

# SEDAR

Southeast Data, Assessment, and Review

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## SEDAR 69

Benchmark Stock Assessment Report

# **Atlantic Menhaden**

January 2020

SEDAR  
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# **Table of Contents**

Pages of each Section are numbered separately.

Section I: Preface	Pg. 4
Section II Assessment Process Report	Pg. 5
Section III: Review Workshop report	Pg. 486
Section IV: Appendices	Pg. 504

## **1. Preface**

The development and peer review of the 2019 Atlantic Menhaden Stock Assessment occurred through a joint Atlantic States Marine Fisheries Commission (ASMFC) and Southeast Data, Assessment, and Review (SEDAR) process. From April 2018 to June 2019, the ASMFC coordinated a Data Workshop and three Assessment Workshops in Arlington, Virginia, and Raleigh, North Carolina, while SEDAR coordinated the Review Workshop in Charleston, South Carolina. The report is the culmination of a two-year effort to gather and analyze available data for Atlantic menhaden from the fishery-independent sampling programs of the Atlantic States, commercial purse-seine reduction fishery, and commercial bait fishery. ASMFC developed the stock assessment through its Atlantic Menhaden Technical Committee (TC) and Stock Assessment Subcommittee (SAS). The ASMFC facilitated numerous conference calls and webinars in preparation for the Data, Assessment, and Review Workshops. Participants in the stock assessment process included TC and SAS members, as well as representatives from the fishing industry and Non-Governmental Organizations with an interest in menhaden.

In addition to the single-species menhaden stock assessment report, an Ecosystem Reference Points (ERP) stock assessment report was developed by the ASMFC Ecosystem Reference Points Work Group, and reviewed by the SEDAR 69 Panel. The ASMFC facilitated several webinars and meetings of the Work Group, coinciding with the Menhaden SAS meetings, to develop the ERP Assessment. The ERP report describes ecosystem monitoring and modeling approaches, and provides reference points designed to address multispecies interactions for a subset of stocks managed by the ASMFC, including management of menhaden for forage services in a broader ecosystem management context.

The SEDAR 69 single-species stock assessment report and ERP stock assessment report were generated and provided to three reviewers appointed by the Center for Independent Experts (CIE), as well as a fourth technical reviewer and the review panel chair appointed by ASMFC. The Review Workshop was held in Charleston, South Carolina, from November 4-8, 2019. At the Workshop, reviewers had opportunities to raise questions to the SAS and ERP WG, and provide critiques and constructive comments on the data and models used. A Review Workshop Report (Section III) was generated with comments and overall opinions about the data sources, models, and assessment results. The Review Report, Single-Species Stock Assessment Report, and Ecosystem Reference Points Stock Assessment Report will be provided to the ASMFC Atlantic Menhaden Management Board in February 2020.

The ASMFC and its committees thank the independent peer reviewers for their time and expertise in providing a thorough review of the Atlantic menhaden stock assessment and the Ecosystem Reference Points stock assessment. Additionally, ASMFC expresses its gratitude to all of the individuals who contributed to the completion of both stock assessments.

# Atlantic States Marine Fisheries Commission

## *Atlantic Menhaden 2019 Stock Assessment Report*



**Vision: Sustainable and Cooperative Management of Atlantic Coastal Fisheries**

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## **EXECUTIVE SUMMARY**

The purpose of this assessment was to evaluate the current status of Atlantic menhaden as a single-species along the U.S. Atlantic coast.

### **Landings**

The Atlantic menhaden commercial fishery has two major components, a purse-seine reduction sector that harvests fish for fish meal and oil and a bait sector that supplies bait to other commercial and recreational fisheries. The first coastwide total allowable catch (TAC) for Atlantic menhaden was implemented in 2013 at 170,800 mt. While the TAC increased to 187,880 mt in 2015, 200,000 mt in 2016, and 216,000 mt in 2017, total coastwide landings have remained under 200,000 mt. Since the implementation of the TAC, reduction landings have ranged from 128,900 mt in 2017 to 143,500 mt in 2015 and the bait landings have ranged from 37,000 mt in 2013 to 45,500 in 2015. In 2017, reduction landings were 128,900 mt and accounted for approximately 74% of coastwide landings. Landings in the reduction fishery are currently at their lowest levels in the time series (1955-2017). In contrast, bait landings have increased in recent years as demand has grown because of recent limitations in other species used as bait (e.g., Atlantic herring), peaking in 2012 at 63,700 mt. In 2017, bait landings were 43,900 mt and comprised 25% of coastwide landings. Recreational landings comprised 1% of the coastwide landings.

### **Indices of Relative Abundance**

#### Young of the Year (YOY) Index

The YOY index developed from 16 fishery-independent surveys shows the largest YOY abundance occurred during the 1970s and 1980s. Abundance has since been lower with notable year classes in the mid-2000s and in 2016. The terminal year, 2017, had the lowest YOY abundance of the time series (1959-2017).

#### Age-1+ Indices

Three coastwide indices of adult abundance were developed from eight fishery independent survey data sets: northern (NAD; age-2+), Mid-Atlantic (MAD; age-1+), and southern (SAD; age-1) adult indices. The SAD indicated that age-1 abundance was high in 1990 and low in recent years, with a notable increase in the terminal year of 2017. The MAD showed high relative abundance in the late 1980s, with variable abundance and then peaks in 2014 and 2015 followed by low abundance in the terminal year. The NAD indicated that age-2+ relative abundance has been variable, but abundance was high in 2014, 2015, and 2016, followed by a decline in the terminal year.

### **Fishing Mortality**

Highly variable fishing mortalities were noted throughout the entire time series and appear dependent upon fishing and management policies. Fishing mortality rate over time was reported as the geometric mean fishing mortality rate at ages-2 to -4. The rate was highest in the 1970s and 1980s and has been declining since approximately 1990.



### **Biomass**

Biomass has fluctuated over time from an estimated high of greater than 6,794,000 mt in 1959 to a low of 1,379,000 mt in 1973. Biomass was estimated to have been largest during the late-1950s and late-2010s, with lows occurring during the 1960s, 1970s, and 1980s. From 1980 to the present, biomass has increased. Biomass increased at a faster rate than abundance because of the increase in the number of older fish at age and an increase in weight-at-age.

### **Fecundity**

Population fecundity (i.e., Total Egg Production) was the measure of reproductive output used. Population fecundity (*FEC*, number of maturing ova) was highest in the early 1960s and from the 1990s to the present. The largest values of population fecundity were in 1955, 1961, and 2012. Throughout the time series, age-2 and age-3 fish have produced most of the total estimated number of eggs spawned annually.

### **Stock Status**

The current management benchmarks are calculated using the full fishing mortality rate (*F*-based) and through spawner-per-recruit calculations (fecundity-based) using the mean values of any time-varying components (i.e., growth, maturity) over the time series 1955-2017. *F* in 2017 (0.11) was below the  $F_{\text{THRESHOLD}}$  (0.60) and  $F_{\text{TARGET}}$  (0.22). In addition, the stock is above the current fecundity target. **The Atlantic menhaden stock status is not overfished and overfishing is not occurring.**

## Table of Contents

TERMS OF REFERENCE .....	28
1 INTRODUCTION .....	36
1.1 Brief Overview and History of the Fisheries .....	36
1.2 Management Unit Definition .....	36
1.3 Regulatory History .....	37
1.4 Assessment History .....	38
1.4.1 Previous stock assessments .....	38
1.4.2 Previous Assessment Data and Models .....	38
1.4.3 Biological Reference Points.....	39
1.4.4 Past Research Recommendations.....	39
2 LIFE HISTORY .....	39
2.1 Stock Definitions .....	39
2.2 Recruitment and Migration Patterns.....	40
2.3 Age .....	41
2.4 Growth .....	41
2.4.1 Length-Weight Relationship.....	41
2.4.2 von Bertalanffy Growth Curve .....	43
2.5 Maturity .....	44
2.6 Fecundity.....	45
2.7 Natural Mortality .....	47
2.7.1 Tag-Based Estimates .....	48
2.7.2 Life-History Based Approaches .....	49
2.7.3 Natural Morality from Multi-Species Approaches.....	50
2.7.4 Base Run Configuration.....	50
3 HABITAT DESCRIPTION.....	51
3.1 Brief Overview of Habitat Requirements.....	51
3.1.1 Spawning, egg, larval habitat .....	53
3.1.2 Juvenile and adult habitats .....	53
3.1.3 Anthropogenic Impacts on Atlantic Menhaden and Their Habitat .....	53
3.2 Habitat Analysis.....	55
3.2.1 Background .....	55
3.2.2 Model Configuration .....	56
3.2.3 Results .....	58
3.3 Ecosystem Context for Atlantic Menhaden .....	59
3.3.1 Temperature .....	60
3.3.2 Salinity .....	60
3.3.3 Chlorophyll .....	60
3.3.4 Zooplankton .....	60
3.3.5 Habitat and Abundance .....	61
3.3.6 Summary .....	62
3.4 Productivity Regimes .....	62
4 FISHERY DEPENDENT DATA SOURCES .....	63
4.1 Commercial Reduction Fishery .....	63

4.1.1 Description of Reduction Fisheries .....	63
4.1.2 Data Collection and Survey Methods.....	64
4.1.3 Selectivity Time Blocks for Modelling .....	65
4.1.4 Commercial Reduction Landings.....	66
4.1.5 Commercial Reduction Catch-at-Age.....	68
4.1.6 Potential Biases, Uncertainty, and Measures of Precision .....	70
4.2 Commercial Bait Fishery .....	71
4.2.1 Description of Bait Fishery .....	71
4.2.2 Data Collection Methods .....	72
4.2.3 Selectivity Time Blocks for Modelling .....	73
4.2.4 Commercial Bait Landings.....	73
4.2.5 Commercial Bait Catch-at-Age.....	74
4.2.6 Potential Biases, Uncertainty, and Measures of Precision .....	75
4.3 Recreational Fishery.....	75
4.3.1 Data Collection and Survey Methods.....	75
4.3.2 Recreational Harvest.....	75
4.3.3 Recreational Discards.....	76
4.3.4 Recreational Catch-at-Age .....	76
4.3.5 Potential Biases, Uncertainty, and Measures of Precision .....	76
4.4 Fishery-Dependent Indices .....	76
5 FISHERY INDEPENDENT DATA SOURCES.....	77
5.1 Stock Assessment Subcommittee Criteria and Index Development .....	77
5.2 Surveys.....	78
5.2.1 Rhode Island Coastal Trawl Survey (Monthly Segment).....	78
5.2.2 Connecticut Long Island Sound Trawl Survey .....	79
5.2.3 Connecticut River Juvenile Alosine Seine Survey.....	80
5.2.4 Connecticut Thames River Seine Survey.....	80
5.2.5 New York Western Long Island Seine Survey.....	81
5.2.6 New York Peconic Bay Small Mesh Trawl Survey .....	82
5.2.7 New York Juvenile Striped Bass Beach Seine Survey .....	83
5.2.8 New Jersey Delaware River Striped Bass Seine Survey.....	84
5.2.9 New Jersey Ocean Trawl Survey .....	85
5.2.10 Delaware Adult Trawl Survey.....	86
5.2.11 Delaware Inland Bays Survey .....	87
5.2.12 Maryland Department of Natural Resources' Chesapeake Bay Juvenile Striped Bass Seine Survey .....	87
5.2.13 Maryland Coastal Bays Trawl Survey .....	88
5.2.14 Maryland Department of Natural Resources' Striped Bass Spring Gill Net Survey.....	89
5.2.15 VIMS Juvenile Fish and Blue Crab Trawl Survey .....	90
5.2.16 VIMS Juvenile Striped Bass Seine Survey.....	91
5.2.17 VIMS American Shad and River Herring Monitoring Program.....	92
5.2.18 North Carolina Program 120 Estuarine Trawl Survey .....	93
5.2.19 North Carolina Program 915 Pamlico Sound Independent Gill Net Survey .....	94
5.2.20 South Carolina Department of Natural Resources Electrofishing Survey.....	95

5.2.21 Georgia Ecological Monitoring Trawl Survey .....	96
5.2.22 Southeast Area Monitoring and Assessment Program, South Atlantic Region Coastal Trawl Survey .....	97
5.2.23 MARMAP and EcoMon.....	98
5.3 Index Correlations.....	100
5.4 Conn Indices.....	100
5.4.1 Background of Analysis and Model Description .....	100
5.4.2 Model Configuration .....	101
5.4.3 Model Results.....	101
6 BEAUFORT ASSESSMENT MODEL (BAM) DESCRIPTION AND CONFIGURATION .....	103
6.1 Treatment of Indices.....	104
6.1.1 Selectivity .....	105
6.2 Parameterization .....	107
6.3 Weighting of Likelihoods.....	109
6.4 Estimating Precision.....	110
6.4.1 Monte Carlo Bootstrap (MCB) Method .....	110
6.4.2 Hybrid Markov Chain Monte Carlo (MCMC) Method.....	111
6.5 Sensitivity Analyses .....	112
6.6 Sensitivity to Input Data.....	112
6.7 Sensitivity to Model Configuration .....	113
6.8 Retrospective Analyses .....	115
6.9 Likelihood Profiling and Simulation Analyses .....	116
6.10 Reference Point Estimation – Parameterization, Uncertainty, and Sensitivity Analysis.	116
6.11 Projections .....	117
7 BAM MODEL RESULTS.....	118
7.1 Goodness of Fit .....	118
7.2 Parameter Estimates.....	119
7.2.1 Selectivities and Catchability.....	119
7.2.2 Fishing Mortality Rates .....	120
7.2.3 Abundance, Fecundity, Biomass, and Recruitment Estimates .....	121
7.3 Sensitivity Analyses .....	121
7.3.1 Sensitivity Analyses Model Runs.....	121
7.3.2 Retrospective Analyses .....	123
7.3.3 Likelihood profiling and simulation analyses.....	124
7.4 Uncertainty Analysis .....	124
7.5 Projections .....	125
8 STOCK STATUS.....	125
8.1 Current Overfishing, Overfished/Depleted Definitions .....	126
8.2 Stock Status Determination .....	126
8.2.1 Overfishing and Overfished Status.....	126
8.2.2 Uncertainty.....	126
8.2.3 Comparison of BAM and ERP Model Results and Management Advice.....	127
9 RESEARCH RECOMMENDATIONS.....	128
9.1 Future Research and Data Collection .....	129

9.1.1 Short Term.....	129
9.1.2 Long Term.....	129
9.2 Assessment Methods.....	130
9.2.1 Short Term.....	130
9.2.2 Long Term.....	130
10 MINORITY OPINION .....	131
11 REFERENCES .....	132
12 TABLES.....	147
13 FIGURES.....	201
14 APPENDICES .....	457
14.1 Reproductive Biology and Fecundity of Atlantic Menhaden.....	457
14.1.1 Introduction .....	457
14.1.2 Methods .....	459
14.1.3 Results & Discussion.....	462
14.1.4 Acknowledgements.....	467
14.1.5 References.....	467
14.1.6 Tables .....	471
14.1.7 Figures .....	472
14.2 BAM AD Model Builder Code.....	481

## LIST OF TABLES

Table 1.	Changes made to model inputs and configuration from SEDAR 40 (2015) to this assessment, SEDAR 69 (2019).....	147
Table 2.	The von Bertalanffy parameters for each cohort year for the bias corrected growth curves from 1955-2015. ....	149
Table 3.	Fork length (mm) at age on March 1 (beginning of fishing year) estimated from year class von Bertalanffy growth parameters with a bias correction..	150
Table 4.	Weight (g) at age on September 1 (middle of fishing year) estimated from overall weight-length parameters and annual lengths at age. ....	152
Table 5.	Atlantic menhaden maturity by year and age based on annual estimates of mean size-at-age and maturity as a function of size. ....	154
Table 6.	Estimates of age-specific annual fecundity for age-1 to age-6 Atlantic menhaden in 2015 using the fecundity-at-length relationship used in past stock assessments (Lewis et al. 1987) and estimates derived from an analysis from Latour & Gartland (VIMS).....	156
Table 7.	Constant $M$ from life history approaches, using $K$ & $L_{\infty}$ bias-corrected averaged across annual values .....	157
Table 8.	Summaries of various age-specific estimates of $M$ including those as inverse function of size-at-age. ....	158
Table 9.	Natural mortality estimates by year and age from the multispecies statistical catch-at-age model developed for the ERP assessment.....	159
Table 10.	Information associated with age 1+ Atlantic menhaden surveys. For some surveys, data from some months were excluded due to very low frequency of nonzero CPUE. ....	160
Table 11.	Years of activity for individual Atlantic menhaden reduction plants along the U.S. Atlantic coast, 1955-2017. ....	161
Table 12.	List of plants and their associated numbers, port numbers, and plant locations for plants participating in the reduction fishery, 1955–2017.....	163
Table 13.	Total Atlantic menhaden landings and effort (vessel-weeks) for 1940-2017. ....	164
Table 14.	Sample size (n), landings in numbers of fish, landings in biomass (C), sampling ‘intensity’ (landings in metric tons per 100 fish measured), and mean weight of fish landed from the Atlantic menhaden reduction fishery, 1955-2017. ....	165
Table 15.	Estimated reduction landings of Atlantic menhaden in numbers by age (in millions), 1955-2017. ....	167
Table 16.	Northern and southern reduction fishery landings in thousands of metric tons 1955–2017. ....	169
Table 17.	Catch-at-age for the northern commercial reduction fishery from 1955-2017. ....	170

Table 18.	Catch-at-age for the southern commercial reduction fishery from 1955-2017. ....	172
Table 19.	Atlantic menhaden bait landings (1000 mt) from 1985-2017.....	174
Table 20.	Atlantic menhaden bait and recreational landings (1000 mt) from 1955-2017 combined and split into northern and southern regions for use in the BAM model. ....	175
Table 21.	Catch-at-age for the northern commercial bait fishery (includes MRIP estimate of recreation catch). ....	176
Table 22.	Catch-at-age for the southern commercial bait fishery (includes MRIP estimate of recreation catch). ....	177
Table 23.	MRIP recreational harvest (A+B1) estimates of Atlantic menhaden for two assessment regions along the U.S. Atlantic coast. ....	178
Table 24.	MRIP recreational total harvest (A+B1+1.0*B2) estimates of Atlantic Menhaden for two assessment regions along the U.S. Atlantic coast.....	179
Table 25.	Fishery-independent surveys considered for inclusion in the assessment and reasons rejected if they were not accepted for use as an abundance index.....	180
Table 26.	Length cutoffs used to distinguish age-0 from age-1+ Atlantic menhaden. Regions refer to those used in the commercial reduction fishery database (Figure 1). ....	182
Table 27.	Monthly length cutoffs used to identify YOY versus age-1+ Atlantic Menhaden in the Georgia Ecosystem Monitoring Trawl Survey (GA EMTS), SC DNR Electrofishing Survey, and the Southeast Area Monitoring and Assessment Program, South Atlantic Region (SEAMAP-SA) Coastal Trawl Survey. ....	182
Table 28.	South Carolina Department of Natural Resources (SC DNR) electrofishing survey based length-length conversions used to convert fish only measured to the nearest mm standard length (SL) or total length (TL) to their predicted fork length in mm. ....	183
Table 29.	Fishery-independent surveys developed into abundance indices, accepted by the SAS, and used to develop regional Conn indices and months used in the index and length of the combined time series.....	184
Table 30.	Young-of-year abundance index (YOY), northern adult index (NAD), Mid-Atlantic adult index (MAD), and southern adult index (SAD) of abundance for Atlantic menhaden developed from the Conn method with associated coefficients of variation (CV). ....	185
Table 31.	List of surveys used in the regional Conn indices and their associated sigma values, or the standard deviation of the process error.....	187
Table 32.	Correlation coefficients and <i>P</i> -values for young-of-year Atlantic menhaden surveys. ....	188

Table 33.	Correlation coefficients and <i>P</i> -values for age-1+ Atlantic menhaden surveys. ....	189
Table 34.	Selectivity slope and $A_{50}$ of the ascending and descending limbs with associated SD for the reduction and bait fisheries and the NAD and MAD indices. ....	189
Table 35.	Geometric mean fishing mortality ( <i>F</i> ) rate of ages-2 to -4 during 1955-2017. ....	190
Table 36.	Full fishing mortality rate at age by year for 1955-2017. ....	191
Table 37.	Numbers at age at the start of the year for Atlantic menhaden during 1955-2017. ....	193
Table 38.	Fecundity at age for the Atlantic menhaden population during 1955-2017.	195
Table 39.	Age-1+ biomass at age at the start of the year during 1955-2017. ....	197
Table 40.	Recruitment in billions of fish during 1955-2017. ....	199
Table 41.	Current fishing mortality and fecundity benchmarks (targets and thresholds) along with terminal year values from the base run of the BAM. ....	200



## LIST OF FIGURES

Figure 1.	Regions used in the biological sampling program for the commercial reduction fishery.....	201
Figure 2.	Number of paired length-weight measurements by cohort year and sampling area (1-5) from the reduction fishery. ....	202
Figure 3.	Comparison between time-varying, with dashed 95% confidence intervals, and time-invariant predicted weight for three fork lengths (150, 200, and 250 mm).....	203
Figure 4.	Average weight of a 200 mm Atlantic menhaden in sampling area 3 (Chesapeake Bay) from 1955-2015 by year with 95% confidence intervals and on average, in yellow. ....	204
Figure 5.	Age and length (FL in mm) for Atlantic menhaden sampled during 1955-2011 (from Schueller et al. 2014). ....	205
Figure 6.	A comparison of the estimated annual, cohort-based von Bertalanffy growth coefficients $L_{\infty}$ (top) and $K$ (bottom) with and without the bias correction as detailed in Schueller et al. (2014). ....	206
Figure 7.	Average maturity-at-age from commercial reduction fishery sampling (black), NEAMAP survey (red), and Higham and Nicholson (1964; green). ...	207
Figure 8.	Predicted logistic regression line for Atlantic menhaden female maturity based on length, with 95% confidence intervals.....	208
Figure 9.	Atlantic menhaden maturity by year and age. Age-0 menhaden are immature, while fish of age-5 and older are 100% mature. ....	209
Figure 10.	Mean monthly gonadosomatic index (GSI) for female Atlantic menhaden collected from 2013-2018.....	210
Figure 11.	Monthly percentage of female Atlantic menhaden in the spawning capable gonad phase (including the actively spawning sub-phase). ....	211
Figure 12.	Annual calculated values of $M$ from age-constant $M$ approaches and average $M$ across ages 1-10.....	212
Figure 13.	Estimates of age-varying natural mortality ( $M$ ) from different methods including the estimate used in this assessment (SEDAR 69) and the method used in the previous benchmark assessment (SEDAR 40).....	213
Figure 14.	Estimates of age-varying natural mortality ( $M$ ) from the Lorenzen (1996) method, scaled either to empirical estimates from tagging (SEDAR 40, SEDAR 69) or to the percent of the population surviving to the maximum age.....	214
Figure 15.	Map depicting the sampling areas and locations of the seven surveys that provided data for the analysis of age 1+ Atlantic menhaden habitat preferences. ....	215

Figure 16.	Annual mean bottom water temperature (°C) associated with each of the seven surveys that provided data for the analysis of age 1+ Atlantic menhaden habitat preferences. ....	216
Figure 17.	Annual mean bottom salinity (ppt) associated with each of the seven surveys that provided data for the analysis of age 1+ Atlantic menhaden habitat preferences. ....	217
Figure 18.	Worm plot of the most empirically supported GAMM, which reflected the fully saturated parameterization for the conditional and zero-inflated model components. ....	218
Figure 19.	Habitat preferences derived from the most empirically supported GAMM calculated as marginal means. ....	219
Figure 20.	Projections of proportional changes available habitat relative to ‘present day habitat conditions’ under various hypothesized climate change scenarios involving increased bottom water temperature (blue), decreased salinity (red), and pairwise combinations of increased bottom water temperature and decreased bottom salinity (dark green). ....	220
Figure 21.	Map of Northeast Fisheries Science Center (NEFSC) bottom trawl survey (BTS) spring and fall strata selected for the Ecosystem Context analysis for Atlantic menhaden (source: NEFSC). ....	221
Figure 22.	Trend and regime mean for spring and fall bottom temperature from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report. ....	222
Figure 23.	Trend and regime mean for spring and fall surface temperature from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report. ....	223
Figure 24.	Trend and regime mean for spring and fall bottom salinity from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report. ....	224
Figure 25.	Trend and regime mean for spring and fall surface salinity from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report. ....	225
Figure 26.	Trend and regime mean for spring and fall chlorophyll concentration from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report. ....	226
Figure 27.	Occupancy probability for Atlantic menhaden for the spring and fall seasons. ....	227
Figure 28.	Time series mean predicted occupancy probability for Atlantic menhaden in the spring (a) and fall (c) using the random forest model with the annual rate of change (Sen slope) in occupancy probability (b and d, spring and fall, respectively). ....	228
Figure 29.	Atlantic menhaden stock habitat area for the spring and fall seasons. ....	229

Figure 30.	Atlantic menhaden ecosystem habitat area for the spring and fall seasons. .....	229
Figure 31.	Minimum population size for Atlantic menhaden in the spring. ....	230
Figure 32.	Minimum population size for Atlantic menhaden in the fall. ....	231
Figure 33.	Atlantic menhaden stock-recruitment data from the base run of the BAM model where recruitment was in billions of age-0s and maturity was applied to biomass-at-age to get spawning stock biomass (SSB) in kt.....	232
Figure 34.	Linearized Ricker stock-recruitment relationship for Atlantic menhaden with log recruitment (R) divided by spawning stock biomass (SSB) and SSB in kt. ....	233
Figure 35.	Kalman filter smoothed productivity time series for Atlantic menhaden with 95% confidence intervals.....	234
Figure 36.	Tree produced by R package RPART to identify regimes for Atlantic menhaden productivity. ....	235
Figure 37.	Plots used to determine how to prune the tree produced in Figure 36. ....	236
Figure 38.	Historical locations of menhaden plants in relation to their NMFS statistical reporting areas.....	237
Figure 39.	Stacked chart of number of menhaden plants by area and year, 1955– 2017. ....	237
Figure 40.	Summary of time series and blocks used for each data source for 1955– 2017. ....	238
Figure 41.	Annual values of menhaden reduction landings (1000 mt) and nominal effort (vessel-week), 1955–2017.....	239
Figure 42.	Atlantic menhaden reduction landings (1000s mt) from 1955-2017.....	239
Figure 43.	Atlantic menhaden bait landings (1000s mt) from 1955-2017. ....	240
Figure 44.	Atlantic menhaden landings by reduction and bait fisheries.....	241
Figure 45.	Percent of total landings (reduction and bait) attributed to the bait fishery. .....	241
Figure 46.	a. Percent of bait landings by major gear types for each region.....	242
Figure 47.	Mean weight of fish in the bait catch by year and region.....	244
Figure 48.	Mean weight of fish in the bait and reduction fisheries by region (pooled over 1985-2017).....	245
Figure 49.	a. Observed proportions at age for the bait fishery for the New England region plotted with proportions at age predicted by the multinomial regression.....	246
Figure 50.	Total bait catch-at-age by region.....	250
Figure 51.	Comparison of the bait catch-at-age developed with the 2019 assessment multinomial gap-filling method and the 2015 assessment pooled data gap- filling method for the northern region. ....	251

Figure 52.	Comparison of the bait catch-at-age developed with the 2019 assessment multinomial gap-filling method and the 2015 assessment pooled data gap-filling method for the southern region.....	252
Figure 53.	Recreational harvest (A+B1) estimates of Atlantic menhaden for two assessment regions along the U.S. Atlantic coast. ....	253
Figure 54.	The Potomac River Fisheries Commission (PRFC) Index and Reduction Fishery CPUE (RCPUE) fishery-dependent indices developed by the ERP WG. ....	253
Figure 55.	Map of Rhode Island Coastal Trawl Survey (monthly segment) with the fixed tow stations represented as red dots.....	254
Figure 56.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the fall portions of the monthly Rhode Island Coastal Trawl Survey with 95% confidence intervals.....	255
Figure 57.	Map of Connecticut Long Island Trawl Survey strata. ....	255
Figure 58.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the Connecticut Long Island Trawl Survey with 95% confidence intervals.....	256
Figure 59.	Standardized index of relative abundance of Age-1+ Atlantic menhaden developed from the Connecticut Long Island Trawl Survey with 95% confidence intervals.....	257
Figure 60.	Standardized index of Age-1+ Atlantic menhaden abundance plotted against standardized index of YOY abundance developed from the Connecticut Long Island Trawl Survey with linear regression line (blue).....	258
Figure 61.	Fixed station sites for the Connecticut River Juvenile Alosine Seine Survey. ....	259
Figure 62.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the Connecticut River Juvenile Alosine Seine Survey with 95% confidence intervals.....	260
Figure 63.	Fixed station sites for the Thames River Seine Survey. ....	261
Figure 64.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the Connecticut Thames River Seine Survey with 95% confidence intervals.....	262
Figure 65.	Sites sampled by the New York Western Long Island Seine Survey.....	263
Figure 66.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the New York Western Long Island Seine Survey with 95% confidence intervals.....	264
Figure 67.	Stations sampled by the New York Peconic Bay Small Mesh Trawl Survey. ..	265
Figure 68.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the New York Peconic Bay Small Mesh Trawl Survey with 95% confidence intervals.....	266

Figure 69.	Sites sampled by the New York Juvenile Striped Bass Seine Survey. ....	267
Figure 70.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the New York Juvenile Striped Bass Seine Survey with 95% confidence intervals.....	268
Figure 71.	Map of New Jersey’s Delaware River Striped Bass Seine Survey’s sampling regions. ....	269
Figure 72.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the New Jersey Delaware River Striped Bass Seine Survey with 95% confidence intervals.....	270
Figure 73.	Map of the sampling area and strata from the New Jersey Ocean Trawl Survey. ....	271
Figure 74.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the New Jersey Ocean Trawl Survey with 95% confidence intervals. ....	272
Figure 75.	Standardized index of relative abundance of age-1+ Atlantic menhaden developed from the New Jersey Ocean Trawl Survey with 95% confidence intervals. ....	272
Figure 76.	Map of the sampling area for Delaware Fish and Wildlife’s Adult Trawl Survey with the nine fixed station sampling sites indicated with numbers...	273
Figure 77.	Standardized index of relative abundance of age 1+ Atlantic menhaden developed from the fall months of the Delaware Bay Adult Trawl Survey with 95% confidence intervals.....	274
Figure 78.	Map of the sampling sites for Delaware Fish and Wildlife’s Juvenile Trawl Inland Bays Survey. ....	275
Figure 79.	Standardized index of relative abundance of YOY Atlantic menhaden developed from Delaware’s Inland Bays Survey with 95% confidence intervals. ....	276
Figure 80.	Map of the survey sites from Maryland Department of Natural Resources Juvenile Striped Bass Survey.....	277
Figure 81.	Standardized index of relative abundance of YOY Atlantic menhaden developed from Maryland Department of Natural Resources Juvenile Striped Bass Survey with 95% confidence intervals. ....	278
Figure 82.	Map of the Maryland Coastal Bays Survey sampling sites. ....	279
Figure 83.	Standardized index of relative abundance of YOY Atlantic menhaden developed from Maryland Department of Natural Resources Coastal Bays Survey with 95% confidence intervals.....	280
Figure 84.	Map of Maryland Department of Natural Resources Striped Bass Spring Gill Net Survey sampling sites. ....	281
Figure 85.	Standardized index of relative abundance of age 1+ Atlantic menhaden developed from Maryland Department of Natural Resources Striped Bass	

	Spring Gill Net Survey for the months of March-May with 95% confidence intervals. ....	282
Figure 86.	Sampling sites for the VIMS Juvenile Fish and Blue Crab Trawl Survey (source: VIMS).....	283
Figure 87.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the VIMS Juvenile Fish and Blue Crab Trawl Survey with 95% confidence intervals.....	284
Figure 88.	Sampling sites for the VIMS Juvenile Striped Bass Seine Survey. Site numbers denote the approximate river mile from the mouth of the Bay (source: VIMS).....	285
Figure 89.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the VIMS Juvenile Striped Bass Seine Survey with 95% confidence intervals.....	286
Figure 90.	Sampling sites for the VIMS Alosine Monitoring Program in the James, York, and Rappahannock rivers (source: VIMS).....	287
Figure 91.	Standardized index of relative abundance of age 1+ Atlantic menhaden developed from the VIMS Alosine Monitoring Program with 95% confidence intervals.....	288
Figure 92.	Core station locations sampled by the North Carolina Program 120 Estuarine Trawl Survey from 1989 to 2017. ....	289
Figure 93.	Standardized index of relative abundance of YOY Atlantic menhaden developed from the North Carolina Program 120 Estuarine Trawl Survey. The grey ribbon is the 95% confidence interval. ....	290
Figure 94.	Sample locations by area and color conducted by the North Carolina Program 915 Pamlico Sound Independent Gill Net Survey from 2001 to 2017. Pamlico Sound sites (reds and blues) established in 2001; Pamlico, Pungo, and Neuse Rivers (greens) added in 2003; New and Cape Fear Rivers (yellows) added in 2008. ....	291
Figure 95.	Standardized index of relative abundance of age 1+ Atlantic menhaden developed from the North Carolina Program 915 Pamlico Sound Independent Gill Net Survey. The grey ribbon is the 95% confidence interval. ....	292
Figure 96.	Map of the South Carolina Department of Natural Resources (SC NDR) electrofishing survey sampling strata. ....	293
Figure 97.	Standardized index of relative abundance of YOY Atlantic Menhaden developed from the SC DNR monthly electrofishing survey with 95% confidence intervals.....	294
Figure 98.	Map of the Georgia Ecosystem Monitoring Trawl Survey with the fixed tow locations identified. ....	295
Figure 99.	Standardized index of relative abundance of age-1+ Atlantic Menhaden developed from the spring and early summery (April-July) portions of the	

	monthly Georgia Ecosystem Monitoring Trawl Survey with 95% confidence intervals. ....	296
Figure 100.	Map of the Southeast Area Monitoring and Assessment Program, South Atlantic Region (SEAMAP-SA) coastal trawl survey strata.....	297
Figure 101.	Standardized index of relative abundance of age-1+ Atlantic Menhaden developed from the SEAMAP-SA coastal trawl survey, only using data collected during the months of April-July. Dashed lines represent 95% confidence intervals.....	298
Figure 102.	MARMAP and EcoMon survey area between Cape Cod, MA and Cape Hatteras, North Carolina.....	299
Figure 103.	Standardized index of relative spawning stock biomass abundance of Atlantic menhaden developed from the MARMAP ichthyoplankton survey. ....	300
Figure 104.	Standardized index of relative spawning stock biomass abundance of Atlantic menhaden developed from the EcoMon ichthyoplankton survey. ..	300
Figure 105.	Correlation coefficients and scatter plots for the Atlantic menhaden YOY abundance indices. ....	301
Figure 106.	Correlation coefficients and scatter plots for the Atlantic menhaden age-1+ abundance indices. ....	302
Figure 107.	PCA on the length compositions of the eight different age-1+ Atlantic menhaden surveys.....	303
Figure 108.	Time series of the young-of-year (YOY) Atlantic menhaden relative abundance index as estimated from hierarchical analysis (Conn 2009).....	304
Figure 109.	Time series of the Northern region (a) and southern region (b) young-of-year Atlantic menhaden relative abundance indices as estimated from hierarchical analysis (Conn 2009). ....	305
Figure 110.	Time series of the northern adult Atlantic menhaden relative abundance index (NAD) as estimated from hierarchical analysis (Conn 2009). ....	306
Figure 111.	Time series of the Mid-Atlantic adult menhaden relative abundance index (MAD) as estimated from hierarchical analysis (Conn 2009). ....	307
Figure 112.	Time series of the southern adult Atlantic menhaden relative abundance index (SAD) as estimated from hierarchical analysis (Conn 2009). ....	308
Figure 113.	Length composition of the Northern Adult (NAD) index plotted with the length composition of fishery samples (pooled over all regions). ....	309
Figure 114.	Length composition of the Mid-Atlantic Adult (MAD) index plotted with the length composition of fishery samples (pooled over all regions). ....	310
Figure 115.	Length composition of the Southern Adult (SAD) index plotted with the length composition of the fishery samples (pooled over all regions). ....	311

Figure 116.	Comparison between the base run and non-linear time series analysis (Deyle et al. 2018) recruitment prediction for Atlantic menhaden for 2007-2017. ....	312
Figure 117.	Commercial reduction landings (1000s mt) for the northern region for 1955-2017. ....	313
Figure 118.	Commercial reduction landings (1000s mt) for the southern region for 1955-2017. ....	314
Figure 119.	Commercial bait landings (1000s mt) for the northern region for 1955-2017. ....	315
Figure 120.	Commercial bait landings (1000s mt) for the southern region for 1955-2017. ....	316
Figure 121.	Annual age composition fits for the commercial reduction fishery for 1955-2017 in the northern region. ....	317
Figure 122.	Annual age composition fits for the commercial reduction fishery for 1955-2017 in the southern region. ....	322
Figure 123.	Annual age composition fits for the commercial bait fishery for 1985-2017 in the northern region. ....	327
Figure 124.	Annual age composition fits for the commercial bait fishery for 1985-2017 in the southern region. ....	330
Figure 125.	Annual age composition fits for the commercial reduction fishery for 1955-2017 in the northern region. ....	334
Figure 126.	Annual age composition fits for the commercial reduction fishery for 1955-2017 in the southern region. ....	335
Figure 127.	Annual age composition fits for the commercial bait fishery for 1985-2017 in the northern region. ....	336
Figure 128.	Annual age composition fits for the commercial bait fishery for 1985-2017 in the northern region. ....	337
Figure 129.	The relative abundance index for recruitment or young of the year (YOY) for 1959-2017. ....	338
Figure 130.	The relative abundance index for the northern adult index (NAD) for 1990-2017. ....	339
Figure 131.	The relative abundance index for the mid-Atlantic adult index (MAD) for 1985-2017. ....	340
Figure 132.	The relative abundance index for the southern adult index (SAD) for 1990-2017. ....	341
Figure 133.	The relative abundance index for fecundity based on the MARMAP and EcoMon larval data (MARECO) for 1981-1988 and 2000-2017. ....	342
Figure 134.	Annual length composition fits for the NAD index for 1990-2017. ....	343
Figure 135.	Annual length composition fits for the MAD index for 2013-2017. ....	345



Figure 136.	Pooled length compositions for the NAD (upper) and MAD (lower) indices. .....	346
Figure 137.	Annual length composition fits for the NAD index for 1990-2017.....	347
Figure 138.	Annual length composition fits for the MAD index for 2013-2017.....	348
Figure 139.	Selectivity-at-age for the commercial reduction fishery in the northern region.....	349
Figure 140.	Selectivity-at-age for the commercial reduction fishery in the southern region.....	350
Figure 141.	Selectivity-at-age for the commercial bait fishery in the northern region. ...	351
Figure 142.	Selectivity-at-age for the commercial bait fishery in the southern region for 1955-2017.....	352
Figure 143.	Selectivity-at-age for the NAD index for 1990-2017.....	353
Figure 144.	Selectivity-at-age for the MAD index for 1985-2017.....	354
Figure 145.	Full fishing mortality rate for the northern commercial reduction fishery for 1955-2017.....	355
Figure 146.	Full fishing mortality rate for the southern commercial reduction fishery for 1955-2017.....	356
Figure 147.	Full fishing mortality rate for the northern commercial bait fishery for 1955-2017.....	357
Figure 148.	Full fishing mortality rate for the southern commercial bait fishery for 1955-2017.....	358
Figure 149.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017.....	359
Figure 150.	Full fishing mortality rate for the Atlantic menhaden population for 1955- 2017.....	360
Figure 151.	Number of fish by age in the population at the start of the year for 1955- 2017.....	361
Figure 152.	Fecundity (billions of eggs) for the Atlantic menhaden population for 1955- 2017.....	362
Figure 153.	Age-1+ biomass in 1000s of mt for Atlantic menhaden during 1955-2017. ..	363
Figure 154.	Recruitment in billions of fish during 1955-2017.....	364
Figure 155.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015).....	365
Figure 156.	Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015).....	366
Figure 157.	Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015).....	367
Figure 158.	Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015).....	368

Figure 159.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices. ....	369
Figure 160.	Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices. ....	370
Figure 161.	Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices.....	371
Figure 162.	Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices.....	372
Figure 163.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019). ....	373
Figure 164.	Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019). ....	374
Figure 165.	Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019). ....	375
Figure 166.	Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019).....	376
Figure 167.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type. ....	377
Figure 168.	Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type.....	378
Figure 169.	Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type.....	379
Figure 170.	Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type. ....	380
Figure 171.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery. ....	381
Figure 172.	Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery. ....	382
Figure 173.	Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery.....	383

Figure 174.	Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery. ....	384
Figure 175.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored assumptions about required sample sizes for the bait fishery.....	385
Figure 176.	Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored assumptions about required samples sizes for the bait fishery.....	386
Figure 177.	Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored assumptions about required samples sizes for the bait fishery. ....	387
Figure 178.	Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored assumptions about required sample sizes for the bait fishery. ....	388
Figure 179.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality. ....	389
Figure 180.	Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality.....	390
Figure 181.	Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality.....	391
Figure 182.	Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality. ....	392
Figure 183.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the retrospective analysis. ....	393
Figure 184.	Fecundity in billions of ova for 1955-2017 for the retrospective analysis. ....	394
Figure 185.	Recruitment in billions of fish for 1955-2017 for the retrospective analysis. ....	395
Figure 186.	Age-1+ biomass for 1955-2017 for the retrospective analysis.....	396
Figure 187.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the retrospective analysis going back until 2011. ....	397
Figure 188.	Fecundity in billions of ova for 1955-2017 for the retrospective analysis going back until 2011.....	398
Figure 189.	Recruitment in billions of fish for 1955-2017 for the retrospective analysis going back until 2011.....	399
Figure 190.	Age-1+ biomass for 1955-2017 for the retrospective analysis going back until 2011.....	400

Figure 191.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period. ....	401
Figure 192.	Fecundity in billions of ova for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period. ....	402
Figure 193.	Recruitment in billions of fish for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period. ....	403
Figure 194.	Age-1+ biomass for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period. ....	404
Figure 195.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles. ....	405
Figure 196.	Fecundity in billions of ova for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles. ....	406
Figure 197.	Recruitment in billions of fish for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles. ....	407
Figure 198.	Age-1+ biomass for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles. ....	408
Figure 199.	Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles and the MCMC analysis of the base run. ....	409
Figure 200.	Fecundity in billions of ova for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles and the MCMC analysis of the base run. ....	409
Figure 201.	Recruitment in billions of fish for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles and the MCMC analysis of the base run. ....	410
Figure 202.	Age-1+ biomass for 1955-2017 for the MCB runs with 95 <sup>th</sup> percentiles and the MCMC analysis of the base run. ....	410
Figure 203.	Selectivity estimates with 95% confidence intervals for the reduction fleets from the BAM MCB and MCMC analyses. ....	411
Figure 204.	Selectivity estimates with 95% confidence intervals for the bait fleets from the BAM MCB and MCMC analyses. ....	412
Figure 205.	Fecundity, recruits, geometric mean fishing mortality rate, and landings for projections done with a constant TAC of 216,000 mt for 2019-2021. ....	413
Figure 206.	Fecundity, recruits, geometric mean fishing mortality rate, and landings for projections done to reach the $F_{TARGET}$ during 2019-2021. ....	414
Figure 207.	Static spawning potential ratio (SPR) for Atlantic menhaden for 1955-2017. ....	415
Figure 208.	Geometric mean fishing mortality rate of ages-2 to -4 during 1955-2017. ....	416
Figure 209.	Fecundity time series for 1955-2017. ....	417

Figure 210.	Fishing mortality rate divided by the threshold $F$ for the suite of sensitivity runs related to continuity with the last update and benchmark assessments. ....	418
Figure 211.	Fishing mortality rate divided by the target $F$ for the suite of sensitivity runs related to continuity with the last update and benchmark assessments. ....	419
Figure 212.	Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to continuity with the last update and benchmark assessments. ....	420
Figure 213.	Fecundity divided by the target fecundity for the suite of sensitivity runs related to continuity with the last update and benchmark assessments. ....	421
Figure 214.	Fishing mortality rate divided by the threshold $F$ for the suite of sensitivity runs related to index choice. ....	422
Figure 215.	Fishing mortality rate divided by the target $F$ for the suite of sensitivity runs related to index choice. ....	423
Figure 216.	Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to index choice. ....	424
Figure 217.	Fecundity divided by the target fecundity for the suite of sensitivity runs related to index choice. ....	425
Figure 218.	Fishing mortality rate divided by the threshold $F$ for the suite of sensitivity runs related to index choice and the ERP models. ....	426
Figure 219.	Fishing mortality rate divided by the target $F$ for the suite of sensitivity runs related to index choice and the ERP models. ....	427
Figure 220.	Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to index choice and the ERP models. ....	428
Figure 221.	Fecundity divided by the target fecundity for the suite of sensitivity runs related to index choice and the ERP models. ....	429
Figure 222.	Fishing mortality rate divided by the threshold $F$ for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve. ....	430
Figure 223.	Fishing mortality rate divided by the target $F$ for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve. ....	431
Figure 224.	Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve. ....	432
Figure 225.	Fecundity divided by the target fecundity for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve. ....	433
Figure 226.	Fishing mortality rate divided by the threshold $F$ for the suite of sensitivity runs related to fishery selectivity. ....	434
Figure 227.	Fishing mortality rate divided by the target $F$ for the suite of sensitivity runs related to fishery selectivity. ....	435

Figure 228.	Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to fishery selectivity. ....	436
Figure 229.	Fecundity divided by the target fecundity for the suite of sensitivity runs related to fishery selectivity. ....	437
Figure 230.	Fishing mortality rate divided by the threshold $F$ for the suite of sensitivity runs related to minimum sample size for bait age compositions. ....	438
Figure 231.	Fishing mortality rate divided by the target $F$ for the suite of sensitivity runs related to minimum sample size for bait age compositions. ....	439
Figure 232.	Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to minimum sample size for bait age compositions. ....	440
Figure 233.	Fecundity divided by the target fecundity for the suite of sensitivity runs related to minimum sample size for bait age compositions. ....	441
Figure 234.	Fishing mortality rate divided by the threshold $F$ for the suite of sensitivity runs related to start year and time-varying $M$ . ....	442
Figure 235.	Fishing mortality rate divided by the target $F$ for the suite of sensitivity runs related to start year and time-varying $M$ . ....	443
Figure 236.	Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to start year and time-varying $M$ . ....	444
Figure 237.	Fecundity divided by the target fecundity for the suite of sensitivity runs related to start year and time-varying $M$ . ....	445
Figure 238.	Fishing mortality rate divided by the threshold $F$ for each of the MCB runs. ....	446
Figure 239.	Fishing mortality rate divided by the target $F$ for each of the MCB runs. ....	447
Figure 240.	Fecundity divided by the threshold fecundity for each of the MCB runs. ....	448
Figure 241.	Fecundity divided by the target fecundity for each of the MCB runs. ....	449
Figure 242.	Terminal year fishing mortality and fecundity divided by the threshold values for each of the MCB runs. ....	450
Figure 243.	Fishing mortality rate divided by the threshold fishing mortality rate for the MCB analysis and for the MCMC analysis. ....	451
Figure 244.	Fishing mortality rate divided by the target fishing mortality rate for the MCB analysis and for the MCMC analysis. ....	451
Figure 245.	Fecundity divided by the threshold fecundity for the MCB analysis and for the MCMC analysis. ....	452
Figure 246.	Fecundity divided by the target fecundity for the MCB analysis and for the MCMC analysis. ....	452
Figure 247.	Fishing mortality rate target and threshold distributions for the MCB analysis and for the MCMC analysis. ....	453
Figure 248.	Fecundity target and threshold distributions for the MCB analysis and for the MCMC analysis. ....	453

Figure 249.	Estimates of age-1+ biomass from the BAM model and the ERP models on an absolute scale (top) and scaled to their time series mean (bottom). .....	454
Figure 250.	Estimates of age-1+ exploitation rate from the BAM model and the ERP models on an absolute scale (top) and scaled to their time series mean (bottom).....	455
Figure 251.	Striped bass age 6+ biomass ratio ( $B/B_{TARGET}$ ) in the terminal year of the EwE projections as a function of fishing mortality on both Atlantic menhaden and striped bass.....	456

## TERMS OF REFERENCE

For the 2019 ASMFC Atlantic Menhaden Benchmark Stock Assessment and Peer Review

Board Approved May 2018

### ***Terms of Reference for the Single-Species Atlantic Menhaden Assessment and Report Summary***

**TOR1. Define population structure based on available data. If alternative population structures are used in the models (e.g., coast-wide or regional), justify use of each population structure.**

Atlantic menhaden are considered a single stock based on size-frequency information, tagging studies, and genetic studies (Section 2.1).

While the population is a single-stock, data is handled within geographical regions in the assessment. Adult relative abundance indices developed from fishery-independent surveys were split into three regions (northern, Mid-Atlantic, and southern) based on length frequency analyses (Section 5.4.2), which indicated differences in gear selectivity and age-specific seasonal migrations of Atlantic menhaden. This benchmark, like SEDAR 40 (2015), incorporated “fleets-as-areas” components where the fisheries (i.e., reduction and bait) were subdivided into northern and southern regions. Commercial reduction landings were split into a northern and southern region as defined by waters north and south of Machipongo Inlet, Virginia, where the Chesapeake Bay is in the southern region. Bait and recreational landings attempted to mimic that geographical break but have a coarser resolution, using coastal Maryland and north as the northern region, and the Chesapeake Bay and south as the southern region. The northern and southern regions reflect differences in age and size composition of the catches, time and duration of fishing, and range of vessels from Atlantic menhaden plants for the reduction fisheries (Section 4.1.5.2).

**TOR2. Evaluate new information on life history such as growth rates, size at maturation, natural mortality rate, and migrations and review potential impacts of environmental change on these characteristics.**

The stock assessment subcommittee (SAS) reviewed current literature and made changes in the Life History (Section 2) from SEDAR 40 (2015). Time-varying fecundity-at-age values were estimated to reflect recent research from Virginia Institute of Marine Science, which resulted in higher estimated fecundity, a spawning stock biomass metric (Section 2.6). Age-varying natural mortality ( $M$ ) was estimated using Lorenzen (1996), as it was in SEDAR 40 (2015), but for this assessment  $M$  was scaled to a recent analysis of historic tagging data (Liljestrand et al. 2019a, 2019b), which resulted in a higher  $M$ -at-age (Section 2.7). The methods for estimating maturity



(Section 2.5) and growth (Section 2.4) were re-evaluated but were not revised from the previous benchmark assessment (SEDAR 2015).

The SAS also evaluated environmental variables and Atlantic menhaden habitat several ways in Section 3. This section provides a literature search (Section 3.1), an analysis of environmental variables available from the fishery-independent surveys used to develop relative abundance indices (Section 3.2), an Ecosystem Context for Atlantic Menhaden report (Section 3.3), and an analysis on productivity regimes (Section 3.4).

**TOR3. Characterize precision and accuracy of fishery-dependent and fishery-independent data used in the assessment, including the following but not limited to:**

- a. Provide descriptions of each data source (e.g., geographic location, sampling methodology, potential explanation for outlying or anomalous data)**
- b. Describe calculation and potential standardization of abundance indices. Consider the consequences of environmental factors on the estimates of abundance or relative indices derived from surveys.**
- c. Discuss trends and associated estimates of uncertainty (e.g., standard errors)**
- d. Justify inclusion or elimination of available data sources.**
- e. Discuss the effects of data strengths and weaknesses (e.g., temporal and spatial scale, gear selectivities, ageing accuracy, sample size) on model inputs and outputs.**

Fishery-dependent data for Atlantic menhaden are available from the commercial reduction (1955-2017; Section 4.1), commercial bait (1955-2017; Section 4.2), and recreational (1981-2017; Section 4.3) fisheries. For each fishery, a description of the fishery, data collection program, landings, catch-at-age, and potential data limitations have been provided.

Nearly 50 fishery-independent surveys were reviewed by the SAS for the development of young-of-year (YOY) or adult (age-1+) abundance indices. Two ichthyoplankton surveys were used to develop a relative index for fecundity. Surveys that met the criteria developed by the SAS for evaluating available data were developed into indices of relative abundance for Atlantic menhaden (Section 5.1). All surveys were standardized using a variety of statistical models and environmental covariates (Sections 5.2.1-5.2.23). Adult abundance indices were combined regionally (northern, Mid-Atlantic, and southern) and YOY indices were combined coastwide using the methods of Conn (2009) to develop composite indices for modelling (Section 5.4). Regions were based on length frequency analyses (Section 5.4.2), which indicated differences in gear selectivity and age-specific seasonal migrations of Atlantic menhaden.

**TOR4. Develop models used to estimate population parameters (e.g.,  $F$ , biomass, abundance) and biological reference points, and analyze model performance.**

- a. Briefly describe history of model usage, its theory and framework, and document associated peer-reviewed literature. If using a new model, test using simulated data.
- b. Clearly and thoroughly explain model strengths and limitations.
- c. Justify choice of CVs, effective sample sizes, or likelihood weighting schemes.
- d. Describe stability of model (e.g., ability to find a stable solution, invert Hessian)
- e. Perform sensitivity analyses for starting parameter values, priors, etc. and conduct other model diagnostics as necessary.
- f. If multiple models were considered, justify the choice of preferred model and the explanation of any differences in results among models.

The Beaufort Assessment Model (BAM) was used in this assessment like the previous 2015 benchmark stock assessment and the 2017 stock assessment update. BAM is a statistical catch-at-age model that estimates population size-at-age and recruitment, using 1955 as the start year, and then projects the population forward in time. The model estimates trends in the population, including abundance-at-age, recruitment, spawning stock biomass, egg production, and fishing mortality rates. BAM was configured to be a fleets-as-areas model with each of the fleets broken into areas to reflect differences in size and age structure along the coast. Model description is discussed in Section 6, along with treatment of indices (6.1), parameterization (6.2), and likelihood weighting schemes (6.3). Several sensitivity analyses were performed and described in Sections 6.5-6.7 and 7.3.

This single-species benchmark assessment was developed in tandem with an ecological-based benchmark, which includes both alternative and complementary models for assessment of Atlantic menhaden. A comparison of single-species results and results from the Ecological Reference Points Workgroup's (ERP WG) models is discussed in Section 8.2.3.

**TOR5. State assumptions made for all models and explain the likely effects of assumption violations on synthesis of input data and model outputs. Examples of assumptions may include (but are not limited to):**

- a. Choice of stock-recruitment function.
- b. No error in the catch-at-age or catch-at-length matrix.
- c. Calculation of  $M$ . Choice to use (or estimate) constant or time-varying  $M$  and catchability.
- d. Choice of equilibrium reference points or proxies for MSY-based reference points.

**e. Choice of a plus group for age-structured species.**

A description of the model configuration is discussed in Section 6. To address each of the bullets above:

- a) The SAS tried to fit a Beverton-Holt stock-recruitment curve; however, the steepness parameter always ended up on a bound near 1.0. Given the interim reference points, the panel decided to fix the steepness value at 0.99, which allowed for the estimation of a median recruitment and estimated deviations over time. The SAS noted, however, that the stock-recruitment relationship observed to date is weak at best. The SAS performed two sensitivity runs that considered different functional forms for recruitment: 1) the Ricker stock recruitment curve and 2) the Shepherd form of the stock-recruitment curve.
- b) Error for each of the inputs into the BAM, including catch-at-age matrices, is summarized in Section 6.2.
- c) A thorough description of the calculation and SAS discussion around estimating  $M$  is discussed in Section 2.7. Ultimately, a Lorenzen (1996) age-varying but time-invariant  $M$  was estimated and scaled to estimates from a tagging study (Liljestrand et al. 2019a, 2019b).
- d) The choice of reference points is discussed in Section 6.10 and the stock status determination can be found in Section 8.2.
- e) SEDAR 40 (2015) and this assessment used ages 6+ as the plus group for modeling based on the ages of Atlantic menhaden observed in the fishery dependent data (the only source of age data). On average from 1955-2017, ages 7 and 8 represent 0.01% of the catch and have rarely been caught since the 1960s.

**TOR6. Characterize uncertainty of model estimates and biological or empirical reference points.**

Uncertainty was examined in the results in three ways: by considering each data source, in turn, in a series of sensitivity runs (Section 7.3), by using a Monte Carlo Bootstrap (MCB) procedure (Section 7.4), and by using a Markov chain Monte Carlo (MCMC) procedure (Section 7.4). The MCB and MCMC approaches quantified different aspects of uncertainty. The MCB approach focused on uncertainty in fixed life history inputs such as  $M$  and fecundity, while the MCMC approach focused on uncertainty in model parameter estimates. The MCB analysis resulted in higher uncertainty in the scale of population estimates (fecundity, recruitment, average  $F$ , and biological reference points), while the MCMC analysis resulted in higher uncertainty in estimated parameters like selectivity, as well as around relative quantities like stock status

determinations. The SAS considered the estimates of uncertainty around population metrics from the MCMC analysis to be a minimum estimate of uncertainty, and ultimately decided to use the MCB procedure for the projections to more fully account for the uncertainty in scale.

**TOR7. Perform retrospective analyses, assess magnitude and direction of retrospective patterns detected, and discuss implications of any observed retrospective pattern for uncertainty in population parameters (e.g.,  $F$ , SSB), reference points, and/or management measures.**

Retrospective analyses were performed as discussed in Section 7.3.2. The retrospective was run by peeling off data back to 2014. The limited years of data removal were due to several base run assumptions that started in 2013 (fishery selectivity time blocks) and data that started in 2013 (MAD length comps). The retrospective exhibited small changes in terminal years of 2016 and 2015 when compared to the base run for the metrics of interest. However, this pattern was not consistent for a terminal year of 2014 whereby the scale of the metrics of interest were substantially different than the base run. The SAS explored this further with additional runs. Based on the exploration of data inputs, the data element found to be causing the change in scale was the fishery age compositions for the northern region. For future assessments, the SAS recommends that the terminal year age compositions should be examined to determine if a similar scale change could be occurring.

**TOR8. Recommend stock status as related to reference points (if available). For example:**

- a. Is the stock below the biomass threshold?
- b. Is  $F$  above the threshold?

Reference point estimation is discussed in Section 6.10 and stock status is in Section 8. The current benchmarks include fishing mortality and fecundity target and threshold values which are based on the geometric mean full fishing mortality rate ( $F$ -based) for ages-2 to -4 and fecundity calculated using the mean values of time-varying components (i.e., growth, maturity) in spawner-per-recruit calculations. Fishing mortality in 2017 (0.11) was below the  $F_{\text{THRESHOLD}}$  (0.60) and  $F_{\text{TARGET}}$  (0.22). In addition, the stock is above the current fecundity target. The Atlantic menhaden stock status is not overfished and overfishing is not occurring.

**TOR9. Compare trends in population parameters and reference points with current and proposed modeling approaches, including the results of the ecological-based benchmark stock assessment. If outcomes differ, discuss potential causes of observed discrepancies.**

A comparison between the single-species and ERP approaches is discussed in Section 8.2.3. The ERP WG explored several different models capable of producing ecological reference points for Atlantic menhaden, ranging from mechanistically very simple with minimal data inputs (time-varying  $r$  and Steele-Henderson surplus production models) to moderately complex

(multispecies statistical catch-at-age and Ecopath with Ecosim models with only key finfish predators) to mechanistically very complex with intensive data needs (full Ecopath with Ecosim model). All of the ERP models agreed with the single-species assessment model about the overall trend of Atlantic menhaden population size and exploitation rates over the last 30 years: a generally increasing trend in biomass and a decreasing trend in exploitation rate.

The ERP models produced similar assessments of stock status to the single-species assessment results, which determined that Atlantic menhaden were not overfished and were not experiencing overfishing in 2017. Current levels of Atlantic menhaden removal were not projected to cause declines in predator biomass.

The ERP assessment recommended a combination of methods as a tool to help managers and stakeholders evaluate the tradeoffs between Atlantic menhaden harvest and predator biomass. The final values for ERPs and Total Allowable Catch (TAC) will be a management decision based on the evaluation of these tradeoffs and stakeholder input. However, the ERP WG put forward example values of an ERP target and an ERP threshold based on existing management objectives for striped bass, the species that was most sensitive to levels of Atlantic menhaden biomass. The ERP target was defined as the maximum  $F$  on Atlantic menhaden that would sustain striped bass at their biomass target when striped bass were fished at their  $F_{TARGET}$ . The ERP threshold was defined as the maximum  $F$  on Atlantic menhaden that would keep striped bass at their biomass threshold when striped bass were fished at their  $F_{THRESHOLD}$ .

These example ERPs suggested that if managers want to achieve their current management objectives for striped bass, the  $F_{TARGET}$  and  $F_{THRESHOLD}$  for Atlantic menhaden should be 30-40% lower than the single-species values. The current single-species reference points are based on a period of stability for the fishery and the Atlantic menhaden population. Predation mortality is incorporated in the estimate of  $M$  used to parameterize the single-species model, but there is no consideration of the effects of Atlantic menhaden biomass on other species in the ecosystem when setting the single-species reference points. However, because of the *ad hoc* buffering approach used by the Atlantic Menhaden Management Board to set the TAC in recent years, current removals of Atlantic menhaden are sustainable under the current management objectives of the key predator species, and  $F$  in 2017 was below the ERP target and threshold.

**TOR10. If a minority report has been filed, explain majority reasoning against adopting approach suggested in that report. The minority report should explain reasoning against adopting approach suggested by the majority.**

A minority report has not been filed (Section 10).

**TOR11. Develop detailed short and long-term prioritized lists of recommendations for future research, data collection, and assessment methodology. Highlight improvements to be made by next benchmark review.**

The SAS developed research recommendations for future research and data collection and assessment methodology. While all recommendations are high priority, the first recommendation is the highest priority. Each category is further broken down into

recommendations that can be completed in the short term and recommendations that will require long term commitment (Section 9).

**TOR12. Recommend timing of next benchmark assessment and intermediate updates, if necessary relative to biology and current management of the species.**

For the single-species assessment, the SAS recommends an update be considered in three years and a new benchmark be considered in six years (Section 9).

***Terms of Reference for the Atlantic Menhaden Peer Review***

1. Evaluate the thoroughness of data collection and the presentation and treatment of fishery-dependent and fishery-independent data in the assessment, including the following but not limited to:
  - a. Presentation of data source variance (e.g., standard errors).
  - b. Justification for inclusion or elimination of available data sources,
  - c. Consideration of data strengths and weaknesses (e.g., temporal and spatial scale, gear selectivities, aging accuracy, sample size),
  - d. Calculation and/or standardization of abundance indices.
  
2. Evaluate the methods and models used to estimate population parameters (e.g.,  $F$ , biomass, abundance) and biological reference points, including but not limited to:
  - a. Evaluate the choice and justification of the preferred model(s). Was the most appropriate model (or model averaging approach) chosen given available data and life history of the species?
  - b. If multiple models were considered, evaluate the analysts' explanation of any differences in results.
  - c. Evaluate model parameterization and specification (e.g., choice of CVs, effective sample sizes, likelihood weighting schemes, calculation/specification of  $M$ , stock-recruitment relationship, choice of time-varying parameters, plus group treatment).
  
3. Evaluate the diagnostic analyses performed, including but not limited to:
  - a. Sensitivity analyses to determine model stability and potential consequences of major model assumptions
  - b. Retrospective analysis

4. Evaluate the methods used to characterize uncertainty in estimated parameters. Ensure that the implications of uncertainty in technical conclusions are clearly stated.
5. If a minority report has been filed, review minority opinion and any associated analyses. If possible, make recommendation on current or future use of alternative assessment approach presented in minority report.
6. Recommend best estimates of stock biomass, abundance, and exploitation from the assessment for use in management, if possible, or specify alternative estimation methods.
7. Evaluate the choice of reference points and the methods used to estimate them. Recommend stock status determination from the assessment, or, if appropriate, specify alternative methods/measures.
8. Review the research, data collection, and assessment methodology recommendations provided by the TC and make any additional recommendations warranted. Clearly prioritize the activities needed to inform and maintain the current assessment, and provide recommendations to improve the reliability of future assessments.
9. Recommend timing of the next benchmark assessment and updates, if necessary, relative to the life history and current management of the species.
10. Prepare a peer review panel terms of reference and advisory report summarizing the panel's evaluation of the stock assessment and addressing each peer review term of reference. Develop a list of tasks to be completed following the workshop. Complete and submit the report within 4 weeks of workshop conclusion.

## **1 INTRODUCTION**

The 2019 benchmark stock assessment for Atlantic menhaden (*Brevoortia tyrannus*) was initiated by the Atlantic States Marine Fisheries Commission (ASMFC or Commission) Atlantic Menhaden Management Board (Board), prepared by the ASMFC Atlantic Menhaden Stock Assessment Subcommittee (SAS), and reviewed and approved by the ASMFC Atlantic Menhaden Technical Committee (TC) as part of the interstate fisheries management and assessment process. The previous stock assessment was similarly completed by ASMFC and peer reviewed through the Southeast Data, Assessment, and Review (SEDAR) process in 2015, and then updated using the same methodology in 2017.

This assessment models the population dynamics of Atlantic menhaden from 1955 to 2017. In this benchmark assessment, the same modelling approach as SEDAR 40 (2015) was used, the Beaufort Assessment Model (BAM). However, changes were made to some model inputs and configurations during this assessment, which are summarized in Table 1 and discussed throughout this report.

### **1.1 Brief Overview and History of the Fisheries**

Atlantic menhaden have supported one of the largest fisheries in the U.S. since colonial times and menhaden have repeatedly been listed as the most important commercial fishery on the U.S. Atlantic coast in terms of annual landings.

Native Americans were the first to use menhaden, primarily as fertilizer. Colonists soon recognized the value of menhaden as fertilizer and local seine fisheries gradually developed from Maine to New York. The menhaden oil industry began in Rhode Island in the early 1800s (Frye 1999) and numerous small factories were located along the Northeast coast soon after. Supply was limited to fish that could be captured by the traditional shore-based seines until the advent of purse seines in 1845, which enabled fishermen to harvest larger quantities of menhaden further from shore. By 1870, the industry had expanded southward with several plants in the Chesapeake Bay and North Carolina areas (Whitehurst 1973). The industry continued to develop during the late 1800s and early 1900s and is described in considerable detail prior to World War I by Greer (1915). After World War I, the primary use of menhaden changed from fertilizer to animal feed due to the development of a process known as fish reduction. Menhaden meal began to be mixed into poultry, swine, and cattle feeds as the amount used for fertilizer decreased (Harrison 1931). The current commercial fishery is divided into the reduction fishery, in which menhaden are produced into fish meal and fish oil, and the bait fishery, in which menhaden are harvested and used as a bait source in other commercial and recreational fisheries.

### **1.2 Management Unit Definition**

The management unit is defined as the range of Atlantic menhaden within U.S. waters of the Northwest Atlantic Ocean, from the estuaries eastward to the offshore boundary of the Exclusive Economic Zone (EEZ). All Atlantic coast states from Maine to Florida, including Pennsylvania and the Potomac River Fisheries Commission, have a declared interest in the ASMFC Interstate Fishery Management Plan for Atlantic menhaden.



Since 1981, the Commission, under the authority of the Atlantic Coastal Fisheries Cooperative Management Act, is responsible for managing Atlantic menhaden in state waters (0-3 nautical miles from shore) from Maine through Florida. Management authority in the Exclusive Economic Zone (3-200 nautical miles from shore) lies with NOAA Fisheries.

### **1.3 Regulatory History**

Atlantic menhaden management authority is vested in the states because historically the vast majority of landings came from state waters. In recent years, a larger portion of the landings have come from federal waters (48% in 2017 and 60% in 2018; R. Mroch, NOAA, personal communication). All Atlantic coast states and jurisdictions, with the exception of the District of Columbia, have a declared interest in the Atlantic menhaden management program.

The first coastwide fishery management plan (FMP) for Atlantic menhaden was passed in 1981 (ASMFC 1981). The FMP did not recommend or require specific management actions, but provided a suite of options should they be needed. After the FMP was approved, a combination of additional state restrictions, imposition of local land use rules, and changing economic conditions resulted in the closure of most reduction plants north of Virginia by the late 1980s. In 1988, the ASMFC concluded that the 1981 FMP had become obsolete and initiated a revision to the plan. The 1992 Plan Revision included a suite of objectives to improve data collection and promote awareness of the fishery and its research needs (ASMFC 1992).

Amendment 1, approved in 2001, provides specific biological, social, economic, ecological, and management objectives (ASMFC 2001). No recreational or commercial management measures were implemented as a result of Amendment 1; however, subsequent addenda instituted a harvest cap on Atlantic menhaden by the reduction fishery in Chesapeake Bay. Addendum II initially implemented the harvest cap for the 2006-2010 seasons; Addendum III revised the harvest cap amount just prior to the 2006 season; and Addendum IV extended the harvest cap three additional years (2011-2013) at the same cap levels as established in Addendum III (ASMFC 2005; ASMFC 2006; ASMFC 2009). Addendum I and Addendum V addressed biological reference points for menhaden, the frequency of stock assessments (every three years), and updated the habitat section of the FMP (ASMFC 2004a; ASMFC 2011).

Amendment 2, approved in 2012, established a 170,800 metric ton total allowable catch (TAC) for the commercial fishery beginning in 2013 (ASMFC 2012a). This TAC represented a 20% reduction from average landings between 2009 and 2011, and an approximately 25% reduction from 2011 harvest. The 2009-2011 time period was also used to allocate the TAC among jurisdictions. States are required to close their respective fisheries when the state-specific portion of the TAC (quota) has been reached. Amendment 2 also established requirements for timely reporting of commercial landings and required states to be accountable for their respective quotas by paying back any overages the following year. Additionally, Amendment 2 included provisions that allowed for the transfer of quota between jurisdictions and a bycatch allowance of 6,000 pounds per day for non-directed fisheries that operate after a jurisdiction's quota has been landed. Further, it reduced the Chesapeake Bay reduction fishery harvest cap by 20% to 87,216 metric tons. Finally, the Amendment set aside 1% of the overall TAC for

episodic events. Episodic events are times and areas where Atlantic menhaden are available in more abundance than they normally occur. The set aside is designed to enable increased harvest of Atlantic menhaden during episodic events. Technical Addendum I to Amendment 2 establishes a mechanism for New England states to use the set aside (ASMFC 2013). Addendum 1, approved in 2016, modified the bycatch provision to allow two authorized individuals working together from the same vessel, and using stationary multi-species gear to land up to 12,000 pounds per day (ASMFC 2016).

Amendment 3, approved in 2017, completely replaced Amendment 2 and currently sets the management program for Atlantic menhaden. The Amendment continues to manage the stock via single-species biological reference points until the review and adoption of menhaden-specific ecological reference points as part of the 2019 benchmark stock assessment process (ASMFC 2017a). Amendment 3 also changed TAC allocations to strike an improved balance between gear types and jurisdictions. Specifically, the Amendment allocated a baseline quota of 0.5% to each jurisdiction, and then allocated the rest of the TAC based on historic landings during the 2009-2011 time period. This measure provided fishing opportunities to states which previously had little quota, while still recognizing historic landings in the fishery. The Amendment also maintained the quota transfer process, prohibited the rollover of unused quota, maintained the 6,000 pound trip limit for non-directed and small-scale gears following the closure of a directed fishery, and maintained the episodic events set aside program for the states of Maine through New York. Lastly, Amendment 3 reduced the Chesapeake Bay cap from 87,216 metric tons to 51,000 metric tons. However, the terminal year of this stock assessment is 2017, before the implementation of Amendment 3.

## **1.4 Assessment History**

### **1.4.1 Previous stock assessments**

Since the stock assessment peer review process was adopted by the ASFMC in 1998, Atlantic menhaden have been assessed several times (ASMFC 1999, 2004b, 2010, 2012b; SEDAR 2015; ASMFC 2017b). The most recent peer reviewed benchmark stock assessment was SEDAR 40 (2015), which was updated in 2017 (ASMFC 2017b).

### **1.4.2 Previous Assessment Data and Models**

The most recent Atlantic menhaden assessment (SEDAR 2015, ASMFC 2017b) used both fishery-dependent and -independent data as well as information about Atlantic menhaden biology and life history. Fishery-dependent data came from the commercial reduction and bait fisheries, while fishery-independent data were collected through scientific research and surveys. The data were used to inform both juvenile and adult abundance within the model.

The Beaufort Assessment Model (BAM) was used to provide management advice during the 2015 benchmark stock assessment (SEDAR 2015) and the 2017 update. BAM is a statistical catch-at-age model that estimates population size-at-age and recruitment, using 1955 as the start year, and then projects the population forward in time. The model estimates trends in the population, including abundance-at-age, recruitment, spawning stock biomass, egg production, and fishing mortality rates. BAM was configured to be a fleets-as-areas model with each of the

fishing sectors (bait, reduction) broken into areas to reflect differences along the coast. This means that both reduction and bait fleets were split into north and south regions because each fishery operated differently along the coast and through time.

### **1.4.3 Biological Reference Points**

Based on the assessment update (ASMFC 2017b), Atlantic menhaden were neither overfished nor experiencing overfishing. Stock status was evaluated against the assessment's reference points, which used historical performance of the population during 1960-2012. This time-frame was a period during which the TC considers the population to have been sustainably fished.

Fishing mortality rates (geometric mean for ages 2-4) remained below the overfishing threshold (1.85) since the 1960s and hovered around the overfishing target (0.8) through the 1990s. In 2003, fishing mortality dropped below the target and was estimated to be 0.51 in 2016 (the last year in the assessment update). Generally, fishing mortality was decreasing throughout the history of the fishery, was below the threshold since the early 1960s, and was below the target since the early 2000s.

The biological reference point used to determine the fecundity target was defined as the mature egg production when the population is being fished at the threshold fishing mortality rate. Population fecundity, a measure of reproductive capacity, has been well above the threshold (57,295 billion eggs) and at or near the target (99,467 billion eggs) in recent years. In 2016, fecundity was estimated to be 83,486 billion eggs, well above the threshold but below the target.

### **1.4.4 Past Research Recommendations**

Both the 2015 benchmark assessment and the 2017 update identified a number of data and research needs for future Atlantic menhaden stock assessments. Some recommendations included the development of a coastwide fishery-independent survey to replace or supplement the existing indices. Also, development of a spatially explicit (e.g., regional) stock assessment model would be beneficial once sufficient age-specific data on movement rates of menhaden are available. The stock assessment also suggested conducting a management strategy evaluation and multi-objective decision analysis. Developing ecological reference points for Atlantic menhaden has been a research recommendation for some time.

## **2 LIFE HISTORY**

### **2.1 Stock Definitions**

Atlantic menhaden is a euryhaline species (i.e., tolerates a wide range of salinity) that inhabits nearshore and inland tidal waters from Nova Scotia, Canada, to Florida. Atlantic menhaden are considered a single stock. Historically, there was considerable debate relative to stock structure of Atlantic menhaden on the U.S. East Coast, with a northern and southern stock hypothesized based on meristics and morphometrics (Sutherland 1963; June 1965). Based on size-frequency information and tagging studies (Nicholson 1972 and 1978; Dryfoos et al. 1973), the Atlantic

menhaden resource is believed to consist of a single unit stock or population. Genetic studies also (Anderson 2007; Lynch et al. 2010a) support the single stock hypothesis.

## **2.2 Recruitment and Migration Patterns**

Several studies have examined Atlantic menhaden migration patterns (Roithmayr 1963; Dryfoos et al. 1973; Nicholson 1978; ASMFC 2004b). The population of Atlantic menhaden is widely distributed from Nova Scotia to Florida. Adults begin migrating inshore and north in early spring following the end of the major spawning season off the Carolinas during December-February. The oldest and largest fish migrate farthest, reaching southern New England by May and the Gulf of Maine by June. Adults that remain in the south Atlantic region for spring and summer migrate south later in the year, reaching northern Florida by fall. In the fall, Atlantic menhaden begin a migration to the Carolinas. During November and December, most of the adult population that summered north of Chesapeake Bay moves south of the Virginia and North Carolina capes. Atlantic menhaden spawn as a population off the coast of the Carolinas in the winter months (Nicholson 1978; Lewis et al. 1987), although they are multiple spawners that can also spawn again along the migration route (Ahrenholz 1991).

Historical tagging data from 1966-1969 was recently reanalyzed by Liljestrand et al. (2019a, 2019b), which indicated that while the pattern of Atlantic menhaden's movement was similar to previous findings, the magnitude of movement during the winter in the northern region differed. For example, previous literature (Roithmayr 1963; Nicholson 1971) stated that the majority of Atlantic menhaden in the north migrate south to overwinter in North Carolina whereas Liljestrand et al. suggested about 55% of Atlantic menhaden in the northern region migrates southward. Therefore, there may be less southward movement of Atlantic menhaden in the winter than previously described by the literature and more residency in the northern area throughout the year.

After spawning on the coastal shelf, Atlantic menhaden rely on ocean currents to deliver larvae to inshore nursery grounds along the coast where juveniles develop before recruiting to the adult population. Depending on physical processes and ocean circulation, larvae can be transported hundreds of kilometers from the spawning ground to estuaries (Epifanio and Garvine 2001). Nursery ground productivity may vary annually due to environmental and biological factors such as the amount of larvae near estuarine mouths, time and location of spawning, number of eggs produced and the size of the spawning stock biomass, changes in the Gulf Stream, temperature, accessibility of estuarine mouths, and winter storms (Nelson et al. 1977; Miller et al. 1984; Checkley et al. 1988; Quinlan et al. 1999; Werner et al. 1999). Apart from physical conditions in the ocean, migrations by size and age classes may increase the spatial and temporal placement of eggs and larvae. While the majority of Atlantic menhaden spawning occurs off of North Carolina, some spawning does take place throughout most of the year along the migratory tract of the older, larger, more fecund fish in northern regions, possibly ensuring recruitment from a variety of locations (Ahrenholz 1991). An analysis of historical ichthyoplankton survey data from 1977-2013 confirmed that while the highest larval abundance was indeed off the coast of North Carolina, shallow areas along the Atlantic coast had comparable abundance estimates (Simpson et al. 2016). Additionally, Simpson et al. (2016)

found that the number of larval Atlantic menhaden has increased in the last decade although pre-recruit survival appears to have decreased, likely due to changes in temperature in estuaries and coastal waters.

## **2.3 Age**

In 1955, the NOAA Laboratory at Beaufort, North Carolina, began monitoring the Atlantic menhaden purse-seine fishery for size and age composition of the catch (June and Reintjes 1959). Scales were selected as the ageing tool of choice for Atlantic menhaden due to ease of processing and reading and an age validation study confirming reliable age marks on scales (June and Roithmayer 1960). During the early decades of the Menhaden Program at the Beaufort Laboratory, scales from individual menhaden specimens were read multiple times by several readers. Since the early 1970s, only a single reader was retained on staff to age menhaden scales. The Beaufort lab still ages all reduction fishery samples. The maximum age of Atlantic menhaden is 10 years, although Atlantic menhaden over age 6 are rarely found in the fisheries.

State agencies collect scales from their bait fisheries and fishery independent programs. In the past, Beaufort was ageing the bait samples for stock assessments and the states aged some of the fishery independent samples, although those were not used in the assessment. To address future plans for states to age Atlantic menhaden scales and the research recommendation to conduct an ageing workshop, the ASMFC organized and held a workshop in 2015 (ASMFC 2015). An exchange of scale samples took place and was followed with an in-person workshop to discuss the results. Despite the fact that most participating agers were new to ageing Atlantic menhaden or had never aged the species, agreement between readers was, on average, 73% and increased to 95% within one year. False annuli, poor storage of samples, and damaged scales were common issues identified at the workshop.

Atlantic menhaden scales were also examined at ASMFC's 2017 and 2018 Quality Assurance/Quality Control Fish Ageing Workshops (ASMFC 2017c, 2018). Average percent error between agers along the Atlantic coast was 15% in 2017 and 13% in 2018, although many readers had no previous experience ageing Atlantic menhaden.

To prepare for supplying this assessment with ages, Atlantic menhaden agers from Maine to Florida and representatives from the Beaufort lab took part in an ageing call in January 2018 to decide how to proceed with ageing Atlantic menhaden samples. Participants decided to have Beaufort continue to age all bait samples for this benchmark, in addition to the reduction fishery samples. After this assessment is completed, agers and ASMFC anticipate developing an exchange set of scales and otoliths and organizing another workshop.

## **2.4 Growth**

### **2.4.1 Length-Weight Relationship**

For SEDAR 40 (2015) and ASMFC 2017b, a time-invariant length-weight relationship was developed from the reduction fishery's biological data set. For this assessment, the SAS re-evaluated whether the relationship should be time-varying or time-invariant.

Paired length-weight data were evaluated from the reduction fishery sampling program using the cohort years of 1955-2015. Refer to section 4.1.2 for a more thorough discussion of the methods for biological sampling in the reduction fishery. Briefly, biological samples including age, weight, and length are collected throughout the year and categorized into five areas: North Atlantic (1), Middle Atlantic (2), Chesapeake Bay (3), South Atlantic (4), and the fall fishery off North Carolina (5; Figure 1). Using ages, the samples were assigned to their cohort year. There were over 470,000 paired lengths and weights, although the number of samples available ranged by year and region (Figure 2) as the sampling protocols changed (section 4.1.2) and the fishery changed over time. For example, region 4 was sampled heavily during the 1960s – 1980s, sampled less frequently in the 1990s and early 2000s, and then not sampled from 2005-2017.

An annual regression of weight ( $W$  in g) on fork length ( $FL$  in mm) for port samples of Atlantic menhaden were fit, based on the natural logarithm transformation:

$$\ln W = a + b \ln FL.$$

and was corrected for transformation bias (root MSE) when retransformed back to the form:

$$W = a(FL)^b.$$

The root MSE was calculated to be 0.11.

The length-weight regressions were tested to determine if the fit was statistically different between cohort years and the results indicated that the relationship has significantly changed throughout time (ANOVA:  $F_{1,61} = 228$ ,  $P < 0.001$ ). However, the SAS had concerns that these differences were an artifact of the changes in sampling both spatially and temporally. The SAS evaluated the predicted weight from the time-invariant and time-varying relationships for several given lengths to see if the time-invariant fell within the time-varying confidence interval. Because the predicted weights had very small confidence intervals given the large samples sizes from the reduction fishery, the time-invariant weight did not fall within the confidence intervals of time-varying for most years and lengths (Figure 3). But since sampling varied across years and regions, looking at the average weight of a 200-mm menhaden, for example, through time in one area, the time-invariant average weight fell within the confidence intervals of the time-varying (Figure 4). Due to the suspected effects of sampling on the relationship, and also that growth is time-varying in the assessment model, the SAS decided that the time-invariant relationship for length-weight ( $a = 7.03E-6$  and  $b = 3.17$ ) was sufficient.

Catch in numbers by year, season, and fishing area was developed for weighting corresponding sampled weights of Atlantic menhaden. This was then used to calculate the mean weight-at-age for fish from 1955-2017, which was used in the stock assessment for matching to landings. These “weighted” mean weights increased during the 1960s, declined dramatically during the 1970s, and remained low during most of the 1980s. Increasing mean weights were estimated

during the 1990s followed by declines in mean weight to the present. Weighting by catch in numbers by year, season, and fishing area was also applied to calculate average fork lengths (mm) by age and year.

#### 2.4.2 von Bertalanffy Growth Curve

As in previous menhaden assessments, regressions of fork length (mm) on age were based on the von Bertalanffy growth curve:

$$FL = L_{\infty}(1 - \exp(-K(\text{age} - t_0))).$$

Von Bertalanffy fits were made with the size-at-age data aligned by cohort (year class). Because of concerns that density-dependent growth is a characteristic of the cohort, cohort-based analyses were thought to be a better approach. Attempts were made to fit the von Bertalanffy growth equation to each year class from 1947 (age-8 in 1955) to 2015 (age-2 in 2017). For most cohorts, a full range of ages were available (1955-2011). For the incomplete cohorts at the beginning of the time period (1947-1955) all fits converged, although specific parameter estimates became progressively unrealistic for the earlier years. Similarly, incomplete cohorts for the recent time period (2012-2017) generally converged with the exception of the last two years (2016-2017). Thus, for age-0 during 2016-2017 and age-1 during 2017, the size- and weight-at-age were the average of the three years preceding.

Annual estimates of length-at-age for the population were bias corrected using the methods in Schueller et al. (2014). Specifically, the methods correct for the absence of samples at the youngest and oldest ages and smallest and largest sizes. Evidence is available from the fishery-independent data that both smaller and larger fish are available for capture in the population, yet are not represented in the commercial reduction fishery database (the only data available to estimate growth parameters, Figure 5). Therefore, the growth curves for the population would be biased to smaller maximum sizes than naturally occur in the population. The correction was done on the cohort-based annually estimated growth curves with a minimum size of 100 mm FL (unless samples had a larger minimum size) and the maximum size was set at the 99.95% size for encountered fish rounded to the nearest whole number ending in 0 or 5. In a few cases,  $t_0$  was fixed at the uncorrected value. The reference age selected was age-2 as that age reflects the full distribution of sizes-at-age. The corrected values of  $L_{\infty}$  and  $K$  were within the range of uncorrected values (Figure 6, Table 2). The growth curve parameters vary year to year and are influenced by both density dependent processes and differing growth conditions.

Annual estimates of fork length-at-age were interpolated from the annual, cohort-based von Bertalanffy growth fits with a bias correction to represent the population or start of the fishing year (March 1) for use in estimating population fecundity (Table 3). Annual estimates of length-at-age were interpolated based on the non-biased corrected von Bertalanffy estimates to represent the fishery or middle of the fishing year (September 1), and converted to weight-at-age for use in the statistical catch-at-age models when comparing model estimated catch to observed catch (Table 4).

Growth for Atlantic menhaden is variable over time and a few scientists have tried to link the changes to environmental conditions. Turner (2017) related growth rates of both Atlantic and Gulf menhaden to climate change; however, that paper garnered a response from Schueller et al (2018) who claimed that biased data were used in the analyses, as well as the analyses not addressing the stated objectives. In response, Midway et al. (in review) modeled changes in growth over time with appropriate data and hierarchical Bayesian models (A. Schueller, NOAA, personal communication). Midway et al. (in review) found that landings, and thus density dependence, seemed to be the most influential coastwide driver of changes in growth for Atlantic menhaden, while other environmental factors such as wind and AMO had differing effects spatially.

## **2.5 Maturity**

Maturity information for Atlantic menhaden used in this assessment is based on the comprehensive analysis of maturity data completed during SEDAR 40 (2015) and reconsidered and reevaluated for this assessment. In past assessments, maturity had been treated as age-specific and time-invariant based on estimates from Higham and Nicholson (1964). Additional review indicated that the maturity ogive based on this study was not representative of maturity in the population because the classification of maturity by Higham and Nicholson was “active” versus “inactive,” rather than “mature” versus “immature.” In 2014, two new data sets were made available to the assessment team for determining maturity-at-age: commercial reduction fishery data and Northeast Area Monitoring and Assessment Program (NEAMAP) data.

Commercial reduction fishery data collected by the Beaufort Laboratory contain records on more than 240,000 fish sampled between 1955 and 1970 through the harvest monitoring sampling program (Huntsman and Chapoton 1973). Reduction plants from Maine to Florida were sampled every month except February and March. Fish size, age, location of sample, and maturity data were recorded for both males and females. Female maturity stages in the database were coded as 1 = immature, 2 = resting, 3 = ripening, 4 = ripe, 5 = spent, and 6 = unknown (Huntsman and Chapoton 1973). Menhaden are known to spawn throughout most of the year, but the peak of the spawning activity is believed to occur during fall to early winter, with spawning aggregations primarily off the coast of North Carolina south of Cape Hatteras (Nelson et al. 1977; Ahrenholz et al. 1987b; Checkley et al. 1999). To match the peak of spawning and the center of spawning population distribution, data for maturity analysis were subset by time (September through January) and geographic location (only plants located in Virginia and North Carolina). Data for all years were combined to have the most accurate representation of maturity, resulting in a total sample size of 79,076. Maturity stages were recoded as immature (stage 1) and mature (stages 2 - 5). The maturity process was modeled as a function of age or size with the logistic regression. This resulted in average maturity-at-age very similar to the estimates that were based on the fishery-independent NEAMAP survey (Figure 7). Considering that NEAMAP employs a stratified random survey design (Bonzek et al. 2012), the SAS concluded that the maturity estimates from NEAMAP and the reduction fishery data were unbiased.



The SAS discussed the role of size and age in the maturation process and concluded that Atlantic menhaden maturation is more likely to commence upon reaching a certain size and energy content than a specific age. Consequently, maturity was further modeled as a length-based process. Logistic regression was used to model maturity as a function of length:

$$P = \frac{1}{1 + \exp(-(\alpha + \beta L))}$$

where the intercept and slope of the logistic regression model were estimated to be  $\alpha = -9.929$  and  $\beta = 0.0476$ , respectively (Figure 8).

Previous studies reported that Atlantic menhaden growth is density dependent and varies greatly among years (Ahrenholz et al. 1987b; Schueller and Williams 2017). As the average size of fish within an age group varies from year to year, the maturity must also vary among years. Thus, the year-specific mean lengths-at-age on March 1 (the start date of a fishing year in the model, Table 3) were used as inputs to the logistic regression to provide time-varying estimates of maturity-at-age for 1955-2017 (Figure 9, Table 5).

## 2.6 Fecundity

A reevaluation of fecundity was a high-priority research recommendation following SEDAR 40 (2015) due to a number of concerns with the fecundity-at-length relationship used to estimate annual fecundity. The fecundity-at-length information used in past assessments was developed based on sampling that occurred between 1956 and 1981 and was restricted to the coastal ocean in the vicinity of Beaufort, North Carolina, during fall (Higham and Nicholson 1964; Dietrich 1979; Lewis et al. 1987). Annual egg production has been shown to exhibit plasticity in response to variability in both biotic and abiotic factors (Brown-Peterson and Warren 2001), and as such a contemporary evaluation of Atlantic menhaden fecundity from throughout a broad range of the stock is warranted. Further, while evaluation of Atlantic menhaden ovary samples collected in the 1950s suggested that this species may exhibit indeterminate batch spawning, the approach used to quantify the aforementioned fecundity-at-length relationship employed methodology associated with determinate total spawning species (Higham and Nicholson 1964; Lewis et al. 1987).

Since SEDAR 40 (2015), work has been completed by VIMS (R. Latour and J. Gartland, unpublished data) to address the research recommendation and update fecundity values. The objective of the investigation was to generate a contemporary evaluation of female Atlantic menhaden reproductive biology that represented a broad spatiotemporal spawning range, and subsequently updated estimates of fecundity using methodology that is consistent with the spawning mode of this species. A complete description of the VIMS research project and methods is in Appendix 14.1 and summarized briefly here.

Latour and Gartland collected female Atlantic menhaden across all seasons and throughout the Mid-Atlantic Bight, between Cape Cod, Massachusetts, to Cape Hatteras, North Carolina, from 2013-2018. The study implemented standard gonad histology techniques to assess ovarian maturity phases, provide insight into spawning mode, and information on spawning seasonality, interval, and frequency. Ova were counted using methodology consistent with the

spawning mode of this species. Fecundity was modeled as a function of fish length and coupled with information on size-at-age, spawning frequency, and maturity data to yield age-specific estimates of annual fecundity.

The VIMS study found that for each of the female Atlantic menhaden in the developing, spawning capable, and actively spawning phases, the presence of ova in the most advanced stage of development was accompanied by oocytes in all earlier stages of development. These observations indicated that oocyte development is asynchronous in Atlantic menhaden and confirms that this species exhibits batch spawning (Brown-Peterson et al. 2011). The spawning season was defined by evaluating the monthly mean gonadosomatic index (GSI), the ratio of total ovary weight to ovary-free fish weight, which showed peaks from October to December (Figure 10). The percentage of spawning capable fish was highest during these months as well (Figure 11), although May also had a notable peak in both graphs indicating that spawning season is likely longer. The size-frequency distributions of oocytes in the ovaries of spawning capable Atlantic menhaden collected near the beginning of the peak (i.e., October) and end of the peak (December) of the spawning season were evaluated to characterize the spawning mode of this species and the distributions were consistent with indeterminate spawning. Given the evidence, it is likely that Atlantic menhaden exhibit indeterminate batch spawning, and this finding is consistent with the determinations of spawning mode for both Gulf and Brazilian menhaden (Macchi and Acha 2000; Brown-Peterson et al. 2017).

Estimates of age-specific annual fecundity for Atlantic menhaden spanning age-0 to age-6+ were provided for this assessment. Fecundity-at-age for each year was fixed and based on a function of mean weight by age for the population. The annual fecundity-at-age in year  $i$  ( $AF_{ai}$ ) was estimated as:

$$AF_{ai} = RBF * WT_{ai} * SF * PM_{ai}$$

where RBF (relative batch fecundity) was 236.92 eggs/g ovary-free body weight, SF (spawning frequency) was 11.70 spawns/season, and where  $WT_{ai}$  (weight-at-age) and  $PM_{ai}$  (maturity-at-age) were the weight-at-age  $a$  and proportion of fish mature at age  $a$  for a given  $i$  at the start of the fishing year (i.e., March 1). Uncertainty in these annual fecundity estimates was characterized to yield lower and upper bounds on these estimates. An example of these fecundity estimates for 2015 is provided (Table 6). Note that when compared with the age-specific annual fecundity estimates generated from the fecundity-at-length relationship used previously (Lewis et al. 1987), increases in age-specific annual fecundity range from 554.7% - 680.8%, with a mean increase of 623.5%. Estimates of annual fecundity for Gulf menhaden using a similar methodology resulted in increases on the order of 1100%-2300% (Brown-Peterson et al. 2017), indicating that the results of this investigation are not unreasonable.

Simpson et al. (2016) documented Atlantic menhaden larval distribution and abundance along Atlantic coast from between Cape Hatteras, North Carolina, and Cape Cod, Massachusetts, and Keller et al. (1999) showed that Atlantic menhaden larvae occur in Narragansett Bay, Rhode Island, in June/July and again in October through December. The VIMS study did document a single actively spawning Atlantic menhaden in the southern New England area in May, which is consistent with the presence of larvae and juveniles in northern estuaries during summer

(Simpson et al. 2016, Keller et al. 1999). However, given the sample size ( $n = 1$ ), spring months were excluded from the spawning season estimate. It is likely that Atlantic menhaden spawn during their spring northerly migration, and additional specimen collections are ongoing to further resolve the spawning seasonality.

## 2.7 Natural Mortality

Age-structured models attempt to reconstruct the fish population and fishing mortality rates by age and year, where total instantaneous mortality rate ( $Z$ ) is the sum of instantaneous rates of fishing ( $F$ ) and natural ( $M$ ) mortality. Historically, natural mortality has been assumed to be constant over ages and years. In many stock assessments, constant values for  $M$  have been obtained from life history analogies (e.g. maximum age, growth rate parameters). Because it is thought that younger fish are more vulnerable to predation, natural mortality may decline with size or age. Several approaches have been considered to provide such size-varying estimates of natural mortality. For purposes of stock assessments, sizes are related to age to provide age-varying estimates of natural mortality.

Because menhaden are abundant in coastal waters and are a common prey species to many predatory fishes, sea birds, and marine mammals, predation mortality is probably the greatest component of natural mortality. This high rate of mortality is particularly acute among the youngest age classes, due to mouth gape limitation of most piscivorous fishes. Menhaden are preyed upon by a variety of predators such as bluefish, striped bass, king mackerel, Spanish mackerel, pollock, cod, weakfish, silver hake, tunas, swordfish, bonito, tarpon, and a variety of sharks (ASMFC 2001). In turn, menhaden are valuable forage for many commercial and recreationally important East Coast fishes. Given the importance of menhaden as a forage species and the assumed high predation that presumably occurs on young of the year and juvenile fish, age-varying natural mortality rates may be more appropriate for this species.

Coastal pollution and habitat degradation threaten marine fish species, such as Atlantic menhaden, which spend their first year of life in estuarine waters and the rest of their life in both ocean and estuarine waters. Other poorly understood sources of natural mortality for Atlantic menhaden are diseases and parasites. A partial list of parasites was given in Reintjes (1969), but no information is available concerning the extent of parasitism or its possible effect on survival. Ahrenholz et al. (1987a) described the incidence of ulcerative mycosis (UM), a fungal infestation that was observed in menhaden over much of their range in 1984 and 1985 and in a more restricted area in 1986. A large fish kill in Pamlico Sound, North Carolina in November 1984 was associated with UM, but its primary effect may be to weaken fish, making them more susceptible to other causes of mortality, such as predation, parasites, other diseases, and low dissolved oxygen concentrations. The overall impact of UM on the 1984 and 1985 year classes could not be assessed, but it was not believed to be significant (Ahrenholz et al. 1987a). Vaughan et al. (1986) believed that the mortality effects of a disease or other event must be "truly catastrophic" to be detectable.

Another source of natural mortality for Atlantic menhaden (and many other species) may be 'red tide.' The term refers to the color of water caused by the rapid multiplication or 'bloom' of single-celled planktonic organisms called dinoflagellates, which produce a toxic compound. The

toxin accumulates in the tissues of filter-feeding animals, which ingest the dinoflagellate. An outbreak of red tide occurred along the coast of the Carolinas during November 1987 - April 1988 when Gulf Stream water containing the dinoflagellates was transported into coastal waters. Menhaden recruitment in Beaufort Inlet during this period was severely reduced (S. Warlen, NMFS, personal communication as cited in ASMFC 1992). A new species of toxic dinoflagellate was identified as the causative agent in a major menhaden kill in the Pamlico River, North Carolina, in May 1991. Problems with toxic phytoplankton organisms may increase in the future since their appearance has been correlated with increasing nutrient enrichment in estuarine and coastal waters that are subject to increasing organic pollution (Smayda 1989).

An additional source of mortality are fish 'kills', which occur when schools of menhaden enter enclosed inshore bodies of water in such large numbers that they consume all available oxygen and suffocate. The mean lethal dissolved oxygen concentration for menhaden has been reported to be 0.4 mg/l (Burton et al. 1980). Bluefish are known to follow (or even chase) schools of menhaden inshore, feeding on them, and may contribute to their mortality by preventing them from leaving an area as the oxygen supply is depleted. High water temperatures, which increase the metabolic rate of the fish and accelerate oxygen depletion. Menhaden that die from low oxygen stress can immediately be recognized by the red coloration on their heads caused by bursting blood capillaries. Just before death, the fish can be seen swimming very slowly in a disoriented manner just below the surface of the water. This is a common phenomenon that has been observed throughout the range of the species. Menhaden spotter pilots have reported menhaden 'boiling up' from the middle of dense schools and washing up on the beach, apparently from oxygen depletion within the school. This phenomenon was observed during December 1979 in the ocean off Atlantic Beach, North Carolina (M. Street, NC DMF, personal communication as cited in ASMFC 1992). Smith (1999) reported a similar event off Core Banks, North Carolina, in December 1997. Other species are not nearly as susceptible simply because they do not enter enclosed inshore waters in such large numbers.

### **2.7.1 Tag-Based Estimates**

To examine life-history and migration of Atlantic menhaden, Liljestrand et al. (2019a, 2019b) reanalyzed historical tagging data using new analytical methods that were not available during the initial analysis of the data. The original dataset was the result of a comprehensive large scale mark-recovery study of Atlantic menhaden conducted by NMFS from 1966–1969. A total of 1,066,357 fish were injected with individually numbered ferromagnetic tags which were recovered by magnets at 17 of the 18 processing facilities in operation on the Atlantic coast during that time. Tagging ranged from Massachusetts to northern Florida and had an approximate 15-20% return rate which varied by season, area, and year (Dryfoos et al., 1973). Empirical estimates of tag shedding/tag mortality rates and reporting rates (i.e., magnet efficiency) were developed from supplementary studies conducted to estimate values for these processes.

Liljestrand et al. (2019a) used a Bayesian model that estimated natural mortality, region- and time- specific fishing mortality, and monthly movement. As part of the model development, the study tested the ability of the Bayesian model to estimate natural mortality and movement

rates with simulated data, and the model was able to produce unbiased estimates with good accuracy and precision. Liljestrand et al. (2019a) estimated a natural mortality of  $1.17 \text{ yr}^{-1}$  (95% CI: 1.09–1.23). This was higher than previous estimates based on the same dataset, which ranged from  $0.50\text{--}0.52 \text{ yr}^{-1}$  (Dryfoos et al. 1973; Reish et al. 1985). However, the Bayesian model used by Liljestrand et al. (2019a) represents an improvement over the older catch-curve-based (Dryfoos et al. 1973) and VPA-based (Reish et al. 1985) approaches for estimating  $M$  from tagging data.

## 2.7.2 Life-History Based Approaches

While methods that relate life history traits with natural mortality were reviewed in Vetter (1987), newer methods have been developed since that landmark paper. A variety of methods have been explored during past menhaden SEDAR data workshops, and the results of some of these methods are summarized in this section. Often  $M$  is related to the parameters from the von Bertalanffy growth equation ( $K, L_\infty$ ), or as an inverse function of size-at-age, so consideration of growth of Atlantic menhaden is relevant to this section.

### 2.7.2.1 Age-Constant $M$ Approaches

Several methods are available for determining an age-constant  $M$  based on life history characteristics, notably maximum age ( $t_{max}$ ), von Bertalanffy growth parameters ( $K, L_\infty$ ), and average water temperature ( $T^\circ\text{C}$ ). Results from the following approaches are summarized in Table 7.

Mean environmental temperature ( $T^\circ\text{C}$ ), or mean annual temperature where the fish is caught, used here was  $19^\circ\text{C}$ . Quinn and Deriso (1999) have converted Pauly's equation from base 10 to natural logarithms as presented above. The "rule of thumb" method has a long history in fisheries science, but it is difficult to pin down its source. Hewitt and Hoenig (2005) compared this approach to that of Hoenig (1983) and noted that the Hoenig method provided an estimate of  $M$  only when fishing mortality can be assumed small ( $F \sim 0$ ) otherwise it was suggested to be an upper bound on  $M$ . Annual values of  $M$  for those equations above were calculated when there were annual values of input parameters; e.g., Alverson and Carney (1975), Jensen (1996) and Pauly (1980) (Figure 12). Then et al. (2014) re-estimated many of the common age-constant estimators of  $M$  with more robust statistical methods and data vetting.

Estimates of  $M$  in the early literature on Atlantic menhaden vary, though not widely (Ahrenholz 1991). Schaaf and Huntsman (1972) estimated  $M = 0.37 \text{ yr}^{-1}$  based on an ad hoc approach regressing  $Z$  on fishing effort. Estimates were  $M = 0.52 \text{ yr}^{-1}$  from a preliminary tag-recovery analysis (Dryfoos et al. 1973) and  $M = 0.50 \text{ yr}^{-1}$  from a more extensive tag-recovery analysis (Reish et al. 1985). The mean of the range ( $M = 0.45 \text{ yr}^{-1}$ ) has been used routinely in Atlantic menhaden assessments beginning with Ahrenholz et al. (1987b).

### 2.7.2.2 Age-Varying $M$ Approaches

Several approaches have been developed to provide age-varying estimates of  $M$  (Peterson and Wroblewski 1984; Boudreau and Dickie 1989; Lorenzen 1996; Charnov et al. 2013). All of the approaches use an inverse relationship between size or weight and  $M$ . To apply these methods, weight-at-age is calculated for the middle of the calendar year (September 1).

The method of Peterson and Wroblewski (1984) was used to describe natural mortality for young-of-year Atlantic menhaden (Heimbuch et al. 2007), and uses a dry weight as its independent variable. The method of Boudreau and Dickie (1989) has been applied in several assessments, notably for Gulf menhaden in Vaughan et al. (2007). In some SEDAR assessments, the method of Charnov et al. (2013) has been used whereby the weight relationship, growth and natural mortality, prior to and after maturity, are used to estimate natural mortality.

The method of Lorenzen (1996) has been used in recent years (SEDAR 2015, ASMFC 2017d, NEFSC 2018, and SEDAR 2018). When applying the method of Lorenzen (1996), estimates of age-varying  $M$  are scaled such that cumulative survival from age 1 through the maximum age is equal to 1.5%. This cumulative survival value comes from the fixed  $M$  method of Hoenig (1983) as described in Hewitt and Hoenig (2005). When similarly scaled, the resulting  $M$  from Peterson and Wroblewski (1984), Boudreau and Dickie (1989), and Lorenzen (1996) provide very similar results (Figure 13).

More recently Then et al. (2014) examined different methods of estimating  $M$  from life history traits. They suggested a lower survival at maximum age (0.3% - 0.6%) versus earlier work by Hoenig (1983) as described in Hewitt and Hoenig (2005).

Unscaled and scaled estimates of  $M$  based on the approaches of Lorenzen (1996) were developed using the von Bertalanffy growth equation applied to ages 1 through maximum age (age 10) separately, by age.

To scale the Lorenzen estimates to longevity, a Hoenig-based age-invariant estimate of  $M$  equal to 0.42 was used. A survival of 1.5% from age 1 through age 10 was assumed. Corresponding percentages were developed to scale  $M$  ranging from  $M = 0.37$  to  $0.52$  (or 2.5% and 0.6% survival, respectively). Additionally,  $M$  scaled to survival from the more recent work by Then et al. (2009) is also provided (Figure 14). Various scaled and unscaled age-varying estimates of  $M$  are summarized for ages 0-6 in Table 8.

### **2.7.3 Natural Mortality from Multi-Species Approaches**

In previous benchmark assessments, a Multi-species Virtual Population Analysis (MSVPA-X) was used to derive an  $M$  matrix by both age and year for Atlantic menhaden (Garrison et al 2010), which was then used as input to inform the current single species approach. During the most recent benchmark (SEDAR 2015), this approach was discontinued. Reasons for this included the sensitivity of the MSVPA-X results to changes in spatial and temporal overlap between predators and prey, divergent results with some single species assessments, as well as inherent problems using the MSVPA-X output from 1982 onward and using an average back to 1955.

As part of the ERP efforts, a time-varying and age-varying matrix of  $M$  was developed from the Virtual Assessment for the Description of Ecosystem Responses (VADER), a multi-species statistical catch-at-age model (ERP Report, SEDAR 2019; Table 9). This  $M$  matrix was used in a sensitivity run for the single-species assessment.

### **2.7.4 Base Run Configuration**

Given Atlantic menhaden's role as a forage species and the need to account for increased natural mortality at the younger ages, the SAS considered an age-varying  $M$  the best approach

to parameterize natural mortality in the base run. Liljestrand et al.'s (2019a) estimate of natural mortality was not age specific. The mean age of the tagged fish was 1.35 years. In order to develop age-specific estimates for use in the assessment, the SAS scaled the estimates of  $M$ -at-age calculated using Lorenzen (1996) so that the estimate of  $M$  at age 1.5 was equal to Liljestrand et al.'s (2019a) estimate of  $1.17 \text{ yr}^{-1}$ . This was the same approach used in SEDAR (2015), but the tag-based  $M$  scaler was updated to reflect the most recent estimate.

The age-varying  $M$  scaled by Liljestrand et al.'s (2019a) estimate is significantly higher than estimates of  $M$  used in the previous assessment, as well as age-constant and age-varying estimates derived from common literature approaches based on maximum age, von Bertalanffy growth parameters, or weight-at-age (Table 7 - Table 8, Figure 13 - Figure 14). The age-varying estimate of  $M$  used in the base run of the assessment model would result in approximately 0.01% of the population surviving to a maximum age of 10 years, while Then et al.'s (2014) recommended maximum age estimator would result in approximately 0.3% of the population surviving to a maximum age of 10 years. The unscaled Lorenzen (1996) would result in approximately 0.15% of the population surviving to age 10.

The choice of  $M$  is a decision with significant implications for the scale of the assessment. The SAS determined that the empirical estimate of  $M$  derived from a robust, large-scale tagging project analyzed with the most up-to-date model was the best estimate of  $M$  for use in the stock assessment, and preferred it to literature-based estimates of  $M$  derived from meta-analysis of a range of species, most of which were not short-lived, forage fish species. A sensitivity analysis was conducted using the lower estimate of  $M$  from the previous benchmark assessment.

### **3 HABITAT DESCRIPTION**

#### **3.1 Brief Overview of Habitat Requirements**

Estuarine and nearshore waters along the Atlantic coast from Florida to Nova Scotia serve as important habitat for juvenile and adult Atlantic menhaden. Within this wide geographic range, hydrographic and circulation features constrain population distribution (Maryland Sea Grant 2009). Adult menhaden distribution is bounded by the Gulf Stream Front on the seaward side and by water temperatures greater than  $10^{\circ}\text{C}$  (Maryland Sea Grant 2009).

Adult Atlantic menhaden spawn in oceanic waters along the continental shelf, as well as in sounds and bays in the northern extent of their range (Judy and Lewis 1983). Winds and tides transport larvae shoreward from the shelf (Checkley et al. 1988; Werner et al. 1999) toward nursery grounds in the estuaries. Larvae are between one and three months old, usually closer to two months, at first ingress into estuaries (Warlen et al. 2002; Maryland Sea Grant 2009). After entering the estuary, larvae congregate in large concentrations near the upstream limits of the tidal zone, where they metamorphose into juveniles (June and Chamberlin 1959; Houde 2011).

While Atlantic menhaden occur throughout a wide range of physicochemical conditions, several studies have explored the species' environmental limits and optimum conditions. In particular, studies have noted an affinity of young menhaden for low salinity waters. Wilkens and Lewis

(1971) speculated that larval menhaden require low salinity water to metamorphose properly, and Lewis (1966) found that, although larvae metamorphosed in salinities of 15-40 ppt, one-third of the juveniles developed slightly crooked vertebral columns. Furthermore, larvae reared by Hettler (1976) at a lower salinity of 5-10 ppt exhibited significantly higher activity levels, metabolic rates, and growth rates than those reared at 28-34 ppt. Rogers et al. (1984) noted that pre-juveniles of many fishes, including those of *Brevoortia* species, enter estuarine habitats during seasonal peaks of freshwater influx when the area of low salinity and fresh tidal water is greatest.

Studies also suggest that temperature has an important effect on larval development and dispersion. In the South Atlantic region, sea surface temperature readings during the months of highest egg capture were generally 12-20°C (Walford and Wicklund 1968). In the North Atlantic, the lowest temperature at which Atlantic menhaden eggs and larvae were collected was between 10 and 13°C (Ferraro 1980). The temperature range for the Mid-Atlantic region was 0-25°C, but most eggs and larvae were collected at 16-19°C (Kendall and Reintjes 1975). Studies suggest that the limits of larval temperature tolerance are affected by acclimation time. Survival above 30°C (Lewis and Hettler 1968) and below 5°C (Lewis 1966) was progressively extended by acclimation temperatures closer to test values, suggesting that rapid changes to extreme temperatures are more likely to be lethal than prolonged exposure to slowly changing values. Mortality of juvenile Atlantic menhaden to a temperature decrease of 10°C (from 15 to 5°C) was less when temperature was decreased at a rate of 6.7°C/h or lower.

Historically, estuarine zones received freshwater from contiguous wetlands and riverine systems. However, channelization, diking of river courses, ditching and draining of marginal wetlands, and urbanization have reduced the freshwater retention capacities of coastal wetlands. Furthermore, extensive filling of estuarine marshlands has diminished the area receiving runoff in many locations. In combination, these changes cause the rapid discharge of freshwater during brief periods and reduced amounts of freshwater at other times. High inflows, particularly those that occur in early spring after the arrival of pre-juvenile menhaden, can expose fish to extreme fluctuations of temperature, turbidity, and other environmental conditions. Although the effects of altered freshwater flow regimes on Atlantic menhaden are not known, effects on other estuarine dependent, offshore spawned fishes range from disappearance (Rogers et al. 1984) to death (Nordlie et al. 1982).

Dissolved oxygen, particularly at low levels, can also impact the survival of menhaden. Lewis and Hettler (1968) observed increased survival of juveniles at 35.5°C with increased dissolved oxygen (DO) saturation. Burton et al. (1980) reported a mean lethal DO concentration of 0.4 mg/l, but warned against interpretation of this value as “safe” in view of the interactive nature of environmental factors.

Amendment 3 (2017a) has an extensive and thorough habitat description for Atlantic menhaden including environmental requirements, physical description of habitat by region, descriptions of programs to preserve Atlantic menhaden habitat, and habitat conservation and restoration recommendations that are not included in this document.



### **3.1.1 Spawning, egg, larval habitat**

Currents and circulation features play an important role in cueing reproduction, and in controlling dispersal of larval stages, assuring that some larvae are transported to the coastal estuaries and embayments that serve as juvenile nurseries. Most larval menhaden are found shoreward of the Gulf Stream Front (GSF); those sampled in the GSF, or seaward of it, presumably are rapidly advected northeast and lost to the population although it is possible that warm-core rings and onshore streamers could return some larvae to the shelf (Hare and Govoni 2005). There is ample evidence, based on observations and models, that coastward transport of larvae is supported by favorable winds and currents on the shelf (Checkley et al. 1988; Werner et al. 1999). Models and observations of advective mechanisms at estuary mouths present a less-clear picture of how menhaden larvae move into estuaries, although it is apparent that winds, tides, and larval behavior control the ingress.

Inter-annual variability in recruitment is believed to be, at least partly, controlled by variability in oceanographic conditions that affect hydrography, circulation, and possibly biological productivity. Weather and climate patterns are probable drivers of such variability. Wood et al. (2004) demonstrated that prevalence of a late-winter climate pattern that brings dry and warm weather to the Mid-Atlantic region is associated with high recruitment of Atlantic menhaden. This weather pattern may promote favorable shoreward transport or feeding conditions for early-stage menhaden larvae while on the continental shelf.

### **3.1.2 Juvenile and adult habitats**

Abundance of young-of-year (YOY) juvenile menhaden is strongly and positively correlated with chlorophyll *a* and primary production in the Chesapeake Bay (Houde and Harding 2009). Although recent research indicates that age-1+ menhaden may derive most energy from zooplankton food (Lynch et al. 2010b; Friedland et al. 2011), it is apparent that YOY menhaden can efficiently filter small phytoplankton (Friedland et al. 2006) and that it is their primary food. The timing, intensity, quality, and spatial variability of the spring phytoplankton bloom in the Chesapeake Bay show high inter-annual variability and are strongly affected by climate (Adolf et al. 2006; Miller and Harding 2007). This variability in primary production is likely a key factor controlling production potential of young menhaden in estuarine habitats.

Juvenile habitat is unconsolidated bottom consisting mostly of sand and mud, with various mixtures of organic material. In more northerly areas, juveniles can be found in rocky coves, with mixtures of cobble, rock, and sand bottoms. Sub-adult habitats are found in temperate, nearshore marine and estuarine areas that have a bottom composition of sand and mud, and more organic material than in marine areas. Adult habitat ranges from a bottom composition of sand, mud, and organic material to marine sand and mud with increasing amounts of rocks in the more northerly areas.

### **3.1.3 Anthropogenic Impacts on Atlantic Menhaden and Their Habitat**

The human population along the coast is steadily increasing, and the average number of people per square mile in coastal counties has nearly doubled since 1960 (U.S. Census Bureau 2010). Increasing human presence precipitates industrial and municipal expansion, thus intensifying anthropogenic pressure on resources and accelerating competition for use of land and water.

Consequently, estuarine and coastal habitats have been significantly reduced and continue to be stressed by dredging, filling, coastal construction, energy plant development, pollution, waste disposal, nutrient loading, and other human-related activities.

Perhaps the most significant physical alteration of the Chesapeake Bay watershed in recent decades has been the increase in impervious surfaces. More than 400,000 hectares are currently categorized as impervious surfaces and that value continues to climb (Brush 2009). These surfaces increase the nutrient, sediment, and contaminant flow rate to the Chesapeake Bay (Clagett 2007), and exacerbate eutrophication and expansion of hypoxic and anoxic zones. Although not well studied at present, reduced water quality associated with increases in impervious surfaces could diminish habitat quality for menhaden or their predators.

Menhaden fish kills, both human-caused and naturally occurring, are a persistent problem in bays and estuaries throughout the range. Most states keep records of fish kills, documenting water quality, number of fish killed, and likely causes. Localized die-offs often occur due to critically low dissolved oxygen (DO) levels, which may result from a variety of factors including high temperature, low flow, overcrowding, or algal blooms. Infectious diseases, parasites, toxicants, or miscellaneous human activity (e.g. thermal shock or fishing discards) may also cause localized mortality. In Maryland, nearly 50 years of records document annual Atlantic menhaden kills ranging from tens to tens-of-millions of fish, caused by a variety of factors from concussive explosions to disease and toxicants from spills or discharge (ASMFC 2017a). The most common factor was low DO in the presence of algal blooms, which causes an annual spring die-off. In the Neuse and Tar-Pamlico River estuaries in North Carolina, low oxygen events cause significant mortality of Atlantic menhaden and other fish species nearly every summer (ASMFC 2017a). In Florida, nutrient inputs, exacerbated by low flushing in the Indian River Lagoon, result in Harmful Algal Blooms (HABs) and, ultimately, menhaden kills (ASMFC 2017a).

At one time, fish kills may have solely been a natural occurrence, but anthropogenic impacts to water quality and flow have certainly exacerbated the frequency and intensity of these mortality events. State efforts to track fish kills can provide information on patterns and trends. North Carolina, for example, instituted a fish kill investigation procedure in 1996 to collect and track fish kill information. Data are maintained in a central database and are reviewed as part of an effort to monitor water quality trends.

A growing body of literature is beginning to describe shifts in species distributions and spawning locations and seasons, possibly due to a changing climate on the Atlantic coast (e.g. Walsh et al. 2015; Kleisner et al. 2016). Menhaden ingress to estuaries is sensitive to changes in wind patterns and temperatures, which are known to be variable and may be influenced by climate change (Quinlan et al. 1999; Austin 2002). Moreover, nursery habitats within bays and estuaries are likely to be altered by the effects of climate change, in some cases potentially enhancing menhaden productivity and other cases, resulting in lower production and recruitment. The effects of climate change are predicted to include: increased water temperatures, sea-level rise, and changes in precipitation patterns and climate variability (Sherman et al. 2009). These changes can influence salinity, temperature, and nutrients throughout nursery grounds.

In addition to long-term climate change, the Atlantic coast has also experienced shorter-term, decadal fluctuations in weather, shifting between cold-wet and warm-dry periods. Austin (2002) showed that the 1960s were warmer and wetter than the 1970s and 1990s in the Mid-Atlantic. Menhaden recruitment success tends to be relatively high in years when late winter-spring conditions are warm and dry (Wood 2000). Although Atlantic menhaden recruitment has been correlated with the Atlantic Multidecadal Oscillation (Buchheister et al. 2016), the correlation between Chesapeake Bay and southern New England is reversed and the mechanisms of influence are unknown. The generally low recruitment of YOY menhaden in recent years appear to be constrained by frequent cool and wet winter-spring conditions that favor recruitment of anadromous spawners, but not offshore-spawning fishes such as Atlantic menhaden (Kimmel et al. 2009).

## **3.2 Habitat Analysis**

### **3.2.1 Background**

Marine organisms have undergone shifts in distributions in response to climate change (Nye et al. 2009; Pinsky et al. 2013; Morley et al. 2018), with warming causing movements poleward and into deeper waters (Sunday et al. 2012; Poloczanska et al. 2013). The geographic distributions of marine species are strongly linked to the hydrographic conditions that collectively dictate habitat conditions, and the implications of geographic shifts have been observed in the magnitude and composition of global fisheries catches (Cheung et al. 2010). The North American continental shelf supports some of the most productive fisheries in the world, but this area is also subject to some of the most rapidly changing hydrographic conditions, most notably increases in temperature (Burrows et al. 2011). Global ocean temperatures are expected to continue increasing, and some of the most significant increases may occur along the northeast U.S. coast (Saba et al. 2016). Accordingly, projections of species distributions under various hydrographic conditions can be helpful in evaluating potential impacts of climate change on marine species.

In this habitat analysis, a coarse evaluation of potential impacts of climate change on the available habitat for age 1+ Atlantic menhaden was provided. The analysis involved two steps: 1) develop an understanding of habitat preferences by modeling extant survey catch-per-unit-effort (CPUE) data from several sampling programs, and 2) generate projected changes in available age 1+ Atlantic menhaden habitat under various hypothetical changes in key habitat parameters that broadly represent expected directional changes in hydrographic conditions due to climate change. This analysis is viewed as course because it has not yet coupled the habitat model with a general circulation model that reflects various Representative Concentration Pathway (RCPs) tied to specific greenhouse gas emission scenarios, and because uncertainty in estimated habitat preferences and projections of future available habitat lack a rigorous treatment of uncertainty. Both of these areas represent important areas of future work.

## 3.2.2 Model Configuration

### 3.2.2.1 Survey data

CPUE data expressed as counts for age 1+ Atlantic menhaden were compiled from seven sampling programs (Table 10, Figure 15). Summary statistics along with monthly and spatial plots of survey catches were used to filter the combined data set. Since all of these surveys target species other than Atlantic menhaden, months with less than 5% of the total survey catch were eliminated from the analysis in an effort to remove uninformative zero observations. CPUE values associated with nonsensical latitudes/longitudes (i.e., spatial locations well outside a survey's sampling frame) were also eliminated. Finally, CPUE observations without accompanying measures of bottom water temperature, bottom salinity, and depth were excluded. The final combined data set contained a total of 31,645 survey observations.

### 3.2.2.2 Habitat variables

From the combined data set, annual mean bottom water temperature and bottom salinity were calculated for each survey to provide a characterization of temporal patterns in habitat variables over the respective sampling time periods.

### 3.2.2.3 Habitat preferences

The statistical modeling framework provided by the *gamlss* R package (Generalized Additive Models for Locations, Scale, and Shape; Rigby and Stasinopoulos 2005) was chosen for analyzing CPUE in relation to habitat variables. *Gamlss* can accommodate probability distributions for the response variable beyond those in the exponential family, zero-inflated mixture distributions, mixed effects, and an additive model structure to allow for nonlinearity among the response and explanatory variables. To guide the choice of the probability distribution for the CPUE data, the *fitDist* function was used to fit all relevant parametric count distributions to the CPUE data using maximum likelihood, and Akaike's Information Criterion (AIC; Akaike 1973; Burnham and Anderson 2002) strongly favored the zero-inflated Sichel distribution (ZISICHEL). The standard Sichel distribution is useful for over-dispersed Poisson count data exhibiting high positive skewness, and is also known as the generalized inverse Gaussian Poisson (GIGP) distribution. The probability function of the Sichel distribution, denoted by SICHEL ( $\mu, \sigma, \nu$ ), is given by (Rigby et al. 2008):

$$P(Y = y|\mu, \sigma, \nu) = \frac{(\mu/c)^y K_{y+\nu}(\alpha)}{y! (\alpha\sigma)^{y+\nu} K_\nu\left(\frac{1}{\sigma}\right)}$$

for  $y = 0, 1, 2, 3, \dots$ , where  $\mu > 0$ ,  $\sigma > 0$ ,  $-\infty < \nu < \infty$ ,  $\alpha^2 = \sigma^{-2} + 2\mu(c\sigma)^{-1}$ ,  $c = R_\nu\left(\frac{1}{\sigma}\right)$ ,  $R_\lambda(t) = K_{\lambda+1}(t)/K_\lambda(t)$ , and  $K_\lambda(t)$  is the modified Bessel function of the third kind. By extension, the zero-inflated Sichel distribution, denoted ZISICHEL ( $\mu, \sigma, \nu, \tau$ ), is given by:

$$P(Y = y|\mu, \sigma, \nu, \tau) = \begin{cases} \tau + (1 - \tau)P(Y_1 = 0|\mu, \sigma, \nu), & \text{for } y = 0 \\ (1 - \tau)P(Y_1 = y|\mu, \sigma, \nu), & \text{for } y = 1, 2, 3, \dots \end{cases}$$

for  $0 < \tau < 1$  and where  $P(Y_1 = 0|\mu, \sigma, \nu) = K_\nu(\alpha)/[(\alpha\sigma)^\nu K_\nu(\frac{1}{\sigma})]$ ,  $\alpha^2 = \sigma^{-2} + 2\mu(b\sigma)^{-1}$ , and  $b = K_{\nu+1}(\frac{1}{\sigma})/K_\nu(\frac{1}{\sigma})$ .

Given the ZISICHEL distribution for the CPUE data, a generalized additive mixed model (GAMM) was implemented to characterize habitat preferences for age 1+ Atlantic menhaden. Fixed effects for both the conditional and zero-inflated model components included bottom water temperature, bottom salinity, and depth. A categorical indicator variable denoting survey was also included in both components to broadly account for differences in sampling gear and methods (i.e., survey catchability). The categorically defined variable year was treated as a random effect in both model components (random intercept structure), and cubic splines were used to give the additive structure such that:

$$\begin{aligned} g_1(\mu) &= X\beta + \sum_{i=1}^p s_i(x_i) + Zb \\ g_2(\tau) &= X\beta + \sum_{j=1}^q s_j(x_j) + Zb, \end{aligned}$$

where  $X$  is the linear fixed effects model matrix,  $\beta$  is the vector of linear fixed effects coefficients,  $s_k$  is the cubic spline function for the  $k^{th}$  habitat variable,  $Z$  is the model matrix for the linear random effect,  $b$  is the vector of linear random effects such that  $b \sim N(0, D)$ , with  $D$  being the symmetric, positive-definite variance-covariance matrix, and  $g_1$  and  $g_2$  are link functions taken to be the *log* and *logit*, respectively. Multiple model parameterizations that reflected various combinations of the habitat covariates were fitted and AIC was used for model selection. All models included the categorical survey covariate and the random effect year in both the conditional and zero-inflated model components. Predictions of mean CPUE across the observed domains of the covariates retained in the most supported model were computed as marginal means (Searle et al. 1980).

#### 3.2.2.4 Projections

Prior to developing projections reflecting potential climate change impacts on available habitat for age 1+ Atlantic menhaden, it was first necessary to create a geostatistical layer based on observed data. Using ArcGIS, a polygon was constructed around each of the seven survey areas to establish the respective sampling frames. Within each sampling frame, a spatial grid was created where each grid cell represented 0.01 decimal degrees (approximately 0.5 nm<sup>2</sup>). Empirical Bayesian kriging was used to assign values of bottom water temperature, bottom salinity, and depth to the center point of each grid cell, based on observed values associated with the full time-series for each survey. The habitat values for each survey's grid were then combined into a complete data set taken to represent 'present day habitat conditions.' The most supported GAMM parameterization was then used to generate predicted abundances for all grid cells in the geostatistical layer, and the sum of those abundances was taken as an index of 'present day habitat conditions.'

To explore the effects of changing habitat conditions resulting from climate change, the ‘present day habitat conditions’ data were modified. A total of three scenarios were considered: 1) increased bottom water temperature (0.5 to 5 °C at 0.5 °C increments due primarily to atmospheric warming; Muhling et al. 2018), 2) decreased bottom salinity (-0.5 to -2.0 ppt at -0.2 ppt increments due primarily to sea level rise; Hong and Shen 2012), and 3) pairwise combinations of the increased bottom water temperatures and decreased bottom salinities. The modified decreased bottom salinities were set to 0 in areas where the incremental decrease created negative values (e.g., Maryland’s Gill Net Survey). New geostatistical layers were created for each scenario by manipulating the ‘present day habitat conditions’ data by the specified incremental change. The most supported GAMM parameterization was again used to generate predicted abundance for each grid cell in the modified layers, and the sum of those abundances was taken as an index of ‘potential future habitat conditions.’ Percent changes relative to the summed abundances associated with ‘present day habitat conditions’ were calculated to characterize potential alterations in the available habitat for age 1+ Atlantic menhaden under climate change.

### **3.2.3 Results**

#### **3.2.3.1 Habitat variables**

Increasing trends in annual mean bottom water temperature were present for the Connecticut Long Island Sound Trawl (CT LISTS), New Jersey Ocean Trawl (NJ OT), Delaware Adult Trawl (DE Adult), and North Carolina’s Program 915 (NC p915) surveys, although the slopes of fitted linear regressions were not statistically significant (Figure 16). Conversely, the Maryland Gill Net (MD GN), Georgia Ecological Monitoring (GA EMTS), and Southeast Area Monitoring and Assessment Program (SEAMAP) surveys showed equivocal to slightly decreasing trends in annual mean bottom water temperature, but again fitted regressions were not significant. The directionality of patterns in mean annual bottom salinity varied across surveys, with positive regressions associated with CT LISTS, DE Adult, GA EMTS, and SEAMAP, and negative regressions for NJ OT and NC p915 (Figure 17). The MD GN survey occurs in virtually freshwater and showed an equivocal temporal pattern.

#### **3.2.3.2 Habitat preferences**

Based on AIC model selection, the fully saturated GAMM parameterization for both the conditional and zero-inflated components received the most empirical support. This result suggests that all habitat variables were important in terms of explaining variation in the underlying CPUE data. Overall, the model fit the data reasonably well as indicated by worm plot, although the deviations above the zero line for positive quantiles suggests some underestimation of the mean (Figure 18). Marginal means predictions revealed appreciably broad habitat envelopes with peak mean abundance occurring around 10°C bottom temperature, 30 ppt salinity, and 8 ft of depth (Figure 19). The presence of ascending and descending limbs in the predicted habitat preference curves indicates that the observed data spanned the preferred domains of the habitat variables. The need for a zero-inflated mixture distribution does raise concern regarding the presence of false zeros in the observed CPUE data. Although attempts were made to filter each survey data set to exclude the so-called

'naughty zeros' (bad zeros – absence of age 1+ Atlantic menhaden due to seasonal migration patterns preventing presence), it is possible that additional data filtering is needed. Future work to better understand the spatial distribution and seasonal movements would be helpful in this regard.

### **3.2.3.3 Projections**

Results of the projection analyses strongly indicated that changes in bottom water temperature was more influential on available habitat when compared to changes in bottom salinity. All warming scenarios lead to reductions in available habitat, ranging from proportional changes of 0.98 to 0.74 across the domain of incremental increases (Figure 20). Conversely, all scenarios involving decreased bottom salinity lead to slight increases in available habitat such that proportional changes ranged from 1.01 to 1.04. As expected, the combined scenarios lead to overall decreases in available habitat as driven by the temperature effects, but to a slightly lesser degree when compared to the temperature scenario alone due to the influence of the salinity effects.

These projections represent first cut sensitivities in how available habitat for age 1+ Atlantic menhaden might change under climate change. Although the incremental changes in the habitat variables considered fall within ranges of environmental changes expected in the northwest Atlantic under various RCPs, they were uniformly applied to all survey areas without regard for localized effects of climate change. They also assume that the internal population dynamics of Atlantic menhaden (i.e., recruitment, growth, natural and fishing mortality, movement) remain constant over time.

### **3.3 Ecosystem Context for Atlantic Menhaden**

An ecosystem context report was developed for this assessment by the Northeast Fisheries Science Center (NEFSC) with data from the spring and fall trawl survey confined to Atlantic menhaden stock area based on survey strata sets (Figure 21). Similar reports have been provided for other species and informed their assessments, such as summer flounder, black sea bass, bluefish, monkfish, and scup. The information is intended to span a range of potential factors affecting the productivity and distribution of Atlantic menhaden including physical factors, lower trophic level changes, and habitat distribution. These factors can be used to qualitatively inform the interpretation of population status and/or quantitatively to improve model responsiveness to ecosystem factors.

Report findings are abbreviated and summarized below. For the full Ecosystem Context for Stock Assessments methods and report for Atlantic menhaden, see:

<https://noaa-edab.github.io/ECSA/atlantic-menhaden.html>

After reviewing the information, the SAS concluded that the report provides valuable information for understanding the connection between Atlantic menhaden and environmental variables. The SAS was concerned about the use of the NEFSC trawl survey since it had been evaluated by the SAS for an abundance index and eliminated due to low occurrence of Atlantic menhaden in the survey (i.e., less than 2% positive tows in the spring inshore data), with about two thirds of Atlantic menhaden caught in four tows from 1963-2017. The authors of the report

stated that the range and complexity of ecosystem data makes it unlikely to find the most relevant and comprehensive factor variables with a first evaluation; this process will require an iterative approach of evaluation and feedback. Additional indices can be included to address the needs of the SAS in the future.

### **3.3.1 Temperature**

In both spring and fall, bottom water temperatures have significantly increased, with the suggestion of abrupt changes in temperature early in the time series (Figure 22). The rate of increase has been twice as high in the fall. There does not appear to be any trend associated with spring surface temperature conditions, however, fall temperatures have increased over time (Figure 23).

### **3.3.2 Salinity**

There is a long-term trend in spring bottom salinity in the stock area and the suggestion of an abrupt change in salinity around the year 2000 (Figure 24). The fall bottom salinity does not appear to have a long-term trend, however, there are two change points present in the time series. The spring surface salinity, like the bottom conditions, also show a long-term increasing trend and a change point in 2013 (Figure 25). The fall surface salinity time series was without trend or any change points. These changes in salinity conditions are likely indicators of changes in source water on the shelf and may have ramifications for patterns of primary production.

### **3.3.3 Chlorophyll**

The concentration of chlorophyll is an indicator of lower trophic level productivity and may be of particular importance to menhaden considering both juvenile and adults directly use phytoplankton as a food resource. There is no apparent trend in spring chlorophyll concentration; however, there is a significant trend in fall chlorophyll associated with a regime change to lower levels in 2012 (Figure 26). During this new regime, fall chlorophyll has been at the lowest levels in this time series.

Based on the most recent menhaden assessment, the chlorophyll time series overlaps the recruitment series for the years 1998-2016. The two largest year classes during that period appear to have occurred in 2005 and 2010 (based on age-0 numbers). The correlation between April polyhaline chlorophyll concentration in the Chesapeake Bay and recruitment was 0.43 ( $P=0.066$ ).

### **3.3.4 Zooplankton**

Menhaden consume zooplankton during all their life history stages, but have a dependency on zooplankton as larval fish and a preference for zooplankton as adults (Friedland et al. 2011). The most commonly encountered copepod genera were *Centropages*, *Acartia*, *Temora*, *Caligus*, and *Labidocera*. Numerically, the most important prey were copepods, which accounted for approximately 46-70% of the prey, followed by barnacle nauplii and cladocerans, which ranged from 10-30% of the diet. After the metamorphosis from larval particle feeding to filter feeding, the nature of their gill raker feeding apparatus would suggest they would feed on any size zooplankton and not be limited by any minimum size like some herring species (Friedland et al.



2006). So generally, whatever taxa are abundant would likely be a useful prey resource for both larval and adult fish.

### **3.3.5 Habitat and Abundance**

#### **3.3.5.1 Occurrence Probability**

The probability of occurrence was estimated using random forest classification models and provide an estimate of the potential use of the habitat associated with the stock definition. The most dramatic change in occupancy probability occurred in the spring (Figure 27 and Figure 28). In the beginning of the time series, occupancy probability was less than 0.08 and has increased to well over 0.1 in recent decades. This suggests greater use of the continental shelf by menhaden during the spring period. Fall occupancy has remained relatively constant of the time series range between 0.12-0.13.

#### **3.3.5.2 Habitat Area**

The area of the Northeast Shelf with an estimated occurrence probability for menhaden of 0.25 was determined for the stock area and the ecosystem. The area of habitat with the stock area generally ranged from 2,000-4,000 km<sup>2</sup> with a notable peak in habitat associated with 2012 spring conditions (Figure 29 and Figure 30). With the exception of 2012, spring habitat appears to have been represented by a larger area during the 1980s. Fall habitat has increased in recent years and was also at high levels in the early 1980s. The fall habitat area for menhaden over the ecosystem is larger than the areas restricted to the stock definition. Fall habitat approached 5,000 km<sup>2</sup> reflecting a greater use of the ecosystem during the warmer part of the year. The spring habitat over the ecosystem were similar to the stock area dimensions.

#### **3.3.5.3 Minimum Population Size**

Estimates of the numbers and biomasses for the minimum population size of menhaden stocks were determined by re-stratifying the habitat each year depending on the distribution of occupancy habitat. The procedure provides eight population size estimates for each stock, by season, based on the use of three estimation options.

The spring minimum population size in numbers suggests the stock continues the trend of high abundance that began with the 2005 recruitment (Figure 31). When disaggregated by northern and southern subareas, it appears the southern subunit approximates the unit abundance for most of the time series. Collectively, both the abundance and biomass data suggest a shift in spring population distribution, with more of the population now distributed in the northern subareas. The fall population estimates are dissimilar to the spring estimates in terms of both localized abundance and trends (Figure 32). The fall data suggest an abundance peak in the early 2000s that is not seen in the spring data. Furthermore, a peak in fall biomass does not accompany this peak in abundance. The fall data do not suggest any trend in abundance or biomass in the unit estimate or in the subareas estimates either. The fall unit estimate is most closely approximated by the northern subarea estimate in all cases.

### 3.3.6 Summary

Substantial changes have occurred in the coastal environment supporting the menhaden population. Thermal conditions have changed in both spring and fall seasons, with high rates of change in fall temperatures. Further physical change in the environment can be seen in a shift in salinity during the spring.

There have also been changes in lower trophic level productivity with a significant decline in fall chlorophyll concentration. Zooplankton taxa used by menhaden show varying patterns of time series changes, with some of the principal taxa increasing and others in decline. Zooplankton biomass has not declined during the spring, which would suggest the food resources for menhaden larvae have remained abundant. However, fall zooplankton biomass has declined over the most recent decade and may be a factor for adult feeding.

Abundance estimates based on a habitat model suggest the stock is presently at a high level although regional abundance patterns may have changed. During spring, it appears more of the population is in the northern end of the stock area than in earlier years.

### 3.4 Productivity Regimes

State-space models were used to examine time-varying productivity, or the maximum reproductive rate, for Atlantic menhaden using methods adapted from Tableau et al. (2018). Briefly, estimated biomass-at-age and recruitment (number of age-0 Atlantic menhaden) were taken from the base run of the BAM and maturity was applied to the estimated biomass-at-age to get spawning stock biomass (SSB). The recruitment time-series was lagged by one year to match recruits with spawners. The resulting plot shows the stock-recruitment data and that the 1958 year-class was the highest in the time series (Figure 33).

A linearized Ricker function, where log of recruitment divided by SSB was plotted against the SSB, indicated a strong depensation relationship where an increase in SSB led to a decrease in production (Figure 34). A time-varying Ricker stock-recruitment model was fit using a state-space framework (Peterman et al. 2003) with the R DLM (Dynamic Linear Models; Petris et al. 2009) package. A Kalman filter was fit to the stock-recruitment data to estimate Atlantic menhaden productivity. The common signal-to-noise ratio of the process to observation error variances from Tableau et al. (2018) of 0.75 was used. The calculated ratio for the Atlantic menhaden was 0.33 but the differences in the ratio did not impact the final results. The smoothed productivity values indicate high values in the early part of the time series followed by a steady decrease into the 1970s when productivity began to rise again (Figure 35). Estimated productivity has been fairly steady since the 1970s through the terminal year.

Tableau et al. (2018) incorporated environmental variables into the Kalman filter for predicting productivity but cautioned that relationship may change over time and covariates do not provide straight-forward answers. Ultimately, Tableau et al. (2018) stated that their study found few relationships between environmental covariates and productivity for the stocks they evaluated. The SAS decided not to pursue incorporating variables, such as the Atlantic multidecadal oscillation, chlorophyll  $a$ , or sea surface temperature, at this time but perhaps would consider it in future assessments.

Regime shifts in the Atlantic menhaden productivity time series were detected using chronological clustering (Legendre and Legendre 2012). This method uses a clustering algorithm that divides the productivity time series into regimes where the clusters are chosen to minimize the sum of squares within the clusters. Perretti et al. (2017) used this method to identify shifts in recruitment from stock assessment outputs. The analysis was run using the RPART package in R (Therneau et al. 2015), which built the classification tree for Atlantic menhaden productivity (Figure 36). To determine how many clusters provided the best model for understanding the regimes for productivity, the tree was pruned to include 3 clusters, or 2 splits, based on accompanying plots from the analysis (Figure 37). Therefore, the productivity regimes, or time blocks, were 1955-1961 when productivity was increasing, 1962-1973 when productivity was decreasing, and 1974-2017 when productivity was stable.

## **4 FISHERY DEPENDENT DATA SOURCES**

### **4.1 Commercial Reduction Fishery**

#### **4.1.1 Description of Reduction Fisheries**

Commercial fishing for Atlantic menhaden occurred at a relatively low level during colonial times, but the use of purse-seine gear began in New England about 1850 (Ahrenholz et al. 1987b) and expanded the fishery. The purse-seine fishery spread south to the Mid-Atlantic States and the Carolinas by the late 1800s. Purse-seine landings reached their peak in the 1950s, with 712,100 metric tons landed in 1956; menhaden factories at the time numbered over 20 (ASMFC 2004a), and ranged from southern Maine to northern Florida (Table 11, Table 12, Figure 38, Figure 39). In the 1960s, the Atlantic menhaden stock contracted geographically, and many of the fish factories north of Chesapeake Bay closed because of a scarcity of fish (Nicholson 1975).

During the 1970s and 1980s, the Atlantic menhaden population began to expand primarily because of a series of abundant year classes entering the fishery. Adult Atlantic menhaden were again abundant in the northern half of their range, from the southern Gulf of Maine to Long Island Sound. By the mid-1970s, reduction factories in Rhode Island, Massachusetts, and Maine again landed Atlantic menhaden until the 1980s (Table 11). By 1989, all shore-side reduction plants in New England had closed mainly because of odor abatement issues with local municipalities. The gap in menhaden harvest was filled by foreign companies. In 1987, after many of the United States plants closed, a reduction plant in New Brunswick, Canada, landed Atlantic menhaden harvested in southern Maine. A second Canadian plant in Nova Scotia also processed Atlantic menhaden caught in southern Maine in 1992-1993. In 1988, Maine entered into an Internal Waters Processing venture (IWP) with the Soviet Union, which brought up to three foreign factory ships into Maine territorial waters (< 3 miles from the coast). American vessels harvested the Atlantic menhaden and unloaded the catch for processing on the factory ships. The Russian-Maine IWP and the Canadian plants last processed Atlantic menhaden during summer 1993.

During the 1990s the Atlantic menhaden stock contracted again (as in the 1960s). Fish became scarce again north of Long Island Sound. After 1993, only three factories remained in the

fishery, two factories in Reedville, Virginia, and one factory in Beaufort, North Carolina. Virginia vessels (about 18-20) ranged north to New Jersey and south to about Cape Hatteras, North Carolina, while the North Carolina vessels (generally two) fished mostly in North Carolina waters.

Major changes in the industry began following the 1997 fishing season, when the two reduction plants operating in Reedville consolidated into a single company and a single factory. This significantly reduced effort and overall production capacity. Seven of the 20 vessels operating out of Reedville were removed from the fleet prior to the 1998 fishing year and 3 more vessels were removed prior to the 2000 fishing year, reducing the Virginia fleet to 10 vessels during 2000 to 2012 (although an eleventh vessel at Reedville fished sparingly during fall 2005 and again 2010-12). Efforts were further reduced and consolidated in Reedville when the last menhaden plant in North Carolina closed in 2005, leaving Reedville as the sole reduction fishing operation in the Atlantic Ocean. In 2013, the factory at Reedville further reduced its fleet to seven vessels because of the coastwide TAC imposed by Amendment 2 (2012a).

The reduction fishery for Atlantic menhaden employs purse-seine gear to encircle schools of menhaden. Two purse boats (approximately 12 m long), each holding one-half of the seine, are deployed from a large carrier vessel (approximately 50-60 m long; also called a 'steamer'). A pilot in a spotter aircraft directs the purse boats via radio to the fish schools. Spotter pilots assist with about 80% of purse-seine sets (Smith 1999). The fish are 'hardened' into the bunt of the net, and then pumped onboard the steamer. The purse-seine fleet averages about five sets per fishing day (Smith 1999). At the end of the fishing trip, the catch is pumped at dockside into the fish factory, where it is reduced into the three main processed products of the menhaden industry: fish meal, fish oil, and fish solubles.

Prior to World War II, most menhaden were dried and sold as 'fish scrap' for fertilizer. By the early 1950s, the demand for fish meal as an ingredient in poultry feeds increased as the 'fryer' chicken industry expanded. During the latter half of the twentieth century, the menhaden meal market expanded as it became an integral component in swine and ruminant feeds. By the 1990s, the primary market shifted again to include greater quantities into aquaculture feeds. Historically, most menhaden oil was exported to Europe where it was processed into cooking oil or margarine. Beginning in the late 1990s, greater quantities of menhaden oil, a high-grade source of omega-3 fatty acids, were used by the pharmaceutical and processed-food industries of the U.S. Currently, large amounts of menhaden oil are formulated by the aquaculture industry into fish feeds, especially for the culture of salmonids.

#### **4.1.2 Data Collection and Survey Methods**

Fishery-dependent data for the Atlantic menhaden purse-seine reduction fishery have been collected by the Beaufort Laboratory of the National Marine Fisheries Service since 1955 and consist of three major data sets: 1) fishery landings or catch records, 2) port samples for age and size composition of the catch, and 3) daily logbooks, or Captains Daily Fishing Reports (CDFRs).

Detailed landings data for the reduction purse-seine fishery are available 1940-2017. The biostatistical data, or port samples, for length- and weight-at-age are available from 1955

through 2017, and represent one of the longest and most complete time series of fishery data sets in the nation. The CDFRs itemize purse-seine set locations and estimated at-sea catches; vessel compliance is 100%. CDFR data for the Atlantic menhaden fleet are available for 1985-2017.

Biological sampling for the menhaden purse-seine fishery is based on a two-stage cluster design conducted over the range of the fishery, both temporally and geographically (Chester 1984). The number of fish sampled in the second cluster was reduced after 1971 from 20 fish to 10 fish to increase sampling of the first cluster (number of purse-seine sets). Port agents randomly select vessels at dockside to retrieve a bucket of fish from the top of the vessel's fish hold and determine the location and date of this set from the crew or logbook. The sample is assumed to represent fish from the last purse-seine set of the day, not the entire boat load or trip. From the bucket the agent randomly selects ten fish (second cluster). These fish are measured (fork length in mm), weighed (g), and the scales are removed for age estimation. An age validation/verification study determined that the annulus rings on menhaden scales are reliable age marks (June and Roithmayr 1960).

#### **4.1.3 Selectivity Time Blocks for Modelling**

Consistent with SEDAR 40 (2015), the SAS addressed selectivity in the reduction fishery and potential time blocks or breaks by considering residual patterns in the age composition data and major changes within the fishery. These changes are reflected in Figure 38 along with the spatial divisions in the fishery. With regard to the latter, the SAS adopted four time blocks for the reduction fishery in the northern region (defined as waters north of Machipongo Inlet, Virginia).

The first time block is 1955- 1969. Comprehensive and coastwide data collection for the reduction fishery began at the Beaufort Laboratory in 1955. The 1950s were also the years of peak landings for the fishery. After the 1958 year class phased through the fishery (by about 1963), what followed in the 1960s were a series of poor to mediocre recruitment years. The stock contracted and many fish plants north of New Jersey closed. Year 1969 was chosen as the end of this first time block for the northern region due to the consistent poor recruitment and the contraction of the fishery.

The second time block for the northern region is 1970-1993. During the 1970s the stock once more expanded into the northern half of its range. Fish plants in New England reopened and fish were abundant there through about 1993. The end of this time block was when the Russian factory ships ceased operating in Maine waters because of lack of fish. The third time block is 1994-2012 when there were no factories and no reduction landings in the northern region, although there were removals off the Mid-Atlantic coast by Virginia vessels that landed their catch in Reedville. The final time block, 2013-2017, was included due to Amendment II and the changes in fishery behavior with the implementation of the coastwide TAC.

The SAS also adopted four time blocks for the reduction fishery in the southern region (defined as waters south of Machipongo Inlet, including Chesapeake Bay). The first was 1955-1971 as 1971 was when several factories closed in the southern region. The second time block for the southern region began in 1972 and ended in 2004 when the last menhaden factory in North

Carolina closed, leaving only one active fish plant on the U.S. East Coast at Reedville. The third time block for the southern region is 2005-2012. The final time block, 2013-2017, was included due to Amendment II and the changes in fishery behavior with the implantation of the coastwide TAC. In both regions, the introduction of selectivity time blocks noticeably improved the residual pattern apparent in the age composition data.

A chronology of plant activity from 1955 to present is found in Table 11 and Figure 39. A summary of time blocks used for each data source can be found in Figure 40.

#### **4.1.4 Commercial Reduction Landings**

Commercial landings of Atlantic menhaden from the reduction purse-seine fleet have been maintained by the Beaufort Laboratory of the National Marine Fisheries Service (NMFS) since 1955. These reduction landings are compiled by fishing year (March 1 through February 28 of the following year). Landings of Atlantic menhaden for reduction are reported to the Beaufort Laboratory monthly or more frequently during the fishing year. Daily vessel unloads are provided in thousands of standard fish (1,000 standard fish = 670 lbs), which are converted to kilograms.

Landings and nominal fishing effort (vessel-weeks, measured as number of weeks a vessel unloaded at least one time during the fishing year) are available since 1940 (Table 13 and Figure 41). Landings rose during the 1940s (from 167,000 to 376,000 t), peaked during the late 1950s (> 600,000 mt for four of five years), and then declined to low levels during the 1960s (from 576,000 mt in 1961 to 162,000 mt in 1969). After 1969, landings began an increasing trend through much of the 1970s, and reached a local maximum of 418,600 mt in 1983 and another small peak in 1990 of 401,200 mt before declining through much of the 1990s. By 1998, the fishery had contracted to only two factories, one in Virginia and one in North Carolina. Landings dipped to 167,200 mt in 2000, rose to 233,700 mt in 2001, and then varied annually from 174,000 mt to 166,100 to 183,400 mt through 2004. Landings during 2000-2004, when the fishery was relatively stable with two plants and about twelve vessels, averaged 184,900 mt. The Beaufort plant closed for the 2005 season, and the period from 2005–2012 had the remaining menhaden factory averaging 156,900 mt. Beginning in 2013, the reduction fishery was constrained by the coastwide TAC and landings have remained close to each year's TAC. Landings were split into northern and southern regions (defined as waters north and south of Machipongo Inlet, Virginia) for use in the modelling (Figure 42).

##### **4.1.4.1 Effort Based on Vessel-Week, 1940–2017**

Historic catch summations and estimates of fishing effort in the menhaden purse-seine fishery for reduction are based on company records of individual vessel unloads. Normally, menhaden vessels unload their catches daily; however, trips of 2-3 days are common. The menhaden plants record the date and amount of fish unloaded per vessel, but do not list number of days at sea, nor days actively fishing, nor days when the catch is zero. Logbooks were placed on menhaden vessels during the late 1950s and early 1960s to try and capture better information on 'fishing' and 'non-fishing' days at sea (Roithmayr 1963), but compliance was incomplete (Nicholson 1971). Therefore, until the 1970s there was no satisfactory way to acquire a complete at-sea history of each vessel.

Considering that menhaden vessels generally operate continuously over the course of a fishing season and fish every day that weather permits, vessel-week (one vessel fishing at least one day of a given week) was considered a satisfactory unit of nominal fishing effort for the Atlantic menhaden purse-seine fishery (Nicholson 1971). Vessel-weeks for all vessels in the fleet are calculated across the spatial and temporal range of the fishing season and summed for an estimate of annual nominal fishing effort for the fishery.

The trend in nominal fishing effort showed a pattern similar to that of landings from the beginning of the program until the 1980s (Table 13 and Figure 41). In 1949, an increase in effort coincided with a slight decrease in landings. Shortly after that, along with landings, effort increased to their peak of 2,878 vessel-weeks in 1956. A steep decline in effort followed, coinciding with plant closings in the 1960s. A small rebound in effort occurred in the 1970s followed by another decline in the 1980s. Further consolidation of plants in the 1990s and the closing of the IWF efforts in New England further reduced effort. From 1997 on, effort remained steady at the new levels with two remaining menhaden processing plants on the east coast. After 2005, effort was further reduced with the closing of the penultimate factory on the coast. The final changes in effort have coincided with the implementation of Amendment II to the Atlantic menhaden FMP and adjustments to the TAC.

In a general sense for many fisheries, CPUE is used as an index of abundance, where a proportional change in CPUE is expected to represent the same proportional change in stock size. However, for purse-seine fisheries it has been demonstrated that CPUE and nominal or observed fishing effort can be poor measures of population abundance, and this is especially true for those fisheries that use spotter aircraft (Clark and Mangel 1979). Therefore, fishery-independent data indices, rather than fishery-dependent CPUEs were used to estimate measures of population abundance in the single species assessment.

#### **4.1.4.2 Measuring Devices Used to Unload Menhaden**

During the SEDAR 27 Review Workshop Report for Gulf Menhaden (2011), review panelists expressed concern over the fact that the industry self-reports landings in 1,000s of standard fish. This convention dates to the early days of the fishery on the Atlantic coast when 1,000 standard fish were taken to weigh 670 pounds and the volume of a standardized hopper used at reduction plants to offload landings held 1,000 standard fish (Greer 1915). Review panelists expressed some concern about the consistency of fish hopper dimensions, and therefore landings estimates across the menhaden time series.

The question of consistency among measuring devices for landings at menhaden factories on the Atlantic coast no doubt concerned staff during the early years of the Menhaden Program at the NMFS Beaufort Laboratory. The traditional unit of measurement for landings in the menhaden fishery is the 'quarter-box' dump (or hopper), which volumetrically, by the menhaden industry's definition, measures 22,000 cubic inches, was estimated to hold 670 lbs with a coefficient of variation of 3.7% suggested a high degree of accuracy for the landings (Kutkuhn 1966). This unit of measure was further shown to be in almost universal use by the industry (June and Reintjes 1976). Based on the information above, the conversion factor of 0.670 (1,000 standard fish = 670 lbs) was adopted by Beaufort's Menhaden Program.

The fish hoppers at the factory in Reedville, Virginia, were rebuilt in 2008; the paired fish hoppers were redesigned to each hold 2,000 standard fish (M. Deihl, plant manager, personal communication). A local metal fabricator built the hoppers from a set of mechanical drawings. A second engineering company was hired to certify the hoppers as holding 44,000 cubic inches. They found the hoppers slightly oversized and installed a smaller spacer in the bottom to bring them to the desired 44,000 cubic inches.

In summary, the fish measuring convention for landings in the menhaden industry has been exceptionally conservative over the course of the fishery's century-long history. The basic unit of measure remains the fish hopper, or dump, which measures 22,000 in<sup>3</sup> and holds 1,000 'standard' fish, estimated to be one-third of a short ton (0.3039 mt or 667 lbs). Vessel crews, and to some extent spotter pilots, are paid based on each hopper, or dump, of fish unloaded. Reduction landings of menhaden since the 1940s are believed to be both accurate and precise relative to most other U.S. fisheries.

#### **4.1.5 Commercial Reduction Catch-at-Age**

Refer to the SEDAR 40 (2015) document for more information on the commercial reduction catch-at-age data collection program. An average 2,215 Atlantic menhaden from the reduction fishery have been processed annually for size and age composition since implementation of Amendment 2 in 2013 (Table 14). In comparing menhaden sampling intensity to the rule-of-thumb criteria used by the Northeast Fisheries Science Center (e.g. <200 mt/100 n), this sampling level might be considered low, although the results of Chester (1984) suggest this sampling level is adequate.

Since the implementation of Amendment 2, age-1 fish have made up the highest percentage of fish landed for reduction, averaging 46.4% of the coastwide landings. The second highest percentage was age-2 fish with 40.4%, followed by age-3+ fish with 12.2% of the landings and finally age-0 fish comprising 0.9% (Table 15).

##### **4.1.5.1 Captain's Daily Fishing Reports (CDFRs) or Logbooks**

Beginning in the late 1970s, the menhaden industry, state fisheries agencies, and the NMFS entered into a joint CDFR program to better document menhaden catch and fishing effort. For each fishing day, captains are asked to specify, among other things, time and location of each purse-seine set, estimated at-sea catch, and distance from shore. Since the mid-1980s, compliance by menhaden fleets in Virginia and North Carolina has been almost 100%. Paper CDFR data sets for fishing years 1985 through 2017 have been converted to electronic data files and stored at the Beaufort Laboratory.

Smith (1999) summarized the distribution of Atlantic menhaden purse-seine catches and sets during 1985-1996 using the CDFR data sets for the Virginia and North Carolina vessels. He found that on average the fleet (up to 22 vessels) made 10,488 sets annually. Virginia vessels made at least one set on 67-83% of the available fishing days between May and December. In most years, five was the median number of sets attempted each fishing day. Median catch per set ranged from 15-30 mt annually. Spotter aircraft assisted in 83% of the sets. Regionally, median catch per set was 24 mt off Rhode Island, New York, New Jersey and Delaware; 23 mt off the



ocean beaches of Virginia; 18 mt in the Virginia portion of Chesapeake Bay; 26 mt off North Carolina in summer; and 38 mt off North Carolina in fall.

In the 1990s, removals by the reduction fleet from the Chesapeake Bay averaged 145,700 mt per year. Between 2000 and 2005, removals from Chesapeake Bay by the reduction fleet reduced to an average 104,400 mt annually, a 28% decline from the previous decade. Beginning in 2006, a 'Cap' on removals by the reduction fleet (109,020 mt) was imposed through Amendment 1 to the FMP for the Chesapeake Bay. During 2006-2013 the harvest for reduction in Chesapeake Bay averaged 71,300 mt. In 2012, the 'Cap' was further reduced by 20% (along with the coastwide decrement to landings in Amendment 2) to about 87,200 mt. In 2018, Amendment 3 further reduced the 'Cap' to 51,000 mt. The fishery has never exceeded the 'Cap' through the terminal year of this assessment (2017).

Since 2005, menhaden reduction vessels have reported the GPS coordinates of their purse-seine set locations on CDFRs. This information has demonstrated Virginia is the center of the extant reduction fishery and that a majority of sets in Virginia waters recently have been near the mouth of the Chesapeake Bay and along the barrier islands of the Eastern Shore. These data also show that the Virginia fleet ranges north to the central New Jersey coast, but remains in federal waters three miles or greater from shore.

#### **4.1.5.2 Landings, Removals by Areas, and the Beaufort Assessment Model (BAM)**

For the current benchmark assessment, the menhaden fishery is addressed in terms of a northern and a southern fishery versus solely as a reduction and a bait fishery as in earlier assessments. To this end, this benchmark assessment incorporates 'fleets-as-areas' components where both the bait and reduction fisheries are divided into northern and southern regions (Table 14 - Table 18). By consensus, the SAS divided the northern and southern fisheries using a line that runs due east from Great Machipongo Inlet on the Eastern Shore of Virginia. Historically and for statistical reporting purposes, this has been the dividing line for the Mid-Atlantic and Chesapeake Bay areas for the Menhaden Program at the Beaufort Laboratory (June and Reintjes 1959). Nicholson (1971) noted that "similarities in age and size composition of the catches, time and duration of fishing, and range of vessels from home port tended to set each area apart." Through about the 1970s, reduction vessels from menhaden plants in New Jersey and Delaware rarely fished below this line; conversely, reduction vessels from Chesapeake Bay rarely fished north of this line. Therefore, it is a convenient line of demarcation to sort port samples and landings data for the fleet-as-areas model. For the 'fleets-as-areas' model, assignment of reduction landings and port samples by region (north vs. south) was relatively straightforward through 1993 when the Russian factory ships last operated in the southern Gulf of Maine. However, after 1981 the last menhaden factory in the Mid-Atlantic area closed (Port Monmouth, New Jersey) and by the mid-1980s reduction vessels from Chesapeake Bay in mid-summer tended to fish farther north in the Atlantic Ocean up to the coast of New Jersey. Technically, there were no reduction landings in the northern 'fleets-as-areas' region after 1993, although there were removals of fish for reduction purposes by Virginia-based vessels. These removals in the northern region were estimated beginning in 1985 using the CDFRs and for the purposes of this assessment were treated as reduction landings in the northern region. Similarly and beginning in the mid-1980s, port samples from

the northern region (by Virginia vessels returning from more northern waters) were used to develop age compositions of removals from the northern region.

#### **4.1.6 Potential Biases, Uncertainty, and Measures of Precision**

When the Menhaden Program began in the early 1950s at Beaufort, staff visited menhaden plants along the Atlantic coast to obtain detailed catch/effort information back to 1940. These landings and those subsequently collected are thought to be quite accurate. Early in the program, a study was conducted to address concerns about the precision of the hopper as an instrument for measuring fish offloaded at the plant for processing. The results suggest that individual hopper dumps were precise and had a reasonable 3.7% coefficient of variation (Kutkuhn 1966). It was noted that greater uncertainty was associated with fish spoilage (more likely in the years before widespread refrigeration of the holds) than into variation due to compression in the hopper or other factors that may affect the repeatability of hopper measurements. Reported or estimated landings from years prior to 1955, particularly the earliest years of the fishery and those reconstructed through either linear interpolation for missing year data or through proportion of landings of Atlantic menhaden vs Gulf menhaden are clearly subject to greater uncertainty. Reduction landings since 1940 are believed to be both accurate and precise relative to most other fisheries for that time.

Development of catch matrices depends on three data sources, including the landings, sampling for weight, and age determination. Sampling for size and age has been conducted weekly by port since 1955. The catch matrix is built from samples by port, week, and area. Concerns about bias related to ‘topping off’ by vessels from Reedville fishing outside its fishing area have been addressed through post stratification using the Captain’s Daily Fishing Reports.

During the early decades of the Menhaden Program at the Beaufort Laboratory scales from individual menhaden specimens were read multiple times by several readers. Disagreements on age estimates were decided by an additional reading. By the early 1970s - probably because of budget constraints - only a single reader was retained on staff to age menhaden scales. This employee, Ethel A. Hall, read menhaden scales for the Beaufort Laboratory from 1969 to 2015. During 2015, Hall was replaced with a new scale reading technician who has continued to age scales through 2017 and was trained by Hall.

In an effort to estimate contemporary precision of Atlantic menhaden age estimates, Hall was asked to re-read scale samples from the 2008 fishing season. Re-ageing efforts occurred during summer 2009. Hall was instructed to re-assign estimated ages, but not to make measurements to successive annuli (as per protocols for general menhaden ageing at the Beaufort Laboratory). Both sets of age estimates were stored and analyzed in SAS.

A total of 3,711 fish were re-aged from the 2008 fishing season; samples from the reduction and bait fisheries were pooled. Ages ranged from age-0 to age-5. Overall, 80.3% (n = 2,978) of the paired readings agreed. Within age classes, younger ages (ages-0 through age-3) showed the best agreement versus older specimens (ages-4 and -5). Paired readings for age-0's agreed 95.2% (n = 40) of the time; age-1's agreed 74.5% (n = 152), age-2's agreed 87.0% (n = 1,850), while age-3's agreed 74.4% (n = 821). Agreement for age-4's was considerably less at 51.9% (n =

111), while agreement for age-5's was poor at 19.1% (n = 4). Most disagreements for ages-1, -2, and -3 were +/- one year (98.1%, 86.3%, and 96.5%, respectively).

Alternate to the percent agreement statistic, an average percent error, APE (Beamish and Fournier 1981), was calculated for all paired readings combined. The APE for paired Atlantic menhaden ageing was 4.1% for Hall, the sole reader for much of the duration of the Atlantic menhaden sampling program, suggesting generally good agreement between readings. A comparison of her ages of the reference set with those of her replacement yielded an APE of 1.5%.

## **4.2 Commercial Bait Fishery**

### **4.2.1 Description of Bait Fishery**

Atlantic menhaden are frequently used for bait in commercial pot fisheries (e.g., American lobster and blue crab), hook and line fisheries (e.g., striped bass and bluefish), and are harvested for bait in most Atlantic Coast states. A variety of gears are used to harvest Atlantic menhaden commercially for bait. Most bait harvest comes from purse seines, pound nets, gill nets, and trawls, with a smaller amount of harvest coming from cast nets, fyke nets, and haul seines (Figure 46). Bait harvest comes from directed fisheries, but is also landed as bycatch in various food-fish fisheries.

Since 1985, the proportion of menhaden landed as bait has increased, averaging 10% of the total Atlantic menhaden landings (bait plus reduction) from 1985-2000 and 20% of total landings from 2001-2017. However, this apparent growth in the Atlantic menhaden bait fishery should be interpreted cautiously as bait landings have historically been incomplete due to the nature of the fishery and its unregulated marketing. The increase in proportion of total landings is likely attributed to better data collection in the fishery, but is also due to other factors including the decline in reduction landings and the decline in Atlantic herring as available bait.

Given the geographic expanse of the Atlantic menhaden bait fishery, there are regional differences in how and when menhaden are harvested. In the New England region, purse seine landings in Maine, Massachusetts, and Rhode Island, account for the majority of the recorded bait landings. The New England operators are fairly small, typically with one harvest vessel, ranging in size from the 30-90 feet in length. In Rhode Island, there is a historic floating fish trap fishery, which harvests the majority of menhaden landed in the state. In Connecticut, smaller directed gill net fisheries also harvest Atlantic menhaden. The bulk of Atlantic menhaden landings for bait in New England are used in the lobster fishery.

In the Mid-Atlantic, an expansion of the purse seine bait fishery has occurred, particularly in New Jersey. The New Jersey menhaden fishery uses about 20 carry vessels and about 15 catch vessels per year. Most operations have a catch vessel paired with a specific carry vessel, but some vessels are both catch and carry. Carry vessel length ranges from 59-90 feet and catch vessel length ranges from 40-88 feet. Net length is restricted to 150 fathoms (900 feet) by regulation. In New York and Delaware, Atlantic menhaden bait landings are primarily caught in pound nets, gill nets, cast nets, and seines.

In Virginia, Atlantic menhaden bait landings are dominated by purse seine vessels referred to as 'snapper rigs.' These vessels range from about 80-135 feet long and primarily sell bait to the sport and crab fisheries, but also sell a portion to the reduction factory. In contrast, the Maryland and Potomac River bait fisheries are primarily executed by pound nets. The pound net fishery in the Chesapeake Bay region is carried out by numerous small, non-refrigerated vessels with maximum hold capacity of 9 metric tons or less, but daily catches rarely reach capacity. The majority of these fish supply the bait demands for the local blue crab fishery.

In the southeast, menhaden landings are dominated by Florida and North Carolina. Florida historically had significant bait landings from gill nets and purse seines. In 1994, however, Florida implemented a net ban and now menhaden are primarily landed with cast nets. In North Carolina, fishermen primarily use cast nets, gill nets, and pound nets to harvest menhaden. Most menhaden harvested for bait in North Carolina are used in the blue crab fishery. Some anglers keep menhaden alive in holding tanks for 'slow trolling' of species such as king mackerel. There are no directed menhaden fisheries in South Carolina or Georgia.

#### **4.2.2 Data Collection Methods**

Systems for reporting bait landings have historically been incomplete because of the nature of the fishery and its unregulated marketing. Data limitations also exist because menhaden taken as bycatch in other commercial fisheries are often reported as 'bait' together with other fish species. Additionally, menhaden harvested for personal bait use or sold 'over-the-side' likely go unreported. As a result, the TC and previous assessments (ASMFC 2004b, 2012b, 2017b; SEDAR 2015) have determined that even though bait landing records date back to 1955, the most reliable bait landings are available since 1985 because of recent improvements made to harvester and dealer reporting programs.

Despite problems associated with estimating menhaden bait landings, data collection has improved in many areas. Some states license directed bait fisheries and require detailed landings records. More recently, harvest data reporting requirements changed through the implementation of Amendment 2 (2012) to the Atlantic Menhaden FMP because of the need for states to monitor in-season harvest relative to their newly implemented state specific quotas. Beginning in 2013, several states went from monthly reporting to weekly or daily reporting to avoid exceeding their allocated quota. Amendment 3 (2017a) reinforced those guidelines requiring states to, at a minimum, maintain the quota monitoring systems in place from Amendment 2 and submit CDFR or similar daily trip level reports for purse seine and bait seine (or snapper rig) vessels.

Sampling of the bait fishery for length and age has generally improved since 1988, especially beginning in 1994 when the Atlantic Menhaden Advisory Committee (AC, precursor to the TC) emphasized greater biological sampling of the bait fishery. The AC recommended that sampling be stratified by major gear type (purse-seine, pound net, and gill net) and that samples be taken in proportion to bait landings. Although the goals of these recommendations were not uniformly met at that time, the number of samples from the bait fishery generally increased (Figure 46).

Based on the results of a power analysis to statistically determine the level of sampling needed in the bait fishery to adequately represent the age structure of the catch, Amendment 2 (2012a) implemented monitoring requirements as follows:

- One 10-fish sample (age and length) per 300 metric tons landed for bait purposes for ME, NH, MA, RI, CT, NY, NJ, and DE; and
- One 10-fish sample (age and length) per 200 metric tons landed for bait purposes for MD, PRFC, VA, and NC.

The TC recommended that samples should be stratified by gear type; while this was not formally implemented, samples have generally been collected in proportion to the major gear types in the regional fisheries (Figure 46).

#### **4.2.3 Selectivity Time Blocks for Modelling**

SEDAR 40 (2015) had a single time block for the northern and southern bait fisheries, but due to the changes in the fishery made by Amendment 2 (2012a), the SAS considered the use of a second time block for 2013-2017. The SAS addressed selectivity in the bait fishery and potential time blocks or breaks by looking at residual patterns in the age composition data and major changes within the fishery. After reviewing likelihood profiles where there were differences in the selectivity for ages 4, 5, and 6+, the SAS determined that the northern region bait fishery should have two time blocks (1955-2012 and 2013-2017) to reflect changes in fishing behavior following the change in management. In the southern region, fishery behavior did not appear to have changed and only one time block (1955-2017) was used.

A summary of time blocks used for each data source can be found in Figure 40.

#### **4.2.4 Commercial Bait Landings**

Bait landings from 1955-1984 were compiled using the Atlantic Coastal Cooperative Statistics Program's (ACCSP) data warehouse, which houses historical data but is admittedly incomplete. For 1985-2017, commercial bait landings for each state were validated with state partners through ACCSP and compared with the annual compliance reports. Because bait landings from 1985-2017 were validated, these bait landings represent the most accurate dataset (Table 19). Virginia did not collect data on the snapper-rig bait seine fishery until 1998, so bait landings from 1993-1997 were adjusted to account for this fishery (Smith and O'Bier 2011, SEDAR 2015, ASFMC 2017b). Bait and recreational landings (Section 4.3) were combined and then split into northern and southern regions for inclusion in the BAM model (Table 20). The northern region includes landings from Maine to Maryland's Eastern Shore, excluding the Chesapeake Bay. The southern region includes landings from the Chesapeake Bay to Florida.

Coastwide bait landings of Atlantic menhaden have generally increased from 1985 through 2017 (Table 19, Figure 43). During 1985 to 2017, bait landings averaged 37,795 mt, with a high of 63,885 mt landed in 2012 and a low of 21,968 mt landed in 1986. Bait landings comprised of about 8% of coastwide landings in the mid-1980s and has steadily increased throughout the time series (Figure 44). In 2017, bait landings were 43,858 mt and comprised 25% of coastwide landings (Figure 45).

#### 4.2.5 Commercial Bait Catch-at-Age

The bait fisheries along the Atlantic coast have not been consistently sampled over time (Figure 46). Because of the limited biological data, characterizing the age distribution of the removals by the bait fishery was done at the region/year level, rather than port/week/area fished used for the reduction fishery. Four regions were defined as follows: (1) New England (Connecticut and north); (2) Mid-Atlantic (coastal Maryland, and Delaware through New York); (3) Chesapeake Bay (including coastal waters of Virginia); and (4) South Atlantic (North Carolina to Florida). Samples were pooled across gears for each region. Separate catch-at-age matrices were constructed for each region. The New England and Mid-Atlantic catch-at-age matrices were pooled to create a northern bait fishery catch-at-age, and the Chesapeake Bay and South Atlantic catch-at-age matrices were pooled to create a southern bait fishery catch-at-age.

Although there are bait landings from all regions in all years, there are not age samples from all regions in all years (Figure 46), and so some gap-filling must be done. There is a latitudinal gradient in the mean weight of fish in the catch across all four regions, with the northern regions catching larger fish than the southern regions (Figure 47). As a result, samples from one region cannot be used as a proxy for the age structure of another region. Similarly, although the reduction fishery samples show a similar size gradient, the distributions of mean weight in each region is not the same across the bait and reduction fisheries, and so reduction fishery samples cannot be used a proxy for the bait fishery in a given year and region (Figure 48).

In previous assessments, when the number of samples for a given region and year was less than 50, data were pooled across the years available for that region and substituted for that year (SEDAR 2015). For this assessment, and to avoid pooling data over years, a multinomial model was developed to predict age as a function of year, region, and fishery (bait or reduction):

$$\text{Age} \sim \text{Year} + \text{Region} + \text{Fishery}$$

The regression matched the observed age composition very well for most years (Figure 49). For years and regions where less than 30 samples were collected, the multinomial regression was used to predict the proportions-at-age. The population weights-at-age were combined with the predicted proportion-at-age to calculate a mean weight of fish in the catch for that year and region to convert the catch in weight to catch in numbers-at-age. If 30 or more samples were available for that year and region, the observed proportions-at-age and the observed mean weight were used to convert the catch in weight for that year and region into catch-at-age in numbers.

The age proportions of the bait catch were applied to the MRIP estimates of recreationally caught menhaden by year and region, and this recreational catch-at-age was pooled with the bait catch-at-age.

Overall, the bait catch-at-age in the north was dominated by ages 2-4, while the bait catch-at-age in the south was dominated by ages 1-3 (Figure 50, Table 21-Table 22). Comparisons between the bait catch-at-age developed with this assessment's multinomial gap-filling method and SEDAR 40 (2015)'s pooled data gap-filling method can be seen in Figure 51 and Figure 52. The results are generally similar, but the new method allows for more variability in the age structure in years with low sample sizes.

#### **4.2.6 Potential Biases, Uncertainty, and Measures of Precision**

Greater uncertainty is expected for the bait fishery as compared to the reduction fishery. Landings reconstructed for 1955-1984 likely underestimate actual bait landings because of a lack of information on purse-seine fishing for bait during this period. Bait landings since 1985 are significantly better, particularly for purse-seine landings. The catch matrix is built from limited sampling for 1985 to present (computed by region and year), and is therefore subject to much greater uncertainty than the catch matrix for reduction landings. However, information on bait size and age has improved in recent years.

#### **4.3 Recreational Fishery**

Menhaden are important bait in many sport fish fisheries and, as a result, some recreational fishermen use cast nets to capture menhaden or snag them with hook and line. Recreational harvest is not well captured by the Marine Recreational Information Program (MRIP) because there is not a known direct harvest for menhaden, other than for bait. MRIP intercepts typically capture the landed fish from recreational trips as fishermen come to the dock or on the beach. Since the menhaden caught by recreational fishermen are used as bait during their trip, they typically are not part of the catch that is seen by the surveyor completing the intercept.

##### **4.3.1 Data Collection and Survey Methods**

The MRIP data set was used to derive a time series of recreational landings of Atlantic menhaden for 1981 – 2017. Estimated recreational catches are reported as numbers or weights (kg) of fish harvested (Type A+B1) and numbers of fish released alive (Type B2). The fundamental cell structure for estimating recreational catches is by state (Maine – Florida), mode of fishing (beach/bank, manmade, shore, private/rental, charter), fishing area (inland, ocean (<=3mi), ocean (>3mi)), and wave (six 2-month periods). MRIP estimates were obtained from the NMFS Recreational Fisheries Statistics database and were fully calibrated for the Access Point Angler Intercept Survey (APAIS) 2013 design change as well as the transition from the Coastal Household Telephone Survey (CHTS) to the Fishing Effort Survey (FES). Harvested fish (A+B1) and released fish (B2) were reported separately for the two assessment regions (North: Maine to Delaware; and South: Maryland to Florida). The majority of landings from Maryland were assumed to come from Chesapeake Bay; therefore, those landings were allocated to the southern region.

##### **4.3.2 Recreational Harvest**

The recreational harvest (A+B1) estimates of Atlantic menhaden are reported for the two assessment regions in Table 21. Estimates of recreational harvest averaged over the past ten years were 798 mt in the northern region and 359 mt in the southern region. Harvest in the northern region increased to greater levels between 1986 and 1992 then decreased again and became variable but stable through 2005; harvest then increased in trend from 2006 – 2017. Harvest in the southern region was variable with greater levels of harvest occurring since about 2004 (Figure 53). Available recreational data were insufficient to calculate recreational catch rates.

### 4.3.3 Recreational Discards

To determine total harvest, the number of dead discards is estimated by applying a release mortality rate to the numbers of released fish ( $B2$ ). The judgment of the data workshop participants was to increase the mortality estimate used in previous assessments to a rate of 100%. Recreational total harvest in units of numbers of fish is therefore calculated as  $(A + B1)_{num} + (1.0 * B2_{num})$  and reported in Table 24. Since MRIP only collects estimates of released fish in units of numbers of fish, the non-imputed weights of individual fish measured (in kilograms) by each state each year were used to obtain estimates of released fish in weight. Since neither measurement of fish weight nor estimates of released fish were reported every year, the non-imputed weights of individual fish ( $w$ ) were averaged across all years for each state ( $s$ ) to obtain a state-specific estimate of average fish weight ( $\bar{w}_s$ ). State-specific fish weights were then multiplied by  $B2_{num}$  to obtain estimates of released fish in units of weight:  $B2_{kg} = \bar{w}_s \times B2_{num}$ . Thus, recreational total harvest in units of weight can be obtained using  $(A + B1)_{kg} + (1.0 * B2_{kg})$  and are reported in units of metric tons in Table 24. Estimates of recreational total harvest averaged over the past ten years were 1,382 mt in the north region and 446 mt in the south region.

### 4.3.4 Recreational Catch-at-Age

Insufficient biological samples were available to develop a recreational catch-at-age matrix. As in the 2010 and 2015 benchmarks and the 2017 update, recreational landings were combined with bait landings, and the bait catch at-age matrix was expanded to reflect these additional landings in numbers applied regionally and then combined.

### 4.3.5 Potential Biases, Uncertainty, and Measures of Precision

The MRIP provides estimates of PSE (proportional standard error) as a measure of precision. The PSE values associated with MRIP estimates for Atlantic menhaden were substantial (>50%) in most years. Potential biases are unknown.

## 4.4 Fishery-Dependent Indices

The SAS reviewed six fishery-dependent datasets from Atlantic coast states that were submitted along with fishery-independent data to support the stock assessment. The fishery-dependent data the SAS reviewed and time series provided were:

1. Rhode Island's daily harvester reports from floating fish trap fishery (2007-2017)
2. Massachusetts' pound net fishery (2002-2013)
3. Maryland's pound net fishery (1992-2012)
4. North Carolina's bait fishery (1994-2017)
5. Delaware's drift gill net fishery (1985-2017)
6. Delaware's fixed gill net fishery (1985-2017)

The SAS discussed the inclusion of these data sets in the assessment but ultimately came to the same conclusion as SEDAR 40 (2015), which was not to include these in the assessment.



Fishery-dependent indices lacked both age and length data; thus information to determine selectivity were not available. Furthermore, because the fishery-independent datasets had longer time series and were generally of a higher quality (i.e., fewer issues of concern; e.g., one data set was one permit holder), all fishery-dependent indices were removed from consideration in assessment models.

Two fishery-dependent CPUEs were developed to support ERP modelling, a commercial reduction CPUE (RCPUE) and the Potomac River Fishery Commission commercial bait CPUE (PRFC) index (Figure 54, refer to the ERP report for more details on CPUE development). These indices were developed as input to the ERP WG's surplus production models which required an index with a long time series. The SAS reviewed these indices, but had concerns about the reliability of these indices as measures of relative abundance. These concerns included how to define a consistent unit of effort, the limited spatial scale (of the PRFC index), and the potential for hyperstability (of the RCPUE index). Ultimately, the SAS decided to exclude the RCPUE and PRFC indices and only use fishery-independent indices in the base run of the BAM. Sensitivity analyses were run with the RCPUE or PRFC indices for comparison (Section 6.6).

## **5 FISHERY INDEPENDENT DATA SOURCES**

### **5.1 Stock Assessment Subcommittee Criteria and Index Development**

The SAS reviewed 49 fishery-independent surveys (Table 25) for inclusion in this assessment as young-of-year (YOY) or adult (age-1+) abundance indices. Surveys were categorized as YOY or age-1+ based on regional length cutoffs (Table 26) as developed by the TC in 2003 and used in subsequent stock assessments (ASMFC 2004b, 2012b; SEDAR 2015; ASMFC 2017b). All surveys were evaluated using a standard set of criteria. Indices were removed from consideration for development into an abundance index if they did not meet the following:

- Absence of hyperstability or gear saturation (unless it could be corrected)
- Sufficient time series (minimum 10 years)
- Defined spatial extent
- Includes trips with zero catches unless evidence can be provided that the lack of zeroes does not impact the index
- Consistent data collection over time or ability to account for changes with model or through correction
- Proper identification of catches to species level
- Standardization model converges
- Information on gear selectivity available to determine if the index is YOY or adult
- Availability of length data

Surveys that met these criteria were developed into indices of abundance for further consideration. The SAS also compared percent of positive tows, weighted CVs, average CPUE,

average catch, and number of collections per year of each survey to make sure surveys were accepted or rejected based on similar criteria. All surveys were standardized by the SAS using R code developed by SAS member Rob Latour (VIMS) to consider a variety of statistical models, including generalized linear models (GLM), generalized linear mixed models (GLMM), and generalized additive models (GAM) as well as zero-inflated and hurdle models and nominal indices. These methods more fully accounted for uncertainty, but also led to higher coefficients of variation (CVs) than in SEDAR 2015. The SAS reviewed work on several fishery-independent surveys and selected the following as abundance indices for YOY and adult Atlantic menhaden.

## **5.2 Surveys**

### **5.2.1 Rhode Island Coastal Trawl Survey (Monthly Segment)**

#### **5.2.1.1 Survey Design and Methods**

The Rhode Island Coastal Trawl Survey began operating in 1990. The monthly segment of the survey is conducted year-round and samples 13 fixed stations - 12 inside Narragansett Bay and 1 in Rhode Island Sound (Figure 55). At each station, an otter trawl is towed for twenty minutes.

#### **5.2.1.2 Biological and Environmental Sampling**

Finfish are sorted by species, counted, weighed, and lengths are taken. If a large catch of a single species is collected, a sub-sample is taken for length measurements. Temperature, salinity, dissolved oxygen, cloud cover, and wind direction and speed are collected at each station.

#### **5.2.1.3 Evaluation of Survey Data and Index Standardization**

A fall (August-November) index of YOY Atlantic menhaden abundance was developed from this survey. Atlantic menhaden were caught in the fall with 42% positive tows whereas the spring months had 2% positive tows. There were six tows in the time series that caught over 5,000 Atlantic menhaden that were causing the GLM model not to converge, so these six tows were set at 5,000 Atlantic menhaden. A full model that predicted catch as a linear function of year, month, depth, bottom water temperature, and station was compared with nested submodels using AIC. Based on several diagnostics (AIC, dispersion, percent deviance explained, and resulting CVs), the model chosen was a negative binomial that included year and temperature.

#### **5.2.1.4 Abundance Index Trends**

The survey of relative abundance of YOY Atlantic menhaden in Rhode Island coastal waters showed low abundance in the early 1990s with some peaks in abundance in the late 1990s (Figure 56). The index was variable through the 2000s followed by very low values from 2009-2013. Abundance increased after 2013 and was at its highest value in the terminal year of 2017.

## **5.2.2 Connecticut Long Island Sound Trawl Survey**

### **5.2.2.1 Survey Design and Methods**

The Connecticut Long Island Sound Trawl Survey (CT LISTS) began operating in 1984. The survey operates in the Connecticut and New York waters of Long Island Sound (Figure 57), and uses a stratified random design. The sampling area is divided into 1x2 nautical mile sites with each site assigned to one of 12 strata defined by depth interval (0-9.0 m, 9.1-18.2 m, 18.3- 27.3 m, or 27.4+ m) and bottom type (mud, sand, or transitional). The survey is conducted during the spring (April – June) and fall (September – October), with 40 samples taken per month. No tows were conducted in fall 2010, resulting in a missing value for that year.

### **5.2.2.2 Biological and Environmental Sampling**

Catch is sorted by species. Finfish, lobsters, squid, and other selected invertebrates are counted and weighed in aggregate by species. All finfish, lobsters, and squid and selected invertebrates are measured. Prior to 1992 weights are not available. All menhaden were measured starting in 1996. Surface and bottom temperature, surface and bottom salinity, and depth are collected with each tow, starting in 1989.

### **5.2.2.3 Evaluation of Survey Data and Index Standardization**

The CT LISTS catches both YOY and age-1+ menhaden. Monthly length cutoffs were used to assign individuals as either YOY or age-1+ menhaden, and separate indices were developed for each. Because menhaden could not be separated into YOY or age-1+ prior to 1996, both indices start in 1996. The data were subset to stratum that had 5% or more positive tows in the fall over the entire time series. Samples from April, September, and October were used for the YOY index, based on proportion positive tows and when YOY menhaden would be expected to be present in Long Island Sound. Fall samples (September and October only) were used for the age-1+ index. After the subset, approximately 15% of tows were positive for YOY and 18% were positive for age-1+. A zero-inflated negative binomial GLM was chosen for both indices based on AIC and dispersion metrics. Stratum, depth, water temperature, and salinity were explored as factors, and effort (tow duration) was used as an offset. The final model for the YOY index used year, stratum, and bottom temperature in the count model and year and stratum in the zero-inflation component. The final model for the age-1+ index used year, month, and depth for the count model and year and stratum for the zero-inflation component.

### **5.2.2.4 Abundance Index Trends**

The index of relative abundance of YOY Atlantic menhaden in Long Island Sound varied without trend; it showed strong year classes in 2000, 2004, and 2016 (Figure 58). The index of relative abundance of Age-1+ menhaden was variable, but showed a slight increasing trend over the time series, with 4 of the 5 highest values of the time series occurring in the last 6 years, and the 2011 – 2017 average being higher than the time series mean (Figure 59).

The YOY index is reasonably well correlated with the Age-1+ index the following year (Figure 60), suggesting both indices are picking up on a coherent population trend.

## **5.2.3 Connecticut River Juvenile Alosine Seine Survey**

### **5.2.3.1 Survey Design and Methods**

The Connecticut River Juvenile Alosine Seine Survey began operating in 1978, with methods becoming standardized by 1987. The survey is a fixed site seine survey that operates in the Connecticut River (Figure 61). The sampling sites for this survey were chosen based on location, physical conditions, and accessibility. One seine haul per station was made during daylight hours with an 18.3-m nylon bag seine (0.5-cm delta mesh) and 30.5-m lead ropes. The seine was fished with the aid of a boat to deploy it upstream and offshore. One seine haul is made per site, and 7 sites sampled per week from mid-July to mid-October.

### **5.2.3.2 Biological and Environmental Sampling**

Species in the family *Clupeidae* (American shad, blueback herring, alewife, and Atlantic menhaden) are collected and brought to the laboratory for species identification, count by species and total length measurement. Temperature is the only environmental co-variate recorded.

### **5.2.3.3 Evaluation of Survey Data and Index Standardization**

Survey data were subset to the lower four stations (Figure 61) where menhaden are commonly captured. Only records with complete data on year, month, and temperature were used. All menhaden captured in this survey are YOY. Approximately 40% of hauls were positive for menhaden, with frequent large catches - about 15% of positive hauls caught more than a thousand menhaden. A zero-inflated negative binomial GLM was chosen to develop the index based on AIC and dispersion metrics. Year, month, temperature, and station were explored as factors. The final model included year, month, and station for both components of the model.

### **5.2.3.4 Abundance Index Trends**

The index of relative abundance for YOY menhaden from the Connecticut River Juvenile Alosine Seine survey did not show a strong trend, but the index has been below the time series average for most of the last 10 years, although 2015 was above average (Figure 62). The index showed strong year classes in 1992, 2002, and 2003.

## **5.2.4 Connecticut Thames River Seine Survey**

### **5.2.4.1 Survey Design and Methods**

The Thames River Seine Survey was started in 1998 and uses the same method and design as the Connecticut River Juvenile Alosine Seine Survey (Section 5.2.3.1). The survey is conducted at 8 fixed-site stations on the Thames River, from Norwich, Connecticut, to the mouth of the river (Figure 63). The sampling sites for this survey were chosen based on location, physical conditions, and accessibility. One seine haul per station was made during daylight hours with an 18.3-m nylon bag seine (0.5-cm delta mesh) and 30.5-m lead ropes. The seine was fished with the aid of a boat to deploy it upstream and offshore. Sites were sampled weekly (1998 – 2001) or biweekly (2002 – present) from mid-July to mid-October.

#### **5.2.4.2 Biological and Environmental Sampling**

Species in the family Clupeidae (American shad, blueback herring, alewife, and Atlantic menhaden) are collected and brought to the laboratory for species identification, count by species and total length measurement. Temperature is the only environmental co-variate recorded.

#### **5.2.4.3 Evaluation of Survey Data and Index Standardization**

All menhaden captured in this survey are YOY. Data were subset to the 7 stations that were consistently sampled over the time series. Only data through 2016 were available at the time of index development. Approximately 43% of hauls were positive for menhaden, with frequent large catches: about 35% of positive hauls caught more than a thousand menhaden. A zero-inflated negative binomial GLM was chosen to develop the index based on AIC and dispersion metrics. Year, month, temperature, and station were explored as factors. The final model included year and station for both components of the model.

#### **5.2.4.4 Abundance Index Trends**

The index of relative abundance of YOY menhaden from the Connecticut Thames River Seine Survey showed a similar pattern to the index from the Connecticut River Juvenile Alosine Survey (Section 5.2.3). The index has been low in recent years, although 2015 was above average, with the strongest year classes occurring in 1998, 2000, and 2002 (Figure 64).

### **5.2.5 New York Western Long Island Seine Survey**

#### **5.2.5.1 Survey Design and Methods**

The Western Long Island Seine Survey was started in 1984. It is a fixed station beach seine survey that uses a 200-foot x 10-foot beach seine with ¼-inch square mesh in the wings, and 3/16-inch square mesh in the bunt. The seine is set by boat in a “U” shape along the beach and pulled in by hand. Sites in Little Neck and Manhasset Bays on the north shore of Long Island, and Jamaica Bay on the south shore have been sampled since the beginning of the survey while other bays have been sampled on a shorter time frame (Figure 65). Pre-2000 sampling was conducted 2 times per month during May and June, once a month July through October. Now, Little Neck, Manhasset, and Jamaica Bays are sampled 2 times per month (bi-weekly) from May through October. Hempstead Harbor and Oyster Bay are sampled 1 time each month. Generally 5-10 seines are sampled in each bay on each sampling trip.

#### **5.2.5.2 Biological and Environmental Sampling**

All finfish species identified and counted, and starting in 1987, invertebrates have been consistently counted. As many finfish as possible were measured at each station until 2000 when either all, if less than 30, or a subset of 30 individuals were measured for each species. Environmental information (air and water temperature, salinity, dissolved oxygen, tide stage, wind speed and direction, and wave height) has been recorded at each station. Bottom type, vegetation type, and percent cover have been recorded qualitatively since 1988. Young-of-the-year vs. older menhaden are identified through month-specific length cutoffs.

### **5.2.5.3 Evaluation of Survey Data and Index Standardization**

YOY menhaden make up 90-100% of the menhaden captured for most years in this survey, so only a YOY index was developed for this survey. YOY menhaden could not be distinguished prior to 1986, as no length samples were taken, so 1984 and 1985 were dropped from the index. Data were subset to the three bays that were consistently sampled over the entire time series (Little Neck, Manhasset, and Jamaica Bay). The percent of positive hauls in those bays was 21% over the time series. A zero-inflated negative binomial GLMM was chosen to develop the index based on AIC and dispersion metrics. Air and water temperature, salinity, dissolved oxygen, tide stage, wind speed and direction, and wave height were explored as factors, and the final model included year, month, and bay with station as a random effect for the count component and year, month, salinity, and bay for the zero-inflation component.

### **5.2.5.4 Abundance Index Trends**

The index of relative abundance of YOY menhaden developed from the Western Long Island Seine Survey has generally been flat with more moderately abundant year classes after 1998, and a few strong year classes in 1999, 2015, and 2016 (Figure 66).

## **5.2.6 New York Peconic Bay Small Mesh Trawl Survey**

### **5.2.6.1 Survey Design and Methods**

The New York Peconic Bay Small Mesh Trawl Survey has operated with a consistent design since 1987. The survey operates in Peconic Bay Estuary from Flanders Bay in the west to the western side of Shelter Island (Figure 67). The survey uses a fixed station design, with 16 randomly selected stations sampled per week from May – October. The sampling net is a ~16-foot semi-balloon shrimp trawl with a 1-inch body and cod end, fitted with a 3/8-inch cod end liner. Each tow is done for 10 minutes at approximately 2-2.5 knots, depending on current tidal conditions.

### **5.2.6.2 Biological and Environmental Sampling**

At the beginning of each tow, temperature (°C), dissolved oxygen (mg/l), saturation % (surface and bottom), depth, and secchi disc readings are taken. After each tow, the cod end is emptied into a walled culling table with running sea water that keeps the samples alive until release. All species are identified and counted. Large catches of finfish are subsampled, measuring 30 randomly selected individuals from that species and plus counting the rest, and species where multiple year classes are caught are subsampled by year class. All finfish, as well as mantis shrimp, horseshoe crabs, and squid, are measured to the nearest millimeter. Young-of-the-year vs. older menhaden are identified through month-specific length cutoffs.

### **5.2.6.3 Evaluation of Survey Data and Index Standardization**

YOY menhaden make up 90-100% of the menhaden captured for most years in this survey, so only a YOY index was developed for this survey. Most of the menhaden captured by the survey were encountered in July, August, and September, so the index was subset to those months. Data from those months were also subset to records that had complete environmental data. Overall, 8% of the tows in those months were positive for YOY menhaden. No YOY menhaden were captured in 1989, 1993, or 2008. A negative binomial GLMM was chosen to develop the

index based on AIC and dispersion metrics. Depth, water temperature, dissolved oxygen, oxygen saturation, and turbidity (secchi disk reading) were considered as factors in the standardization process. The final model included year, surface temperature, surface salinity, turbidity, and bay as factors with station as a random effect.

#### **5.2.6.4 Abundance Index Trends**

The index of relative abundance of YOY menhaden developed from the New York Peconic Bay Small Mesh Trawl Survey has varied without trend over the entire time series, although there have been more frequent strong year classes since 2000 (Figure 68). The three strongest year classes occurred in 2002, 2015, and 2016, which is consistent with several other YOY indices from this region.

### **5.2.7 New York Juvenile Striped Bass Beach Seine Survey**

#### **5.2.7.1 Survey Design and Methods**

The New York Juvenile Striped Bass Beach Seine Survey has been conducted since 1985. This survey is a fixed site survey that targets young-of-year striped bass in the lower brackish tidal portion of the Hudson River Estuary (river miles 22-39/rkm 35-63; Figure 69). From 1985-2013, 25 fixed stations were sampled every week; in 2014, the number of stations was reduced to 13 due to staffing constraints, unsafe sites, and redundant habitat sampled, but the broad geographical range of the nursery area was retained. Sites are sampled bi-weekly from July through early November. The survey uses an off-center 200 foot x 10 foot beach seine that is deployed from the shore with a boat.

#### **5.2.7.2 Biological and Environmental Sampling**

All fish collected are identified to species, counted and returned to the river. A subset of 30 individuals per seine haul of Atlantic menhaden and other high priority fish are measured for both fork and total length (mm). Length, weight and scales are also taken from any game fish thought to be over one year of age. Water quality data such as temperature, salinity, pH, dissolved oxygen, conductivity and total dissolved solids is taken at each site as are prevailing conditions such as wave height, wind velocity, cloud cover, and tide stage. Young-of-the-year vs. older menhaden are identified through month-specific length cutoffs.

#### **5.2.7.3 Evaluation of Survey Data and Index Standardization**

Only a YOY index was developed for this survey. Lengths were not collected for menhaden prior to 2000, so YOY menhaden cannot be distinguished from age 1+ menhaden prior to 2000. YOY menhaden make up 90-100% of the catch of menhaden in most years, but in some years, age-1+ menhaden are more abundant, so years prior to 2000 were dropped from the index. Approximately 13% of hauls from 2000 onward were positive for menhaden. Catch rates were low in November, so that month was dropped from the index. A negative binomial GLMM was chosen to develop the index based on AIC and dispersion metrics. Tide stage, region, surface temperature, salinity, substrate, and dissolved oxygen were considered as factors. The final model included year, month, salinity, and dissolved oxygen as factors with station as a random effect.

#### **5.2.7.4 Abundance Index Trends**

The index of relative abundance for YOY menhaden from the New York Juvenile Striped Bass Beach Seine Survey showed no trend over the time series; it showed strong year classes in 2005 and 2015 (Figure 70).

### **5.2.8 New Jersey Delaware River Striped Bass Seine Survey**

#### **5.2.8.1 Survey Design and Methods**

Since 1980, New Jersey has conducted a striped bass young-of-year seine survey in the Delaware River. This survey catches a variety of other species of fish and invertebrates, including significant numbers of Atlantic menhaden. The survey area extends from river mile 53.5 to 126 (Salem Nuclear Plant to Trenton; Figure 71), and is divided into three regions based on salinity. Stations are sampled twice per month using a 100-foot bagged seine with 0.25" mesh. Survey methodology has changed considerably since the survey began in 1980. Modifications include changes to station selection, distribution of stations among regions, single/replicate tows, and months sampled. Standardized methodology employed since 1998 includes sampling 32 fixed stations twice per month from June to November.

#### **5.2.8.2 Biological and Environmental Sampling**

Catches are sorted by species, counted, and up to 30 individuals measured per tow. Prior to 2001, length data for menhaden consisted of only minimum and maximum length per tow. Other information collected includes tide, water temperature, salinity, and dissolved oxygen.

#### **5.2.8.3 Evaluation of Survey Data and Index Standardization**

Data from this survey were subset in a number of ways to develop an appropriate index of YOY menhaden. Station selection was relatively haphazard for the years 1980-1985, so these years were removed. Stations furthest up river, in the tidal fresh portion of the survey area, were excluded from the index calculation because very few (less than 0.1%) of the menhaden caught were from this region. Similarly, the index was restricted to the months of August to October when the majority of menhaden catch occurs. Replicate tows, which were conducted at each station for a number of years, were removed so only the first set at each station was included. Finally, after many changes to station selection, a fixed set of stations was developed in 1998 and have been used consistently since. Although not all of these stations have been sampled over the entire survey time period, only data from these stations were used in the analysis.

Available covariates for the index include station, temperature, salinity, and dissolved oxygen; however, since temperature and DO are often collinear, DO was excluded from the model. Several functional forms were investigated, including GLM, GLMM, and GAM. Based on several diagnostics (AIC, dispersion, percent deviance explained, and resulting CVs), the model chosen was a GAM with nonlinear functions for salinity, temperature, and station.

#### **5.2.8.4 Abundance Index Trends**

The index of relative abundance of YOY Atlantic menhaden in the Delaware River appears to show two different patterns between early and recent periods (Figure 72). From 1986 to 1999,



abundance was variable, ranging from <10 to over 300 fish per tow (peak 620 in 1999), and an average of 140 fish per tow. Since 2000, abundance has been lower and much less variable, with an average of just 14 fish per tow, and a peak of 144 in 2010.

## **5.2.9 New Jersey Ocean Trawl Survey**

### **5.2.9.1 Survey Design and Methods**

New Jersey has conducted a seasonal trawl survey of nearshore ocean waters since 1988 (Figure 73), with standardized methods since 1990. Five cruises occur each year during January/February, April, June, August, and October. The survey employs a stratified random design based on three depths (<10, 10-20, 20-30 meters) and five latitudinal divisions between Henlopen Channel (Delaware Bay) and Ambrose Channel (Hudson River). Tows are 20 minutes long using a three-in-one trawl with a 30.5-m footrope and ¼" liner.

### **5.2.9.2 Biological and Environmental Sampling**

Catch is sorted by species and weighed to get a total species weight (no individual weights). Length data are collected for up to 50 individuals per species. Other information collected from each tow include surface and bottom readings of temperature, salinity, and DO, as well as start and end depth and location.

### **5.2.9.3 Evaluation of Survey Data and Index Standardization**

Atlantic menhaden catches from the New Jersey Ocean Trawl Survey were first parsed into catches of YOY and adult (age-1+) using tow specific length frequency data and approved YOY cutoffs by month (Table 26). Catches of YOY and age-1+ menhaden in time and space were then evaluated to determine if subsetting was appropriate. For the YOY index, based on timing and location of catches, all strata were used from the January and October cruises. October catches were lagged forward one year to develop a Jan-1 index. For the age-1+ index, based on timing and location of catches, data from all cruise months were used except tows from the deepest strata (20-30m). October catches were lagged forward one year to develop a Jan-1 index.

For the YOY index, available covariates for the index include salinity, temperature, depth, and stratum. Several functional forms were investigated, including GLM, GLMM, and GAM. Based on several diagnostics (AIC, dispersion, percent deviance explained, and resulting CVs), the model chosen was a GAM using stratum and nonlinear functions for salinity and temperature.

For the age-1+ index, available covariates for the index include salinity, temperature, depth, and stratum. Several functional forms were investigated, including GLM, GLMM, and GAM. Based on several diagnostics (AIC, dispersion, percent deviance explained, and resulting CVs), the model chosen was a GAM using nonlinear functions for temperature and depth.

### **5.2.9.4 Abundance Index Trends**

Relative abundance of YOY menhaden in the New Jersey Ocean Trawl Survey shows a period of low catches during the 1990s, a shift to generally higher catches during the early 2000s, returning back to lower catches since 2010 (Figure 74). The long term average is approximately 1.8 fish per tow, with a range of 0.01 to 15.32.

Relative abundance of adult (age-1+) menhaden in the New Jersey Ocean Trawl Survey shows a period of low and stable catches (<1 fish/tow) during the 1990s followed by a gradual increase in abundance in the early 2000s (Figure 75). Since 2005, catches have averaged over 14 fish/tow, with a peak of approximately 40 fish/tow in 2012.

## **5.2.10 Delaware Adult Trawl Survey**

### **5.2.10.1 Survey Design and Methods**

Delaware Fish and Wildlife's Adult Trawl Survey operated in the years 1966-1971, 1979-1984, and 1990-present, although only the 1990-2017 years of data were used for this assessment due to inconsistent methods throughout the time series. The survey operated year-round initially but since 1990 it has operated from March through December. It is a fixed station sampling design with sites throughout Delaware waters of the Delaware Bay from 7 to 35 m in depth (Figure 76). At each station, an otter trawl is towed for twenty minutes.

### **5.2.10.2 Biological and Environmental Sampling**

Catch is sorted by species and aggregate weights are taken for each species. Finfish species with less than 50 individuals were measured for fork length to nearest half-centimeter. Finfish species with more than 50 individuals were randomly sub-sampled (50 measurements) for length with the remainder counted. Temperature, salinity, dissolved oxygen, depth, and tide are collected at each station.

### **5.2.10.3 Evaluation of Survey Data and Index Standardization**

A fall (September-December) index of age-1+ Atlantic menhaden abundance was developed from this survey for 1990-2017. Length cutoff values for the region and time of year were used to omit YOY Atlantic menhaden from the data set so that only ages 1+ were included in the index. Several stations were eliminated before the index was developed due to low or no catches of Atlantic menhaden, including stations 42, 54, 61, 63, and 73. After subsetting, the survey had 50% positive tows for Atlantic menhaden. Several models were explored that predicted catch as a function of year, month, station, temperature, depth, tide, salinity, dissolved oxygen, latitude, and longitude. Submodels within model types were chosen based on AIC. Several model diagnostics were considered and the model chosen for this survey was a GAM that included year, month, temperature, and station using a spline with random effects on the latter. This model was chosen over the GLM because it was slightly less dispersed and reduced the CVs associated with the annual index values.

### **5.2.10.4 Abundance Index Trends**

The survey of relative abundance of adult Atlantic menhaden in Delaware Bay showed varying abundance throughout the time series with the largest abundance occurring in 1999 and lowest in 2003-2004 (Figure 77). The terminal year in the index, 2017, indicates low abundance.

## **5.2.11 Delaware Inland Bays Survey**

### **5.2.11.1 Survey Design and Methods**

Delaware Fish and Wildlife's (Juvenile Trawl) Inland Bays Survey began in 1978, although only the 1986-2017 were used for this assessment due to inconsistent methods throughout the time series. The survey operates from April through October with a fixed station sampling design. For the Inland Bays portion, 12 stations are sampled a month for a total of 84 annually (Figure 78). At each station, an otter trawl is towed for twenty minutes.

### **5.2.11.2 Biological and Environmental Sampling**

Catch is sorted by species. Finfish species with less than 30 individuals were measured for fork length to nearest half-centimeter. Finfish species with more than 30 individuals were randomly sub-sampled (30 measurements) for length with the remainder counted. Temperature, salinity, weather, depth, and tide are collected at each station.

### **5.2.11.3 Evaluation of Survey Data and Index Standardization**

An index of YOY Atlantic menhaden abundance was developed from this survey for the months of June-October. Atlantic menhaden were predominantly captured by this survey in those months with 19% positive tows. The data set was subset to include only stations 2-14. A full model that predicted catch as a linear function of year, month, depth, temperature, salinity, tide, and station was compared with nested submodels using AIC. Based on several diagnostics (AIC, dispersion, percent deviance explained, and resulting CVs), the model chosen was a negative binomial that included year and salinity.

### **5.2.11.4 Abundance Index Trends**

The abundance index of YOY Atlantic menhaden developed from this survey indicates high abundance in the late 1980s, low abundance through most of the 1990s, followed by some variability in the 2000s (Figure 79). The highest abundance of YOY Atlantic menhaden was observed in the terminal year, 2017.

## **5.2.12 Maryland Department of Natural Resources' Chesapeake Bay Juvenile Striped Bass Seine Survey**

### **5.2.12.1 Survey Design and Methods**

The Maryland Department of Natural Resources' Chesapeake Bay Juvenile Striped Bass Seine Survey was initiated in 1954 to document annual year-class success for young-of-the-year (YOY) striped bass (*Morone saxatilis*) in Chesapeake Bay. The juvenile striped bass survey also documents relative abundance of many other fish species in Chesapeake Bay, including menhaden.

Juvenile indices are derived annually from sampling at 22 fixed stations within Maryland's portion of the Chesapeake Bay (Figure 80) with a 30.5-m x 1.24-m bagless beach seine set by hand. Samples are taken in four of the major spawning and nursery areas: seven each in the Potomac River and Head of Bay areas and four each in the Nanticoke and Choptank rivers. Stations have been sampled continuously since 1954, with changes in some station locations.

Due to the changes in the survey, the SAS decided to use 1959-2017 for use as an abundance index for Atlantic menhaden. Sampling is completed monthly, with rounds occurring during July (Round I), August (Round II), and September (Round III). Replicate seine hauls, a minimum of thirty minutes apart, are taken at each site on each sample round, resulting in a total of 132 samples.

#### **5.2.12.2 Biological and Environmental Sampling**

All striped bass and selected other species, including menhaden, are counted and a random sample of 30 fish per species is measured for length. Menhaden were consistently measured for size distribution only beginning in 2005. Prior to that only minimum and maximum size were recorded (1954-1979) and for a period of years no length measurements were taken (1980-2004). Additional data collected at each site and sample round include time of first haul, maximum distance from shore, weather, maximum depth, surface water temperature (°C), tide stage, surface salinity (ppt), primary and secondary bottom substrates, and submerged aquatic vegetation within the sample area (ranked by quartiles). Dissolved oxygen (DO), pH, and turbidity (secchi disk) were added in 1997.

#### **5.2.12.3 Evaluation of Survey Data and Index Standardization**

A summer–fall (July, August and September) index of age-0 Atlantic menhaden abundance was developed from this survey for 1959–2017. A separation of age 0 from age 1+ was not possible for the full time series because length frequencies were available only from in 2005. Analysis of length distribution for available period indicated that age-1+ menhaden comprised on average 11% of the total catch. Hence the decision was made to treat all menhaden counts as age 0 fish. Prior to index development site numbers with zero catch and sites that were sampled in less than 50% of time series were eliminated. Several models (GLM, GLMM, GAM, zero inflated GLM, zero inflated GLMM) were explored that predicted catch as a function of year, month, station, temperature, depth, salinity, and distance from shore. Nested models within model types were also considered. Based on AIC and dispersion values, zero-inflation GLMM model was selected as the best fit model:

Catch ~ Year + Station + Temperature | Year + Station, where station was treated as a random intercept in both the model components.

#### **5.2.12.4 Abundance Index Trends**

The index of relative abundance of age-0 Atlantic menhaden in Upper Chesapeake Bay tributaries suggested low abundance during the first third of the time series (1959-1970; Figure 81). This was followed by the period of very high abundance during 1970s and 1980s. At the end of 1980s the index dropped again to low levels and remained low through the end of time series.

### **5.2.13 Maryland Coastal Bays Trawl Survey**

#### **5.2.13.1 Survey Design and Methods**

The Coastal Bays Fisheries Investigation Program was initiated in 1972 to characterize fishes and their abundances in Maryland’s coastal bays. Trawl and beach seine surveys were

conducted since 1972, but sampling protocol was standardized in 1989. Trawl samples are taken at 20 fixed sites (Figure 82) on a monthly basis from April through October. A 16-foot semi-balloon trawl is towed for 6 minutes (0.1 hr) at a speed of approximately 2.8 knots.

#### **5.2.13.2 Biological and Environmental Sampling**

For each sampling site the following environmental parameters were recorded: dissolved oxygen (mm/l), salinity (ppt), and water temperature (°C). Physical parameters included: speed (kts), tide state, water clarity (Secchi disk; cm), water depth (ft), weather conditions, and wind direction. Fishes and invertebrates were identified, counted and measured for total length. At each site, a subsample of the first 20 fish (when applicable) of each species were measured and the remainder counted.

#### **5.2.13.3 Evaluation of Survey Data and Index Standardization**

Data collected in April through October were used to develop an index of age-0 Atlantic menhaden abundance from this survey for 1972–2017. Prior to index development years and sites with zero catch as well as sites that were sampled less than 50% of time series were eliminated from analysis.

Several models (GLM, GLMM, GAM, zero inflated GLM, zero inflated GLMM) were explored that predicted catch as a function of year, month, station, temperature, depth, salinity, and distance from shore. Nested models within model types were also considered. There was no support for station random effect. Based on AIC and dispersion values, a zero-inflation GLMM model was selected as the best fit model:  $\text{Catch} \sim \text{Year} + \text{Month} + \text{Station} + \text{Temperature} \mid \text{Station} + \text{Temperature}$ , where station was treated as a random intercept in both model components.

#### **5.2.13.4 Abundance Index Trends**

The survey index of relative abundance of age-0 Atlantic menhaden in Maryland Coastal Bays shows high abundance with several peaks in early part of time series (1972-1980; Figure 83), followed by a drop and consistently low abundance from 1980s through the most recent period.

### **5.2.14 Maryland Department of Natural Resources' Striped Bass Spring Gill Net Survey**

#### **5.2.14.1 Survey Design and Methods**

Since 1985, the Maryland Department of Natural Resources has employed multi-panel experimental drift gill nets to monitor the Chesapeake Bay component of the Atlantic coast striped bass population. Multi-panel drift gill nets are deployed in the Potomac River and in the Upper Chesapeake Bay (Figure 84) and fished 6 days per week from late March through May totaling 30-40 sample days. Individual net panels are 150 feet long. The panels are constructed of multifilament nylon webbing in 3.0, 3.75, 4.5, 5.25, 6.0, 6.5, 7.0, 8.0, 9.0, and 10.0-inch stretch mesh. Sampling locations are assigned using a stratified random design. The Potomac River and Upper Bay spawning areas are each considered a stratum. In both systems, all 10 panels are fished twice daily at randomly selected site within the strata.

#### **5.2.14.2 Biological and Environmental Sampling**

Atlantic menhaden caught in the gill nets are counted and measured for total length (mm TL), when possible, and released. At each site, depth, air and surface water temperatures, surface salinity, and water clarity (Secchi depth) are measured and recorded.

#### **5.2.14.3 Evaluation of Survey Data and Index Standardization**

Based on random sampling design and catch frequency distribution, a GLM model with negative binomial link function was chosen to develop an index of menhaden abundance. All menhaden caught in the survey were above the cutoff size that separates Age 0 and Age 1+ menhaden, therefore, all sampled fish were used to calculate the Age 1+ index of abundance. March samples and all samples for the Potomac River were excluded due to low occurrence of menhaden. In addition, records with missing observations of environmental covariates were excluded, as well as records for the 3.1.3 inch mesh panel because it was not consistently used throughout the time series. Following TC decision, years with zero menhaden catch (1996, 2003, and 2004) were removed from the analysis. Significant explanatory variables were determined based on a run of full GLM negative binomial model. Based on AIC criteria and tests of significance, the final version of negative binomial GLM model predicted catch as a linear function of year, mesh size, depth, salinity, water temperature, and an offset for logarithm of effort. Calculated index is in 1,000 sq yards per hour.

#### **5.2.14.4 Abundance Index Trends**

The index of relative abundance of adult Atlantic menhaden in Upper Chesapeake Bay gillnet survey suggested higher abundance at the beginning of the time series (1985-1989; Figure 85), followed by the period of low abundance through 1990s and 2000s. There was an increase in adult abundance in recent years (2009-2016), followed by a drop to a low level for the two most recent years. The terminal year in the index, 2018, indicates low abundance.

### **5.2.15 VIMS Juvenile Fish and Blue Crab Trawl Survey**

#### **5.2.15.1 Survey Design and Methods**

The VIMS Juvenile Fish and Blue Crab Trawl Survey has been operating since the 1950s, but the program has experienced several gear and vessel changes over the years and calibration studies to understand the impacts of those changes on catch rates were not conducted. Accordingly, the SAS abbreviated this time series to 1990-2017. In 2015, the survey was moved to a new research vessel and the sampling gear was changed to reflect a more modernized design, however, a significant calibration study was conducted so that the effects of these protocol changes could be accounted for in the data standardization. Presently, the survey uses a trawl net with a 5.8-m head line with 40-mm stretch-mesh body made of dyneema and a 6.4-mm liner. Tows are 5 minutes in duration, conducted during daylight hours. Sampling sites are chosen according to a random stratified design based on depth and latitude (bay mainstem) or longitude (tributaries; Figure 86). Each bay mainstem region spans 15 latitudinal minutes and consists of six strata, while each tributary is partitioned into four regions of approximately 10 longitudinal minutes, with four strata in each. Approximately 1,300 sites are sampled during a full year.

#### **5.2.15.2 Biological and Environmental Sampling**

After each 5-minute tow, the catch is sorted and fishes are identified and measured for fork length. In the case of large catches, subsampling occurs and lengths are assigned to the full catch using expansion factors based on the length distribution of measured fish. Habitat type of each tow is also noted. Hydrographic and station data are also collected, including latitude and longitude, depth, tidal current stage, secchi depth, air temperature, wind direction, wind speed, weather conditions, sea state, water temperature, salinity and dissolved oxygen.

#### **5.2.15.3 Evaluation of Survey Data and Index Standardization**

A zero-inflated negative binomial GLM model was chosen to develop an index of YOY menhaden abundance. The overall data set was filtered to remove sampling regions and months with very low nonzero catches, and the resulting data included the three main Virginia rivers (James, York, and Rappahannock) and the colder months (Nov-March). Explanatory variables included: year (categorical), month (categorical), river (categorical), depth (continuous), salinity (continuous), dissolved oxygen (continuous), and temperature (continuous). Various combinations of explanatory variables for both the conditional and zero-inflated model components were considered and AIC was used for model selection. The final model included all explanatory variables for the conditional component, and all but DO for the zero-inflated component.

#### **5.2.15.4 Abundance Index Trends**

The index of relative abundance of YOY Atlantic menhaden showed a peak in 1993, followed by low abundance in the late 1990s and early 2000s (Figure 87). Abundance has incrementally increased since the mid-2000s through 2014 when it began to decrease through the terminal year of 2017.

### **5.2.16 VIMS Juvenile Striped Bass Seine Survey**

#### **5.2.16.1 Survey Design and Methods**

The VIMS Juvenile Striped Bass (*Morone saxatilis*) Seine Survey began in 1967 and operates in the major tributaries of the lower Chesapeake Bay. Survey operations were discontinued from 1974-1979 creating a break in the time series, and YOY Atlantic menhaden are captured as bycatch. The survey samples 18 historic and 21 auxiliary sites along the shores of the James, York, and Rappahannock river systems during five approximately biweekly sampling periods from July through mid-September (Figure 88). At each site, collections are made by deploying a 100 ft. (30.5 m.) long, 4 ft. (1.22 m.) deep, 1/4 in. (0.64 cm.) bar mesh minnow seine perpendicular to the shoreline (either until the net is fully extended or a depth of approximately four feet is encountered) and then leaving the onshore brail in a fixed position while pulling the offshore end down current and back to the shore, resulting in the sweeping of a quarter-circle quadrant.

#### **5.2.16.2 Biological and Environmental Sampling**

Counts are taken for captured menhaden and up to 25 are measured for fork length. For large catches (> 25 individuals), lengths are assigned to the full catch using expansion factors based

on the length distribution of measured fish. Hydrographic and station data are recorded: salinity, water temperature, pH, dissolved oxygen, sampling time, tidal stage, and weather conditions.

### **5.2.16.3 Evaluation of Survey Data and Index Standardization**

A zero-inflated negative binomial GLMM model was chosen to develop an index of YOY menhaden abundance. Explanatory variables included: year (categorical), month (categorical), river system (categorical), salinity (continuous), and temperature (continuous). Sampling site (categorical) was treated as a random effect. The years 1967, 1973, 1981, 1983, and 1984 were eliminated from analyses due to zero menhaden catch. Various combinations of explanatory variables for both the conditional and zero-inflated model components were considered and AIC was used for model selection. The final model included all explanatory variables for the conditional component, and year and month for the zero-inflated component.

### **5.2.16.4 Abundance Index Trends**

The index of relative abundance of YOY Atlantic menhaden showed variable but higher abundances in the 1980s followed by low abundance since 1990 through the terminal year of 2017 (Figure 89).

## **5.2.17 VIMS American Shad and River Herring Monitoring Program**

### **5.2.17.1 Survey Design and Methods**

The VIMS Alosine Monitoring Program began in 1998 to assess the spawning run of American shad (*Alosa sapidissima*) in the James, York, and Rappahannock rivers. Sampling occurs from mid Feb to early May, and age 1+ Atlantic menhaden are captured as bycatch. In the James and York rivers, fish are collected using a 273-m staked gill net (9.1-m panel length) located at river miles 10 (36°59.0'N, 76°28.8'W) and 14 (37°20.8'N, 76°37.7'W), respectively (Figure 90). In the Rappahannock River, a 277-m staked gill net (14.6-m panel length) located at river mile 36 (37°55.9'N, 76°50.4'W) is used for sampling. The nets in the York and James rivers are constructed of 12.4-cm stretched-mesh monofilament netting, while the net used in the Rappahannock River is constructed of 12.7-cm netting. From 1998-2014, each net was fished for approximately 24 h twice a week, however, sampling effort was reduced to once per week for 2015-2017.

### **5.2.17.2 Biological and Environmental Sampling**

All menhaden captured are enumerated and fork length data exist for 1998 and 2013-2017. Hydrographic and station data are recorded: salinity, water temperature, sampling time, and weather conditions.

### **5.2.17.3 Evaluation of Survey Data and Index Standardization**

A negative binomial GLM model was chosen to develop an index of menhaden abundance. Explanatory variables included: year (categorical), month (categorical), and river (categorical). Hydrographic variables were often missing in the data which precluded their inclusion in the modeling, and a mixed model with station as a random effect was not considered due to there



being only three sites. Various combinations of explanatory variables were considered and AIC was used for model selection. The final model included all explanatory variables.

#### **5.2.17.4 Abundance Index Trends**

Despite a high proportion of nonzero catches, the index of relative abundance of age 1+ Atlantic menhaden showed a variable trend through the time series from 1998-2017 with no discernable pattern (Figure 91). There was a peak in abundance in 2015, but it was followed by two low values in 2016 and 2017.

### **5.2.18 North Carolina Program 120 Estuarine Trawl Survey**

#### **5.2.18.1 Survey Design and Methods**

The North Carolina Program 120 Estuarine Trawl Survey began in 1971 and operates in shallow coastal waters from the Roanoke Sound south to the Shallotte River (Figure 92). In the beginning, various gears and sampling methodologies were used but sampling standardizations would later be established. Starting in 1978, trawling occurred during daylight hours and tow times were set to one minute with total area coverage of 75 yards. In 1989, sampling occurred at 104 core stations only using an otter trawl with 10.5-ft of headrope; each station was sampled in May and June. For this assessment, the survey data were restricted to years 1989 through 2017 for methodological consistency within the survey timeseries.

#### **5.2.18.2 Biological and Environmental Sampling**

Finfish are sorted by species and counted. If a large catch of economically important species is collected, a sub-sample of each size group is taken, and lengths are measured to the nearest millimeter. Environmental measurements taken at each site include temperature, salinity, dissolved oxygen, bottom composition, sediment size, and turbidity.

#### **5.2.18.3 Evaluation of Survey Data and Index Standardization**

Only YOY Atlantic menhaden were vulnerable to the sampling gear according to the age 1+ length cutoff values developed for North Carolina. Therefore, an index of YOY abundance was developed from this survey for the months of May and June from 1989 through 2017. The data were filtered by omitting stations ( $n = 8$ ) where Atlantic menhaden were never observed throughout the timeseries, removing 3 observations where catches were greater than 1,300 fish, and removing outlier observations of temperature and depth. After filtering the survey timeseries, 42% of the catch observations, on average, contained at least one individual (proportion positive). Across all years, the proportion positive ranged from 21% to 62%. Several model types that predicted catch as a function of year, month, depth, salinity, and temperature were explored. When applicable, station was included as a random effect. Nested submodels within respective model types were selected using AIC. Based on model diagnostics (e.g. AIC, residuals, dispersion, percent deviance explained, and CVs), a fully parameterized negative binomial generalized linear mixed-effects model (NB GLMM) with a log-link was selected as the final model.

#### **5.2.18.4 Abundance Index Trends**

The index of abundance for YOY Atlantic menhaden developed from this survey was highly variable with an average decreasing trend through 2017 (Figure 93). Years of high abundance include 1989, 1998, 1999, and 2005. Abundance from 2015 – 2017 was stable but low.

### **5.2.19 North Carolina Program 915 Pamlico Sound Independent Gill Net Survey**

#### **5.2.19.1 Survey Design and Methods**

The North Carolina Program 915 Pamlico Sound Independent Gill Net Survey began operating in Pamlico Sound in 2001. Sampling was expanded to include the Pamlico, Neuse, and Pungo Rivers in 2003 and the New and Cape Fear Rivers in 2008 (Figure 94). The survey uses a stratified-random-sampling design with strata defined by area and depth with each area sampled twice per month from February through December. Sink gill nets are 240 yards long with 8 panels (30 yards each) consisting of 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, and 6.5-inch square mesh and set for 12 hours and each sampling location. For this assessment, the survey data was restricted to years 2008 through 2017 for spatial and temporal consistency across all areas surveyed.

#### **5.2.19.2 Biological and Environmental Sampling**

Finfish are sorted by species, counted, weighed, and lengths are taken. If a large catch of a single species is collected, a sub-sample is taken for length measurements per mesh size. Environmental measurements taken at each site include temperature, salinity, dissolved oxygen, pH, bottom composition, sediment size, and turbidity.

#### **5.2.19.3 Evaluation of Survey Data and Index Standardization**

An index of age 1+ Atlantic menhaden abundance was developed from this survey for the months of April to July from 2008 through 2017. Since both YOY and age 1+ Atlantic menhaden are vulnerable to the gear used in this survey, age 1+ length cutoff values developed for North Carolina were used to omit YOY individuals from the index. The data were additionally filtered by omitting the Cape Fear River area where the numbers of individuals collected were comparably lower than the other areas and by removing outlier observations where nets were set in depths greater than 8.8 m. Lastly, the dataset was disaggregated from the level of whole gill net set to the level of mesh size panel to allow for mesh size variable categorization in the analysis. After filtering the survey time series, 42% of the catch observations, on average, contained at least one individual (proportion positive). Across all years, the proportion positive ranged from 31% to 57%. Several model types that predicted catch as a function of year, month, area, mesh size, depth, and salinity were explored. Nested submodels within respective model types were selected using AIC. Based on model diagnostics (e.g. AIC, residuals, dispersion, percent deviance explained, and CVs), a fully parameterized negative binomial generalized additive model (GAM) with a log-link and splines on depth and salinity was selected as the final model.

#### **5.2.19.4 Abundance Index Trends**

The index of abundance for age 1+ Atlantic menhaden developed from this survey increased in trend from 2008 through 2015. The index increased steadily until an abrupt decrease in 2016 (Figure 95).

### **5.2.20 South Carolina Department of Natural Resources Electrofishing Survey**

#### **5.2.20.1 Survey Design and Methods**

The South Carolina Department of Natural Resources (SC DNR) electrofishing survey began operating in 2001 to assess the relative abundance of recreationally and ecologically important finfish species found in upper estuary, tidally influenced habitats that traditionally are difficult to sample with gill nets or trammel nets due to high currents and presence of substantial submerged structure. The survey currently covers five (four since May 2001; fifth added in November 2003 (Waccamaw River/Winyah Bay)) upper estuarine strata along the coast of South Carolina (Figure 96). Each month (January through December) up to six stations per stratum are selected at random from ½-nautical mile (926-m) sections of river bank, restricted to sections where electrofishing is possible (usually less than 5 ppt; Arnott et al. 2010). Fish are collected using an electrofishing boat (Smith-Root) operating at approximately 3,000-W pulsed direct current. Stunned fish are caught with dip nets (4.5-mm square-mesh) over a 15-minute period while the boat moves with the current at drift or idle speed along the riverbank.

#### **5.2.20.2 Biological and Environmental Sampling**

At the end of each 15-minute set, fish are identified, counted, and measured (SL) before being released alive. In the case of large catches, a random subset of 25 individuals are measured for length prior to release. Environmental data are recorded, including tidal stage, surface water temperature, salinity, dissolved oxygen, depth, and Secchi disk depth.

#### **5.2.20.3 Evaluation of Survey Data and Index Standardization**

The SC DNR electrofishing survey catches both YOY and age-1+ menhaden. Monthly length cutoffs were used to assign individuals as either YOY or age-1+ menhaden (Table 27), subsequently developing only an index of YOY Atlantic menhaden abundance from this survey. Prior to applying the monthly length cutoffs, which are in fork length (FL), FL (in mm) was predicted all using survey specific length-length conversion equations (Table 28). Prior to index development, data were subset based on effort (10-30 minutes), tidal stage (excluded collections made during late flood tides or at high tide), depth (< 3 m), salinity (<13 PSU), secchi disk depth ( $\leq 1.64$  m), month (February – November), and water temperature (6-32.9°C). Any sampling station where there were no observed YOY menhaden was excluded. This data censoring removed 1,664 collections (32% of available collections) but only 2.6% of all YOY menhaden encountered in the survey, while increasing the overall proportion positive from 21% to 30%. A zero-inflated negative binomial generalized additive mixed model (ZINB GAMM) was chosen based on AIC, CV estimates, and dispersion metrics. Covariates considered included year and tidal stage as discrete variables, depth, water temperature, salinity, day of year, and secchi disk depth as continuous variables, stratum as a random effect, and effort (sampling duration) as an offset term in both sub-models of the ZINB GAMM. The final model retained the

covariates year, water temperature, salinity, day of year, and the random effect of stratum in the conditional model and the covariates year, tidal stage, depth, water temperature, salinity, day of year, and the random effect of stratum in the zero-inflation component.

#### **5.2.20.4 Abundance Index Trends**

The index of relative abundance of YOY Atlantic menhaden in the SC DNR electrofishing survey gives an overall impression of a decreasing trend throughout the time series (Figure 97). However, much of this impression may be driven by evidence of two strong year classes early in the time series, one in 2001 and another in 2003. Since then the only evident strong year class occurred in 2011.

### **5.2.21 Georgia Ecological Monitoring Trawl Survey**

#### **5.2.21.1 Survey Design and Methods**

The Georgia Ecological Monitoring Trawl Survey (GA EMTS) began operating in 1976 to assess commercially important shrimp (Penaeid shrimp) and blue crabs, though it wasn't until 2003 that this survey was expanded to assess and monitor all marine organisms encountered, including shrimp, crabs, finfish, and other biota with the primary objective of providing a comprehensive, long-term fisheries-independent monitoring program for finfish and invertebrates residing within Georgia's territorial waters. The monthly survey is conducted year-round in six of Georgia's commercially important estuarine sound systems (Figure 98). At each station, an otter trawl configured with a naked (i.e., no BRD or TED) 40' flat net is towed behind the R/V Anna for approximately 15 minutes. Since 2005, additional stations have been added to the original 36 stations sampled historically, bringing a coast-wide total of 42 stations sampled monthly (Figure 98).

#### **5.2.21.2 Biological and Environmental Sampling**

After each tow, catches are deposited on deck and sorted to the species level. Total weights are recorded for each species and a representative random sample of up to 30 individuals of each species are measured. Tidal stage, depth, temperature, and salinity are collected at each station.

#### **5.2.21.3 Evaluation of Survey Data and Index Standardization**

The GA EMTS catches both YOY and age-1+ menhaden. Monthly length cutoffs were used to assign individuals as either YOY or age-1+ menhaden (Table 27), subsequently developing only a spring and early-summer (April-July) index of age-1+ Atlantic menhaden abundance from this survey. Only data from the months of April-July were retained to match the other southern adult Atlantic menhaden abundance indices. During these months, the proportion of collections positive for age-1+ menhaden ranged from 23-39%. Prior to index development, the data were subset based on tow duration (5-24 minutes), depth (2-18 m), salinity (2-40 PSU), temperature (5-34°C) and collections where tidal stage was recorded, removing 48 collections (2.0% of available collections). After the subset, approximately 32% of tows were positive for age-1+ Atlantic menhaden. A zero-inflated negative binomial generalized additive mixed model (ZINB GAMM) was chosen based on AIC, CV estimates, and dispersion metrics. Covariates considered

included year and tidal stage as discrete variables, depth, water temperature and salinity as continuous variables, station as a random effect, and effort (tow duration) as an offset term in both sub-models of the ZINB GAMM. The final model retained the covariates year, tidal stage, salinity, water temperature and the random effect of station in the conditional model and year, tidal stage, depth, water temperature, and salinity in the zero-inflation component.

#### **5.2.21.4 Abundance Index Trends**

The index of relative abundance of age-1+ Atlantic menhaden in the GA EMTS was highly variable in the early part of the time series followed by an overall decreasing trend since the late 2000s. Catches (Figure 99). Catches have been below the series average since 2012.

### **5.2.22 Southeast Area Monitoring and Assessment Program, South Atlantic Region Coastal Trawl Survey**

#### **5.2.22.1 Survey Design and Methods**

The Southeast Area Monitoring and Assessment Program, South Atlantic Region (SEAMAP-SA) coastal trawl surveys the coastal zone of the South Atlantic Bight between Cape Hatteras, North Carolina, and Cape Canaveral, Florida (Figure 100). Trawling occurs in six regions (Florida, Georgia, South Carolina, Long Bay, Onslow Bay, and Raleigh Bay) split into twenty-four nearshore strata (an additional 17 offshore strata were not sampled in all years, and are not considered further in this report). Stations are randomly selected from a pool of trawlable stations within each stratum. The number of stations in each stratum is proportionally allocated according to the surface area of the stratum. Inner strata were delineated by the 4-m depth contour inshore and the 10-m depth contour further offshore. At each station, the R/V Lady Lisa, a 75-foot (23m) wooden-hulled, double-rigged, St. Augustine shrimp trawler owned and operated by the SC DNR is used to tow paired 22.9-m mongoose-type Falcon trawl nets without TED/BRDs. The body of the trawl is constructed of #15 twine with 1.875-inch (47.6-mm) stretch mesh. The cod end of the net is constructed of #30 twine with 1.625-inch (41.3-mm) stretch mesh and is protected by chafing gear of #84 twine with 4-inch (10-cm) stretch 'scallop' mesh. Trawls are towed for twenty minutes exclusively during daylight hours (1 hour after sunrise to 1 hour before sunset), with the exception of spring 1989 when tows were performed at night time. The survey has operated continuously since 1989, with multi-legged cruises being conducted in spring (mid-April to mid-May), summer (mid-July to early-August) and fall (early-October to mid-November) seasons.

#### **5.2.22.2 Biological and Environmental Sampling**

The contents of each net are sorted separately to species, and total biomass and number of individuals are recorded for all species of finfish, elasmobranchs, decapod and stomatopod crustaceans, and cephalopods. When large numbers of specimens of a species occur in a collection, the entire catch is sorted and all individuals of that species are weighed, but only a randomly selected subsample is processed and total number is calculated. For trawl catches where visual estimation of weight of total catch per trawl exceeds 500 kg, the contents of each net are weighed prior to sorting and a randomly chosen subsample of the total catch is then sorted and processed. In every collection, each of the twenty-seven target species is weighed

collectively and individuals are measured to the nearest centimeter. For large collections of the target species, a random subsample consisting of thirty to fifty individuals is weighed and measured. Hydrographic data collected at each station include surface and bottom water temperature and salinity measurements taken with a CTD profiler and sampling depth.

### **5.2.22.3 Evaluation of Survey Data and Index Standardization**

The SEAMAP-SA coastal trawl survey primarily catches age-1+ Atlantic menhaden, though a small percentage of YOY menhaden were identified using monthly length cutoffs (Table 27) and removed prior to development of an age-1+ index of relative abundance. Only data from the months of April-July were retained to match the other southern adult Atlantic menhaden abundance indices. Prior to index development, the data were subset based on trawl depth (3-12 m), removing 2 collections (0.04% of available collections). After the subset, approximately 18% of tows were positive for age-1+ Atlantic menhaden. A zero-inflated negative binomial generalized additive model (ZINB GAM) was chosen based on AIC, CV estimates, and dispersion metrics as best fitting the observed data. Covariates considered included year and season as discrete variables and depth, water temperature, salinity, and latitude as continuous variables. The final model retained the covariates year, season, water temperature, salinity, and latitude in the conditional model and the covariates year, depth, water temperature, salinity and latitude in the zero-inflation component.

### **5.2.22.4 Abundance Index Trends**

The index of relative abundance of age-1+ Atlantic menhaden in the SEAMAP-SA coastal trawl survey has varied without obvious trend (Figure 101). The major signal evident in the index is higher abundances in 1990, 2006, 2009, and 2017.

## **5.2.23 MARMAP and EcoMon**

### **5.2.23.1 Survey Design and Methods**

An index of Atlantic menhaden spawning biomass was developed using larval abundance data collected from two regional ichthyoplankton surveys (Figure 102). Although this method has never been implemented for menhaden previously, indices of fecundity based on larval abundance have been developed for other species in the U.S. and internationally (e.g. Heath 1993, Gledhill and Lyczkowski-Schulz 2000, Richardson et al. 2010, Simpson 2016, Ingram et al. 2010, McManus et al. 2017).

Data from the Marine Resource Monitoring, Assessment, and Prediction (MARMAP) and Ecosystem Monitoring (EcoMon) programs were obtained from NMFS for the years 1977-1987 and 1999-2017, respectively. For both surveys, the survey area extended from Cape Sable, Nova Scotia to Cape Hatteras, North Carolina; however, MARMAP employed a fixed station design while EcoMon uses a stratified random design (Walsh et al 2015). Sampling was conducted year round with generally four to eight cruises per year, depending largely on ship availability and weather. Both surveys perform double oblique tows, from the surface to within 5 m of the bottom or 200 m maximum depth, using a 61-cm bongo net towed at 1.5 knots. Mesh size of the net differed between the surveys, with MARMAP using a 505- $\mu$ m mesh and EcoMon using a 333- $\mu$ m mesh (Walsh et al 2015).

### **5.2.23.2 Biological and Environmental Sampling**

Species identification of ichthyoplankton samples was primarily conducted by the Polish Sorting Center, Morski Instytut Rybacki, in Szczecin (Walsh et al 2015). Up to 50 individuals of each species were sampled for length. In addition, both programs collected station depth and the EcoMon program consistently took surface and bottom temperature and salinity readings.

### **5.2.23.3 Evaluation of Survey Data**

Larval catch per tow was standardized to the total abundance under a 10-m<sup>2</sup> quadrat of sea surface using the method of Smith and Richardson (1977) and Morse (1989). Length frequency data collected during each tow were then used to parse total abundance to number at size. For tows with no length data length samples were randomly sampled from other tows made during the same cruise. Consistent with many other fecundity indices, abundance at size was then recalibrated to abundance at hatch through application of estimated growth and mortality rates. Growth rates of Atlantic menhaden measured during 2005-2008 in Virginia (Lozano et al 2012) were used to estimate time since hatch for each size bin. Subsequently, instantaneous mortality rates for clupeids from Houde and Zastrow (1993) were applied to numbers in each size (i.e. age) bin to back calculate abundance at hatch. Results were then summed across size bins for each tow to estimate total tow-level abundance at hatch used for index development.

Sampling occurs from the Gulf of Maine to Cape Hatteras, but the data were initially subset to Cape Cod to Cape Hatteras (strata 1-25; Figure 102) due to low occurrence of Atlantic menhaden outside this region. Subsequent analysis of catch data from strata 1-25 resulted in additional subsetting to primarily inshore and midshore strata, consistent with Simpson et al (2016).

To account for variability in timing of cruises, surveys were grouped by 2-month 'seasons' (e.g., January-February, March-April) (Walsh et al 2015). Seasonally, very few menhaden have been captured during the July-August time period, and winter sampling (November-December, January-February) has not occurred consistently in recent years. Further, preliminary results indicated that spring catches had minimal effect on index trends. As such, the assessment team concluded that an index based on September-October cruises was most appropriate. To coincide with a March 1 birthdate, data were lagged forward one year to provide a March 1 index of fecundity. Because of the different gears used (mesh size), the assessment team evaluated the two programs separately.

### **5.2.23.4 Abundance Index Trends**

Because standardization of observed catch to abundance at hatch resulted in non-integer values and presence of a large number of zero-catch observations, indices were developed using delta lognormal models. Available covariates for the MARMAP model included year, stratum, and depth, while EcoMon also evaluated surface temperature and salinity. Final models for both programs were:

#### MARMAP

Abundance ~ Year + Season + Stratum (positive model)

Success ~ Year + Season + Stratum (binomial model)

### EcoMon

Abundance ~ Year + Temp + Stratum (positive model)

Success ~ Year + Temp + Salinity + Stratum + Depth (binomial model)

A number of early years of the MARMAP index had no positive catches, requiring truncation of the time series to 1981-1988. During this period, Atlantic menhaden fecundity was variable but generally flat (Figure 103). Results of the EcoMon index suggest that fecundity was relatively stable between 2000 and 2012, but has increased rapidly in recent years (Figure 104).

## **5.3 Index Correlations**

All YOY and adult indices were compared for the years of overlap using a Pearson correlation test. For YOY indices, there were 14 significant ( $P < 0.05$ ) positive correlations and no significant negative correlations (Table 32, Figure 105). Many of these correlations were for surveys that operate near each other. However, some indicate more coastwide congruence. In concert, the recruitment index suite seems to provide supporting evidence of specific year classes having good recruitment. This indication of similar years with large year classes is valuable to the assessment as these indices are being used to create a recruitment index, which influences the estimation of recruitment deviations each year.

For age-1+ indices, there were five significant positive correlations and no significant negative correlations (Table 33, Figure 106). Many show common trends in adult abundance across regions. The three indices from the northern region all show declining or neutral trends in recent years and the Mid-Atlantic and southern region indices show an increasing trend in abundance in the most recent years of the time series.

## **5.4 Conn Indices**

### **5.4.1 Background of Analysis and Model Description**

When several population abundance indices provide different signals, hierarchical analysis can be used to estimate a single population trend. The abundance indices for Atlantic menhaden were combined into regional composite indices using hierarchical modeling as described in Conn (2009). This method assumes each index samples relative abundance but that the abundance is subject to sampling and process errors. It can be used on surveys with different time series. This approach does assume that indices are measuring the same relative abundance and that the surveys have similar selectivities. The Conn method was also used to combine individual abundance indices into regional indices in for previous menhaden assessments (SEDAR 2015, ASMFC 2017b, and SEDAR 2018). For the previous assessments, three composite indices were developed using the Conn approach: a northern adult index (NAD), a southern adult index (SAD), and a young-of-year abundance index (YOY). A summary of all data source time series, including the Conn indices, can be found in Figure 40.



## 5.4.2 Model Configuration

The SAS expressed concerns about the potential for selectivity differences among the adult surveys, particularly those that operated with different gears (i.e., trawl versus gill net), that should be identified before combining surveys using the Conn approach. A Principal Component Analysis (PCA) was run on the length compositions of the surveys to determine which had the most similar sized captures of Atlantic menhaden – the same approach used in SEDAR 40 (2015) to group surveys regionally. While SEDAR 40 (2015) used only trawl surveys to develop adult indices, this assessment also considered some gill net surveys to determine if the length compositions were similar to other surveys. According to the PCA, three groups of indices fell out as having the most consistent selectivities (Figure 107). Based on the results of the PCA, adult indices were combined into three regional surveys (Table 29): a northern adult index (NAD), a Mid-Atlantic adult index (MAD), and a southern adult index (SAD).

Abundance indices for Atlantic menhaden from each region were standardized to their means before being combined using the methods of Conn in R and WinBUGS. The estimates of process error variance for each of the indices were also examined. High sigma ( $\sigma^p$ ) values, or the standard deviation of the processes errors, suggest that the index may be a poor index for tracking abundance or may be measuring a different subpopulation whereas lower values indicate indices that may be better tracking the population or are consistent with the other indices included.

## 5.4.3 Model Results

### 5.4.3.1 YOY

Sixteen fishery-independent surveys met the criteria for inclusion in a coastwide index of recruitment, or the young-of-year abundance index (YOY), for use in modeling. For the YOY, all data sets were censored to only include age-0 individuals using the region specific length cutoffs specified in Table 26.

The YOY hierarchical index predicted low abundance in the mid-1960s, high recruitment in the 1970s through mid-1980s, and lower recruitment from the mid-1990s through the terminal year (Figure 108). The wider confidence intervals early in the time series reflects fewer surveys available for those years with only Maryland's Juvenile Striped Bass Survey informing the YOY from 1959-1967 and then Virginia's Striped Bass Seine Survey beginning in 1968 and Maryland's Coastal Trawl beginning in 1972. Most of the YOY surveys are available by the 1990s through 2017, thus the tighter confidence intervals. The standard deviation of the process errors for the surveys used in the YOY were highest for the Delaware Bay Inner Bays, New York Peconic Bay Trawl, Connecticut Thames River Alosine, and Virginia Striped Bass Seine Surveys (Table 31), indicating that these surveys may not be tracking the population or it may be reflecting differences in sampling programs (see Conn 2009 for a more thorough discussion).

For use in a sensitivity run, a Northern (including YOY surveys from Rhode Island to coastal Maryland) and Southern (including YOY surveys from the Chesapeake Bay to South Carolina) regional Conn indices were developed. Due to the time series of surveys that went into the regional YOY Conn indices, the Northern index went from 1985-2017 and the Southern index went from 1959-2017. The Northern YOY index was variable with no discernable pattern (Figure

109). The Southern YOY index indicated low YOY relative abundance in the 1960s, high abundance in the 1970s and 1980s followed by a decline in the 1990s with low but steady abundance through the terminal year.

#### **5.4.3.2 NAD**

Three fishery-independent surveys met the criteria for inclusion in the NAD and for use in modeling: Connecticut Long Island Sound Trawl Survey (CT LISTS; 1996-2017), New Jersey Ocean Trawl (NJ OT; 1990-2017), and Delaware Adult Trawl Survey (1990-2017). Adult surveys were censored to only include age-1+ Atlantic menhaden using the cutoffs specified in Table 26. Additionally, these surveys were subset to the months of September through January (lagged) before being combined using the methods of Conn (2009). These months represent the time of the year when Atlantic menhaden were most abundant in this region.

The NAD hierarchical index predicted variable abundance throughout the time series with notable peaks in 1999, 2002, and the mid-2010s (Figure 110). Despite the highest abundance occurring in 2015, the final two years of the index (2016-2017) indicate a decreasing adult abundance. All three of the individual abundance indices used in the NAD indicated a declining abundance in the terminal years. The standard deviation of the process errors for the surveys used in the NAD were highest for NJ OT and lowest for Delaware's Adult Trawl, although the sigmas were similar among indices (Table 31), indicating that these surveys were mostly congruent with each other or discrepancies between the indices were easily reconciled (Conn 2009). The annual length composition for each of the surveys was weighted by the inverse of the sigma value squared and then combined to develop a NAD length composition for use in the BAM.

#### **5.4.3.3 MAD**

Two fishery-independent surveys met the criteria for inclusion in the MAD and for use in modeling: Maryland's Striped Bass Spring Gill Net Survey (MD GN; 1985-2017) and Virginia's Shad Gill Net Survey (VA GN; 1998-2017). Adult surveys were censored to only include age-1+ Atlantic menhaden using the cutoffs specified in Table 26. Additionally, these surveys were subset to the months of March through May before being combined using the methods of Conn (2009). These months represent the time of the year when Atlantic menhaden were most abundant in this region.

The MAD hierarchical index predicted high abundance in the beginning of the time series followed by low abundance in the early 1990s (Figure 111). From 1985 until the VA GN began in 1998, the MAD relied on only the MD GN and thus there are larger errors associated with those years. The index then bounces around from the mid-1990s to the 2010s. Despite the highest abundance occurring in 2015, the final two years of the index (2016-2017) indicate a decreasing adult abundance just like the NAD predicted. Both of the individual abundance indices used in the MAD indicated a declining abundance in the terminal years. The standard deviation of the process errors for the surveys used in the MAD were very different between indices (Table 31). The VA GN had a very low sigma value (<1) and the MD GN had a high sigma value(>2), possibly indicating that these surveys may not be tracking the same population or it may be reflecting differences in sampling programs (Conn 2009) even though the PCA indicated the surveys

caught similar sized menhaden. The annual length composition for each of the surveys was weighted by the inverse of the sigma value squared and then combined to develop a MAD length composition for use in the BAM.

#### **5.4.3.4 SAD**

Three fishery-independent surveys met the criteria for inclusion in the SAD and for use in modeling: North Carolina Program 915 Gill Net Survey (NC p915; 2008-2017), Southeast Area Monitoring and Assessment Program (SEAMAP; 1990-2017), and Georgia Ecological Monitoring Trawl Survey (GA EMTS; 2003-2017). Adult surveys were censored to only include age-1+ Atlantic menhaden using the cutoffs specified in Table 26. Additionally, these surveys were subset to the months of April through July before being combined using the methods of Conn (2009). These months represent the time of the year when Atlantic menhaden were most abundant in this region.

The SAD hierarchical index predicted high abundance in 1990 followed by low abundance from 1991-2004 when the abundance begins to increase to a high in 2006 (Figure 112). The index is variable from 2006-2015 with a low abundance in 2016 with a slight uptick in the terminal year of 2017. All three of the individual abundance indices used in the SAD indicated an increasing or neutral abundance in the terminal year. The standard deviation of the process errors for the surveys used in the SAD were highest for NC p915 and lowest for SEAMAP, although the sigmas were similar among indices (Table 31), indicating that these surveys were mostly congruent with each other or discrepancies between the indices were easily reconciled (Conn 2009). The annual length composition for each of the surveys was weighted by the inverse of the sigma value squared and then combined to develop a SAD length composition for use in the BAM.

## **6 BEAUFORT ASSESSMENT MODEL (BAM) DESCRIPTION AND CONFIGURATION**

The Beaufort Assessment Model (BAM) is a forward-projecting statistical catch-at-age model. The essence of such a model is to simulate a population that is projected forward in time like the population being assessed. Aspects of the fishing process (e.g., gear selectivity) are also simulated. Quantities to be estimated are systematically varied from starting values until the simulated population's characteristics match available data on the real population as closely as possible. Such data include total catch by year, observed age composition by year, observed indices of abundance, and observed length composition by year.

The method of forward projection has a long history in fishery models. It was introduced by Pella and Tomlinson (1969) for fitting production models. Additionally, forward projection was used by Fournier and Archibald (1982) and Deriso et al. (1985) in their CAGEAN model and by Methot (1989) in his stock-synthesis model. Forward-projecting age-structured models share many attributes with ADAPT-style tuned and untuned VPAs. The model developed for this assessment is an elaboration of the CAGEAN and stock-synthesis models and very similar in structure to models used for assessments of Gulf of Mexico cobia (Williams 2001, SEDAR 2012), South Atlantic red porgy (SEDAR 2002), South Atlantic black sea bass (SEDAR 2003, SEDAR Update 2005, SEDAR 2011, and SEDAR Update 2013), South Atlantic snowy grouper and tilefish (SEDAR 2004, SEDAR 2011), South Atlantic red snapper (SEDAR 2008, SEDAR 2010), Atlantic

menhaden (SEDAR 2010, SEDAR 2015), and Gulf menhaden (SEDAR 2013, SEDAR 2018). The BAM was the forward-projecting age-structured model used in the previous Atlantic menhaden assessments, has multiple options for benchmark computation, has many model diagnostics, and can account for uncertainty through sensitivity runs and Monte Carlo bootstrapping.

### **6.1 Treatment of Indices**

Several sources of information were used to create five abundance indices for use in the BAM model (see Section 5.4). Three adult indices were created using time series from a number of state fishery-independent surveys. A single recruitment index was created across several gear types using several different fishery-independent surveys from a number of states. In addition, an index of fecundity was created using two ichthyoplankton surveys. Each of these indices was included in the base run of the BAM, along with length compositions for two of the adult indices, because they were deemed as accurate representations of the portion of the population represented over time and best available science.

The three adult surveys (the SAD, MAD, and NAD) included data from southern, mid-Atlantic, and northern states separately. These data sets were parsed out using principle components analysis on the length compositions, which clearly showed smaller fish sampled in the south, larger fish sampled in the north, and consistent sizes of fish in the mid-Atlantic region gears. Age-specific selectivity schedules were estimated for the MAD and NAD indices. Selectivities for the MAD and the NAD were estimated by fitting to length composition data sampled during the surveys. The MAD index selectivity was estimated as a double logistic as there was an absence of the largest individuals in the length compositions when compared to other data. The NAD index selectivity was estimated as logistic selectivity as many of these surveys captured some of the largest individuals sampled by either fishery-independent or –dependent gears. Length compositions were available for the SAD index, but were removed from the base run due to lack of fit given time-varying growth and likely mismatch for the timing during the year. Specifically, the length compositions indicated that the gears used to create the SAD index captured age-1 fish and an absence of large fish in the length samples. The SAD selectivity was therefore fixed at 1.0 for age-1. The level of error in each index was based on the precision surrounding the annual values produced by the hierarchical method used to standardize and combine the component indices. In the BAM model, the estimates of the product of total numbers of fish at the appropriate time of the year (April 15 for SAD, April 15 for MAD, and October 15 for NAD), a single catchability parameter, and the selectivity schedule were fit to the index value in that same year for each respective index. The error in these abundance indices was assumed to follow a lognormal distribution.

The recruitment index used in the BAM model comes from a series of state-specific surveys. These surveys, ostensibly designed for other species, capture primarily juvenile or age-0 menhaden. In the model, the YOY index was treated as an age-0 CPUE recruitment index, by fitting the product of the model estimated annual age-0 numbers part way through the year (June 1) and a constant catchability parameter to the computed index values. The catchability parameter for this index was blocked to accommodate data streams contributing to the index. Therefore, two constant catchability parameters were estimated for this index, one for 1959-

1986 and one for 1987-2017. This allowed for changing spatial coverage in the index (the spatial coverage changes as survey time series were added) as well as changes due to habitat with increasing spatial coverage of the index. The error in the YOY index was assumed to follow a lognormal distribution.

The fecundity index used in the BAM model comes from two time series of ichthyoplankton data: MARMAP (1981-1988) and EcoMon (2000-2017; Section 5.2.23). These surveys cover a large part of the Atlantic Coast and sample ichthyoplankton including larval Atlantic menhaden. In the model, the MARMAP/EcoMon combined index (MARECO) was treated as an indicator of fecundity for the population, by fitting the product of the model estimated annual fecundity (the sum across ages of the product of abundance-at-age, maturity-at-age, sex ratio, and number of eggs by age) at the beginning of the year (March 1) and a constant catchability for each of the surveys. The catchability parameter for this index had two time blocks based on the sampling survey (MARMAP versus EcoMon), which had slightly different gear specifications. The error in the MARECO index was assumed to follow a lognormal distribution.

### **6.1.1 Selectivity**

Because of the migratory behavior of Atlantic menhaden (Section 2.2), changes in the spatial distribution of the fishery likely impacted fishery selectivity over time (Sampson and Scott 2011; Sampson 2014; Waterhouse et al. 2014). The use of dome-shaped selectivity to capture these dynamics of the commercial fisheries was discussed during the assessment process, as well as during SEDAR 40 (2015).

#### **6.1.1.1 Comparison of fishery-independent and -dependent data**

During SEDAR 40 (2015), length data were available for Atlantic menhaden from a number of sources including fishery-dependent (1955-2013) and fishery-independent (years vary) data collection. These sources spanned the majority of the range of the species and provided information to guide the decisions regarding selectivity of both the indices and fisheries within the stock assessment model.

The combined fishery-independent data sets were compared to available fishery-dependent data to determine if larger menhaden were available than had been sampled from the fishery. The presence of larger fish in the fishery-independent data sets indicated that the fishery may not have captured the full range of sizes from the population, providing evidence for dome-shaped selectivity (Figure 113 - Figure 115). Comparisons were completed both for common years among the data sets and across all years of available fishery data. Comparisons among the common years of data between the fishery-dependent and each individual fishery-independent dataset provided information on the overlap of sizes sampled given a specific time frame. Comparisons among the fishery-independent data and all years of the fishery-dependent data provided information on historical sampling relative to collective information on sizes from fishery-independent surveys. Because it was thought that the fishery would be harvesting the entire range of sizes during the 1950s and 1960s, the comparison across all years provided information on the likely shape of the selectivity for those early years.

Although the SAS concluded that fishery selectivities were dome-shaped due to the spatio-temporal overlap of the fish and fishery and potential targeting of the fishery, the SAS was unsure as to the extent of the doming and whether the model would have the information to estimate the dome; therefore, likelihood profiling and simulation analyses were used to determine that selectivity was indeed estimable. While these analyses and decisions were made during SEDAR 40 (2015), the SAS carried it through to this assessment and ran additional likelihood profiles.

#### **6.1.1.2 Selectivity Conclusions**

The selectivity for the fishery-independent indices was defined from the length composition data available and specified functional forms. The selectivity of the recruitment index was set at 1.0 for age-0, while all other ages were set at 0.0. The recruitment selectivity was specified as such because it was intended to reflect only the abundance of age-0s (recruitment) over time. The SAD index was considered to have dome-shaped selectivity because its component indices catch predominantly smaller fish due to the gear's configuration. As a consequence, the selectivity for the SAD index was fixed at 1.0 for age-1 and zero for other ages. The MAD index was considered to have dome-shaped selectivity because its component indices catch smaller fish. Finally, selectivity of the NAD index was considered to be flat-topped because some of the largest lengths observed in any of the datasets came from the surveys included in this index.

All fisheries in the model were considered to have dome-shaped selectivity. Support for this conclusion comes from the presence of larger fish in fishery-independent data, particularly in the northern and Mid-Atlantic regions, and the decreasing variation in length with respect to age (from fishery-dependent data). Several recently published papers demonstrate that dome-shaped selectivity can occur because of heterogeneity in age compositions in the population across space and heterogeneity in fishing that population. Based on the work completed by Sampson and Scott (2011), dome-shaped selectivity is to be expected for a spatially heterogeneous stock such as Atlantic menhaden (Sampson 2014; Waterhouse et al. 2014). Atlantic menhaden undertake extensive migrations throughout the year. Larger individuals migrate farther north as the summer proceeds; therefore, older individuals are less likely to be harvested in a fishery typically centered in Chesapeake Bay (see Section 2.2).

In addition, the fishery-independent data indicate that there are lengths unsampled by the fishery, and the dearth of those sizes in the growth curve information supports that notion. Missing lengths generally imply dome-shaped selectivity even if selectivity is age-based because some ages may be incompletely sampled (based on the lack of lengths). However, these observations do not provide information on the extent of the doming, which was further explored in SEDAR 40 (2015) and in this stock assessment.

Atlantic menhaden fishery purse seines may have dome-shaped selectivity for several reasons. One reason already discussed is that Atlantic menhaden undertake extensive migrations. Another potential reason is fishery targeting practices. If the fishery targets the largest schools to set a purse seine on, those schools are likely comprised of the most abundant ages or sizes of fish, which would likely be smaller and younger fish. Thus, even though schools of age-4 to -6 individuals may be present in an area, the schools may not be harvested because they are

smaller than the optimum school size for the fishery to set on. Finally, larger fish are typically found farther offshore; therefore, if the fishery is located within 3 miles from the coast, they are more likely to encounter smaller fish than sets taken farther offshore.

## 6.2 Parameterization

A summary table of major data sources and time blocks can be found in Figure 40. The ADMB model code and input data file for the base run are attached in Appendix 14.2. All model equations may be found in SEDAR 2015 Appendix C. The major characteristics of the model formulation were as follows:

- *Start year and terminal year:* The start year of the model was 1955, and the terminal year of the model was 2017. Alternative start year configurations were explored using sensitivity analyses.
- *Ages:* The model included ages 0 to 6 with age-6 being treated as a plus group.
- *Natural mortality:* The age-specific natural mortality rate was assumed constant. A Lorenzen curve was scaled such that the mortality of age 1.5 was that estimated in a tagging study (Liljestrand et al. 2019a, 2019b; see Section 2.7).
- *Stock dynamics:* The standard Baranov catch equation was applied. This assumes exponential decay in cohort size because of fishing and natural mortality processes.
- *Sex ratio:* The ratio of males to females was fixed in the model at 1:1 because of the 251,330 fish sampled from the reduction fishery from 1955-1970, 49% were male and 51% were female.
- *Maturity and Fecundity:* The percent of females mature and fecundity were age- and time-varying, but fixed in the model. Maturity was based on length-at-age for the population at the start of the fishing year, while fecundity was based on weight-at-age for the population at the start of the fishing year. Annual, cohort-based von Bertalanffy growth parameters ( $L_{\infty}$ ,  $K$ , and  $t_0$ ) were estimated with a bias correction using the fishery data. These annual growth parameters were then used to estimate mean lengths and weights-at-age over time. Female fecundity-at-age (see Section 2.6) for each year was fixed in the model and was based on a function of mean weight by age for the population given recent sampling for life history information (R. Latour, VIMS, *personal communication*). Lengths were used in an estimated logistic regression function for determining maturity for each year (see Section 2.5), which were fixed in the model.
- *Weights-at-age:* The weight-at-age during spawning and during the middle of the fishery were input into the model and were based on the overall estimates of the parameters for the weight-length equation.
- *Recruitment:* Spawning was assumed to occur on March 1 in the model; hence the spawning time in months was 0.0, as March 1 was the start date for the model. Recruitment to age-0 was estimated in the assessment model for each year with a set of annual deviation parameters, conditioned about a median recruitment, which was estimated in log-space. The SAS tried to fit a Beverton-Holt stock-recruitment curve; however, the steepness parameter always ended up on a bound near 1.0. Given the interim reference points, the panel decided to fix the steepness value at 0.99, which allowed for the estimation of a median recruitment and estimated deviations over time.

Estimated deviations were informed by age composition data and a recruitment index.

- *Fishing*: Four fisheries were explicitly modeled. Southern and northern fleets of both the reduction fishery and the bait fishery were explicitly modeled to account for differences in selectivity due to size and age based migratory patterns. Being such a small proportion of the landings in each year, recreational landings were combined with the bait fishery landings. Fishing mortality rates were estimated for each year for each fishery by estimating a mean log fishing mortality rate and annual deviations.
- *Selectivity functions – indices*: Selectivity for the recruitment index was 1.0 for age-0 and 0.0 for all other ages. Selectivity for the SAD index was 1.0 for age-1 and 0.0 for all other ages. Selectivity for the NAD and MAD indices was age-varying, but constant over time. The NAD index selectivity was estimated as a flat-topped logistic function, while the MAD index selectivity was estimated as a double logistic or dome-shaped function. See Section 6.1 for further discussion.
- *Selectivity functions - fishery*: Selectivity for each of the fishery fleets was estimated using a functional form of dome-shaped selectivity. Specifically, the selectivity for each fleet was estimated as a four parameter double logistic. Selectivity was dome-shaped for each fishery for all years 1955-2017. Selectivity for both the northern and southern commercial reduction fisheries was time-varying using time blocks. For the northern fleet, selectivity was blocked as follows 1955-1969, 1970-1993, 1994-2012, and 2012-2017. For the southern fleet, selectivity was blocked as follows 1955-1971, 1972-2004, 2005-2012, and 2013-2017. Time blocks were based on the contraction and changes in the fishery over time (Section 4.1.3). See also Section 6.1.1 above. Selectivity for the northern bait fishery was blocked as follows 1955-2012 and 2013-2017 to account for the changes in fishery behavior after the implementation of Amendment II. Selectivity for the southern bait fishery was constant with time and didn't have any apparent changes in age structure or fishery behavior after the implementation of Amendment II (Section 4.2.3).
- *Discards*: Discards of Atlantic menhaden were believed to be negligible and were therefore ignored in the assessment model.
- *Abundance indices*: The model used five indices of abundance that were each modeled separately: a recruitment (age-0) index series (1959-2017; YOY), a southern adult index series (1990-2017; SAD), a mid-Atlantic adult index series (1985-2017; MAD), a northern adult index series (1990-2017; NAD), and an ichthyoplankton index series representing fecundity (1981-1988 and 2000-2017; MARECO). Each index except MARECO represents a composite of multiple survey datasets that were standardized/combined using the hierarchical method of Conn (2010).
- *Ageing uncertainty*: Ageing uncertainty was not included in the base run of the assessment due to an absence of information on the true age of sampled fish. However, a sensitivity run was included to explore repercussions of ageing uncertainty with respect to precision (see below).
- *Fitting criterion*: The fitting criterion was a total likelihood approach in which catch, the observed age compositions from each fishery, the observed length compositions from each index, and the patterns of the abundance indices were fit based on the assumed



statistical error distribution and the level of assumed or measured error (Section 5.4).

- *Model testing:* Experiments with a reduced model structure indicated that parameters estimated from the BAM model were unbiased and could be recovered from simulated data with little noise (cf., SEDAR 2007). Simulations were undertaken during SEDAR 40 (2015) to first reproduce results from the assessment and then to determine if selectivity was estimable. Additionally, the general model structure has been extensively peer reviewed. As an additional measure of quality control, code and input data for Atlantic menhaden were examined by multiple analysts to ensure accuracy. This combination of testing and verification procedures suggests that the assessment model has been implemented correctly and provides an accurate assessment of Atlantic menhaden stock dynamics.
- *Biological benchmarks:* Current benchmarks adopted for Atlantic menhaden are SPR based benchmarks based on the geometric mean fishing mortality for ages 2 to 4. The threshold value is the maximum geometric mean value from 1960-2012, while the target value is the median geometric mean value from 1960-2012. Further discussion of benchmarks is in Section 6.10.

### 6.3 Weighting of Likelihoods

The likelihood components in the BAM model include northern and southern reduction landings, northern and southern bait landings, northern and southern reduction catch-at-age, northern and southern bait catch-at-age, the NAD index, the MAD index, the SAD index, the YOY index, the MARECO index, NAD length compositions, and MAD length compositions. For each of these components, a statistical error distribution was assumed as follows:

Likelihood Component	Error Distribution	Error Levels
N & S reduction landings	Lognormal	Constant CV = 0.04
N & S bait landings	Lognormal	Constant CV = 0.15 (1955-1984); Constant CV = 0.10 (1985-2012); Constant CV = 0.05 (2013-2017)
N & S reduction catch-at-age	Dirichlet multinomial	Annual number of trips sampled
N & S bait catch-at-age	Dirichlet multinomial	Annual number of trips sampled
NAD length compositions	Dirichlet multinomial	Annual number of sampling events
MAD length compositions	Dirichlet multinomial	Annual number of sampling events
NAD index	Lognormal	Annual CV values from 0.58 to 0.88
MAD index	Lognormal	Annual CV values from 0.36 to 1.22
SAD index	Lognormal	Annual CV values from 0.36 to 0.82
Recruitment index (YOY)	Lognormal	Annual CV values from 0.41 to 1.12
MARECO index	Lognormal	Annual CV values from 0.41 to 1.85

In addition to these components, the likelihood also contained some penalty terms. The penalties were on recruitment deviations and the deviations in the initial age structure from equilibrium.

The likelihood used for composition data has changed rapidly over the last decade. The BAM model was developed with the multinomial likelihood for the age and length composition data. As more work was done to assess the correlation of composition data, the BAM was updated to include the robust multinomial likelihood following work done by Francis (2011). The robust likelihoods were suggested to reduce the influence of outliers. Most recently the Dirichlet multinomial likelihood has been used for composition data (Francis 2014; Thorson et al 2017). The Dirichlet is self-weighting and addresses correlations in the data.

#### **6.4 Estimating Precision**

The BAM model was implemented using the ADMB software, which allowed for easy calculation of the inverse Hessian matrix, which provides approximate precision of estimated parameters. However, in this case where some key values were fixed (e.g., natural mortality), it is believed that precision measures from the inverse Hessian matrix are underestimates of the true precision. Instead, the BAM model employed a parametric Monte Carlo bootstrap (MCB) procedure in which the input data sources were re-sampled using the measured or assumed statistical distribution and error levels provided. The data sources that were re-sampled in 5,000 bootstrap iterations included natural mortality and fecundity. The SAS explored alternative MCB runs that included uncertainty in additional components including northern and southern reduction and bait landings; the NAD, MAD, SAD, YOY, and MARECO indices; natural mortality; NAD and MAD length compositions; northern and southern commercial reduction and bait age compositions; and fecundity. Those runs were explored to illustrate the different levels of uncertainty that could be included.

The MCB approach resulted in a single maximum likelihood estimate of the model parameters for each set of sampled life history inputs, and as a result, it did not fully explore the uncertainty in the model parameter estimates themselves. To address this issue, the SAS elected to run a Markov Chain Monte Carlo (MCMC) analysis with the base run as well. ADMB's MCMC functionality is commonly used in fisheries modeling to provide a more robust estimate of uncertainty than the asymptotic standard errors from the maximum likelihood estimation process. However, as it relied on the same fixed life history input as the base model run, it did not provide a full picture of model uncertainty, either; the two approaches were complementary.

##### **6.4.1 Monte Carlo Bootstrap (MCB) Method**

For the MCB runs including uncertainty in natural mortality and fecundity (the base/preferred MCB runs), the values were varied based on the uncertainty in the underlying equations and estimates. Variability in natural mortality was included based on variability in natural mortality based on the Lorenzen curve using the ocean option and as estimated by Liljestrand et al. (2019a, 2019b). Specifically, the functional form of the Lorenzen curve was allowed to vary based on the uncertainty from Lorenzen (1996) using the ocean based species. The Lorenzen curve was then scaled such that the value at age 1.5 was equal to the value randomly sampled from the Liljestrand et al. (2019a, 2019b) estimated distribution. This vector was then used as the time-invariant value of natural mortality for that model run. Finally, fecundity varied over time in the model based on uncertainty described in Section 2.6. Specifically, a number was

chosen for the number of batches spawned from a uniform distribution between 9 and 16.7, while the relative batch fecundity was chosen from a uniform distribution between 218.96 and 254.88. These values along with the weight-at-age matrix produced a matrix for fecundity for each run. Thus, these bootstrap runs incorporated two major sources of uncertainty in the data inputs that had an impact on scale.

For the MCB runs that did include the data components (illustrative runs), the landings and indices were all re-sampled using multiplicative lognormal error using the CVs specified in the model input for each respective component. To implement this approach in the MCB runs, random variables ( $x_{s,y}$ ) were drawn for each year  $y$  of time series  $s$  from a normal distribution with a mean of 0 and a variance of  $\sigma_{s,y}^2$ . Each observation was then perturbed from the original values ( $O_{s,y}$ ) using the equation:

$$O_{s,y} = \hat{O}_{s,y} (\exp(x_{s,y}) - \sigma_{s,y}^2 / 2)$$

where  $\sigma_{s,y}^2 / 2$  is a bias correction that centers the multiplicative error on the value of 1.0. Standard deviations in log space were computed from CVs in arithmetic space:

$$\sigma_{s,y} = \sqrt{\log(1 + CV_{s,y}^2)}$$

The age and length compositions were recreated for each year by distributing the number of fish sampled for each year to each age or length based on the probability observed.

A stepwise approach was taken with respect to inclusion of uncertainty in the MCB analyses. During past stock assessments, many reviewers commented on the possibility of correlated life history data and other data inputs. Reviewers noted that if inputs were correlated in nature, but the MCB analysis wasn't accounting for those correlations, then the MCB analysis may be overestimating uncertainty. To address this concern, the SAS did several runs of the MCB analysis and tried to minimize components that may be correlated. In the end, the base set of runs included only  $M$  and fecundity. While  $M$  and fecundity may be correlated, the SAS was not able to specify how the two factors would be correlated; thus, the SAS provided exploration of this topic as a research recommendation.

This was particularly of interest given that the uncertainty produced with the MCB analysis would be used to compare with results from the ERP work. If inputs were highly correlated and the group did not account for that, then the uncertainty bounds would be too large; but if major sources of uncertainty were not included (e.g.,  $M$ ), then the uncertainty bounds would be too small. The SAS settled on including the two major sources of uncertainty for comparison with the acknowledgement that there may be some unaccounted for correlation between  $M$  and fecundity.

#### 6.4.2 Hybrid Markov Chain Monte Carlo (MCMC) Method

The *adnuts* package (Monnahan and Kristensen 2018) in R was used to implement the no-U-turn-sampling (NUTS) algorithm for the hybrid (aka Hamiltonian) Monte Carlo family of MCMC analyses. The *adnuts* package used the built-in hybrid MCMC capabilities of ADMB. Priors were

not turned on in the base run of the BAM model; to reduce processing time, normal priors were enabled for the majority of model parameters, centered on the base run maximum likelihood estimates. For fishing mortality and recruitment deviations, implicit bounded uniform priors were used. The maximum likelihood results of the BAM model with the priors enabled were virtually identical to the base run of the BAM model with no priors enabled.

Three chains were run, each with 4,000 iterations. The NUTS algorithm does not require thinning of the chains, but the first 2,000 iterations of each chain were considered a warm-up period and dropped from further analysis. The resulting samples were examined to make sure autocorrelation of samples was minimal and that the chains had converged.

The BAM model was run with each of the retained 6,000 sets of parameter estimates to generate time series of fecundity, age-1+ biomass, exploitation rate, average  $F$ , and recruitment, as well as  $F$  and fecundity reference points. The distributions of these time series were compared with the BAM base model results and the distributions resulting from the MCB analysis.

### 6.5 Sensitivity Analyses

A total of 38 sensitivity runs were completed with the BAM model. These sensitivity runs represent those involving input data, those involving changes to the model configuration, and those included as part of the retrospective analyses.

### 6.6 Sensitivity to Input Data

Several sensitivity runs were conducted to examine various effects to changes in the input data. These runs are related to uncertainty in index choice, life history values, and ageing uncertainty. Some of the runs included in this group are meant to address data choices in the ERP models (ERP Report, SEDAR 2019). The following is a list of these sensitivity runs:

Run Number	Sensitivity Examined
Am-034	SAD index excluded
Am-038	NAD index excluded
Am-039	MAD index excluded
Am-040	YOY index excluded
Am-041	MARECO index excluded
Am-042	All indices excluded
Am-043	With Lewis et al. 1987 fecundity values
Am-044	Natural mortality ( $M$ ) from the last stock assessment
Am-045	Including age error/uncertainty
Am-066	Using NAD index only; all others removed
Am-068	Using MAD index only; all others removed
Am-074	RCPUE index added in; constant $q$ ; no selectivity time blocks for fisheries
Am-073	PRFC index added in; constant $q$

To explore the uncertainty related to the inclusion of indices of abundance, several sensitivity runs were completed with data sources excluded or included in addition to the base run suite. First, a set of runs was completed with each of the five indices excluded individually (am-034, am-038, am-039, am-40, and am-041). For each run with an exclusion, the associated lengths composition data, if available, were excluded as well. Second, am-042 was completed to determine the influence of the index data as a suite versus the information contained in the other data sources. Third, two additional runs were completed to address questions that arose when running the indices censored individually. These were done with runs looking at the influence of only the NAD and only the MAD index and compared with the run with all indices censored. Finally, two additional index-based runs were completed where additional adult indices were added to the assessment (am-074 and am-073) for comparison of outputs with the ERP group (ERP report, SEDAR 2019). Specifically the RCPUE and PRFC indices were included with the other indices in the base run to be compared with the surplus production models to address ecosystem reference points. The RCPUE and PRFC indices provide longer time series of information on the adult population trajectory.

To explore the uncertainty related to life history values, two sensitivities were completed: the first related to natural mortality and the second related to fecundity. These sensitivity runs were completed to address changes to the model outputs related to life history inputs that changed based on new research as well as to provide information on a continuity run or transition to this assessment. First, natural mortality values from the last stock assessment were used (am-044). Second, fecundity values from the last stock assessment were used, based on Lewis et al. 1987 (am-043). These two runs provided a good picture of the change in scale since the last assessment predicated on the newly available data on natural mortality and fecundity.

One additional sensitivity run was completed to examine ageing uncertainty. Because no validated age data are available, ageing uncertainty was incorporated for these sensitivity runs based on within-reader error (am-045). These runs assume that the true age is uncertain, but there is little comprehensive data to support that assumption. Therefore, these runs are only explorations of the potential effects of true ageing uncertainty. In the end, the SAS decided to use the information in the age composition data and allow the estimation of dome-shaped selectivity in the base run since there was a trade-off related to age information and estimating of selectivity parameters.

### 6.7 Sensitivity to Model Configuration

Several sensitivity runs were conducted to examine the effects of various model configurations. These are related to uncertainty in minimum samples sizes, selectivity, model start year, recruitment index catchability and composition, likelihood component choices, conversion of length compositions to age compositions, and stock recruitment curve choice. The following is a list of these sensitivity runs:

Run Number	Sensitivity Examined
Am-037	One catchability parameter for the YOY index
Am-046	Minimum sample size for bait fishery = 1 trips

Am-047	Minimum sample size for bait fishery = 30 trips
Am-048	Using a robust multinomial likelihood for the composition data sets
Am-049	Using Ricker form for stock-recruitment curve
Am-053	Start year of 1985 and reference point calculations using 1985-2017
Am-053a	Same as Am-053 but with time-varying $M$ from ERP Report
Am-054	No time blocks for fishery selectivity
Am-055	Logistic selectivity for the fishery time blocks
Am-056	Selectivity used age based estimates instead of a functional form
Am-058	Length compositions for the indices converted to age compositions
Am-059	Used 2 indices for YOY, one for the north and one for the south
Am-060	Removed 2013-2017 time block from fishery selectivities
Am-071	Using Shepherd form for stock-recruitment curve

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The SAS was interested in exploring the impact of minimum samples sizes for fitting the bait catch-at-age. The SAS was looking to balance allowing low sample sizes to be included versus the potential loss of information based on a sample size requirements. As a result, two runs were included that looked at the minimum sample sizes for the bait fishery in terms of number of trips sampled with the two options being one trip (am-046) and 30 trips (am-047). Each trip has on average 10 fish sampled.

Selectivity is always an uncertainty in stock assessments, and that uncertainty was explored with four sensitivity runs related to time blocks and functional form of selectivity. The first was to eliminate time blocks from the northern and southern commercial reduction fishery fleets and the northern commercial bait fishery fleet (am-054); while the run am-060 removed only the terminal time block (years 2013-2017) from the same fleets, but retained the time blocks prior to 2012. The third was to estimate the selectivity for all fisheries as logistic or flat-topped (am-055). The final sensitivity run considered age-based estimation of selectivity parameters (am-056). Each of these runs explore the repercussions of the assumptions that were made about the functional form and time periods of selectivity used in the base case.

To explore the effects of the start year of the model, one sensitivity run was completed. The sensitivity was with a start year of 1985 and was meant to line up with some of the models used for the ERP work (ERP report, SEDAR 2019). In addition, starting the model in 1985 allows for the time series to have improved quality and quantity of data. An additional run was also completed with a start year of 1985 for comparison to the ERP models, and that run included a time-varying matrix of  $M$  from the VADER model (ERP Report, SEDAR 2019).

Two additional runs were completed to look at the effect of recruitment. The first run explored the use of a constant catchability for the YOY index without the time block in the base run (am-037). This first run was used to address the assumption of a catchability time block associated with the addition of data to the recruitment index over time. The second run that was completed included two recruitment indices, one for the southern region and one for the northern region (am-059). This particular run was done to determine whether these two regions could have different recruitment signals given environmental factors, which has been shown by Buchheister et al (2016). Each of these addressed a structural model choice or assumption.

The base run model uses a Dirichlet multinomial likelihood component for the composition data. To determine the impacts of the assumption of the likelihood type chosen, the SAS completed a sensitivity run whereby the composition likelihood component was a robust multinomial (am-048). This sensitivity run provides some continuity with the base run from the most recent stock assessment in 2015 and helps to illustrate differences between the two base case runs.

Next, the SAS completed a sensitivity run converting the length compositions from the indices to age compositions (am-058). Age data were not collected by the fishery independent surveys, therefore the base run of the model fit to index length composition data. This run addressed the ability to fit the length data and whether the model would be able to fit the index composition data better if the lengths were converted to ages. Annual age-length keys were developed from the fishery dependent biosamples. Because the index length compositions included fish outside the size range encountered by the fishery in many years (Figure 113 - Figure 115), a multinomial regression with year as a factor was used to develop the age-length keys to take advantage of historical fishery data where larger fish were sampled. The annual age-length keys were used to convert the index length composition data into age composition data.

Finally, the last set of runs related to model configuration related to the stock-recruitment curve decision. Two runs were done that considered different functional forms for recruitment: the Ricker stock recruitment curve (am-049) and the Shepherd form of the stock-recruitment curve (am-071). These two runs address the assumptions used to estimate recruitment in the base run by allowing the form to be different. While the Ricker form assumes a decrease in recruitment at the highest fecundity or stock levels; the Shepherd form allows for multiple shapes at the highest fecundity or stock levels.

## 6.8 Retrospective Analyses

Retrospective analyses were completed by running the BAM model in a series of runs sequentially omitting years 2017 to 2015, as indicated below:

Run Number	Sensitivity Examined
Am-050	Terminal year = 2016
Am-051	Terminal year = 2015
Am-052	Terminal year = 2014

The retrospective analysis was limited to these years to avoid changing model assumptions that would impact the retrospective analysis. For example, the last selectivity block for the commercial reduction fishery fleets and the northern commercial bait fishery fleet, as well as the MAD length compositions, started in 2013. If further data would be removed, then little to no data would be available to estimate the selectivity for that fishery and time period, nor would the model be able to estimate selectivity for the MAD index.

Retrospective analyses are meant to demonstrate the behavior of the model, and to investigate biases in estimated of population size or fishing mortality when additional years of data are added.

For this retrospective analysis, the run with the terminal year of 2014 showed a different scale than the other runs. This caused discussion about the plausible causes of the differences and led to additional retrospective runs to examine the behavior of the model. The SAS decided to remove the time blocks from the fishery fleets for 2013-2017, to fix the selectivity for the MAD index, and then rerun the retrospective analysis for a longer duration. The retrospective was run with the terminal years of 2016-2011. When doing these runs, the run with a terminal year of 2014 was still at a different scale, thus a few runs were looked at to see what data source(s) were causing the observed change. The run shown below (am-077a) explores the impact of a large year class moving through the population and observed in the northern data sources.

Run Number	Sensitivity Examined
Am-075	Terminal year = 2016
Am-076	Terminal year = 2015
Am-077	Terminal year = 2014
Am-077a	Terminal year = 2014; age-4 point reduced in northern commercial reduction and northern commercial bait age comps
Am-078	Terminal year = 2013
Am-079	Terminal year = 2012
Am-080	Terminal year = 2011

### 6.9 Likelihood Profiling and Simulation Analyses

Prior to estimating dome-shaped selectivity for each of the fisheries during SEDAR 40 (2015), the SAS panel wanted to determine if the extent of the dome was estimable and if it was estimable for each time block. Thus, selectivity was estimated for each fishery as an age-specific value. For each age-specific value, a likelihood profile was run across a range of plausible selectivity options. This allowed the panel to determine if there was a value that would be estimated based on the other data that had a better likelihood. The best likelihood was determined by graphing the change in the negative log-likelihood over the values for the age-based selectivity. Additionally, during the last stock assessment, the assessment model was rebuilt as a simulation model by another analyst (SEDAR 40 2015). This was done for two reasons: 1) to verify that the assessment model was performing as expected and to have another review of the code and 2) to determine if the model can estimate selectivity with simulated variability in the model. These simulation analyses were not redone for this assessment, but were assumed to hold true. These two analyses collectively indicated the notion that there was enough information in the available data to estimate the descending limb of the dome-shaped selectivity curves. These analyses were carried through to this assessment.

### 6.10 Reference Point Estimation – Parameterization, Uncertainty, and Sensitivity Analysis

The current fishing mortality reference points for Atlantic menhaden are the median geometric mean fishing mortality rate for ages-2 to -4 during 1960-2012 (target) and the maximum



geometric mean fishing mortality rate for ages-2 to -4 during 1960-2012 (threshold). Population fecundity (*FEC*, number of maturing or ripe eggs) is the other current reference point and is a measure of reproductive capacity. The reference points for reproductive output are the fecundity values associated with the fishing mortality target and threshold predicated on calculations for spawning potential ratio or SPR. All benchmark calculations were based upon landings weighted selectivity across all fleets and areas, *M*-at-age (which was constant), mean maturity-at-age, a 1:1 sex ratio, and mean fecundity-at-age from the model inputs. All means are across the entire time series of 1955 to 2017. Uncertainty in the benchmark estimates was provided by the bootstrap runs and the MCMC analysis. For each MCB run, MCMC analysis, and sensitivity analysis, the current reference points were calculated and a distribution of the benchmarks was provided.

### 6.11 Projections

Additional projections will be conducted following the Peer Review Workshop pending requests for specific scenarios from the Atlantic Menhaden Management Board. The SAS has provided the following example projections as an illustration of the methods being used for providing information to the Board. Specifically, the SAS has provided projections at the current TAC (216,000 mt) and at the TACs for each year to achieve the target 50% of the time. Since this assessment has a 2017 terminal year, the landings for 2018 were taken from the 2019 compliance reports but were not validated by state partners or ACCSP and were intended solely for the purpose of projections.

Data into and output from the MCB runs of the base run of the BAM were used as the basis for the projections. Projections were run for a total of 4 years (2018-2021). The starting conditions of the projection analysis include initial numbers-at-age, which were the estimated numbers-at-age,  $N_a$ , for year 2018 from the BAM for each MCB run.

Numbers-at-age after the initial year were calculated as:

$$N_{a+1,y+1} = N_{a,y} e^{-Z_{a,y}}$$

where *Z* was age- and year-specific mortality and equals natural mortality for each age for that year plus the fishing mortality rate times the selectivity-at-age. The vector for natural mortality for each projection was the vector from each MCB run. Selectivity was a vector from each MCB run for each fishery with the northern and southern commercial reduction fishery selectivities and the northern commercial bait fishery selectivity all being the values in the last time period. Fishing mortality was estimated using the optimize function in R to match the annual landings (level of landings as denoted above). Annual landings were calculated using the Baranov catch equation and weight of landings.

Recruitment was projected using non-linear time series analysis or empirical dynamic modeling as demonstrated in Deyle et al (2018). This method uses the state space of the current recruitment value to predict the space of the recruitment value in the next year. As a demonstration of this method's predictive capabilities for Atlantic menhaden, the SAS ran a moving window prediction to predict the years of 2007-2017 (Figure 116). This prediction

method does not include uncertainty; however, uncertainty in recruitment was included by using each MCB run and predicting recruitment for each of the individual MCB time series.

The number of projections was the same as the number of filtered MCB runs. Outputs included the median and 5<sup>th</sup> and 95<sup>th</sup> percentiles for fecundity (ova) over time, fishing mortality over time, recruitment over time, and landings over time. Fecundity for each year was the number of fish in each age times the reproductive vector at age. Specifically, maturity (mean values in the base run), a 50:50 sex ratio, and fecundity-at-age (as defined from each MCB run) were used to produce the reproductive vector at age.

As usual, projections should be interpreted in light of the model assumptions, key aspects of the data, a life-history of the stock examined. Some major considerations are the following:

- In general, projections of fish stocks are highly uncertain, particularly in the long term (e.g., beyond 5 years) and particularly for stocks with variable recruitment.
- Although projections included major sources of uncertainty, they did not include structural (model) uncertainty. That is, projection results are conditional on one set of functional forms used to describe population dynamics, selectivity, recruitment, etc.
- Fisheries were assumed to continue fishing at their estimated current proportions of total effort, using the estimated current selectivity patterns. New management regulations that alter those proportions or selectivities would likely affect projection results.
- If future recruitment is characterized by runs of large or small year classes, possibly due to environmental or ecological conditions, stock trajectories may be affected.

Projections apply the Baranov catch equation to relate  $F$  and landings using a one-year time step, as in the assessment. The catch equation implicitly assumes that mortality occurs throughout the year. This assumption is violated when seasonal closures are in effect, introducing additional and unquantified uncertainty into the projection results.

## **7 BAM MODEL RESULTS**

### **7.1 Goodness of Fit**

Goodness-of-fit was governed in the BAM assessment model by the likelihood components in the objective function. The relative fit among the likelihood components was governed by the weighting terms and the assumed error levels for each data source (see Section 6). During the Assessment Workshop, goodness of fit was also judged for each data source through examination of the model residuals.

Observed and model-predicted removals for the northern and southern reduction and bait fisheries (1955–2017; Figure 117–Figure 120) were compared for the base model run. Reduction fishery removals, which are known fairly precisely, fit very well, as do bait fishery removals. Patterns in the annual comparisons of observed and predicted proportion catch-at-age for the northern and southern reduction and bait fisheries (Figure 121–Figure 124) indicate a good overall model fit to the observed data. The bubble plots for the northern and southern

reduction and bait fisheries (Figure 125-Figure 128) indicate that the model fit does fairly well at estimating catch-at-age during the time series. The small amount of patterning observed in the bubble plots did not cause concern, especially since patterning was addressed with time block for selectivity to the best extent possible.

Observed and predicted coastwide recruitment indices were compared for the base model run (1959–2017; Figure 129). The residual pattern suggests that the recruitment index data did not fit well for relatively large year classes, especially those that occurred in the 1970s and 1980s. Visual examination of the fit suggests that the overall pattern fit reasonably well for the time series with respect to higher and lower recruitment periods. The most recent time period fit well with respect to scale, but did not hit the individual years particularly well; however, the values were all within the uncertainty bounds.

The observed and predicted NAD index (1990–2017; Figure 130), MAD index (1985-2017; Figure 131), SAD index (1990-2017; Figure 132), and MARECO index (1981-1988 and 2000-2017; Figure 133) values fit the general patterns in each index with many of the indices being rather flat. However, the model had a difficult time fitting estimates to the highest observed values in the time series, especially the high values in the MAD index at the beginning of the time series and the high points in the SAD index. Patterns in the annual comparisons of observed and predicted proportion NAD and MAD measurements at length for the NAD and MAD indices indicate good fit to the observed data in some years, but problems in fitting to data in other years (Figure 134-Figure 136). Given the nature of these indices as a conglomeration of data from different state fishery-independent data sources, changing patterns in the data are expected, yet are difficult to discern with model specifications. Therefore, although the fits to the data could be better, the SAS only used the length data to get an idea of ages represented by each index, nothing more. For example both sets of length compositions exhibit bi-modality, which would be difficult to capture with selectivity within the model. Additionally, the fits to the length composition data are greatly improved when compared with SEDAR 40 (2015). These improvements in fit were addressed through better index selection procedures, limiting the time frame of the data collections used, matching indices based on their respective length composition information, and matching the data with the best time of year in the model specifications. The bubble plots for the NAD and MAD index length compositions (Figure 137-Figure 138) show some patterning, as would be expected from the annual length composition plots. Chasing the fits to the length composition data would not improve the information being estimated in the stock assessment model on the overall trends in the population over time. The primary role of the length composition data was to inform selectivity for the indices.

## **7.2 Parameter Estimates**

### **7.2.1 Selectivities and Catchability**

Fishery removals were related to an overall level of fishing mortality and the selectivity (or availability) of Atlantic menhaden to the fishery. Model estimates of selectivity for the reduction and bait fisheries are shown graphically in Figure 139-Figure 142. Selectivity parameters were estimated for each fishery and time period as four-parameter, double-logistic models with the parameters being the ascending slope and  $A_{50}$  and the descending slope and

$A_{50}$  (Table 34). The application of fishery-specific dome-shaped selectivities is meant to account for varying degrees of availability of menhaden, given the heterogeneity in both the population and fishing effort. Some of these values have large SEs, but the uncertainties in selectivity were addressed using sensitivity analyses, likelihood profiling, and simulations.

Selectivity for the NAD index was estimated as a two-parameter logistic function as shown in Figure 143 and Table 34. Selectivity for the NAD index was used to fit the NAD length composition data and represents the ages of fish that were captured by the NAD index.

Selectivity for the MAD index was estimated as a four-parameter, double-logistic function as shown in Figure 144 and Table 34. Selectivity for the MAD index was used to fit the MAD length composition data and represents the ages of fish that were captured by the MAD index. Some of these values have large SDs, but the uncertainties in selectivity were addressed using sensitivity analyses, likelihood profiling, and simulations.

The base BAM model estimated a single, constant catchability parameter for the NAD, MAD, and SAD abundance indices, reflecting the assumption that expected catchability for these indices is believed to be constant through time. This is a good assumption for the NAD, MAD, and SAD fishery-independent indices since they are based on consistent, scientific survey collections, albeit the surveys are a mix of state surveys and do not target menhaden and because the indices used to create the NAD, MAD, and SAD were standardized to account for catchability differences. Log-catchability was estimated as -0.26 (0.77 back transformed) for the NAD index with a 0.30 SD; as -1.2 (0.29 back transformed) for the MAD index with a 0.26 SD; and as -2.9 (0.06 back transformed) for the SAD index with a 0.18 SD.

The base BAM model estimated two constant catchability parameters for the recruitment index and for the MARECO index. For the recruitment index, the two time blocks were as follows: 1959-1986 and 1987-2017. For the MARECO index, the two time blocks were as follows: 1981-1988 and 2000-2017. The time blocks represent a change in the combined spatial extent of the component seine surveys that comprise the recruitment index, with the addition of several state fishery-independent surveys after 1987. The time blocks for the MARECO index represent a change in the survey and survey gear. The recruitment index log-catchability was estimated as -3.7 (0.02 back transformed) for the first time period with a SD of 0.2, while the log-catchability of the second time period was -5.1 (0.006 back transformed) with a SD of 0.2. The MARECO index log-catchability was estimated as -13.8 ( $9 \times 10^{-7}$  back transformed) for the first time period with a SD of 0.4, while the log-catchability of the second time period was -15.1 ( $2 \times 10^{-7}$  back transformed) with a SD of 0.2.

### **7.2.2 Fishing Mortality Rates**

Highly variable fishing mortalities were noted throughout the entire time series and dependent upon the fishing. The highest fishing mortalities for the commercial reduction fishery in the north were in the 1950s, 1970s, and 1980s (Figure 145), while the highest fishing mortality rates for the commercial reduction fishery in the south were during the 1970s and 1980s (Figure 146). The highest fishing mortalities for the commercial bait fishery in the north were in the 1980s to the present (Figure 147), while the highest fishing mortality rates for the

commercial bait fishery in the south were during the 1960s to 1980s where the fishing mortality rate has been fairly constant and low (Figure 148).

Fishing mortality rate over time was reported as the geometric mean fishing mortality rate at ages-2 to -4 (Table 35; Figure 149). Geometric mean fishing mortality rate was highest in the 1970s and 1980s and has been declining since approximately 1990. In the most recent decade, the full fishing mortality rate has ranged between 0.12 and 0.22 for either age-2 or age-3 (Table 36; Figure 150). However, not all ages are fully selected, thus the fishing mortality rate on other ages can be much smaller. The estimate of fishing mortality rate for 2017 for age-2 is 0.09 and for age-3 is 0.16 (Table 36).

### **7.2.3 Abundance, Fecundity, Biomass, and Recruitment Estimates**

The base BAM model estimated population numbers-at-age (ages 0-6+) for 1955–2017 (Figure 151 and Table 37). From these estimates, along with growth and reproductive data, different estimates of reproductive capacity were computed. Population fecundity (i.e., Total Egg Production) was the measure of reproductive output used as that is what has been used in the past. Population fecundity (*FEC*, number of maturing ova) was highest in the early 1960s and from the 1990s to the present (Figure 152 and Table 38). The largest values of population fecundity were in 1955, 1961, and 2012. The time period 1955-2017 produced a median population fecundity of  $1.9 \times 10^{15}$  ova with a minimum of  $0.6 \times 10^{15}$  and a maximum of  $3.9 \times 10^{15}$  and an interquartile range of  $1.0 \times 10^{15}$  to  $2.4 \times 10^{15}$ . The estimate for population fecundity in 2017 was  $2.7 \times 10^{15}$ , which is above the 75<sup>th</sup> quantile. Throughout the time series, age-2 and age-3 fish have produced most of the total estimated number of eggs spawned annually (Table 38).

Biomass has fluctuated over time from an estimated high of over 6,794,000 mt in 1959 to a low of 1,379,000 mt in 1973 (Figure 153, Table 39). Biomass was estimated to have been largest during the late-1950s and late-2010s, with lows occurring during the 1960s, 1970s, and 1980s. From 1980 to the present, biomass is increasing in trend. Biomass is likely increasing at a faster rate than abundance because of the increase in the number of older fish at age and an increase in weight-at-age.

Age-0 recruits of Atlantic menhaden (Figure 154 and Table 40) were highest during the 1950s. An extremely large year class was also predicted for 1958. Recruitment has appeared to be rather stable during the late 1970s to the present. More recently, larger year-classes have also been estimated in 2010, 2015, and 2016. The log of  $R_0$  was estimated at 4.62 with a standard deviation of 0.12.

## **7.3 Sensitivity Analyses**

### **7.3.1 Sensitivity Analyses Model Runs**

The results of the sensitivity runs suggest that the base BAM model trends are fairly robust to model and data choices made by the SAS (Figure 155-Figure 182).

A suite of sensitivity runs were completed to compare with the last benchmark and update stock assessments, which were called continuity runs. Some of these continuity runs the natural

mortality from last assessment, the fecundity from the last assessment, and the robust multinomial for the composition likelihood components. The fishing mortality rate estimates were impacted by the natural mortality and the likelihood function. Specifically, the natural mortality impacted the overall scale, while the likelihood choice impacted the estimation of  $F$  during the 1950s. The scale of fecundity was impacted by both  $M$  and the new fecundity information used. Recruitment scale was impacted by the new fecundity information and the likelihood decision. Finally, the biomass was impacted by all of these runs to varying degrees. Collectively, these runs demonstrate changes in scale that would be expected, such as for the change in  $M$  and change in fecundity runs.

Several sensitivity analyses were done to look at the effects of exclusion of indices on the robustness of the model outcomes. In general, many of the runs provided very similar results to the base run. The run that was most different was the run with the NAD index excluded. Specifically, with the removal of the index that provided the only flat-topped selectivity, the model had a difficult time estimating the dome-shaped selectivity for the fishery fleets. Some of the other runs differed during the recent years of 1985-present, which was attributed to the years in which the indices influenced the assessment outcomes. The two runs with the largest difference were the run using only the NAD index and the run using only the MAD index. The expectation is that the indices will impact the overall trends and up and downs in the assessment as they inform population trajectory over time. These runs demonstrated which runs had the most influence and also demonstrated that this assessment is provided a lot of information from alternative data sources.

The next set of runs demonstrated the use of indices from the ecosystem reference point analyses (ERP Report, SEDAR 2019). The inclusion of the PRFC and RCPUE indices provided different outlooks on the historical nature of  $F$ , fecundity, recruitment, and biomass. In general, the run with the PRFC index included had the same scale and trends in recent years, but differed historically for all of the metrics of interest. For the runs that included RCPUE, the scale of the metrics of interest was different as was the trend. The RCPUE runs had  $F$  decreasing at a quicker rate and biomass increasing at a quicker rate. These runs were completed to provide a comparison to the ERP models such as the surplus production models, which needed the longest time series possible for the indices used.

Sensitivity runs were completed to evaluate model robustness to decisions related to ageing error, data configurations, catchability, and assumptions about the stock-recruitment curve. In general, the sensitivity analyses had little impact on the estimates of recruitment except for the runs that explored alternative stock-recruitment curves. Those runs had higher recruitment than the base run, which is to be expected given the structural assumption. The run with a Ricker stock-recruitment curve and the run with one catchability for the YOY index both showed decreased  $F$  values with increased fecundity and biomass. Alternatively, the run with ageing error and the run with two separate YOY indices both showed increased  $F$  values with decreased fecundity and biomass. The stock recruitment curve and catchability runs forced the model to scale up biomass and fecundity to account for fitting the assumption in the stock-recruitment curve and to account for the larger recruitment observations when using one index with no catchability changes over time.

Several runs were completed to examine the impacts of assumptions related to selectivity for the fishery. The runs that used age based selectivity estimates and the run that removed the time block for 2013-2017 showed very little difference from the base run results. The run with age based selectivity shows robustness to the type of functional form or strategy for estimating dome-shaped selectivity. The runs that did have an impact were those that 1) used logistic selectivity for the fishery for all time blocks and 2) the run that excluded all time blocks for selectivity and estimated a time-invariant value. These runs had opposite effects with the logistic selectivity run having higher  $F$  values and lower fecundity; while, the run with no time blocks had lower  $F$  values and higher fecundity. The run with logistic selectivity would have required a higher  $F$  value to harvest proportionately more younger fish than older fish as observed in the catch-at-age. The run with no time blocks did not allow the model to account for changes in the catch-at-age over time and therefore fit a selectivity vector that had a reduced fishing mortality likely to fit the largest sample size time periods.

Two sensitivity runs were completed to assess the information contained within the bait catch-at-age information given the sample sizes. Both runs were robust to this decision in the assessment and showed very little change when compared to the base run.

Finally, two runs were completed that used a start year of 1985. These runs examined quality of data during 1955-2017 versus 1985-2017, and allowed for a time- and age-varying matrix of  $M$  to be applied from the VADER model, a multi-species statistical catch-at-age model (ERP Report, SEDAR 2019). Both runs had slightly different scales from the base run, but the differences diminished over time; with the more recent five years being very similar. The run with the time-varying and age-varying  $M$  showed reduced variability in recruitment estimates during the 1990s and 2000s as compared to the other two runs, which likely demonstrates a tradeoff between  $M$  and recruitment estimation.

The sensitivity runs when compared to the MCB runs discussed below (Section 7.4) are generally similar, if not within the bounds of uncertainty explored for this assessment. The output distributions from the estimated parameters from the MCBs are fairly smooth distributions, albeit with two distinct modes, which suggests that these runs are simply the bounds on the uncertainty of the assessment given the assumptions and data inputs. Some of the sensitivity runs are likely scaled such that they are contained within the second smaller mode.

### **7.3.2 Retrospective Analyses**

The retrospective was run back to 2014 (Figure 183-Figure 186). The limited years of data removal were due to several base run assumptions and data that started in 2013 such as fishery selectivity time blocks and MAD length comps. The retrospective exhibits small changes in terminal years of 2016 and 2015 when compared to the base run for the metrics of interest. However, this pattern is not consistent for a terminal year of 2014 whereby the scale of the metrics of interest were substantially different than the base run. The SAS explored this further with additional runs.

To determine the cause of the change in scale for the terminal year of 2014 a set of retrospective runs was completed through the terminal year of 2011 (Figure 187-Figure 190).

For this set of runs, the selectivity time block was removed for 2013-2017 and the MAD selectivity was fixed with the length comps being removed from the likelihood computations. For this set of runs, the changes were relatively small and variable for all years except a terminal year of 2014, which behaves similarly to the first set of retrospective runs completed.

As a result, the SAS explored the reason for the scale change in 2014 by asking what data input are different such that the large-scale change occurred. Based on the exploration of data inputs, the data piece found to be causing the change in scale was the fishery age compositions for the northern region. A large age-4 age class was present in both the reduction and bait fisheries in the north. To explore the impacts, the age composition for that year (2014) was changed to be similar to surrounding years, and the retrospective analysis was rerun (Figure 191-Figure 194). With this change in the data inputs, the retrospective pattern for the terminal year of 2014 disappeared. Given this information, the SAS recommends that during future assessments the terminal year age compositions are considered to determine if a similar scale change could be occurring.

### **7.3.3 Likelihood profiling and simulation analyses**

Likelihood profiling was used as a supplemental analysis in support of decisions made by the SAS regarding the estimability of dome-shaped selectivity given the data contained in the model. The likelihood profiles included here are from previous iterations of the model during development of a base run.

Likelihood profiling demonstrated that the descending limb of the fishery selectivity curves were estimable and supported by the data contained within the model. Some of the oldest ages had smaller changes in the negative log-likelihood values. However, in the final base run, the panel decided to use a functional form for selectivity, thus this was not a concern.

Simulation analyses from the last stock assessment were also used in support of the decision to freely estimate dome-shaped selectivity (SEDAR 2015). Simulation analyses confirmed that data could be reproduced as ‘truth’ in an operating model and that the assessment model could provide the correct parameter estimates for selectivity.

### **7.4 Uncertainty Analysis**

Uncertainty was examined in the results in three distinct ways: 1) by considering each data source, in turn, in a series of sensitivity runs (Section 7.4.1), 2) by using a MCB procedure, and 3) by using an MCMC procedure.

The parametric bootstrap procedure (MCB) was run for 5,000 iterations. Model iterations that did not converge were not included in results. In addition, some iterations estimated parameter values that were outliers and were also excluded. In the end, about 2.7% of runs did not converge or were excluded for unrealistic parameter estimates. The MCB analysis provided uncertainty bounds that took into account uncertainty in natural mortality and fecundity and provided fairly wide bounds. The resulting estimates from the MCB runs have been summarized in Figure 195-Figure 198, showing the 95% confidence region. In general, the MCB results are not symmetrical distributions about the base run results because the uncertainty specifications were not symmetrical. Additional sets of MCB analyses were also run as specified in Section 6.4



above. These runs included additional uncertainty sources and had wider bounds than the base run configuration provided here.

The MCMC analysis generally had smaller uncertainty bounds around population parameters like average  $F$ , fecundity, recruitment, and age-1+ biomass than the MCB analysis (Figure 199- Figure 202), which was to be expected. The MCMC analysis did not account for uncertainty in fixed data inputs, while the MCB analysis did. The MCMC analysis had more uncertainty around estimated parameters like the selectivity curves (Figure 203 and Figure 204), but the uncertainty propagated through to the population scale for quantities like total biomass, fecundity, and recruitment was much smaller than (and generally within the bounds of) the uncertainty from the MCB analysis. The MCMC analysis was provided here for illustrative purposes with respect to the types of uncertainties that are accounted for and for comparison to the MCB analysis. The SAS considers the estimates of uncertainty from the MCMC analysis a minimum estimate of uncertainty on the population scale, and recommends that the MCMC analysis be a supplementary analysis, but not the analysis used for projections.

## 7.5 Projections

Two sets of projections were provided by the group for illustrative purposes. The SAS recognizes that the Board will likely ask for additional projections to be run in the future. The two examples provided here are 1) a projection at the current, *status quo* TAC of 216,000 mt and 2) a projection at the  $F_{TARGET}$  from the base run of the assessment. For the projections at the current TAC, there is little risk of exceeding the  $F_{THRESHOLD}$  and  $F_{TARGET}$  in the near term future (Figure 205-Figure 206). For the projections whereby the  $F_{TARGET}$  was attained with 50% probability, the associated TAC values were 321,900 mt in 2019, 263,900 mt in 2020, and 272,900 mt in 2021.

## 8 STOCK STATUS

For Atlantic menhaden, benchmarks have been discussed thoroughly by both the SAS and TC. Maximum sustainable yield (MSY) based benchmarks are not estimable for Atlantic menhaden, as the yield curve does not have a downward bend and the lack of a specified stock-recruitment curve. Spawning potential ratio (SPR) has also been considered historically; however, choosing an appropriate value of SPR that recognizes menhaden's forage role and its short life span does not have much precedent. The typical values chosen for SPR include 30, 35, and 40% and are meant for long-lived species, as an MSY proxy. Static SPR, meaning the value of SPR as calculated for each year, was provided to frame the discussion on SPR (Figure 207). These values range from around 50% in the 1970s to near 80% in the most recent years. Given the nature of the life history of menhaden and the lack of a stock-recruitment curve, the SAS and TC turned to using reference points based on historical performance. Given that menhaden have been fished for decades without a significant decline, the SAS and TC used a time period over which the stock was stable as an indicator of long-term performance of the fishery during changing predatory demands and a changing environment. In addition, the SAS and TC maintained the reference points currently in the FMP given the concurrent work that is being completed on ERPs.

## 8.1 Current Overfishing, Overfished/Depleted Definitions

The current overfishing definition is based on a threshold computed as the maximum geometric mean fishing mortality rate for ages-2 to -4 during 1960-2012 and the target is the median geometric mean fishing mortality rate for ages-2 to -4 during 1960-2012. The current fecundity-based overfished definitions are the threshold, which is the equilibrium fecundity associated with the  $F_{\text{THRESHOLD}}$ , and the target, which is the equilibrium fecundity associated with the  $F_{\text{TARGET}}$ . These reference points were intended to be interim reference points while ecological-based reference points (ERP) were developed (ERP Report, SEDAR 2019). The intent is to manage Atlantic menhaden at sustainable levels to support fisheries and meet predator demands by maintaining sufficient reproductive capacity to prevent stock depletion and protect against recruitment failure.

## 8.2 Stock Status Determination

### 8.2.1 Overfishing and Overfished Status

The current benchmarks are calculated using the full fishing mortality rate ( $F$ -based) and through spawner-per-recruit calculations (fecundity-based) using the mean values of any time-varying components (i.e., growth, maturity) over the time series 1955-2017. The base BAM model benchmark estimates and terminal year stock status are indicated in Table 41 and Figure 208 - Figure 209. Based on the current adopted benchmarks, the Atlantic menhaden stock status is not overfished and overfishing is not occurring (Table 41). Total fecundity was estimated at  $2.60 \times 10^{15}$  eggs in 2017, above the  $FEC_{\text{THRESHOLD}}$  of  $1.46 \times 10^{15}$  eggs. The geometric mean  $F$  on ages 2-4 was 0.11 in 2017, below both the  $F_{\text{THRESHOLD}}$  of 0.60. In addition, the current stock is below the current fishing mortality target ( $F=0.22$ ) and above the current  $FEC_{\text{TARGET}}$  ( $1.95 \times 10^{15}$  eggs) (Table 41).

### 8.2.2 Uncertainty

The MCB runs and sensitivity runs support the stock status determination given the current benchmarks, as does the MCMC supplemental analysis (Figure 210 - Figure 248). For each run for the uncertainty analyses, the benchmarks were calculated as described for the base run. The entire time series of estimates of fishing mortality over  $F_{\text{THRESHOLD}}$  and  $F_{\text{TARGET}}$  are shown, which include the 95% confidence intervals for the MCB runs (Figure 238 and Figure 239). The entire time series of estimates of fecundity over  $FEC_{\text{THRESHOLD}}$  and  $FEC_{\text{TARGET}}$  are shown, which also include the 95% confidence intervals for the MCB runs (Figure 240 and Figure 241). Similar time series of stock status are shown for the MCMC runs as well (Figure 243 - Figure 246). The uncertainty bounds on the stock status time series ( $F$  and fecundity relative to their targets and thresholds) was larger for the MCMC analysis than for the MCB analysis, although the MCB analysis had larger uncertainty around the reference point estimates themselves (Figure 247 and Figure 248). Phase plots of base run and each MCB run versus the threshold and target benchmarks were provided (Figure 242).

Each of the sensitivity runs, MCB analysis, and MCMC analysis each indicated the same stock status as the base run. The history of fishing mortality rates in these figures suggests that

overfishing is unlikely to be occurring at present. The history of fecundity over the time series suggests that the population was overfished as recently as 1990, but is not currently overfished.

The uncertainty in the terminal year stock status indicators were expressed using the results of the bootstrap runs of the base BAM model, sensitivity runs, and MCMC analysis. The results indicate that the fecundity estimates for the terminal year are generally above both the target and threshold. The results for the 2017 fishing mortality rate suggests that the base run estimate is above the target and threshold with none of the bootstrap runs below the threshold values in the terminal year.

### **8.2.3 Comparison of BAM and ERP Model Results and Management Advice**

The ERP WG explored several different models capable of producing ecological reference points for Atlantic menhaden, ranging from mechanistically very simple with minimal data inputs (time-varying  $r$  and Steele-Henderson surplus production models) to moderately complex (multispecies statistical catch-at-age and Ecopath with Ecosim, or EwE, models with only key finfish predators) to mechanistically very complex with intensive data needs (full EwE model). All of the ERP models explored here agreed with the single-species assessment model about the overall trend of Atlantic menhaden population size and exploitation rates over the last 30 years: a generally increasing trend in biomass and a decreasing trend in exploitation rate (Figure 249, Figure 250). This consistency in findings is not surprising, since all the ERP models used the same time-series of total removals, life history parameters, and indices of abundance as the single species model, and in some cases (the EwE models) used output from the single-species model directly.

The ERP models produced similar assessments of stock status to the single-species assessment results, which determined that Atlantic menhaden were not overfished and were not experiencing overfishing in 2017. Current levels of Atlantic menhaden removal were not projected to cause declines in predator biomass. However, the ERP models were also consistent in the finding that fishing Atlantic menhaden at the single-species threshold would cause declines in predator biomass, particularly for striped bass and piscivorous birds, which were the most sensitive species to higher levels of Atlantic menhaden harvest.

The ERP WG was charged with developing methods to determine reference points and total allowable catch for Atlantic menhaden that account for Atlantic menhaden's role as a forage fish (Term of Reference 4 for the ERP assessment). To this end, the ERP assessment recommended a combination of methods as a tool to help managers and stakeholders evaluate the tradeoffs between Atlantic menhaden harvest and predator biomass. The recommended approach used the BAM single-species assessment model to estimate Atlantic menhaden  $F$  rates and biomass, and an EwE model of intermediate complexity (i.e., one that only included key predator and prey species with good available data) to assess the long-term ecosystem effects of different levels of Atlantic menhaden fishing mortality.

There is no one right number for an ecological reference point or an ecosystem-based TAC; the final numbers chosen depend on the management objectives not just for Atlantic menhaden but for the entire ecosystem. For example, the level of fishing mortality on Atlantic menhaden that would be considered sustainable for striped bass depends on the biomass and fishing

mortality targets for striped bass: a higher biomass target for striped bass would require a lower level of Atlantic menhaden  $F$ , and a lower biomass target for striped bass would allow for a higher level of  $F$  on Atlantic menhaden (Figure 251).

The final values for ERPs and TACs will be a management decision. However, the ERP WG put forward example values of an ERP target and an ERP threshold based on existing management objectives for striped bass. The ERP target was defined as the maximum  $F$  on Atlantic menhaden that would sustain striped bass at their biomass target when striped bass were fished at their  $F_{\text{TARGET}}$ . The ERP threshold was defined as the maximum  $F$  on Atlantic menhaden that would keep striped bass at their biomass threshold when striped bass were fished at their  $F_{\text{THRESHOLD}}$ .

Striped bass was the focal species for this analysis, as it was one of the most sensitive species in the analysis to Atlantic menhaden  $F$ ; ERPs based on striped bass biomass should also sustain other species in the ecosystem that were less sensitive to levels of Atlantic menhaden removals.

The ERP target and threshold were lower than the current single-species target and threshold. The ERP target was estimated at a full  $F$  of 0.188, compared to a full  $F$  of 0.314 for the single-species target (equivalent to the geometric mean  $F$  of 0.22 on ages 2-4). The ERP threshold was estimated at a full  $F$  of 0.573, compared to a full  $F$  of 0.856 for the single-species threshold (equivalent to the geometric mean  $F$  of 0.60 on ages 2-4). The current estimate of full  $F$  from the BAM model is 0.157, below both the example ERP target and ERP threshold, indicating Atlantic menhaden are not experiencing overfishing even when their role as forage is taken into consideration.

The current single-species reference points are based on a period of stability for the fishery and the Atlantic menhaden population. Predation mortality is incorporated in the estimate of  $M$  used to parameterize the single-species model, but there is no consideration of the effects of Atlantic menhaden biomass on other species in the ecosystem when setting the single-species reference points. The ERP framework suggests that if managers want to achieve their current management objectives for striped bass, the  $F_{\text{TARGET}}$  and  $F_{\text{THRESHOLD}}$  for Atlantic menhaden should be 30-40% lower than the single-species estimates. However, because of the *ad hoc* buffering approach used by the Atlantic Menhaden Management Board to set the TAC in recent years, current removals of Atlantic menhaden are sustainable under the current management objectives of the key predator species.

## 9 RESEARCH RECOMMENDATIONS

Research recommendations are broken down into two categories: future research and data collection and assessment methodology. While all recommendations are high priority, the first recommendation is the highest priority. Each category is further broken down into recommendations that can be completed in the short term and recommendations that will require long term commitment. For the single-species assessment, the SAS recommends an update be considered in three years and a new benchmark be considered in six years.

## **9.1 Future Research and Data Collection**

### **9.1.1 Short Term**

1. Continue current level of sampling from bait fisheries, particularly in the Mid-Atlantic and New England. Analyze sampling adequacy of the reduction fishery and effectively sample areas outside of that fishery (e.g., work with industry and states to collect age structure data and biological data outside the range of the fishery).
2. Place observers on boats to collect at-sea samples from purse-seine sets, or collect samples at dockside during vessel pump-out operations (as opposed to current top of hold sampling) to address sampling adequacy.
3. Evaluate which proportion of bait landings by state are captured by gear versus which proportion are sampled for length and age composition to determine if current biosampling requirements are appropriate and adequate.
4. Continue to improve data validation processes for the bait fishery through ACCSP.
5. Conduct an ageing workshop to assess precision and error among readers with the intention of switching bait fishery age reading to state ageing labs.
6. Re-age historic old age samples (i.e., ages >7) to confirm the max age of Atlantic menhaden.
7. Investigate the relationship between fish size and school size to address selectivity (specifically addressing fisher behavior related to harvest of specific school sizes).
8. Investigate the relationship between fish size and distance from shore (addressing selectivity).

### **9.1.2 Long Term**

1. Develop and implement a menhaden-specific, multi-year coastwide fishery-independent index of adult abundance-at-age with ground-truthing for biological information (e.g., size and age composition). A sound statistical design is essential. Ideally, it should be done coast-wide, but area-specific surveys that cover the majority of the population and are more cost-effective could provide substantial improvements over the indices currently used in the assessment.
2. Continue age-specific studies on spatial and temporal dynamics of spawning (where, how often, how much of the year, batch spawning, etc.)
3. Conduct an ageing validation study, making sure to sample older age classes.
4. Continue to investigate environmental covariates related to productivity and recruitment on a temporal and spatial scale.
5. Consider other ageing methods for the future, such as the use of Fourier transform near infrared spectroscopy (FT-NIRS).

## **9.2 Assessment Methods**

### **9.2.1 Short Term**

1. Investigate index standardization to improve CVs and explore methods of combining indices at a regional or coastwide level.
2. Explore the covariance between life history parameters to improve the understanding of uncertainty in the model.
3. Explore the error structure between MCMC and MCB.
4. Perform simulation testing on the Deyle et al. method used in the projections and determine if recruitment is accurately tracked by the method and improve short term projections.
5. Conduct a Management Strategy Evaluation (MSE).

### **9.2.2 Long Term**

1. Continue to monitor model diagnostics given that the model is not robust to anomalous year-classes in the terminal year.
2. Develop a seasonal spatially-explicit model once sufficient age-specific data on movement rates of menhaden are available.

**10 MINORITY OPINION**

No minority opinion was submitted for this assessment.

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12 TABLES

**Table 1. Changes made to model inputs and configuration from SEDAR 40 (2015) to this assessment, SEDAR 69 (2019).**

Topic	SEDAR 40 (2015)	SEDAR 69 (2019)	Result of Change
Fecundity	Time-varying fecundity-at-age based on Lewis et al. (1987)	Time-varying fecundity-at-age based on R. Latour & J. Gartland (VIMS; 2019)	Higher estimated fecundity (SSB metric) overall
Natural Mortality	Lorenzen (1996) age-varying <i>M</i> scaled to historical tagging estimate of <i>M</i>	Lorenzen (1996) age-varying <i>M</i> scaled to Liljestrand et al. (2019a, 2019b)	Higher <i>M</i> -at-age compared to SEDAR 40 (2015)
Bait Landings	Compiled from the states	Queried by ACCSP and validated with individual state partners	Consistency in compiling bait landings over time
Bait Landing CVs	Used CVs of 0.15 for 1955-1984 and 0.05 for 1985-2013	Used CVs of 0.15 for 1955-1984, 0.10 for 1985-2012, and 0.05 for 2013-2017	Better accounted for the uncertainty in bait landings
Bait Catch-at-Age	Handled missing age data or low sample size (<50) in a region by pooling across years	Handled missing age data or low sample size (<30) in a region by using a multinomial model to predict age as a function of year, region, and fishery	Similar results but the SAS has higher confidence in the modeled method to develop the bait CAA
Abundance Indices	<ul style="list-style-type: none"> <li>▪Two adult fishery-independent indices based on nine state surveys, one each for the northern and southern regions</li> <li>▪Fishery-independent YOY based on state seine, trawl, and other gear surveys</li> </ul>	<ul style="list-style-type: none"> <li>▪Three adult fishery-independent indices based on eight state surveys grouped regionally (northern, Mid-Atlantic, and southern regions)</li> <li>▪One YOY index based on 16 state surveys</li> <li>▪Two spawning stock biomass indices based on two ichthyoplankton surveys</li> </ul>	Indices of abundance represent different regions, have slightly different trends, and higher CVs
Abundance Index Length Compositions	Both adult indices had associated length compositions	Length compositions were developed based on individual survey length compositions weighted by the standard deviation of the process error	Resulted in length compositions that better represented the data so that less informative data were down-weighted

**Table 1 Continued**

<b>Topic</b>	<b>SEDAR 40 (2015)</b>	<b>SEDAR 69 (2019)</b>	<b>Result of Change</b>
Likelihood for multinomial data	Used robust multinomial likelihood for composition data	Used Dirichlet multinomial for composition data	Improved weighting scheme for age and length compositions
Fishery Time Blocks	Used time blocks for the north and south reduction fisheries and no time blocks for the bait fishery	Maintained the time blocks used in SEDAR 40 (2015) but added a time block for 2013-2017 for the northern and southern reduction and northern bait fisheries	Addressed changes in the fishery due to Amendment 2 (2012)
Uncertainty Analysis	Used Monte Carlo Bootstrapping (MCB)	Used MCB and MCMC (did not include additional uncertainty in the data inputs)	Fuller view of the types of uncertainties and plausible range of uncertainty
Projections	Used variability in MCB to project forward	<ul style="list-style-type: none"> <li>▪Used MCBs to project forward</li> <li>▪Application of Deyle et al. (2018) for recruitment prediction</li> </ul>	Best available science being used to project recruitment



**Table 2. The von Bertalanffy parameters for each cohort year for the bias corrected growth curves from 1955-2015. The cohorts of 2016 and 2017 did not have enough ages to estimate growth.**

Year	$L_{\infty}$	$k$	$t_0$
1955	545	0.15	-1.13
1956	393	0.28	-0.68
1957	487	0.17	-1.37
1958	459	0.19	-0.85
1959	444	0.21	-1.3
1960	375	0.33	-0.63
1961	335	0.39	-0.74
1962	350	0.35	-0.88
1963	369	0.32	-0.95
1964	470	0.23	-1.01
1965	627	0.14	-1.17
1966	440	0.29	-0.76
1967	675	0.12	-1.5
1968	620	0.13	-1.5
1969	503	0.25	-0.84
1970	392	0.45	-0.36
1971	540	0.15	-1.36
1972	327	0.54	-0.11
1973	401	0.27	-0.72
1974	562	0.13	-1.29
1975	426	0.19	-0.95
1976	537	0.13	-1.06
1977	593	0.12	-1.05
1978	480	0.14	-1.34
1979	566	0.1	-1.47
1980	394	0.22	-0.84
1981	472	0.16	-1.1
1982	429	0.22	-0.7
1983	541	0.12	-1.31
1984	428	0.19	-0.98
1985	545	0.13	-1.15
1986	398	0.21	-0.92
1987	420	0.21	-0.76
1988	385	0.29	-0.59
1989	333	0.4	-0.56
1990	394	0.26	-0.79

Year	$L_{\infty}$	$k$	$t_0$
1991	461	0.2	-1.25
1992	627	0.13	-1.01
1993	417	0.27	-0.82
1994	405	0.35	-0.25
1995	415	0.34	-0.16
1996	456	0.23	-0.46
1997	396	0.3	-0.46
1998	426	0.24	-1.09
1999	393	0.41	-0.26
2000	326	0.62	0
2001	295	0.59	-0.47
2002	363	0.35	-0.63
2003	376	0.3	-0.83
2004	367	0.36	-0.25
2005	296	0.6	-0.19
2006	302	0.55	-0.38
2007	296	0.57	-0.43
2008	402	0.22	-1.46
2009	297	0.55	-0.5
2010	295	0.52	-0.63
2011	312	0.39	-1.33
2012	281	0.67	-0.45
2013	323	0.37	-0.9
2014	295	0.51	-0.62
2015	278	0.56	-0.72

**Table 3. Fork length (mm) at age on March 1 (beginning of fishing year) estimated from year class von Bertalanffy growth parameters with a bias correction. Shaded cells are the average from the three preceding years.**

Year	Age					
	1	2	3	4	5	6+
1955	155.1	226.3	263.8	280.2	298.5	320.7
1956	151.5	222.7	268.3	290.0	302.3	312.7
1957	147.3	207.3	268.6	296.8	308.6	316.8
1958	157.6	207.3	255.2	299.8	316.1	321.9
1959	138.7	207.7	252.7	296.3	321.1	329.2
1960	169.9	195.2	250.3	287.0	331.6	335.5
1961	156.4	221.8	241.8	286.3	312.9	361.8
1962	164.5	218.1	263.8	280.1	316.9	332.4
1963	169.1	219.5	262.3	297.9	311.7	342.8
1964	171.7	222.7	256.6	294.0	325.5	337.7
1965	171.0	225.8	260.3	281.8	316.8	347.9
1966	162.1	231.2	265.0	286.8	298.9	333.1
1967	175.4	222.0	279.3	293.4	305.4	310.4
1968	168.7	241.8	274.3	317.7	314.1	318.5
1969	174.3	223.7	291.6	319.8	348.3	329.0
1970	184.5	229.5	272.8	328.8	359.5	372.8
1971	179.4	254.5	277.8	316.5	356.8	394.0
1972	161.6	256.5	309.1	320.1	355.5	377.7
1973	147.3	214.6	305.7	351.8	357.2	390.2
1974	149.9	222.3	260.2	337.1	385.1	389.8
1975	141.0	209.8	266.1	299.4	357.0	411.0
1976	132.1	190.9	255.4	291.5	333.1	369.8
1977	127.7	183.1	234.9	290.2	306.4	362.1
1978	129.1	178.4	225.2	273.6	316.7	315.1
1979	134.4	181.5	222.8	260.0	307.8	336.9
1980	128.2	179.6	228.1	261.7	288.8	337.9
1981	131.0	171.4	218.9	269.3	295.8	312.6
1982	136.4	182.9	210.3	253.1	305.9	325.7
1983	132.1	186.6	224.5	245.4	282.8	338.4
1984	134.6	190.0	229.4	257.9	277.0	308.6
1985	131.4	182.0	236.6	265.7	284.7	305.5
1986	129.3	181.5	223.9	274.2	296.7	306.2
1987	133.8	178.5	223.1	260.9	304.4	323.0
1988	130.1	184.7	221.9	257.7	293.6	328.7
1989	140.4	185.0	225.7	260.1	286.4	322.5
1990	154.9	200.9	229.6	258.9	293.8	310.3

**Table 3 Continued**

Year	Age					
	1	2	3	4	5	6+
1991	147.9	213.8	246.5	265.7	285.6	323.5
1992	163.6	204.7	253.2	280.7	294.9	307.2
1993	143.2	216.4	248.4	279.6	306.5	318.7
1994	162.2	201.7	259.8	282.0	297.2	325.9
1995	142.8	222.6	253.2	295.5	307.8	309.0
1996	134.3	219.7	268.7	298.4	324.9	327.6
1997	131.9	214.7	274.1	303.9	338.2	349.1
1998	141.7	199.5	272.1	312.6	330.7	373.1
1999	169.9	208.2	252.9	313.0	339.7	351.2
2000	158.2	225.2	257.4	295.2	342.2	358.9
2001	150.1	237.0	268.6	293.7	328.6	363.1
2002	170.9	231.1	289.3	302.6	320.5	355.1
2003	156.7	226.2	274.7	324.0	329.3	340.3
2004	158.1	217.0	256.9	298.2	347.1	350.2
2005	134.0	214.3	259.7	273.9	310.9	362.3
2006	151.6	204.8	256.1	289.9	283.4	317.7
2007	160.5	216.9	254.2	287.1	311.3	288.6
2008	164.8	220.3	252.6	288.5	310.1	326.4
2009	165.5	221.9	254.8	272.3	312.4	327.1
2010	166.1	211.3	254.2	274.8	283.0	329.1
2011	168.5	221.1	248.3	272.5	286.4	288.9
2012	186.6	219.8	253.0	278.1	282.8	293.0
2013	174.5	227.1	250.3	271.4	302.2	288.7
2014	163.1	226.7	254.5	268.4	282.2	321.6
2015	166.6	212.5	253.4	273.0	279.1	288.4
2016	172.0	218.3	246.6	267.0	285.6	285.5
2017	167.3	217.6	249.2	270.1	274.0	294.0

**Table 4. Weight (g) at age on September 1 (middle of fishing year) estimated from overall weight-length parameters and annual lengths at age.**

Year	Age						
	0.5	1	2	3	4	5	6+
1955	38.5	132.7	294.0	418.9	484.9	562.5	656.9
1956	26.5	111.2	283.4	454.9	529.6	594.3	640.1
1957	45.3	98.8	244.8	432.9	575.4	618.6	669.6
1958	25.1	115.8	239.0	388.7	559.1	657.0	687.2
1959	65.9	81.4	242.8	386.7	521.1	656.7	709.4
1960	37.0	139.1	199.8	382.7	515.5	632.3	728.5
1961	54.2	125.0	268.4	345.6	516.4	617.1	720.9
1962	60.3	134.6	280.0	417.8	497.0	633.8	692.8
1963	65.0	148.2	261.3	429.2	571.9	639.7	731.8
1964	66.9	150.0	280.6	379.6	549.4	720.1	766.2
1965	55.4	151.2	284.3	397.8	475.4	637.6	856.1
1966	68.9	127.2	295.0	413.9	488.0	547.2	699.1
1967	66.9	166.6	264.3	449.7	523.5	552.3	598.6
1968	76.6	131.2	324.2	434.0	596.3	609.6	596.3
1969	79.4	145.6	256.4	477.3	619.9	725.3	674.1
1970	58.4	186.9	272.5	426.0	607.0	808.5	833.4
1971	50.8	176.1	363.1	433.7	636.2	708.6	990.4
1972	26.0	131.9	358.2	539.8	621.2	881.4	784.6
1973	42.4	124.0	277.8	512.7	694.9	826.7	1155.3
1974	30.0	109.3	280.2	437.0	624.0	820.9	1042.3
1975	28.4	88.5	225.0	397.8	587.1	697.8	918.6
1976	18.9	70.7	195.9	345.5	470.1	717.3	744.6
1977	22.2	67.4	152.7	310.6	454.2	510.7	824.5
1978	30.3	71.4	165.5	252.9	414.8	544.3	532.5
1979	26.5	71.1	169.8	276.4	359.9	501.3	615.4
1980	23.1	58.5	148.5	283.4	380.5	465.2	569.2
1981	21.7	72.4	123.5	242.5	393.9	468.9	563.3
1982	26.1	75.5	167.6	212.7	343.1	491.6	539.7
1983	32.1	73.4	180.5	273.8	322.3	442.8	573.0
1984	24.9	71.1	166.0	294.8	373.9	448.0	536.4
1985	23.0	70.9	146.0	275.9	398.5	459.8	584.9
1986	26.7	69.2	158.1	241.0	387.6	483.8	529.5
1987	27.1	77.3	157.7	256.5	348.2	491.5	550.0
1988	28.6	72.4	169.0	256.6	351.7	460.8	582.8
1989	43.2	97.9	158.7	265.6	350.4	435.8	573.1
1990	39.4	120.6	218.6	259.0	352.3	431.5	506.0

**Table 4 Continued**

Year	Age						
	0.5	1	2	3	4	5	6+
1991	55.1	98.7	240.2	332.8	359.9	423.5	497.8
1992	31.6	134.9	203.0	344.6	422.9	452.9	479.0
1993	53.6	100.1	260.3	314.7	422.4	487.9	534.1
1994	26.4	129.1	230.0	377.9	418.7	476.0	532.3
1995	24.7	124.7	255.9	370.8	473.7	508.0	511.3
1996	19.0	103.5	301.9	386.2	499.4	546.0	580.7
1997	31.1	92.8	256.0	458.8	502.9	606.4	598.1
1998	64.1	99.5	238.9	409.4	571.3	599.7	690.6
1999	42.3	141.6	231.0	382.8	535.5	644.5	676.1
2000	29.5	143.2	275.2	376.2	497.1	629.2	689.7
2001	58.1	134.6	307.1	421.8	511.1	578.8	695.0
2002	39.7	153.4	304.7	449.2	564.4	625.1	633.9
2003	50.5	122.9	276.8	437.2	552.3	693.0	716.2
2004	26.0	120.2	254.9	364.5	521.5	620.8	803.7
2005	37.0	92.7	235.8	369.7	418.4	570.5	664.3
2006	45.7	120.1	209.6	352.7	454.0	449.3	597.8
2007	56.4	136.3	245.3	319.3	456.1	510.9	466.5
2008	62.7	141.7	265.9	345.7	404.8	540.8	547.6
2009	56.3	123.6	258.6	366.0	413.4	465.6	606.8
2010	60.4	140.3	226.4	349.4	431.6	455.5	506.6
2011	97.1	141.1	253.7	341.4	410.7	471.5	480.6
2012	71.0	168.2	251.6	340.5	457.2	449.2	494.8
2013	56.7	162.5	266.4	339.7	398.1	566.5	472.4
2014	58.3	124.4	268.7	355.0	401.1	433.8	665.2
2015	71.5	138.1	230.0	338.0	427.9	441.1	455.2
2016	61.9	145.6	247.6	332.0	377.7	484.8	466.2
2017	61.9	135.8	231.1	334.7	418.9	399.3	527.7

**Table 5. Atlantic menhaden maturity by year and age based on annual estimates of mean size-at-age and maturity as a function of size.**

Year	Age						
	0	1	2	3	4	5	6+
1955	0	0.1	0.7	0.9	1	1	1
1956	0	0.1	0.7	0.9	1	1	1
1957	0	0.1	0.5	0.9	1	1	1
1958	0	0.1	0.5	0.9	1	1	1
1959	0	0	0.5	0.9	1	1	1
1960	0	0.1	0.3	0.9	1	1	1
1961	0	0.1	0.7	0.8	1	1	1
1962	0	0.1	0.6	0.9	1	1	1
1963	0	0.1	0.6	0.9	1	1	1
1964	0	0.1	0.7	0.9	1	1	1
1965	0	0.1	0.7	0.9	1	1	1
1966	0	0.1	0.7	0.9	1	1	1
1967	0	0.2	0.7	1	1	1	1
1968	0	0.1	0.8	1	1	1	1
1969	0	0.2	0.7	1	1	1	1
1970	0	0.2	0.7	1	1	1	1
1971	0	0.2	0.9	1	1	1	1
1972	0	0.1	0.9	1	1	1	1
1973	0	0.1	0.6	1	1	1	1
1974	0	0.1	0.7	0.9	1	1	1
1975	0	0	0.5	0.9	1	1	1
1976	0	0	0.3	0.9	1	1	1
1977	0	0	0.2	0.8	1	1	1
1978	0	0	0.2	0.7	1	1	1
1979	0	0	0.2	0.7	0.9	1	1
1980	0	0	0.2	0.7	0.9	1	1
1981	0	0	0.1	0.6	0.9	1	1
1982	0	0	0.2	0.5	0.9	1	1
1983	0	0	0.3	0.7	0.9	1	1
1984	0	0	0.3	0.7	0.9	1	1
1985	0	0	0.2	0.8	0.9	1	1
1986	0	0	0.2	0.7	1	1	1
1987	0	0	0.2	0.7	0.9	1	1
1988	0	0	0.2	0.7	0.9	1	1
1989	0	0	0.2	0.7	0.9	1	1
1990	0	0.1	0.4	0.7	0.9	1	1

**Table 5 Continued**

Year	Age						
	0	1	2	3	4	5	6+
1991	0	0.1	0.6	0.9	0.9	1	1
1992	0	0.1	0.5	0.9	1	1	1
1993	0	0	0.6	0.9	1	1	1
1994	0	0.1	0.4	0.9	1	1	1
1995	0	0	0.7	0.9	1	1	1
1996	0	0	0.6	0.9	1	1	1
1997	0	0	0.6	1	1	1	1
1998	0	0	0.4	1	1	1	1
1999	0	0.1	0.5	0.9	1	1	1
2000	0	0.1	0.7	0.9	1	1	1
2001	0	0.1	0.8	0.9	1	1	1
2002	0	0.1	0.7	1	1	1	1
2003	0	0.1	0.7	1	1	1	1
2004	0	0.1	0.6	0.9	1	1	1
2005	0	0	0.6	0.9	1	1	1
2006	0	0.1	0.5	0.9	1	1	1
2007	0	0.1	0.6	0.9	1	1	1
2008	0	0.1	0.6	0.9	1	1	1
2009	0	0.1	0.7	0.9	1	1	1
2010	0	0.1	0.5	0.9	1	1	1
2011	0	0.1	0.6	0.9	1	1	1
2012	0	0.3	0.6	0.9	1	1	1
2013	0	0.2	0.7	0.9	1	1	1
2014	0	0.1	0.7	0.9	0.9	1	1
2015	0	0.1	0.5	0.9	1	1	1
2016	0	0.1	0.6	0.9	0.9	1	1
2017	0	0.1	0.6	0.9	0.9	1	1

**Table 6. Estimates of age-specific annual fecundity for age-1 to age-6 Atlantic menhaden in 2015 using the fecundity-at-length relationship used in past stock assessments (Lewis et al. 1987) and estimates derived from an analysis from Latour & Gartland (VIMS). Mean, minimum (min.), and maximum (max.) estimates of annual fecundity were derived using mean spawning frequency ( $SF_{\bar{x}}$ ), spawning frequency based on the post ovulatory follicle method ( $SF_{POF}$ ), and spawning frequency based on the oocyte maturation method ( $SF_{OM}$ ). The percent change quantifies the change in estimates of age-specific annual fecundity between Lewis et al. (1987) and this investigation where  $SF_{\bar{x}}$  was used to represent spawning frequency.**

Age	Annual Fecundity			Percent Change	
	Lewis et al. 1987	Latour & Gartland Mean	Latour & Gartland Min.		Latour & Gartland Max.
1	3,770	27,350	21,076	39,086	+625%
2	37,765	270,490	208,437	386,555	+616%
3	98,782	771,287	594,344	1,102,240	+681%
4	137,741	1,044,859	805,156	1,493,198	+659%
5	173,022	1,132,786	872,911	1,618,854	+555%
6+	180,394	1,271,904	980,114	1,817,666	+605%



**Table 7. Constant  $M$  from life history approaches, using  $K$  &  $L_{\infty}$  bias-corrected averaged across annual values, either full period of 1955-2015 (full) or recent period of 2011-2015 (recent). Equations were updated using Then et al. (2014).**

<b>Parameters</b>		
$t_{max} = 10$ years		
$K = 0.5$ (recent); $K = 0.301$ (full)		
$L_{\infty} = 29.8$ cm (recent); $L_{\infty} = 42.2$ cm (full)		
<b>Method</b>	<b>Equations</b>	<b><math>M</math> Estimate</b>
Hoenig <sub>nls</sub>	$4.899t_{max}^{-0.916}$	0.59
Pauly <sub>nls-T</sub>	$4.118K^{0.73}L_{\infty}^{-0.33}$	0.80 (recent); 0.49 (full)
"Rule of thumb"	$5.109/t_{max}$	0.51
One parameter $K$	$1.692K$	0.85 (recent); 0.51 (full)

**Table 8. Summaries of various age-specific estimates of  $M$  including those as inverse function of size-at-age.**

Age	Petersen & Wroblewski 1984	Boudreau & Dickie 1989	Lorenzen 1996	Charnov et al. 2013	Lorenzen 1996 Scaled (SEDAR 40)	Lorenzen 1996 Scaled (SEDAR 69)
0	1.13	1.10	1.18	1.41	1.12	1.76
1	0.89	0.79	0.88	0.84	0.82	1.31
2	0.73	0.62	0.70	0.57	0.65	1.03
3	0.65	0.53	0.60	0.45	0.57	0.90
4	0.60	0.48	0.55	0.38	0.52	0.81
5	0.57	0.44	0.51	0.34	0.50	0.76
6	0.54	0.42	0.49	0.31	0.48	0.72

**Table 9. Natural mortality estimates by year and age from the multispecies statistical catch-at-age model developed for the ERP assessment.**

Year	Age						
	0	1	2	3	4	5	6+
1985	1.71	1.39	1.13	0.92	0.80	0.73	0.67
1986	1.73	1.37	1.09	0.91	0.76	0.69	0.65
1987	1.76	1.39	1.09	0.90	0.77	0.68	0.63
1988	1.72	1.32	1.02	0.85	0.73	0.66	0.61
1989	1.79	1.35	1.01	0.84	0.73	0.67	0.61
1990	1.76	1.30	0.98	0.83	0.73	0.66	0.62
1991	1.71	1.29	0.92	0.78	0.69	0.64	0.60
1992	1.78	1.27	0.95	0.79	0.69	0.65	0.61
1993	1.75	1.34	0.93	0.79	0.69	0.64	0.60
1994	1.95	1.35	1.00	0.80	0.71	0.66	0.61
1995	2.08	1.47	0.98	0.83	0.71	0.66	0.63
1996	2.06	1.58	1.03	0.83	0.72	0.66	0.62
1997	2.06	1.59	1.03	0.81	0.71	0.65	0.61
1998	1.87	1.48	1.00	0.78	0.68	0.63	0.59
1999	2.18	1.40	1.03	0.83	0.70	0.64	0.60
2000	2.26	1.58	1.06	0.87	0.74	0.66	0.62
2001	1.97	1.54	1.00	0.83	0.73	0.66	0.61
2002	1.88	1.38	0.99	0.79	0.71	0.66	0.61
2003	1.82	1.36	0.96	0.79	0.68	0.64	0.60
2004	2.04	1.48	1.04	0.85	0.72	0.64	0.61
2005	1.92	1.54	1.06	0.85	0.76	0.68	0.61
2006	1.84	1.39	1.01	0.81	0.70	0.67	0.61
2007	1.90	1.42	1.01	0.83	0.72	0.66	0.65
2008	1.79	1.35	0.97	0.82	0.71	0.65	0.61
2009	1.82	1.36	0.98	0.82	0.73	0.66	0.61
2010	1.71	1.29	0.97	0.80	0.71	0.67	0.61
2011	1.67	1.29	0.96	0.82	0.72	0.67	0.63
2012	1.72	1.26	0.97	0.82	0.72	0.68	0.64
2013	1.66	1.24	0.94	0.81	0.72	0.65	0.63
2014	1.69	1.25	0.92	0.79	0.71	0.66	0.61
2015	1.62	1.22	0.92	0.78	0.69	0.65	0.61
2016	1.63	1.20	0.92	0.79	0.70	0.65	0.62
2017	1.76	1.29	0.96	0.81	0.72	0.67	0.63

**Table 10. Information associated with age 1+ Atlantic menhaden surveys. For some surveys, data from some months were excluded due to very low frequency of nonzero CPUE.**

<b>Survey</b>	<b>Region</b>	<b>Years</b>	<b>Months Included</b>	<b>#obs</b>
CT LISTS	Long Island Sound	1996 – 1998, 2000 - 2017	5,6,9,10	3,004
NJ OT	New Jersey coast	1988 - 2017	1,4,8,10	3,826
DE Adult	Delaware Bay	1990 - 2017	3 - 12	1,386
MD GN	Upper Ches. Bay	1986 - 2017	3,4,5	1,118
NC p915	NC estuaries	2001 - 2017	2 - 12	10,542
GA EMTS	GA estuaries	2003 - 2017	1 - 12	6,900
SEAMAP	SE coast	1990 - 2017	4,5,7	4,869

**Table 11. Years of activity for individual Atlantic menhaden reduction plants along the U.S. Atlantic coast, 1955-2017.**

Year	Plant #																																				Total Plants	# of Vessels															
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	32	33	34	35	36																		
1955	+	+	+	+	+	+		+		+	+	+	+		+	+	+	+	+	+	+	+	+	+	+	+												23	150														
1956	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+													24	149													
1957	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+												25	144													
1958	+	+	+	+	+			+	+	+	+	+	+	+	+	+	+	+		+	+		+	+	+	+													22	130													
1959	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+		+	+		+	+	+	+													23	144													
1960	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+		+			+		+															20	115												
1961	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+		+			+		+															20	117												
1962	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+		+			+		+															19	112												
1963	+	+	+	+	+			+	+	+	+	+	+	+	+	+	+	+		+			+		+																17	112											
1964	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+		+			+		+																18	111											
1965	+	+		+	+			+		+	+	+	+	+		+	+	+		+	+																				17	84											
1966	+	+		+	+		+	+	+	+	+	+	+	+	+	+	+	+		+	+																					20	76										
1967		+		+			+	+	+	+	+	+	+	+	+	+	+	+		+	+																						18	64									
1968	+	+		+			+			+	+	+	+	+	+	+	+	+		+	+																						17	59									
1969	+	+		+			+			+		+	+	+	+	+	+	+		+																								15	51								
1970		+					+			+		+	+	+	+	+	+	+		+			+		+																			15	54								
1971		+					+			+		+	+	+	+	+	+	+		+			+		+		+																		14	51							
1972		+					+			+		+	+			+		+		+			+		+		+																			11	51						
1973		+					+			+		+	+			+		+		+			+		+		+																				11	58					
1974		+					+			+		+	+			+		+		+			+		+		+																					10	63				
1975		+					+			+		+	+			+		+		+			+		+		+																					12	61				
1976		+					+			+		+	+			+		+		+			+		+		+																					11	62				
1977		+					+			+		+	+			+		+		+			+		+		+																					12	64				
1978		+					+			+		+	+			+		+		+			+		+		+																						12	53			
1979		+					+			+		+	+			+		+		+			+		+		+																						12	54			
1980		+					+			+		+	+			+		+		+			+		+		+																						11	51			
1981		+					+			+		+	+			+		+		+			+		+		+																							11	57		
1982							+			+		+	+			+		+		+			+		+		+																							10	47		
1983							+			+		+	+			+		+		+			+		+		+																								9	41	
1984							+			+		+	+			+		+		+			+		+		+																								8	38	
1985							+			+		+				+		+		+			+		+		+																								6	24	
1986							+			+		+				+		+		+			+		+		+																								6	16	
1987							+			+		+				+		+		+			+		+		+																								6	23	
1988							+			+		+				+		+		+			+		+		+																									6	30
1989							+			+		+				+		+		+			+		+		+																									5	37
1990							+			+		+				+		+		+			+		+		+																									5	35

Table 11 Continued

Year	Plant #																																				Total Plants	# of Vessels					
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	32	33	34	35	36								
1991							+			+			+																							+	+				5	37	
1992							+			+			+																								+	+	+	+	+	8	37
1993							+			+			+																							+	+		+	+	7	31	
1994							+			+			+																												3	20	
1995							+			+			+																												3	20	
1996							+			+			+																												3	21	
1997							+			+			+																												3	23	
1998										+			+																												2	15	
1999										+			+																												2	15	
2000										+			+																												2	12	
2001										+			+																												2	12	
2002										+			+																												2	12	
2003										+			+																												2	12	
2004										+			+																												2	13	
2005										+																															1	11	
2006										+																															1	11	
2007										+																															1	10	
2008										+																															1	10	
2009										+																															1	10	
2010										+																															1	11	
2011										+																															1	10	
2012										+																															1	9	
2013										+																															1	7	
2014										+																															1	7	
2015										+																															1	7	
2016										+																															1	7	
2017										+																															1	7	

**Table 12. List of plants and their associated numbers, port numbers, and plant locations for plants participating in the reduction fishery, 1955–2017.**

Port	Plant	Name	Location
3	1	Atlantic Processing Company	Amagansett, NY
4	2	J. Howard Smith, Inc.	Port Monmouth, NJ
-	3	Fish Products Co.	Tuckerton, NJ
8	4	New Jersey Menhaden Products Co.	Wildwood, NJ
0	5	Fish Products Co.	Lewes, DE
0	6	Consolidated Fisheries	Lewes, DE
5	7	Standard Products, Co.	Reedville, VA
5	8	McNeal-Edwards (Standard Prodcuts Co.)	Reedville, VA
5	9	Menhaden Co. (Standard Products Co.)	Reedville, VA
5	10	Virginia Menhaden Products (Reedville Oil and Guano Co.)	Reedville, VA
5	11	Standard Products, Co.	White Stone, VA
6	12	Fish Meal Co.	Beaufort, NC
6	13	Beaufort Fisheries, Inc	Beaufort, NC
6	14	Standard Products, Co.	Beaufort, NC
6	15	Standard Products, Co.	Morehead City, NC
6	16	North Carolina Menhaden Products	Morehead City, NC
7	17	Standard Products, Co.	Southport, NC
7	18	North Carolina Menhaden Products	Morehead City, NC
9	19	Quinn Menhaden Fisheries, Inc.	Fernandina Beach, FL
9	20	Nassau Oil and Fertilizer Co.	Fernandina Beach, FL
9	21	Mayport Fisheries	Mayport, FL
1	22	Maine Marine Products Co. (Pine State Products)	Portland, ME
2	23	Lipman Marine Prodcuts Co. (Gloucester Marine Protein)	Gloucester, MA
2	24	Gloucester Dehy, Co	Gloucester, MA
11	25	Point Judith Byproducts Co.	Point Judith, RI
10	26	Quinn Fisheries	Yonges Island, SC
5	27	Cockerall's Ice and Seafood	Reedville, VA
6	28	Seashore Packing Co	Beaufort, NC
12	29	Cape Charles Procesing Co.	Cape Charles, VA
13	30	SeaPro, Inc	Rockland, ME
15	32	Connor Brothers	New Brunswick, Canada
14	33	Riga (IWP)	Maine
14	34	Vares (IWP)	Maine
14	35	Dauriya (IWP)	Maine
15	36	Comeau	Nova Scotia, Canada

**Table 13. Total Atlantic menhaden landings and effort (vessel-weeks) for 1940-2017.**

Year	Reduction Fishery		Year	Reduction Fishery	
	Landings (1,000 mt)	Effort (v-w)		Landings (1,000 mt)	Effort (v-w)
1940	236.4	967	1979	388.8	1198
1941	296.6	1291	1980	427.6	1158
1942	185.9	991	1981	404.2	1133
1943	255.9	889	1982	402.7	948
1944	276.6	1167	1983	438.3	995
1945	314.6	1271	1984	341.0	892
1946	381.1	1365	1985	334.6	577
1947	397.0	1582	1986	261.0	377
1948	365.2	1781	1987	353.9	531
1949	382.5	2076	1988	354.6	604
1950	308.5	1650	1989	354.4	725
1951	381.8	1686	1990	430.7	826
1952	424.1	1653	1991	412.8	926
1953	619.0	1972	1992	335.0	794
1954	627.4	2094	1993	353.1	626
1955	659.1	2748	1994	296.1	573
1956	738.5	2878	1995	381.2	600
1957	630.3	2775	1996	328.5	528
1958	527.1	2343	1997	299.4	616
1959	682.8	2847	1998	285.1	437
1960	551.7	2097	1999	206.7	382
1961	603.7	2371	2000	201.5	311
1962	567.2	2351	2001	270.1	334
1963	372.8	2331	2002	212.1	318
1964	290.6	1807	2003	200.5	302
1965	298.2	1805	2004	215.3	345
1966	234.4	1386	2005	192.3	291
1967	206.0	1316	2006	186.8	322
1968	245.3	1209	2007	218.2	333
1969	172.9	995	2008	189.9	262
1970	281.0	906	2009	184.2	300
1971	263.8	897	2010	226.8	356
1972	376.2	973	2011	227.8	324
1973	361.7	1099	2012	226.5	279
1974	306.7	1145	2013	169.0	196
1975	271.9	1218	2014	174.1	201
1976	360.2	1163	2015	190.6	182
1977	364.3	1239	2016	187.3	213
1978	369.9	1210	2017	175.0	185



**Table 14. Sample size (n), landings in numbers of fish, landings in biomass (C), sampling 'intensity' (landings in metric tons per 100 fish measured), and mean weight of fish landed from the Atlantic menhaden reduction fishery, 1955-2017.**

Year	Sample Size (n)	Landings		Intensity (C/100n)	Mean Weight (g)
		(millions)	(1000 mt)		
1955	16,150	3,118.44	644.5	3,990.71	205.7
1956	19,881	3,564.82	715.2	3,597.40	199.8
1957	19,714	3,511.67	605.6	3,071.93	171.7
1958	15,785	2,719.21	512.4	3,246.12	187.6
1959	17,960	5,353.64	662.2	3,687.08	123.1
1960	13,513	2,775.11	532.2	3,938.43	190.9
1961	13,217	2,598.31	578.6	4,377.70	221.6
1962	15,795	2,099.86	540.7	3,423.24	256.1
1963	13,035	1,764.51	348.4	2,672.80	196.6
1964	10,443	1,729.06	270.4	2,589.29	155.7
1965	19,581	1,499.71	274.6	1,402.38	179.9
1966	15,707	1,340.61	220.7	1,405.11	163.8
1967	15,488	984.18	194.4	1,255.17	196.6
1968	26,869	1,143.80	235.9	877.96345	204.5
1969	15,132	868.16	162.3	1,072.56	186.1
1970	8,461	1,400.46	259.4	3,065.83	184.9
1971	8,270	969.098	250.3	3,026.60	258.3
1972	6,559	1,713.95	365.9	5,578.59	213.5
1973	6,369	1,843.36	346.9	5,446.69	188.2
1974	5,610	1,990.63	292.2	5,208.56	146.8
1975	7,300	2,162.30	250.2	3,427.40	115.7
1976	6,730	3,283.47	340.5	5,059.44	103.7
1977	7,280	3,673.71	341.2	4,686.81	92.8
1978	7,111	3,085.20	344.1	4,838.98	111.5
1979	6,368	3,870.13	375.7	5,899.81	97.1
1980	7,292	3,332.32	401.5	5,506.03	120.5
1981	9,220	3,984.02	381.3	4,135.57	95.7
1982	9,070	3,175.72	382.5	4,217.20	120.4
1983	5,180	3,942.11	418.6	8,081.08	106.2
1984	11,690	3,548.04	326.3	2,791.27	92
1985	7,720	3,025.29	306.7	3,972.80	101.4
1986	5,410	1,912.41	238	4,399.26	124.5
1987	7,400	2,315.18	326.9	4,417.57	141.2
1988	7,358	2,157.97	309.3	4,203.59	143.3

**Table 14 Continued**

Year	Sample Size (n)	Landings		Intensity (C/100n)	Mean Weight (g)
		(millions)	(1000 mt)		
1989	6,890	2630.51	322	4,673.44	122.4
1990	6,840	2,157.91	401.1	5,864.04	185.9
1991	7,690	3,166.58	381.4	4,959.69	120.4
1992	5,610	2,052.46	297.6	5,304.81	145
1993	5,320	1,593.99	320.6	6,026.32	201.1
1994	4,710	1,492.05	260	5,520.17	174.3
1995	4,610	1,643.29	339.9	7,373.10	206.8
1996	4,220	1,091.93	292.9	6,940.76	268.2
1997	4,100	995.869	259.1	6,319.51	260.2
1998	3,840	1,007.45	245.9	6,403.65	244.1
1999	3,620	1,056.25	171.2	4,729.28	162.1
2000	3,040	657.417	167.3	5,503.29	254.3
2001	3,920	669.189	233.6	5,959.18	349.2
2002	3,600	803.057	174.1	4,836.11	216.7
2003	3,490	698.289	166.1	4,759.31	237.9
2004	4,170	978.022	178.5	4,280.58	187.5
2005	3,530	648.535	152.9	4,331.44	226.4
2006	3,570	753.951	157.4	4,408.96	208.8
2007	3,790	932.65	174.5	4,604.22	187.1
2008	2,770	577.448	141.1	5,093.86	244.4
2009	2,830	738.321	143.8	5,081.27	223.5
2010	3,270	1023.07	183.1	5,599.39	212.3
2011	3,230	987.255	174	5,387.00	187.1
2012	2,630	796.355	160.6	6,106.46	235.5
2013	2,130	633.605	131	6,150.23	223.9
2014	2,080	671.781	131.1	6,302.88	227.5
2015	2,560	745.226	143.5	5,605.47	227.5
2016	2,500	711.002	137.4	5,496.00	239.2
2017	2,350	623.36	128.9	5,485.11	220.4

**Table 15. Estimated reduction landings of Atlantic menhaden in numbers by age (in millions), 1955-2017.**

Year	0	1	2	3	4	5	6+
1955	761.0	674.2	1057.7	267.3	307.2	38.1	13.0
1956	36.4	2073.3	902.7	319.6	44.8	150.7	37.4
1957	299.6	1600.0	1361.8	96.7	70.8	40.5	42.3
1958	106.1	858.2	1635.4	72.1	17.3	15.9	14.4
1959	11.4	4038.7	851.3	388.3	33.4	11.9	18.7
1960	72.2	281.0	2208.6	76.4	102.2	23.8	11.0
1961	0.3	832.4	503.6	1209.6	19.2	29.4	3.9
1962	51.6	514.1	834.5	217.3	423.4	30.8	28.3
1963	96.9	724.2	709.2	122.5	45.0	52.4	14.3
1964	302.6	704.0	605.0	83.5	17.9	7.9	8.3
1965	259.1	745.2	421.4	77.8	12.2	1.8	2.0
1966	349.5	550.8	404.1	31.7	3.9	0.4	0.3
1967	7.0	633.2	265.7	72.8	5.1	0.5	0.0
1968	154.3	377.4	539.0	65.7	10.7	1.0	0.1
1969	158.1	372.3	284.3	47.8	5.4	0.2	0.0
1970	21.4	870.9	473.9	32.6	4.0	0.1	0.0
1971	72.9	263.3	524.3	88.3	17.8	2.5	0.0
1972	50.2	981.3	488.5	173.1	19.1	1.9	0.0
1973	56.0	588.5	1152.9	38.6	7.0	0.3	0.0
1974	315.6	636.7	986.0	48.6	2.5	1.4	0.0
1975	298.6	720.0	1086.5	50.2	6.6	0.2	0.1
1976	274.2	1612.0	1341.1	48.0	8.0	0.3	0.0
1977	484.6	1004.5	2081.8	83.5	17.8	1.4	0.1
1978	457.4	664.1	1670.9	258.1	31.2	3.5	0.0
1979	1492.5	623.1	1603.3	127.9	21.8	1.5	0.1
1980	88.3	1478.1	1458.2	222.7	69.2	14.4	1.4
1981	1187.6	698.7	1811.5	222.2	47.5	15.4	1.3
1982	114.1	919.4	1739.6	379.7	16.3	5.8	0.9
1983	964.4	517.2	2293.1	114.4	47.4	5.0	0.7
1984	1294.2	1024.2	892.1	271.5	50.3	15.2	0.5
1985	637.2	1075.9	1224.6	44.1	35.6	6.3	1.7
1986	98.4	224.2	1523.1	49.1	10.5	6.1	1.1
1987	42.9	504.7	1587.7	151.9	25.2	2.2	0.7
1988	338.8	282.7	1157.7	301.4	69.8	7.1	0.6
1989	149.7	1154.6	1158.5	108.4	47.5	11.6	0.2

**Table 15 Continued**

Year	0	1	2	3	4	5	6+
1990	308.1	132.8	1553.1	109.0	42.2	12.3	0.4
1991	881.8	1033.9	946.1	254.0	38.0	10.7	2.2
1992	399.7	727.2	795.4	66.1	51.3	10.9	1.9
1993	67.9	379.0	983.1	148.9	10.9	3.9	0.3
1994	88.6	274.5	888.9	165.1	67.2	7.5	0.2
1995	56.8	533.7	671.9	309.1	67.5	4.4	0.0
1996	33.7	209.1	679.1	139.0	29.0	2.0	0.0
1997	25.2	246.9	424.5	237.4	51.6	9.0	1.2
1998	72.8	185.0	540.6	126.3	73.0	9.0	0.8
1999	193.9	301.1	450.8	81.8	25.0	3.2	0.4
2000	77.8	114.2	340.6	111.9	11.1	1.9	0.0
2001	23.0	43.5	369.5	217.6	14.9	0.7	0.0
2002	178.2	211.7	259.8	135.8	17.1	0.5	0.0
2003	60.7	127.5	447.3	53.8	7.8	0.9	0.3
2004	18.0	214.0	652.1	75.7	17.4	0.9	0.0
2005	12.1	78.9	382.9	154.2	18.7	1.8	0.0
2006	9.2	298.9	300.1	121.7	23.6	0.5	0.0
2007	1.1	239.2	609.2	69.4	13.0	0.7	0.0
2008	7.9	52.4	394.9	106.6	14.7	1.0	0.0
2009	4.4	352.4	229.0	130.8	19.9	1.8	0.0
2010	15.5	409.5	201.1	68.1	28.3	0.6	0.0
2011	0.0	418.5	493.1	65.1	8.9	1.7	0.0
2012	4.7	127.2	627.0	33.6	3.9	0.0	0.0
2013	22.1	240.0	284.8	76.3	10.1	0.3	0.0
2014	3.9	268.0	273.3	94.7	30.3	1.6	0.0
2015	0.0	93.3	551.3	91.4	9.3	0.0	0.0
2016	12.5	180.5	347.1	162.9	8.0	0.0	0.0
2017	0.0	1165.6	238.7	26.0	0.0	0.0	0.0

**Table 16. Northern and southern reduction fishery landings in thousands of metric tons 1955–2017.**

Year	North	South	Year	North	South
1955	402.7	241.7	1990	144.1	257.1
1956	478.9	236.4	1991	104.6	276.9
1957	389.8	215.8	1992	99.1	198.5
1958	248.3	264.0	1993	58.4	262.2
1959	318.4	343.7	1994	33.4	226.6
1960	323.9	208.4	1995	96.3	243.6
1961	334.8	243.9	1996	61.6	231.4
1962	321.4	219.3	1997	25.2	234.0
1963	147.5	200.9	1998	12.3	233.6
1964	50.6	219.8	1999	8.4	162.8
1965	58.0	216.6	2000	43.2	124.1
1966	7.9	212.8	2001	39.6	193.9
1967	17.2	177.2	2002	27.2	146.9
1968	33.1	202.8	2003	4.1	162.0
1969	15.4	146.9	2004	25.9	152.6
1970	15.8	243.6	2005	15.4	137.5
1971	33.4	216.9	2006	60.1	97.2
1972	69.1	296.8	2007	36.6	137.8
1973	90.7	256.2	2008	39.3	101.8
1974	77.9	214.3	2009	18.7	125.1
1975	48.4	201.8	2010	28.7	154.4
1976	86.8	253.7	2011	29.6	144.5
1977	53.3	287.8	2012	23.9	136.7
1978	63.5	280.5	2013	32.7	98.3
1979	70.2	305.6	2014	29.9	101.2
1980	83.0	318.5	2015	28.8	114.7
1981	68.1	313.2	2016	45.0	92.4
1982	35.1	347.4	2017	58.4	70.5
1983	39.4	379.3			
1984	35.0	291.3			
1985	111.3	195.4			
1986	42.6	195.4			
1987	83.0	243.9			
1988	73.6	235.6			
1989	98.8	223.2			

**Table 17. Catch-at-age for the northern commercial reduction fishery from 1955-2017.**

Year	0	1	2	3	4	5	6+
1955	0	0.015	0.471	0.217	0.253	0.032	0.012
1956	0	0.133	0.555	0.195	0.025	0.072	0.02
1957	0	0.27	0.61	0.051	0.033	0.017	0.02
1958	0	0.025	0.908	0.042	0.01	0.008	0.009
1959	0	0.531	0.291	0.159	0.009	0.004	0.007
1960	0	0.009	0.892	0.037	0.049	0.009	0.004
1961	0	0.003	0.16	0.803	0.012	0.018	0.003
1962	0	0.015	0.245	0.218	0.457	0.033	0.032
1963	0	0.296	0.438	0.095	0.068	0.08	0.023
1964	0	0.034	0.357	0.345	0.128	0.065	0.072
1965	0	0.16	0.37	0.373	0.071	0.013	0.014
1966	0	0.201	0.467	0.212	0.1	0.009	0.012
1967	0	0.055	0.296	0.567	0.072	0.009	0
1968	0	0.007	0.479	0.388	0.116	0.009	0.001
1969	0	0.001	0.251	0.594	0.149	0.005	0
1970	0	0.15	0.793	0.05	0.007	0	0
1971	0	0.126	0.288	0.433	0.137	0.017	0
1972	0	0.169	0.286	0.452	0.085	0.008	0
1973	0	0.021	0.821	0.133	0.024	0.001	0
1974	0	0.028	0.844	0.117	0.006	0.004	0
1975	0	0	0.798	0.175	0.025	0.001	0
1976	0	0.092	0.823	0.071	0.013	0	0
1977	0	0.022	0.567	0.326	0.079	0.006	0.001
1978	0	0	0.298	0.567	0.12	0.015	0
1979	0	0.007	0.579	0.332	0.076	0.006	0
1980	0	0.002	0.237	0.462	0.243	0.051	0.004
1981	0	0.001	0.357	0.357	0.21	0.07	0.006
1982	0	0.042	0.393	0.473	0.063	0.025	0.004
1983	0	0.012	0.826	0.12	0.037	0.005	0
1984	0	0.024	0.343	0.506	0.097	0.029	0.001
1985	0	0.02	0.76	0.089	0.111	0.017	0.003
1986	0	0.01	0.795	0.107	0.05	0.031	0.006
1987	0	0.005	0.652	0.277	0.058	0.006	0.002
1988	0	0	0.225	0.486	0.26	0.026	0.003
1989	0	0.081	0.623	0.173	0.097	0.025	0

**Table 17 Continued**

Year	0	1	2	3	4	5	6+
1990	0	0.011	0.788	0.134	0.049	0.018	0.001
1991	0	0.085	0.43	0.385	0.072	0.023	0.005
1992	0	0.058	0.687	0.107	0.118	0.026	0.004
1993	0	0.045	0.675	0.226	0.036	0.017	0.002
1994	0	0.017	0.42	0.333	0.183	0.047	0
1995	0	0.02	0.567	0.329	0.079	0.006	0
1996	0	0	0.579	0.32	0.092	0.008	0
1997	0	0	0.495	0.293	0.158	0.055	0
1998	0	0	0.657	0.281	0.062	0	0
1999	0	0	0.389	0.428	0.168	0.015	0
2000	0	0.005	0.559	0.406	0.019	0.011	0
2001	0	0	0.15	0.796	0.055	0	0
2002	0	0.04	0.347	0.491	0.12	0.002	0
2003	0	0	0.474	0.378	0.139	0.01	0
2004	0	0.004	0.615	0.32	0.061	0	0
2005	0	0	0.219	0.605	0.174	0.002	0
2006	0	0.022	0.456	0.422	0.099	0.001	0
2007	0	0.022	0.761	0.174	0.041	0.002	0
2008	0	0.002	0.216	0.668	0.106	0.008	0
2009	0	0.123	0.299	0.463	0.102	0.013	0
2010	0	0	0.456	0.348	0.193	0.003	0
2011	0	0.058	0.726	0.19	0.023	0.003	0
2012	0	0.001	0.778	0.192	0.029	0	0
2013	0	0.028	0.724	0.233	0.015	0	0
2014	0	0.085	0.518	0.274	0.119	0.004	0
2015	0	0.006	0.593	0.362	0.038	0	0
2016	0	0.075	0.413	0.481	0.031	0	0
2017	0	0.017	0.572	0.393	0.015	0.003	0

**Table 18. Catch-at-age for the southern commercial reduction fishery from 1955-2017.**

Year	0	1	2	3	4	5	6+
1955	0.374	0.323	0.269	0.016	0.016	0.002	0
1956	0.017	0.885	0.049	0.018	0.004	0.022	0.004
1957	0.151	0.598	0.217	0.01	0.011	0.007	0.006
1958	0.059	0.466	0.443	0.018	0.005	0.005	0.004
1959	0.003	0.855	0.099	0.034	0.005	0.002	0.002
1960	0.052	0.192	0.701	0.018	0.025	0.008	0.004
1961	0	0.538	0.217	0.234	0.004	0.007	0
1962	0.04	0.387	0.491	0.033	0.044	0.003	0.002
1963	0.079	0.46	0.386	0.059	0.007	0.008	0.002
1964	0.187	0.433	0.349	0.028	0.002	0	0
1965	0.184	0.528	0.269	0.018	0.001	0	0
1966	0.265	0.414	0.299	0.02	0.001	0	0
1967	0.007	0.663	0.269	0.057	0.003	0	0
1968	0.143	0.349	0.468	0.037	0.003	0	0
1969	0.188	0.442	0.33	0.038	0.002	0	0
1970	0.016	0.65	0.309	0.022	0.003	0	0
1971	0.083	0.288	0.569	0.054	0.005	0.001	0
1972	0.033	0.618	0.285	0.061	0.003	0	0
1973	0.036	0.372	0.591	0.001	0	0	0
1974	0.196	0.388	0.413	0.003	0	0	0
1975	0.154	0.371	0.469	0.006	0.001	0	0
1976	0.101	0.572	0.324	0.003	0	0	0
1977	0.14	0.289	0.567	0.003	0	0	0
1978	0.158	0.23	0.558	0.05	0.003	0	0
1979	0.413	0.172	0.403	0.012	0.001	0	0
1980	0.028	0.476	0.452	0.038	0.004	0.001	0
1981	0.316	0.186	0.46	0.038	0	0	0
1982	0.038	0.306	0.558	0.096	0.001	0	0
1983	0.279	0.148	0.547	0.016	0.008	0.001	0
1984	0.396	0.311	0.244	0.04	0.007	0.002	0
1985	0.235	0.394	0.364	0.006	0	0	0
1986	0.056	0.126	0.797	0.019	0.002	0.001	0
1987	0.022	0.253	0.691	0.031	0.003	0	0
1988	0.175	0.146	0.573	0.099	0.006	0.001	0
1989	0.069	0.514	0.402	0.014	0.001	0	0



**Table 18 Continued**

Year	0	1	2	3	4	5	6+
1990	0.19	0.078	0.697	0.023	0.01	0.002	0
1991	0.317	0.36	0.281	0.038	0.004	0.001	0
1992	0.243	0.428	0.313	0.014	0.002	0	0
1993	0.049	0.266	0.608	0.074	0.003	0	0
1994	0.064	0.197	0.609	0.094	0.035	0.002	0
1995	0.044	0.408	0.366	0.15	0.031	0.002	0
1996	0.036	0.226	0.63	0.092	0.015	0.001	0
1997	0.027	0.26	0.423	0.236	0.047	0.007	0.001
1998	0.073	0.187	0.535	0.123	0.073	0.009	0.001
1999	0.188	0.292	0.428	0.069	0.02	0.003	0
2000	0.14	0.205	0.51	0.127	0.016	0.002	0
2001	0.039	0.073	0.604	0.265	0.018	0.001	0
2002	0.242	0.284	0.321	0.14	0.012	0	0
2003	0.088	0.185	0.643	0.073	0.01	0.001	0
2004	0.02	0.234	0.67	0.06	0.015	0.001	0
2005	0.02	0.131	0.618	0.21	0.018	0.003	0
2006	0.016	0.525	0.378	0.072	0.008	0	0
2007	0.001	0.306	0.631	0.054	0.008	0	0
2008	0.017	0.115	0.812	0.053	0.003	0	0
2009	0.007	0.515	0.311	0.147	0.019	0.001	0
2010	0.017	0.447	0.494	0.034	0.008	0	0
2011	0	0.477	0.467	0.048	0.007	0.002	0
2012	0.007	0.183	0.789	0.02	0.001	0	0
2013	0.043	0.457	0.388	0.095	0.016	0	0
2014	0.007	0.482	0.377	0.106	0.026	0.002	0
2015	0	0.141	0.759	0.092	0.009	0	0
2016	0.022	0.303	0.509	0.160	0.006	0	0
2017	0	0.249	0.581	0.144	0.026	0	0

**Table 19. Atlantic menhaden bait landings (1000 mt) from 1985-2017. The northern region includes landings from Maine to Maryland’s Eastern Shore, excluding the Chesapeake Bay. The southern region includes landings from the Chesapeake Bay to Florida (source: ACCSP).**

<b>Year</b>	<b>North</b>	<b>South</b>	<b>Total</b>
1985	7.86	19.56	27.42
1986	8.04	13.93	21.97
1987	8.24	18.13	26.38
1988	12.50	31.70	44.20
1989	11.32	20.57	31.90
1990	14.23	14.84	29.07
1991	16.83	13.45	30.28
1992	21.51	13.57	35.08
1993	17.55	14.44	31.99
1994	19.19	16.54	35.73
1995	22.17	18.47	40.64
1996	16.25	18.85	35.09
1997	18.20	21.86	40.06
1998	15.97	22.81	38.78
1999	13.11	21.89	35.00
2000	15.15	18.81	33.96
2001	13.24	22.89	36.13
2002	13.13	24.06	37.19
2003	8.60	25.18	33.78
2004	10.19	24.31	34.50
2005	10.23	28.95	39.18
2006	12.38	15.54	27.92
2007	20.39	22.27	42.66
2008	26.43	21.44	47.87
2009	19.26	20.60	39.86
2010	25.80	17.17	42.97
2011	34.26	18.69	52.95
2012	39.99	23.90	63.89
2013	19.71	17.32	37.03
2014	20.50	20.49	41.00
2015	24.73	20.79	45.52
2016	25.21	18.16	43.37
2017	26.43	17.42	43.86

**Table 20. Atlantic menhaden bait and recreational landings (1000 mt) from 1955-2017 combined and split into northern and southern regions for use in the BAM model. The northern region includes landings from Maine to Maryland’s Eastern Shore, excluding the Chesapeake Bay. The southern region includes landings from the Chesapeake Bay to Florida (source: ACCSP and MRIP).**

Year	Northern	Southern	Total
1955	10.14	4.50	14.64
1956	17.51	5.74	23.25
1957	10.60	14.11	24.71
1958	3.46	11.23	14.69
1959	7.98	12.61	20.58
1960	7.61	11.83	19.44
1961	8.44	16.63	25.07
1962	10.60	15.98	26.58
1963	6.11	18.28	24.39
1964	4.27	15.97	20.23
1965	3.30	20.32	23.62
1966	1.76	11.96	13.72
1967	1.44	10.17	11.61
1968	0.75	8.71	9.46
1969	1.11	9.50	10.61
1970	1.41	20.23	21.64
1971	1.87	11.60	13.47
1972	2.14	8.21	10.35
1973	2.61	12.16	14.77
1974	2.11	12.43	14.54
1975	1.89	19.80	21.69
1976	1.98	17.65	19.63
1977	1.39	21.70	23.09
1978	1.07	24.80	25.87
1979	1.17	11.85	13.02
1980	1.07	25.05	26.11
1981	1.33	21.52	22.85
1982	1.52	18.67	20.19
1983	1.49	18.17	19.66
1984	1.73	12.96	14.69
1985	8.24	19.68	27.92
1986	8.97	14.03	22.99

Year	Northern	Southern	Total
1987	8.87	18.15	27.02
1988	13.04	32.31	45.35
1989	11.78	20.64	32.42
1990	14.59	15.00	29.58
1991	17.76	13.65	31.41
1992	23.63	13.75	37.38
1993	18.02	14.49	32.51
1994	19.38	16.74	36.12
1995	22.53	18.79	41.32
1996	16.36	19.24	35.60
1997	18.31	21.94	40.25
1998	16.31	22.89	39.20
1999	13.24	22.30	35.54
2000	15.37	18.85	34.22
2001	13.30	23.20	36.50
2002	13.76	24.27	38.03
2003	8.92	25.43	34.35
2004	12.16	24.63	36.79
2005	10.27	29.23	39.49
2006	13.25	16.15	29.39
2007	21.05	22.71	43.76
2008	27.22	21.56	48.78
2009	19.44	20.97	40.41
2010	26.18	17.51	43.69
2011	34.70	19.03	53.74
2012	40.78	25.08	65.86
2013	20.25	17.72	37.97
2014	22.20	20.83	43.03
2015	25.89	21.17	47.06
2016	31.09	18.84	49.93
2017	28.40	17.73	46.13

**Table 21. Catch-at-age for the northern commercial bait fishery (includes MRIP estimate of recreation catch).**

Year	0	1	2	3	4	5	6+
1985	0.00	0.02	0.79	0.10	0.07	0.02	0.00
1986	0.00	0.00	0.29	0.50	0.10	0.08	0.02
1987	0.00	0.00	0.28	0.50	0.20	0.01	0.01
1988	0.00	0.00	0.09	0.52	0.35	0.04	0.00
1989	0.00	0.01	0.22	0.38	0.31	0.09	0.00
1990	0.00	0.00	0.56	0.25	0.13	0.05	0.00
1991	0.00	0.01	0.29	0.53	0.12	0.04	0.01
1992	0.00	0.03	0.41	0.21	0.28	0.06	0.02
1993	0.00	0.01	0.44	0.41	0.09	0.04	0.00
1994	0.00	0.00	0.11	0.50	0.34	0.05	0.00
1995	0.00	0.00	0.09	0.48	0.44	0.00	0.00
1996	0.00	0.00	0.44	0.44	0.12	0.01	0.00
1997	0.00	0.00	0.15	0.32	0.39	0.12	0.02
1998	0.00	0.00	0.11	0.39	0.41	0.08	0.01
1999	0.00	0.00	0.15	0.48	0.32	0.04	0.01
2000	0.00	0.00	0.41	0.31	0.23	0.03	0.01
2001	0.00	0.00	0.11	0.73	0.14	0.01	0.00
2002	0.00	0.00	0.05	0.55	0.34	0.06	0.00
2003	0.00	0.00	0.13	0.66	0.20	0.01	0.00
2004	0.00	0.00	0.25	0.61	0.14	0.00	0.00
2005	0.00	0.00	0.18	0.63	0.16	0.02	0.00
2006	0.00	0.00	0.29	0.59	0.12	0.00	0.00
2007	0.00	0.00	0.38	0.48	0.13	0.01	0.00
2008	0.00	0.00	0.26	0.59	0.14	0.01	0.00
2009	0.00	0.00	0.20	0.61	0.17	0.01	0.00
2010	0.00	0.00	0.37	0.38	0.23	0.03	0.00
2011	0.00	0.00	0.14	0.49	0.33	0.04	0.00
2012	0.00	0.00	0.39	0.47	0.13	0.01	0.00
2013	0.00	0.00	0.26	0.55	0.16	0.03	0.00
2014	0.00	0.00	0.07	0.52	0.39	0.02	0.00
2015	0.00	0.00	0.38	0.52	0.10	0.00	0.00
2016	0.00	0.02	0.41	0.52	0.05	0.01	0.00
2017	0.00	0.02	0.60	0.35	0.03	0.00	0.00

**Table 22. Catch-at-age for the southern commercial bait fishery (includes MRIP estimate of recreation catch).**

Year	0	1	2	3	4	5	6+
1985	0.00	0.36	0.62	0.01	0.00	0.00	0.00
1986	0.00	0.07	0.86	0.06	0.01	0.00	0.00
1987	0.00	0.10	0.83	0.06	0.01	0.00	0.00
1988	0.00	0.07	0.67	0.22	0.03	0.00	0.00
1989	0.00	0.38	0.55	0.05	0.01	0.00	0.00
1990	0.01	0.07	0.90	0.02	0.00	0.00	0.00
1991	0.01	0.32	0.58	0.08	0.00	0.00	0.00
1992	0.00	0.55	0.45	0.00	0.00	0.00	0.00
1993	0.01	0.39	0.51	0.09	0.00	0.00	0.00
1994	0.00	0.15	0.65	0.14	0.05	0.00	0.00
1995	0.00	0.39	0.37	0.22	0.02	0.00	0.00
1996	0.00	0.01	0.76	0.20	0.04	0.00	0.00
1997	0.00	0.05	0.53	0.35	0.06	0.01	0.00
1998	0.04	0.07	0.54	0.24	0.11	0.01	0.00
1999	0.00	0.11	0.66	0.17	0.05	0.01	0.00
2000	0.01	0.22	0.66	0.11	0.00	0.00	0.00
2001	0.00	0.04	0.66	0.27	0.02	0.00	0.00
2002	0.00	0.05	0.26	0.49	0.17	0.02	0.00
2003	0.01	0.10	0.74	0.14	0.01	0.00	0.00
2004	0.00	0.07	0.73	0.17	0.03	0.00	0.00
2005	0.00	0.01	0.52	0.45	0.03	0.00	0.00
2006	0.00	0.33	0.45	0.19	0.02	0.00	0.00
2007	0.00	0.25	0.67	0.07	0.02	0.00	0.00
2008	0.01	0.04	0.81	0.11	0.02	0.01	0.00
2009	0.00	0.25	0.37	0.34	0.05	0.00	0.00
2010	0.00	0.31	0.52	0.10	0.06	0.00	0.00
2011	0.00	0.34	0.47	0.12	0.05	0.02	0.00
2012	0.00	0.07	0.83	0.08	0.02	0.00	0.00
2013	0.01	0.45	0.29	0.17	0.05	0.03	0.00
2014	0.00	0.44	0.36	0.14	0.05	0.01	0.00
2015	0.01	0.31	0.59	0.09	0.00	0.00	0.00
2016	0.00	0.23	0.42	0.32	0.02	0.01	0.00
2017	0.00	0.28	0.47	0.24	0.01	0.00	0.00

**Table 23. MRIP recreational harvest (A+B1) estimates of Atlantic menhaden for two assessment regions along the U.S. Atlantic coast.**

Year	North (ME - DE)		South (MD - FL)	
	Harvest (mt)	Harvest (numbers)	Harvest (mt)	Harvest (numbers)
1981	236.977	703,836	132.568	634,034
1982	201.887	653,057	72.193	1,869,090
1983	127.979	331,651	246.981	2,493,266
1984	129.048	304,589	66.947	727,515
1985	337.865	963,374	20.722	184,870
1986	896.124	2,866,290	81.043	290,155
1987	571.306	2,852,814	11.714	117,477
1988	516.072	1,325,890	601.299	2,639,419
1989	443.148	1,251,481	24.976	224,452
1990	303.139	920,877	139.530	1,234,658
1991	852.993	2,405,388	154.746	1,449,707
1992	1,953.325	4,320,030	183.278	1,825,157
1993	449.577	1,589,230	35.213	336,254
1994	170.851	732,431	196.679	1,100,919
1995	337.261	1,079,202	297.329	1,186,673
1996	108.802	327,445	397.450	1,670,900
1997	107.002	344,458	81.615	599,052
1998	337.831	845,231	74.376	388,029
1999	72.347	145,391	158.500	631,265
2000	127.689	247,915	24.259	155,456
2001	55.843	98,460	222.879	1,362,492
2002	426.193	1,012,795	127.796	900,776
2003	309.958	612,635	42.459	4,428,594
2004	80.437	173,180	241.943	2,418,783
2005	29.599	57,111	208.201	2,028,924
2006	563.503	1,430,644	385.210	3,750,319
2007	590.924	1,862,431	340.000	2,786,070
2008	725.266	3,460,945	110.641	1,123,610
2009	165.458	465,316	243.617	2,173,084
2010	262.090	893,532	236.048	2,515,340
2011	432.526	1,345,275	247.132	2,535,923
2012	785.192	2,102,320	1,155.377	4,050,795
2013	348.353	1,081,072	328.814	2,724,862
2014	1,135.107	3,666,107	228.842	3,077,786
2015	774.254	2,072,077	248.056	2,470,563
2016	1,862.107	5,421,498	570.717	4,368,449
2017	1,487.503	4,007,625	216.533	1,554,878

**Table 24. MRIP recreational total harvest (A+B1+1.0\*B2) estimates of Atlantic Menhaden for two assessment regions along the U.S. Atlantic coast.**

Year	North (ME - DE)		South (MD - FL)	
	Total Harvest (mt)	Total Harvest (numbers)	Total Harvest (mt)	Total Harvest (numbers)
1981	250.613	744,033	160.256	934,032
1982	202.475	654,912	130.321	2,531,703
1983	136.781	356,587	458.881	5,042,349
1984	145.354	351,989	216.326	2,359,587
1985	375.779	1,071,278	124.276	1,172,620
1986	928.576	2,959,569	98.584	531,607
1987	630.309	3,021,788	17.492	197,246
1988	542.733	1,402,360	609.496	2,741,075
1989	456.467	1,289,427	71.298	807,867
1990	357.124	1,077,048	159.257	1,464,393
1991	920.469	2,583,548	205.897	1,751,567
1992	2,119.246	4,797,851	186.216	1,859,484
1993	470.492	1,649,204	51.691	547,526
1994	189.124	783,085	198.898	1,120,857
1995	357.221	1,136,106	320.401	1,336,112
1996	111.829	336,093	397.713	1,672,796
1997	107.990	347,168	82.582	607,006
1998	343.545	861,548	79.806	447,020
1999	133.325	317,752	408.290	3,367,977
2000	221.739	540,130	35.061	258,578
2001	58.965	107,642	309.727	2,052,264
2002	626.626	1,588,779	213.340	1,590,007
2003	317.710	634,852	247.908	6,059,127
2004	1,968.612	6,057,124	315.171	2,999,853
2005	36.425	76,926	276.429	2,594,284
2006	870.161	2,310,390	608.962	5,527,305
2007	662.735	2,067,996	441.620	3,653,385
2008	787.352	3,643,438	126.083	1,246,816
2009	175.073	495,109	372.621	3,209,141
2010	386.108	1,251,959	337.511	3,321,951
2011	443.096	1,376,068	343.141	3,298,700
2012	795.151	2,132,358	1,179.198	4,247,172
2013	537.785	1,648,400	396.602	3,263,680
2014	1,692.942	5,290,171	337.727	4,249,897
2015	1,159.114	3,177,381	383.951	3,809,070
2016	5,881.312	17,897,392	675.955	5,214,862
2017	1,965.995	5,380,486	306.435	2,960,156

**Table 25. Fishery-independent surveys considered for inclusion in the assessment and reasons rejected if they were not accepted for use as an abundance index.**

State	Survey	Age	Status		Reason(s) Rejected					
			Accepted	Rejected	Time series too short or broken	Rare occurrence of menhaden	Years with zero menhaden caught	Inconsistent methods, gear changes	Limited spatial/temporal coverage	Another survey available with similar coverage
ME-NH	ME-NH Inshore Trawl Survey	YOY		X		X	X			
	NEFSC Trawl			X		X		X		
RI	Narragansett Bay Juvenile Finfish Seine Survey	YOY		X		X				
RI	Coastal Pond Juvenile Finfish Seine Survey	YOY		X		X				
RI	Spring Trawl Survey (Seasonal Survey)	YOY		X		X	X			
RI	Fall Trawl Survey (Seasonal Survey)	YOY		X			X			X
RI	Monthly Trawl Survey (Fall Months)	YOY	X							
MA	Inshore Bottom Trawl	YOY		X		X	X			
CT	CT DEEP Connecticut River Juvenile Alosine Seir	YOY	X							
CT	CT Long Island Sound Trawl Survey (LISTS)	YOY	X							
CT	CT Long Island Sound Trawl Survey (LISTS)	Age 1+	X							
CT	Thames River Seine Survey	YOY	X							
NY	WLI Seine Survey	YOY	X							
NY	Peconic Bay Small Mesh Trawl Survey	YOY	X							
NY	Alosine Beach Seine Survey			X		X	X			
NY	Striped Bass Beach Seine Survey			X				X	X	
NJ	Striped Bass Seine Survey	YOY	X							
NJ	Ocean Trawl	YOY	X							
NJ	Ocean Trawl	Age 1+	X							
NJ	DB Juvenile Finfish Trawl Survey or DB Trawl	YOY		X		X				X
NJ	PSEG			X						
DE	DB Adult Trawl Survey (30')	Age 1+	X							
DE	DB Juvenile Trawl (16')	YOY		X		X				X
DE	DB Juvenile Trawl (16')	Adult		X		X				X
DE	Inland Bays (16', IB)	YOY	X							
DE	Inland Bays (16', IB)	Adult		X			X			



**Table 25 Continued**

State	Survey	Age	Status		Reason(s) Rejected					
			Accepted	Rejected	Time series too short or broken	Rare occurrence of menhaden	Years with zero menhaden caught	Inconsistent methods, gear changes	Limited spatial/temporal coverage	Another survey available with similar coverage
MD	Juvenile striped bass beach seine survey	YOY	X							
MD	Coastal Bays (Trawl)	YOY	X							
MD	Coastal Bays (seine)	YOY		X						X
MD	Gill net survey	Age 1+	X							
ChesBay	CHESFIMS	Age 1+		X						X
VA	VA Shad Gillnet	Age 1+	X							
VA	VA Juvenile Trawl	YOY	X							
VA	VA Juvenile Trawl	Age 1+		X						
VA	VA Seine Survey	YOY	X							
VA	NEAMAP	YOY		X	X		X			
VA	NEAMAP	Age 1+		X	X					X
VA	ChesMMAP			X						X
NC	Pamlico Sound Independent Gill Net (p915) - Riv	Age 1+	X					X		X
NC	Pamlico Sound Survey (p195)	YOY		X	X		X	X		X
NC	Striped Bass Independent Gill Net Survey (p135)	Age 1+		X			X	X	X	X
NC	Juvenile Anadromous Survey (p100) - Trawl	YOY		X	X		X	X	X	X
NC	Juvenile Anadromous Survey (p100) - Seine	YOY		X			X	X	X	X
NC	Estuarine Trawl Survey (p120)	YOY	X				X			X
SC	SEAMAP	Age 1+	X							
SC	Trammel	Age 1+		X		X				
SC	Electrofishing	YOY	X							
GA	Ecological Monitoring Trawl Survey (EMTS)	YOY		X		X				
GA	Ecological Monitoring Trawl Survey (EMTS)	Age 1+	X							

**Table 26. Length cutoffs used to distinguish age-0 from age-1+ Atlantic menhaden. Regions refer to those used in the commercial reduction fishery database (Figure 1).**

Region	Month	Cutoff ( $\leq$ fork length mm)
1-3	May	90
	June	110
	July	125
	Aug-April	150
4	April	108
	May	113
	June	119
	July	126
	Aug-March	135

**Table 27. Monthly length cutoffs used to identify YOY versus age-1+ Atlantic Menhaden in the Georgia Ecosystem Monitoring Trawl Survey (GA EMTS), SC DNR Electrofishing Survey, and the Southeast Area Monitoring and Assessment Program, South Atlantic Region (SEAMAP-SA) Coastal Trawl Survey.**

Month	Fork Length	
	GA-EMTS and SCDNR Electrofishing Surveys	SEAMAP-SA Coastal Trawl Survey
January	108	110
February	108	110
March	108	110
April	108	110
May	108	110
June	113	110
July	119	120
August	126	130
September	135	140
October	135	140
November	135	140
December	135	140

**Table 28. South Carolina Department of Natural Resources (SC DNR) electrofishing survey based length-length conversions used to convert fish only measured to the nearest mm standard length (SL) or total length (TL) to their predicted fork length in mm. As the majority of fish were only measured to the nearest mm SL, a SL to FL conversion equation was used, then applied the TL to FL conversion equation to any fish having only a TL measurement. Numbers in parenthesis represent standard errors about the length-length linear regression coefficient estimates.**

<b>Order</b>	<b>X-variable</b>	<b>n</b>	<b>Intercept</b>	<b>Slope</b>
1	SL	1701	-0.314 (0.0546)	1.105 (0.00136)
2	TL	1701	2.963 (0.0485)	0.831 (0.000976)

**Table 29. Fishery-independent surveys developed into abundance indices, accepted by the SAS, and used to develop regional Conn indices and months used in the index and length of the combined time series.**

<b>Conn</b>	<b>Fishery-Independent Survey</b>	<b>Months</b>	<b>Length</b>
<b>NAD</b>	CT LISTS	Sept-lagged Jan	1990-2017
	DB Adult Trawl		
	NJ Ocean Trawl		
<b>MAD</b>	MD Gill Net	March-May	1985-2017
	VA Shad Gill Net		
<b>SAD</b>	NC p915	April-July	1990-2017
	SEAMAP		
	GA EMTS		
<b>YOY</b>	RI Trawl	Varies by survey	1959-2017
	CT LISTS		
	CT River Alosine		
	CT Thames River Alosine		
	NY Juvenile Striped Bass Seine		
	NY Peconic Bay Trawl		
	NY WLIS Seine		
	NJ Ocean Trawl		
	NJ Striped Bass YOY Seine		
	DB Inner Bays		
	MD Coastal Trawl		
	MD Juv Striped Bass		
	VA Juvenile Trawl		
	VA Striped Bass Seine		
	NC p120		
	SC Electrofishing		

**Table 30. Young-of-year abundance index (YOY), northern adult index (NAD), Mid-Atlantic adult index (MAD), and southern adult index (SAD) of abundance for Atlantic menhaden developed from the Conn method with associated coefficients of variation (CV).**

Year	YOY		NAD		MAD		SAD	
	Index	CV	Index	CV	Index	CV	Index	CV
1959	1.48	1.06						
1960	0.50	1.09						
1961	0.45	1.11						
1962	1.57	1.07						
1963	1.21	1.08						
1964	0.88	1.13						
1965	0.52	1.08						
1966	0.66	1.06						
1967	0.54	1.09						
1968	0.57	1.05						
1969	0.96	0.98						
1970	0.46	1.04						
1971	1.20	1.00						
1972	2.25	0.91						
1973	1.33	0.92						
1974	3.27	0.95						
1975	2.98	0.95						
1976	3.27	0.94						
1977	2.56	0.93						
1978	1.44	0.93						
1979	2.55	0.93						
1980	3.66	0.91						
1981	1.70	0.94						
1982	2.22	0.92						
1983	0.98	0.92						
1984	0.97	0.92						
1985	2.50	0.90			1.80	1.15		
1986	1.75	0.82			1.77	1.14		
1987	0.38	0.76			1.94	1.18		
1988	1.41	0.75			1.86	1.14		
1989	0.94	0.57			1.20	1.18		
1990	0.57	0.51	1.14	0.74	0.94	1.15	3.69	0.63
1991	0.77	0.50	0.43	0.75	0.78	1.16	1.16	0.59
1992	0.52	0.51	1.10	0.76	1.32	1.16	0.86	0.63
1993	0.20	0.56	0.90	0.73	0.58	1.19	0.47	0.68

**Table 30 Continued**

Year	YOY		NAD		MAD		SAD	
	Index	CV	Index	CV	Index	CV	Index	CV
1994	0.30	0.53	0.69	0.77	1.39	1.14	0.36	0.75
1995	0.28	0.52	1.17	0.74	1.35	1.13	0.17	0.82
1996	0.23	0.52	0.75	0.58	0.58	1.20	0.27	0.73
1997	0.24	0.49	0.40	0.59	0.58	1.22	0.22	0.74
1998	0.46	0.50	0.33	0.88	0.72	0.40	0.75	0.64
1999	0.51	0.50	1.98	0.61	0.51	0.43	0.25	0.74
2000	0.62	0.48	0.91	0.66	1.44	0.36	0.85	0.81
2001	0.32	0.45	0.65	0.83	0.85	0.38	0.81	0.74
2002	0.50	0.43	1.56	0.59	0.46	0.43	0.89	0.65
2003	0.87	0.43	0.48	0.68	1.01	0.36	1.08	0.50
2004	0.69	0.42	0.52	0.73	0.52	0.38	0.45	0.51
2005	0.85	0.42	1.15	0.59	1.35	0.39	1.20	0.46
2006	0.31	0.43	0.80	0.67	0.40	0.42	3.19	0.41
2007	0.51	0.44	1.20	0.59	0.86	0.42	0.41	0.47
2008	0.34	0.41	0.95	0.63	0.39	0.45	0.63	0.39
2009	0.26	0.42	0.41	0.61	0.90	0.41	2.34	0.44
2010	0.40	0.44	0.88	0.80	0.85	0.39	0.80	0.39
2011	0.31	0.43	0.92	0.65	0.63	0.38	1.45	0.39
2012	0.15	0.45	1.78	0.59	0.56	0.44	1.22	0.36
2013	0.17	0.42	0.62	0.62	0.91	0.40	0.86	0.40
2014	0.40	0.42	1.62	0.62	1.53	0.38	0.80	0.44
2015	0.40	0.44	2.33	0.72	1.98	0.45	1.16	0.41
2016	0.53	0.46	1.56	0.60	0.57	0.43	0.33	0.54
2017	0.11	0.46	0.75	0.64	0.46	0.41	1.33	0.41

**Table 31. List of surveys used in the regional Conn indices and their associated sigma values, or the standard deviation of the process error.**

<b>Stage</b>	<b>Survey</b>	<b>Sigma (<math>\sigma^p</math>)</b>
YOY	RI Trawl	2.96
	CT LISTS	2.50
	CT River Alosine	3.16
	CT Thames River Alosine	1.34
	NY Juvenile Striped Bass Seine	3.78
	NY Peconic Bay Trawl	2.99
	NY WLIS Seine	1.18
	NJ Ocean Trawl	1.85
	NJ Striped Bass YOY Seine	1.81
	DB Inner Bays	11.34
	MD Coastal Trawl	2.17
	MD Juv Striped Bass	1.64
	VA Juvenile Trawl	1.31
	VA Striped Bass Seine	3.05
	NC p120	0.82
SC Electrofishing	0.92	
Age 1+	CT LISTS	0.96
	DB Adult Trawl	0.88
	NJ OT	1.53
	MD Gill Net	2.23
	VA Shad Gill Net	0.24
	NC p915	0.92
	SEAMAP	0.40
	GA EMTS	0.50

**Table 32. Correlation coefficients and *P*-values for young-of-year Atlantic menhaden surveys. Correlation coefficients are above the grey, diagonal line for the pairwise comparisons and *P*-values are below the line. Significant (*P*<0.05) correlations are highlighted in orange cells.**

		Correlation Coefficients															
		RITrawl	CTRivAlo	CTTh	CTLISTS	NYPec	NYWLIS	NYJSB	NJSB	NJOT	DBIB	MDCstl	MDJuvSB	VAJvTwl	VA SB	NCp120	SCElect
p-value	RITrawl		0.27	<b>0.63</b>	-0.19	0.15	0.30	-0.12	0.06	0.22	<b>0.53</b>	-0.08	-0.18	-0.15	-0.27	-0.17	-0.21
	CTRivAlo	0.168		<b>0.73</b>	-0.02	0.22	0.18	-0.08	0.06	0.34	-0.24	0.01	-0.13	-0.31	-0.18	0.04	<b>0.57</b>
	CTTh	0.004	0.000		-0.06	<b>0.52</b>	0.09	-0.02	0.07	0.14	-0.13	0.33	-0.19	-0.39	-0.24	-0.16	0.00
	CTLISTS	0.414	0.923	0.826		<b>0.47</b>	0.34	0.06	-0.15	0.16	-0.05	0.31	0.10	0.07	0.30	-0.11	-0.06
	NYPec	0.461	0.244	0.023	0.032		<b>0.40</b>	0.00	-0.10	0.13	-0.09	0.18	-0.30	-0.07	-0.20	-0.36	-0.17
	NYWLIS	0.119	0.324	0.725	0.134	0.025		<b>0.49</b>	0.33	0.36	-0.11	-0.12	-0.16	-0.11	-0.19	0.11	-0.06
	NYJSB	0.640	0.762	0.938	0.820	0.993	0.039		0.06	-0.03	0.04	0.11	0.25	-0.02	0.21	<b>0.60</b>	0.01
	NJSB	0.780	0.763	0.771	0.518	0.576	0.063	0.805		-0.07	-0.04	-0.06	<b>0.37</b>	-0.30	0.09	0.15	0.01
	NJOT	0.255	0.075	0.556	0.475	0.498	0.058	0.901	0.727		-0.18	-0.06	-0.19	-0.13	-0.20	-0.04	0.26
	DBIB	0.003	0.193	0.587	0.835	0.647	0.563	0.889	0.848	0.362		0.26	0.13	0.08	-0.03	-0.12	-0.26
	MDCstl	0.688	0.974	0.169	0.170	0.323	0.521	0.663	0.760	0.771	0.150		<b>0.57</b>	-0.17	0.15	-0.05	-0.07
	MDJuvSB	0.367	0.502	0.438	0.669	0.104	0.378	0.325	0.038	0.326	0.484	0.000		-0.13	<b>0.34</b>	0.20	-0.29
	VAJvTwl	0.454	0.112	0.102	0.750	0.725	0.581	0.945	0.123	0.517	0.682	0.399	0.508		0.07	-0.05	-0.34
	VA SB	0.162	0.333	0.319	0.188	0.273	0.302	0.399	0.618	0.298	0.882	0.348	0.023	0.716		<b>0.40</b>	-0.05
	NCp120	0.390	0.848	0.519	0.620	0.057	0.584	0.009	0.433	0.840	0.546	0.817	0.290	0.819	0.031		<b>0.53</b>
SCElect	0.428	0.017	0.989	0.816	0.526	0.826	0.978	0.956	0.319	0.321	0.784	0.261	0.181	0.859	0.027		



**Table 33. Correlation coefficients and *P*-values for age-1+ Atlantic menhaden surveys. Correlation coefficients are above the grey, diagonal line for the pairwise comparisons and *p*-values are below the line. Significant (*P*<0.05) correlations are highlighted in orange cells.**

		Correlation Coefficients							
		CT.LISTS	DB Trawl	NJ OT	MD GN	VA GN	NC p195	SEAMAP	GA EMTS
p-value	CT.LISTS		-0.01	0.16	<b>0.52</b>	<b>0.62</b>	<b>0.94</b>	-0.03	-0.29
	DB Trawl	0.980		0.06	0.10	-0.23	0.15	-0.09	-0.07
	NJ OT	0.479	0.773		0.18	0.00	0.03	-0.13	-0.39
	MD GN	0.015	0.606	0.359		0.29	0.47	0.01	-0.28
	VA GN	0.005	0.321	0.992	0.216		<b>0.87</b>	-0.08	-0.16
	NC p195	0.000	0.680	0.934	0.173	0.001		-0.24	-0.33
	SEAMAP	0.902	0.647	0.496	0.956	0.728	0.510		<b>0.80</b>
	GA EMTS	0.317	0.802	0.156	0.315	0.564	0.359	0.000	

**Table 34. Selectivity slope and  $A_{50}$  of the ascending and descending limbs with associated SD for the reduction and bait fisheries and the NAD and MAD indices.**

Fishery/Index	Region	Period	Ascending Limb				Descending Limb			
			Slope	SD	A50	SD	Slope	SD	A50	SD
Reduction	North	1955-1969	17.1	278	1.2	2.8	2.0	1.7	5.3	2.9
Reduction	North	1970-1993	5.0	0.2	2.0	0.05	24	4.6	3.9	0.05
Reduction	North	1994-2012	4.3	0.3	2.1	0.07	19	370	2.9	5.6
Reduction	North	2013-2017	4.1	0.6	2.1	0.3	1.7	1.3	1.8	1.4
Reduction	South	1955-1971	4.1	0.2	1.1	0.07	0.4	0.1	0.01	0.001
Reduction	South	1972-2004	3.1	0.1	1.8	0.06	0.9	0.1	0.01	0.001
Reduction	South	2005-2012	4.4	0.6	1.5	0.1	0.6	0.7	0.2	8
Reduction	South	2013-2017	4.2	0.6	1.4	0.2	1.8	1.7	2.6	1
Bait	North	1955-2012	7.4	1.6	2.3	0.06	3.4	0.7	2.6	0.1
Bait	North	2013-2017	5.2	0.4	2.3	0.04	2.8	0.6	1.8	0.2
Bait	South	1955-2013	4.9	0.4	1.5	0.06	1.1	0.4	2.7	0.5
NAD	North	1990-2017	2.2	0.1	3.0	0.2	-	-	-	-
MAD	Mid-Atlantic	1985-2017	4.3	1.0	2.2	0.2	34	68	2.3	1.1

**Table 35. Geometric mean fishing mortality (*F*) rate of ages-2 to -4 during 1955-2017.**

Year	Geo F	Year	Geo F
1955	0.26	1987	0.28
1956	0.41	1988	0.35
1957	0.34	1989	0.42
1958	0.20	1990	0.38
1959	0.26	1991	0.32
1960	0.13	1992	0.24
1961	0.22	1993	0.17
1962	0.34	1994	0.15
1963	0.30	1995	0.22
1964	0.25	1996	0.17
1965	0.28	1997	0.19
1966	0.17	1998	0.22
1967	0.13	1999	0.16
1968	0.17	2000	0.14
1969	0.15	2001	0.16
1970	0.24	2002	0.14
1971	0.26	2003	0.13
1972	0.57	2004	0.16
1973	0.60	2005	0.16
1974	0.48	2006	0.19
1975	0.36	2007	0.16
1976	0.37	2008	0.13
1977	0.28	2009	0.13
1978	0.28	2010	0.17
1979	0.29	2011	0.15
1980	0.41	2012	0.12
1981	0.45	2013	0.09
1982	0.42	2014	0.13
1983	0.41	2015	0.16
1984	0.44	2016	0.15
1985	0.49	2017	0.11
1986	0.22		

**Table 36. Full fishing mortality rate at age by year for 1955-2017.**

Year	Age						
	0	1	2	3	4	5	6+
1955	0.00	0.06	0.27	0.26	0.24	0.21	0.15
1956	0.00	0.07	0.42	0.42	0.39	0.34	0.25
1957	0.00	0.06	0.35	0.35	0.33	0.28	0.20
1958	0.00	0.06	0.22	0.20	0.18	0.15	0.11
1959	0.00	0.06	0.27	0.26	0.24	0.21	0.15
1960	0.00	0.03	0.14	0.14	0.12	0.11	0.08
1961	0.00	0.06	0.24	0.22	0.20	0.17	0.12
1962	0.00	0.09	0.37	0.35	0.31	0.27	0.19
1963	0.00	0.09	0.34	0.31	0.27	0.22	0.15
1964	0.00	0.11	0.30	0.26	0.21	0.15	0.10
1965	0.00	0.11	0.32	0.28	0.23	0.18	0.12
1966	0.00	0.09	0.21	0.18	0.13	0.09	0.06
1967	0.00	0.07	0.16	0.13	0.10	0.08	0.05
1968	0.00	0.08	0.20	0.17	0.13	0.10	0.07
1969	0.00	0.08	0.19	0.16	0.12	0.09	0.06
1970	0.00	0.12	0.28	0.25	0.19	0.14	0.08
1971	0.00	0.12	0.28	0.27	0.22	0.17	0.09
1972	0.01	0.11	0.66	0.66	0.43	0.29	0.12
1973	0.01	0.09	0.61	0.70	0.51	0.39	0.15
1974	0.00	0.07	0.48	0.56	0.42	0.32	0.13
1975	0.00	0.06	0.38	0.41	0.29	0.21	0.08
1976	0.00	0.05	0.37	0.43	0.32	0.25	0.10
1977	0.00	0.05	0.32	0.32	0.21	0.14	0.06
1978	0.00	0.05	0.32	0.32	0.21	0.15	0.06
1979	0.00	0.06	0.34	0.34	0.22	0.15	0.06
1980	0.00	0.08	0.47	0.48	0.31	0.21	0.09
1981	0.01	0.09	0.52	0.52	0.34	0.23	0.09
1982	0.01	0.09	0.53	0.49	0.29	0.18	0.07
1983	0.01	0.09	0.51	0.47	0.28	0.17	0.07
1984	0.01	0.10	0.54	0.50	0.30	0.18	0.07
1985	0.00	0.05	0.43	0.58	0.47	0.38	0.14
1986	0.00	0.04	0.23	0.26	0.18	0.12	0.05
1987	0.00	0.05	0.29	0.33	0.23	0.17	0.06
1988	0.00	0.06	0.38	0.41	0.28	0.19	0.07
1989	0.00	0.06	0.40	0.49	0.37	0.28	0.11
1990	0.00	0.04	0.33	0.46	0.37	0.29	0.11
1991	0.00	0.04	0.31	0.38	0.28	0.21	0.08
1992	0.00	0.03	0.20	0.29	0.23	0.17	0.06
1993	0.00	0.03	0.18	0.20	0.14	0.09	0.03
1994	0.00	0.03	0.16	0.18	0.12	0.06	0.01
1995	0.00	0.03	0.21	0.27	0.20	0.11	0.01

**Table 36 Continued**

Year	Age						
	0	1	2	3	4	5	6+
1996	0.00	0.03	0.17	0.20	0.14	0.08	0.01
1997	0.00	0.04	0.22	0.22	0.13	0.07	0.02
1998	0.00	0.05	0.27	0.26	0.16	0.07	0.02
1999	0.00	0.03	0.19	0.19	0.12	0.06	0.02
2000	0.00	0.02	0.12	0.17	0.13	0.07	0.01
2001	0.00	0.03	0.17	0.19	0.13	0.06	0.01
2002	0.00	0.02	0.15	0.17	0.11	0.06	0.01
2003	0.00	0.03	0.15	0.15	0.09	0.04	0.01
2004	0.00	0.03	0.17	0.18	0.12	0.06	0.01
2005	0.00	0.03	0.19	0.18	0.13	0.07	0.02
2006	0.00	0.02	0.16	0.23	0.19	0.11	0.02
2007	0.00	0.02	0.15	0.19	0.16	0.08	0.02
2008	0.00	0.01	0.11	0.15	0.13	0.07	0.01
2009	0.00	0.02	0.14	0.15	0.11	0.06	0.02
2010	0.00	0.02	0.16	0.19	0.15	0.08	0.02
2011	0.00	0.02	0.13	0.18	0.15	0.08	0.02
2012	0.00	0.01	0.10	0.14	0.12	0.06	0.01
2013	0.00	0.01	0.09	0.12	0.07	0.02	0.00
2014	0.00	0.01	0.12	0.17	0.10	0.03	0.01
2015	0.00	0.02	0.15	0.22	0.13	0.04	0.01
2016	0.00	0.01	0.13	0.21	0.12	0.03	0.01
2017	0.00	0.01	0.09	0.16	0.09	0.02	0.01

**Table 37. Numbers at age at the start of the year for Atlantic menhaden during 1955-2017.**

Year	Age						
	0	1	2	3	4	5	6+
1955	154.9	15.8	6.2	1.8	2.3	0.4	0.1
1956	256.0	26.6	4.0	1.7	0.6	0.8	0.2
1957	108.5	44.0	6.7	0.9	0.5	0.2	0.3
1958	577.5	18.6	11.2	1.7	0.3	0.1	0.2
1959	81.3	99.2	4.8	3.2	0.6	0.1	0.1
1960	58.3	14.0	25.3	1.3	1.0	0.2	0.1
1961	59.0	10.0	3.7	7.8	0.5	0.4	0.1
1962	68.2	10.1	2.5	1.0	2.6	0.2	0.2
1963	46.9	11.7	2.5	0.6	0.3	0.8	0.1
1964	73.8	8.0	2.9	0.6	0.2	0.1	0.4
1965	70.2	12.7	1.9	0.8	0.2	0.1	0.2
1966	86.4	12.0	3.1	0.5	0.2	0.1	0.1
1967	36.3	14.8	3.0	0.9	0.2	0.1	0.1
1968	49.3	6.2	3.7	0.9	0.3	0.1	0.1
1969	57.8	8.5	1.5	1.1	0.3	0.1	0.1
1970	28.7	9.9	2.1	0.5	0.4	0.1	0.1
1971	62.5	4.9	2.4	0.6	0.1	0.1	0.1
1972	57.2	10.7	1.2	0.6	0.2	0.1	0.1
1973	71.8	9.8	2.6	0.2	0.1	0.1	0.1
1974	122.2	12.3	2.4	0.5	0.0	0.0	0.0
1975	189.8	20.9	3.1	0.5	0.1	0.0	0.0
1976	144.3	32.5	5.3	0.8	0.1	0.0	0.0
1977	152.3	24.7	8.3	1.3	0.2	0.0	0.0
1978	115.0	26.1	6.3	2.2	0.4	0.1	0.0
1979	150.2	19.7	6.7	1.6	0.6	0.1	0.0
1980	104.6	25.8	5.0	1.7	0.5	0.2	0.1
1981	149.6	17.9	6.4	1.1	0.4	0.2	0.1
1982	63.1	25.6	4.4	1.4	0.3	0.1	0.1
1983	121.5	10.8	6.3	0.9	0.3	0.1	0.1
1984	187.9	20.8	2.7	1.3	0.2	0.1	0.1
1985	159.6	32.1	5.1	0.6	0.3	0.1	0.1
1986	97.9	27.4	8.2	1.2	0.1	0.1	0.1
1987	87.4	16.8	7.1	2.3	0.4	0.0	0.1
1988	164.2	15.0	4.3	1.9	0.7	0.1	0.0
1989	99.9	28.1	3.8	1.1	0.5	0.2	0.1
1990	164.8	17.1	7.2	0.9	0.3	0.2	0.1
1991	174.0	28.3	4.4	1.8	0.2	0.1	0.1
1992	135.2	29.8	7.3	1.2	0.5	0.1	0.1
1993	113.6	23.2	7.8	2.1	0.4	0.2	0.1
1994	145.7	19.5	6.1	2.3	0.7	0.1	0.1

**Table 37 Continued**

Year	Age						
	0	1	2	3	4	5	6+
1995	86.5	25.0	5.1	1.8	0.8	0.3	0.1
1996	76.5	14.9	6.5	1.5	0.6	0.3	0.2
1997	75.6	13.1	3.9	2.0	0.5	0.2	0.2
1998	132.0	13.0	3.4	1.1	0.6	0.2	0.2
1999	97.4	22.6	3.3	0.9	0.4	0.2	0.2
2000	68.3	16.7	5.9	1.0	0.3	0.1	0.2
2001	95.2	11.7	4.4	1.9	0.3	0.1	0.2
2002	102.6	16.3	3.1	1.3	0.6	0.1	0.1
2003	83.4	17.6	4.3	0.9	0.5	0.3	0.1
2004	78.2	14.3	4.6	1.3	0.3	0.2	0.2
2005	132.2	13.4	3.8	1.4	0.4	0.1	0.2
2006	123.5	22.7	3.5	1.1	0.5	0.2	0.1
2007	77.3	21.2	6.0	1.1	0.4	0.2	0.1
2008	115.7	13.3	5.6	1.9	0.4	0.1	0.1
2009	107.1	19.9	3.5	1.8	0.6	0.1	0.1
2010	203.4	18.4	5.3	1.1	0.6	0.3	0.1
2011	99.3	35.0	4.9	1.6	0.4	0.2	0.2
2012	76.6	17.1	9.3	1.5	0.5	0.1	0.2
2013	100.2	13.2	4.6	3.0	0.5	0.2	0.2
2014	98.1	17.2	3.5	1.5	1.1	0.2	0.2
2015	177.6	16.9	4.6	1.1	0.5	0.4	0.2
2016	163.9	30.5	4.5	1.4	0.4	0.2	0.3
2017	52.9	28.2	8.1	1.4	0.5	0.1	0.2

**Table 38. Fecundity at age for the Atlantic menhaden population during 1955-2017.**

Year	Age						
	0	1	2	3	4	5	6+
1955	0	143496	1312412	774044	1337095	269013	107143
1956	0	224735	805006	787086	364539	597983	160087
1957	0	339757	761923	439124	323259	134244	294662
1958	0	178273	1279387	665634	198301	126835	176865
1959	0	0	546297	1236818	394959	91777	140872
1960	0	169538	1431522	481353	644751	198081	102871
1961	0	93575	723010	2330246	290752	333412	168904
1962	0	111121	409830	451758	1511788	146409	215092
1963	0	140207	411667	271790	212115	692469	162726
1964	0	100994	576888	258364	129233	95710	401015
1965	0	156877	406464	323231	121018	59133	240666
1966	0	125782	691652	224721	149362	51473	117716
1967	0	397811	586495	519180	117605	71064	67843
1968	0	73913	1114050	498681	277873	58540	69272
1969	0	222774	313899	734053	278781	145236	63676
1970	0	312945	464582	248610	374146	159527	120681
1971	0	142011	934607	327580	126141	177985	151269
1972	0	110925	475862	518064	159135	65205	142761
1973	0	75473	395480	170404	163742	65229	99065
1974	0	100251	480417	212344	46927	58266	68424
1975	0	0	366117	240376	85256	16548	59019
1976	0	0	280723	300138	96096	39893	25963
1977	0	0	255997	355908	132000	36392	29692
1978	0	0	179497	448774	213479	62937	24938
1979	0	0	200534	329513	268003	111575	45113
1980	0	0	145663	367852	204110	148065	81075
1981	0	0	80258	181842	202306	108908	100132
1982	0	0	135992	162388	104202	106772	105553
1983	0	0	309246	192054	118998	54734	111741
1984	0	0	138322	296499	96932	65097	66379
1985	0	0	154239	153455	149343	48511	63668
1986	0	0	245945	242018	69641	65649	46705
1987	0	0	202546	471390	158461	35925	61252
1988	0	0	137065	376227	280105	90216	47707
1989	0	0	121426	221057	215481	145759	67236
1990	0	155225	593458	201707	109040	107997	92413
1991	0	221224	669404	657218	106188	50942	97298
1992	0	321734	800052	451390	307217	55043	61549
1993	0	0	1230902	777864	209653	143392	59372
1994	0	204408	510082	986273	429136	98305	104285

**Table 38 Continued**

Year	Age						
	0	1	2	3	4	5	6+
1995	0	0	1024550	715290	562407	224454	91452
1996	0	0	1077113	691952	417483	277314	167823
1997	0	0	596855	1087900	377241	239079	249631
1998	0	0	275588	605543	539882	191839	290586
1999	0	275122	386505	358152	296026	267849	215141
2000	0	161924	1230028	403695	218211	154830	251361
2001	0	96249	1237750	872184	233597	119509	207125
2002	0	202223	693894	877895	477692	120854	159781
2003	0	165537	906539	525780	433003	248319	131746
2004	0	138496	733115	533768	239674	219621	204941
2005	0	0	572802	587581	246091	107436	220261
2006	0	192371	387875	446915	314954	107392	119161
2007	0	215260	950658	419161	231567	145023	89692
2008	0	146676	933737	714388	233948	112617	135838
2009	0	222186	701626	711640	350375	117737	123979
2010	0	207986	638664	431871	352666	157874	121605
2011	0	413412	815880	581670	200114	153409	111010
2012	0	837893	1528906	586606	313244	86194	126963
2013	0	348475	971829	1120887	286809	160910	98732
2014	0	184103	746443	585079	503499	134107	157123
2015	0	192728	566379	430816	278531	254549	119060
2016	0	385884	721589	501143	166469	125464	179139
2017	0	325891	1300241	518554	220542	78948	157374



**Table 39. Age-1+ biomass at age at the start of the year during 1955-2017.**

Year	Age					
	1	2	3	4	5	6+
1955	1035.7	1352.2	620.3	964.4	194.0	77.3
1956	1620.0	829.4	630.7	262.9	431.3	115.5
1957	2452.6	1099.2	351.9	233.1	96.8	212.5
1958	1285.5	1845.4	533.4	143.0	91.5	127.6
1959	4563.0	787.9	991.2	284.9	66.2	101.6
1960	1223.0	3440.5	385.7	465.0	142.9	74.2
1961	675.1	744.8	2100.7	209.7	240.5	121.8
1962	801.6	492.5	362.0	1090.3	105.6	155.1
1963	1010.7	494.9	217.8	153.0	499.4	117.4
1964	728.2	594.4	207.0	93.2	69.0	289.2
1965	1131.3	418.8	259.0	87.3	42.6	173.6
1966	907.1	712.7	180.1	107.7	37.1	84.9
1967	1434.3	604.4	374.5	84.8	51.2	48.9
1968	532.8	1004.4	359.6	200.4	42.2	50.0
1969	803.1	323.4	529.4	201.1	104.7	45.9
1970	1128.5	478.7	179.3	269.8	115.1	87.0
1971	512.2	748.9	236.3	91.0	128.4	109.1
1972	799.8	381.3	373.7	114.8	47.0	103.0
1973	544.4	475.4	122.9	118.1	47.0	71.4
1974	722.5	494.9	170.1	33.8	42.0	49.3
1975	1015.1	527.9	192.6	61.5	11.9	42.6
1976	1285.3	674.9	240.5	69.3	28.8	18.7
1977	875.7	923.3	320.9	95.2	26.2	21.4
1978	956.3	647.5	462.4	154.0	45.4	18.0
1979	820.3	722.9	339.6	214.8	80.5	32.5
1980	922.0	525.5	378.9	163.6	106.8	58.5
1981	687.6	578.9	218.5	162.1	78.5	72.2
1982	1116.7	490.6	234.2	83.5	77.0	76.1
1983	425.6	743.7	197.9	95.4	39.5	80.6
1984	871.3	332.7	305.5	77.7	47.0	47.9
1985	1246.8	556.1	138.3	119.7	35.0	45.9
1986	1009.9	886.9	249.3	50.2	47.4	33.7
1987	690.5	730.5	485.7	127.0	25.9	44.2
1988	562.7	494.4	387.6	224.5	65.1	34.4
1989	1345.4	438.0	227.8	172.7	105.1	48.5
1990	1118.7	1070.3	207.9	87.4	77.9	66.7
1991	1594.9	804.5	526.7	85.1	36.7	70.2
1992	2319.3	1154.3	361.7	221.6	39.7	44.4
1993	1182.1	1479.9	623.3	151.2	103.4	42.8
1994	1474.9	919.8	790.4	309.5	70.9	75.2

**Table 39 Continued**

Year	Age					
	1	2	3	4	5	6+
1996	616.4	1294.7	554.5	301.1	200.0	121.0
1997	516.1	717.3	784.5	272.0	172.4	180.0
1998	638.7	496.8	436.7	389.4	138.4	209.6
1999	1985.3	557.6	287.0	213.5	193.2	155.2
2000	1167.8	1267.5	323.5	157.4	111.7	181.3
2001	694.5	1115.8	698.9	168.5	86.2	149.4
2002	1457.9	714.9	633.2	344.5	87.2	115.2
2003	1193.3	934.1	379.2	312.3	179.1	95.0
2004	998.5	881.2	427.7	172.9	158.4	147.8
2005	554.9	688.6	470.8	177.5	77.5	158.9
2006	1386.7	559.5	358.2	227.2	77.5	85.9
2007	1552.5	1142.7	335.9	167.0	104.6	64.7
2008	1058.1	1122.3	572.5	168.7	81.2	98.0
2009	1601.5	722.7	570.2	252.7	84.9	89.4
2010	1500.8	921.0	346.1	254.3	113.9	87.7
2011	2980.2	980.7	466.1	144.3	110.6	80.1
2012	2014.3	1837.9	470.1	225.9	62.2	91.6
2013	1256.4	1001.2	898.1	206.9	116.0	71.2
2014	1327.8	769.1	468.9	403.5	96.7	113.3
2015	1390.8	816.8	345.2	200.9	183.6	85.9
2016	2782.5	867.3	401.6	133.4	90.5	129.2
2017	2351.7	1562.7	415.5	176.7	56.9	113.5

**Table 40. Recruitment in billions of fish during 1955-2017.**

Year	Recruits	Year	Recruits
1955	154.9	1987	87.4
1956	256.0	1988	164.2
1957	108.5	1989	99.9
1958	577.5	1990	164.8
1959	81.3	1991	174.0
1960	58.3	1992	135.2
1961	59.0	1993	113.6
1962	68.2	1994	145.7
1963	46.9	1995	86.5
1964	73.8	1996	76.5
1965	70.2	1997	75.6
1966	86.4	1998	132.0
1967	36.3	1999	97.4
1968	49.3	2000	68.3
1969	57.8	2001	95.2
1970	28.7	2002	102.6
1971	62.5	2003	83.4
1972	57.2	2004	78.2
1973	71.8	2005	132.2
1974	122.2	2006	123.5
1975	189.8	2007	77.3
1976	144.3	2008	115.7
1977	152.3	2009	107.1
1978	115.0	2010	203.4
1979	150.2	2011	99.3
1980	104.6	2012	76.6
1981	149.6	2013	100.2
1982	63.1	2014	98.1
1983	121.5	2015	177.6
1984	187.9	2016	163.9
1985	159.6	2017	52.9
1986	97.9		

**Table 41. Current fishing mortality and fecundity benchmarks (targets and thresholds) along with terminal year values from the base run of the BAM. Fecundity (*FEC*) is in billions of eggs.**

Current Reference Points	Benchmark	Terminal year value
$F_{\text{THRESHOLD}}$	0.60	0.11
$F_{\text{TARGET}}$	0.22	0.11
$FEC_{\text{THRESHOLD}}$	1,463,344	2,601,550
$FEC_{\text{TARGET}}$	1,945,613	2,601,550

13 FIGURES

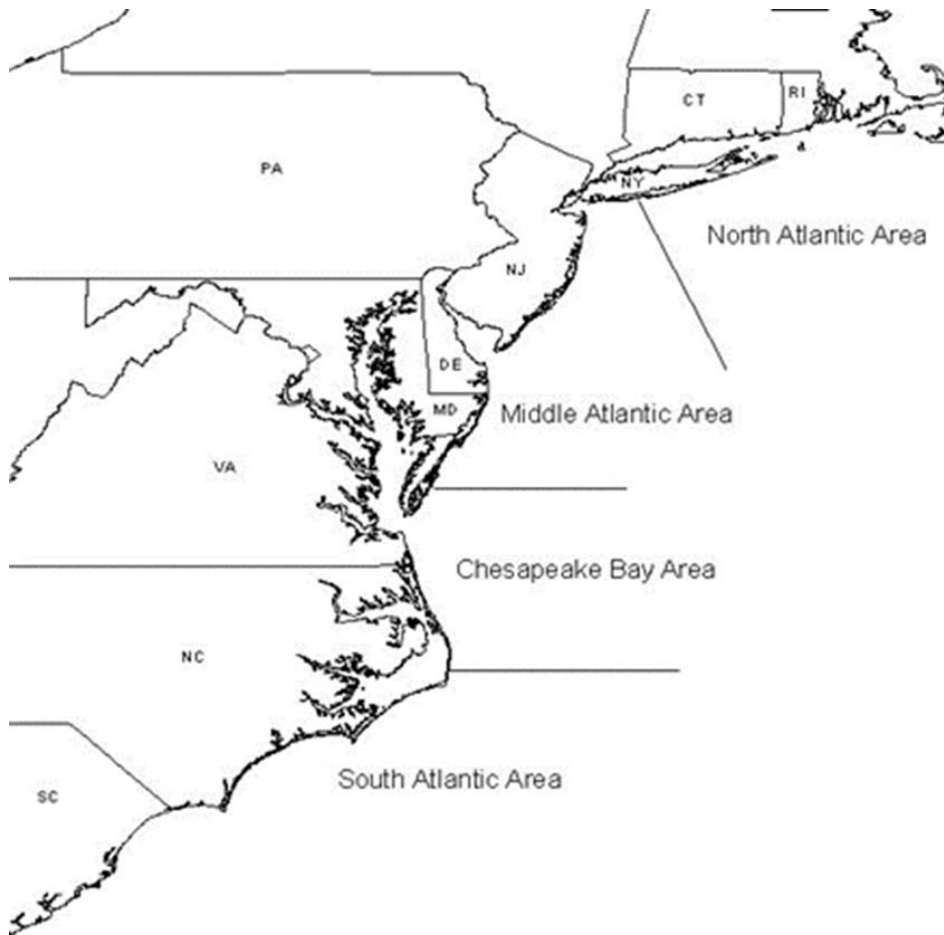
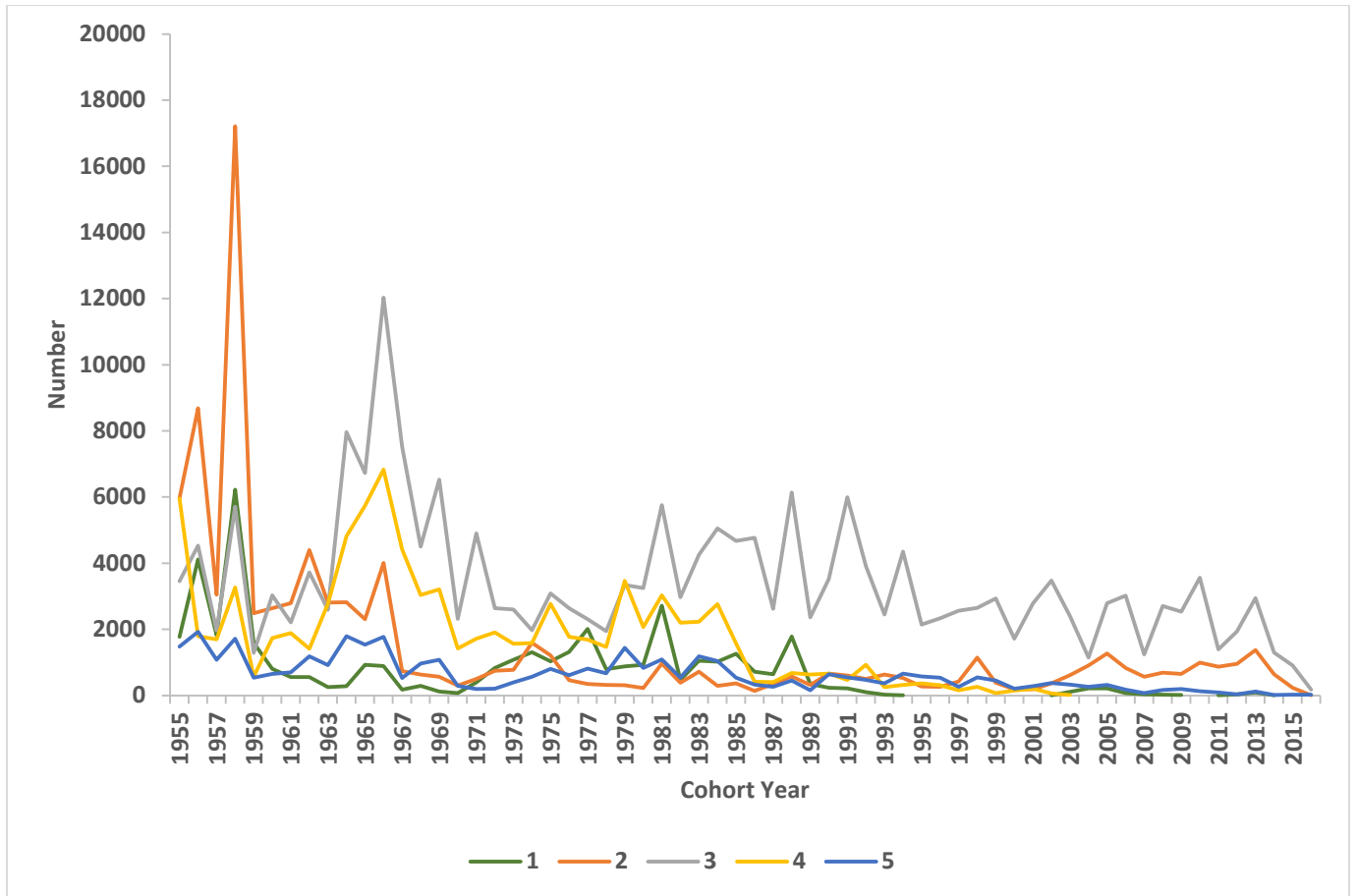
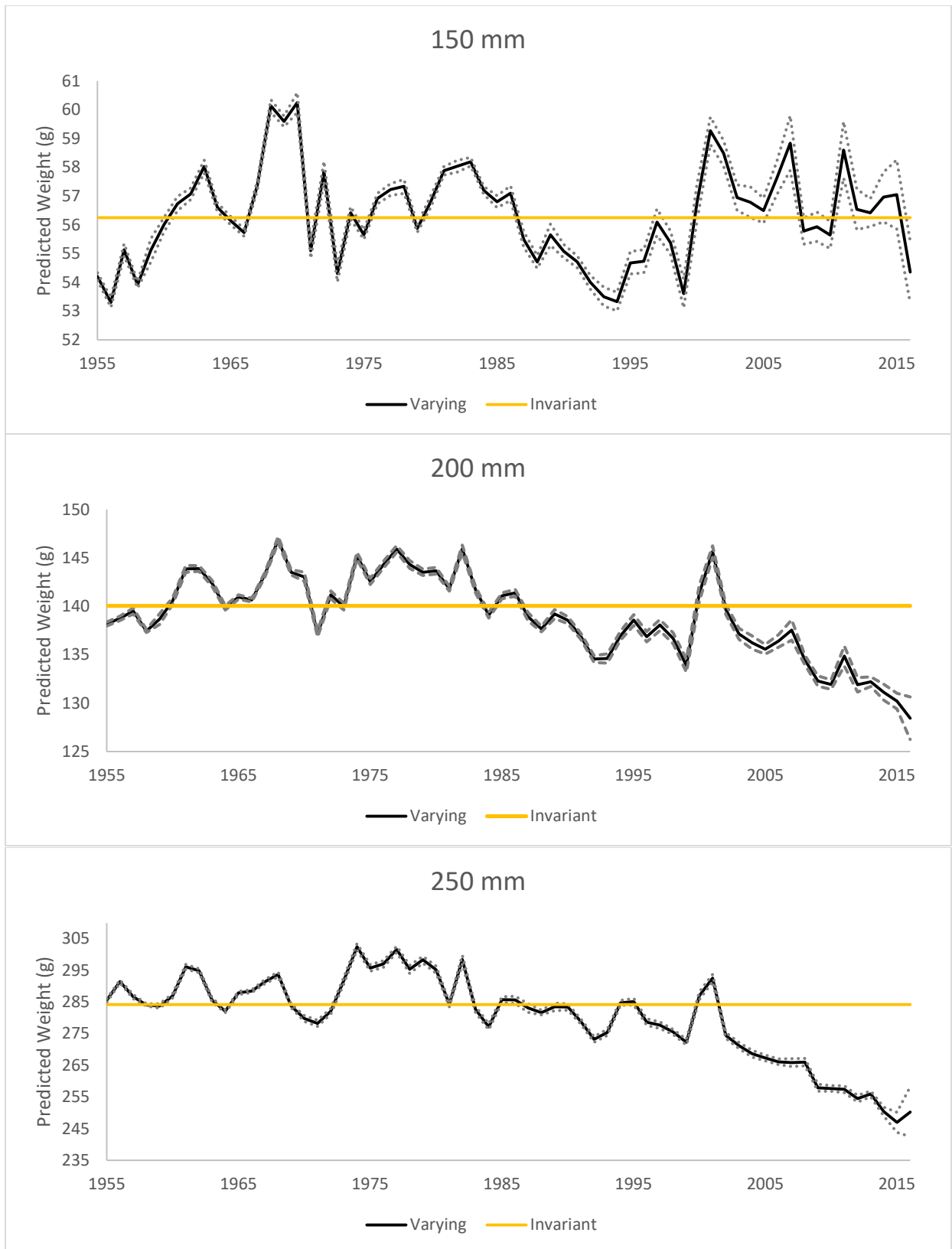


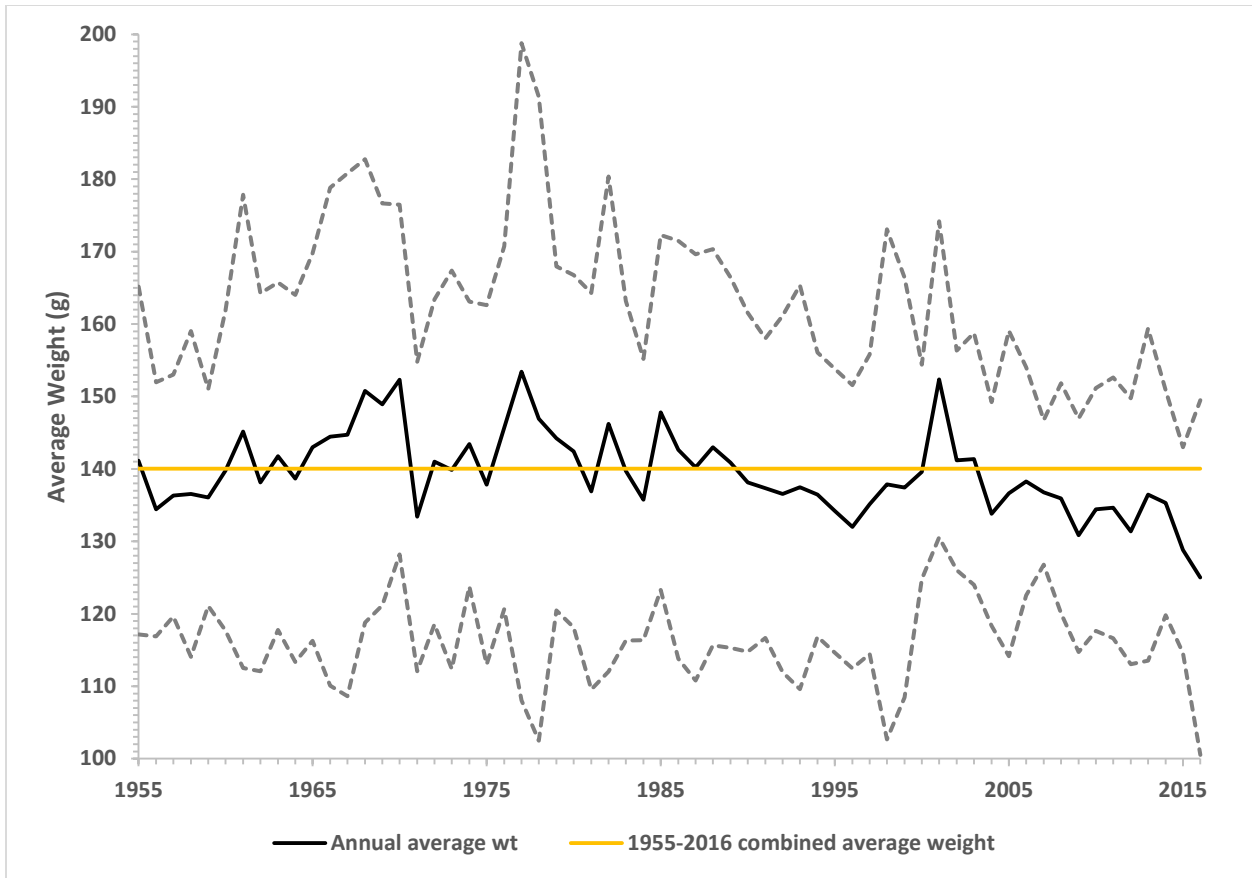
Figure 1. Regions used in the biological sampling program for the commercial reduction fishery.



**Figure 2. Number of paired length-weight measurements by cohort year and sampling area (1-5) from the reduction fishery. The areas represent North Atlantic (1), Middle Atlantic (2), Chesapeake Bay (3), South Atlantic (4), and the fall fishery off North Carolina (5).**

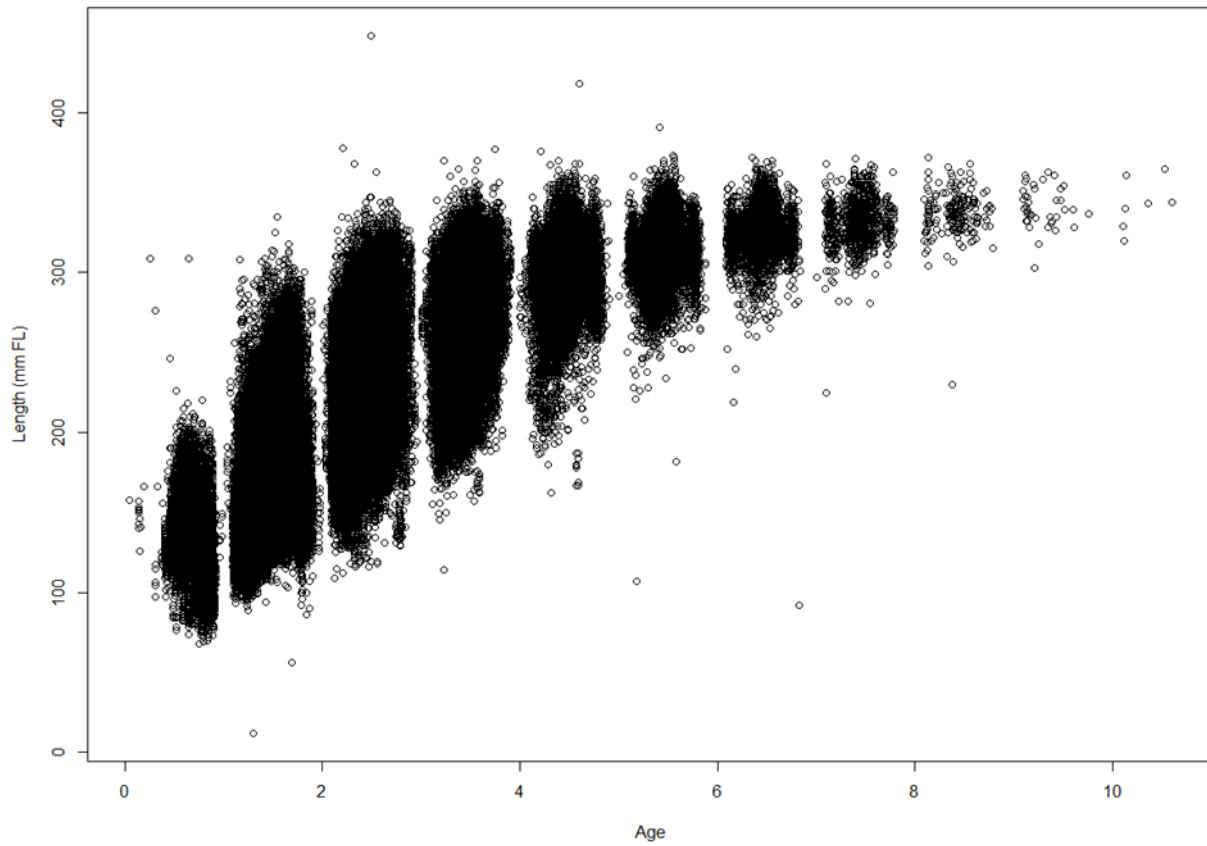


**Figure 3. Comparison between time-varying, with dashed 95% confidence intervals, and time-invariant predicted weight for three fork lengths (150, 200, and 250 mm).**



**Figure 4. Average weight of a 200 mm Atlantic menhaden in sampling area 3 (Chesapeake Bay) from 1955-2015 by year with 95% confidence intervals and on average, in yellow.**





**Figure 5. Age and length (FL in mm) for Atlantic menhaden sampled during 1955-2011 (from Schueller et al. 2014).**

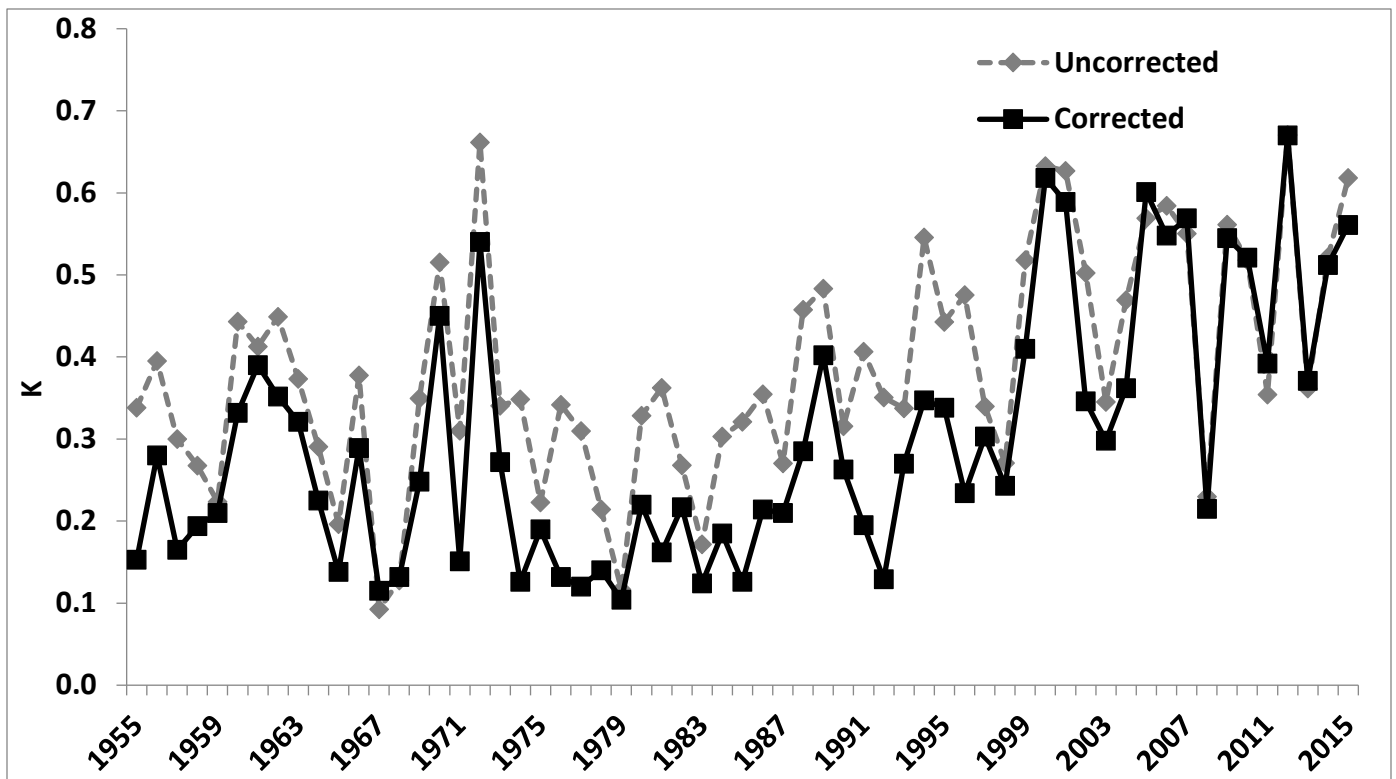
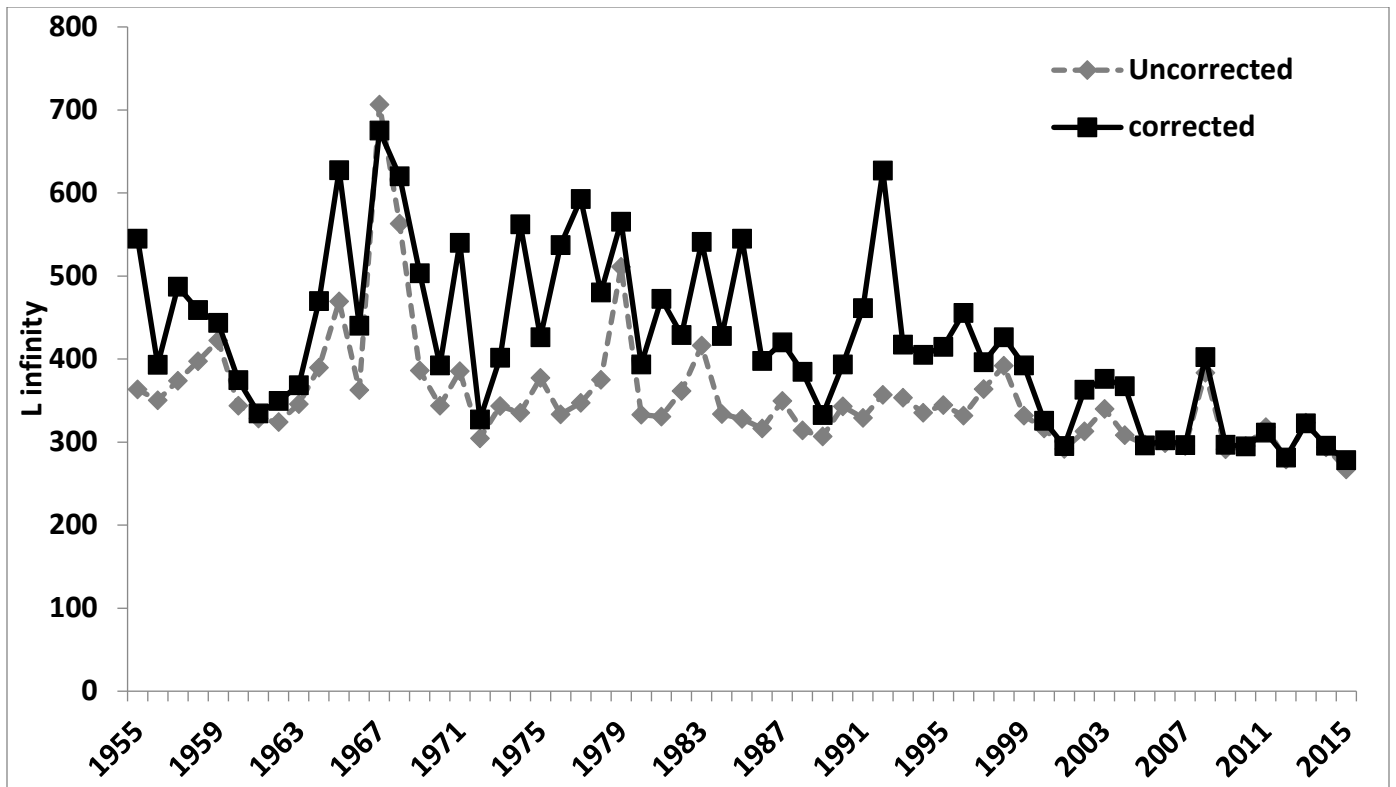


Figure 6. A comparison of the estimated annual, cohort-based von Bertalanffy growth coefficients  $L_{\infty}$  (top) and  $K$  (bottom) with and without the bias correction as detailed in Schueller et al. (2014).

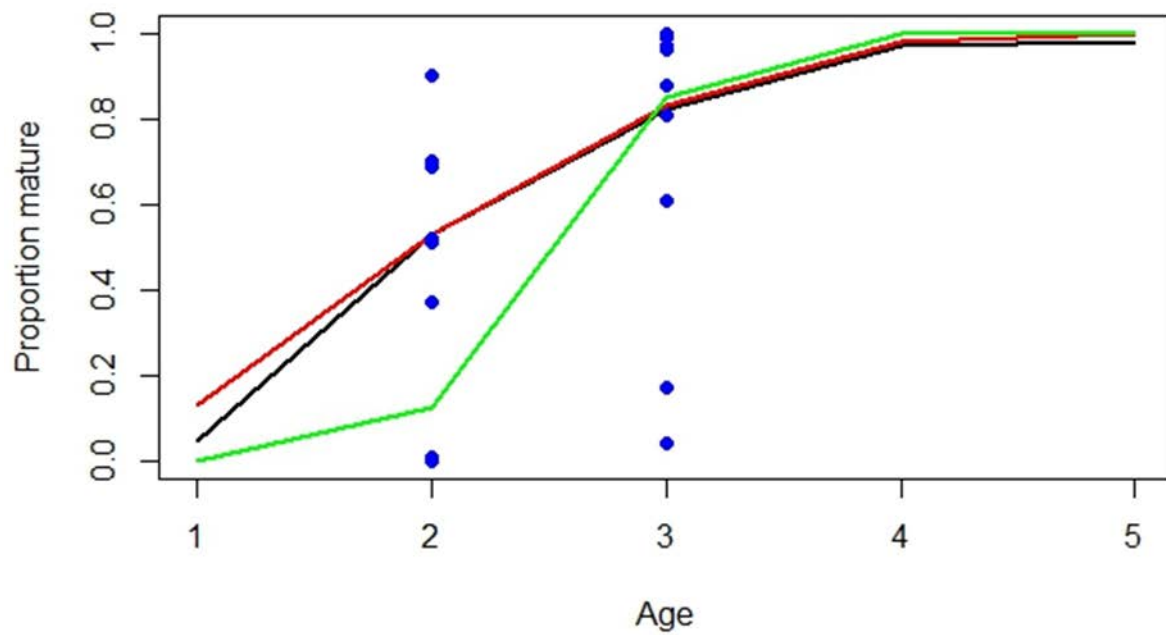
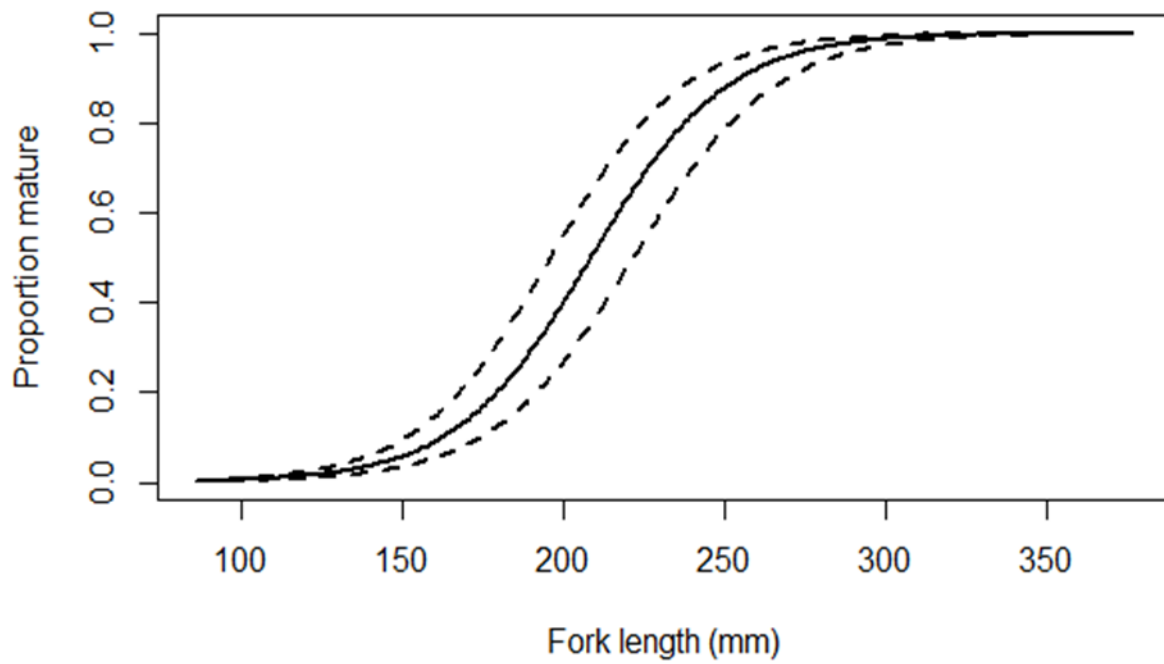
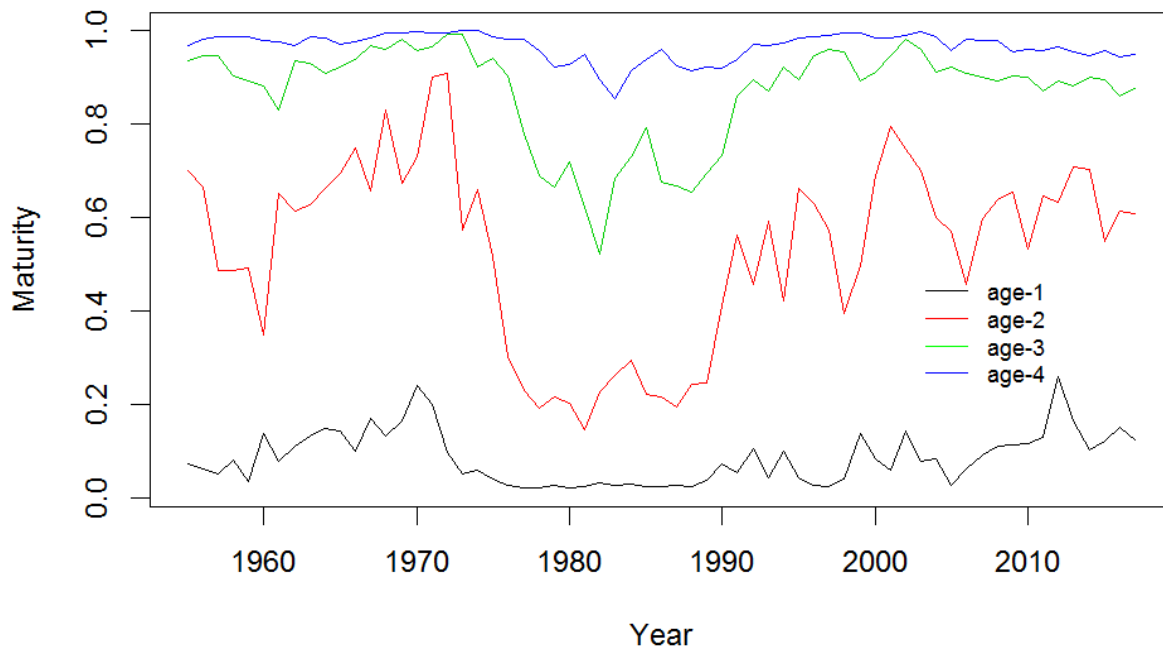


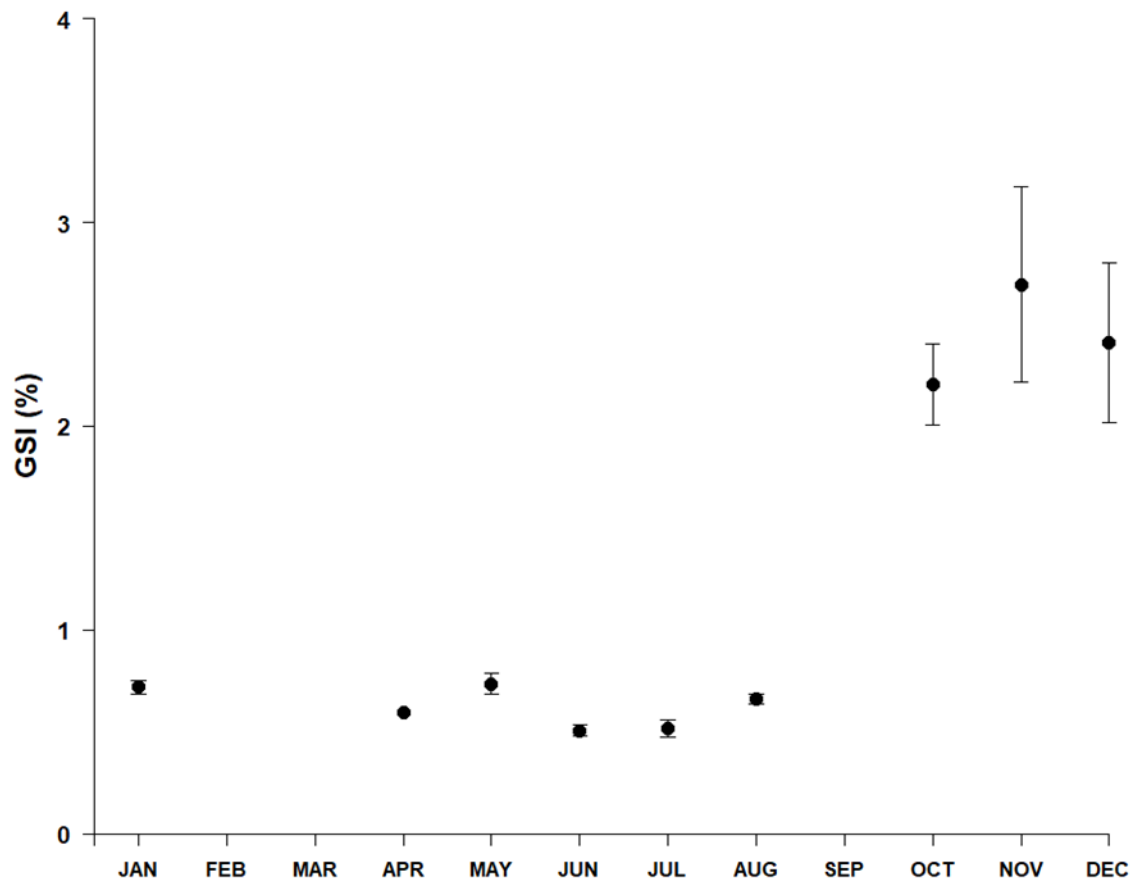
Figure 7. Average maturity-at-age from commercial reduction fishery sampling (black), NEAMAP survey (red), and Higham and Nicholson (1964; green).



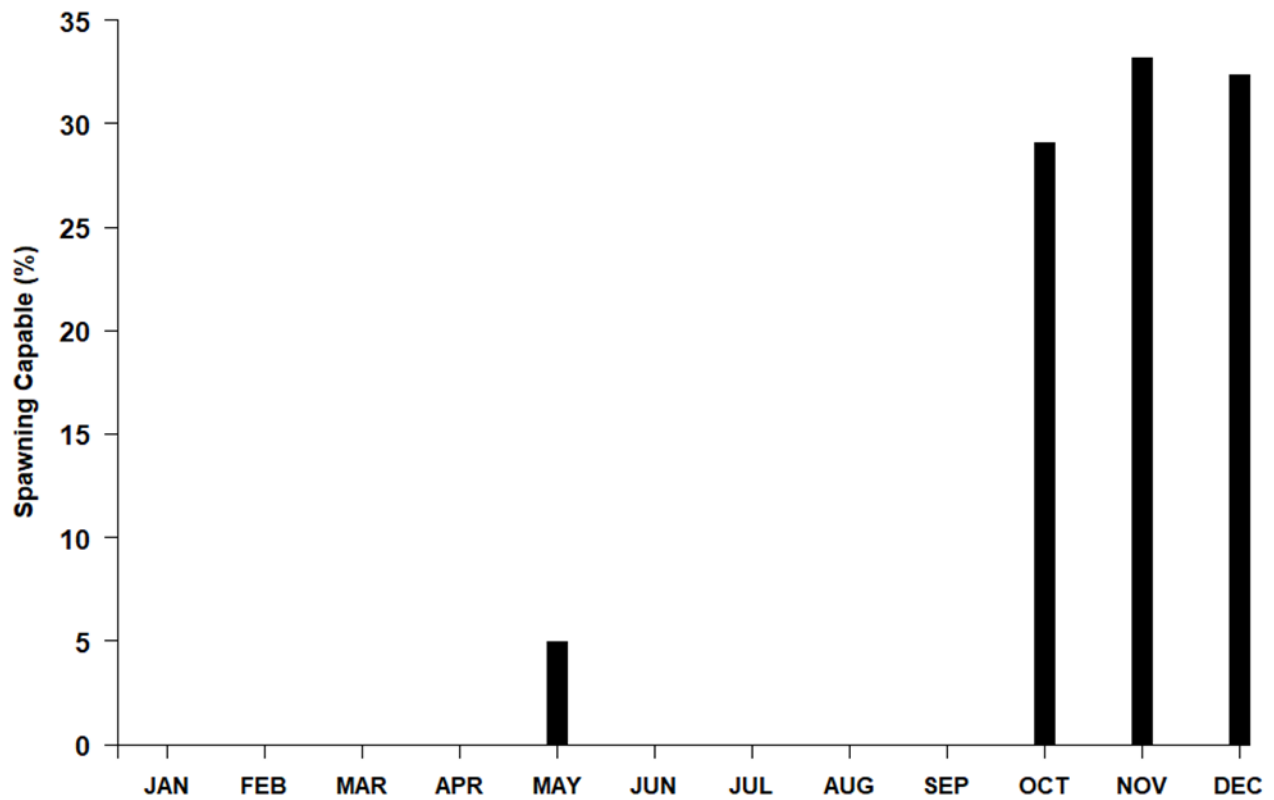
**Figure 8. Predicted logistic regression line for Atlantic menhaden female maturity based on length, with 95% confidence intervals.**



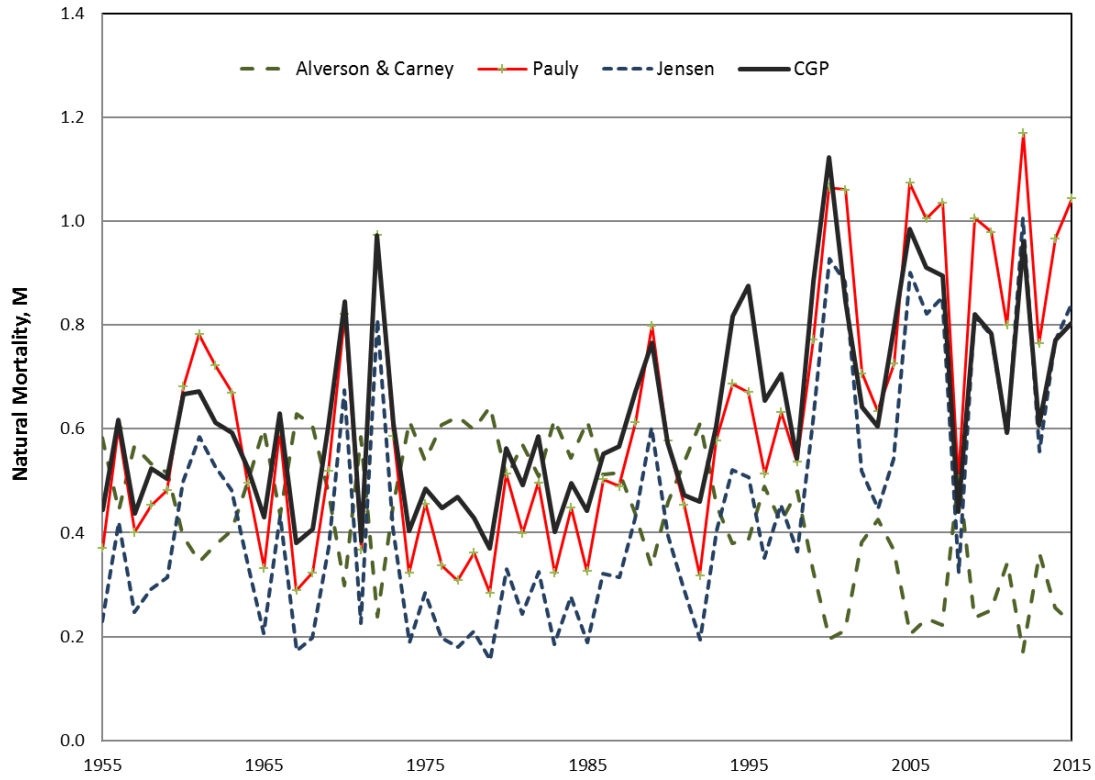
**Figure 9. Atlantic menhaden maturity by year and age. Age-0 menhaden are immature, while fish of age-5 and older are 100% mature.**



**Figure 10. Mean monthly gonadosomatic index (GSI) for female Atlantic menhaden collected from 2013-2018. Error bars represent standard errors of the means.**



**Figure 11. Monthly percentage of female Atlantic menhaden in the spawning capable gonad phase (including the actively spawning sub-phase). Fish were collected from 2013-2018 in an effort to characterize the reproductive biology and fecundity for this species.**



**Figure 12. Annual calculated values of  $M$  from age-constant  $M$  approaches and average  $M$  across ages 1-10.**



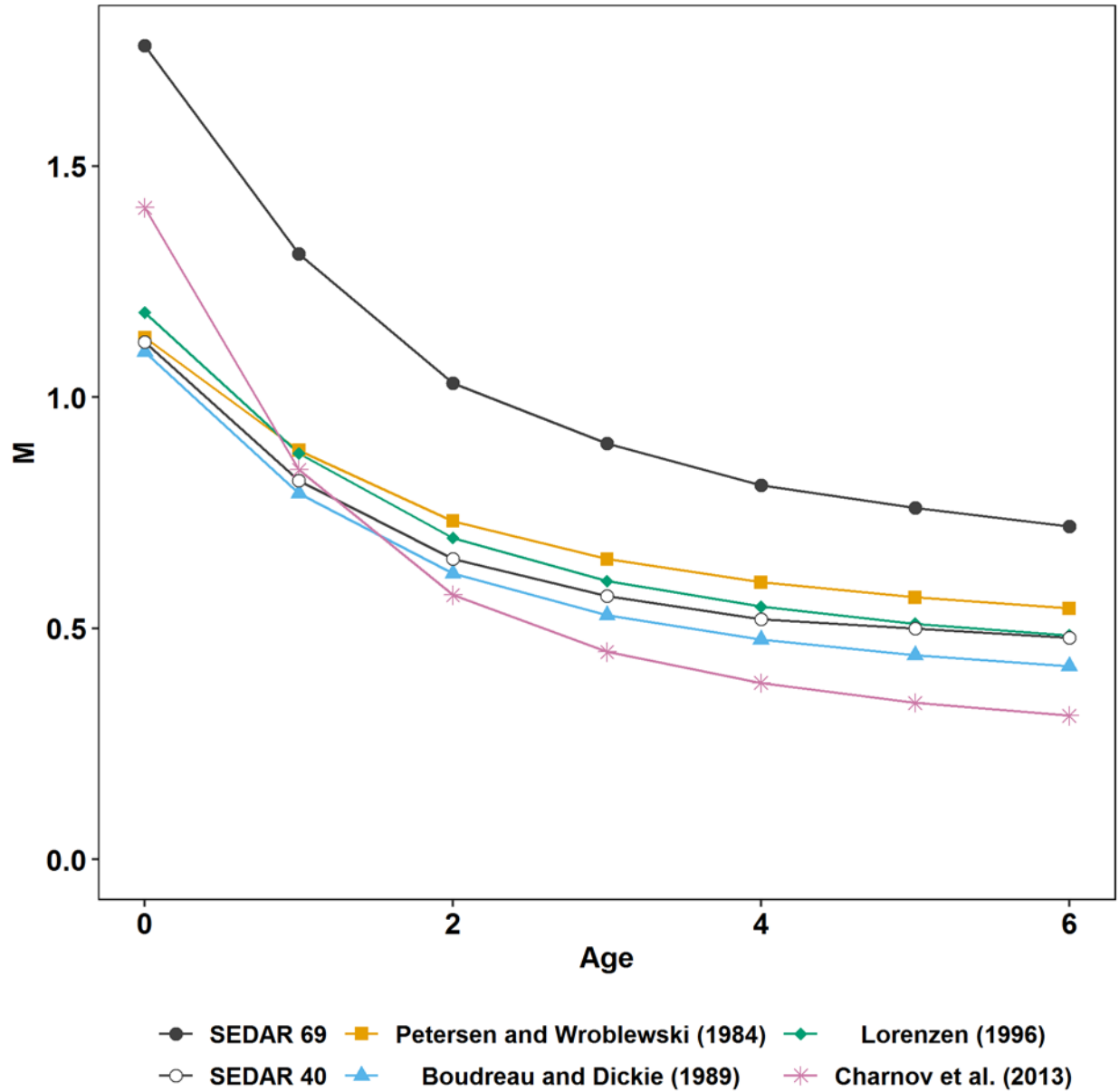


Figure 13. Estimates of age-varying natural mortality ( $M$ ) from different methods including the estimate used in this assessment (SEDAR 69) and the method used in the previous benchmark assessment (SEDAR 40).

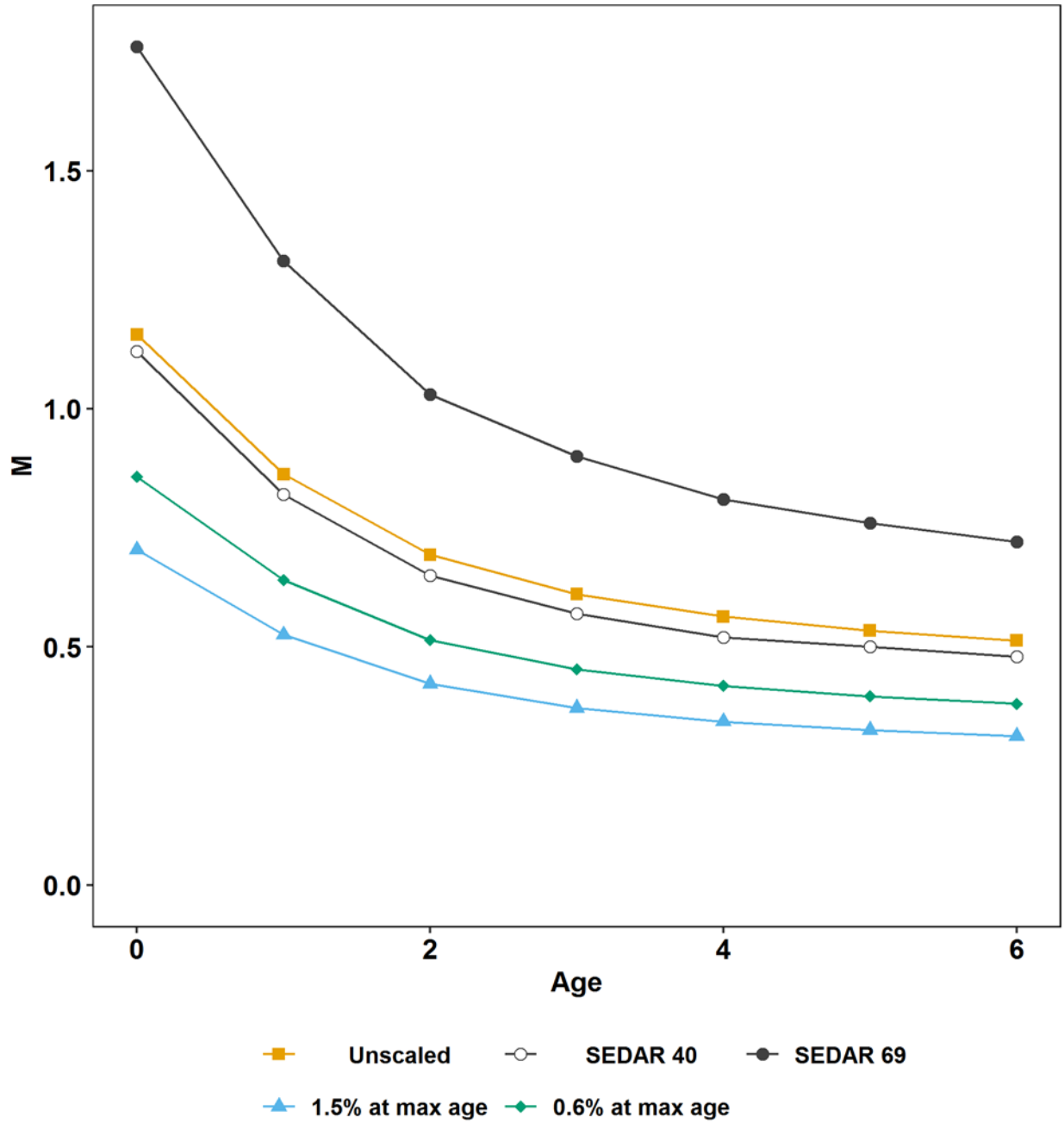
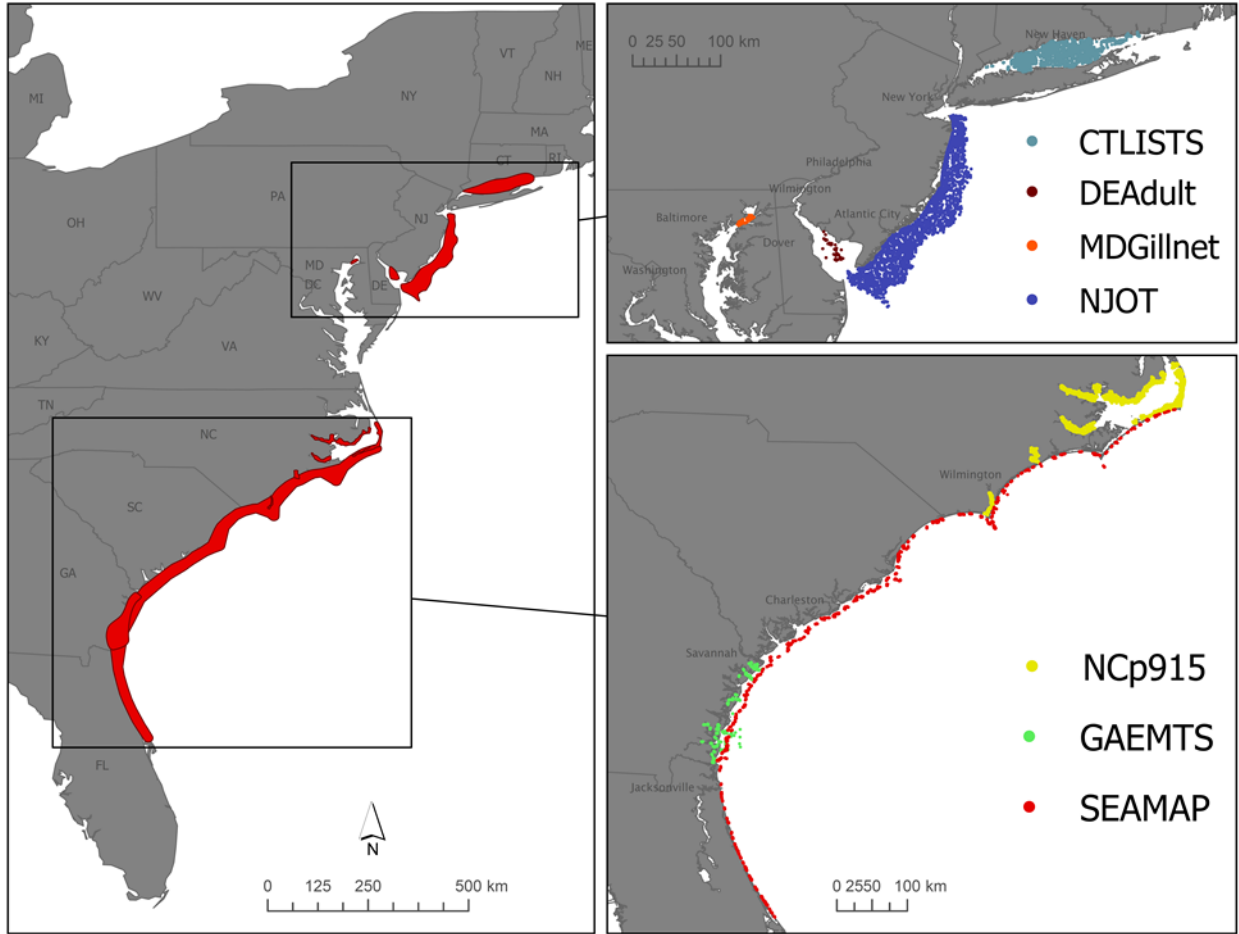
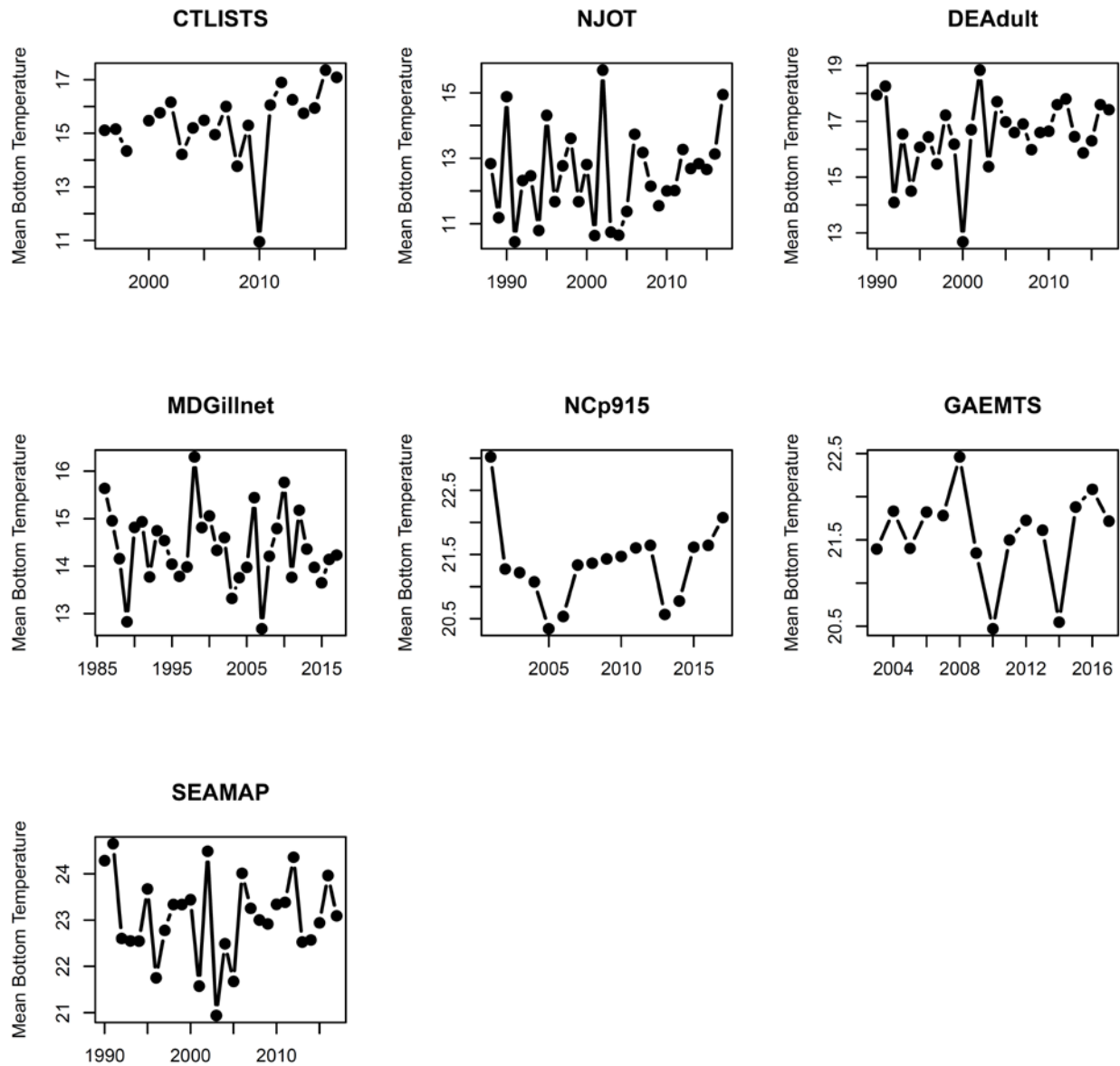


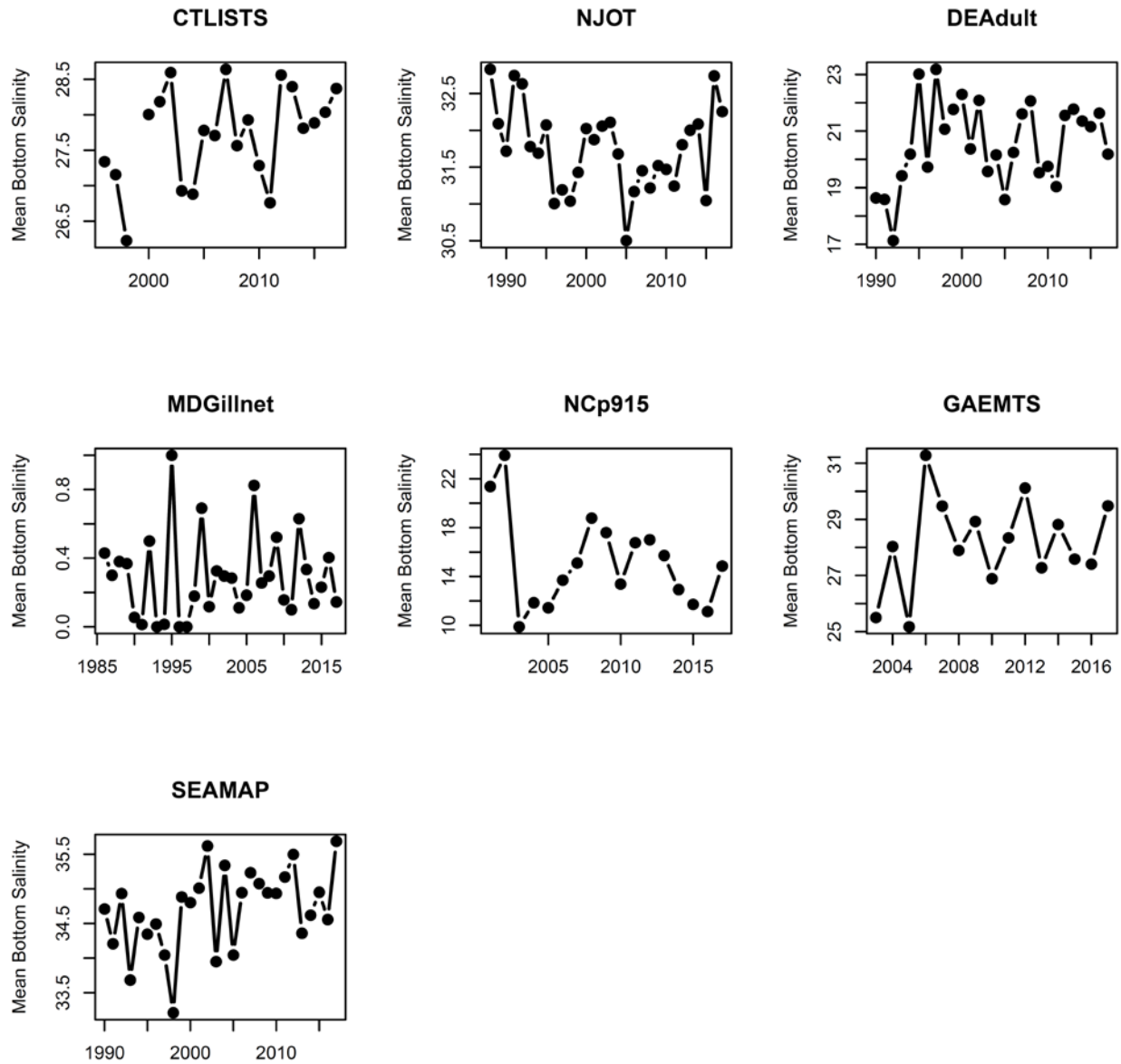
Figure 14. Estimates of age-varying natural mortality ( $M$ ) from the Lorenzen (1996) method, scaled either to empirical estimates from tagging (SEDAR 40, SEDAR 69) or to the percent of the population surviving to the maximum age.



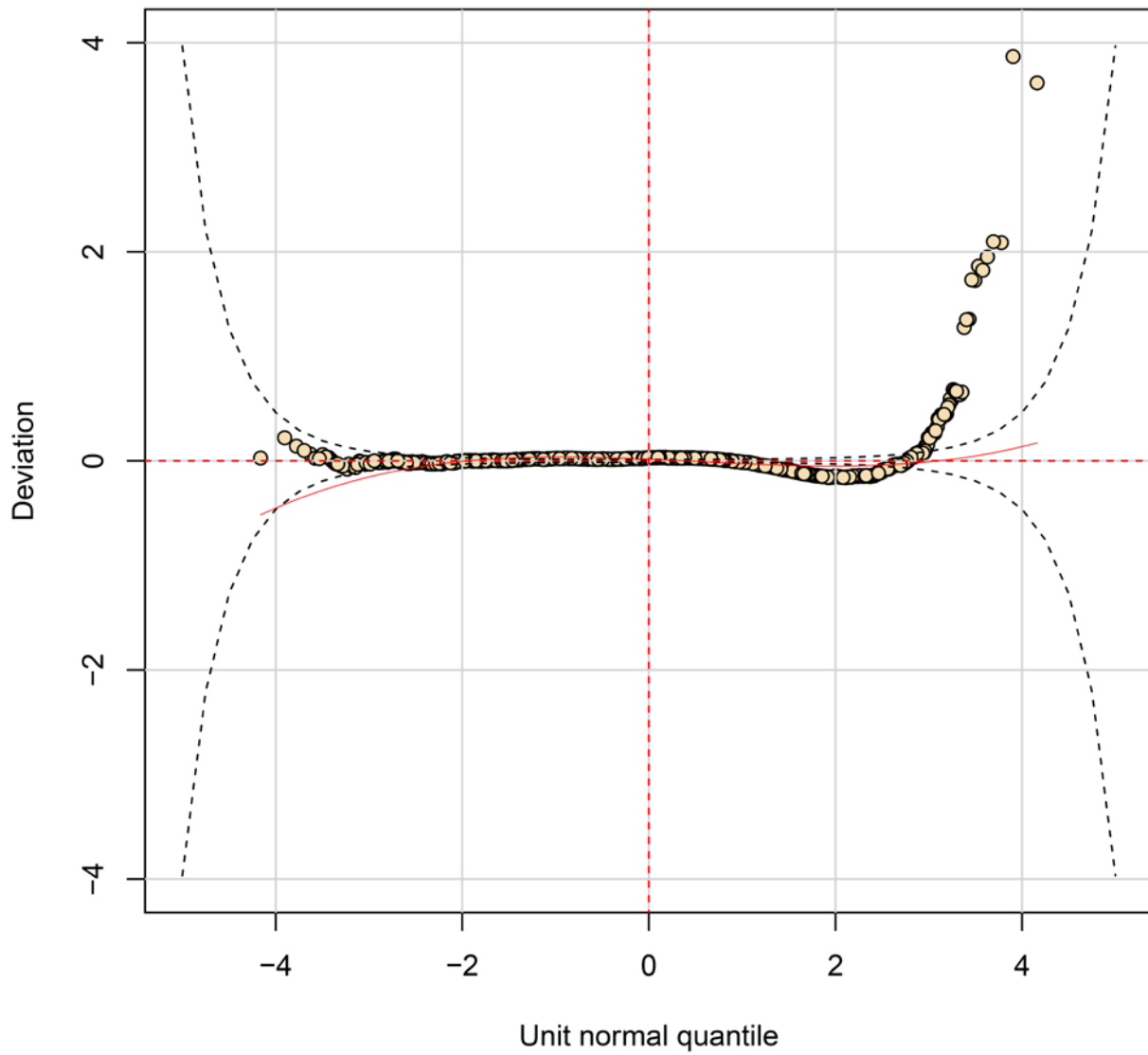
**Figure 15. Map depicting the sampling areas and locations of the seven surveys that provided data for the analysis of age 1+ Atlantic menhaden habitat preferences.**



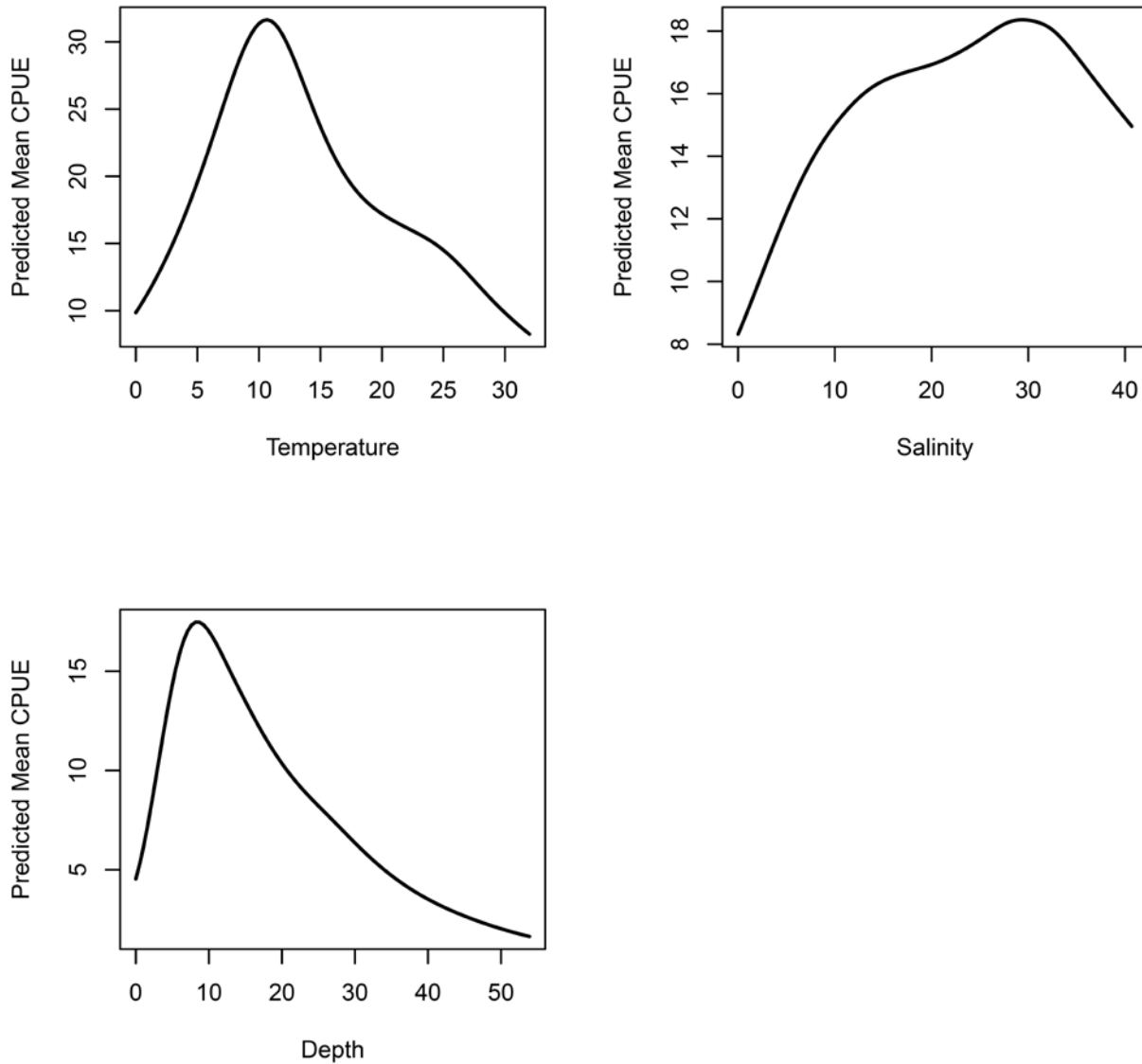
**Figure 16. Annual mean bottom water temperature (°C) associated with each of the seven surveys that provided data for the analysis of age 1+ Atlantic menhaden habitat preferences.**



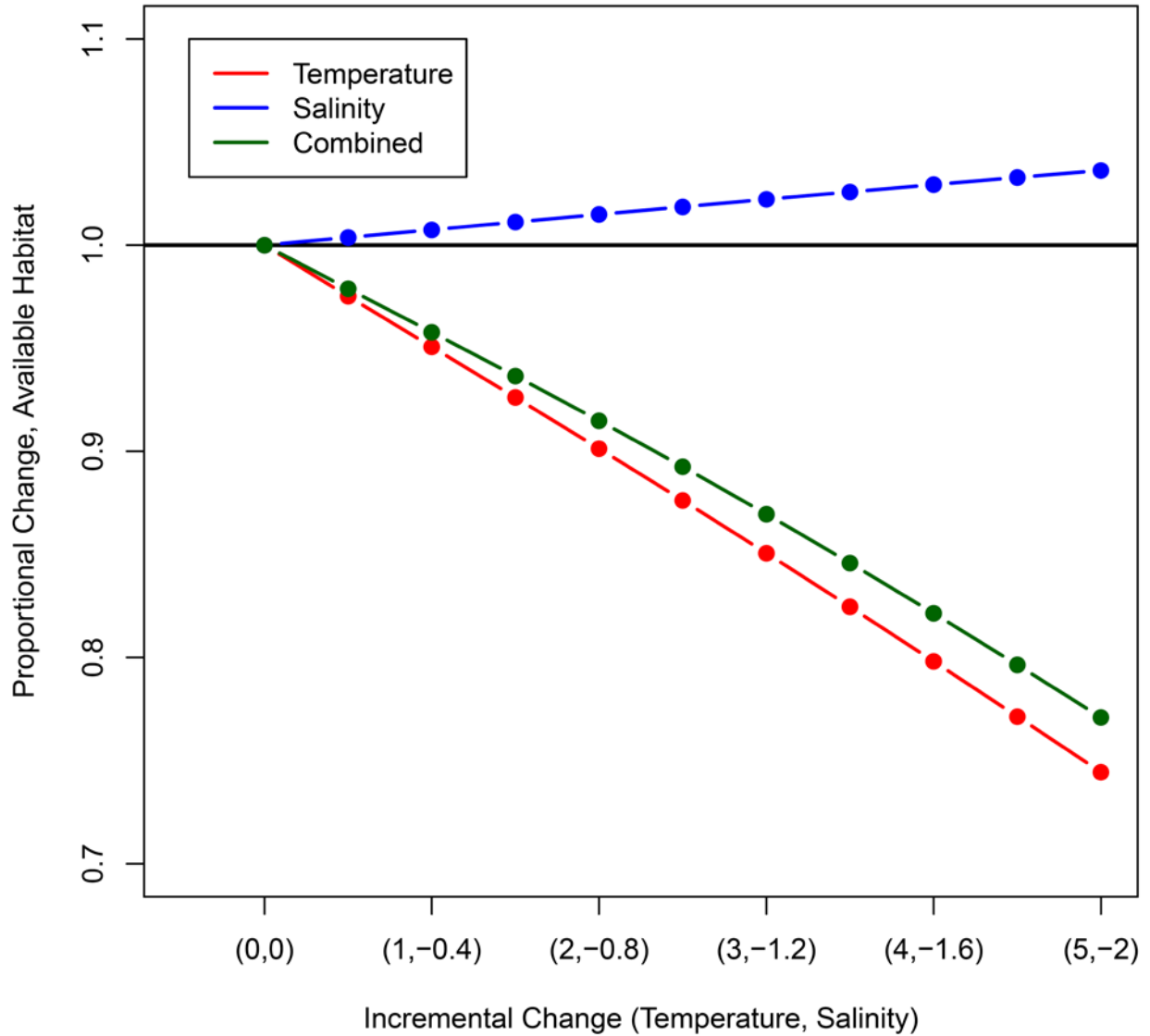
**Figure 17. Annual mean bottom salinity (ppt) associated with each of the seven surveys that provided data for the analysis of age 1+ Atlantic menhaden habitat preferences.**



**Figure 18. Worm plot of the most empirically supported GAMM, which reflected the fully saturated parameterization for the conditional and zero-inflated model components.**



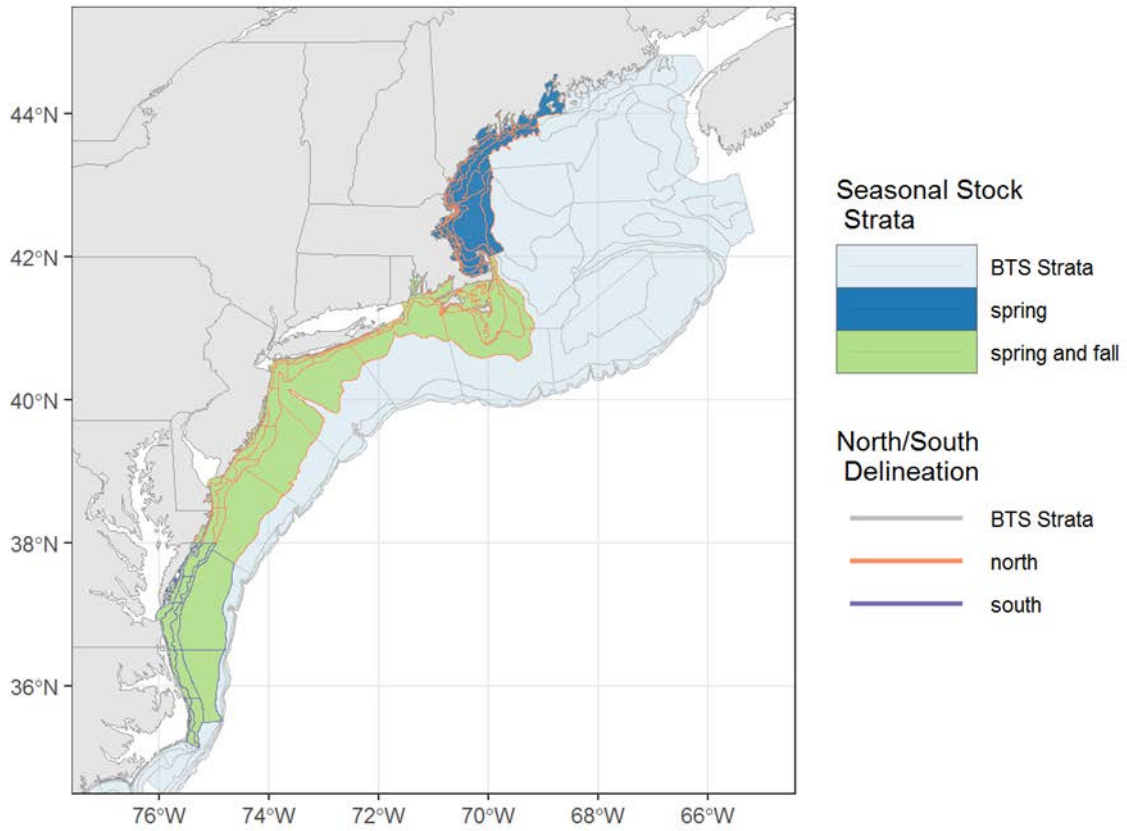
**Figure 19. Habitat preferences derived from the most empirically supported GAMM calculated as marginal means.**



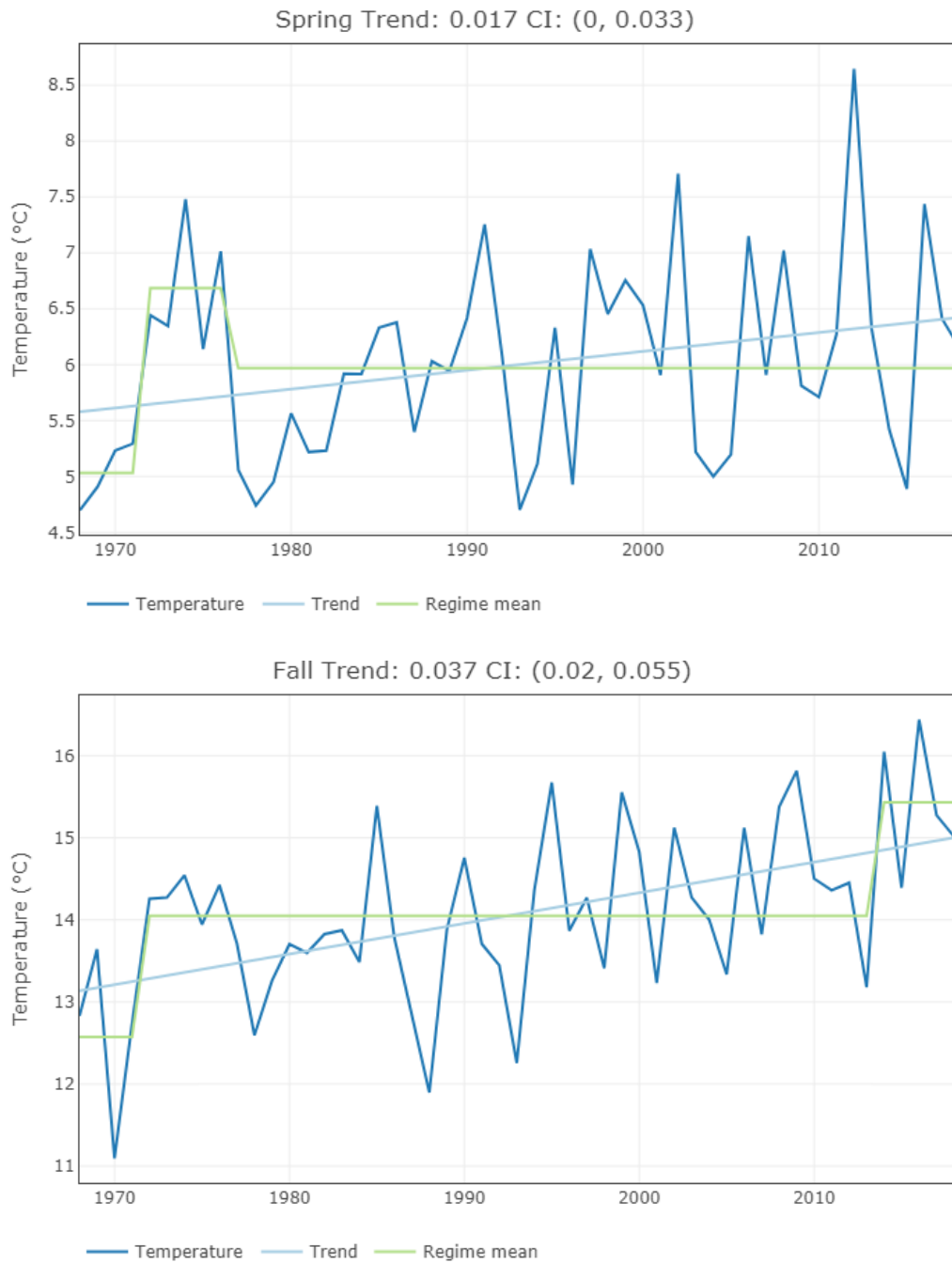
**Figure 20. Projections of proportional changes available habitat relative to ‘present day habitat conditions’ under various hypothesized climate change scenarios involving increased bottom water temperature (blue), decreased salinity (red), and pairwise combinations of increased bottom water temperature and decreased bottom salinity (dark green).**



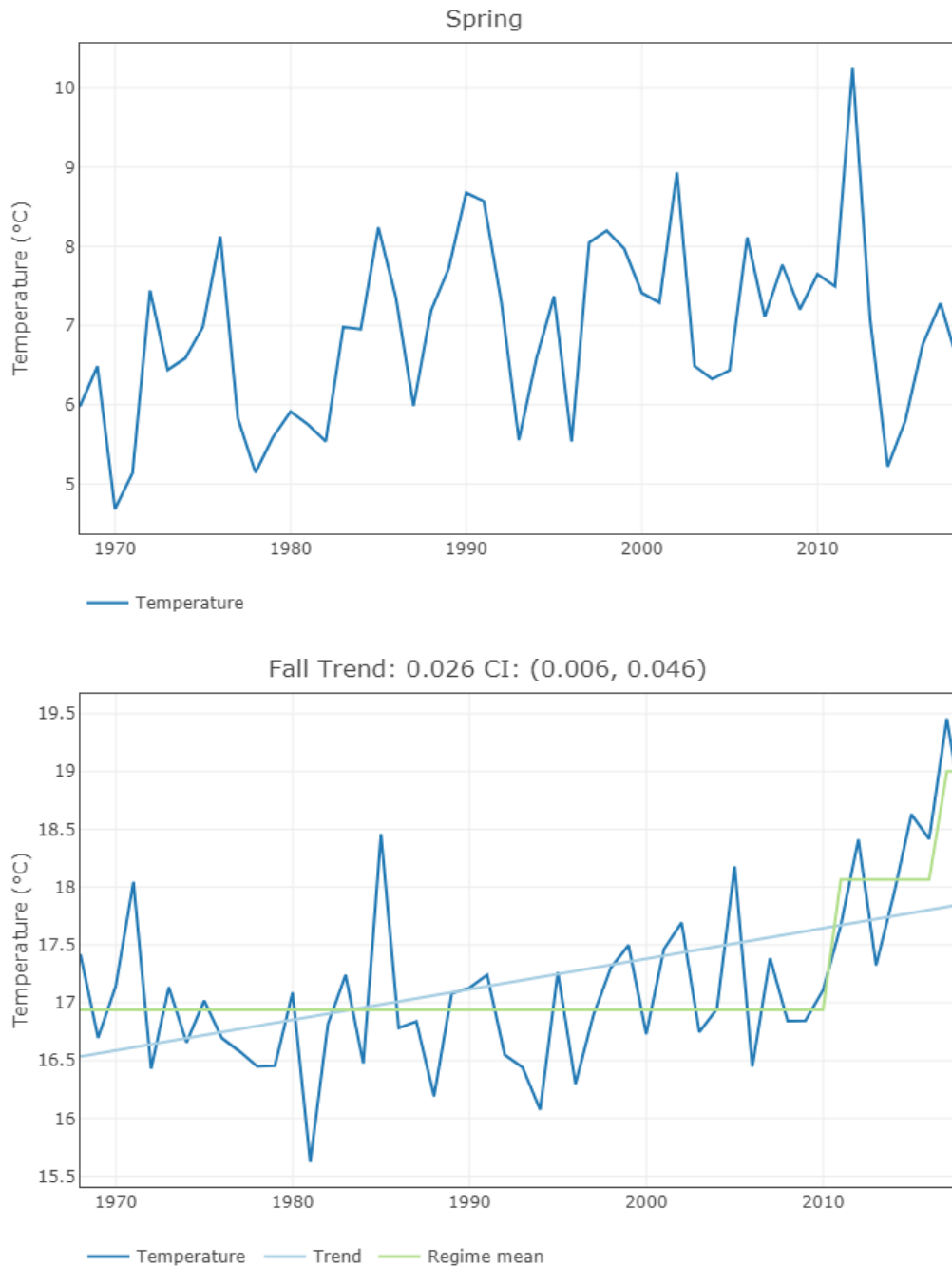
### Atlantic menhaden



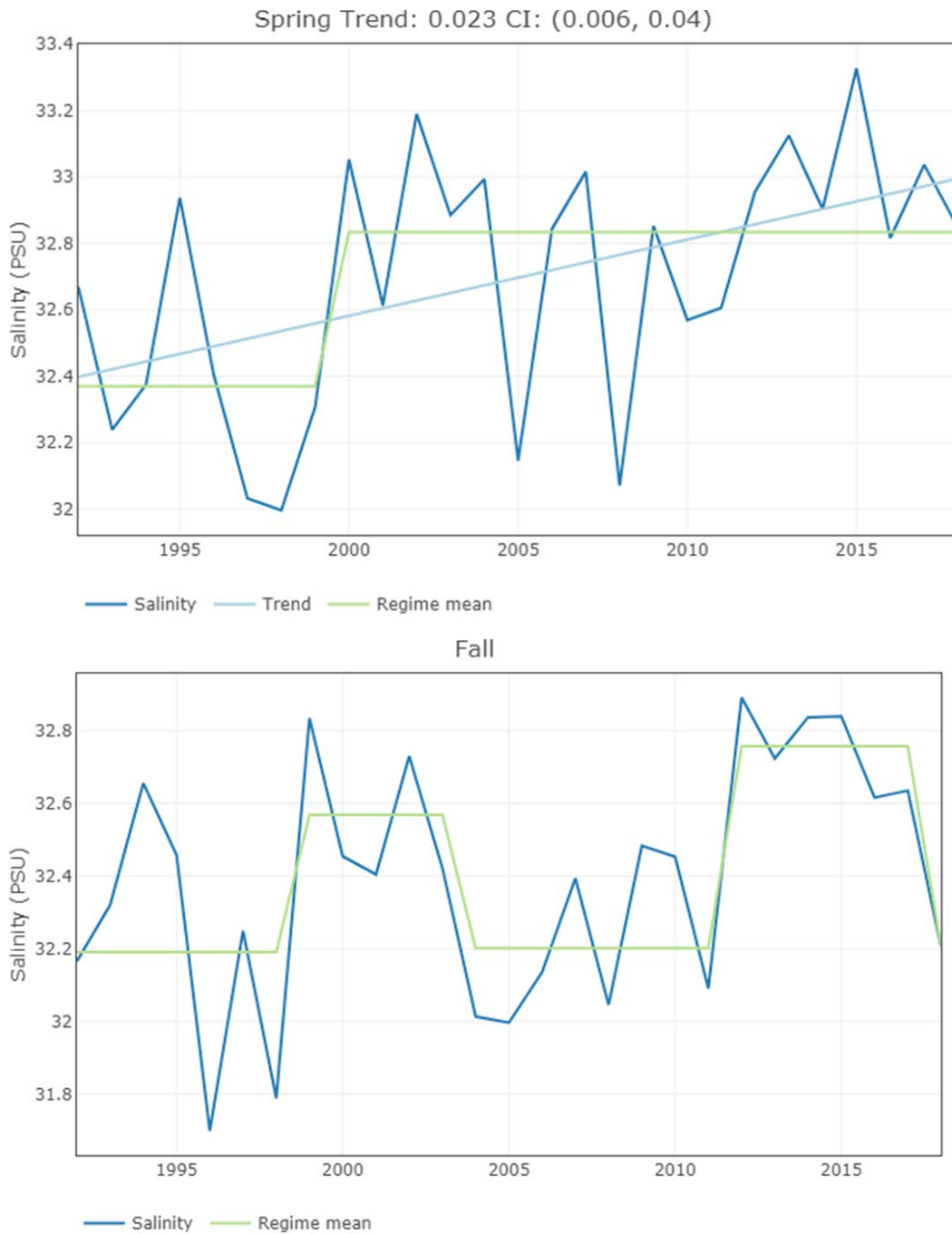
**Figure 21. Map of Northeast Fisheries Science Center (NEFSC) bottom trawl survey (BTS) spring and fall strata selected for the Ecosystem Context analysis for Atlantic menhaden (source: NEFSC).**



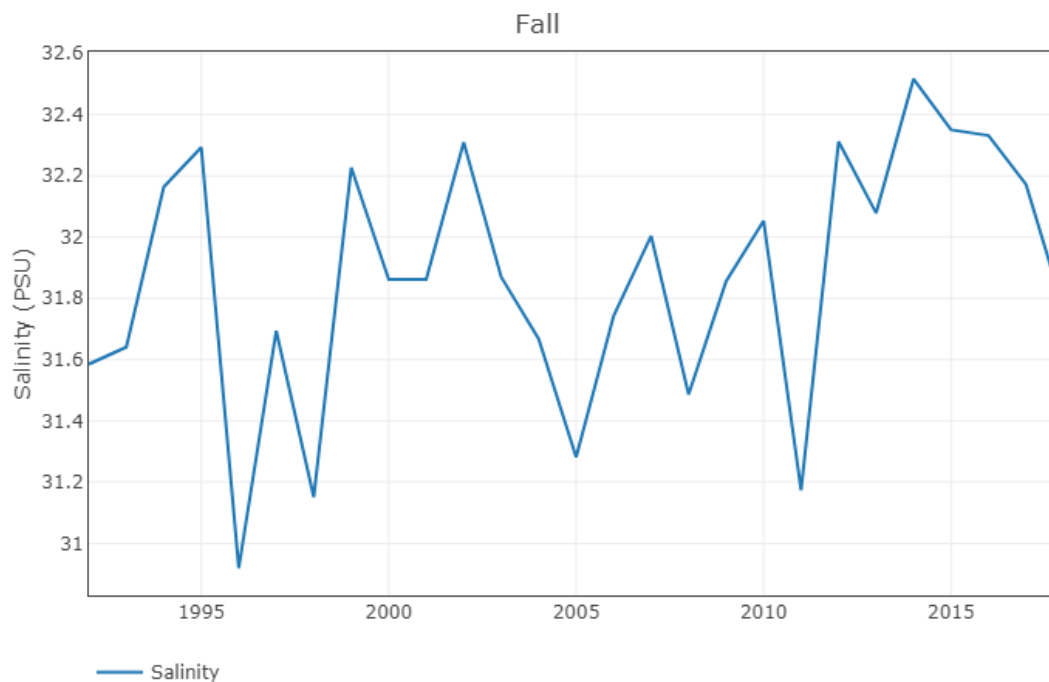
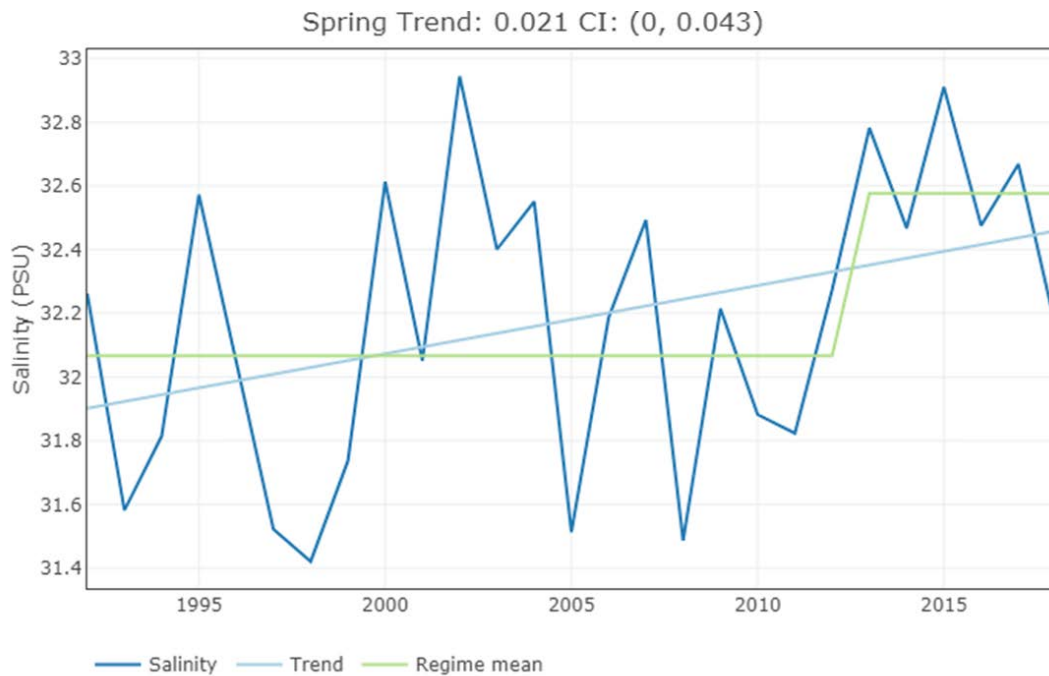
**Figure 22. Trend and regime mean for spring and fall bottom temperature from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report.**



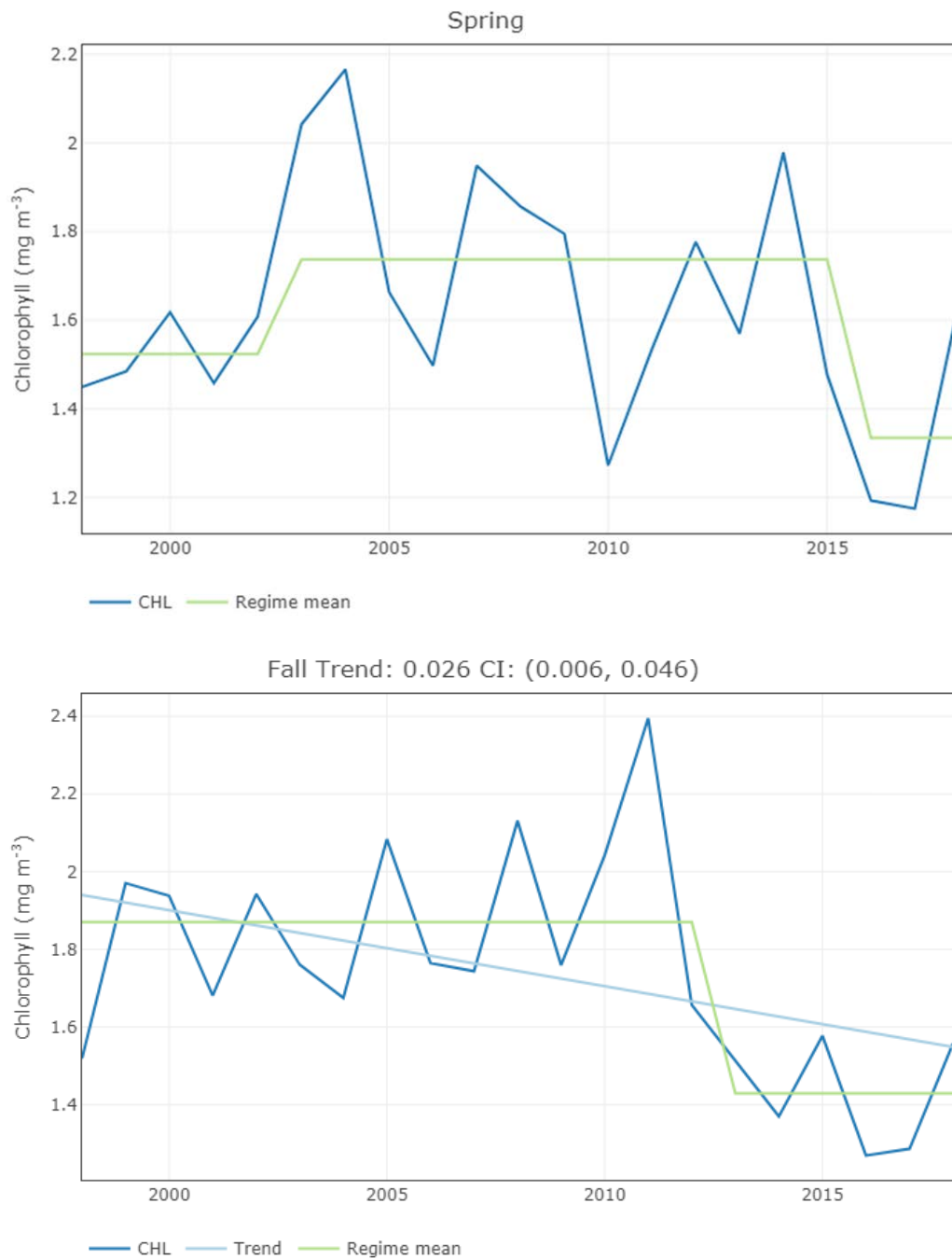
**Figure 23. Trend and regime mean for spring and fall surface temperature from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report.**



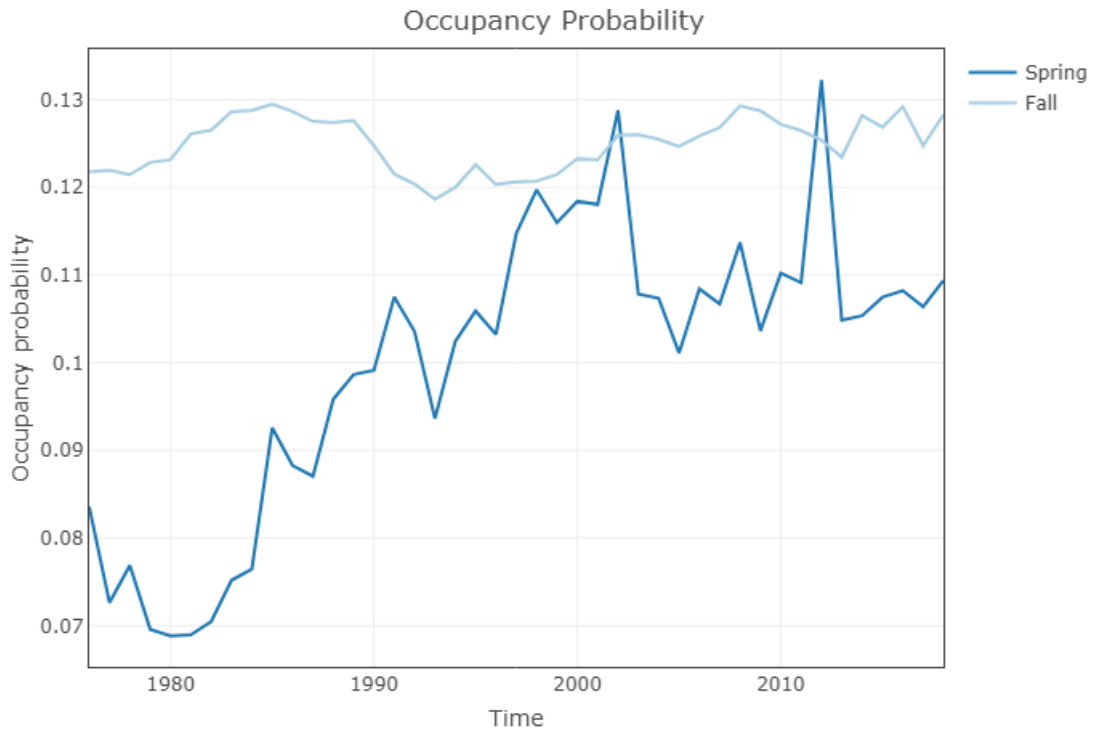
**Figure 24. Trend and regime mean for spring and fall bottom salinity from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report.**



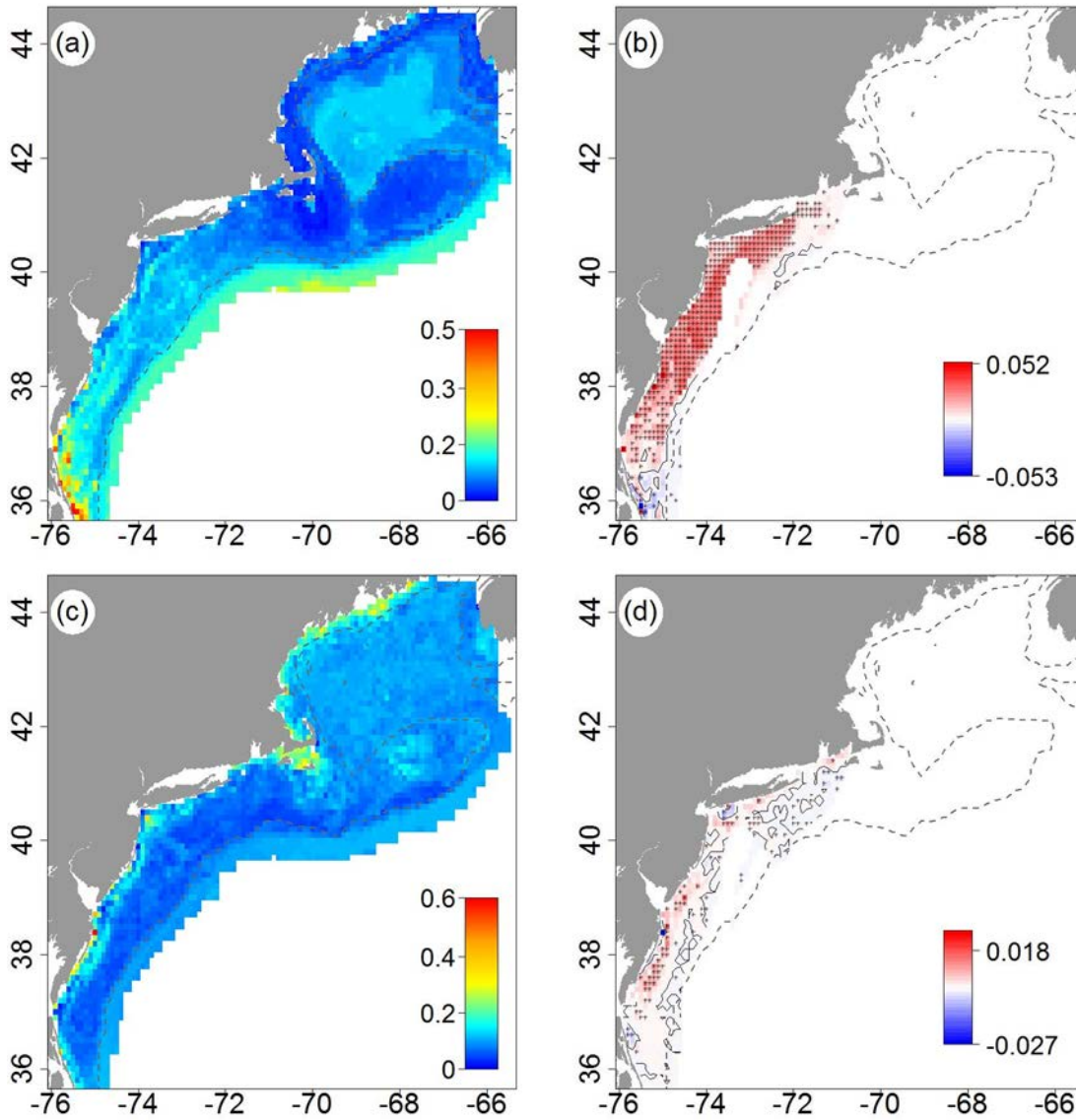
**Figure 25. Trend and regime mean for spring and fall surface salinity from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report.**



**Figure 26. Trend and regime mean for spring and fall chlorophyll concentration from the NEFSC trawl survey strata included in the Atlantic Menhaden Ecosystem Context Report.**

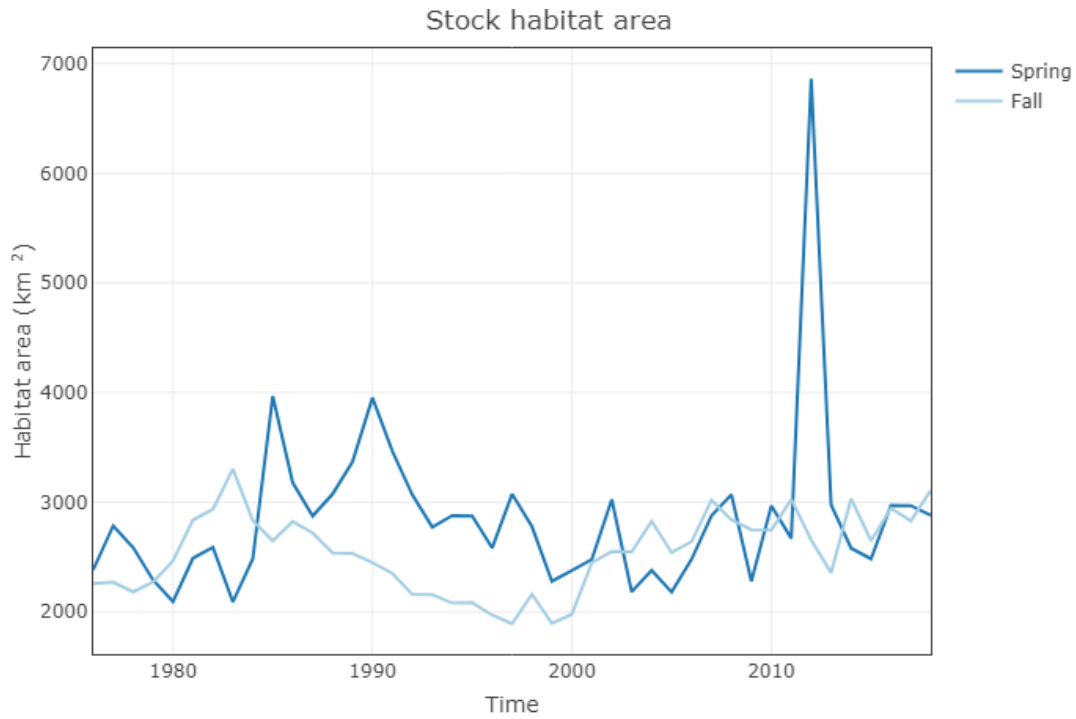


**Figure 27. Occupancy probability for Atlantic menhaden for the spring and fall seasons.**

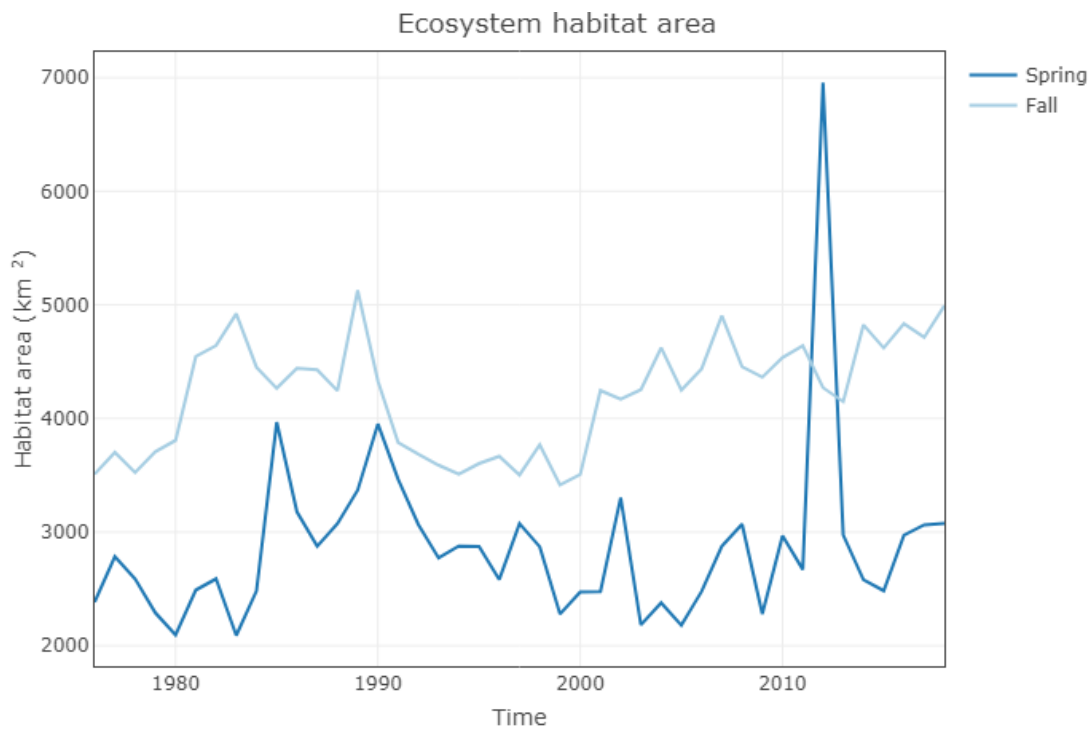


**Figure 28.** Time series mean predicted occupancy probability for Atlantic menhaden in the spring (a) and fall (c) using the random forest model with the annual rate of change (Sen slope) in occupancy probability (b and d, spring and fall, respectively). Black crosses in rate of change panels indicate significant slopes ( $P < 0.01$ ).

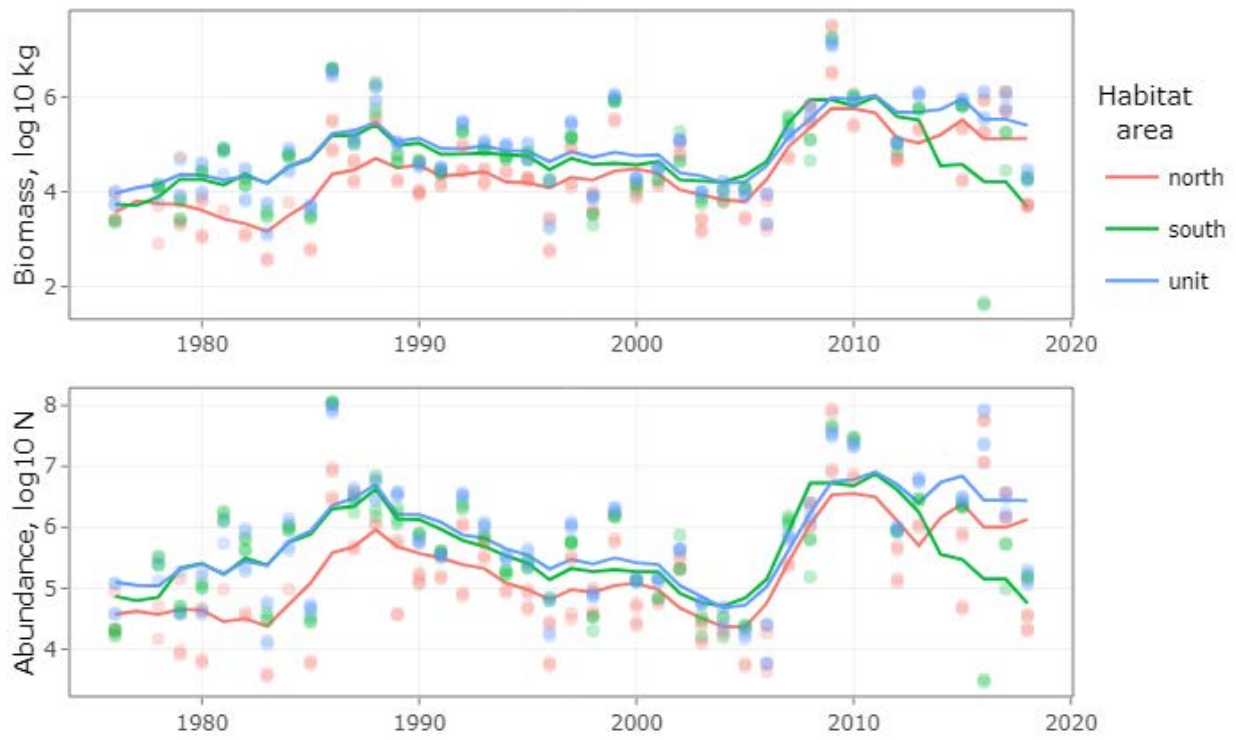




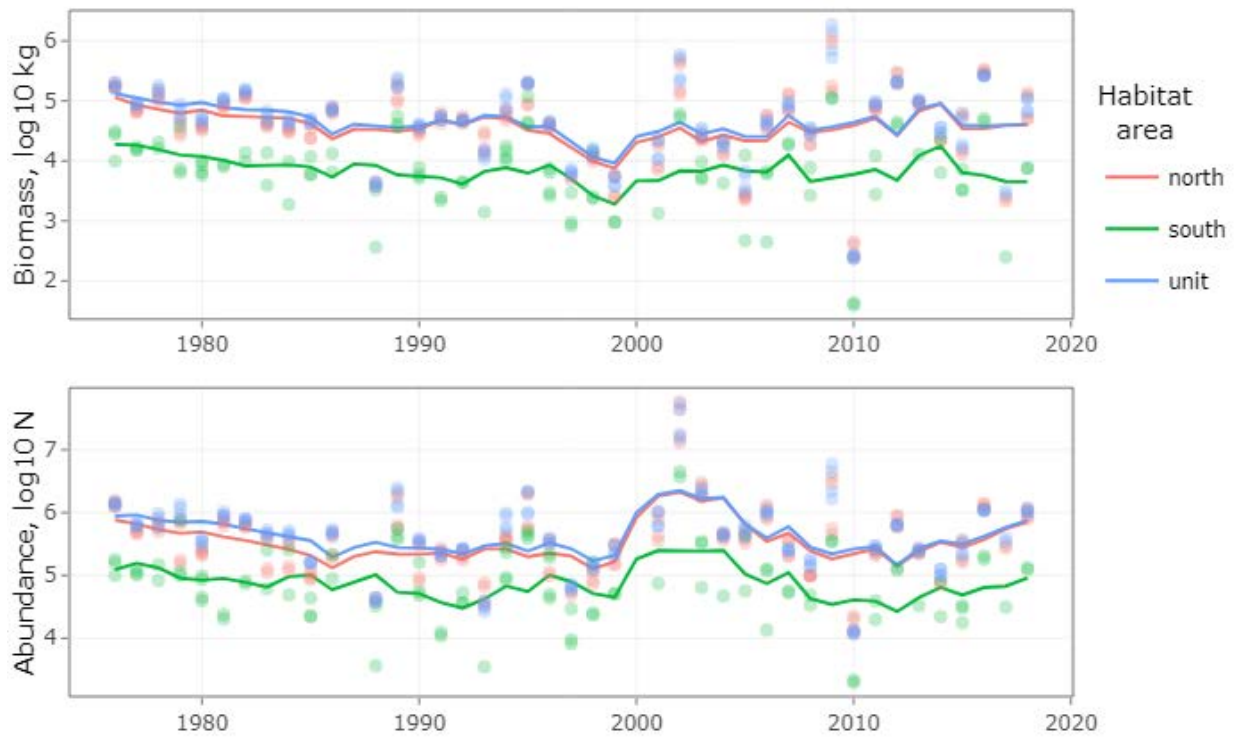
**Figure 29. Atlantic menhaden stock habitat area for the spring and fall seasons.**



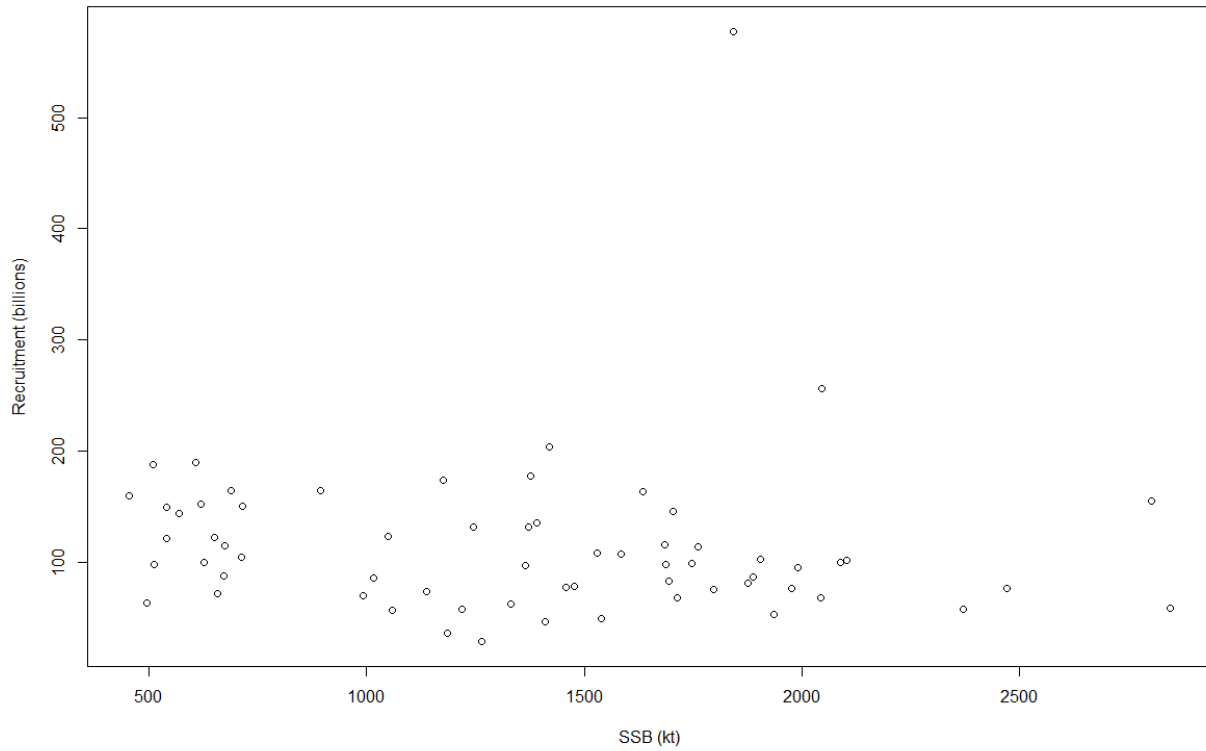
**Figure 30. Atlantic menhaden ecosystem habitat area for the spring and fall seasons.**



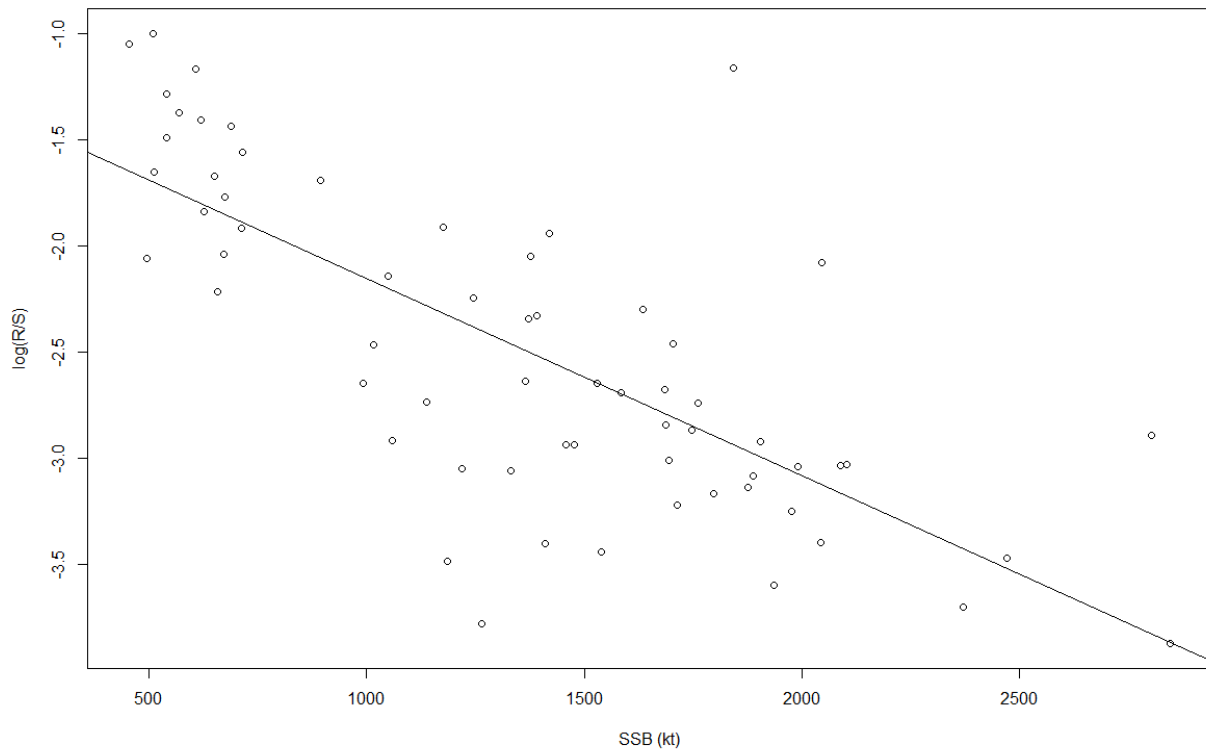
**Figure 31. Minimum population size for Atlantic menhaden in the spring.**



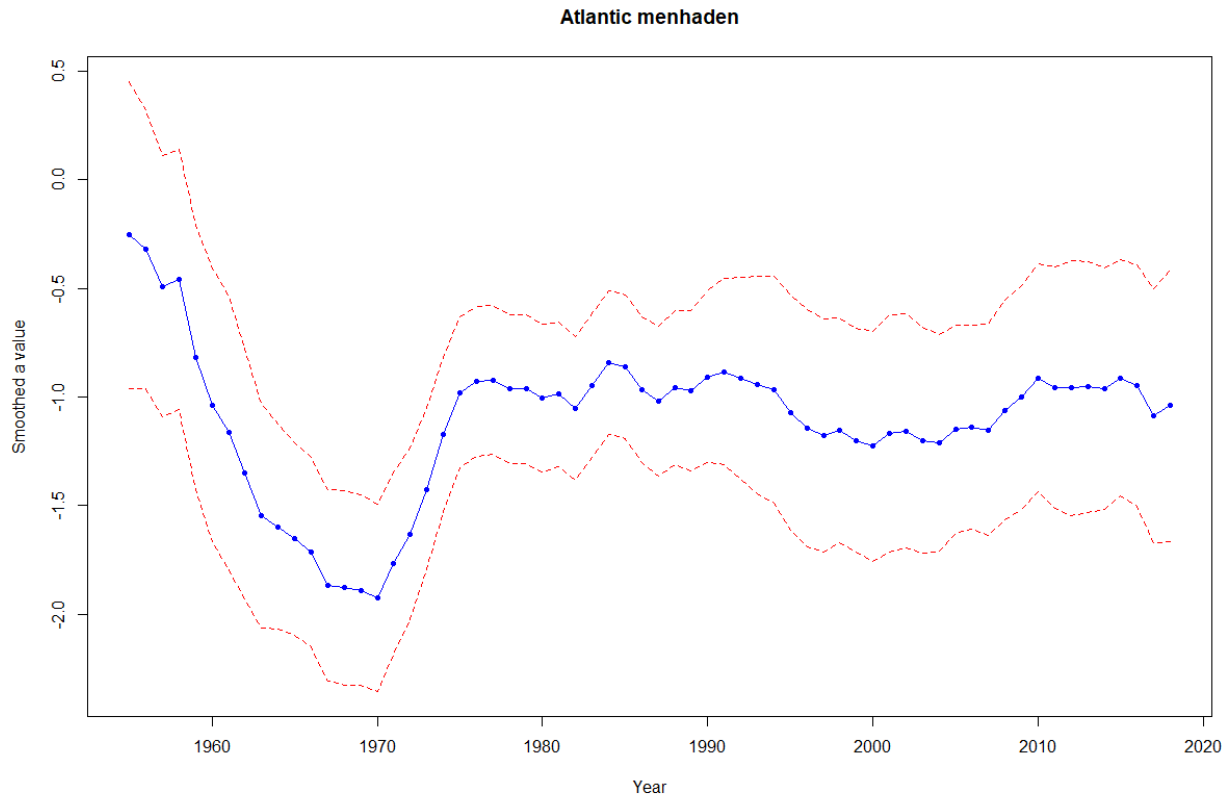
**Figure 32. Minimum population size for Atlantic menhaden in the fall.**



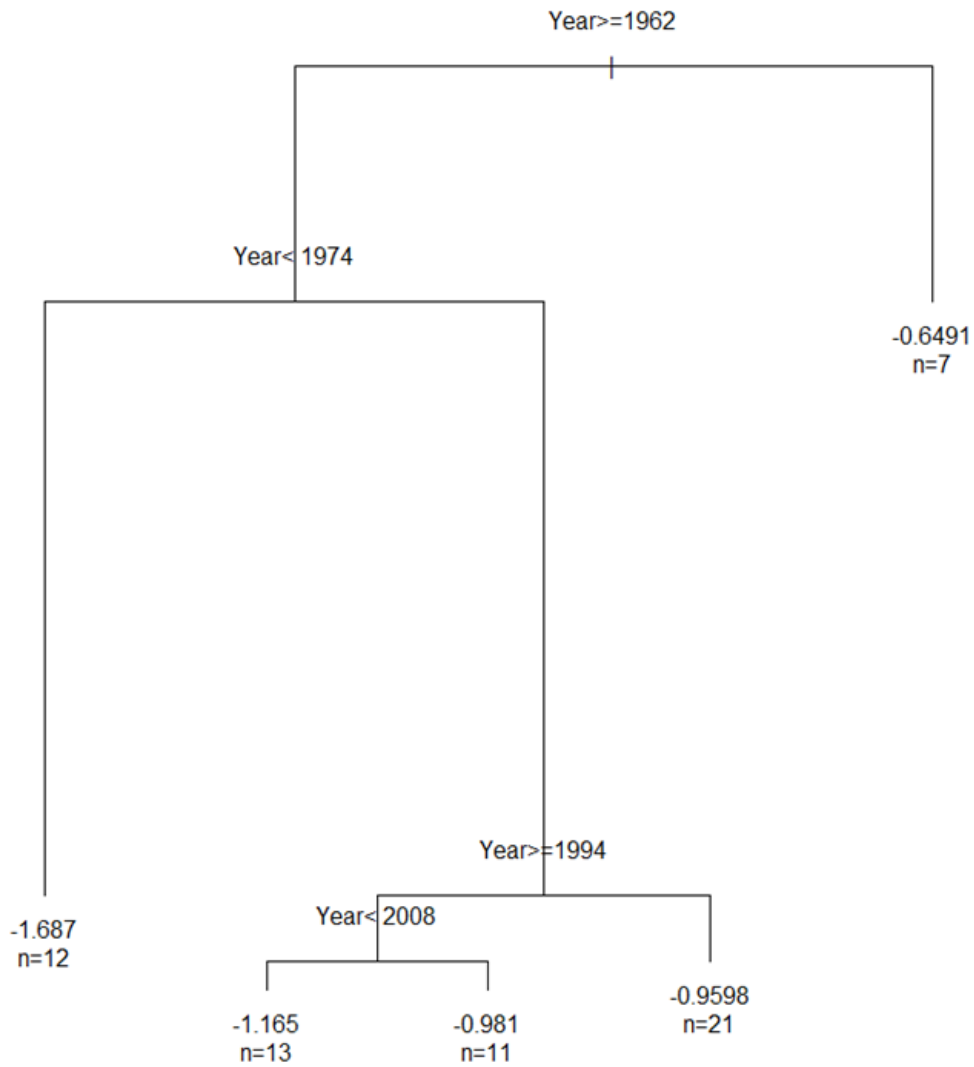
**Figure 33. Atlantic menhaden stock-recruitment data from the base run of the BAM model where recruitment was in billions of age-0s and maturity was applied to biomass-at-age to get spawning stock biomass (SSB) in kt.**



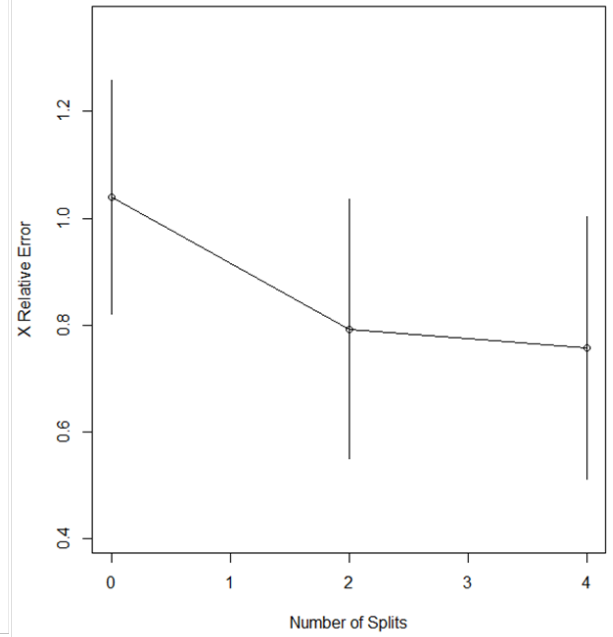
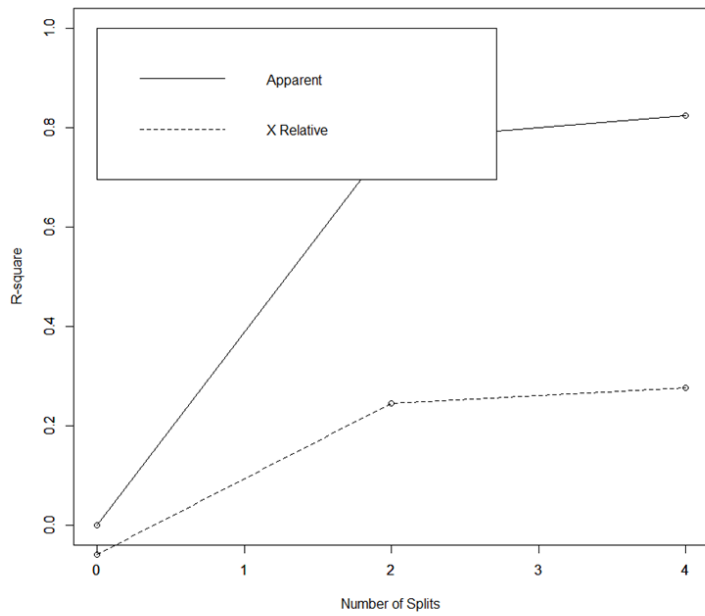
**Figure 34. Linearized Ricker stock-recruitment relationship for Atlantic menhaden with log recruitment (R) divided by spawning stock biomass (SSB) and SSB in kt.**



**Figure 35. Kalman filter smoothed productivity time series for Atlantic menhaden with 95% confidence intervals. The smoothed value corresponds to the recruit number per metric ton of the spawning stock biomass on the logarithmic scale.**



**Figure 36. Tree produced by R package RPART to identify regimes for Atlantic menhaden productivity.**



**Figure 37.** Plots used to determine how to prune the tree produced in Figure 36. The figure on the left shows that the second split offers the most information. The figure on the right suggests that the tree should be pruned to include 2 splits.



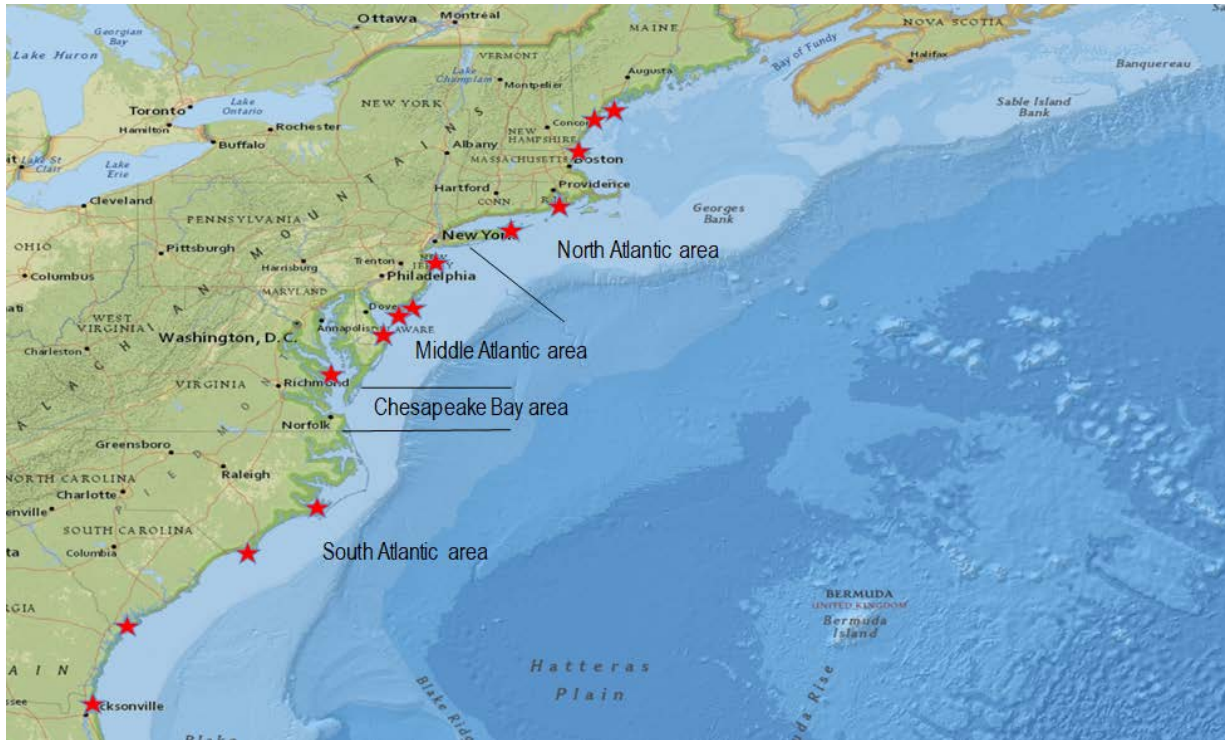


Figure 38. Historical locations of menhaden plants in relation to their NMFS statistical reporting areas.

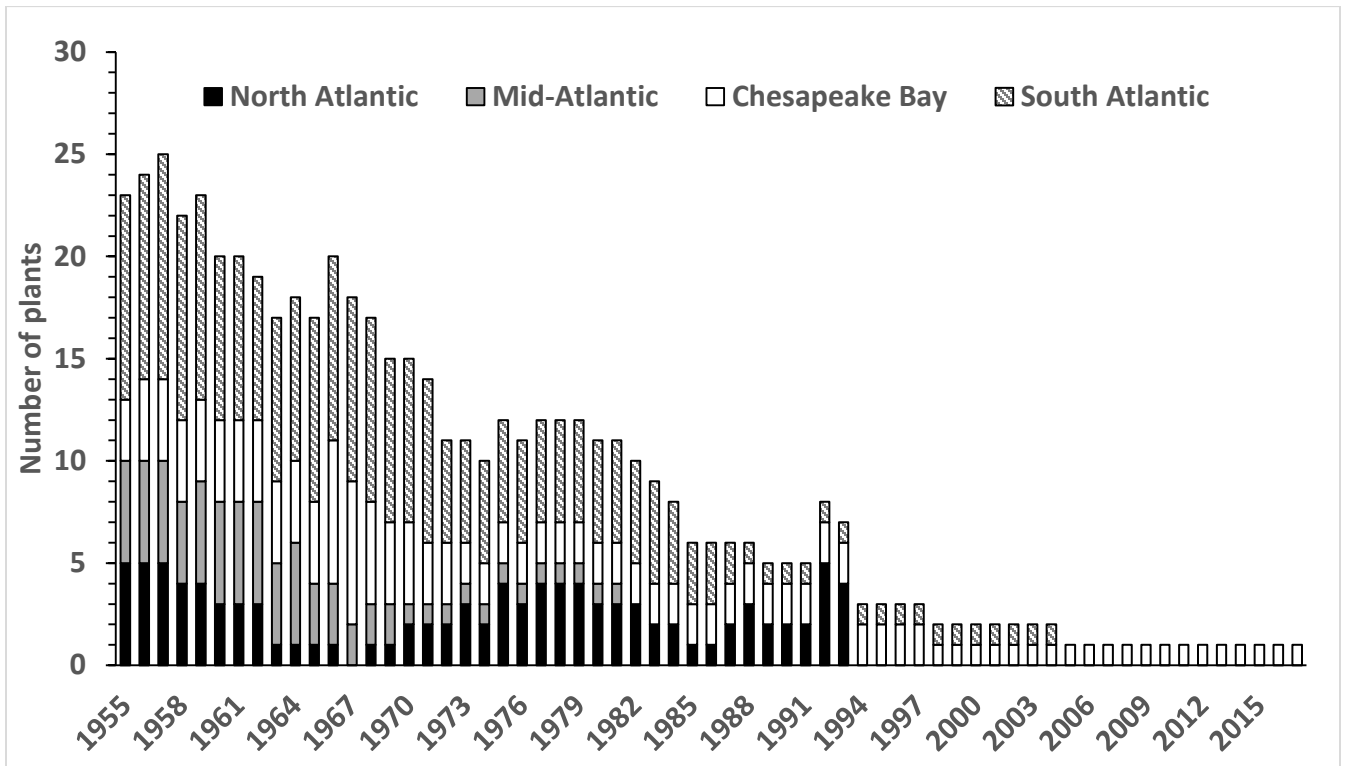
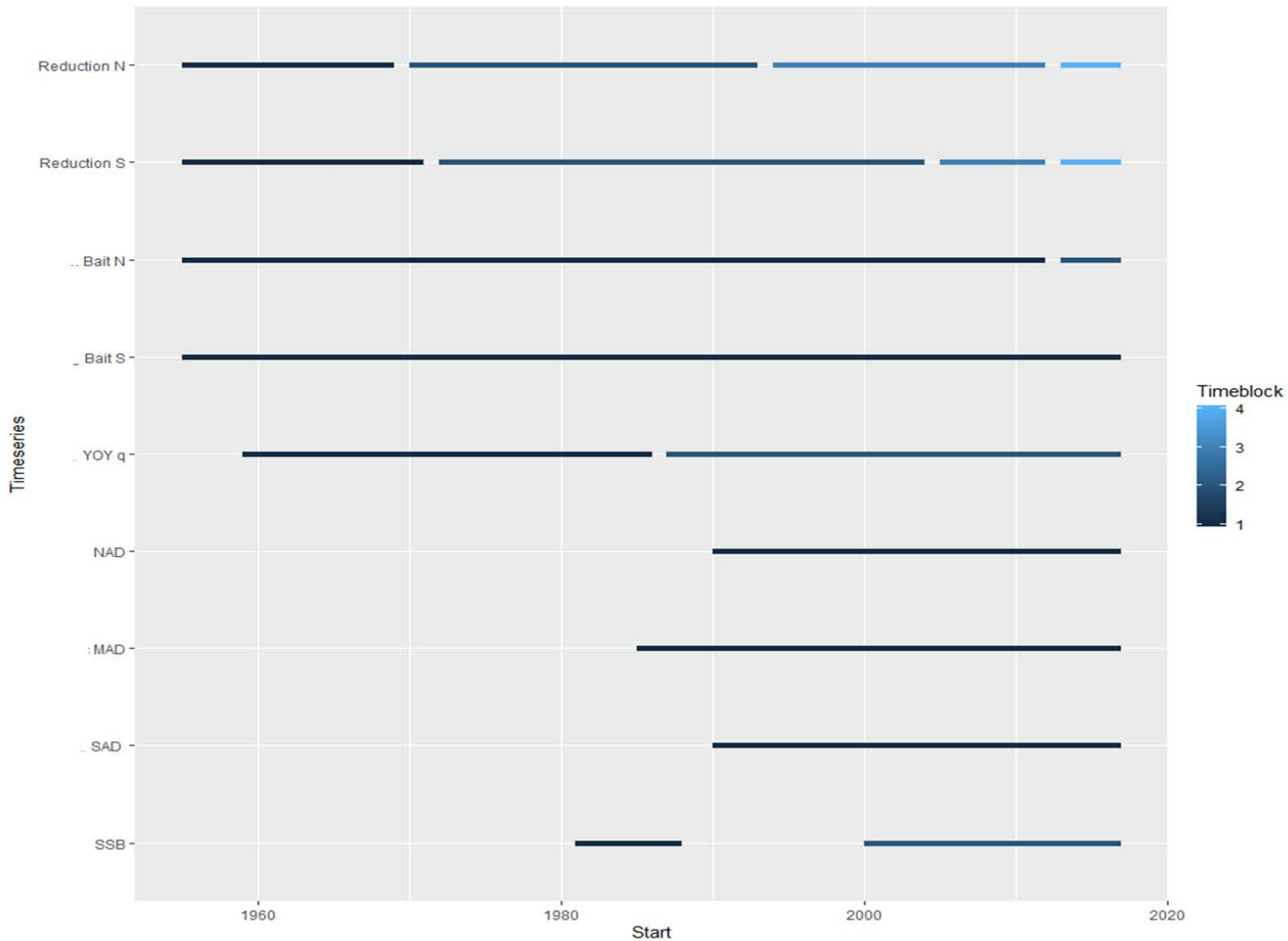


Figure 39. Stacked chart of number of menhaden plants by area and year, 1955–2017.



**Figure 40. Summary of time series and blocks used for each data source for 1955-2017. Reduction and bait fisheries are split into northern (N) and southern (S) regions and the YOY index has two catchability coefficients ( $q$ ) used in the BAM.**

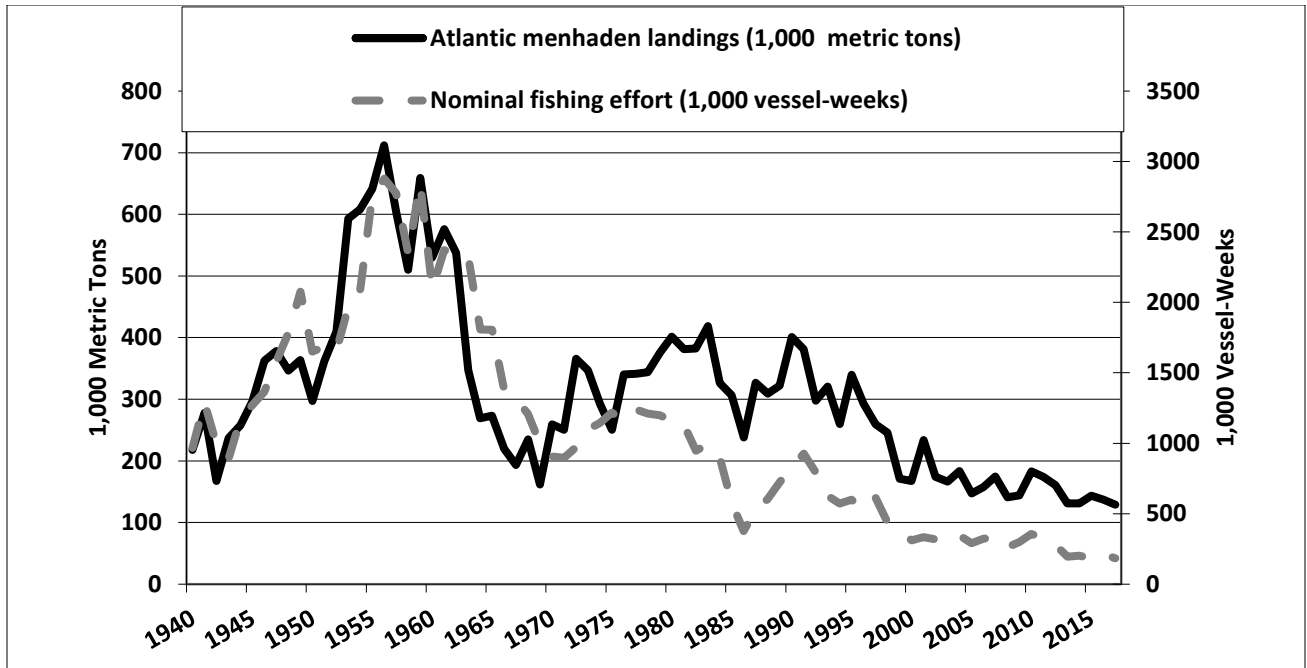


Figure 41. Annual values of menhaden reduction landings (1000 mt) and nominal effort (vessel-week), 1955–2017.

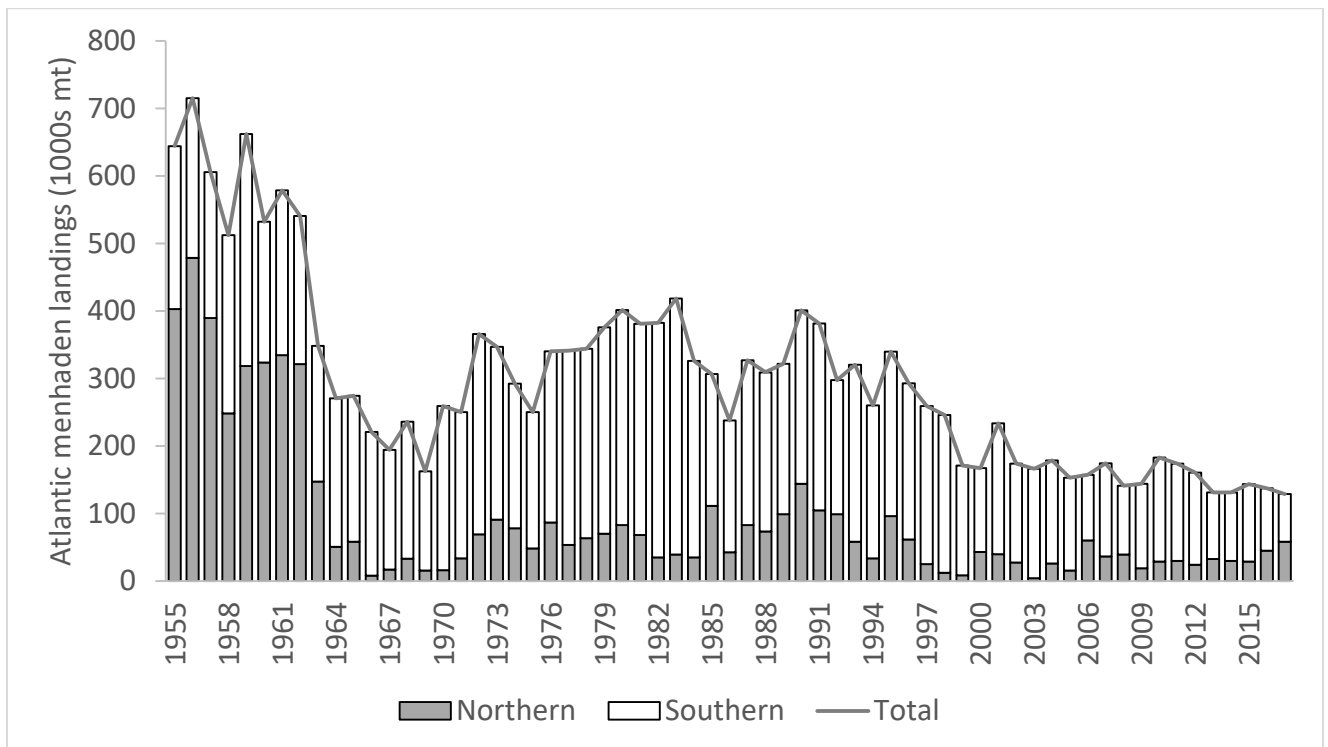
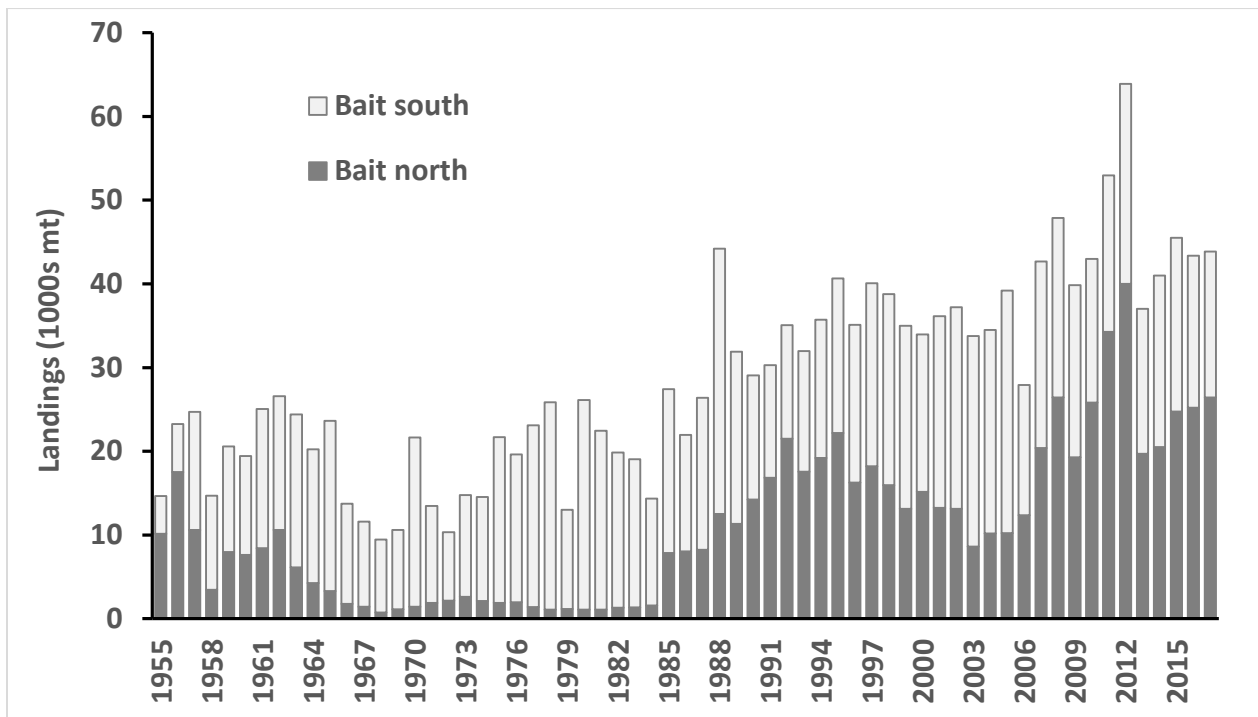


Figure 42. Atlantic menhaden reduction landings (1000s mt) from 1955-2017. The northern region is comprised of landings from north of Virginia Eastern Shore and the southern region is comprised of landings from Virginia Eastern Shore and south (Source: NMFS Beaufort).



**Figure 43. Atlantic menhaden bait landings (1000s mt) from 1955-2017. The northern region includes landings from Maine to Maryland’s Eastern Shore, excluding the Chesapeake Bay. The southern region includes landings from the Chesapeake Bay to Florida.**

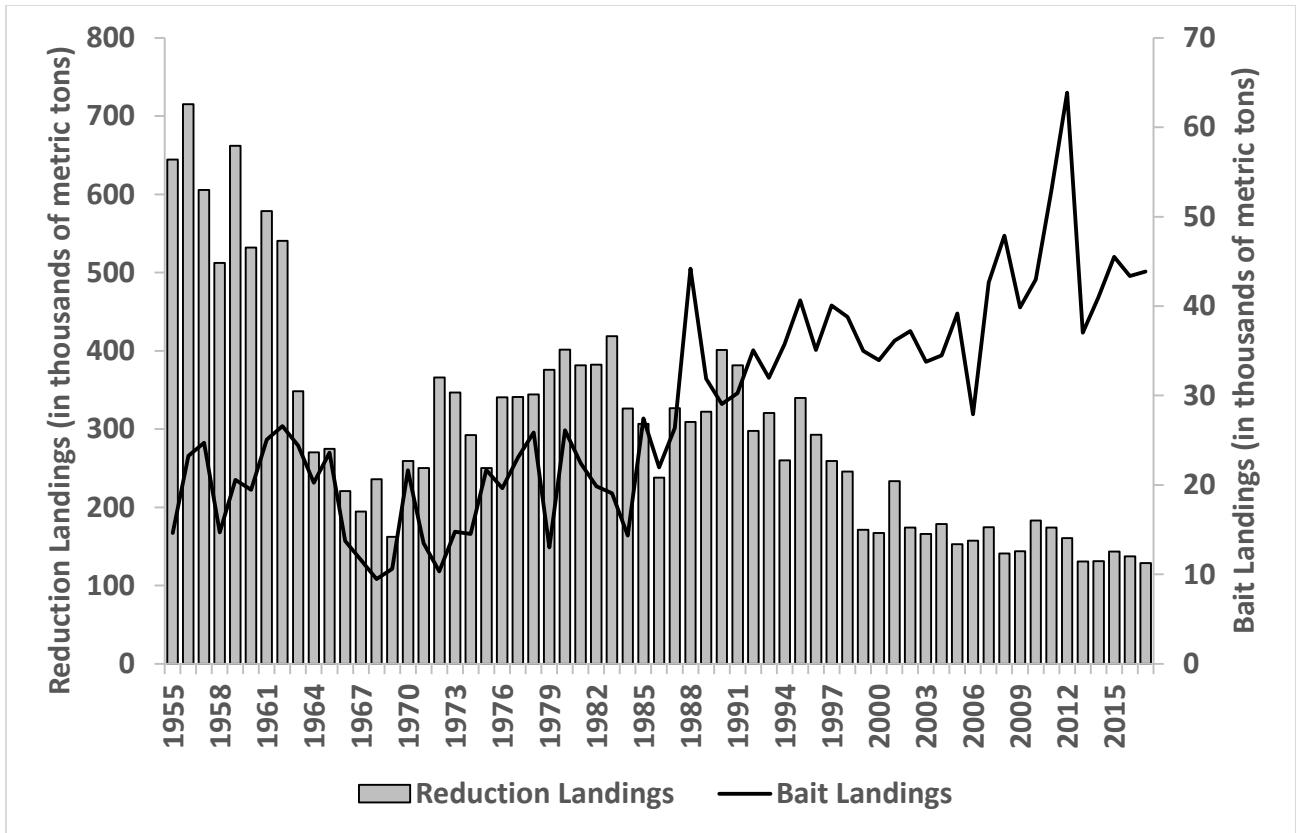


Figure 44. Atlantic menhaden landings by reduction and bait fisheries.

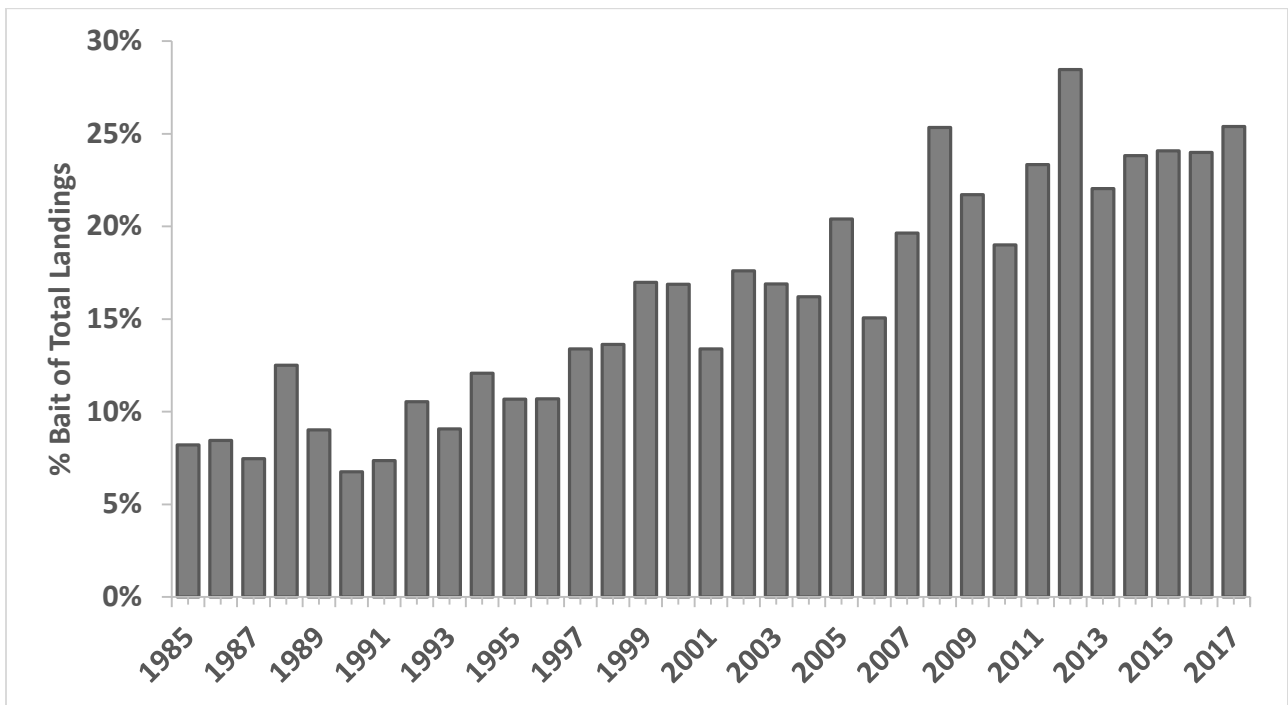


Figure 45. Percent of total landings (reduction and bait) attributed to the bait fishery.

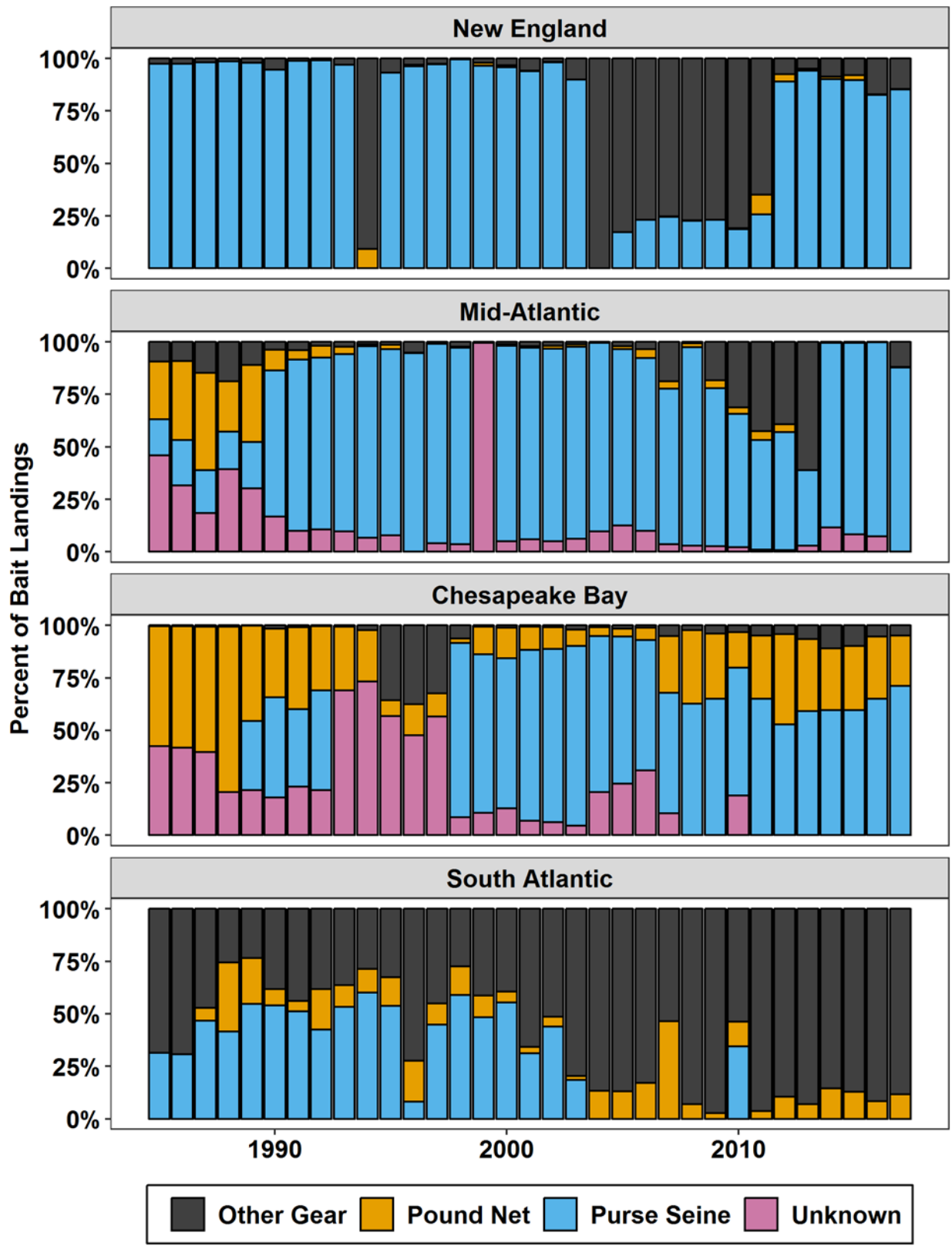


Figure 46. a. Percent of bait landings by major gear types for each region.

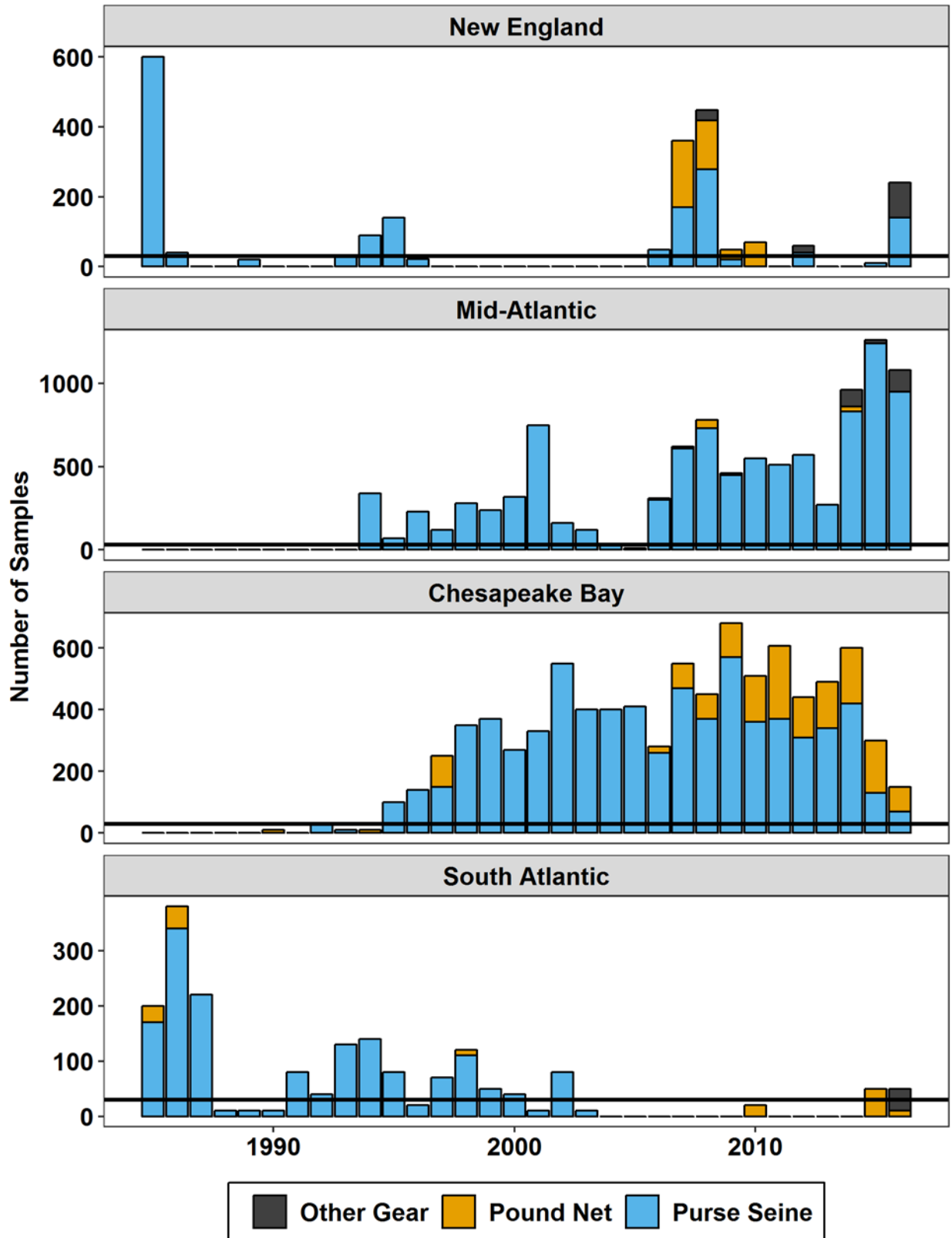
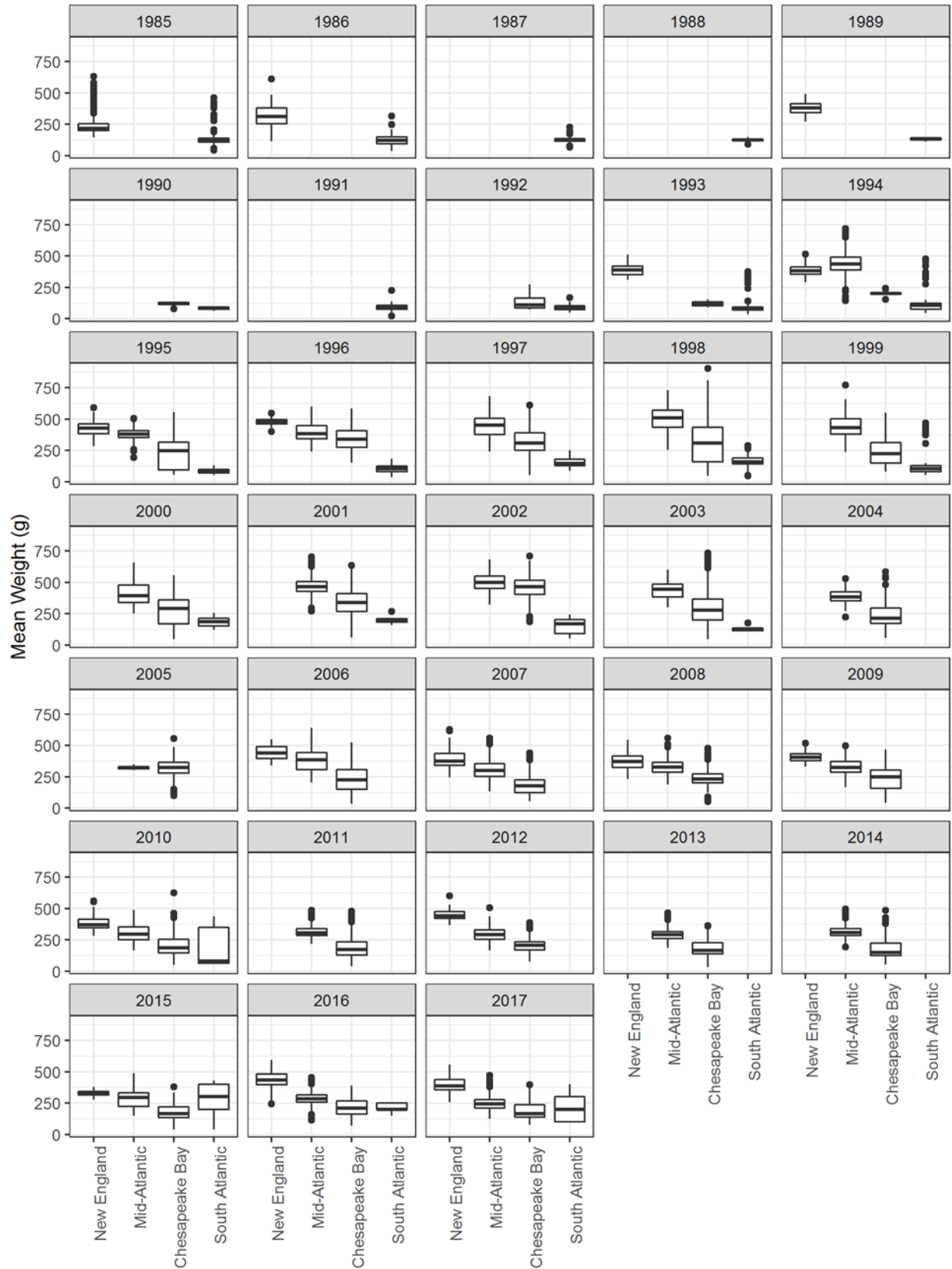


Figure 46. b. Numbers of fish sampled from the bait fishery by year, gear, and region. The horizontal black line indicates the 30 fish sample size cutoff.



**Figure 47. Mean weight of fish in the bait catch by year and region.**



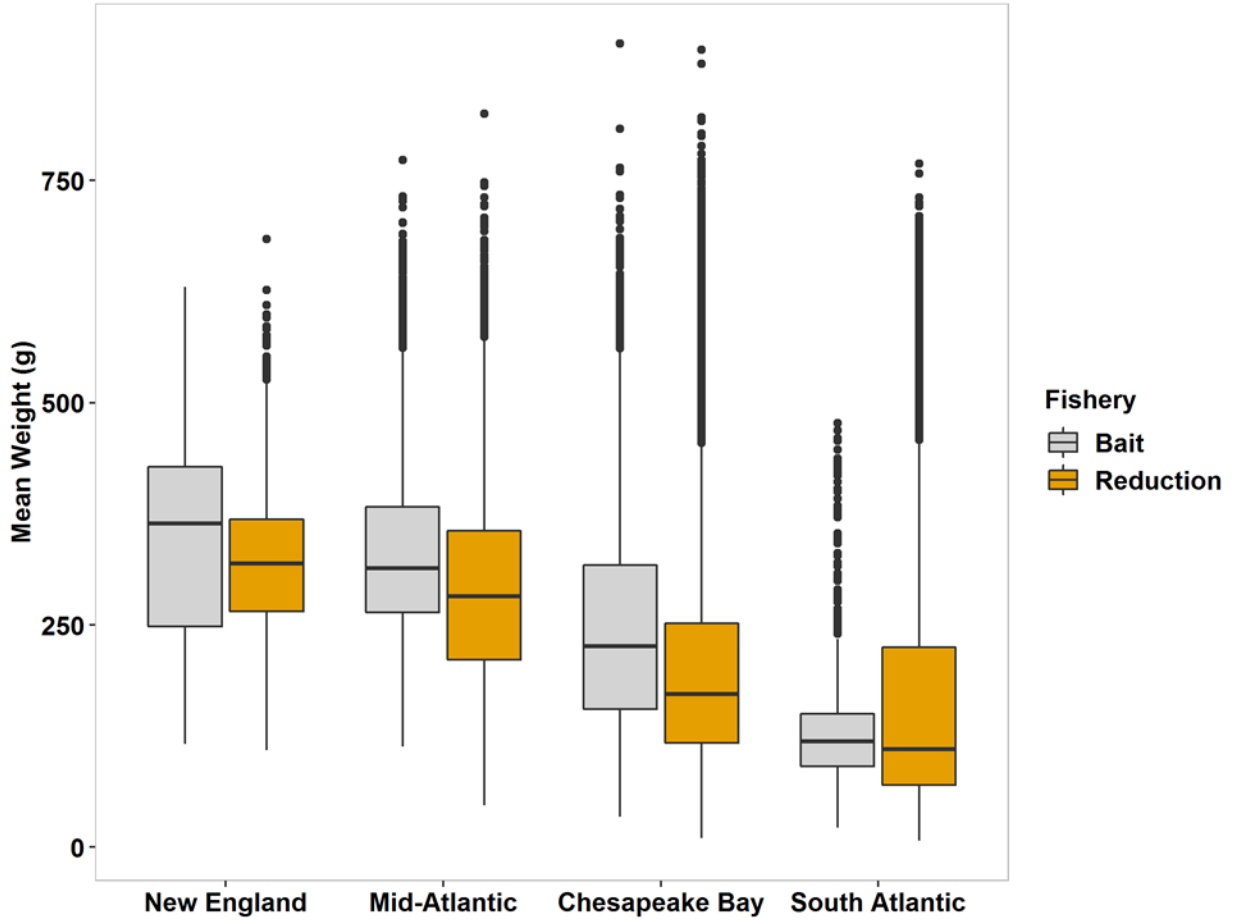


Figure 48. Mean weight of fish in the bait and reduction fisheries by region (pooled over 1985-2017).

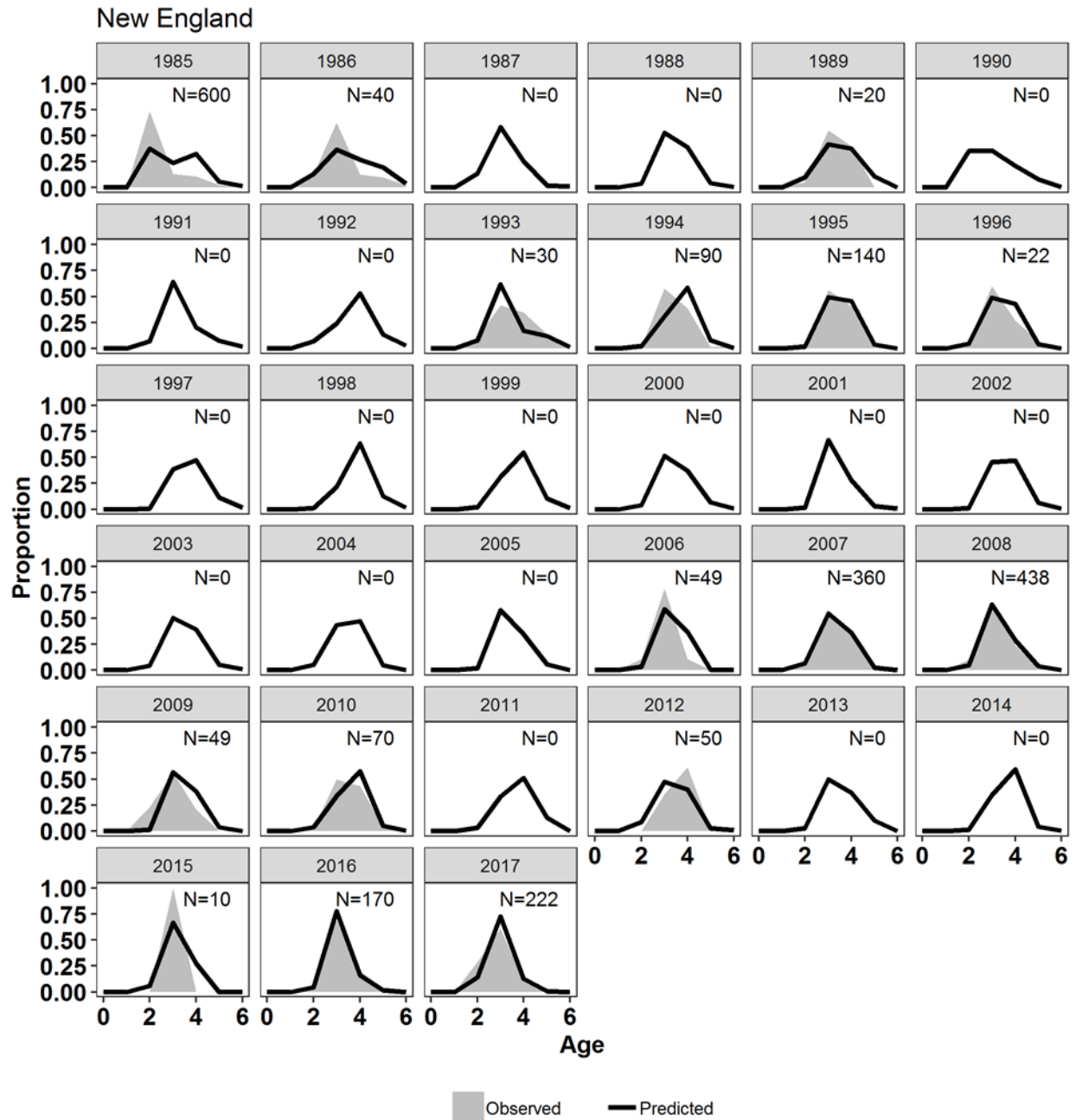


Figure 49. a. Observed proportions at age for the bait fishery for the New England region plotted with proportions at age predicted by the multinomial regression. *N* indicates number of observed ages in that year.

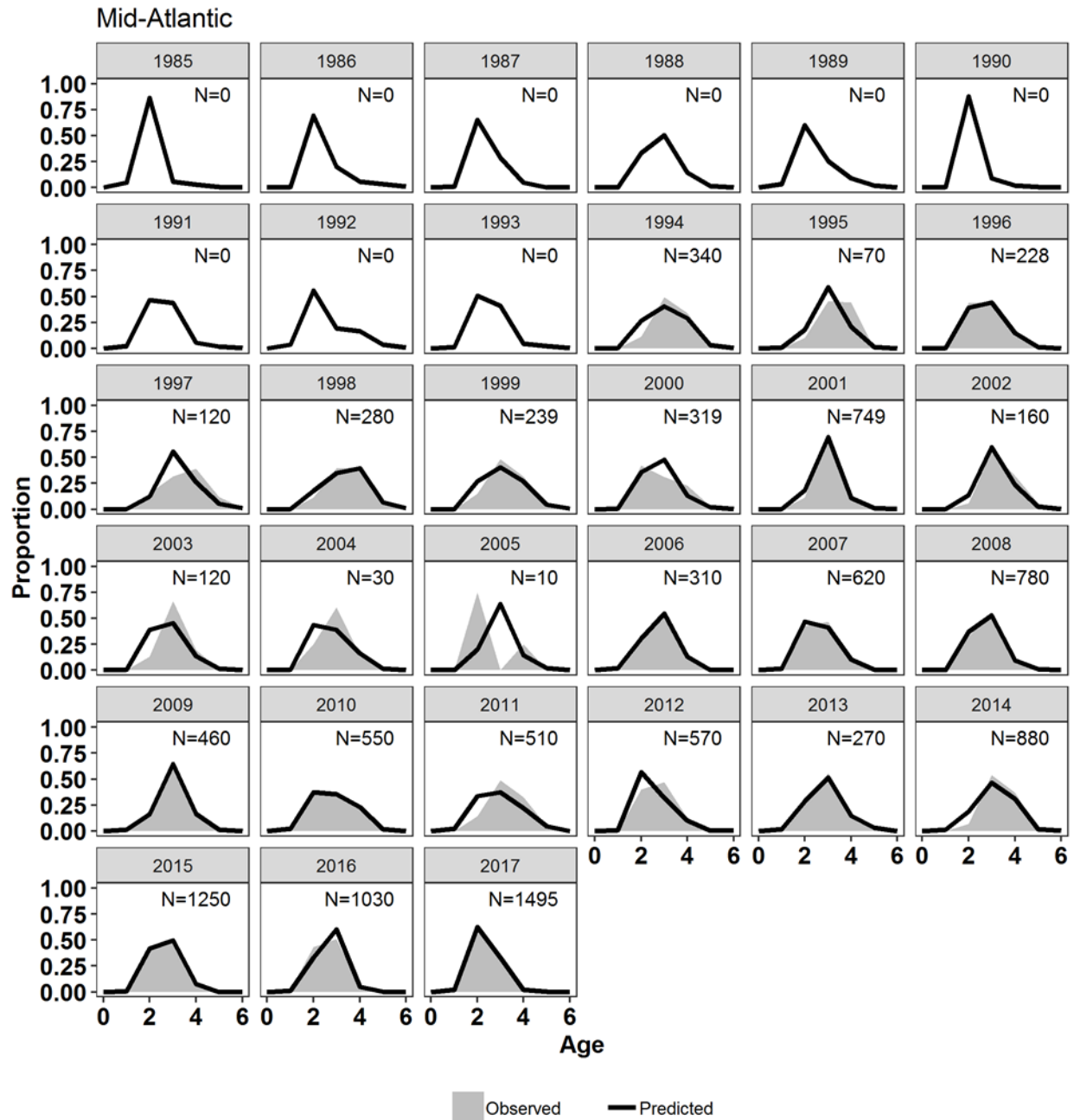


Figure 49. b. Observed proportions at age for the bait fishery for the Mid-Atlantic region plotted with proportions at age predicted by the multinomial regression. *N* indicates number of observed ages in that year.

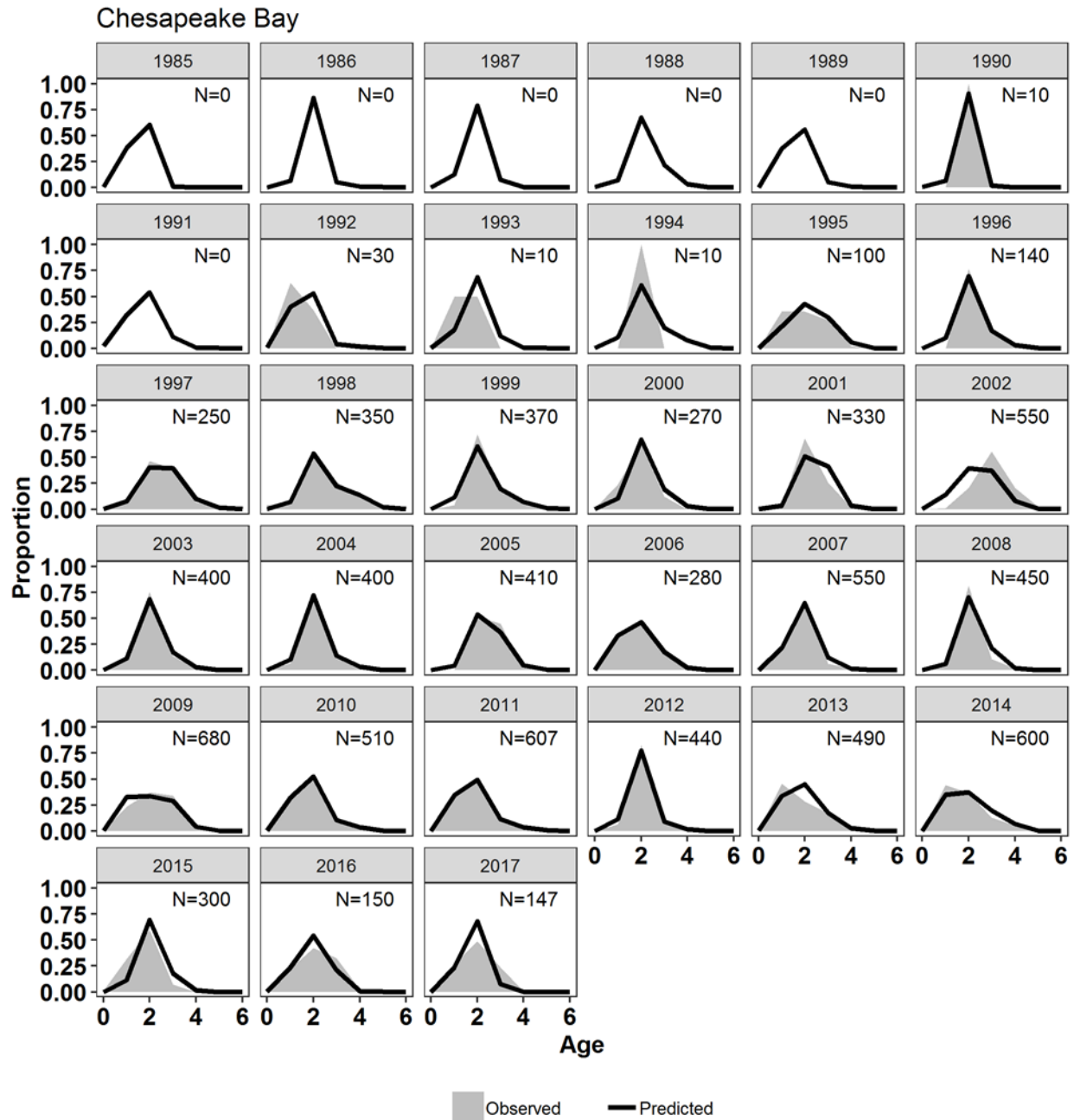


Figure 49. c. Observed proportions at age for the bait fishery for the Chesapeake Bay region plotted with proportions at age predicted by the multinomial regression. *N* indicates number of observed ages in that year.

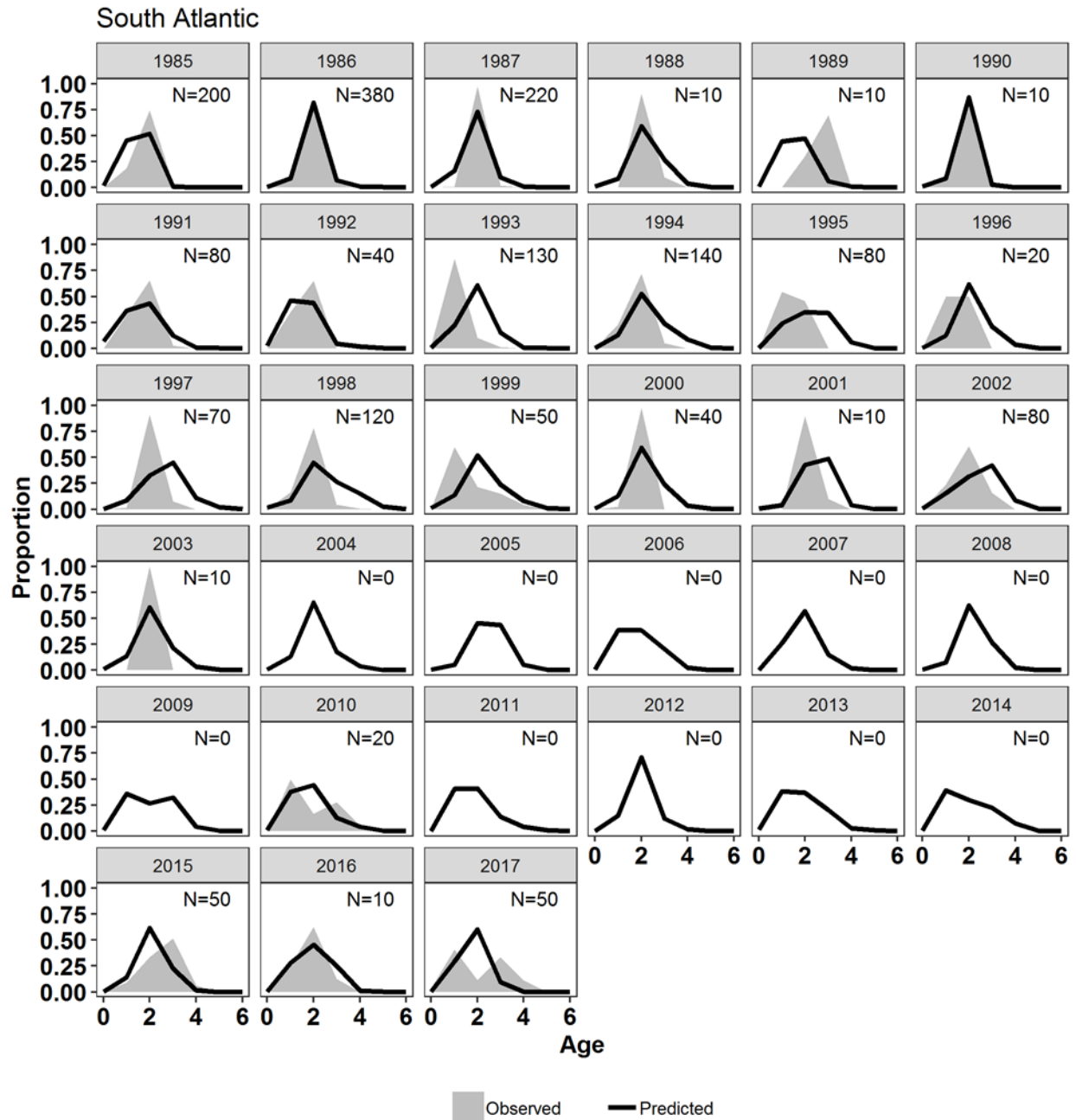


Figure 49. d. Observed proportions at age from the bait fishery for the South Atlantic region plotted with proportions at age predicted by the multinomial regression. *N* indicates number of observed ages in that year.

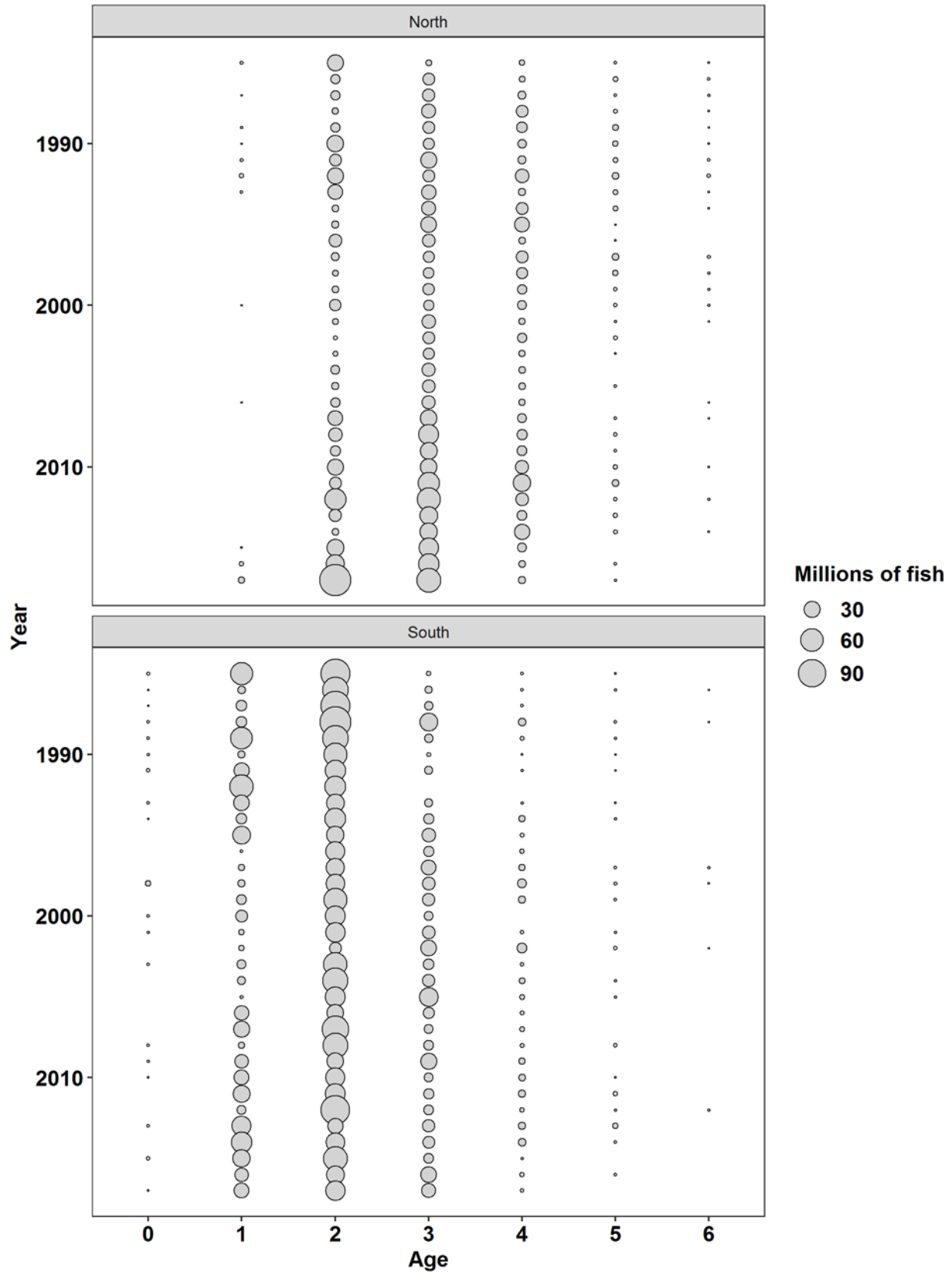


Figure 50. Total bait catch-at-age by region.

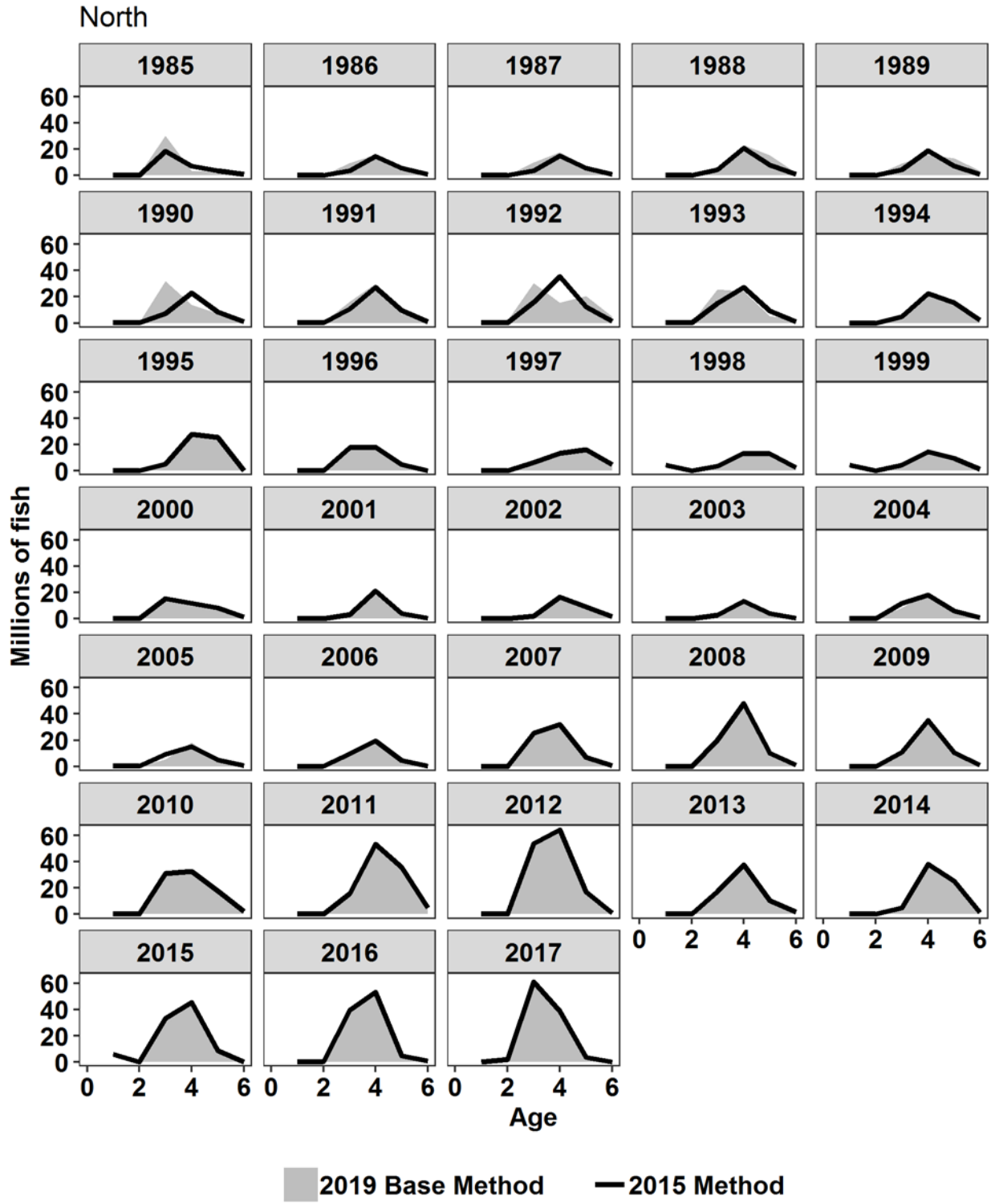


Figure 51. Comparison of the bait catch-at-age developed with the 2019 assessment multinomial gap-filling method and the 2015 assessment pooled data gap-filling method for the northern region.

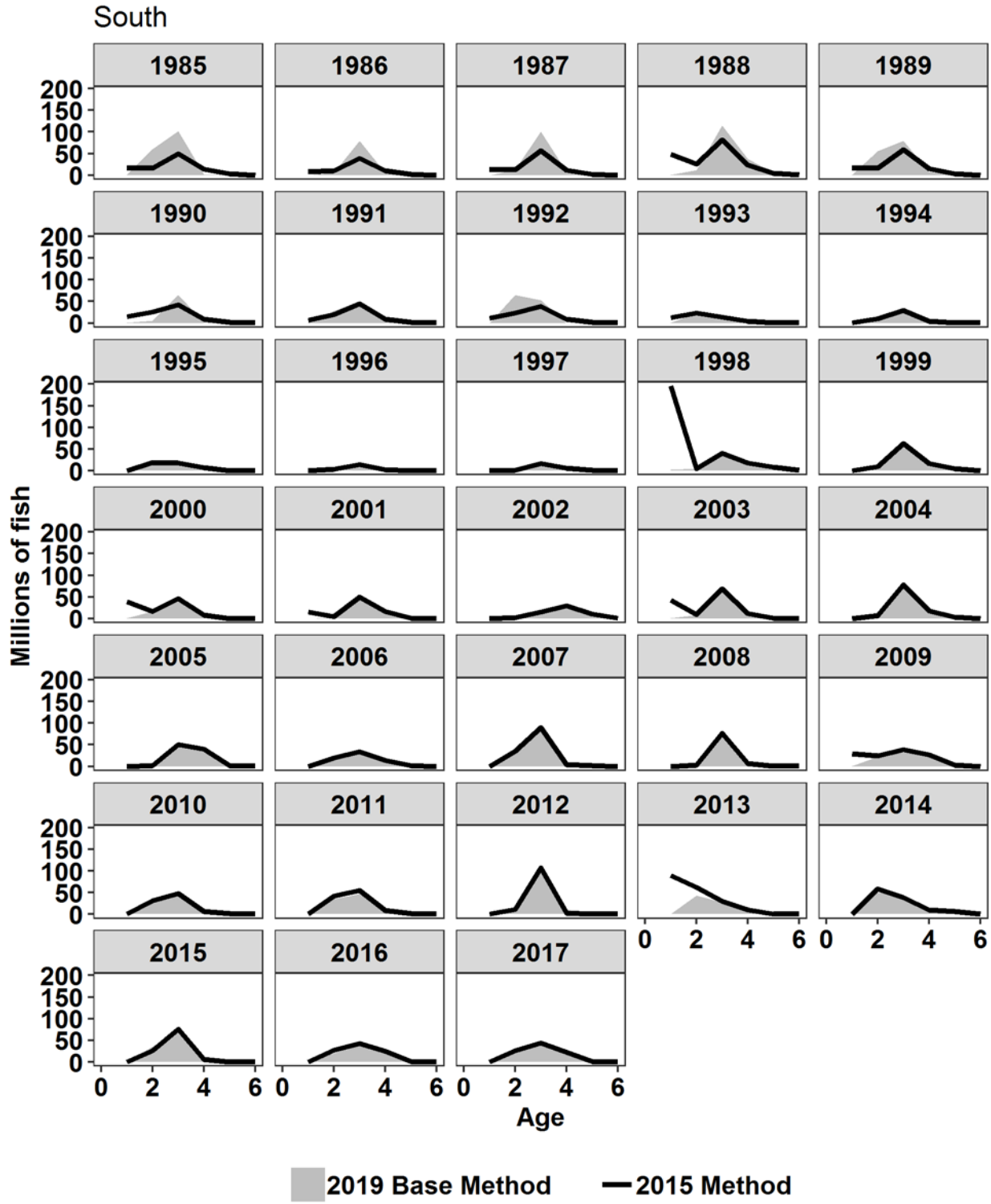


Figure 52. Comparison of the bait catch-at-age developed with the 2019 assessment multinomial gap-filling method and the 2015 assessment pooled data gap-filling method for the southern region.



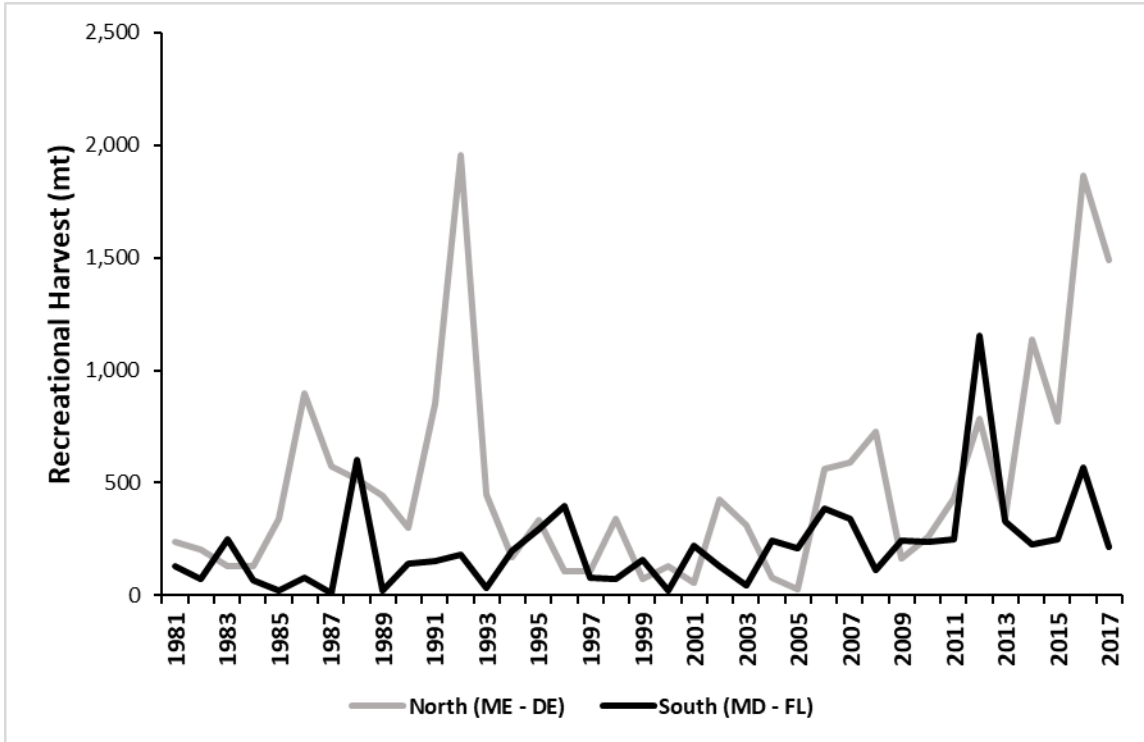


Figure 53. Recreational harvest (A+B1) estimates of Atlantic menhaden for two assessment regions along the U.S. Atlantic coast.

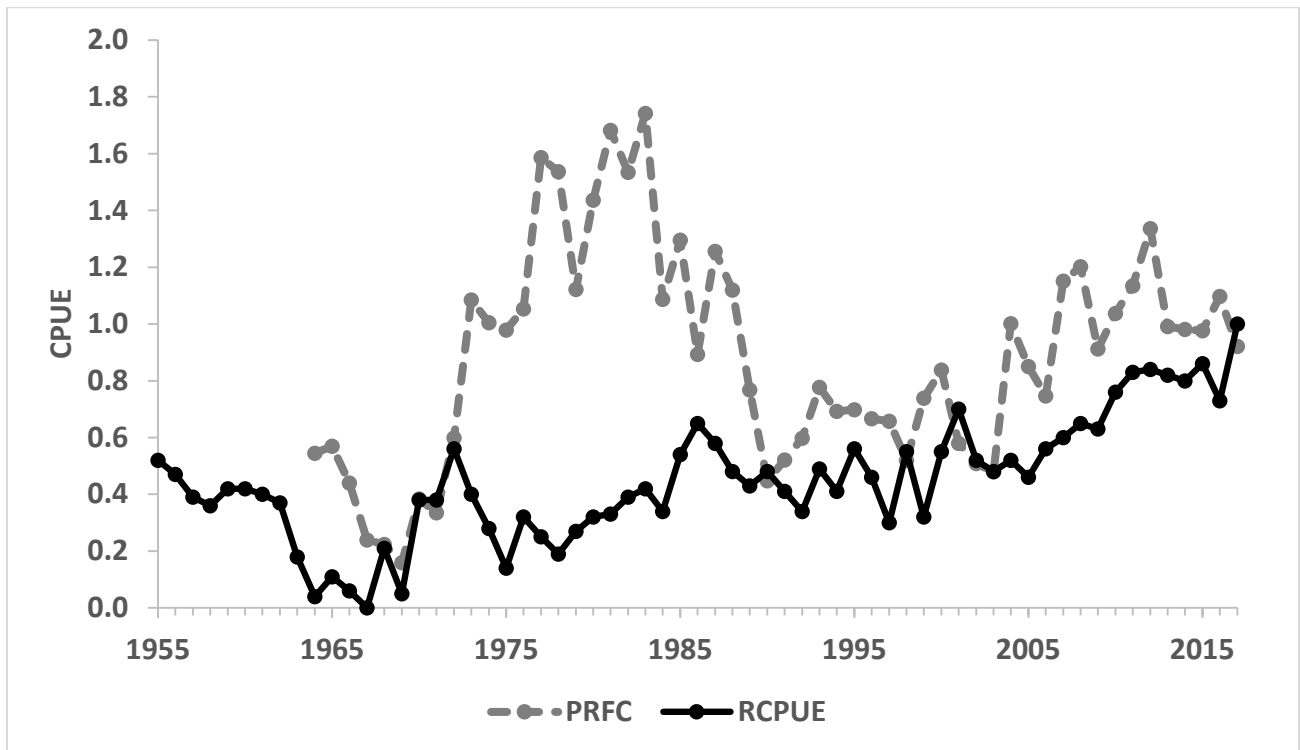
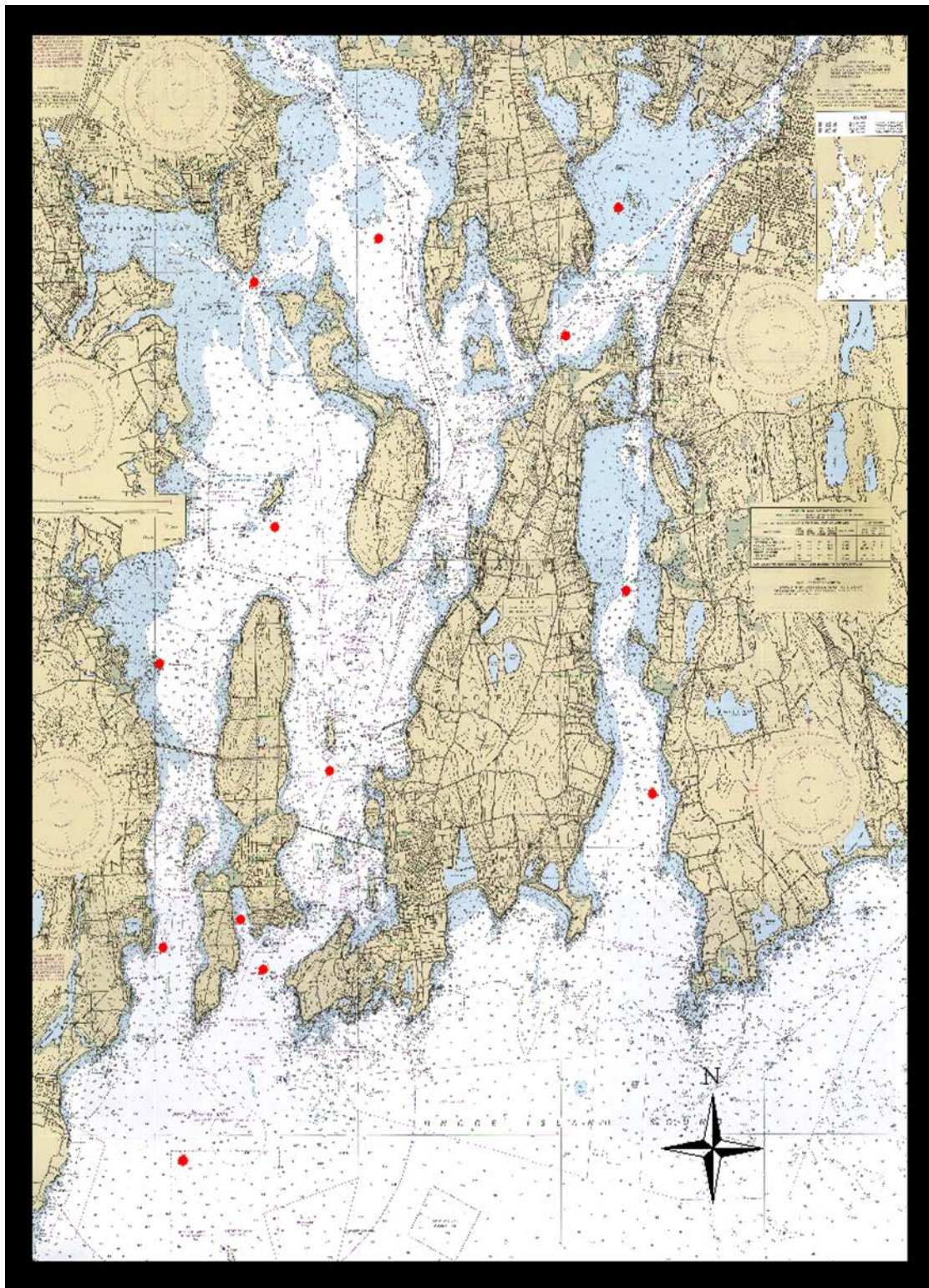
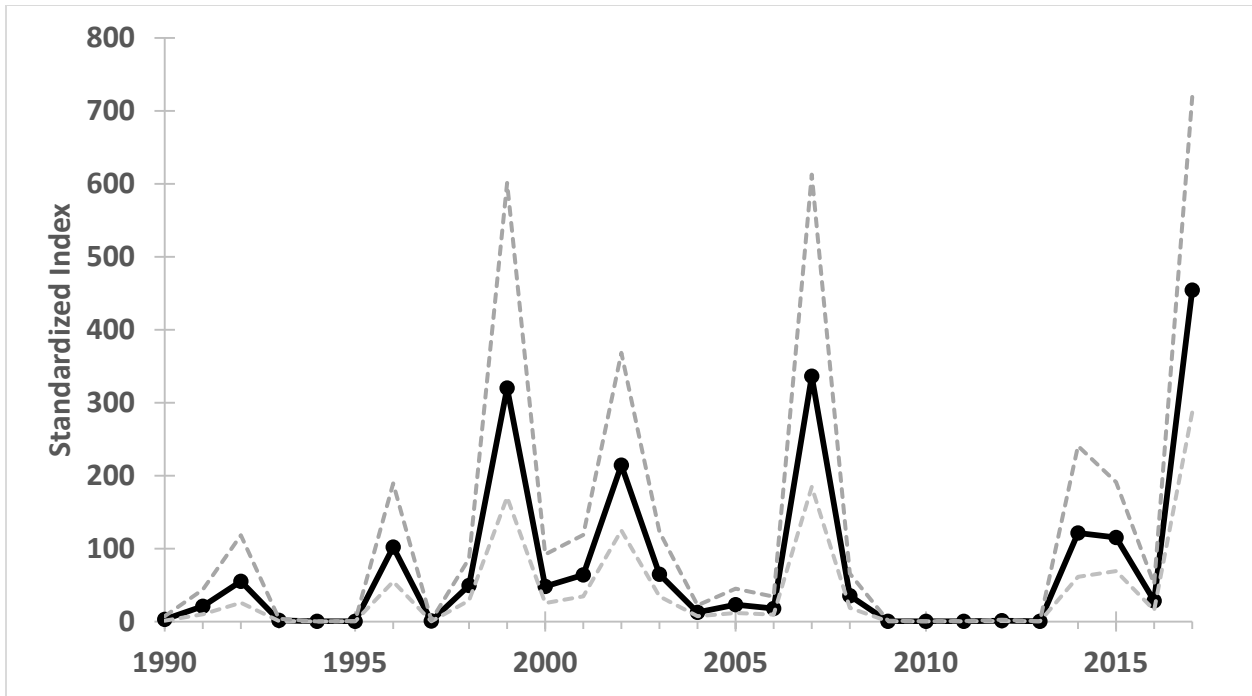


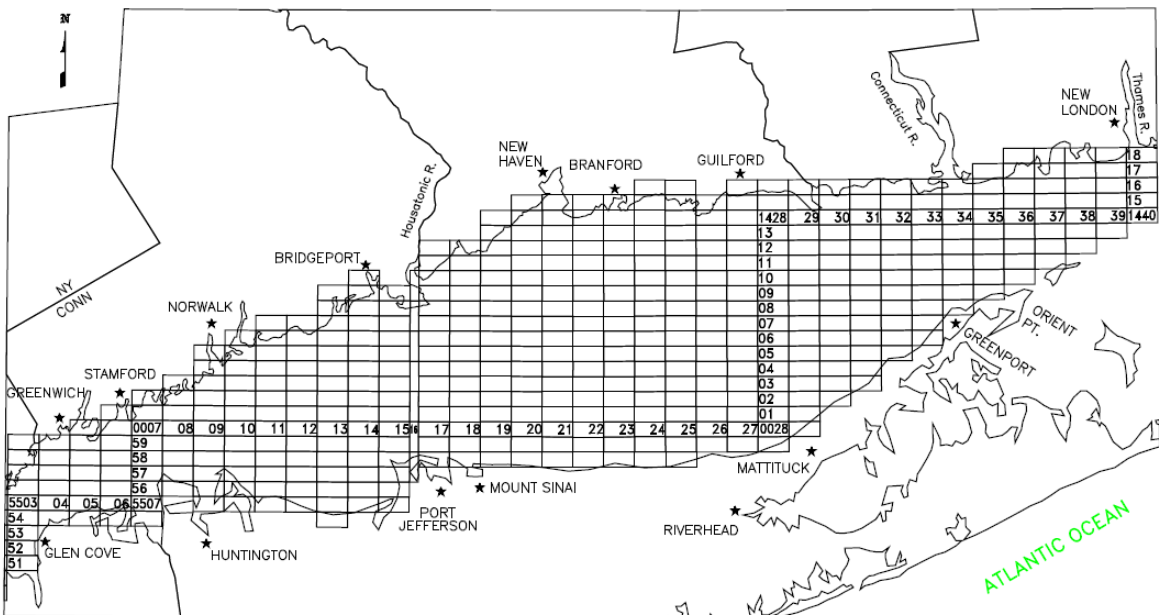
Figure 54. The Potomac River Fisheries Commission (PRFC) Index and Reduction Fishery CPUE (RCPUE) fishery-dependent indices developed by the ERP WG.



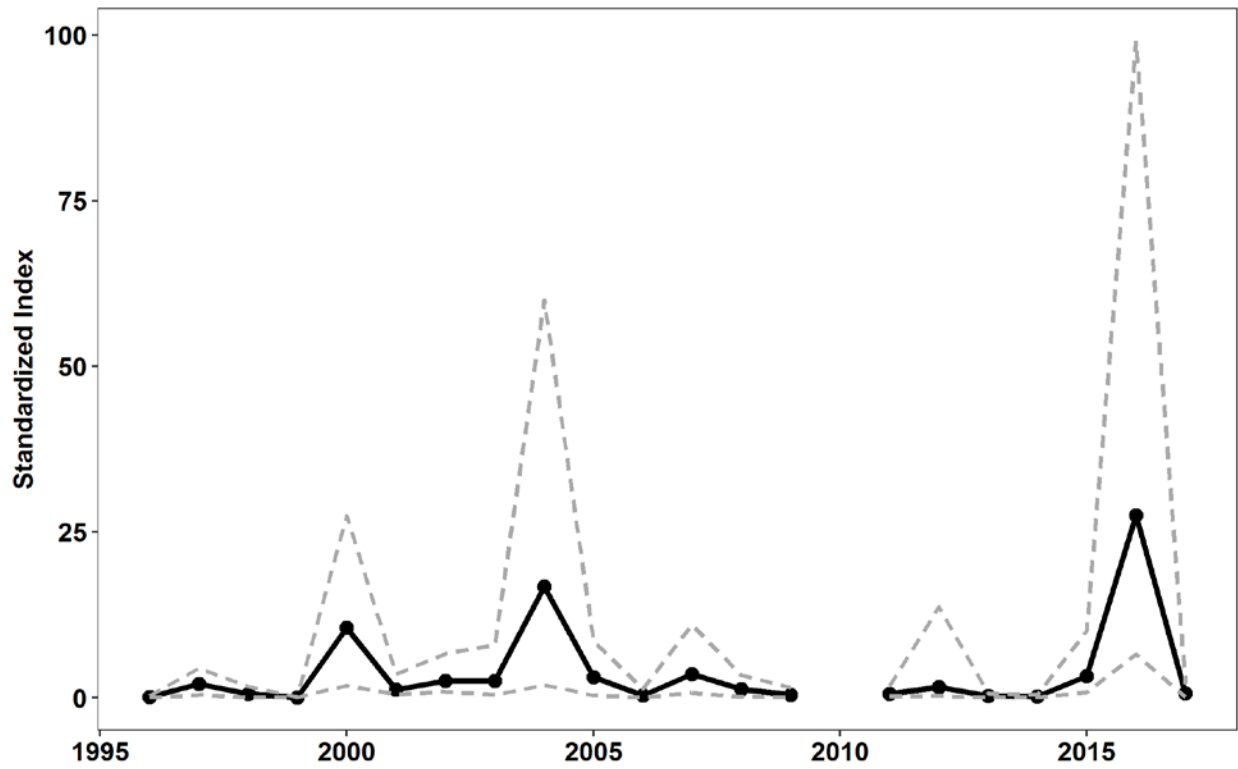
**Figure 55. Map of Rhode Island Coastal Trawl Survey (monthly segment) with the fixed tow stations represented as red dots.**



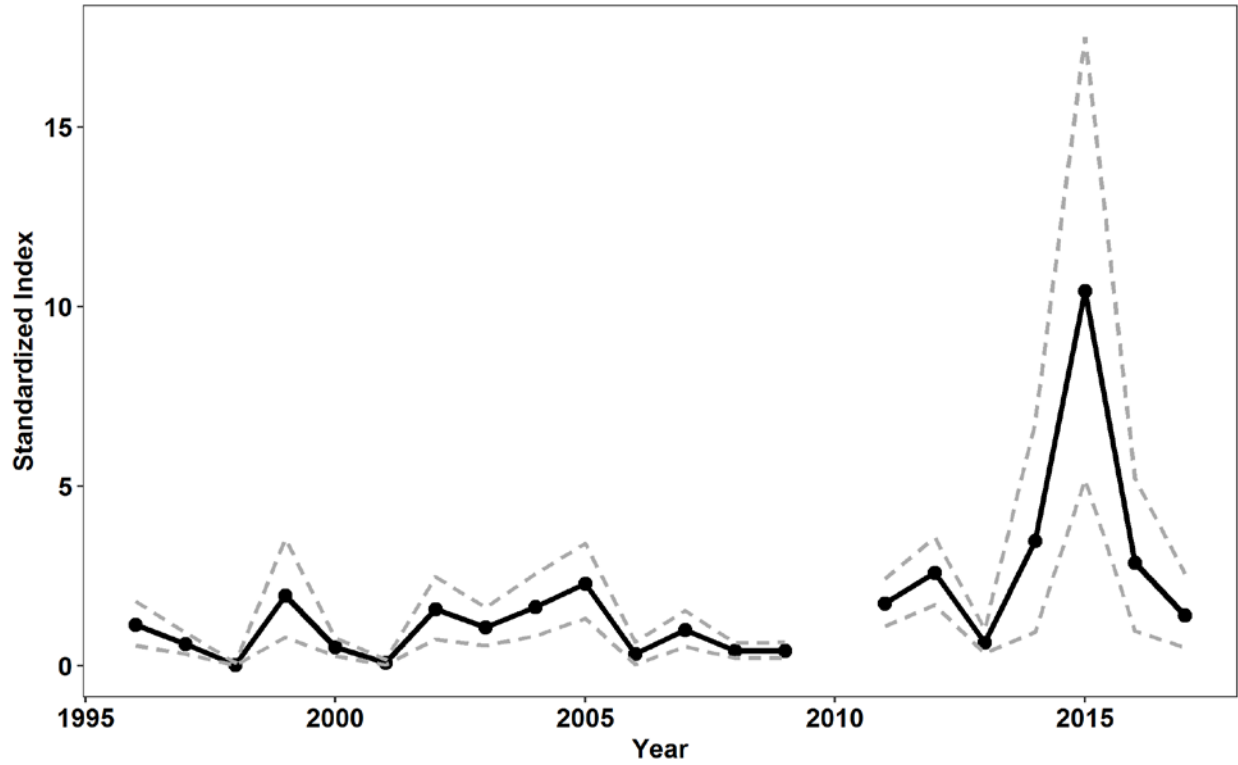
**Figure 56. Standardized index of relative abundance of YOY Atlantic menhaden developed from the fall portions of the monthly Rhode Island Coastal Trawl Survey with 95% confidence intervals.**



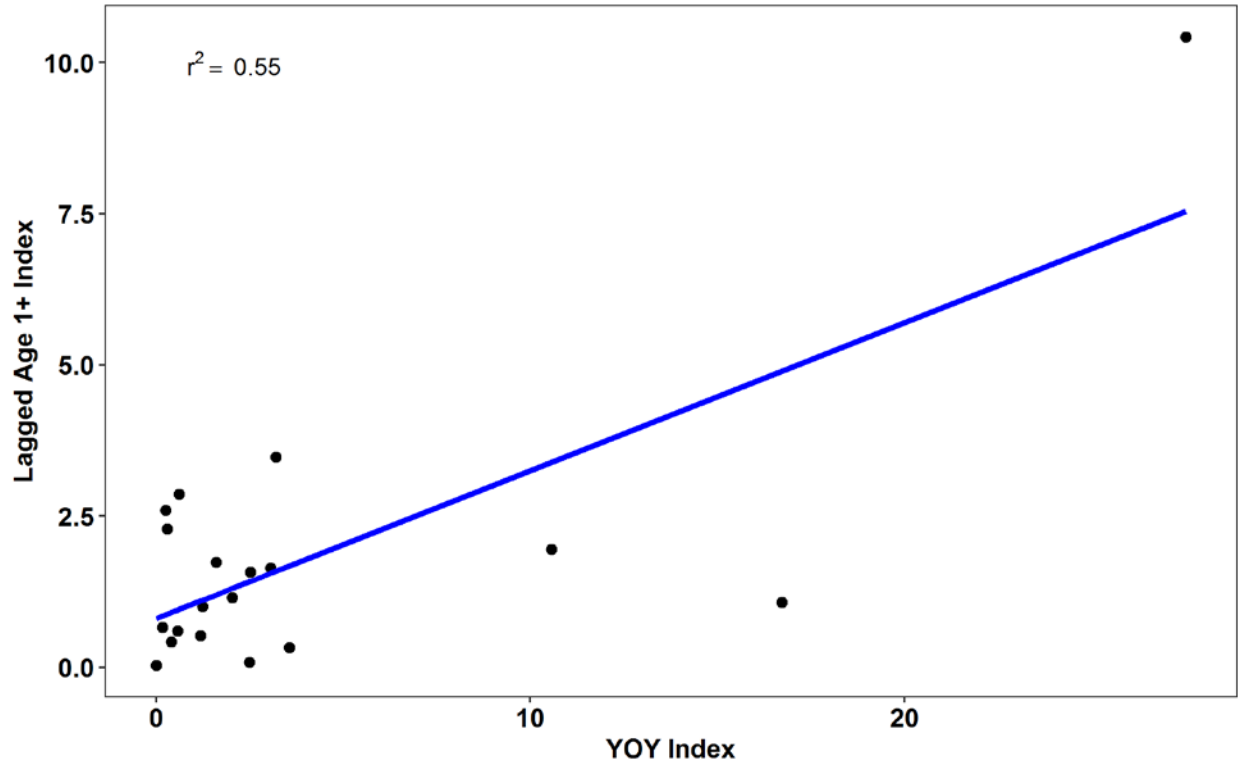
**Figure 57. Map of Connecticut Long Island Trawl Survey strata.**



**Figure 58. Standardized index of relative abundance of YOY Atlantic menhaden developed from the Connecticut Long Island Trawl Survey with 95% confidence intervals.**



**Figure 59. Standardized index of relative abundance of Age-1+ Atlantic menhaden developed from the Connecticut Long Island Trawl Survey with 95% confidence intervals.**



**Figure 60. Standardized index of Age-1+ Atlantic menhaden abundance plotted against standardized index of YOY abundance developed from the Connecticut Long Island Trawl Survey with linear regression line (blue).**

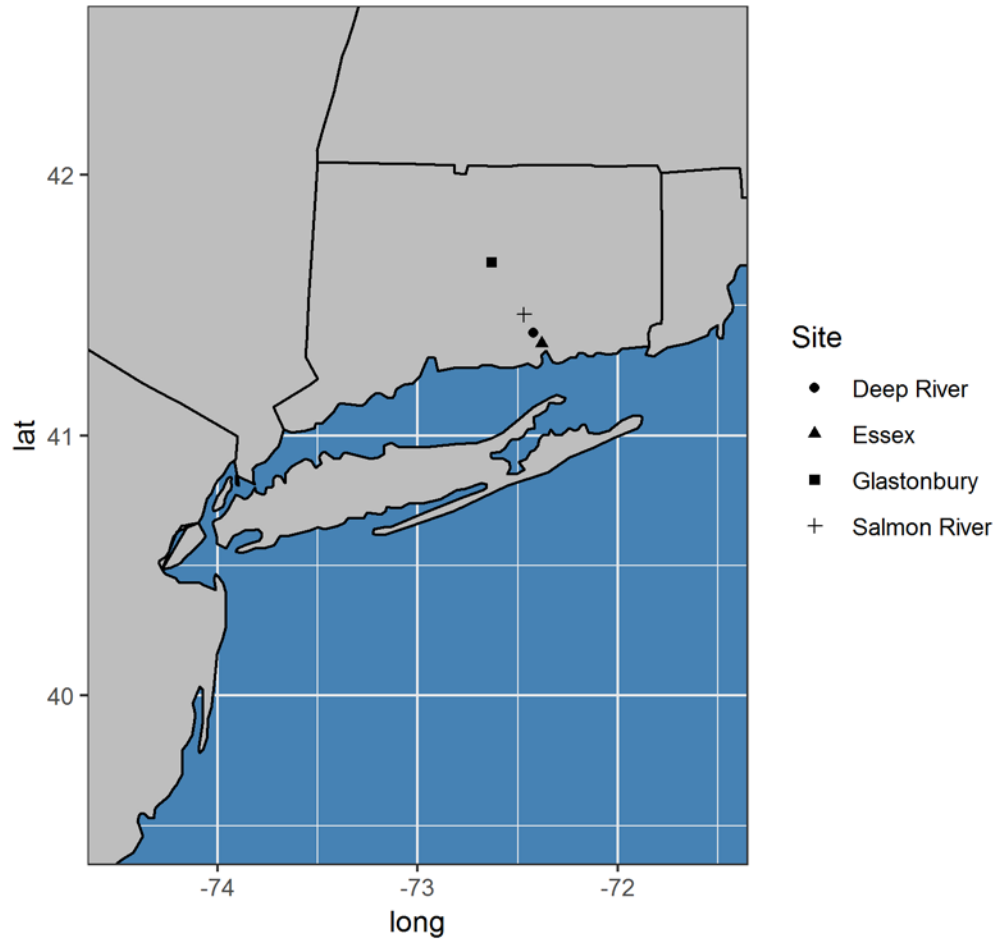
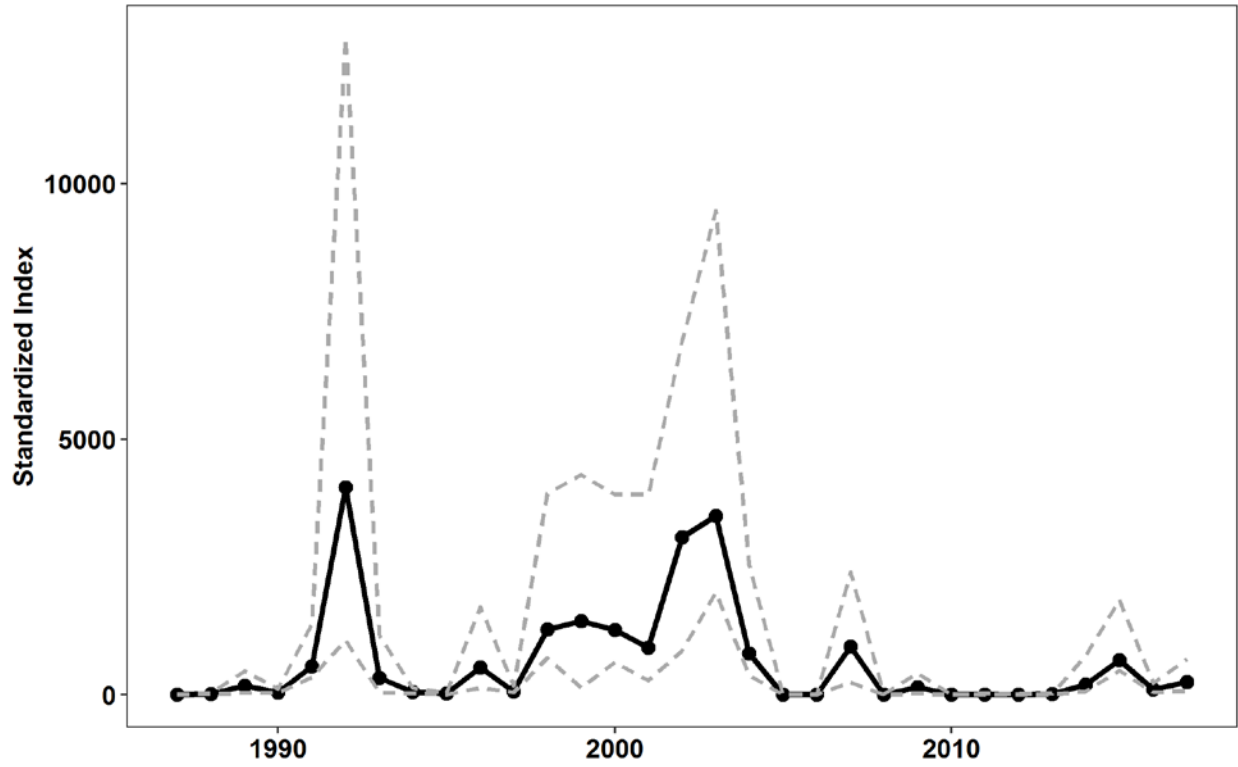
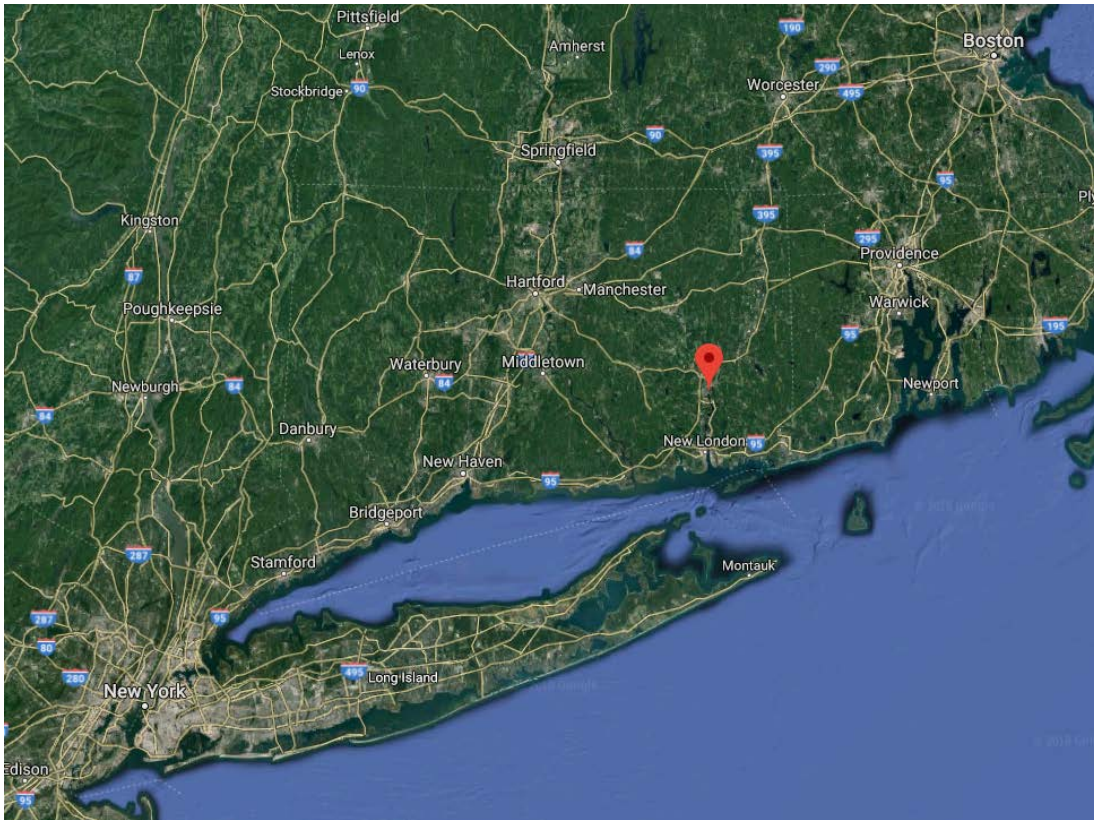


Figure 61. Fixed station sites for the Connecticut River Juvenile Alosine Seine Survey.

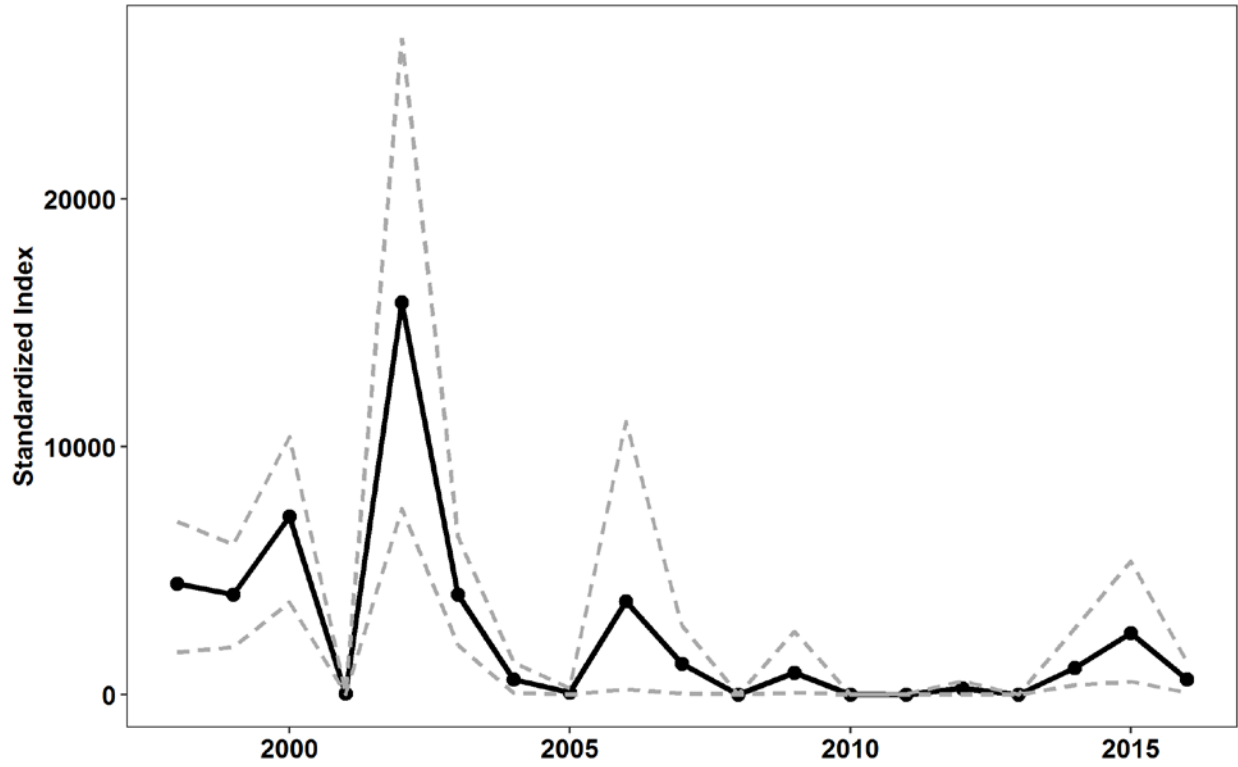


**Figure 62. Standardized index of relative abundance of YOY Atlantic menhaden developed from the Connecticut River Juvenile Alosine Seine Survey with 95% confidence intervals.**

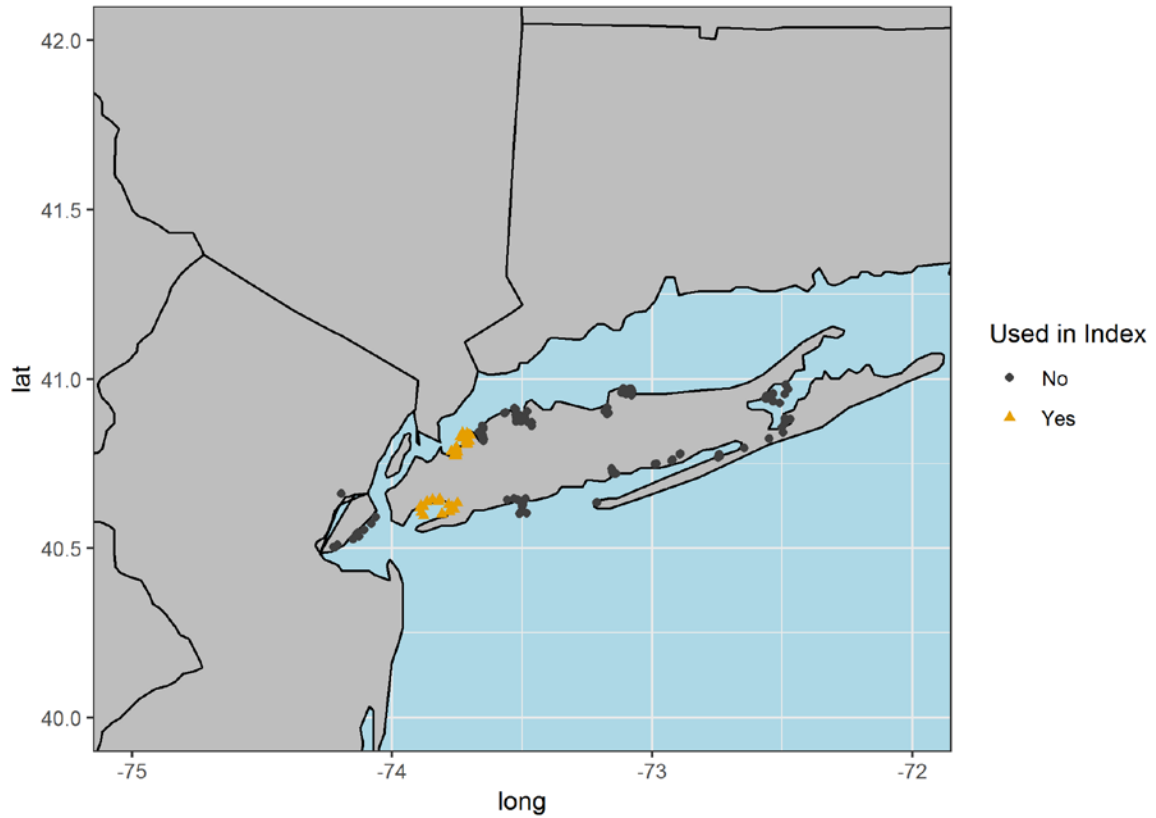




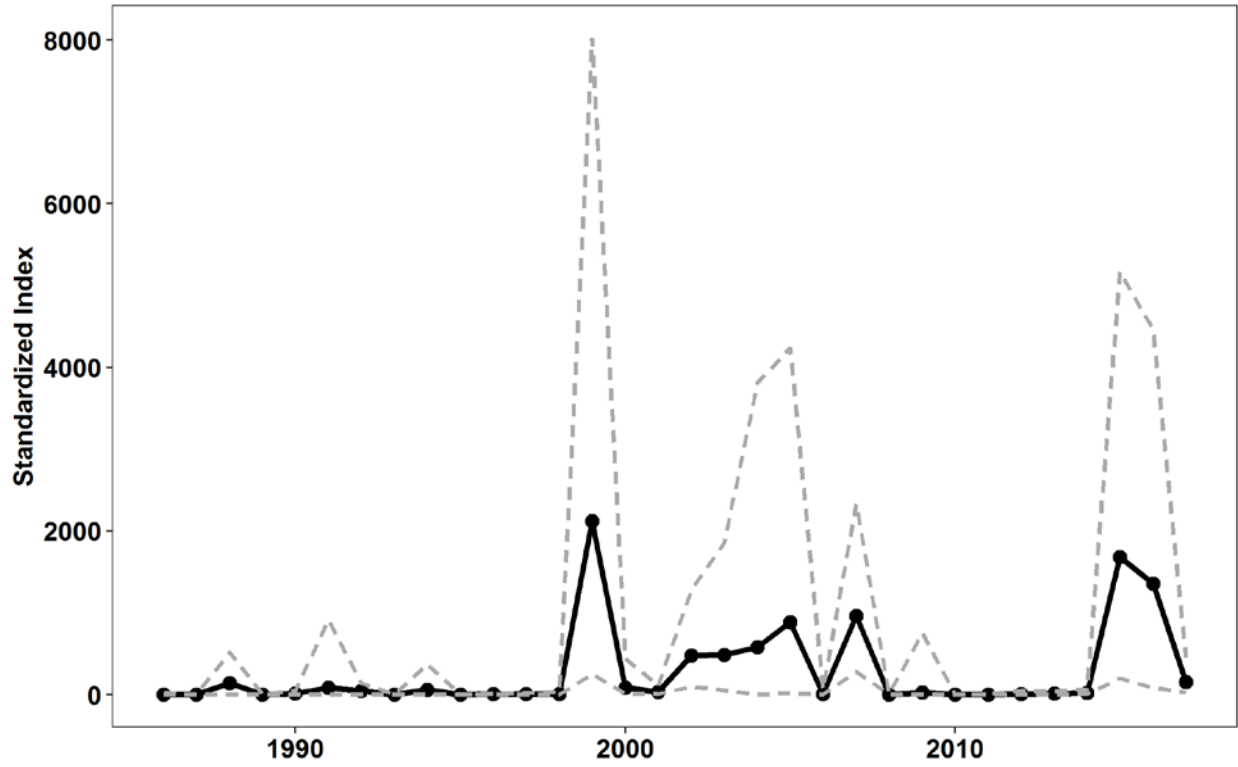
**Figure 63. Fixed station sites for the Thames River Seine Survey.**



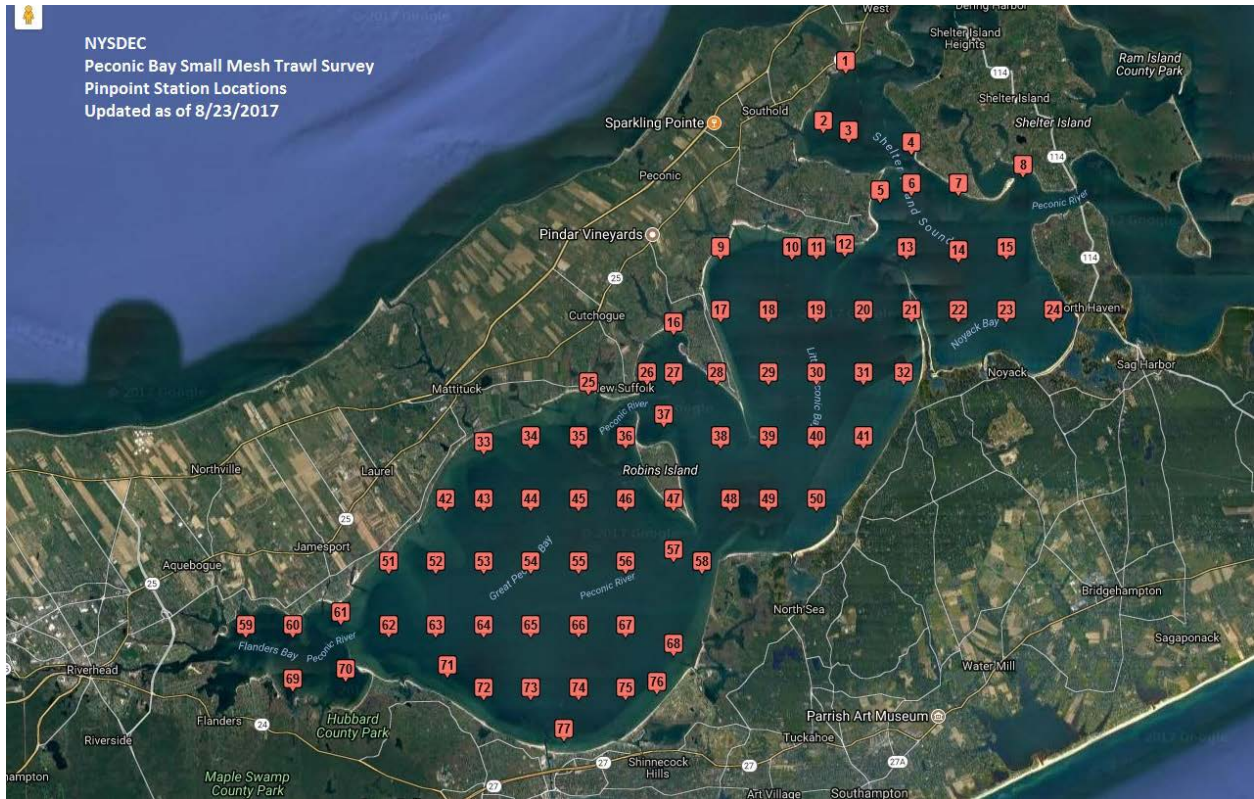
**Figure 64. Standardized index of relative abundance of YOY Atlantic menhaden developed from the Connecticut Thames River Seine Survey with 95% confidence intervals.**



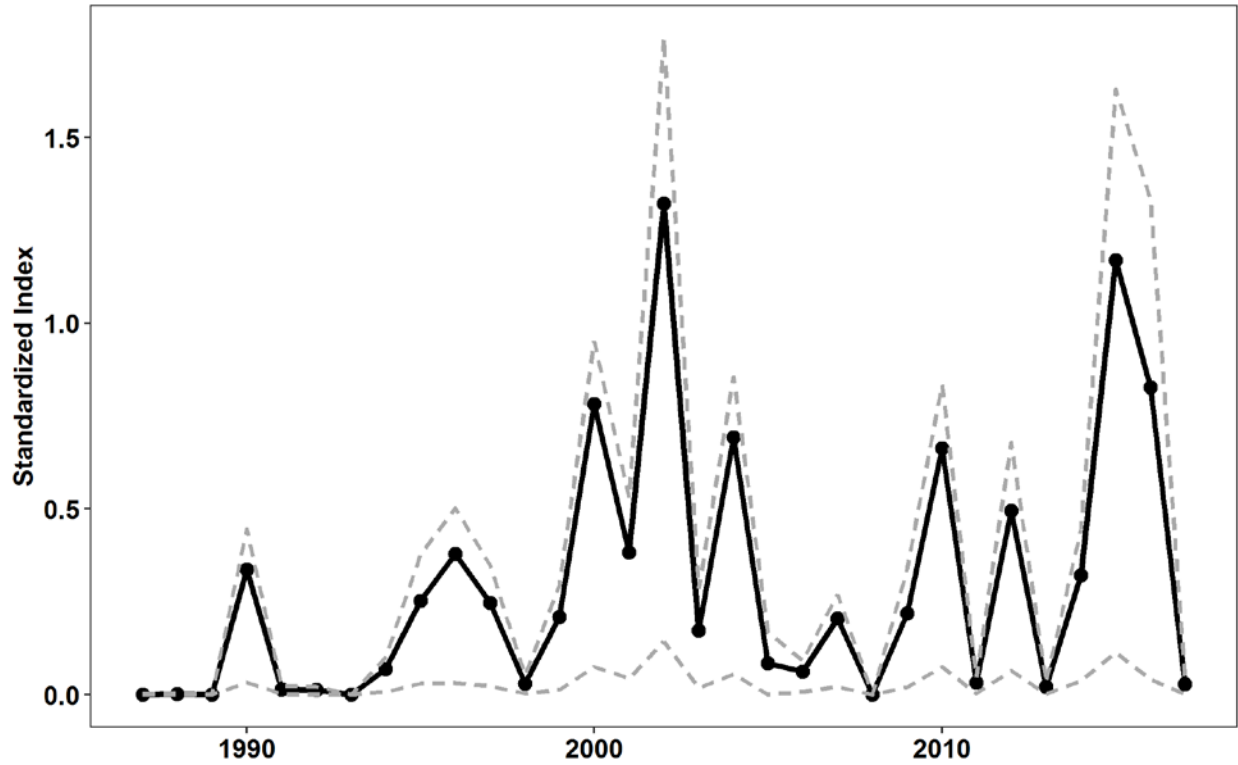
**Figure 65. Sites sampled by the New York Western Long Island Seine Survey. Only sites sampled consistently over the entire time series were used in the index.**



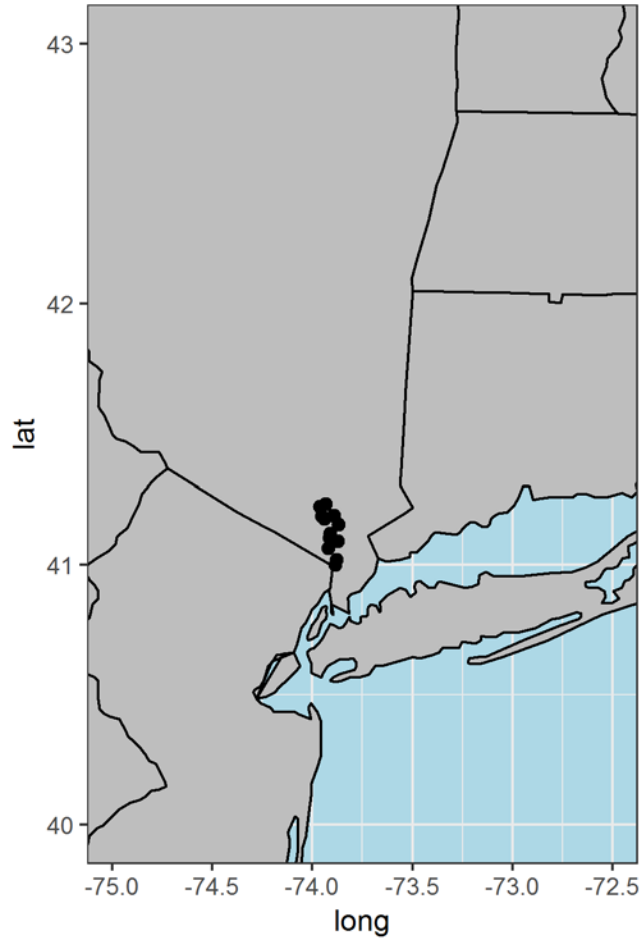
**Figure 66. Standardized index of relative abundance of YOY Atlantic menhaden developed from the New York Western Long Island Seine Survey with 95% confidence intervals.**



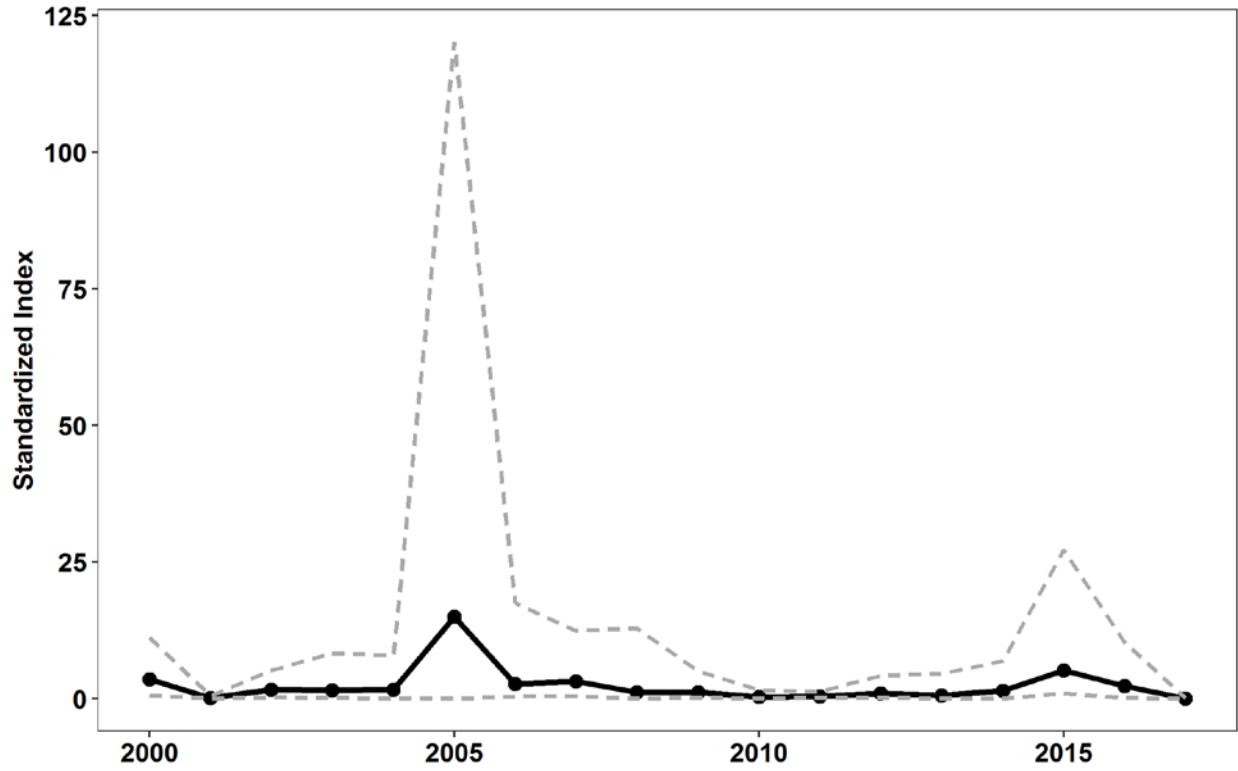
**Figure 67. Stations sampled by the New York Peconic Bay Small Mesh Trawl Survey.**



**Figure 68. Standardized index of relative abundance of YOY Atlantic menhaden developed from the New York Peconic Bay Small Mesh Trawl Survey with 95% confidence intervals.**



**Figure 69. Sites sampled by the New York Juvenile Striped Bass Seine Survey.**



**Figure 70. Standardized index of relative abundance of YOY Atlantic menhaden developed from the New York Juvenile Striped Bass Seine Survey with 95% confidence intervals.**



DELAWARE RIVER RECRUITMENT SURVEY SAMPLING AREA

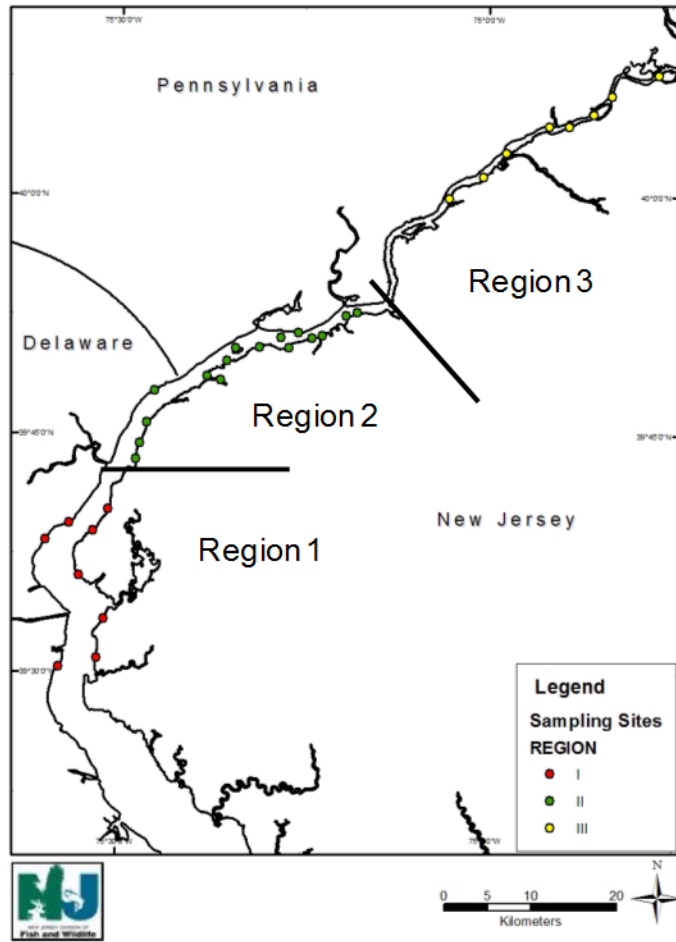
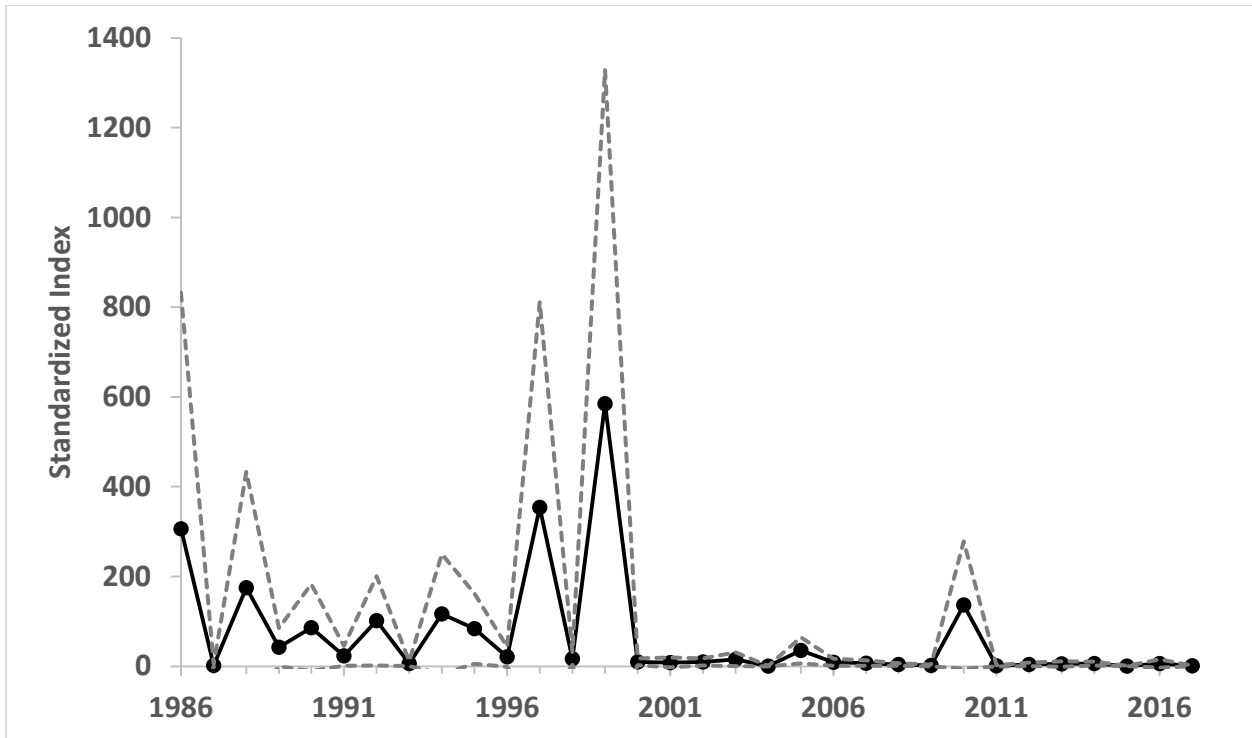


Figure 71. Map of New Jersey's Delaware River Striped Bass Seine Survey's sampling regions.



**Figure 72. Standardized index of relative abundance of YOY Atlantic menhaden developed from the New Jersey Delaware River Striped Bass Seine Survey with 95% confidence intervals.**

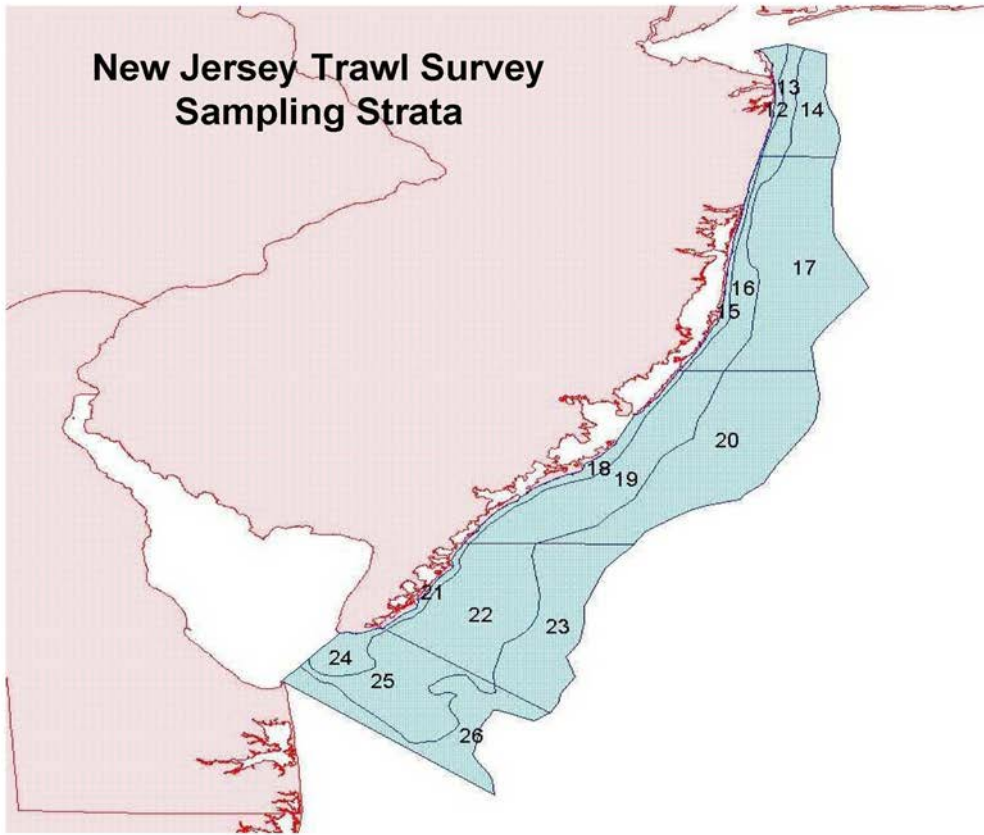


Figure 73. Map of the sampling area and strata from the New Jersey Ocean Trawl Survey.

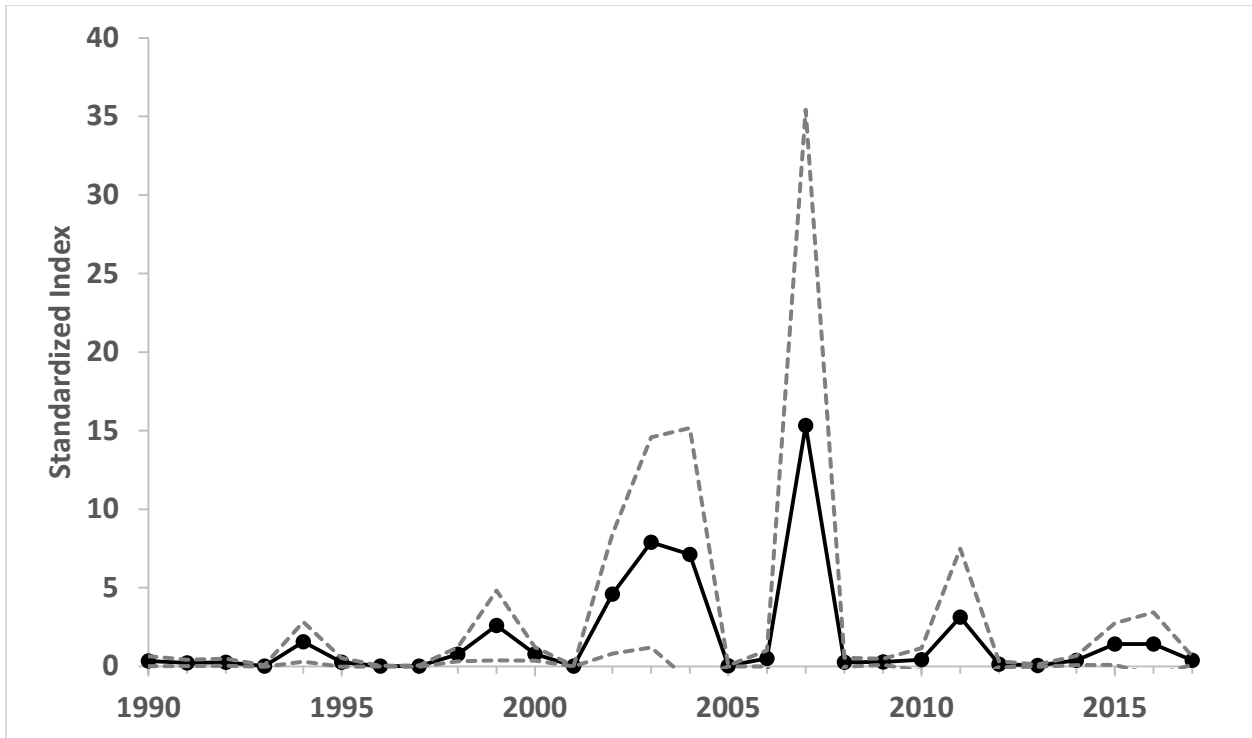


Figure 74. Standardized index of relative abundance of YOY Atlantic menhaden developed from the New Jersey Ocean Trawl Survey with 95% confidence intervals.

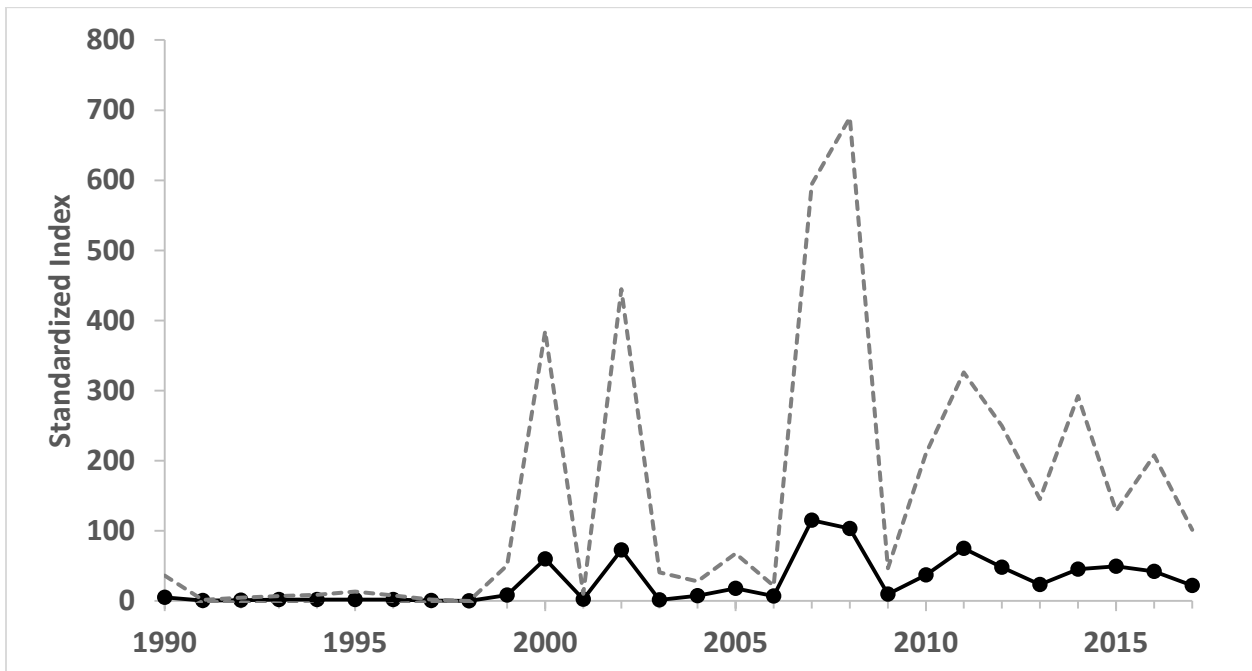
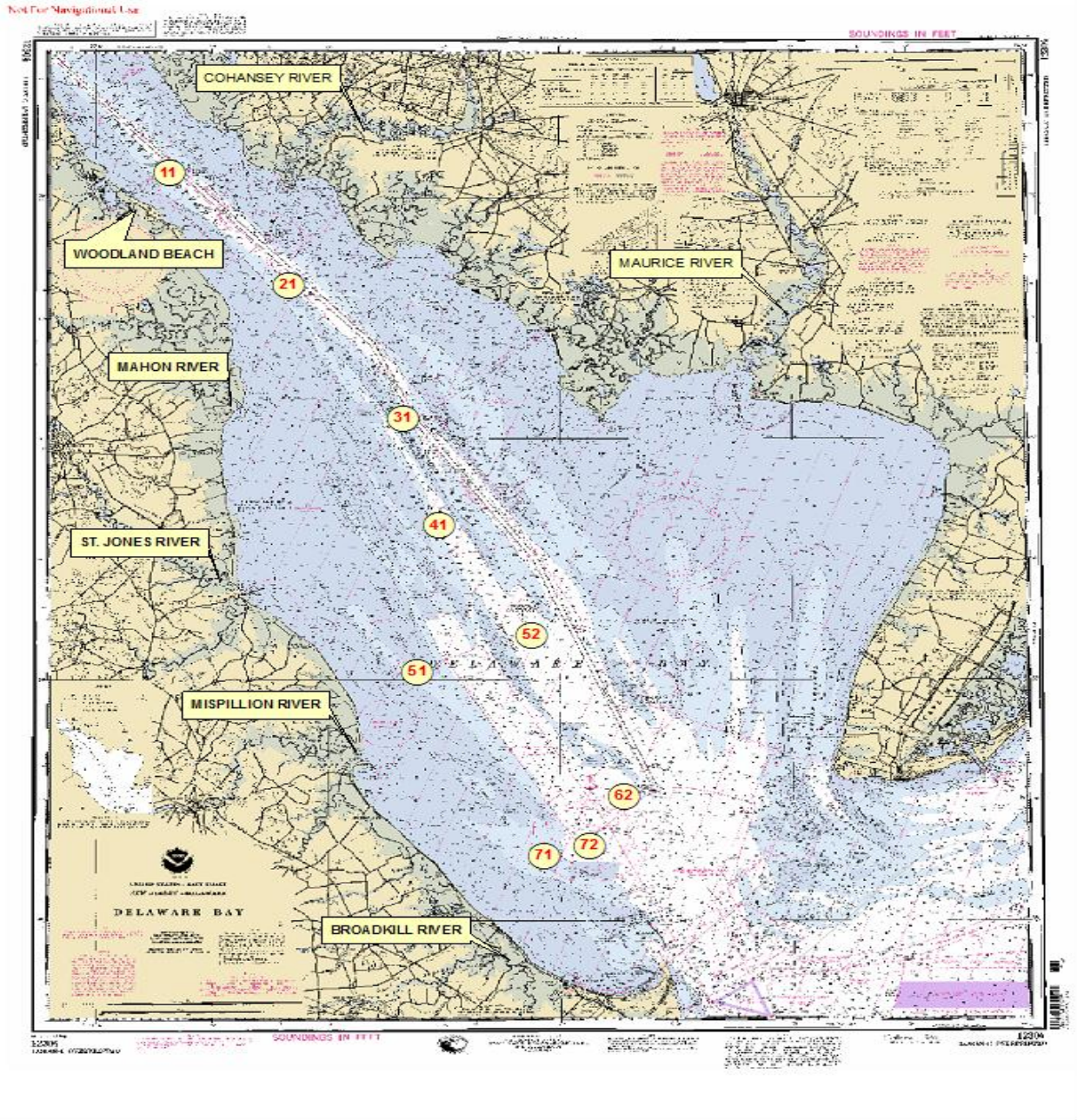
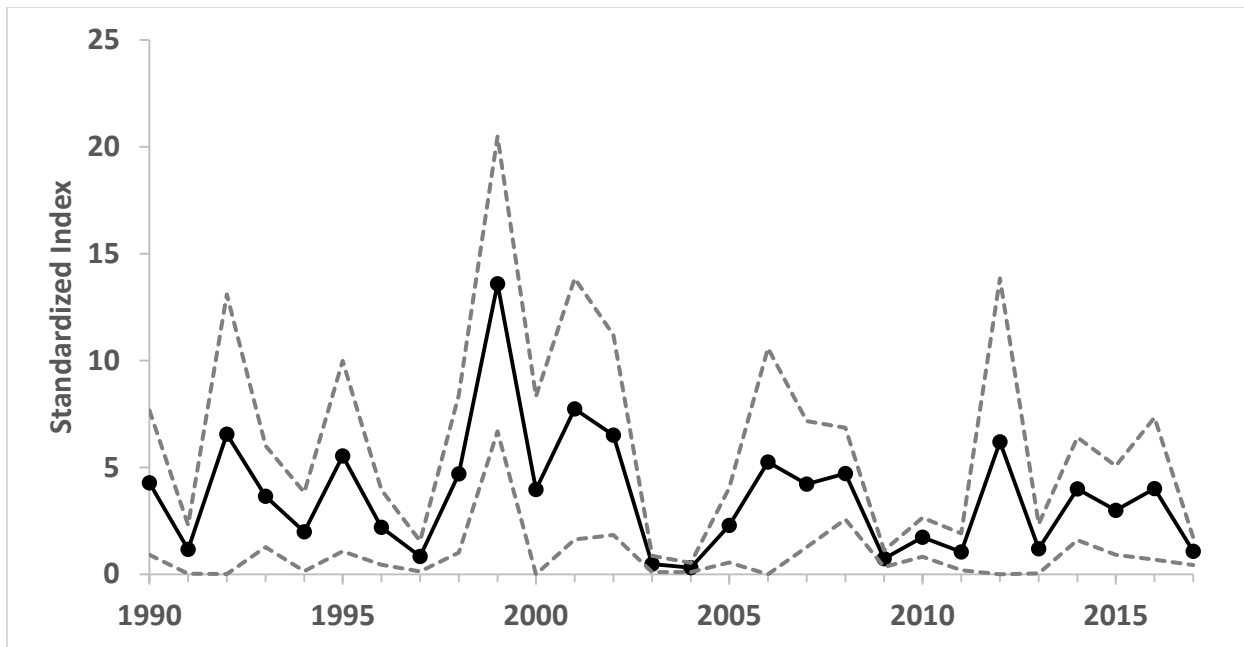


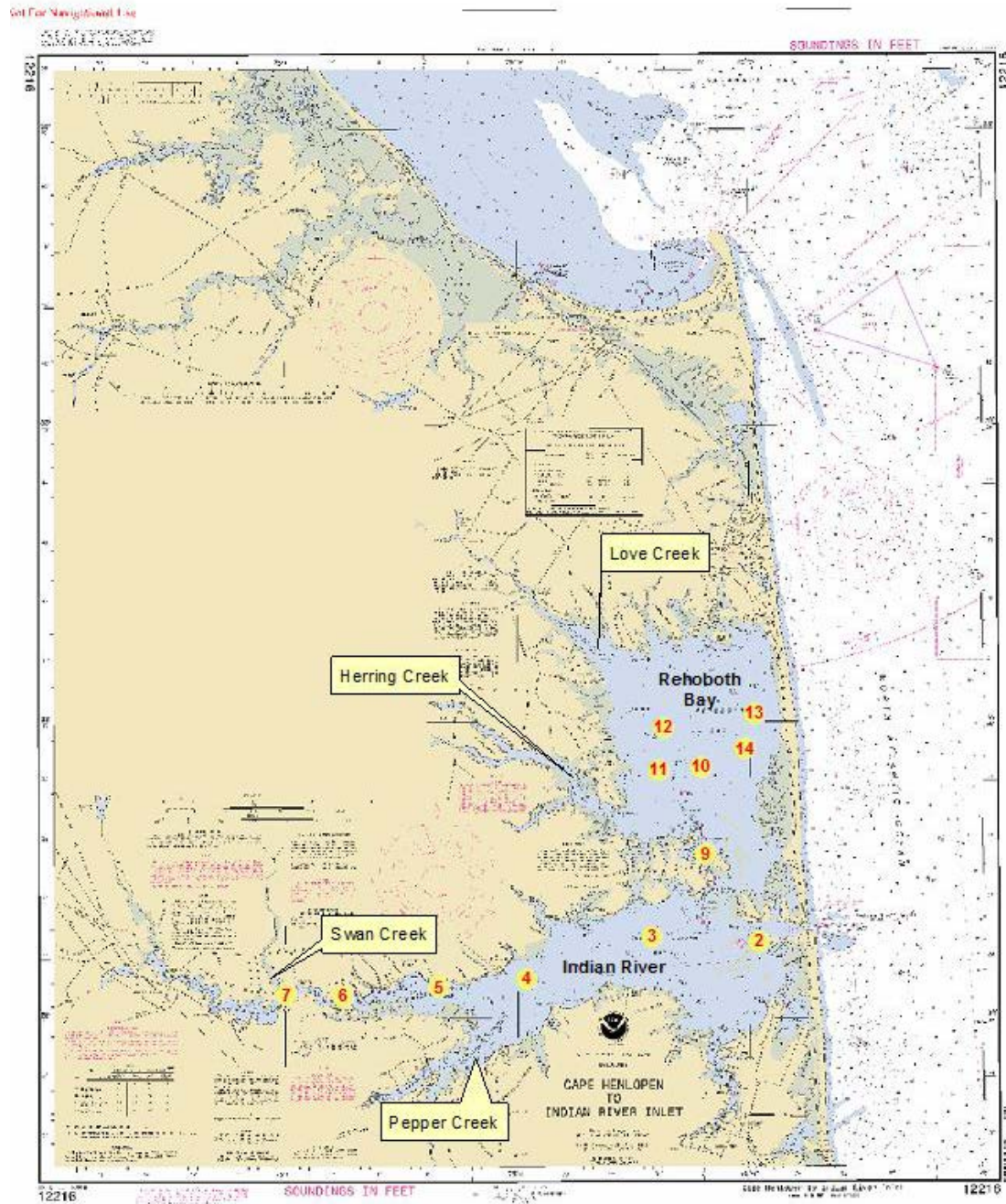
Figure 75. Standardized index of relative abundance of age-1+ Atlantic menhaden developed from the New Jersey Ocean Trawl Survey with 95% confidence intervals.



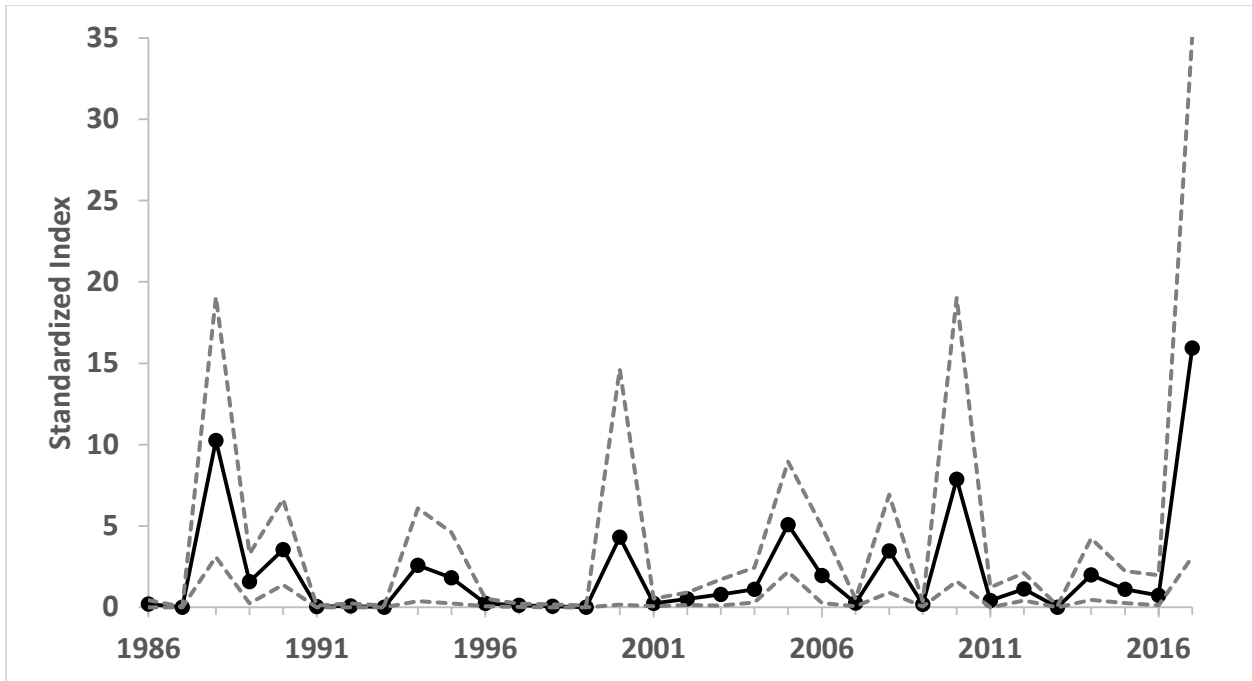
**Figure 76. Map of the sampling area for Delaware Fish and Wildlife’s Adult Trawl Survey with the nine fixed station sampling sites indicated with numbers.**



**Figure 77. Standardized index of relative abundance of age 1+ Atlantic menhaden developed from the fall months of the Delaware Bay Adult Trawl Survey with 95% confidence intervals.**



**Figure 78. Map of the sampling sites for Delaware Fish and Wildlife’s Juvenile Trawl Inland Bays Survey.**



**Figure 79. Standardized index of relative abundance of YOY Atlantic menhaden developed from Delaware’s Inland Bays Survey with 95% confidence intervals.**



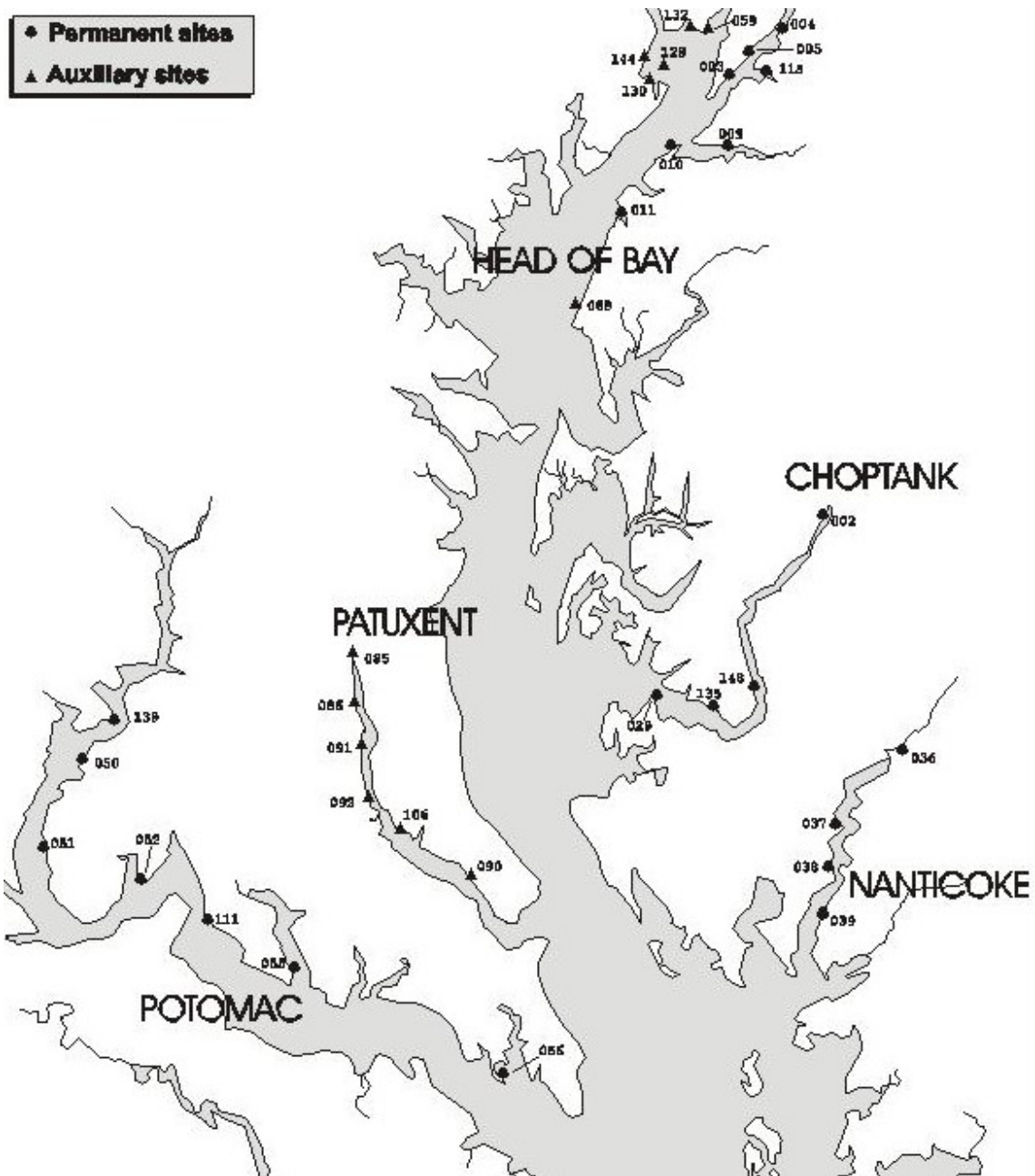
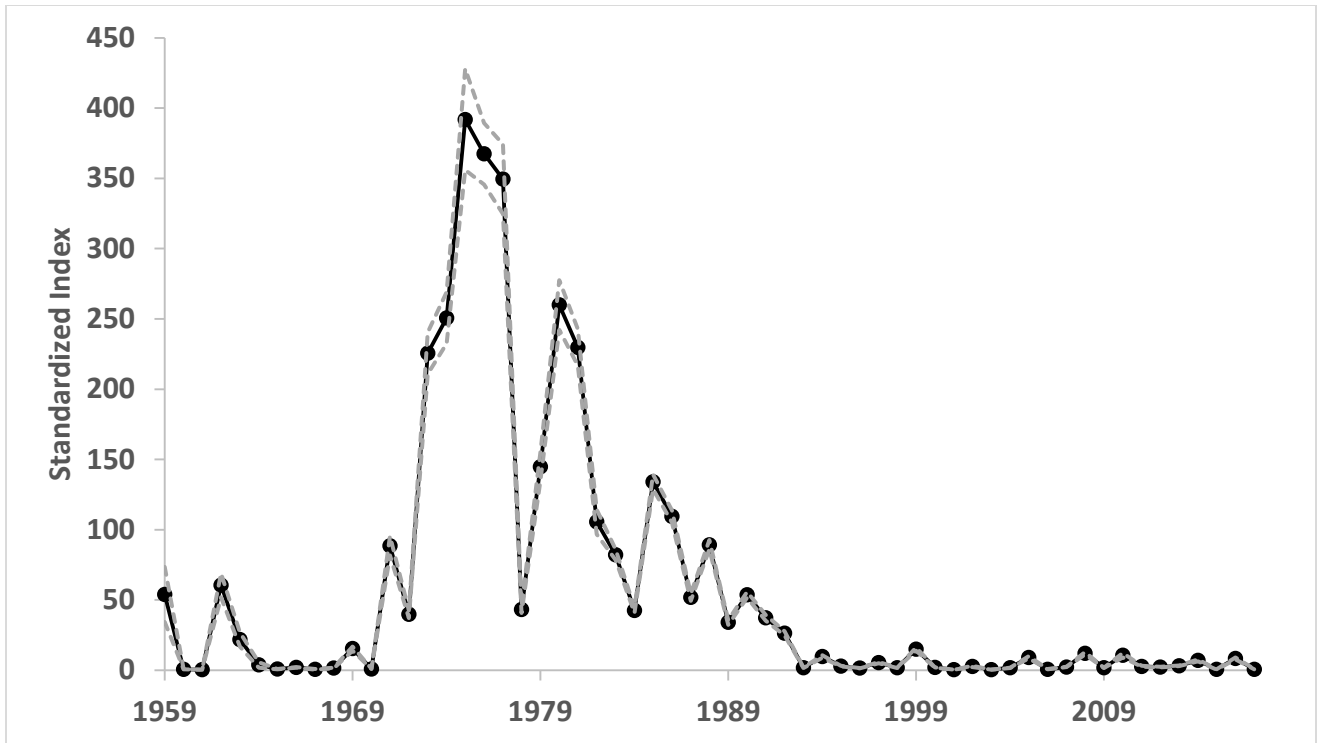


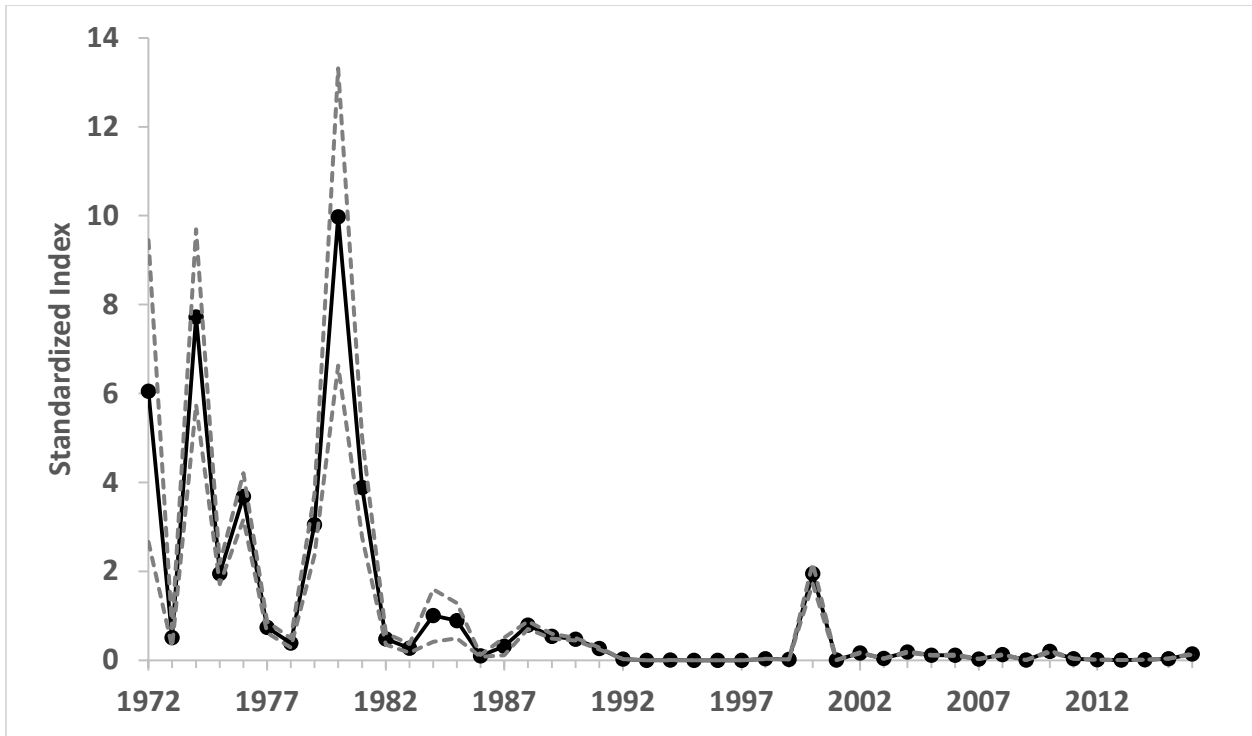
Figure 80. Map of the survey sites from Maryland Department of Natural Resources Juvenile Striped Bass Survey.



**Figure 81. Standardized index of relative abundance of YOY Atlantic menhaden developed from Maryland Department of Natural Resources Juvenile Striped Bass Survey with 95% confidence intervals.**



Figure 82. Map of the Maryland Coastal Bays Survey sampling sites. Trawl sites are labeled with the prefix of “T” (map from MD DNR).



**Figure 83. Standardized index of relative abundance of YOY Atlantic menhaden developed from Maryland Department of Natural Resources Coastal Bays Survey with 95% confidence intervals.**

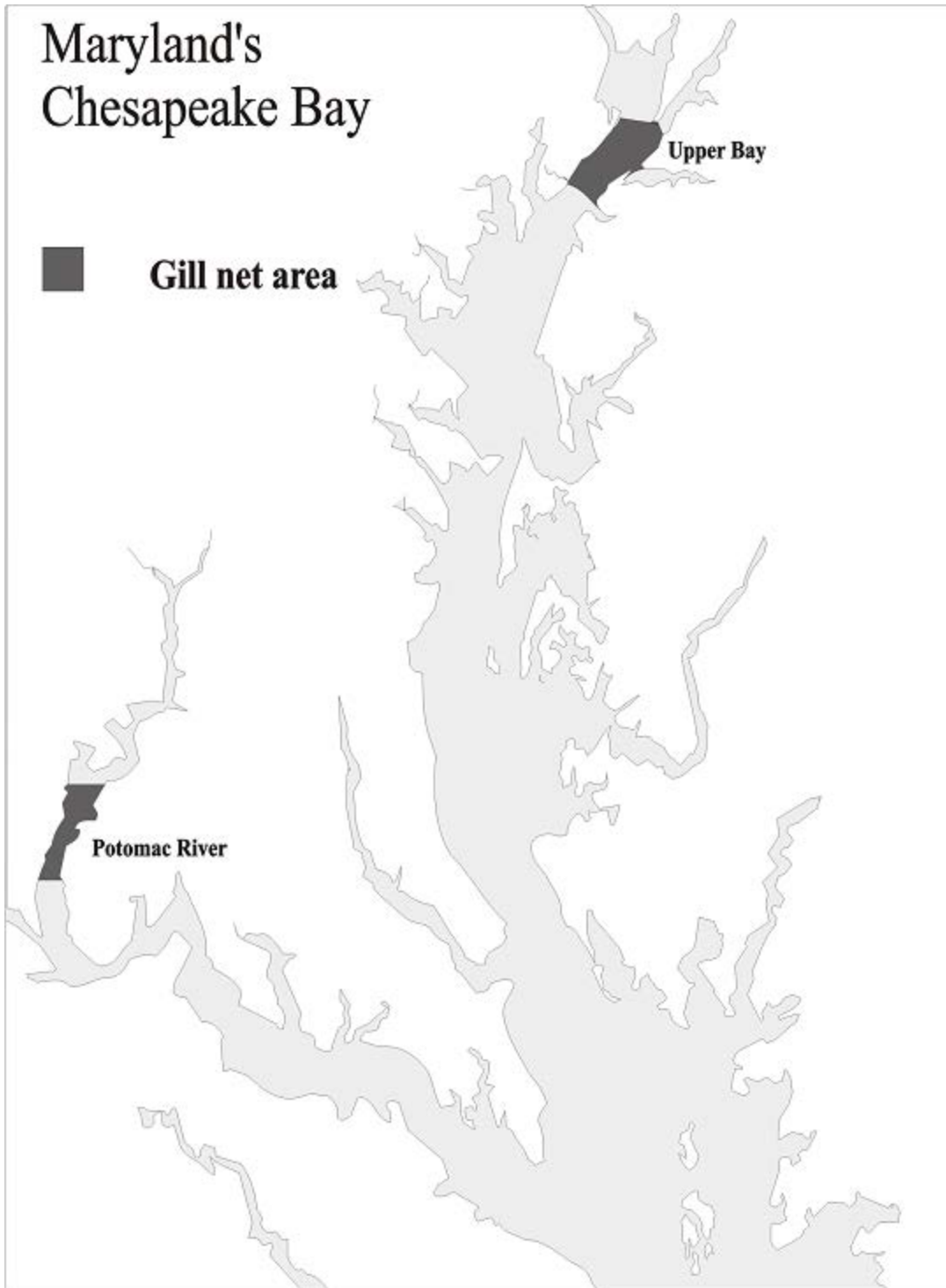
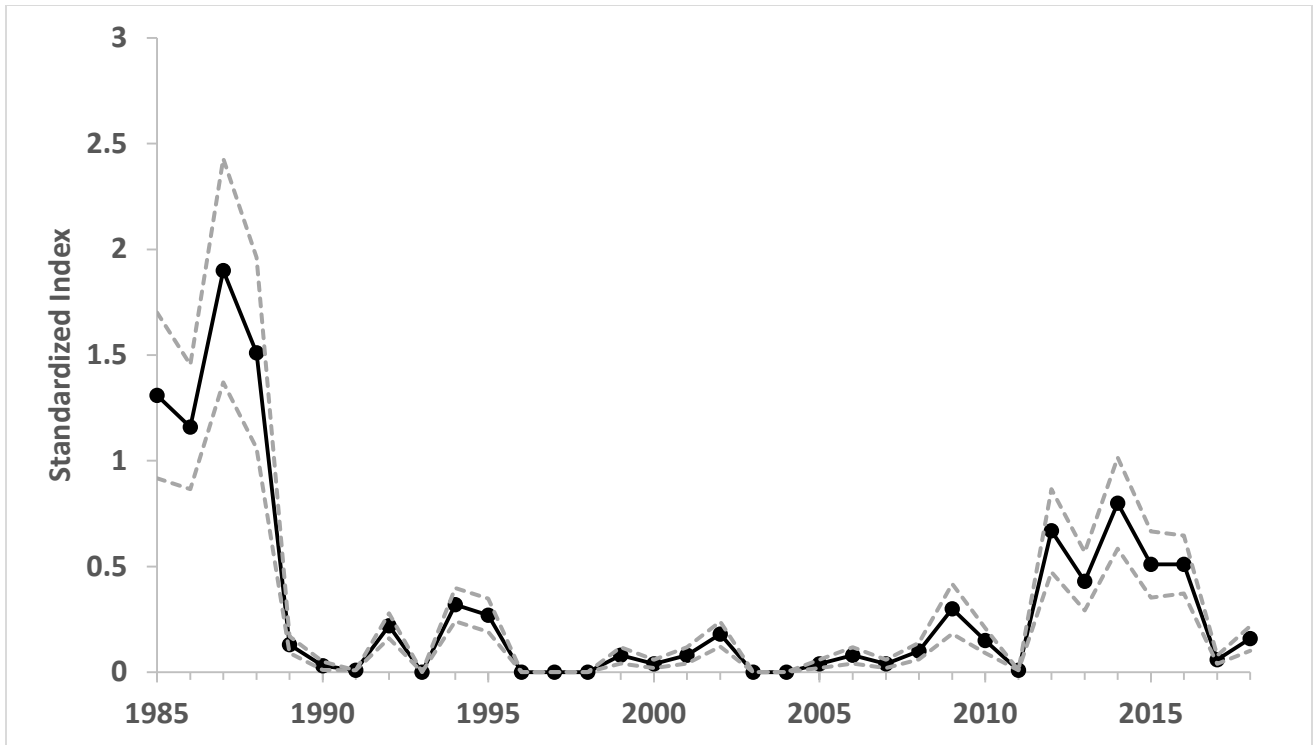


Figure 84. Map of Maryland Department of Natural Resources Striped Bass Spring Gill Net Survey sampling sites.



**Figure 85. Standardized index of relative abundance of age 1+ Atlantic menhaden developed from Maryland Department of Natural Resources Striped Bass Spring Gill Net Survey for the months of March-May with 95% confidence intervals.**

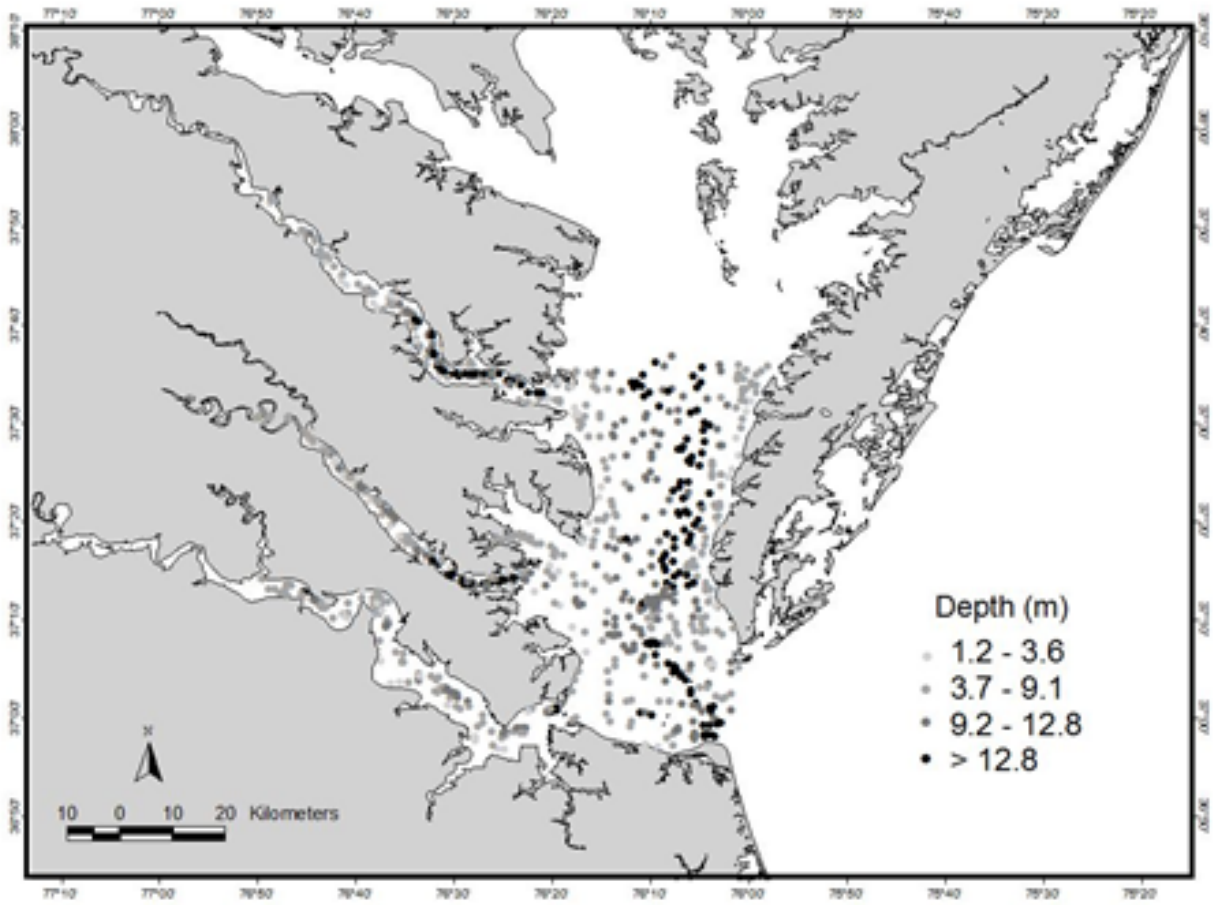
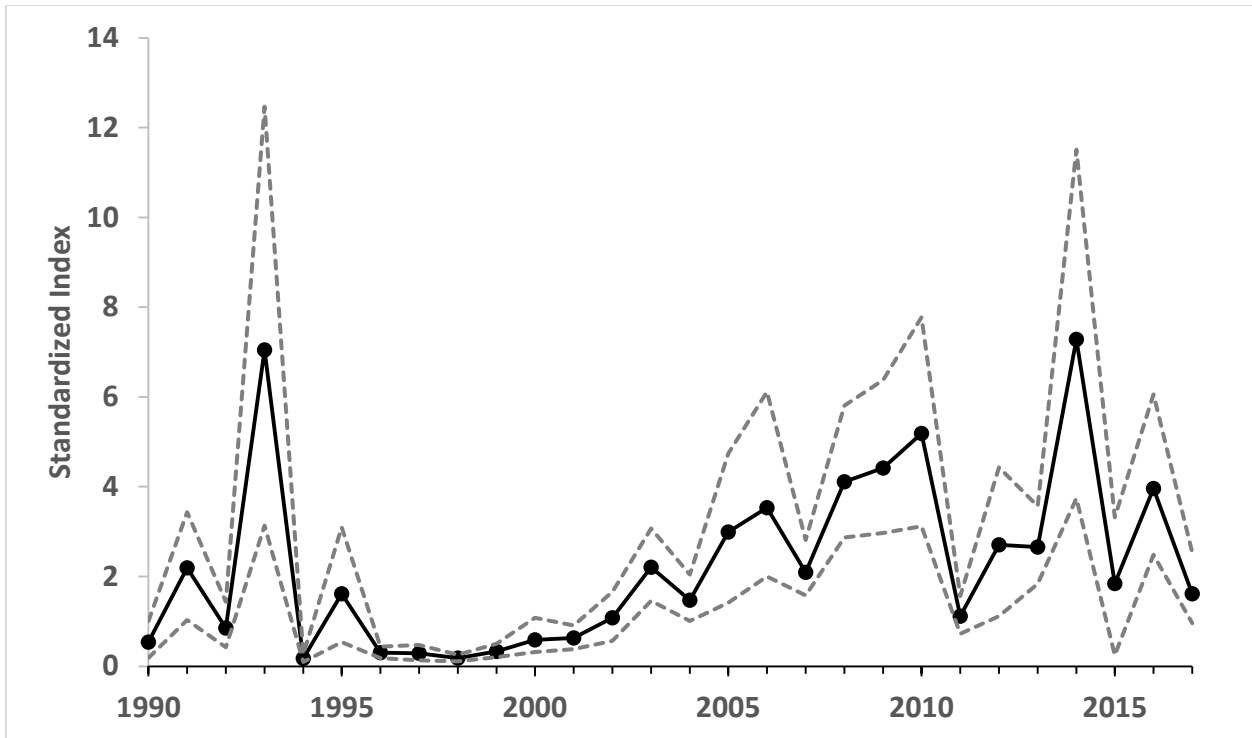


Figure 86. Sampling sites for the VIMS Juvenile Fish and Blue Crab Trawl Survey (source: VIMS).



**Figure 87. Standardized index of relative abundance of YOY Atlantic menhaden developed from the VIMS Juvenile Fish and Blue Crab Trawl Survey with 95% confidence intervals.**



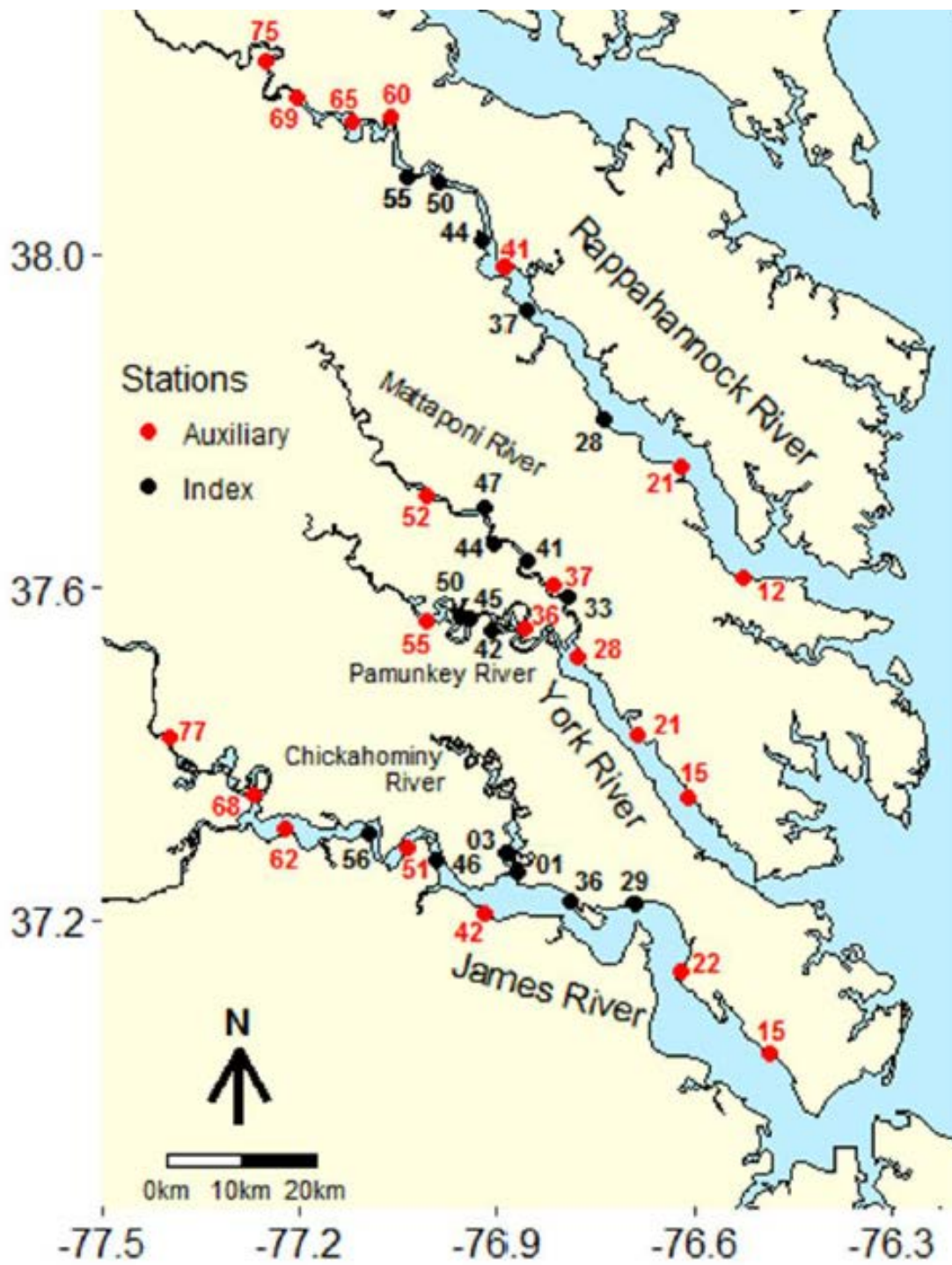


Figure 88. Sampling sites for the VIMS Juvenile Striped Bass Seine Survey. Site numbers denote the approximate river mile from the mouth of the Bay (source: VIMS).

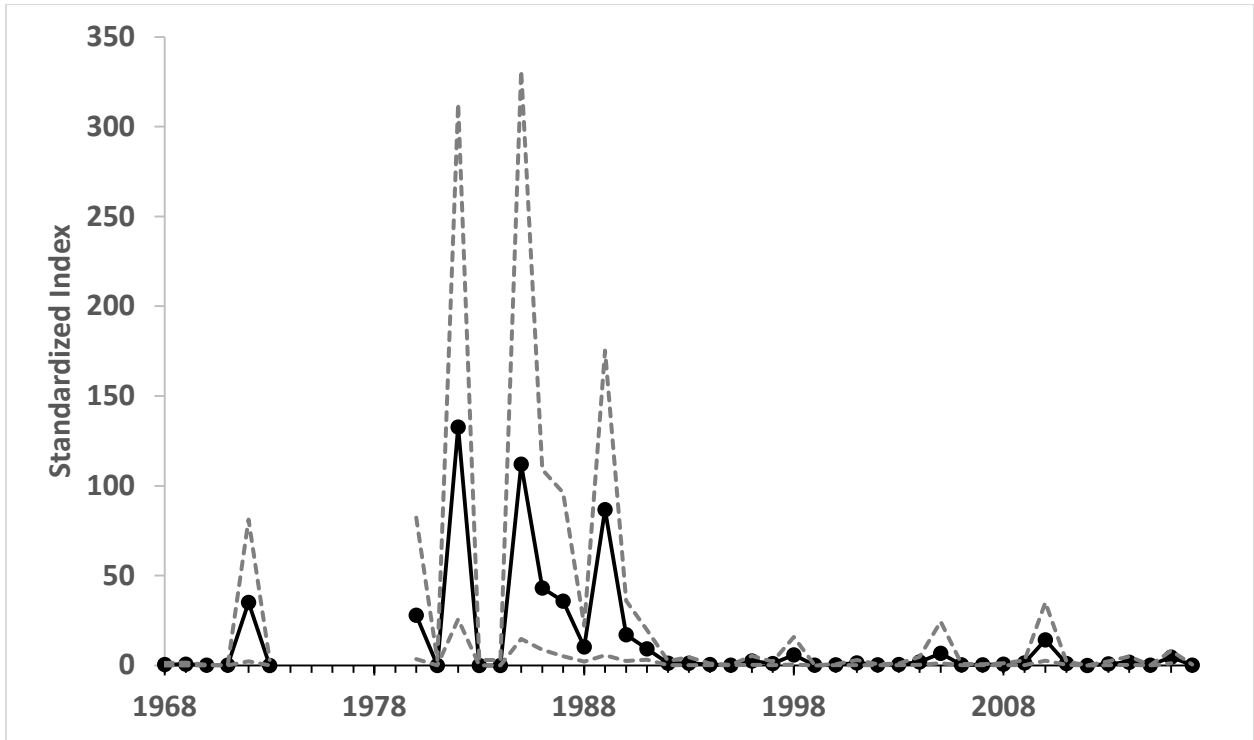
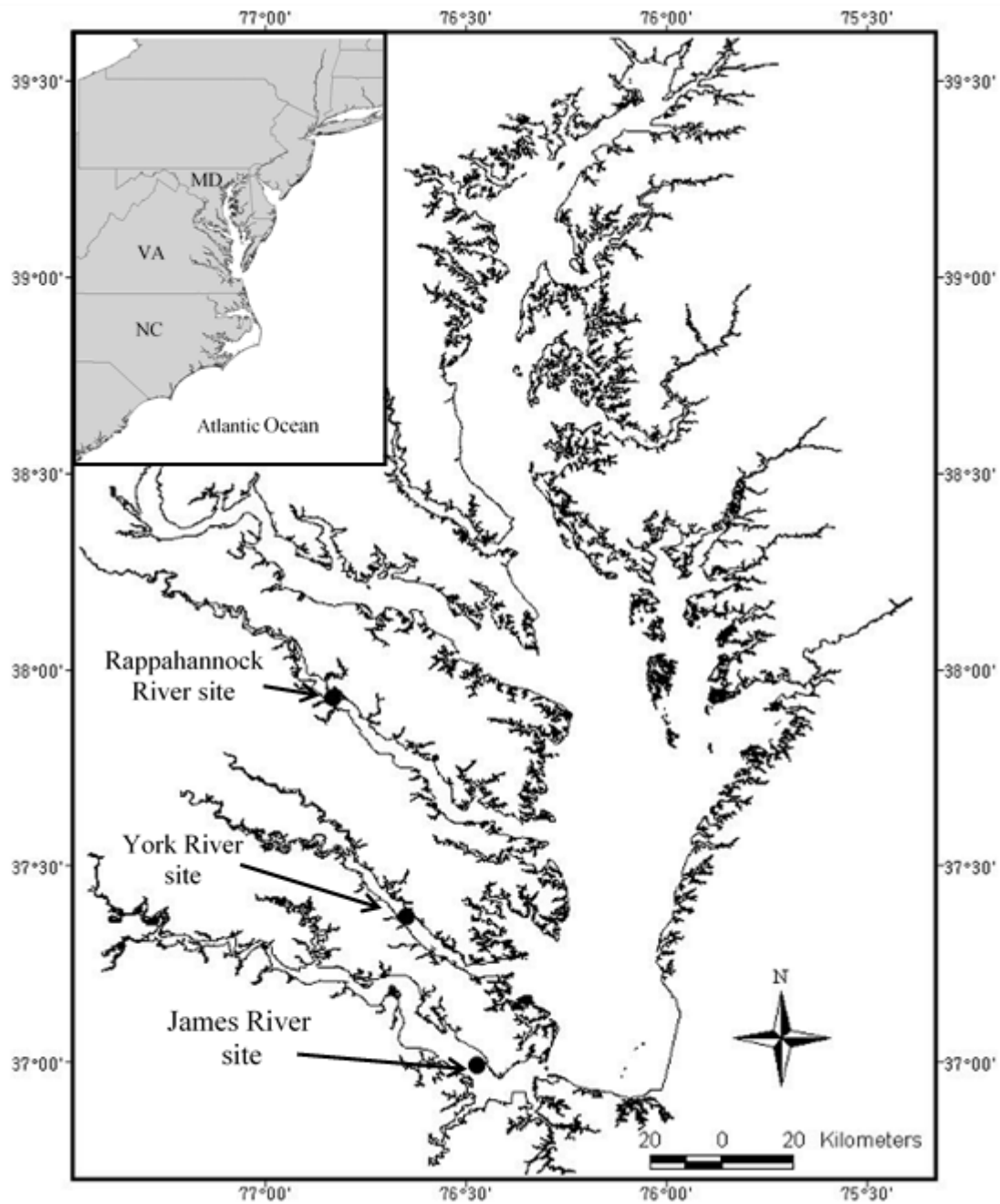
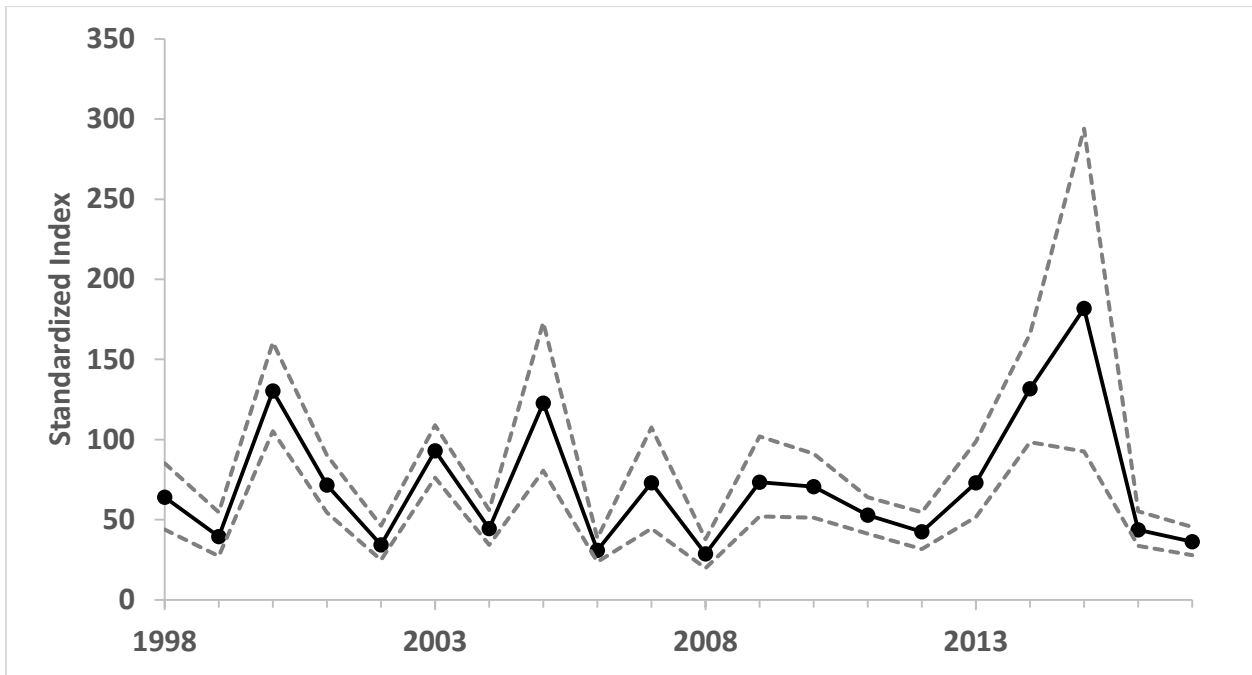


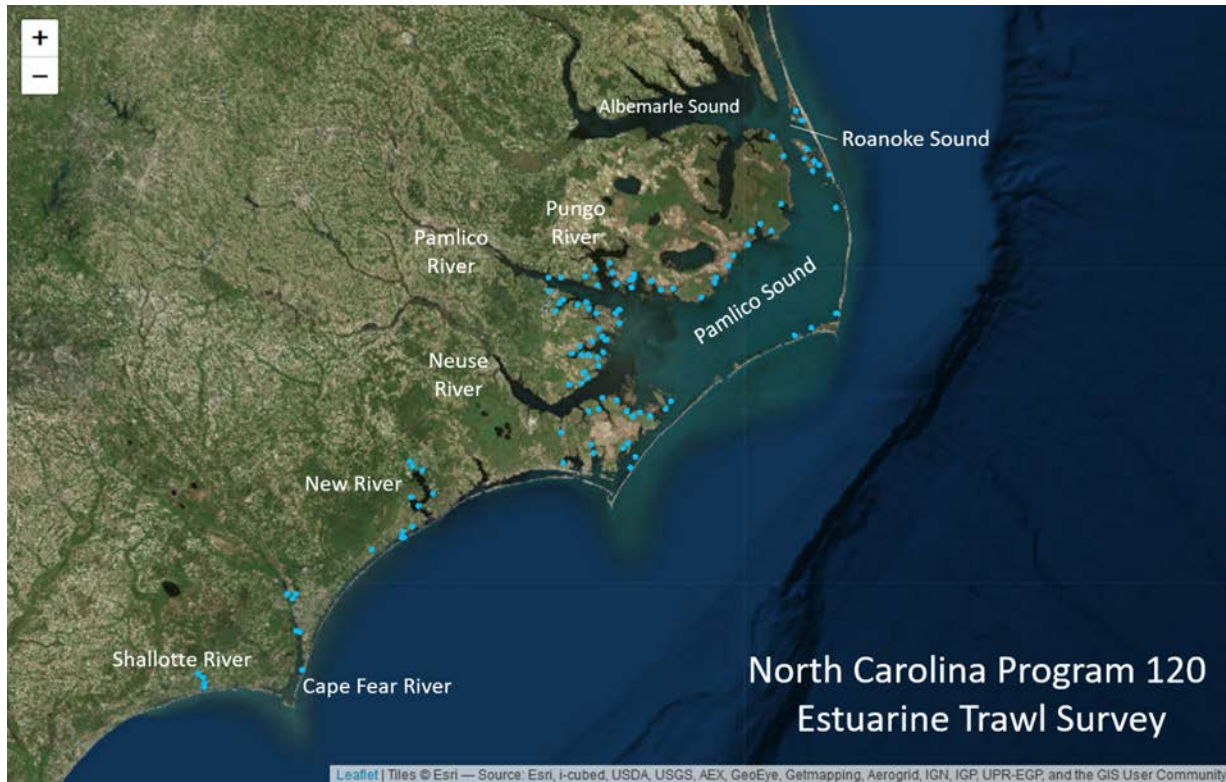
Figure 89. Standardized index of relative abundance of YOY Atlantic menhaden developed from the VIMS Juvenile Striped Bass Seine Survey with 95% confidence intervals.



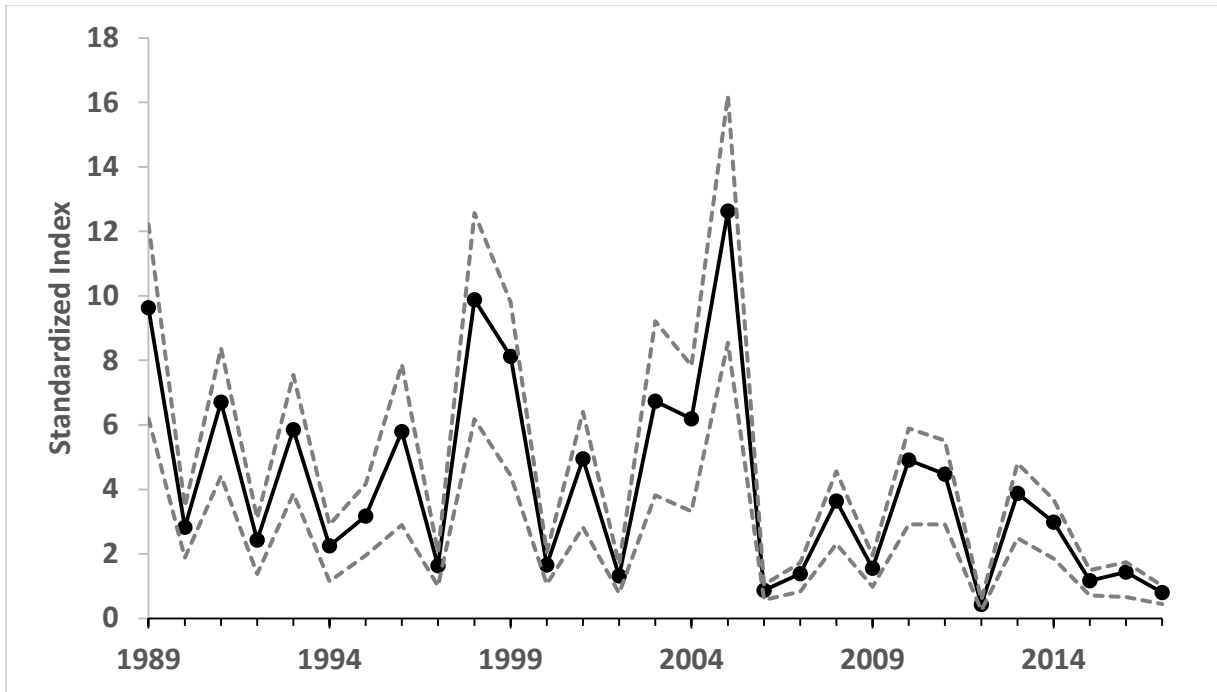
**Figure 90. Sampling sites for the VIMS Alosine Monitoring Program in the James, York, and Rappahannock Rivers (source: VIMS).**



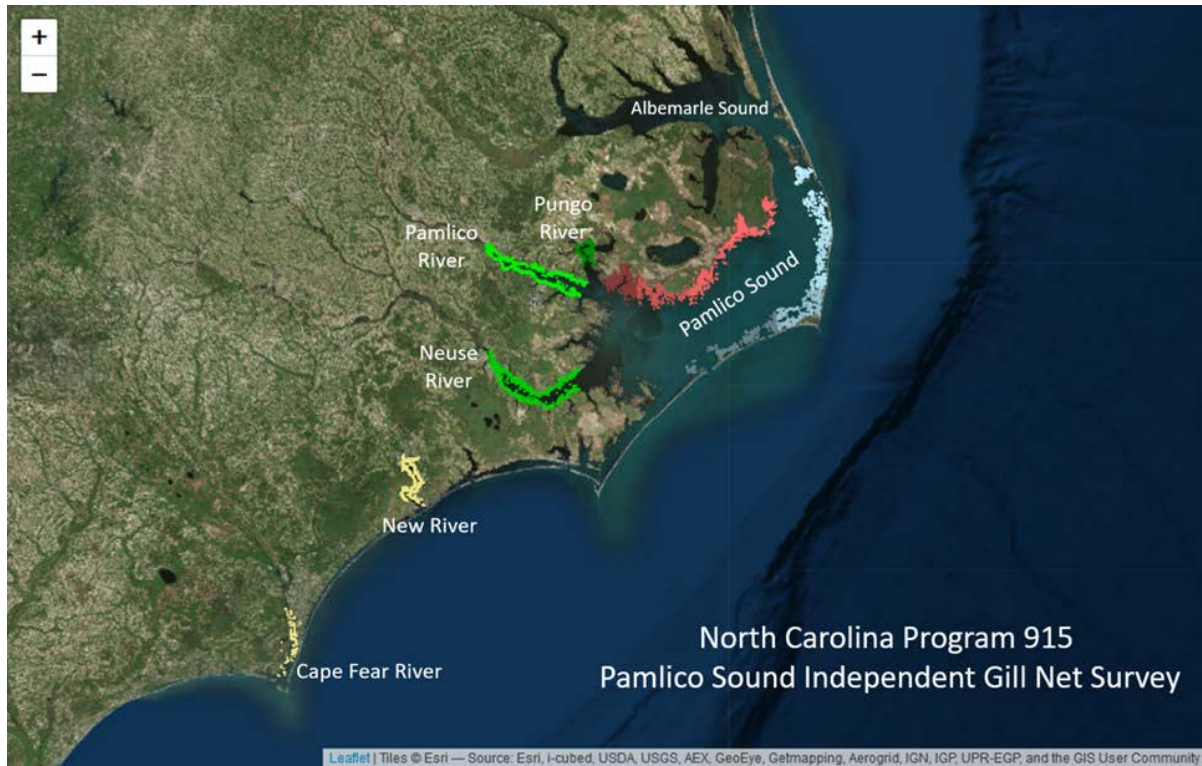
**Figure 91. Standardized index of relative abundance of age 1+ Atlantic menhaden developed from the VIMS Alosine Monitoring Program with 95% confidence intervals.**



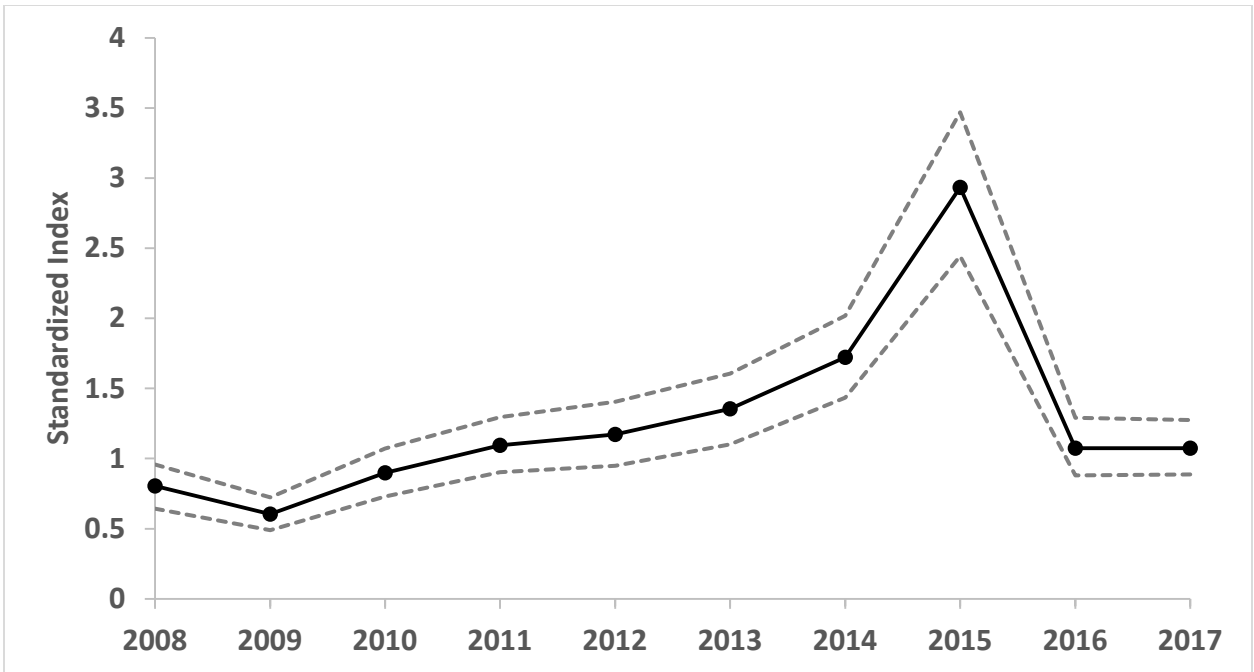
**Figure 92. Core station locations sampled by the North Carolina Program 120 Estuarine Trawl Survey from 1989 to 2017.**



**Figure 93. Standardized index of relative abundance of YOY Atlantic menhaden developed from the North Carolina Program 120 Estuarine Trawl Survey. The grey ribbon is the 95% confidence interval.**

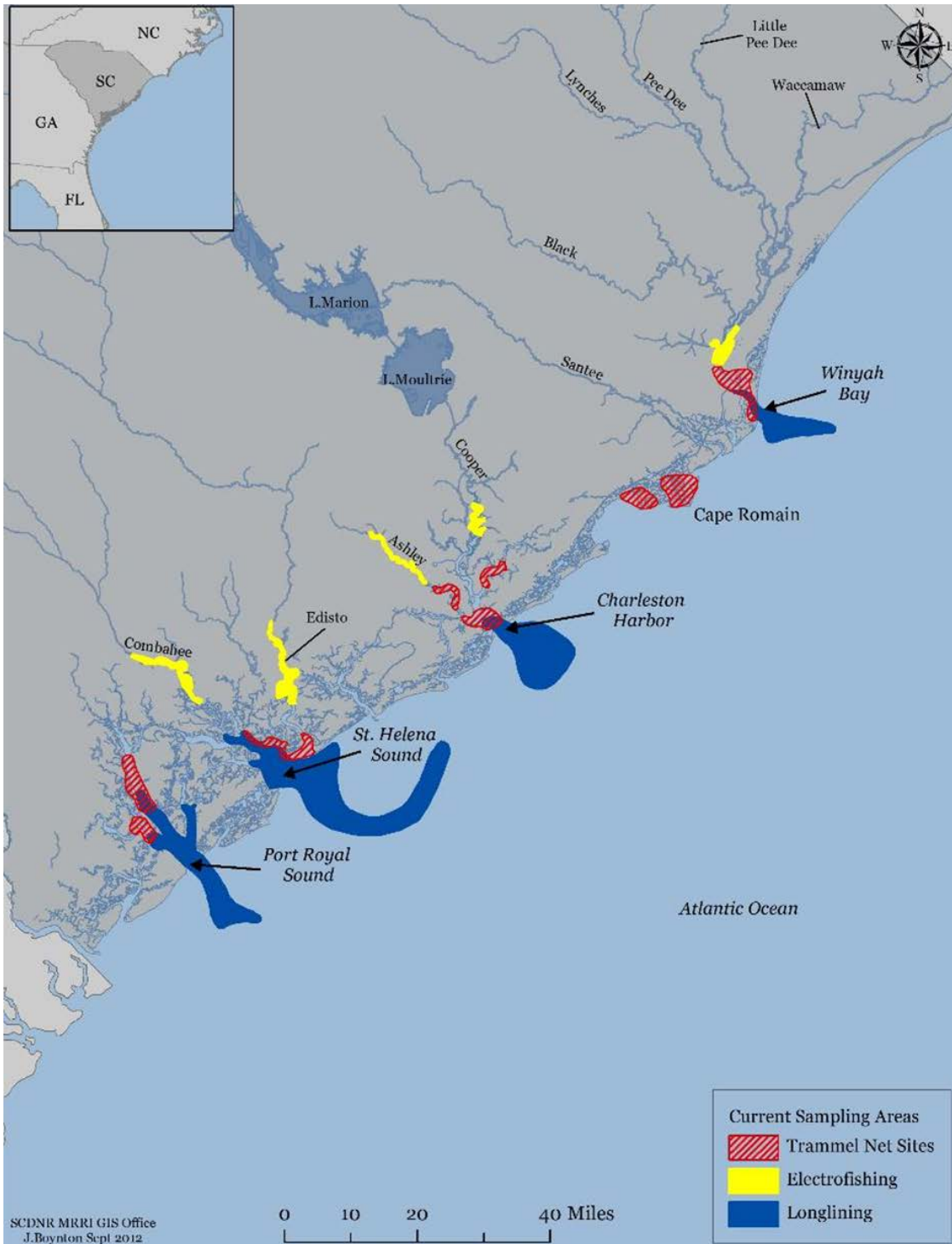


**Figure 94. Sample locations by area and color conducted by the North Carolina Program 915 Pamlico Sound Independent Gill Net Survey from 2001 to 2017. Pamlico Sound sites (reds and blues) established in 2001; Pamlico, Pungo, and Neuse Rivers (greens) added in 2003; New and Cape Fear Rivers (yellows) added in 2008.**

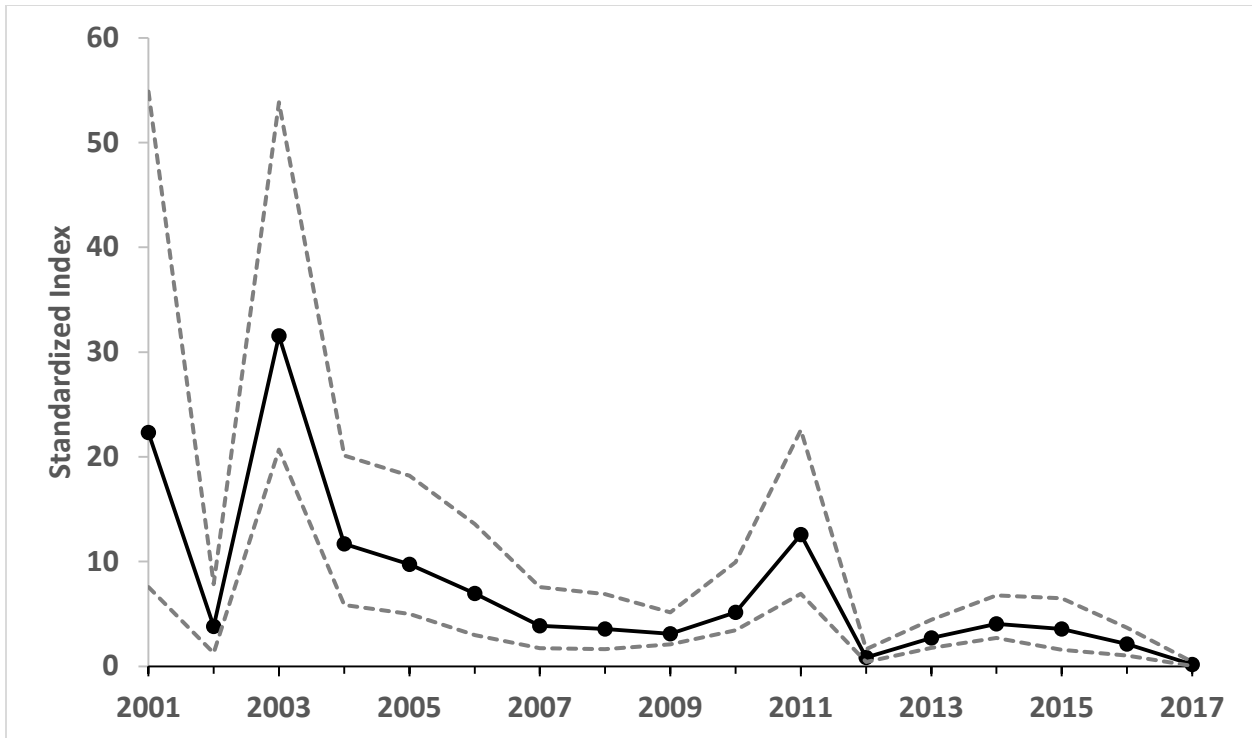


**Figure 95. Standardized index of relative abundance of age 1+ Atlantic menhaden developed from the North Carolina Program 915 Pamlico Sound Independent Gill Net Survey. The grey ribbon is the 95% confidence interval.**





**Figure 96. Map of the South Carolina Department of Natural Resources (SC NDR) electrofishing survey sampling strata. The SC DNR electrofishing survey sample strata are identified by the yellow areas. Other SC DNR fishery-independent survey sampling strata are identified by the red (SC DNR trammel net survey) and blue (SC DNR adult red drum and shark longline survey) areas.**



**Figure 97. Standardized index of relative abundance of YOY Atlantic Menhaden developed from the SC DNR monthly electrofishing survey with 95% confidence intervals.**

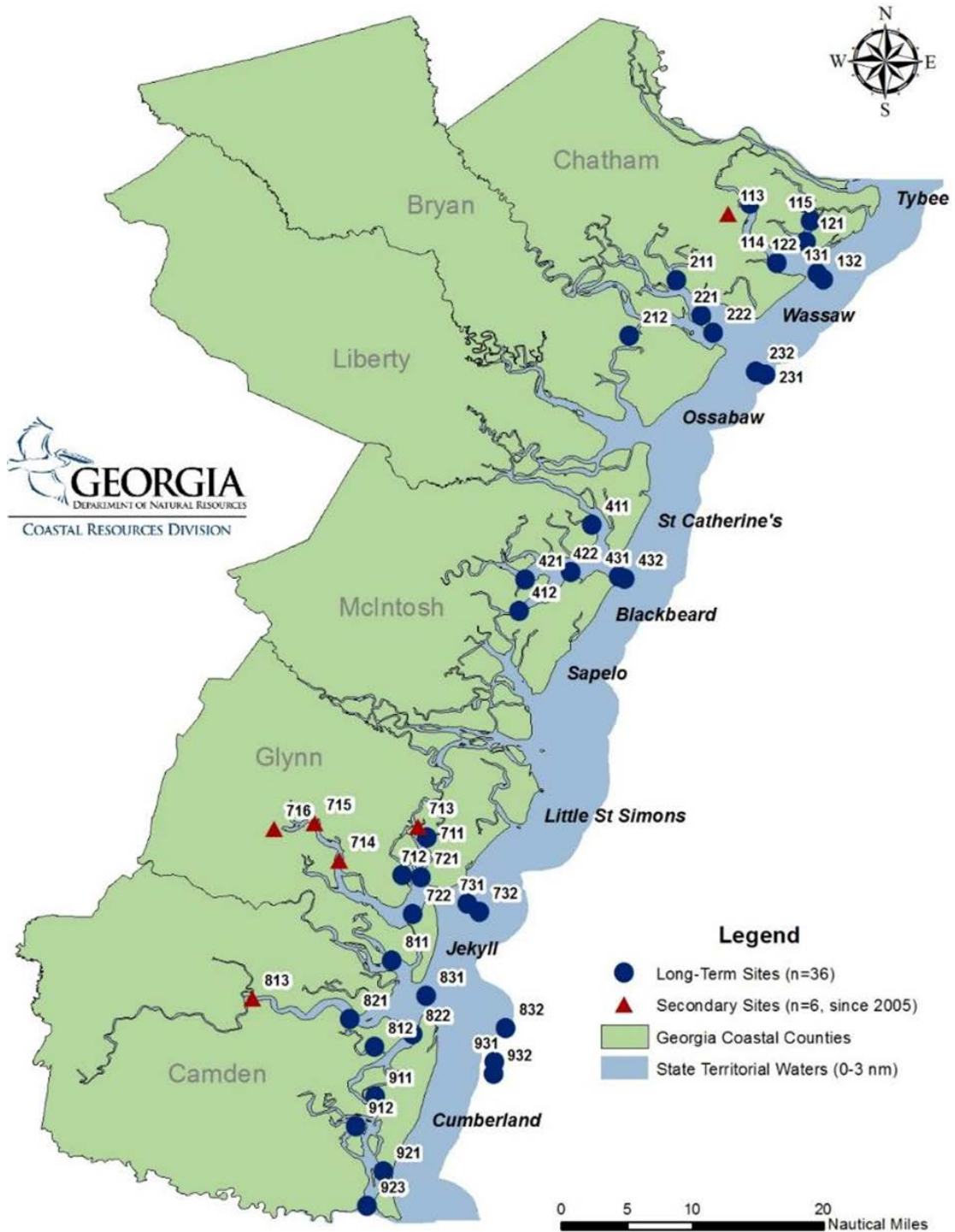
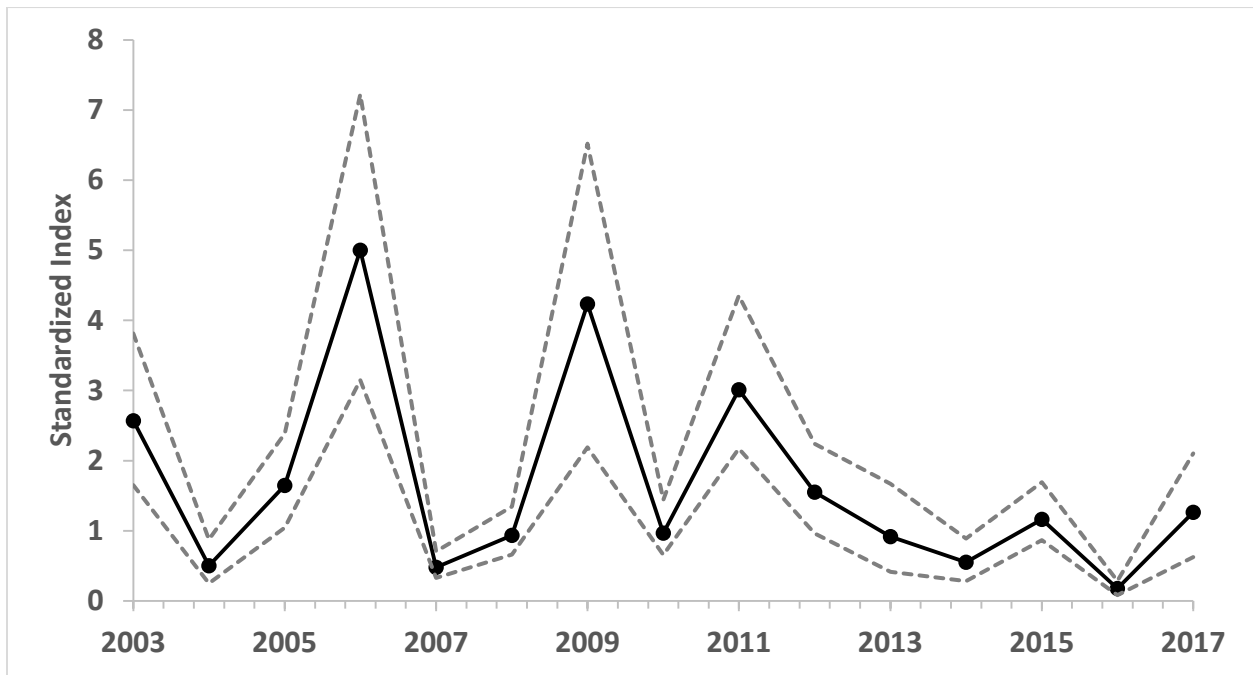
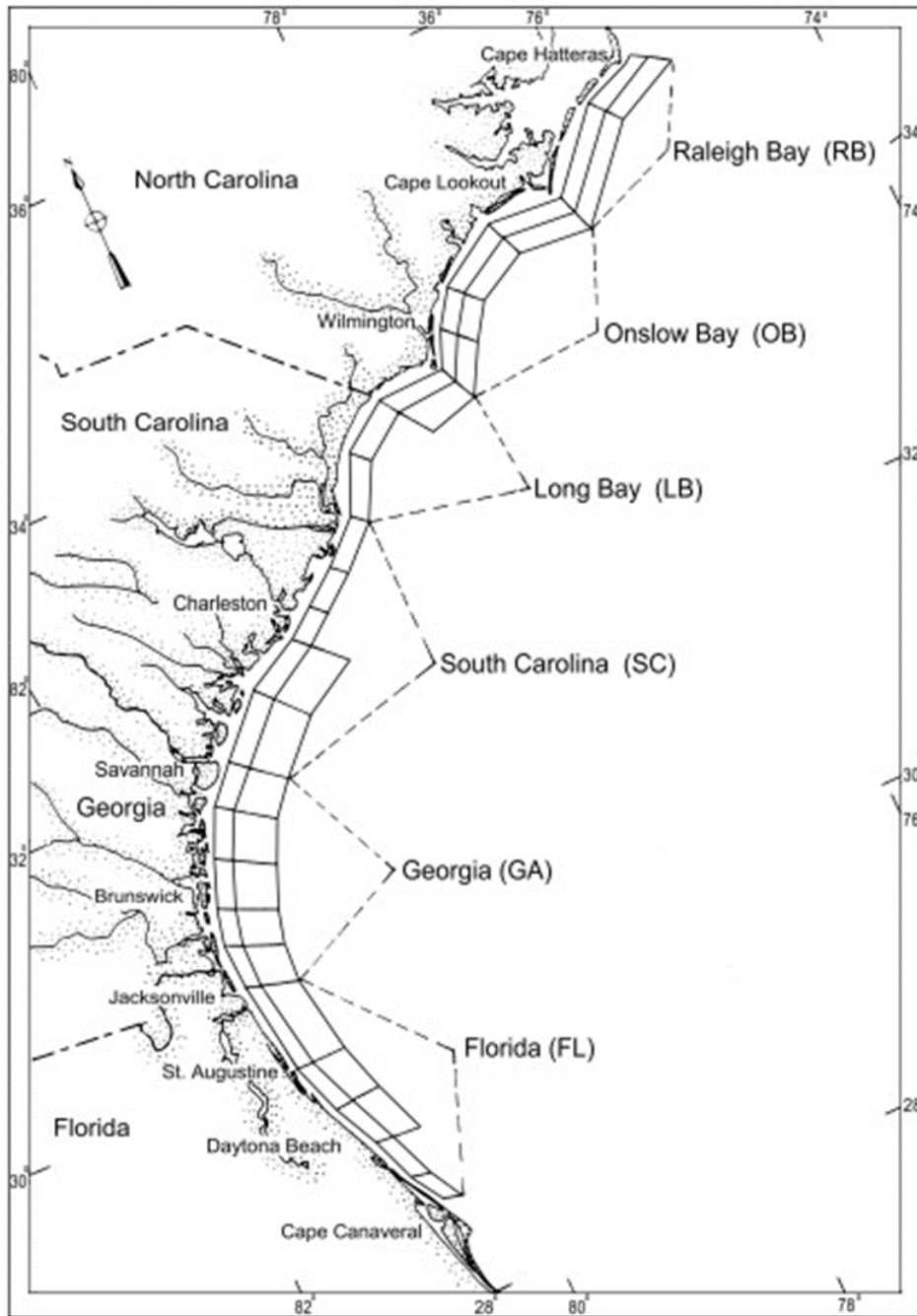


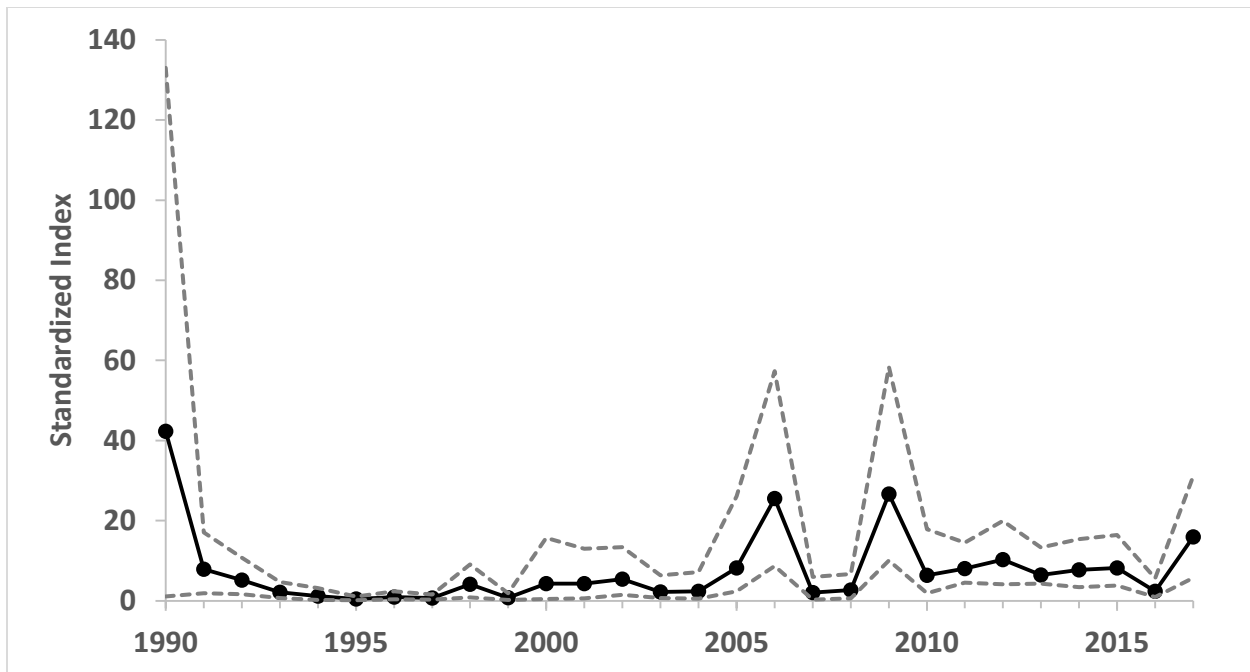
Figure 98. Map of the Georgia Ecosystem Monitoring Trawl Survey with the fixed tow locations identified. Long-term sites are represented by blue circles, while fixed stations added in 2005 are identified as red triangles.



**Figure 99. Standardized index of relative abundance of age-1+ Atlantic Menhaden developed from the spring and early summer (April-July) portions of the monthly Georgia Ecosystem Monitoring Trawl Survey with 95% confidence intervals.**



**Figure 100.** Map of the Southeast Area Monitoring and Assessment Program, South Atlantic Region (SEAMAP-SA) coastal trawl survey strata. The survey operates in the twenty-four inshore strata found from Cape Hatteras, North Carolina, to Cape Canaveral, Florida. The offshore strata found off North Carolina and Georgia/Florida are not currently sampled and are not included in the development of indices.



**Figure 101.** Standardized index of relative abundance of age-1+ Atlantic Menhaden developed from the SEAMAP-SA coastal trawl survey, only using data collected during the months of April-July. Dashed lines represent 95% confidence intervals.

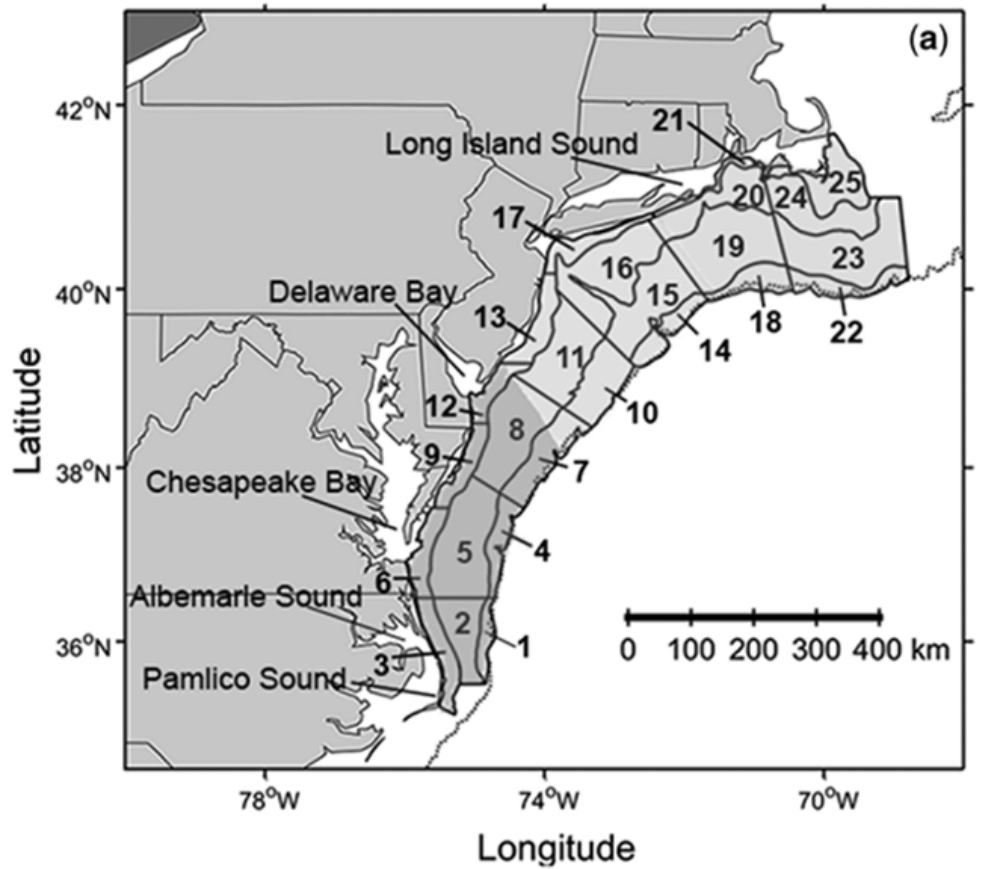
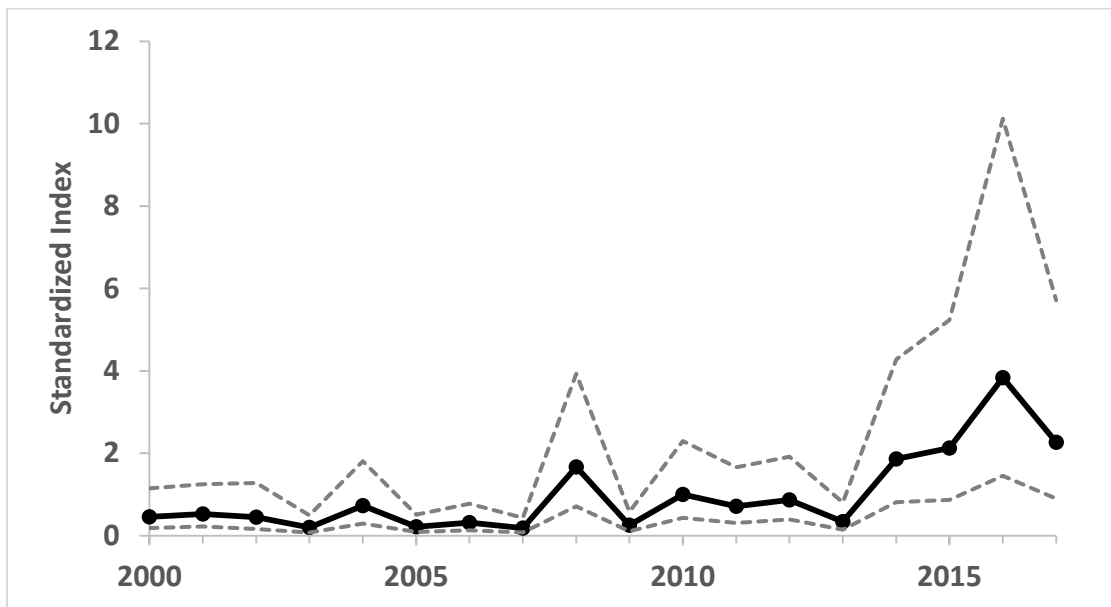


Figure 102. MARMAP and EcoMon survey area between Cape Cod, Massachusetts, and Cape Hatteras, North Carolina. Stations retained for index development (>5% positive tow for menhaden) include strata 2, 3, 5, 6, 8, 9, 11, 12, 13, 16, 17, 20, and 21.

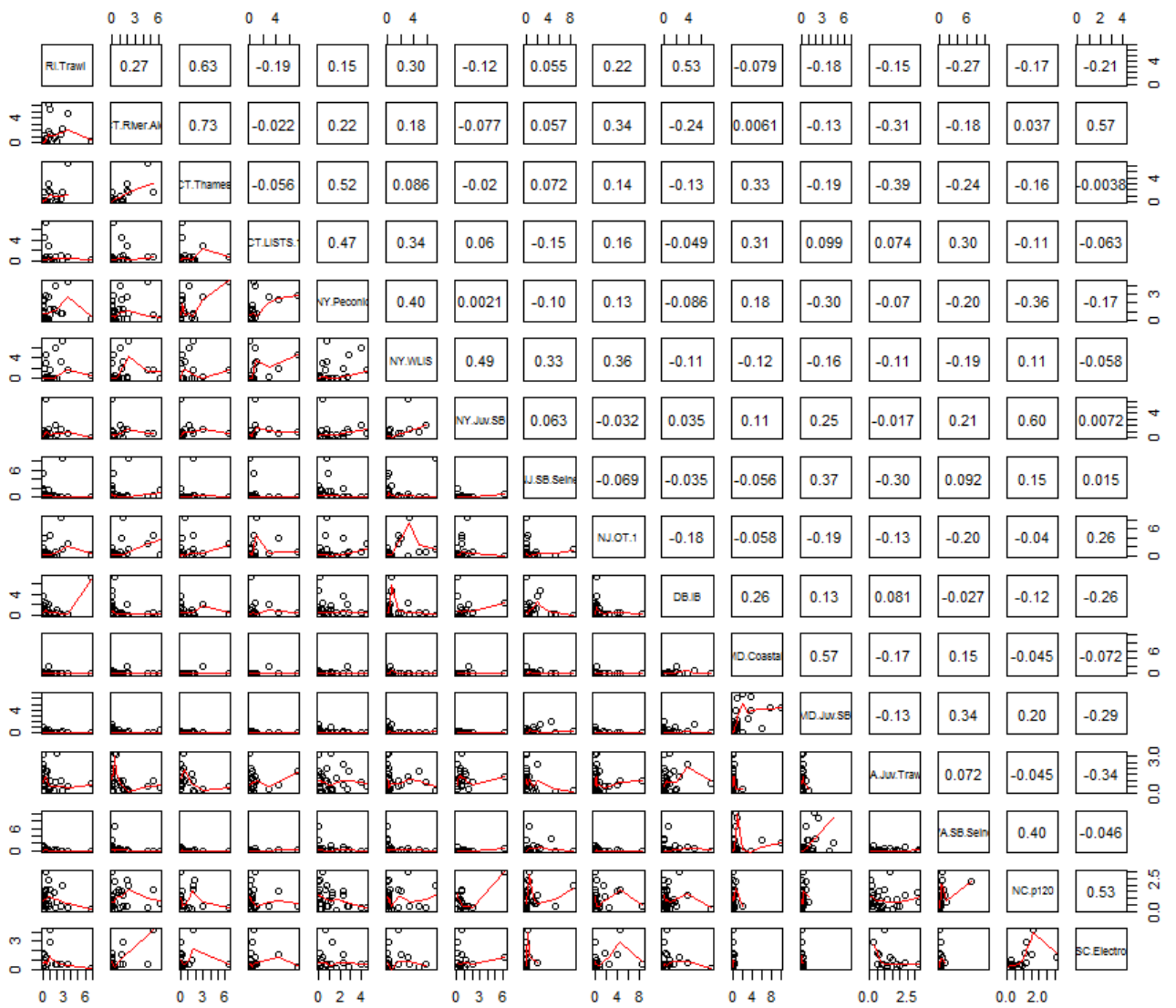


**Figure 103.** Standardized index of relative spawning stock biomass abundance of Atlantic menhaden developed from the MARMAP ichthyoplankton survey. Dashed lines represent 95% confidence intervals and the 1978 upper confidence interval has not been included on the graph because of its large value (94).

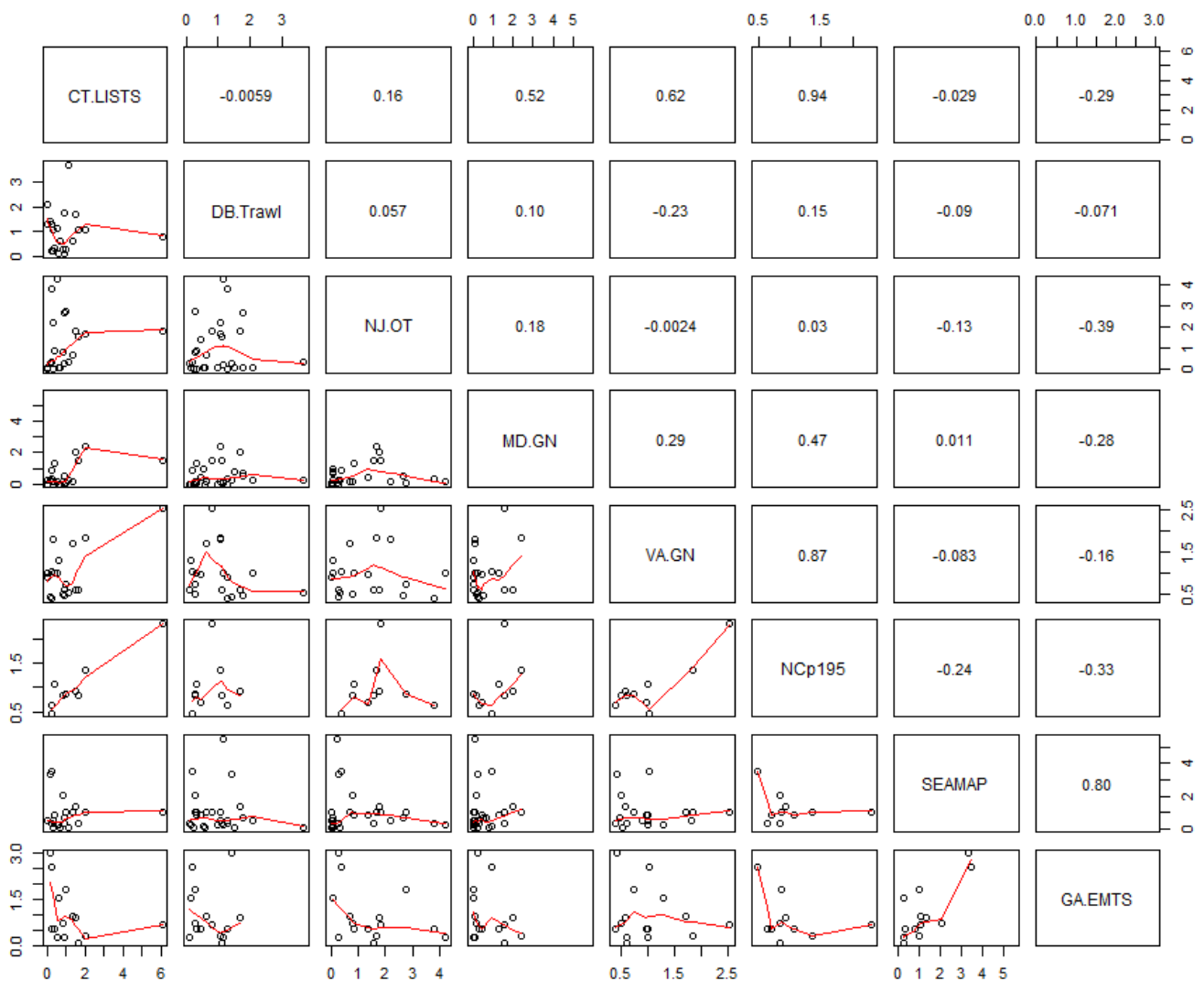


**Figure 104.** Standardized index of relative spawning stock biomass abundance of Atlantic menhaden developed from the EcoMon ichthyoplankton survey. Dashed lines represent 95% confidence intervals.





**Figure 105. Correlation coefficients and scatter plots for the Atlantic menhaden YOY abundance indices. Fourteen correlations are significant ( $P < 0.05$ ) and positively correlated. See Table 32 for  $P$ -values.**



**Figure 106.** Correlation coefficients and scatter plots for the Atlantic menhaden age-1+ abundance indices. Five correlations are significant ( $P < 0.05$ ) and positively correlated. See Table 33 for  $P$ -values.

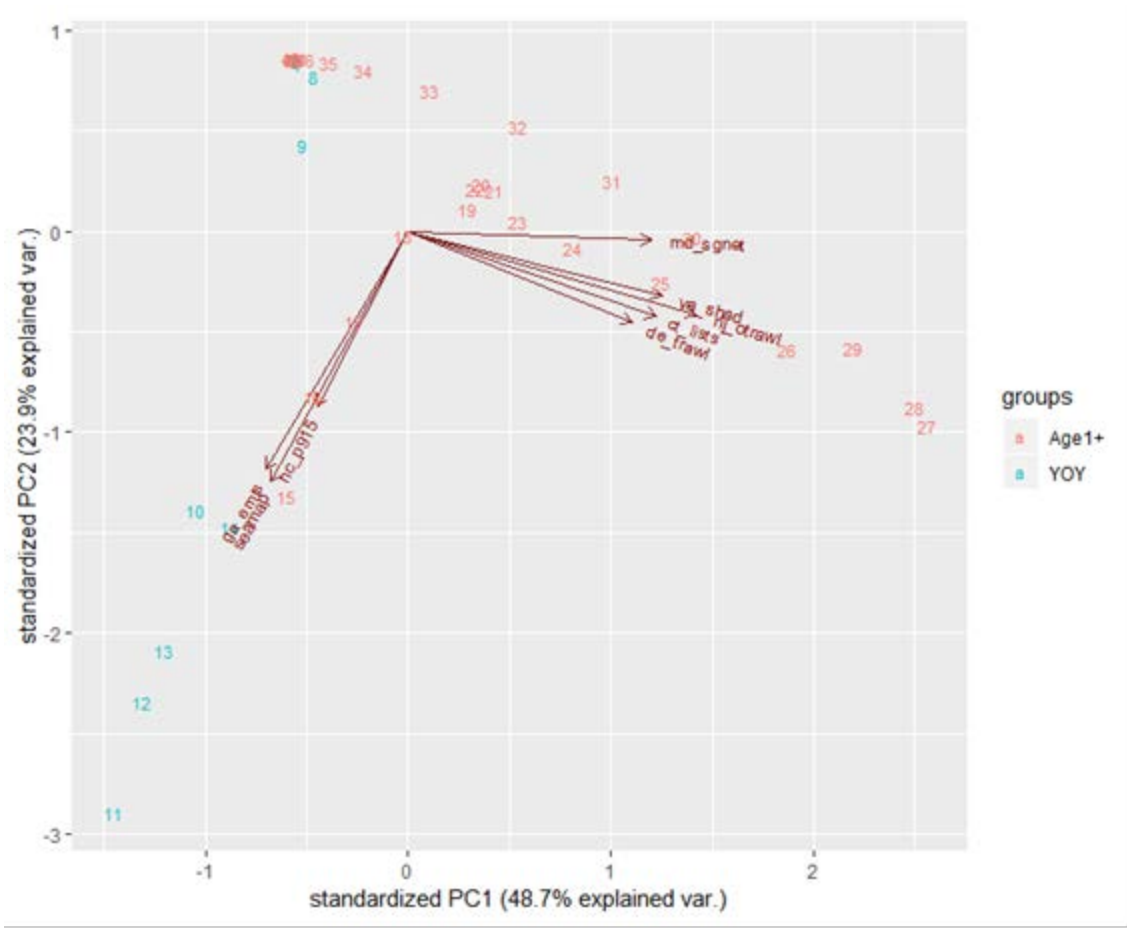
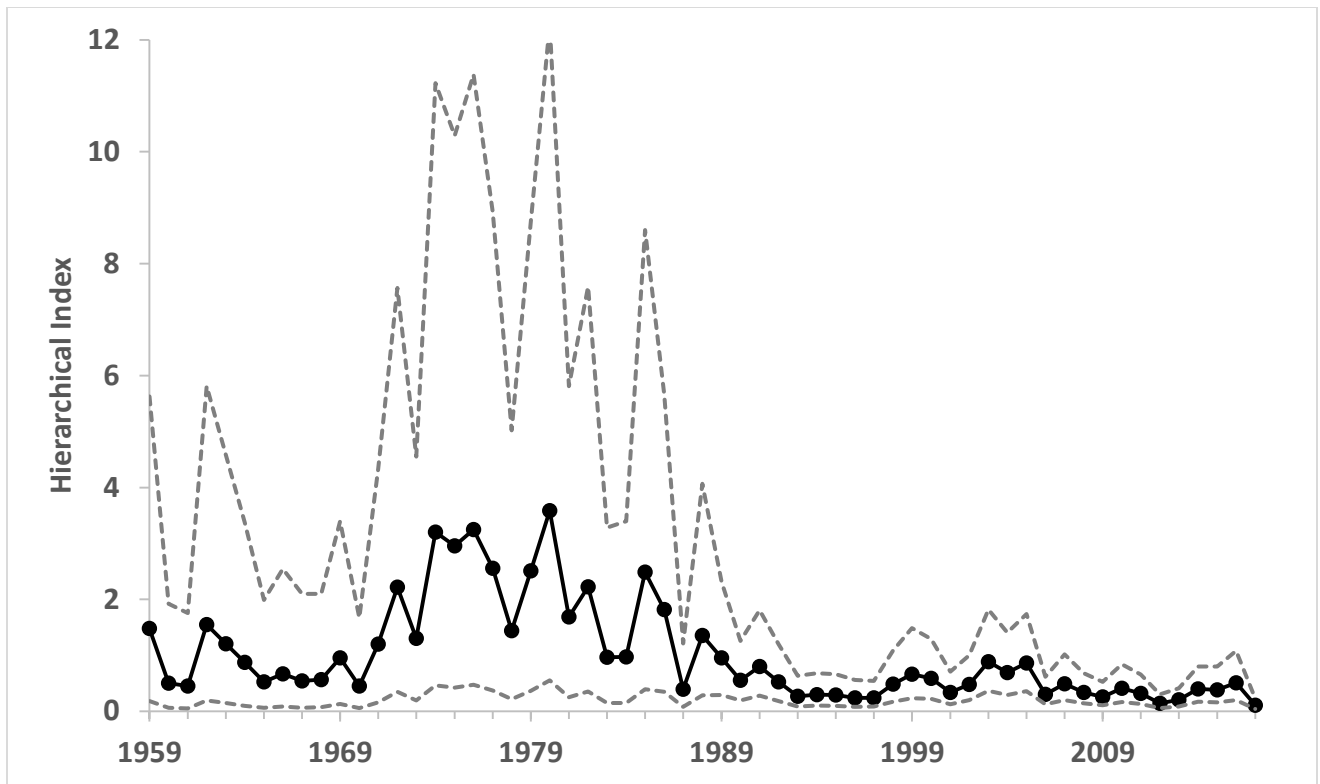
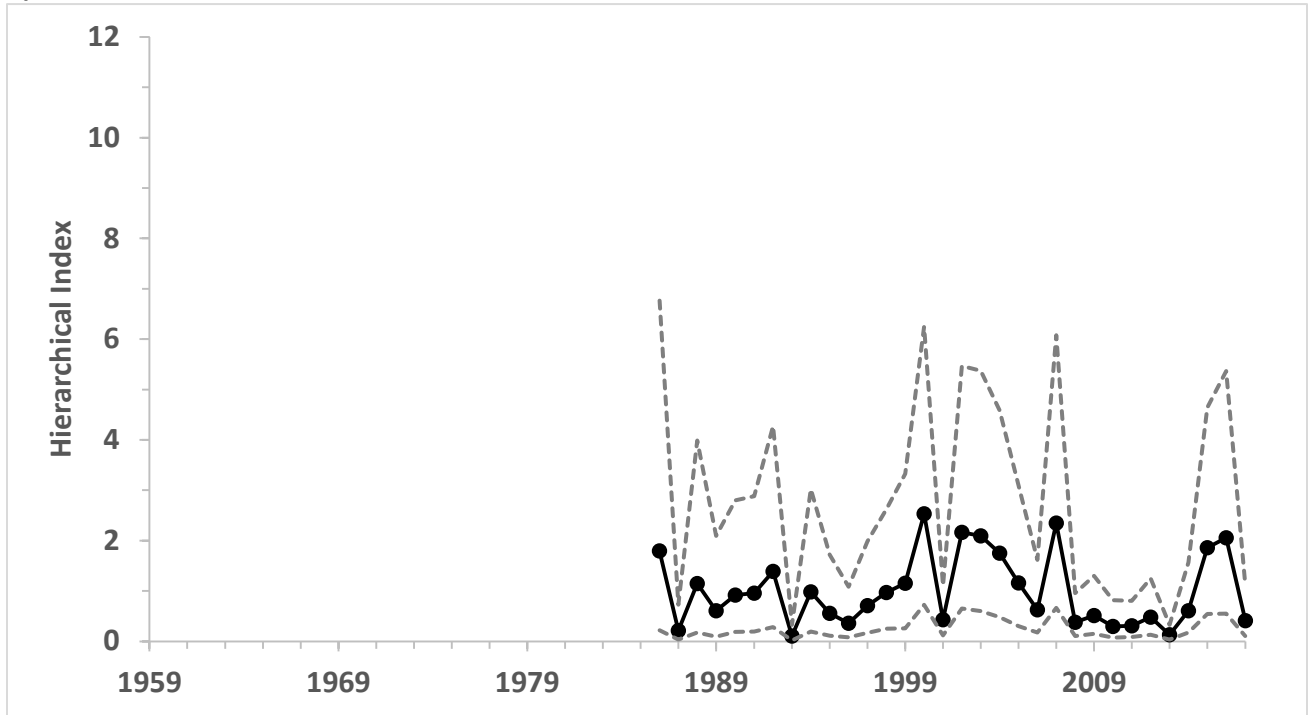


Figure 107. PCA on the length compositions of the eight different age-1+ Atlantic menhaden surveys.

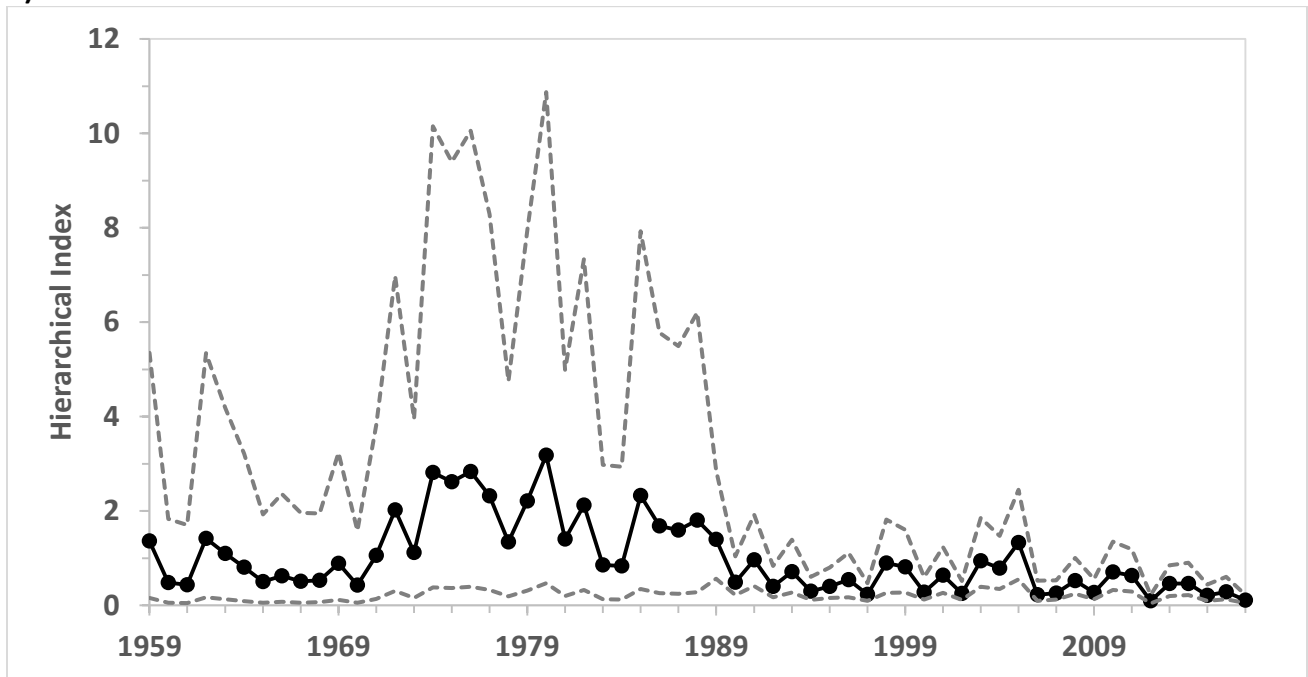


**Figure 108.** Time series of the young-of-year (YOY) Atlantic menhaden relative abundance index as estimated from hierarchical analysis (Conn 2009). The black line gives the posterior mean and the grey, dashed lines represents a 95% credible interval about the time series.

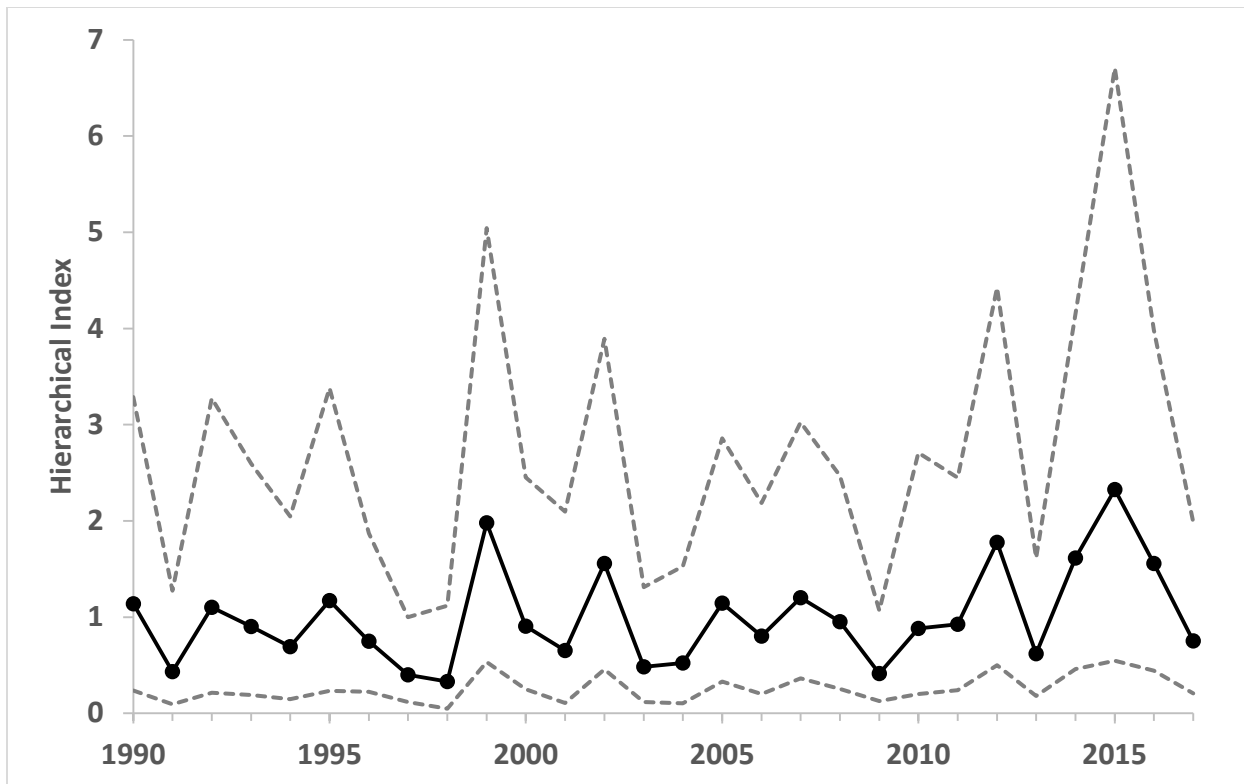
a)



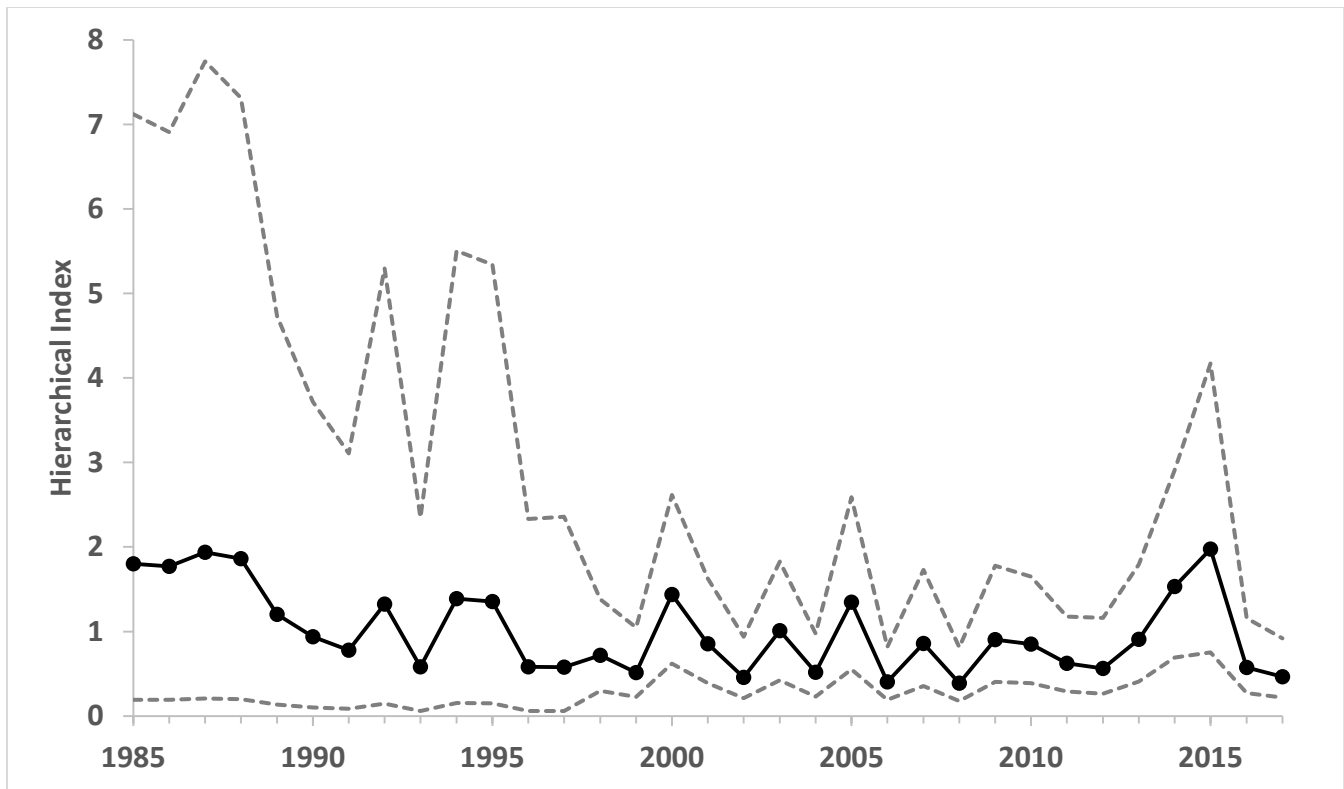
b)



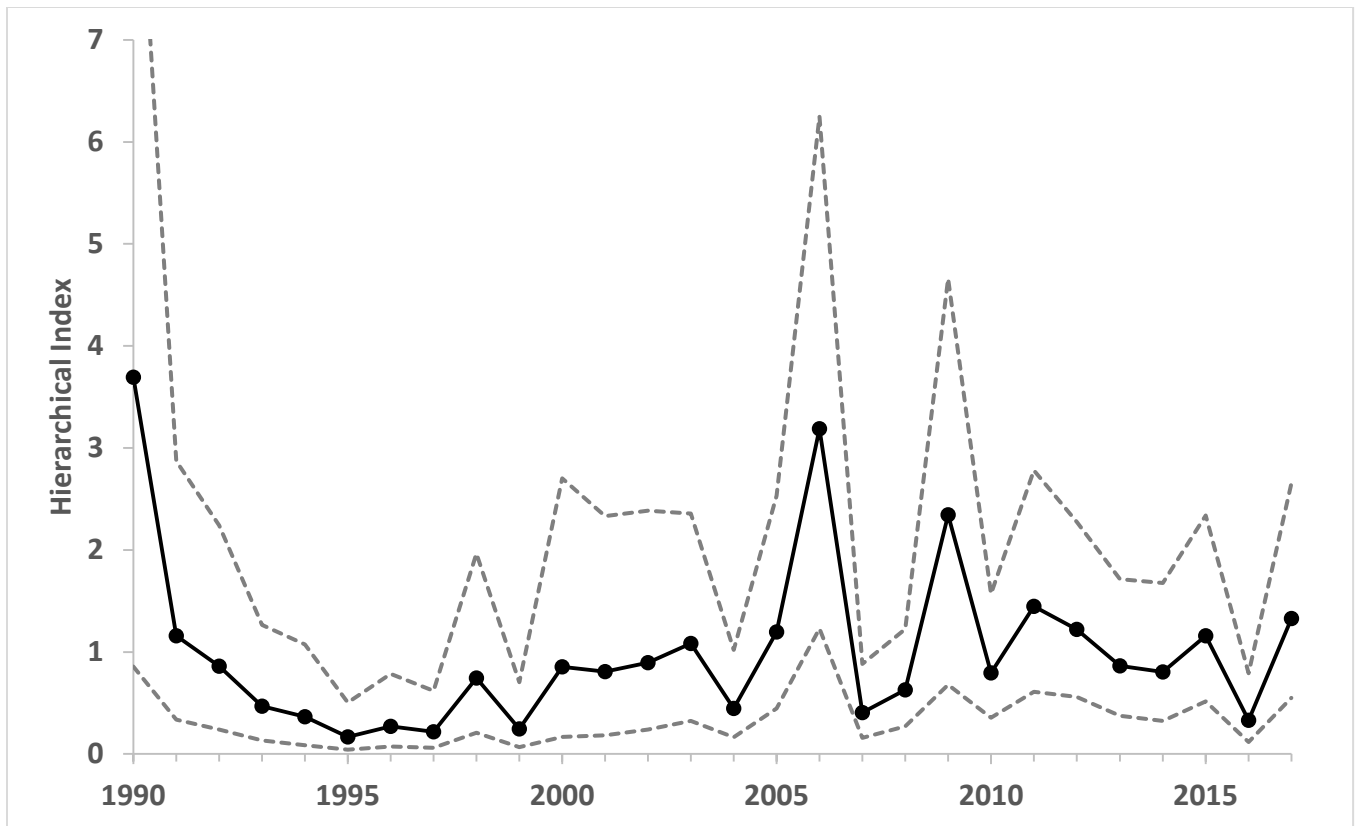
**Figure 109.** Time series of the Northern region (a) and southern region (b) young-of-year Atlantic menhaden relative abundance indices as estimated from hierarchical analysis (Conn 2009). The black line gives the posterior mean and the grey, dashed lines represents a 95% credible interval about the time series.



**Figure 110.** Time series of the northern adult Atlantic menhaden relative abundance index (NAD) as estimated from hierarchical analysis (Conn 2009). The black line gives the posterior mean and the grey, dashed lines represents a 95% credible interval about the time series.

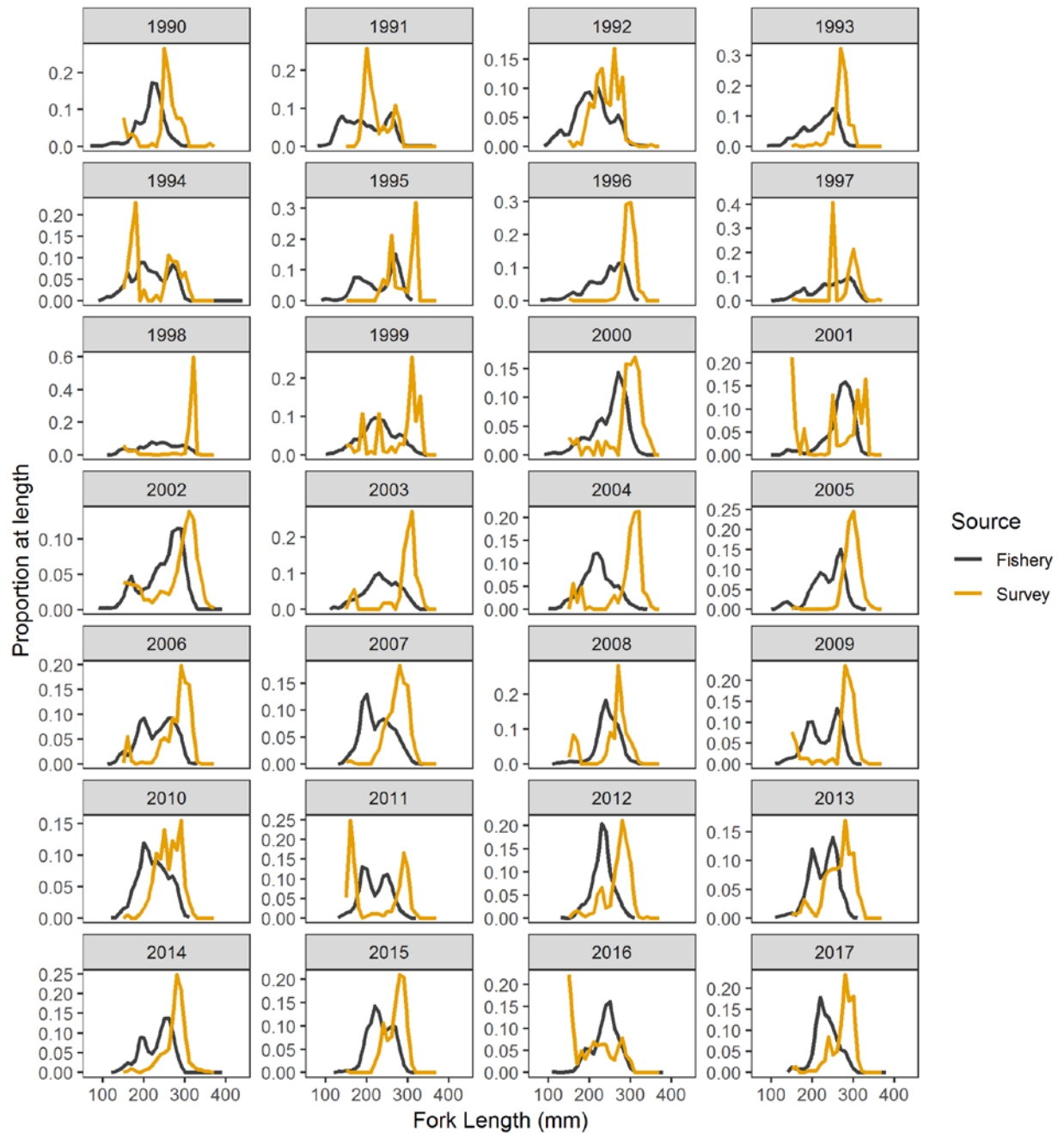


**Figure 111.** Time series of the Mid-Atlantic adult menhaden relative abundance index (MAD) as estimated from hierarchical analysis (Conn 2009). The black line gives the posterior mean and the grey, dashed lines represents a 95% credible interval about the time series.

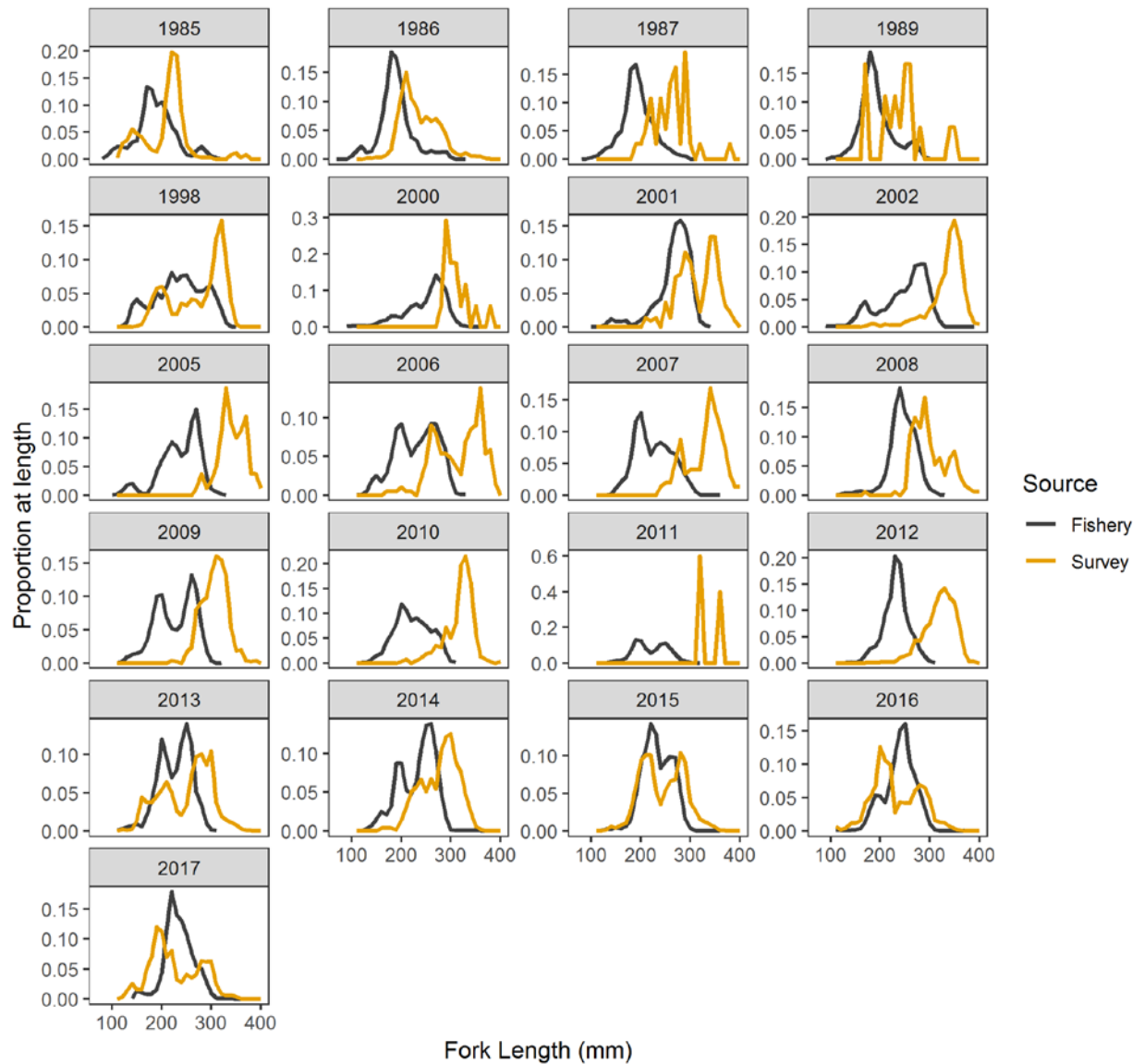


**Figure 112.** Time series of the southern adult Atlantic menhaden relative abundance index (SAD) as estimated from hierarchical analysis (Conn 2009). The black line gives the posterior mean and the grey, dashed lines represents a 95% credible interval about the time series.

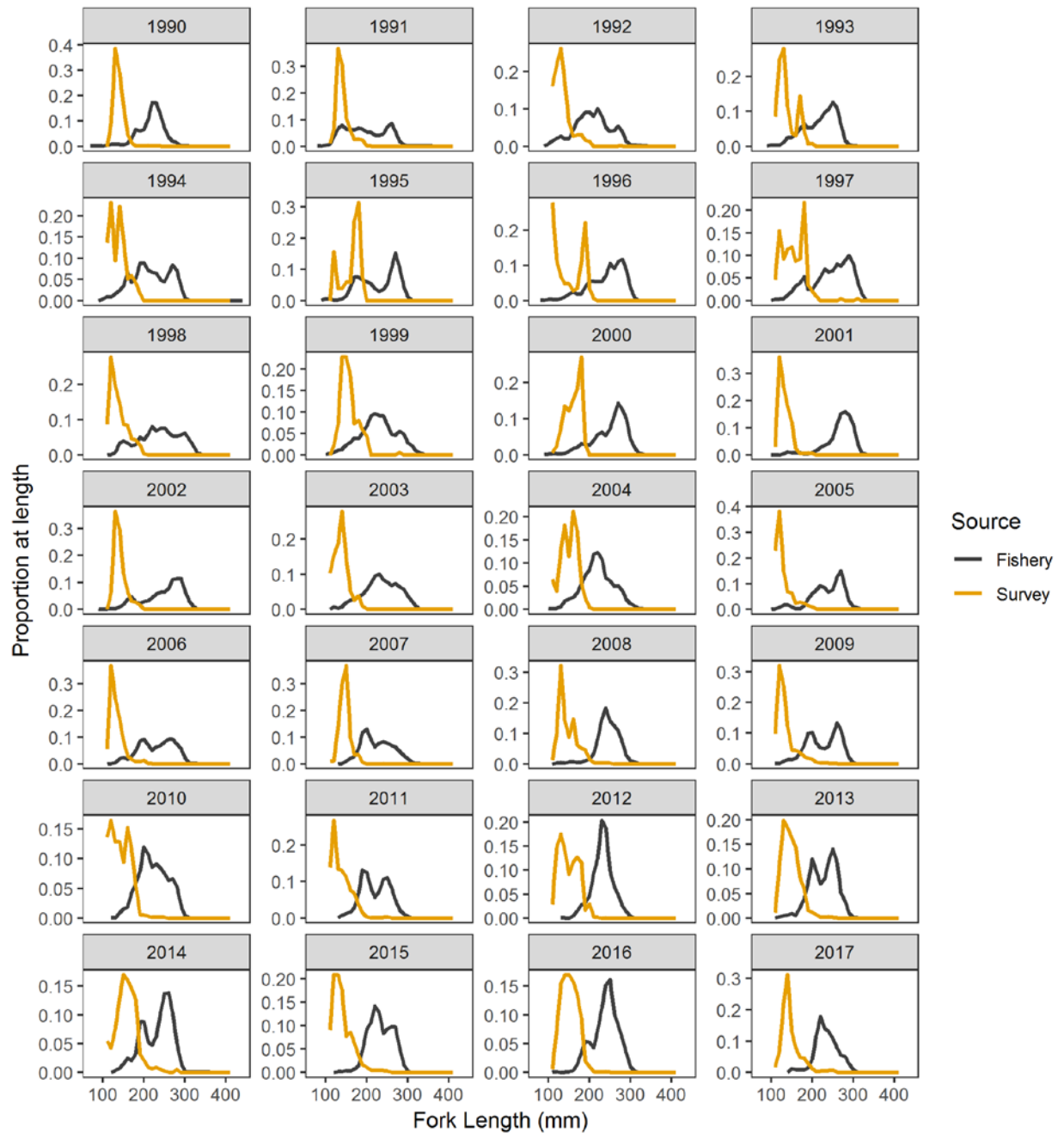




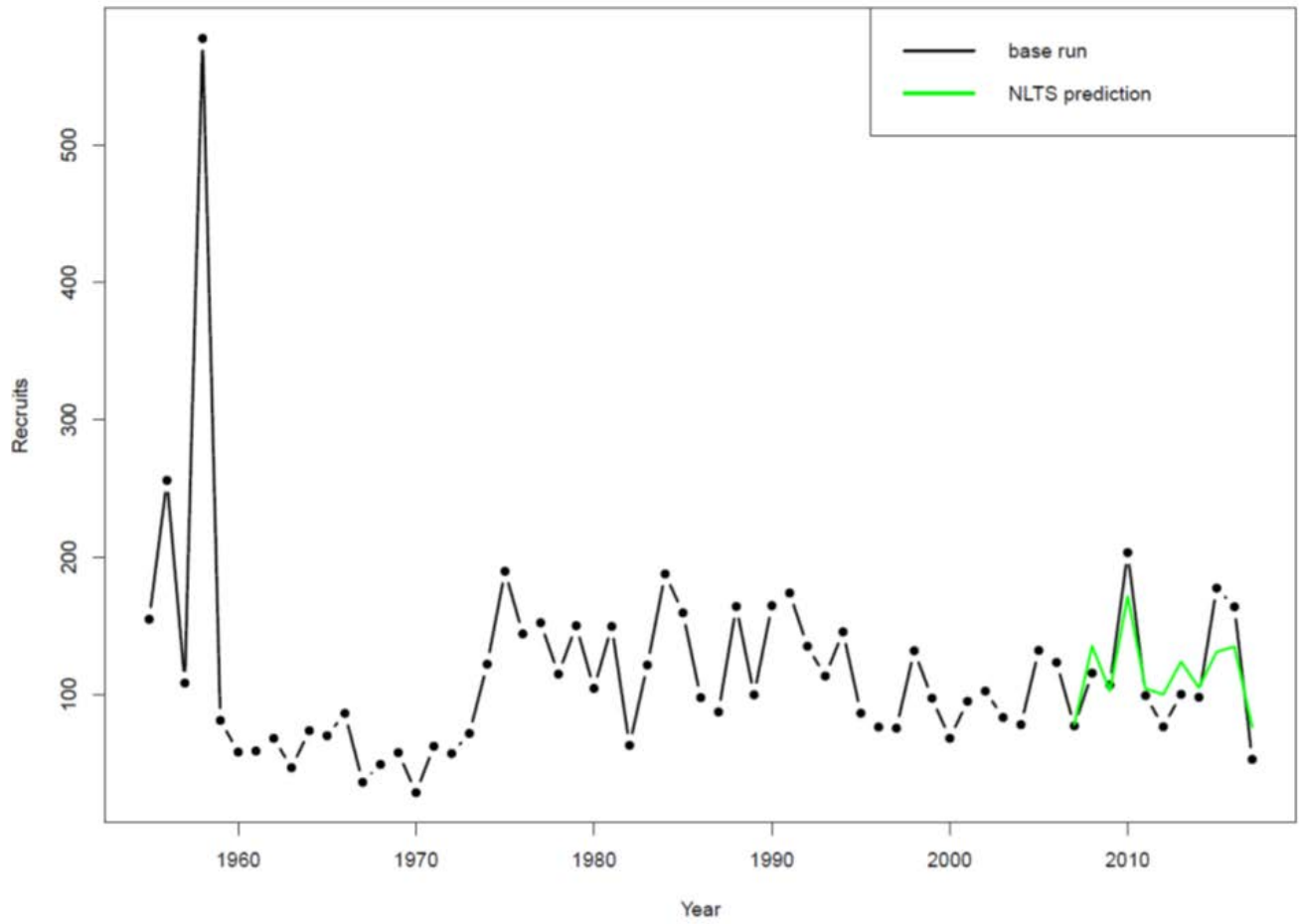
**Figure 113.** Length composition of the Northern Adult (NAD) index plotted with the length composition of fishery samples (pooled over all regions).



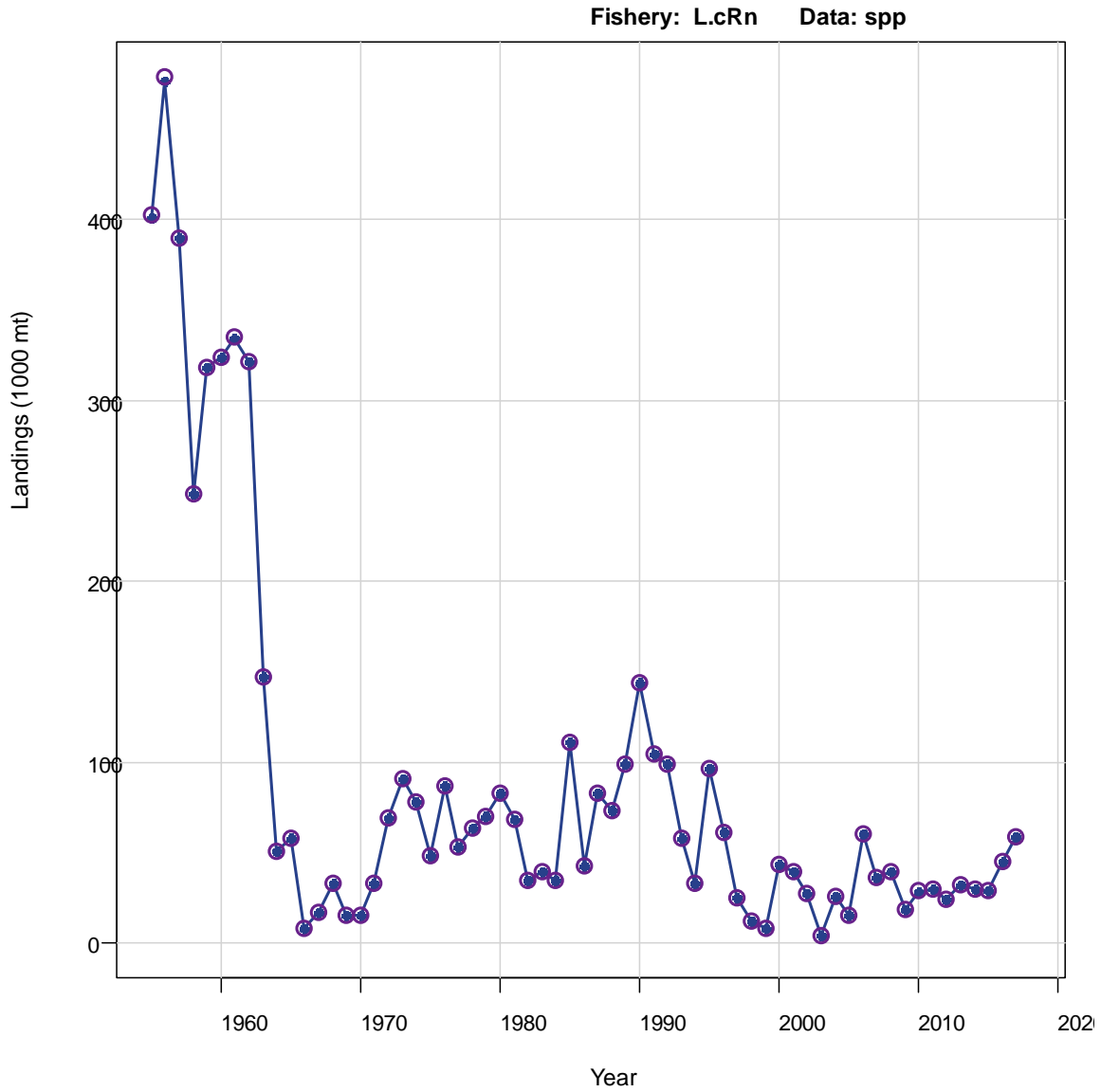
**Figure 114.** Length composition of the Mid-Atlantic Adult (MAD) index plotted with the length composition of fishery samples (pooled over all regions). Length composition data were not available for all years of the MAD index.



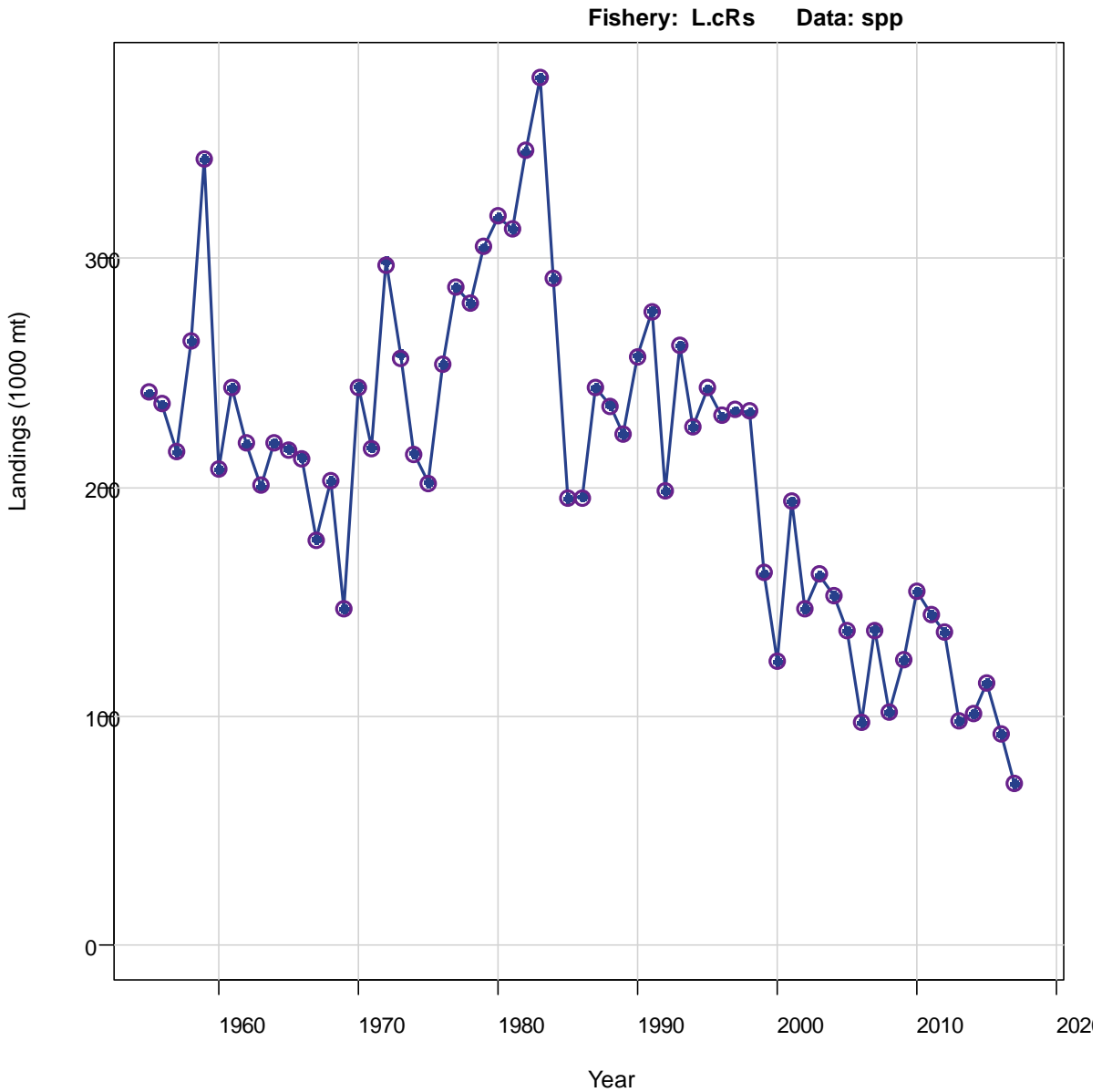
**Figure 115. Length composition of the Southern Adult (SAD) index plotted with the length composition of the fishery samples (pooled over all regions).**



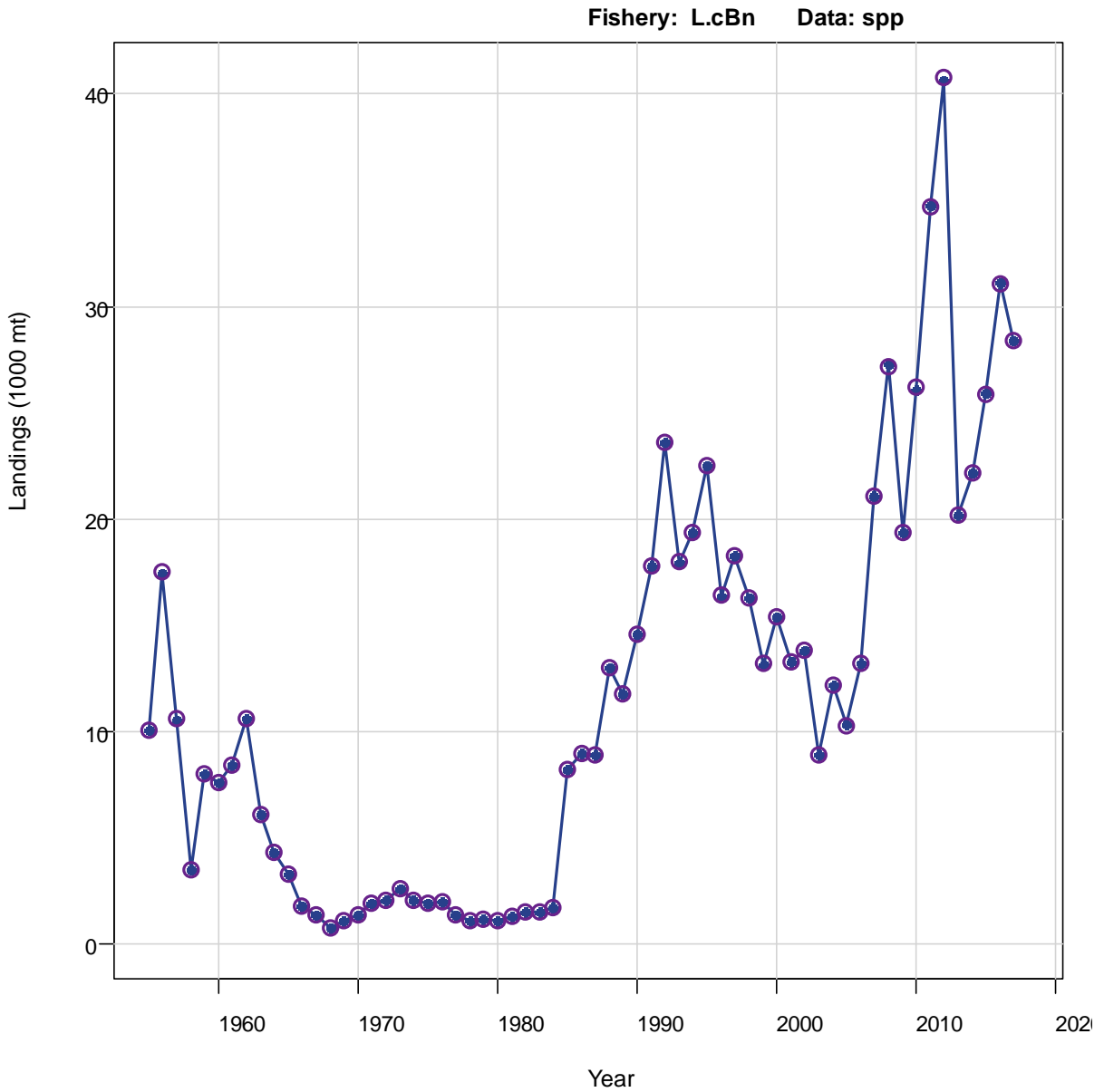
**Figure 116. Comparison between the base run and non-linear time series analysis (Deyle et al. 2018) recruitment prediction for Atlantic menhaden for 2007-2017.**



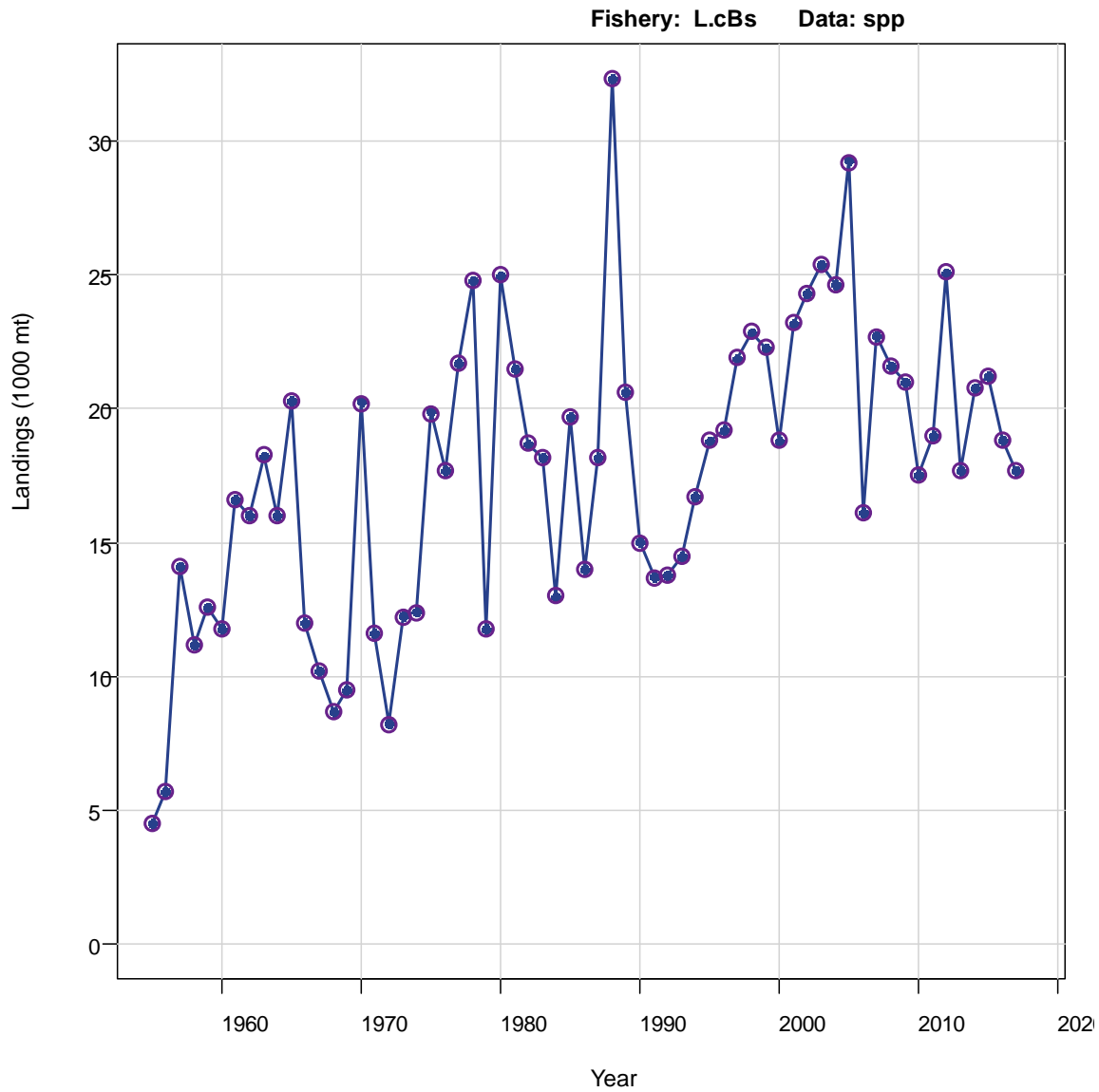
**Figure 117. Commercial reduction landings (1000s mt) for the northern region for 1955-2017. Open circles denote observed landings data, while the filled circles and line represent the fitted landings values.**



**Figure 118. Commercial reduction landings (1000s mt) for the southern region for 1955-2017. Open circles denote observed landings data, while the filled circles and line represent the fitted landings values.**

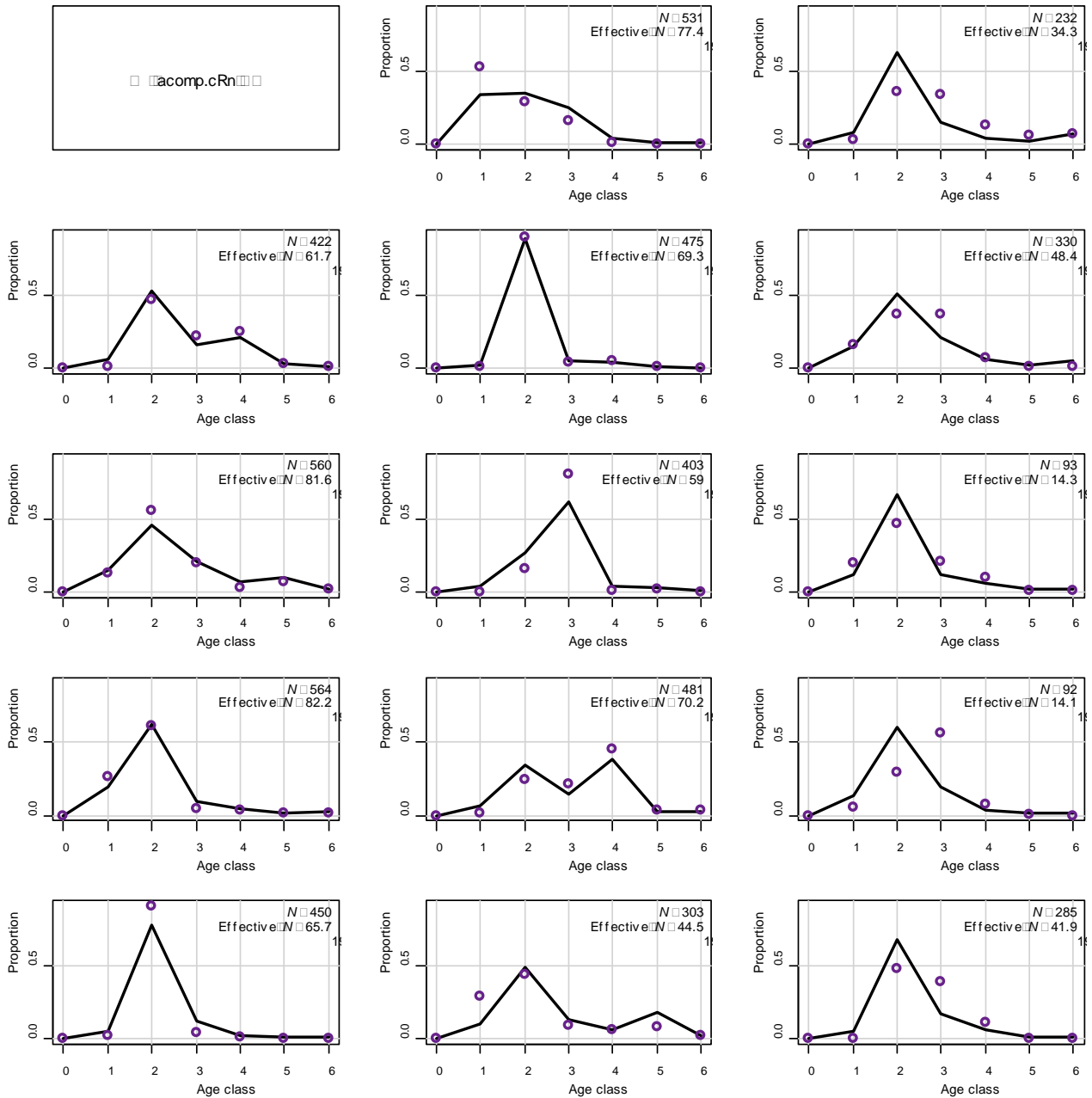


**Figure 119. Commercial bait landings (1000s mt) for the northern region for 1955-2017. Open circles denote observed landings data, while the filled circles and line represent the fitted landings values.**



**Figure 120. Commercial bait landings (1000s mt) for the southern region for 1955-2017. Open circles denote observed landings data, while the filled circles and line represent the fitted landings values.**





**Figure 121.** Annual age composition fits for the commercial reduction fishery for 1955-2017 in the northern region. Open circles indicate the observed data, while the solid line indicates predicted fits to the data. In the upper right corner of each panel there is the number of trips sampled, the effective sample size, and the year.

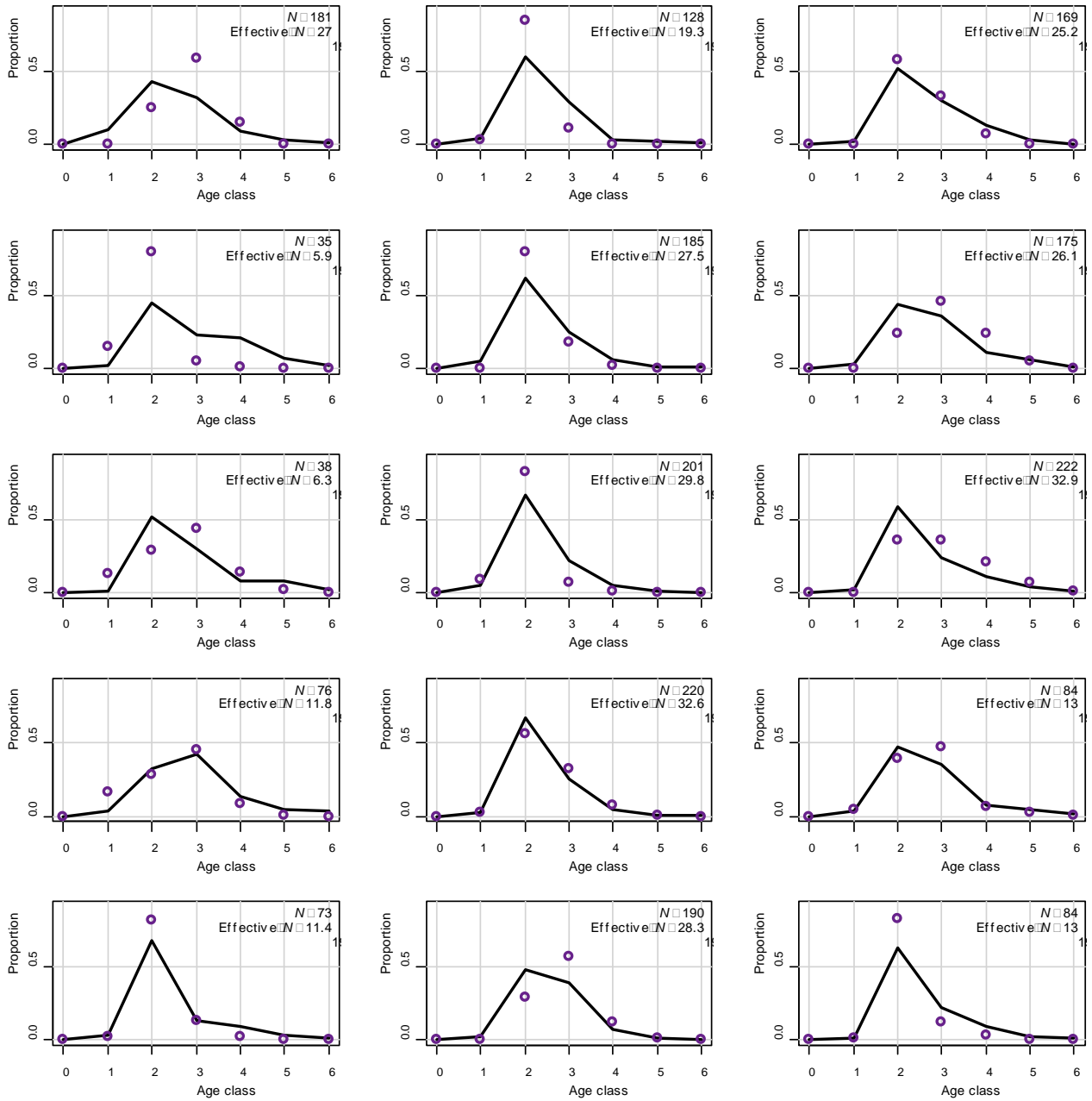


Figure 121 Continued

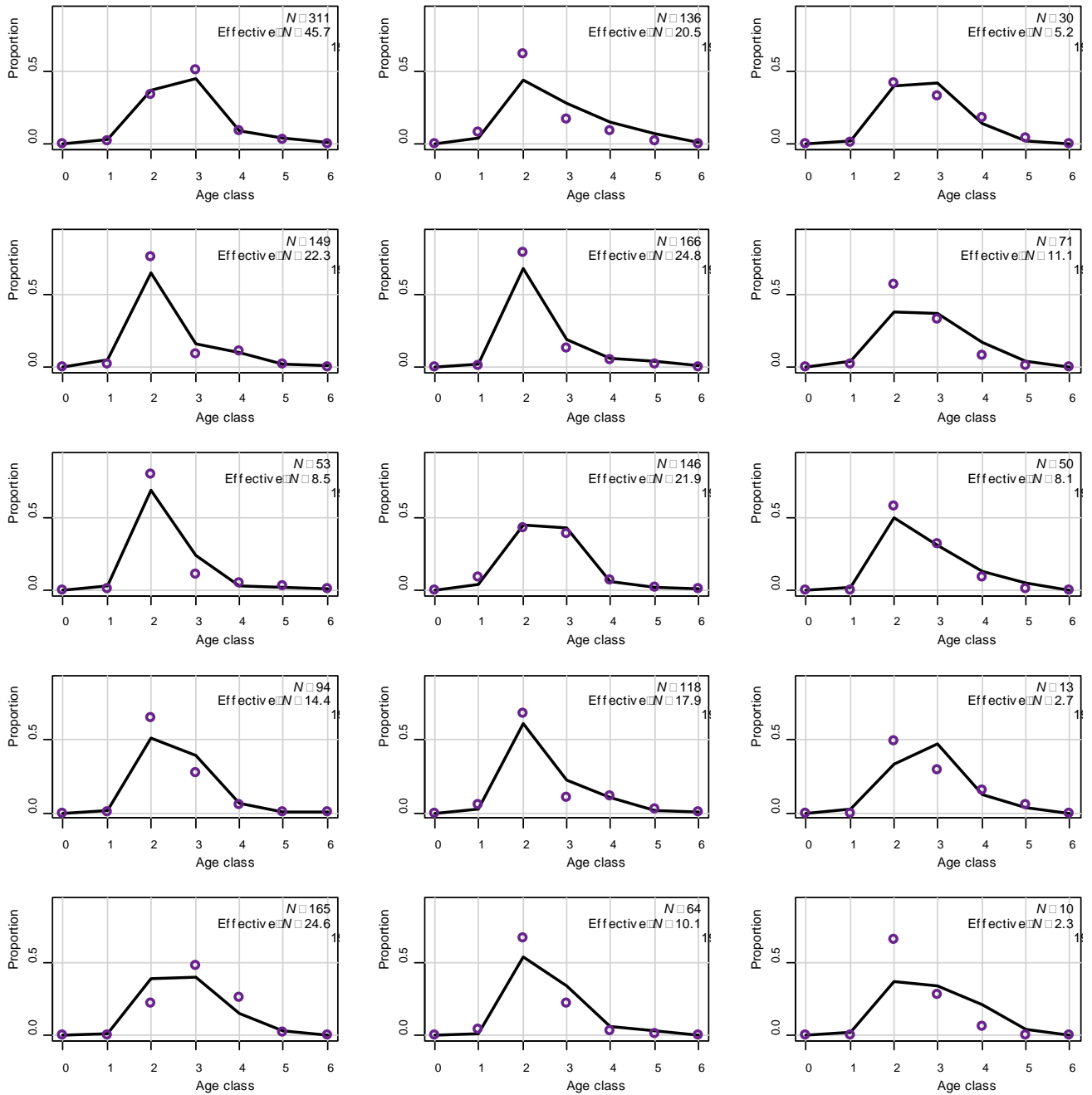


Figure 121 Continued

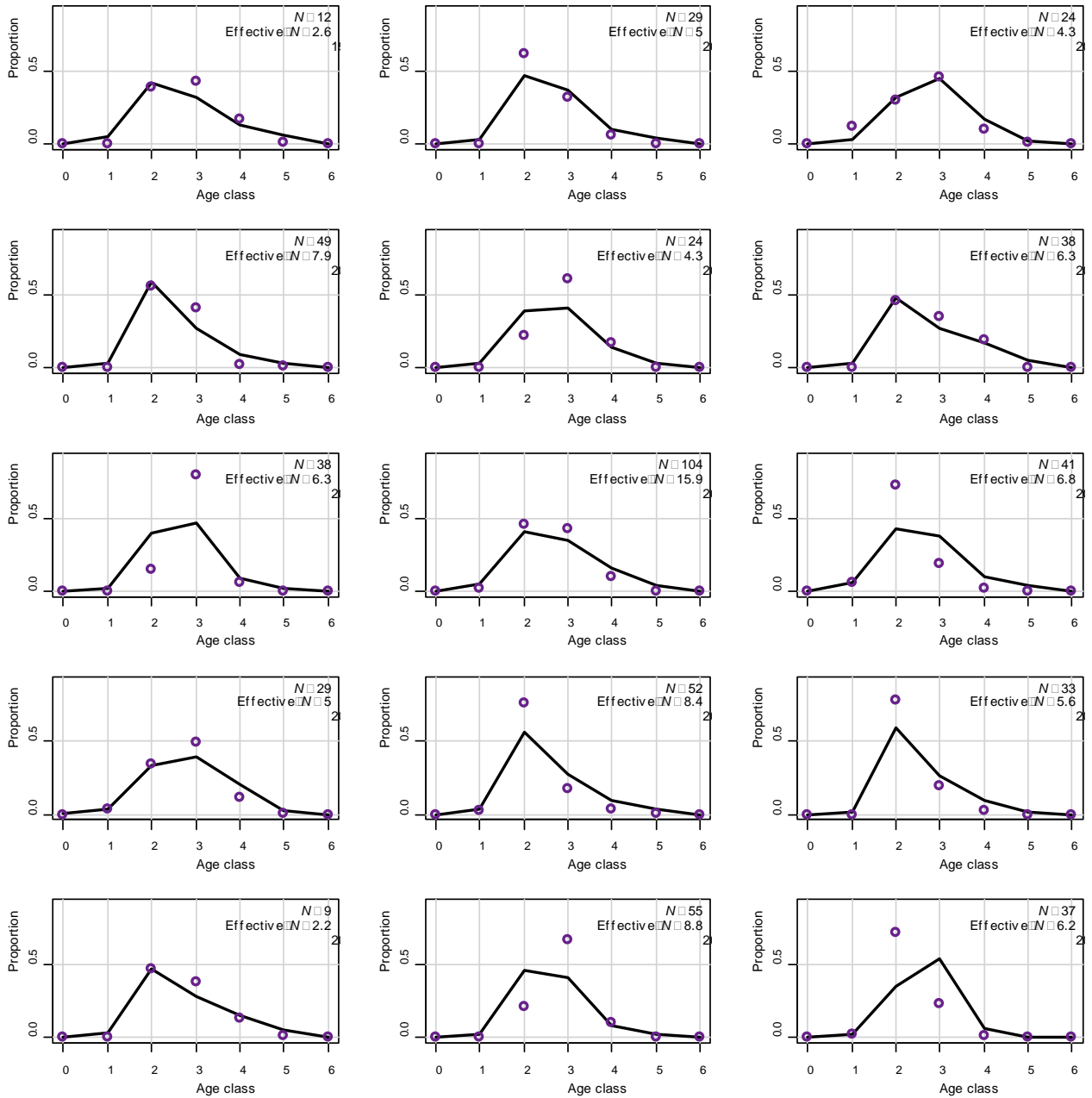
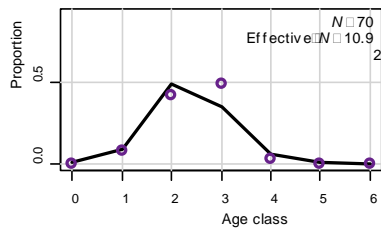
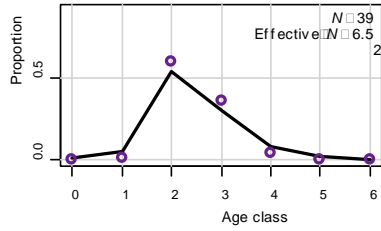
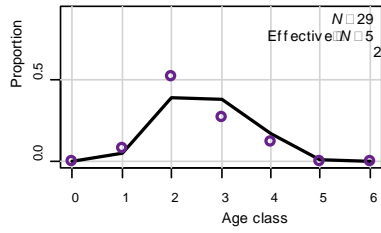
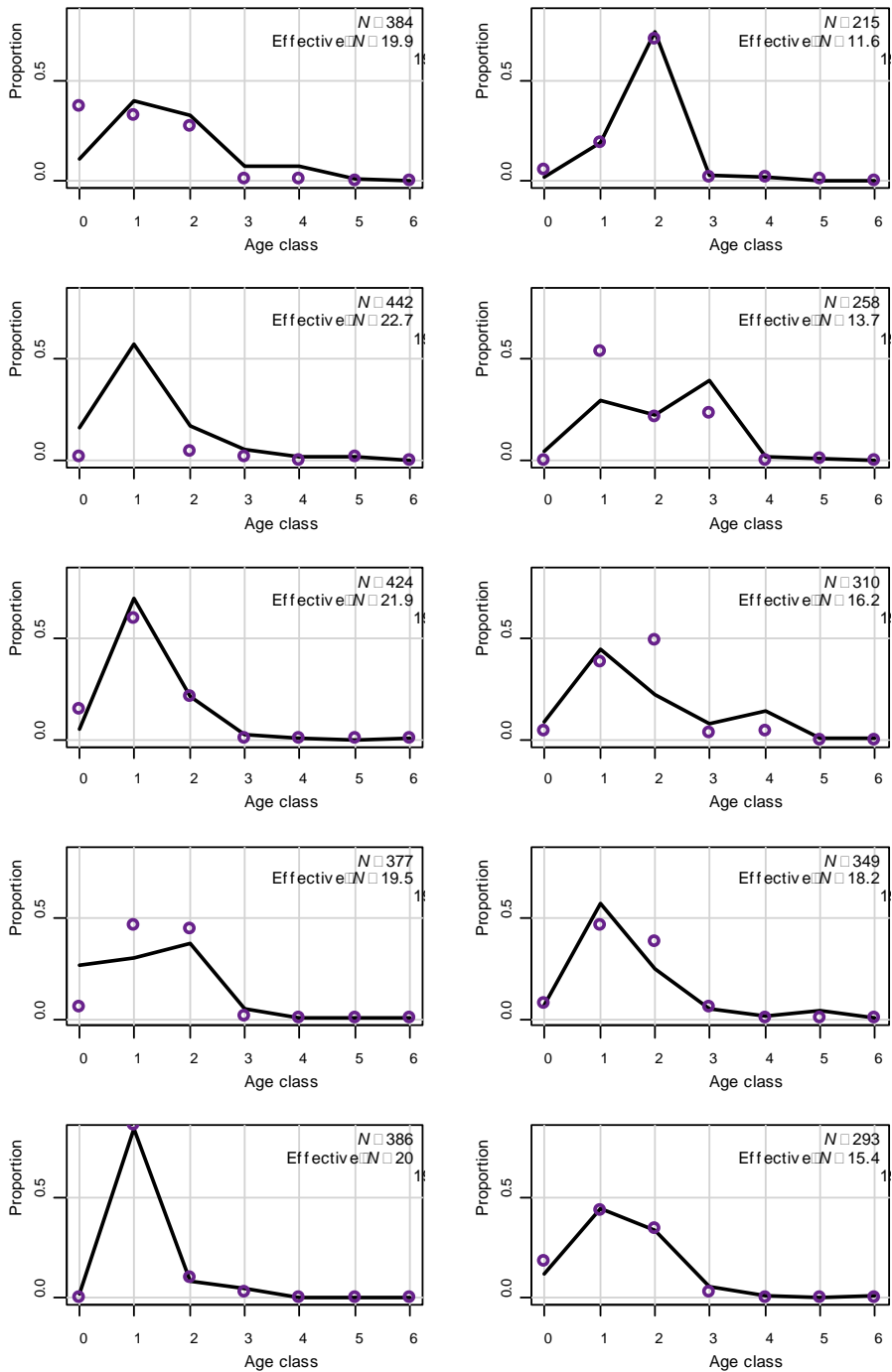


Figure 121 Continued



**Figure 121 Continued**



**Figure 122.** Annual age composition fits for the commercial reduction fishery for 1955-2017 in the southern region. Open circles indicate the observed data, while the solid line indicates predicted fits to the data. In the upper right corner of each panel there is the number of trips sampled, the effective sample size, and the year.

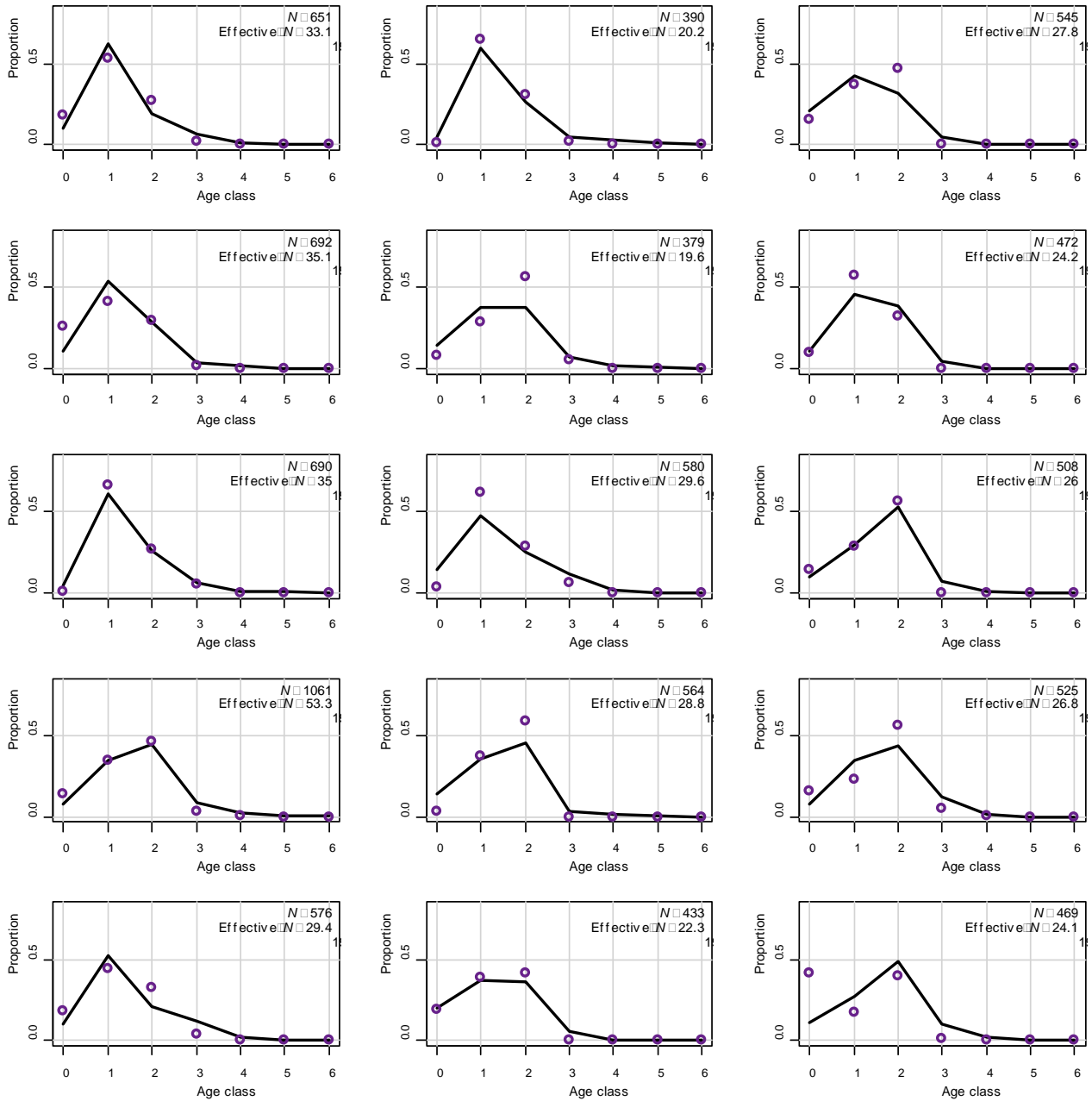


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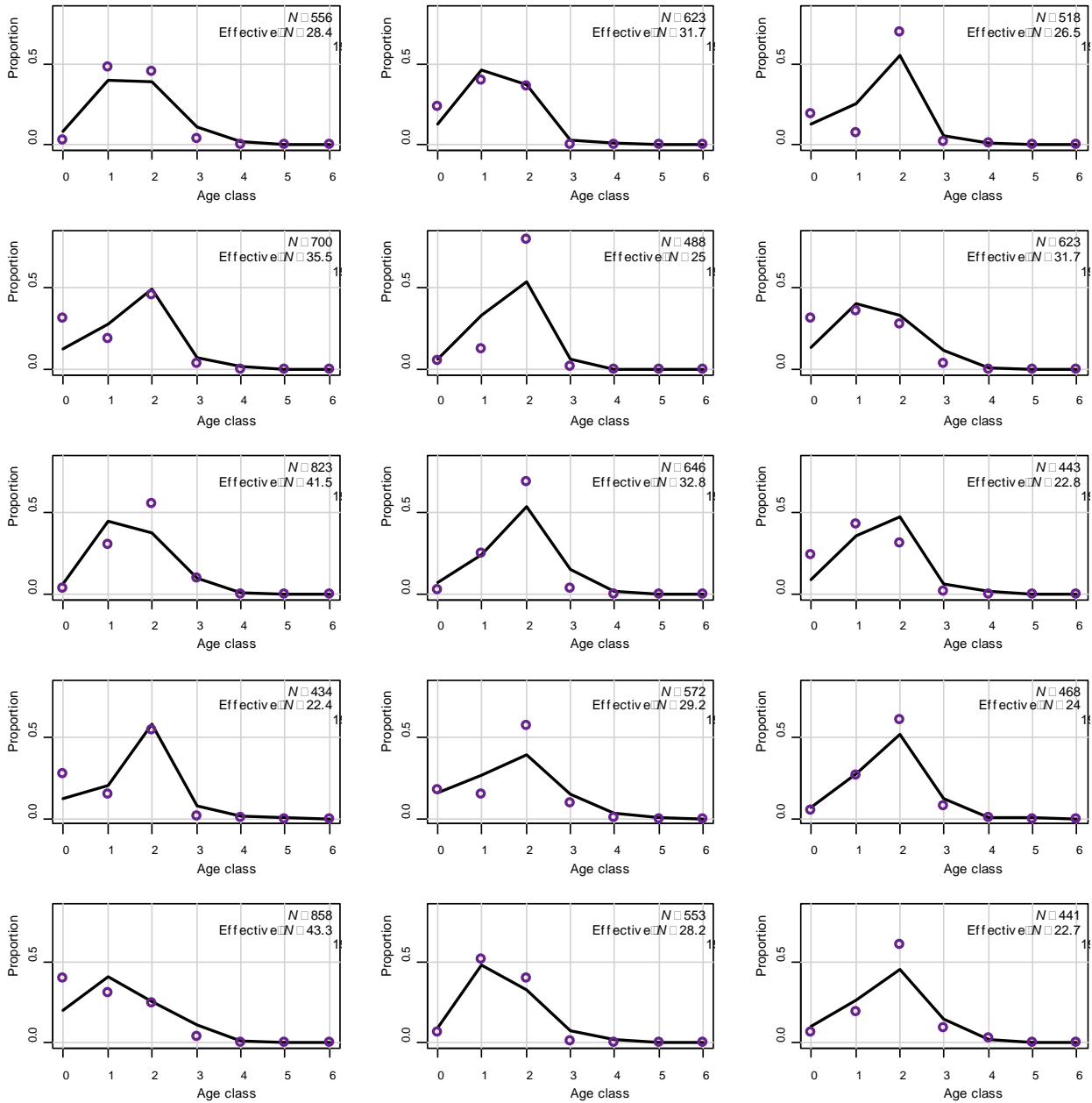


Figure 122 Continued



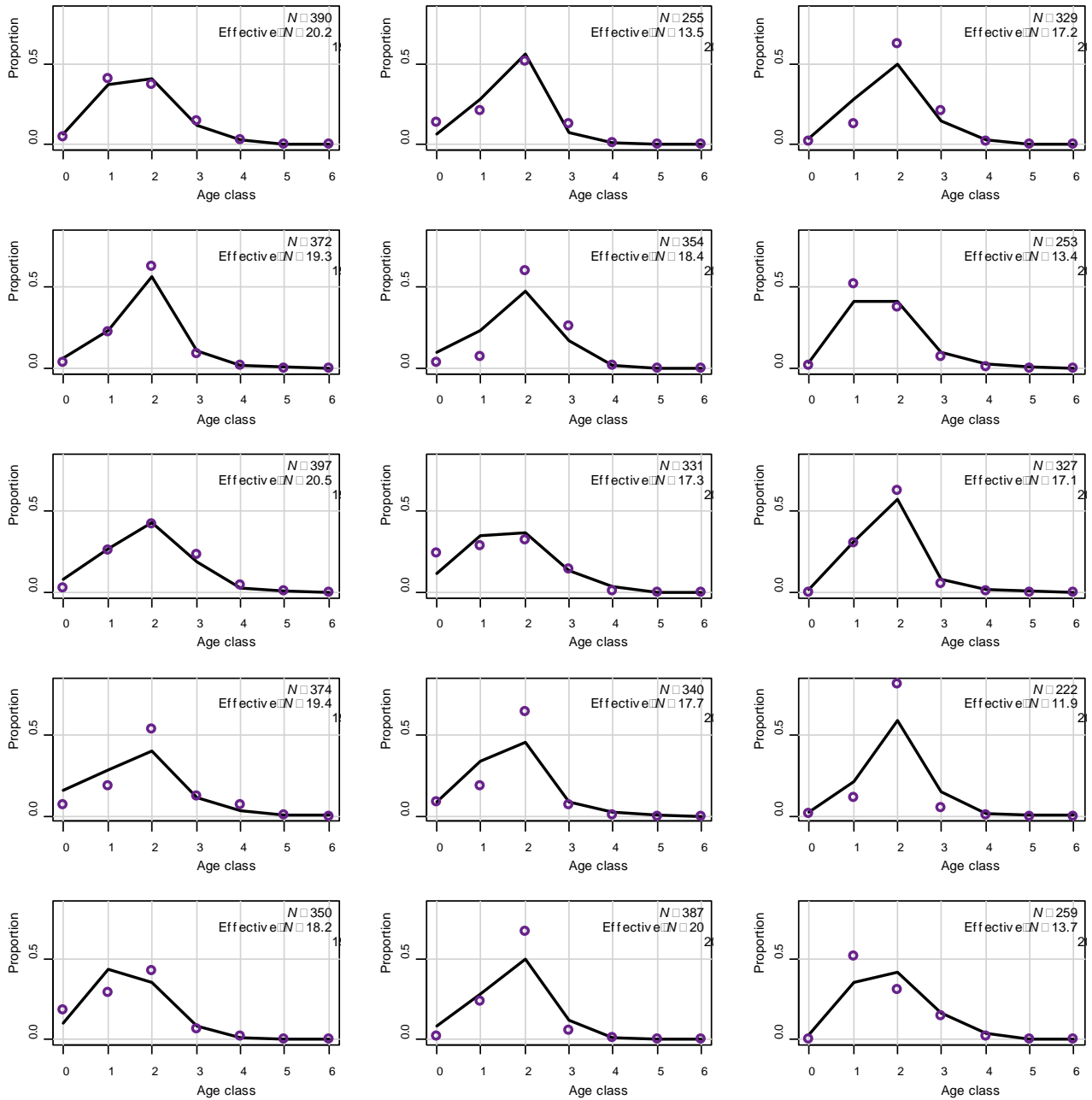


Figure 122 Continued

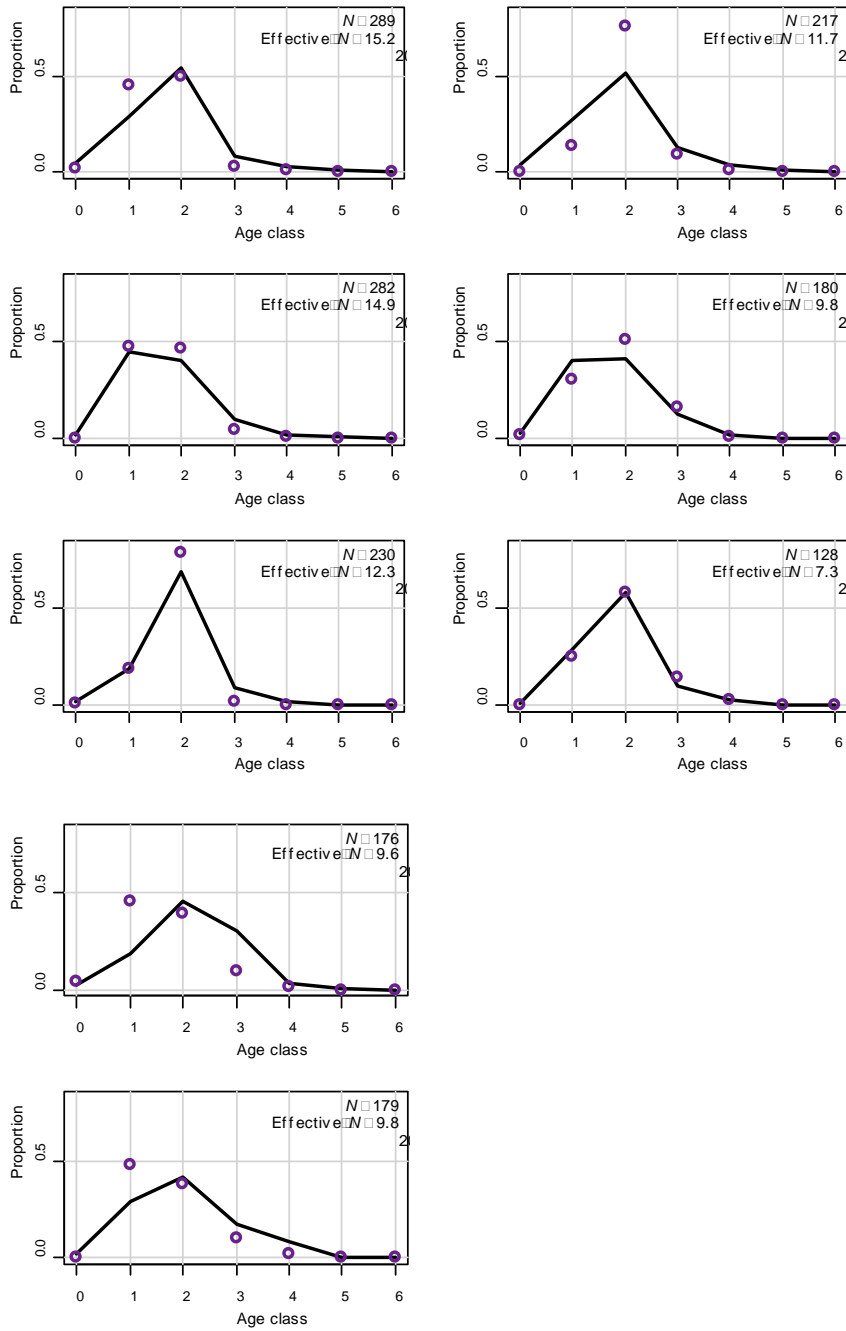
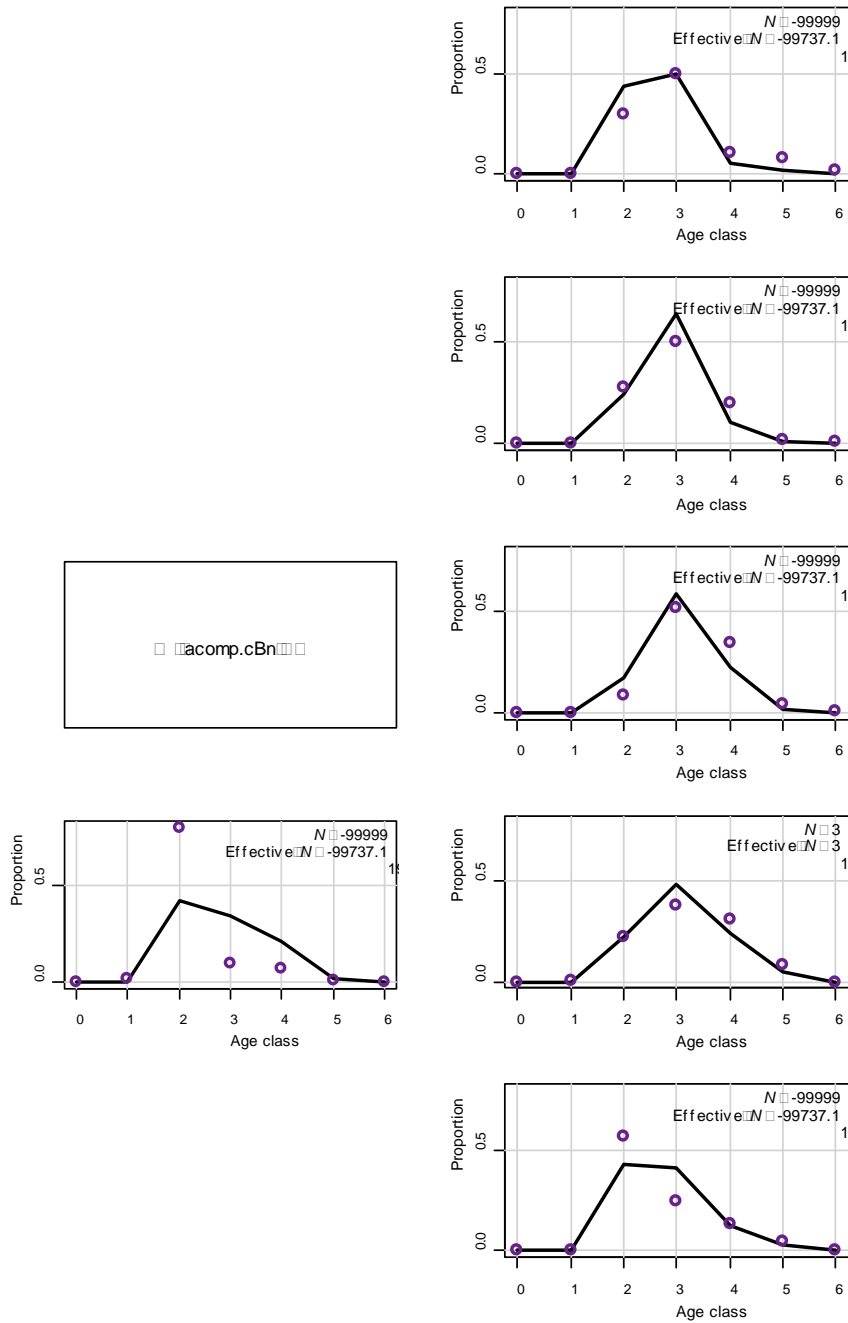


Figure 122 Continued



**Figure 123.** Annual age composition fits for the commercial bait fishery for 1985-2017 in the northern region. Open circles indicate the observed data, while the solid line indicates predicted fits to the data. In the upper right corner of each panel there is the number of trips sampled, the effective sample size, and the year. If the numbers in the upper right hand corner are large and negative that indicates that those years were not used in fitting the likelihood.

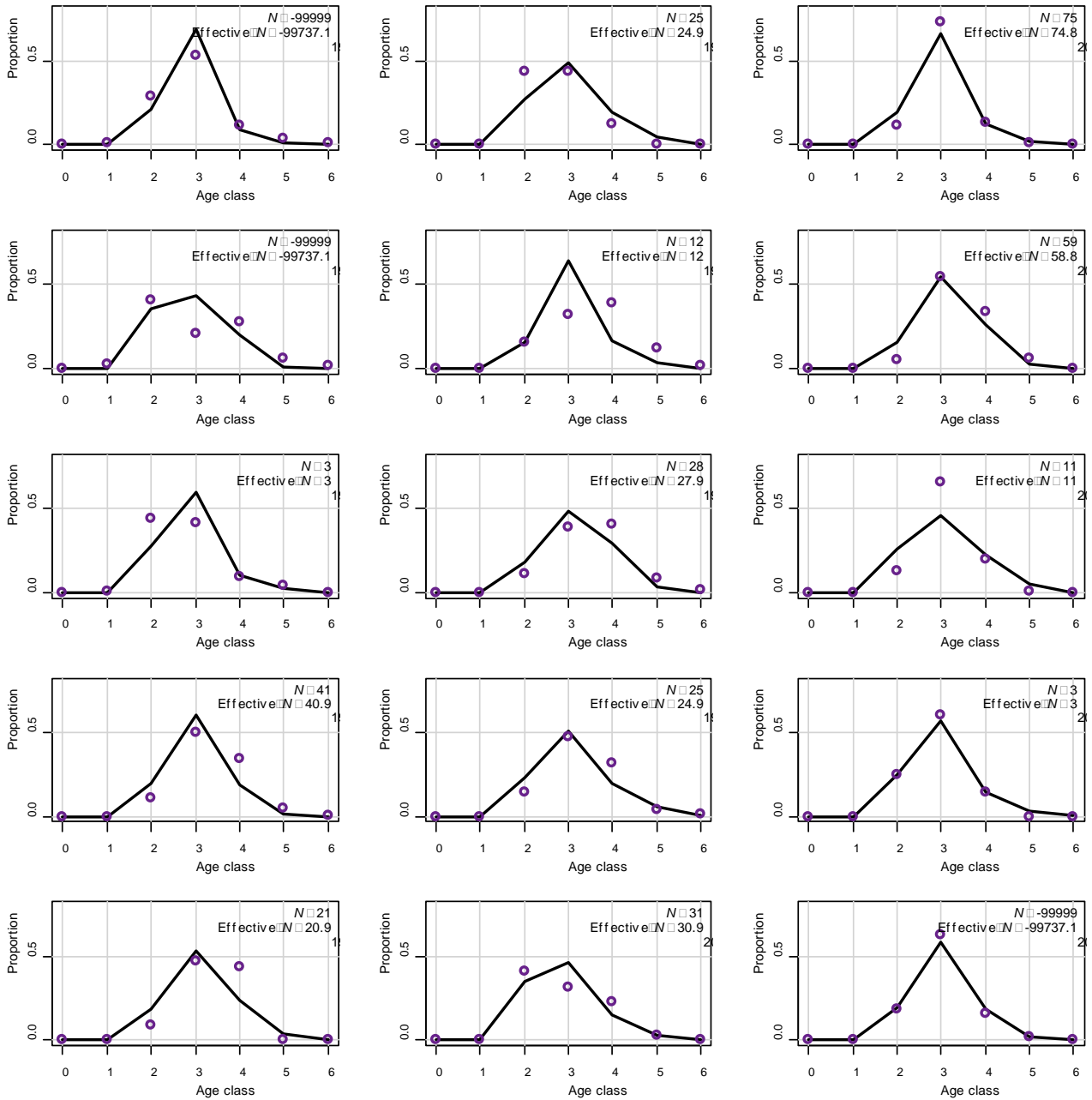


Figure 123 Continued

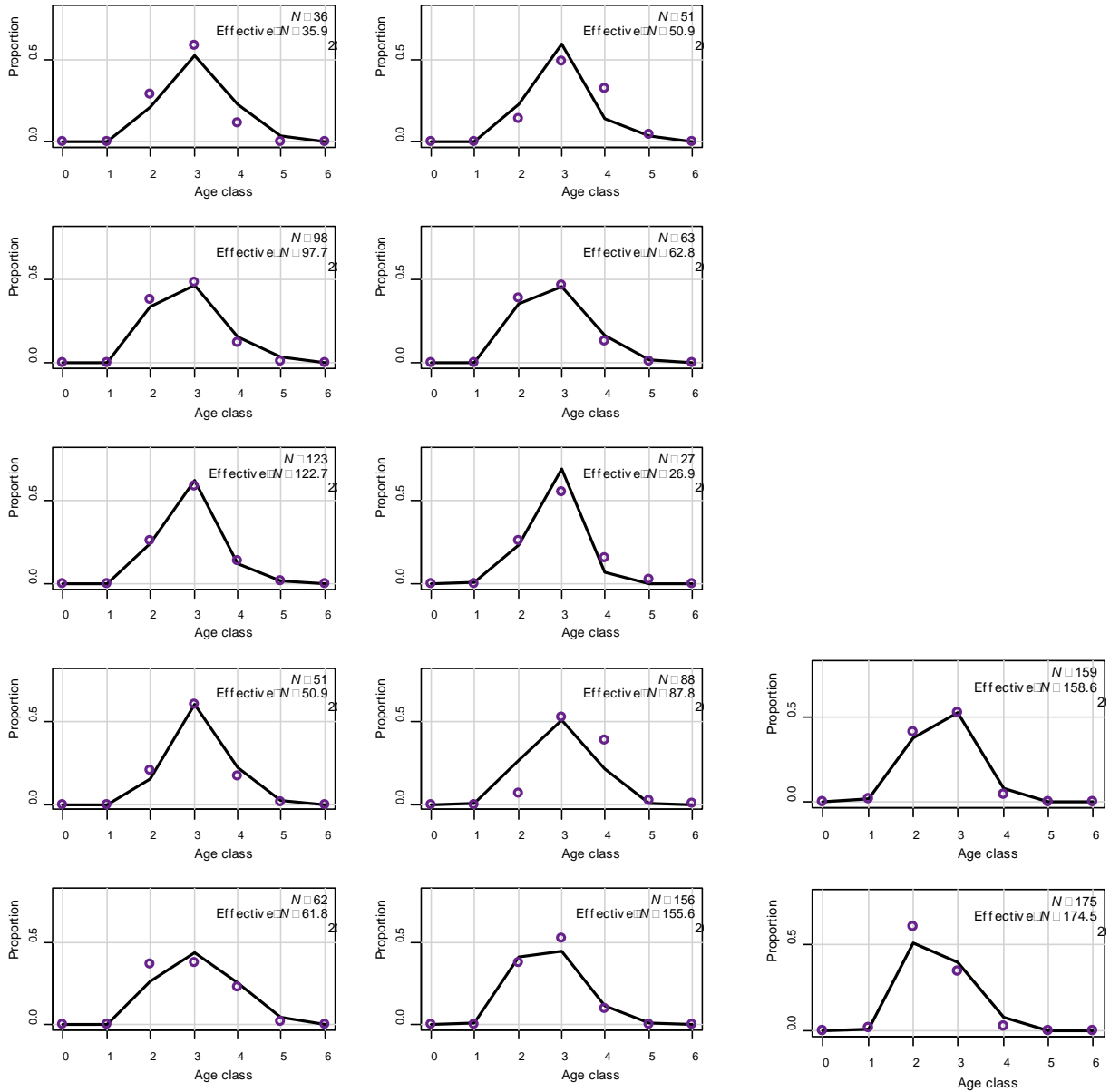
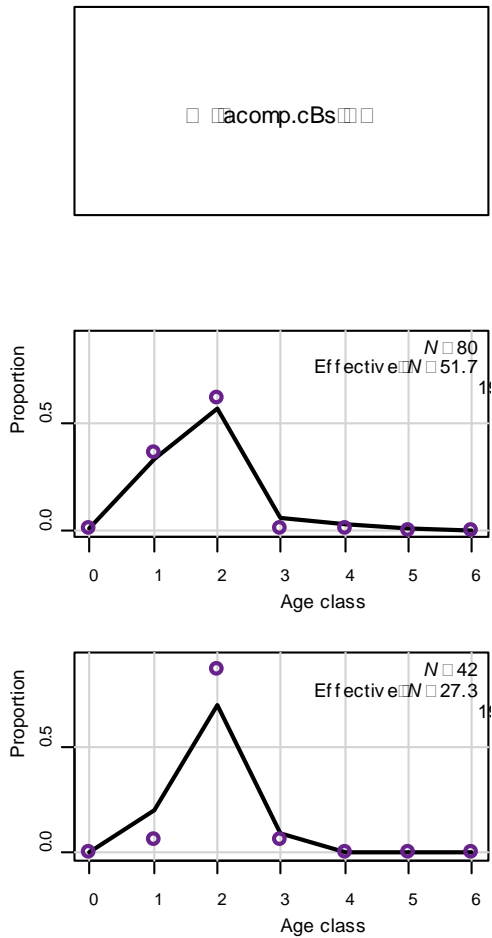


Figure 123 Continued



**Figure 124.** Annual age composition fits for the commercial bait fishery for 1985-2017 in the southern region. Open circles indicate the observed data, while the solid line indicates predicted fits to the data. In the upper right corner of each panel there is the number of trips sampled, the effective sample size, and the year. If the numbers in the upper right hand corner are large and negative that indicates that those years were not used in fitting the likelihood.

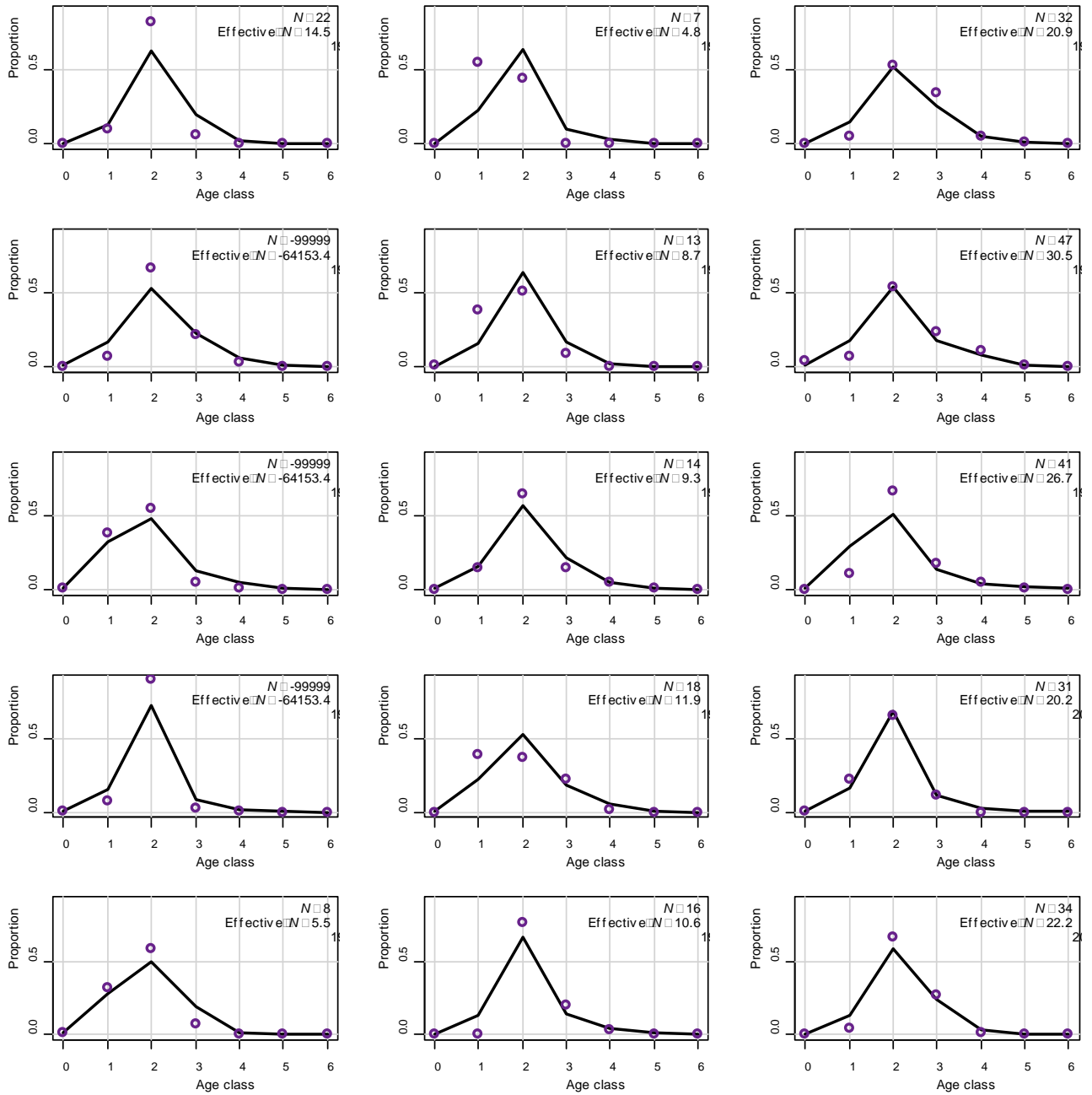


Figure 124 Continued

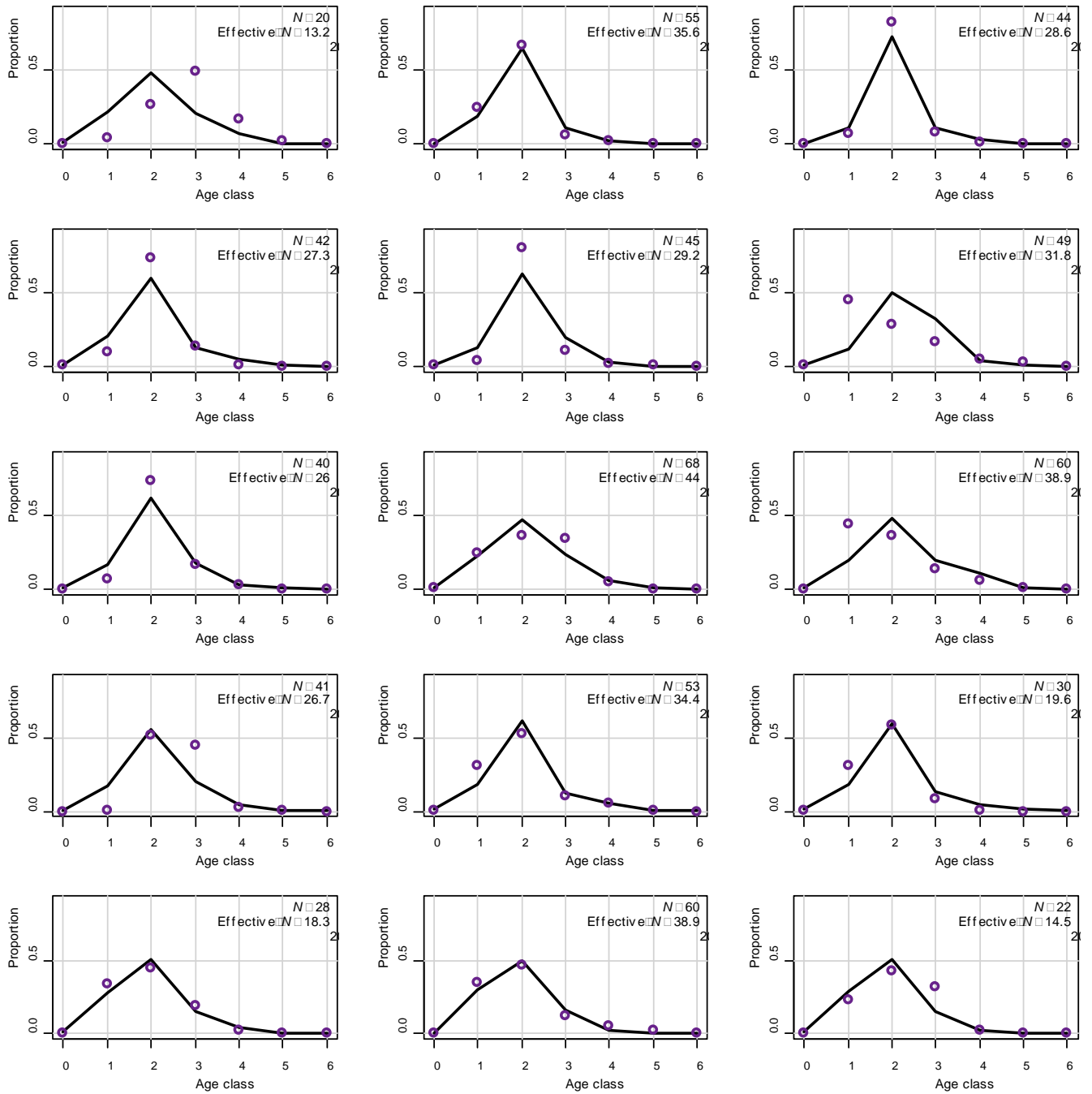
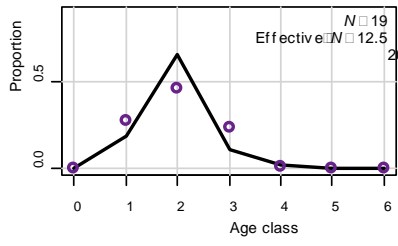
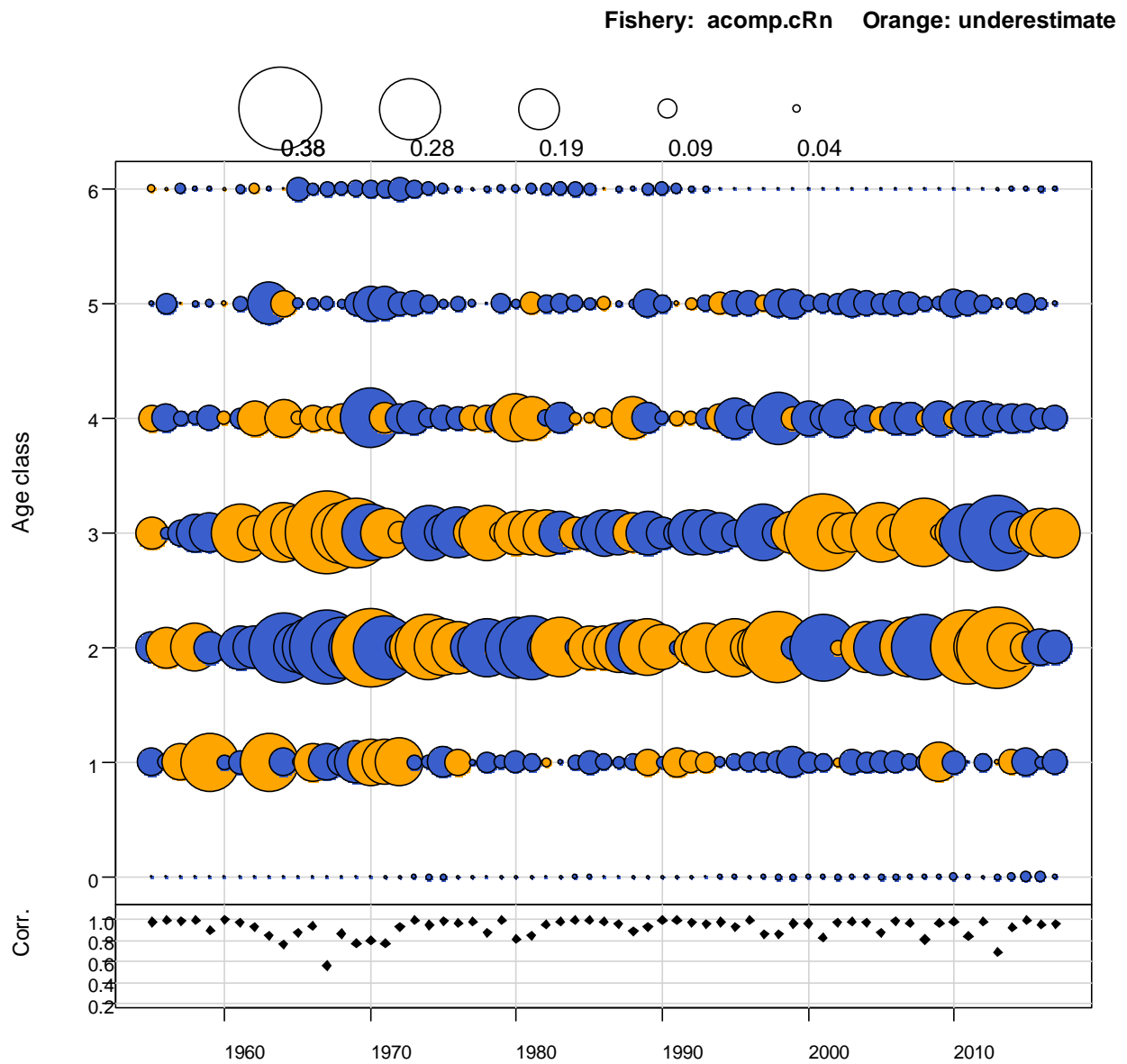


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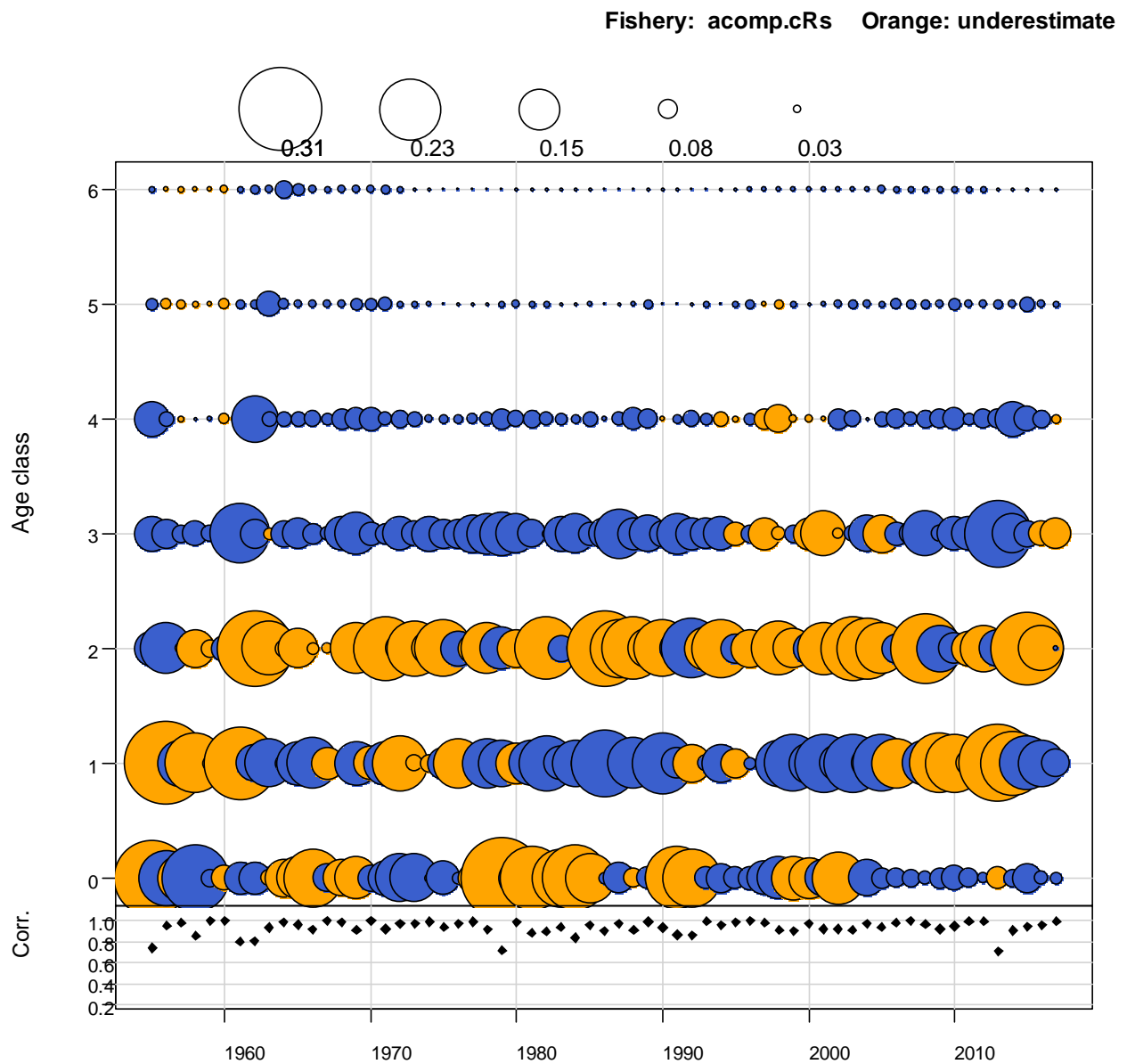




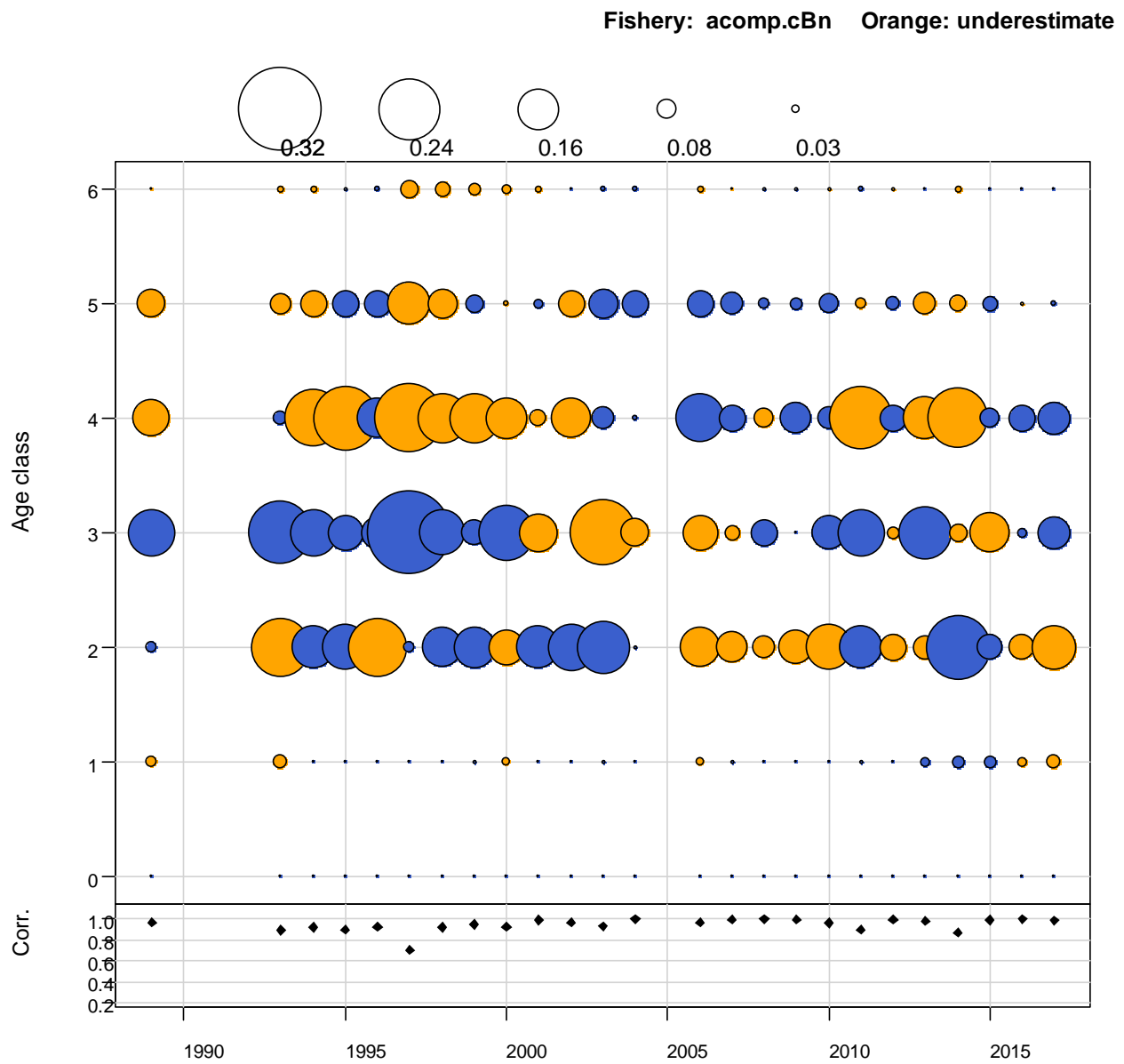
**Figure 124 Continued**



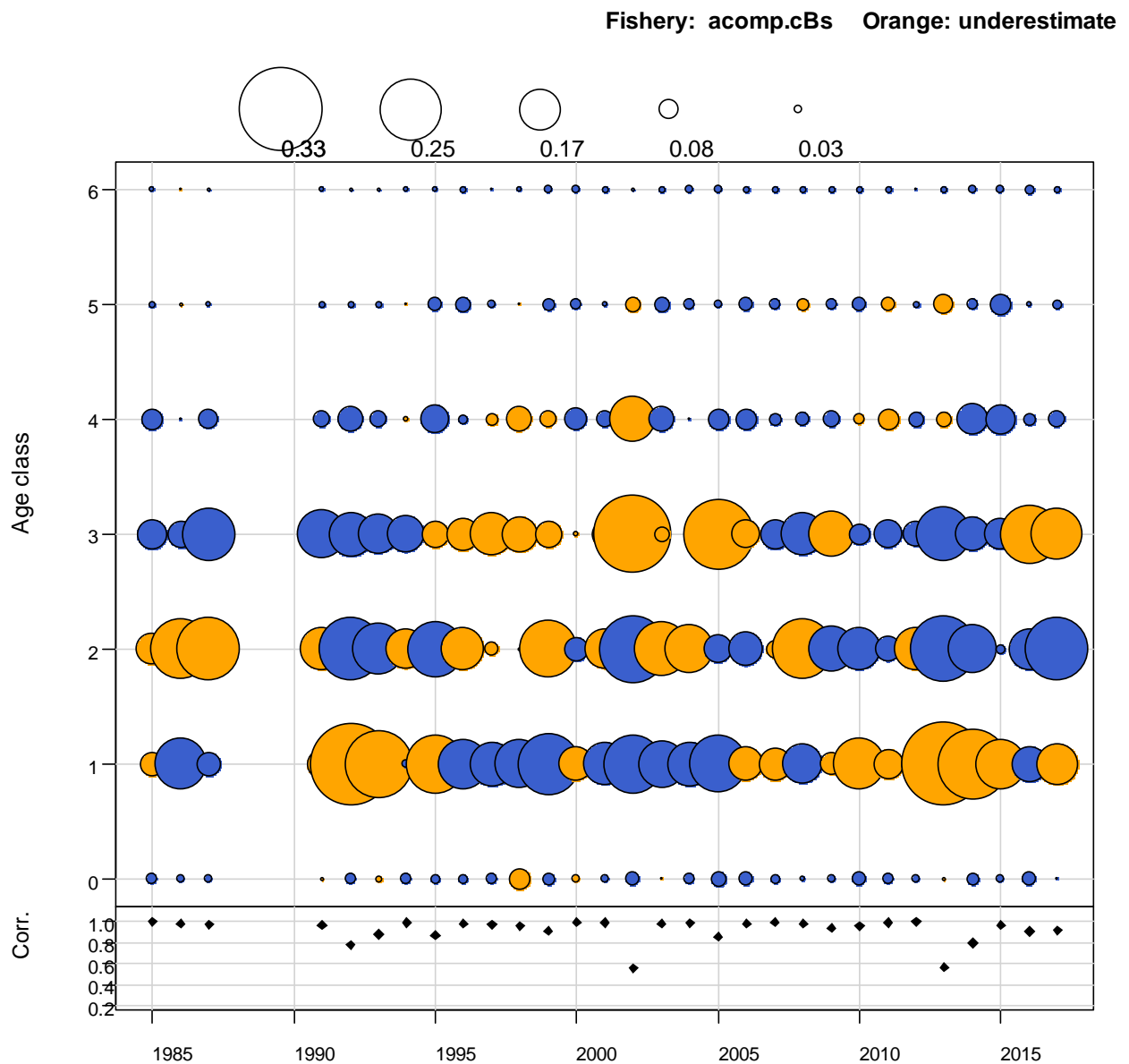
**Figure 125.** Annual age composition fits for the commercial reduction fishery for 1955-2017 in the northern region. Orange circles indicate an underestimate, while blue circles indicate an overestimate. The bottom panel contains the correlation between the observed and predicted data.



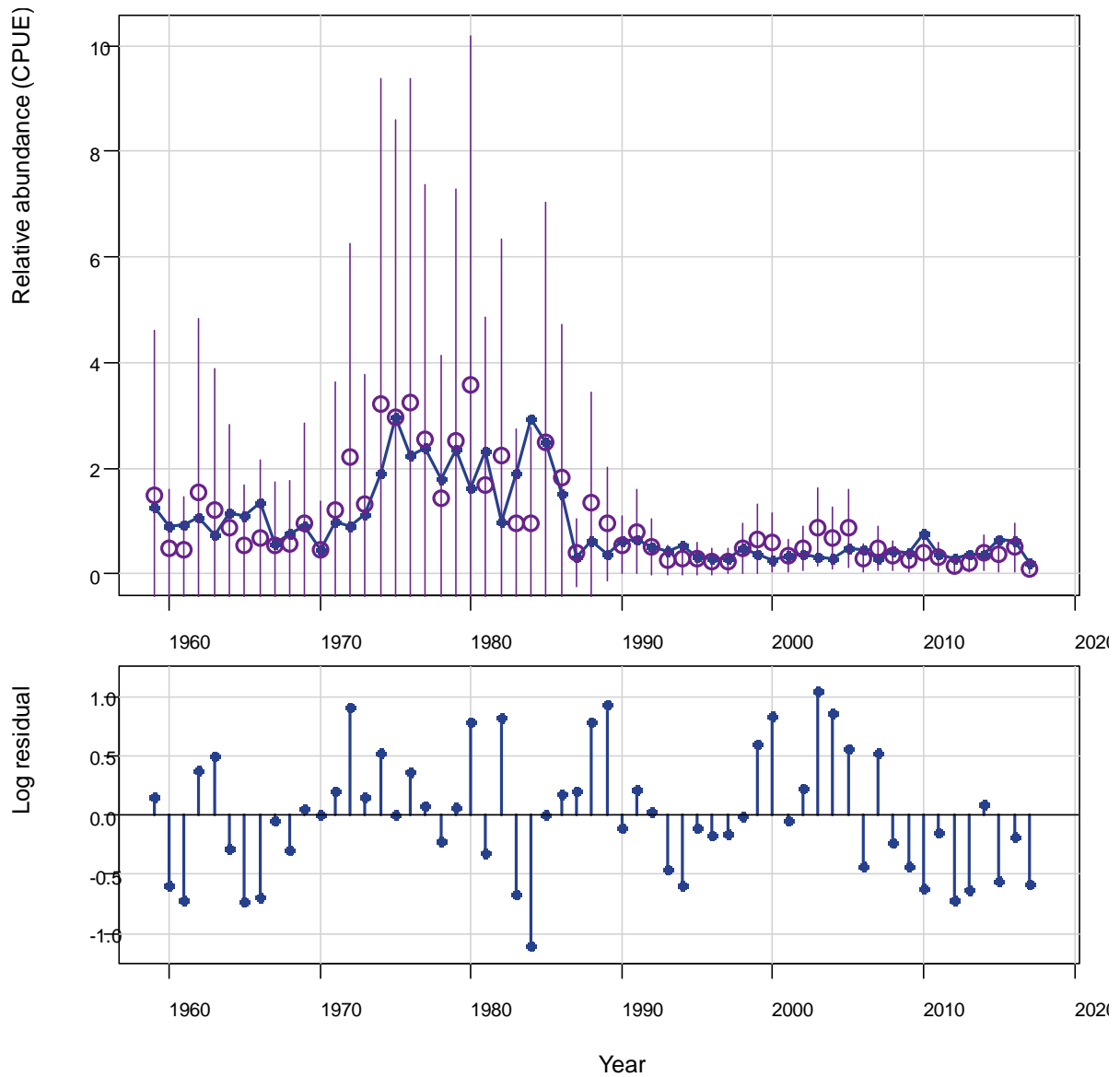
**Figure 126.** Annual age composition fits for the commercial reduction fishery for 1955-2017 in the southern region. Orange circles indicate an underestimate, while blue circles indicate an overestimate. The bottom panel contains the correlation between the observed and predicted data.



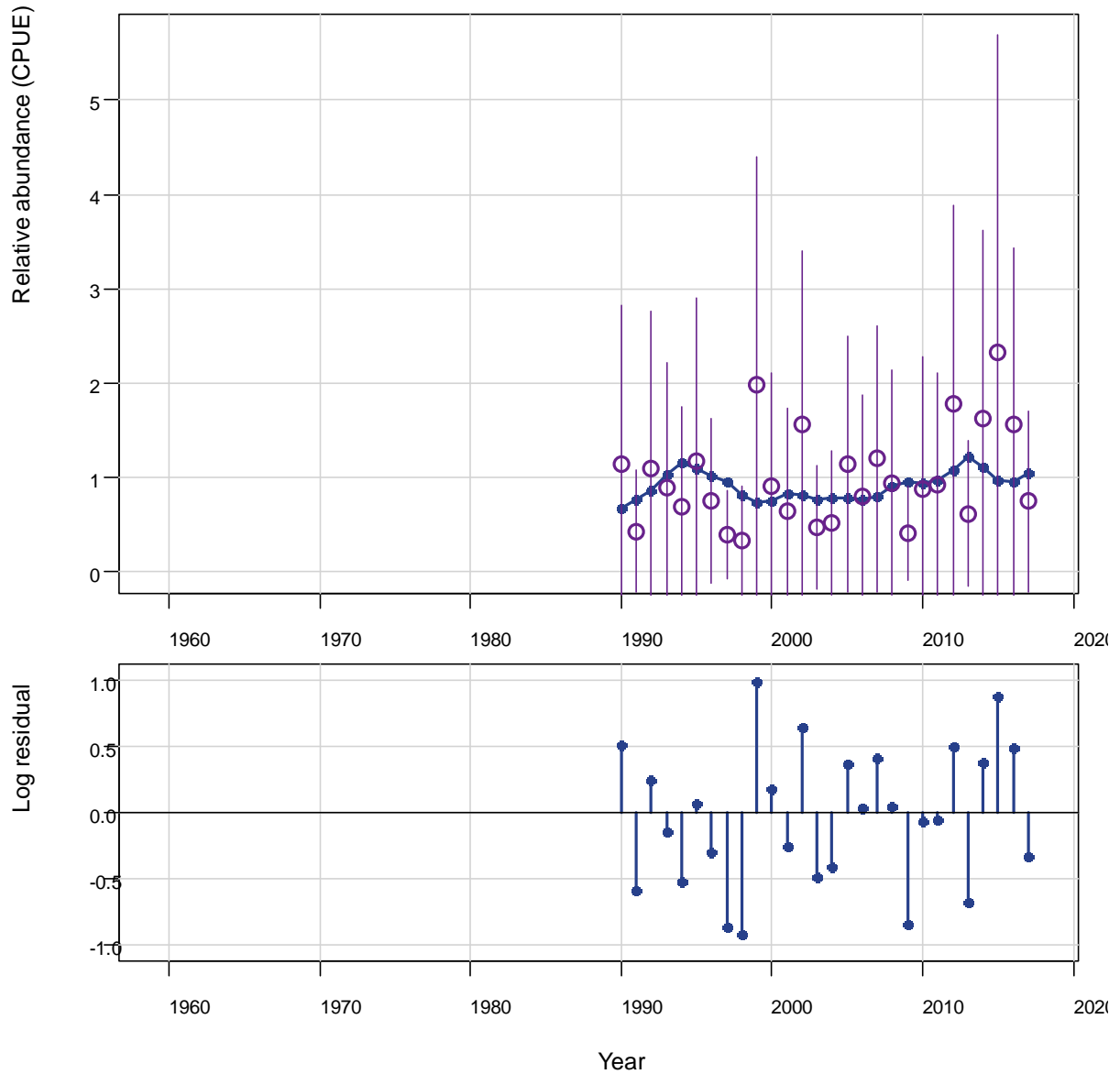
**Figure 127.** Annual age composition fits for the commercial bait fishery for 1985-2017 in the northern region. Orange circles indicate an underestimate, while blue circles indicate an overestimate. The bottom panel contains the correlation between the observed and predicted data.



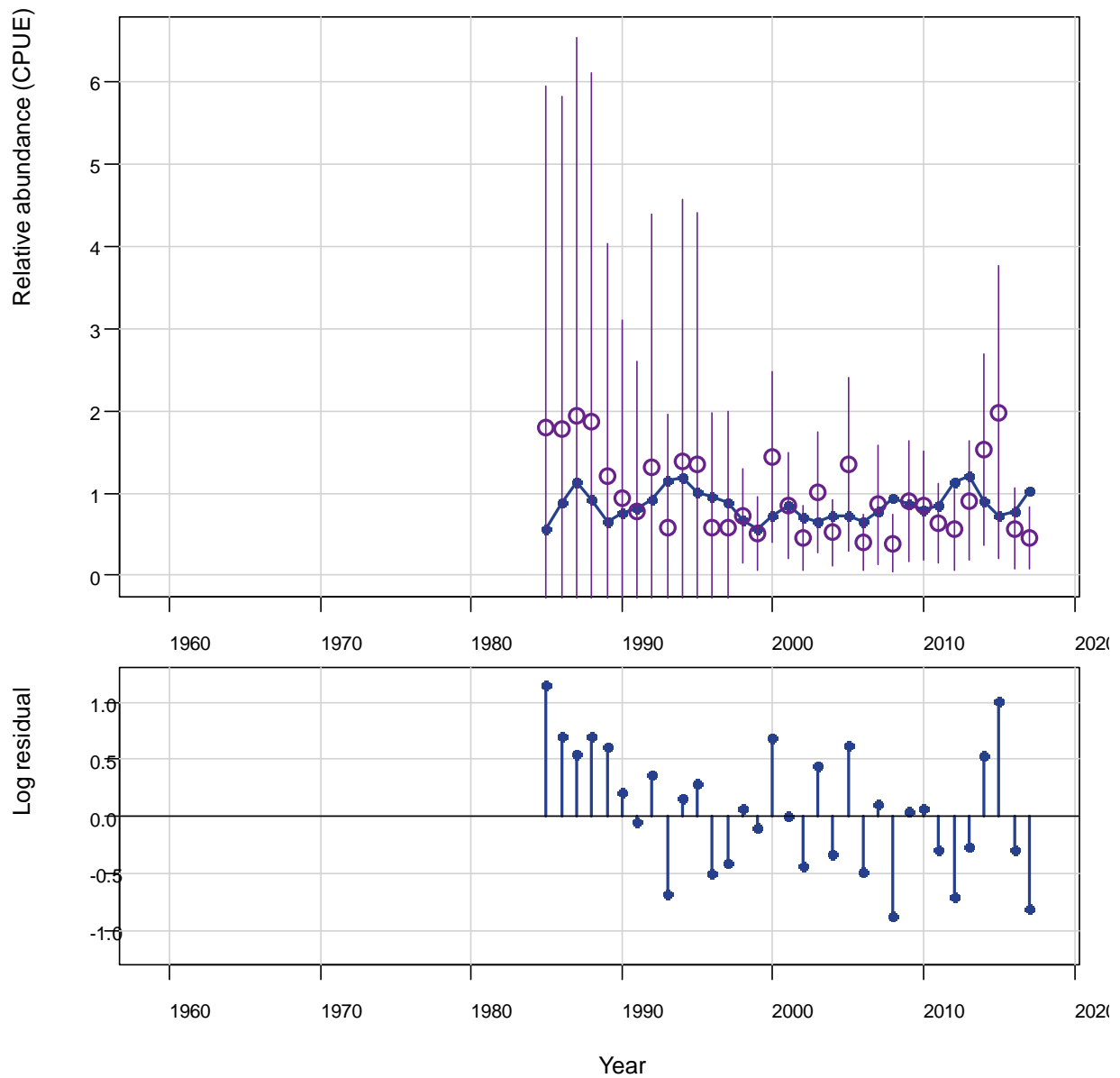
**Figure 128.** Annual age composition fits for the commercial bait fishery for 1985-2017 in the northern region. Orange circles indicate an underestimate, while blue circles indicate an overestimate. The bottom panel contains the correlation between the observed and predicted data.



**Figure 129.** The relative abundance index for recruitment or young of the year (YOY) for 1959-2017. The observed values are the open circles with the vertical lines indicating the uncertainty based on the CV values. The filled circles and blue solid line indicate the predicted or fitted values. The bottom panel contains the annual log residuals.

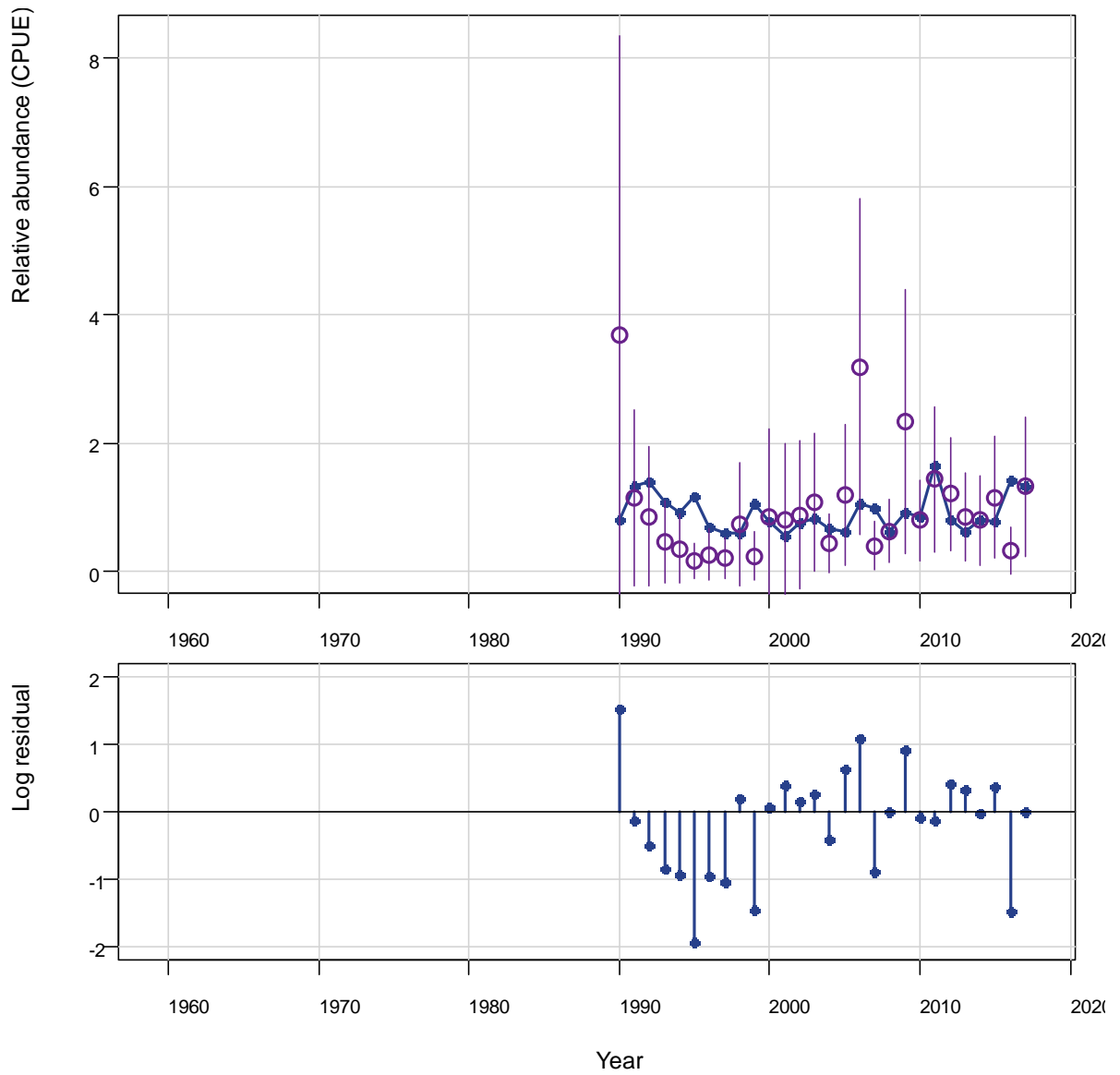


**Figure 130.** The relative abundance index for the northern adult index (NAD) for 1990-2017. The observed values are the open circles with the vertical lines indicating the uncertainty based on the CV values. The filled circles and blue solid line indicate the predicted or fitted values. The bottom panel contains the annual log residuals.

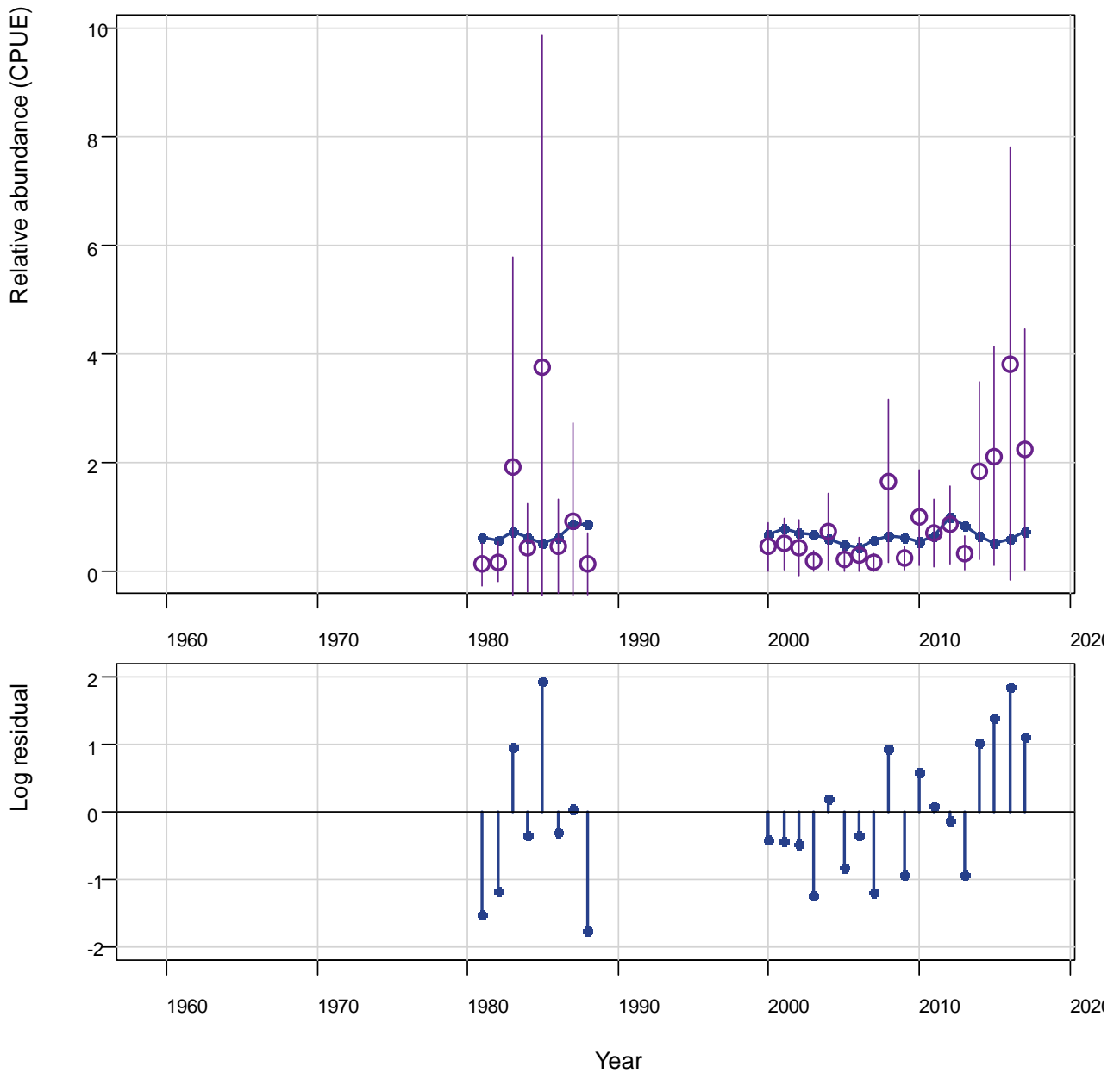


**Figure 131.** The relative abundance index for the mid-Atlantic adult index (MAD) for 1985-2017. The observed values are the open circles with the vertical lines indicating the uncertainty based on the CV values. The filled circles and blue solid line indicate the predicted or fitted values. The bottom panel contains the annual log residuals.

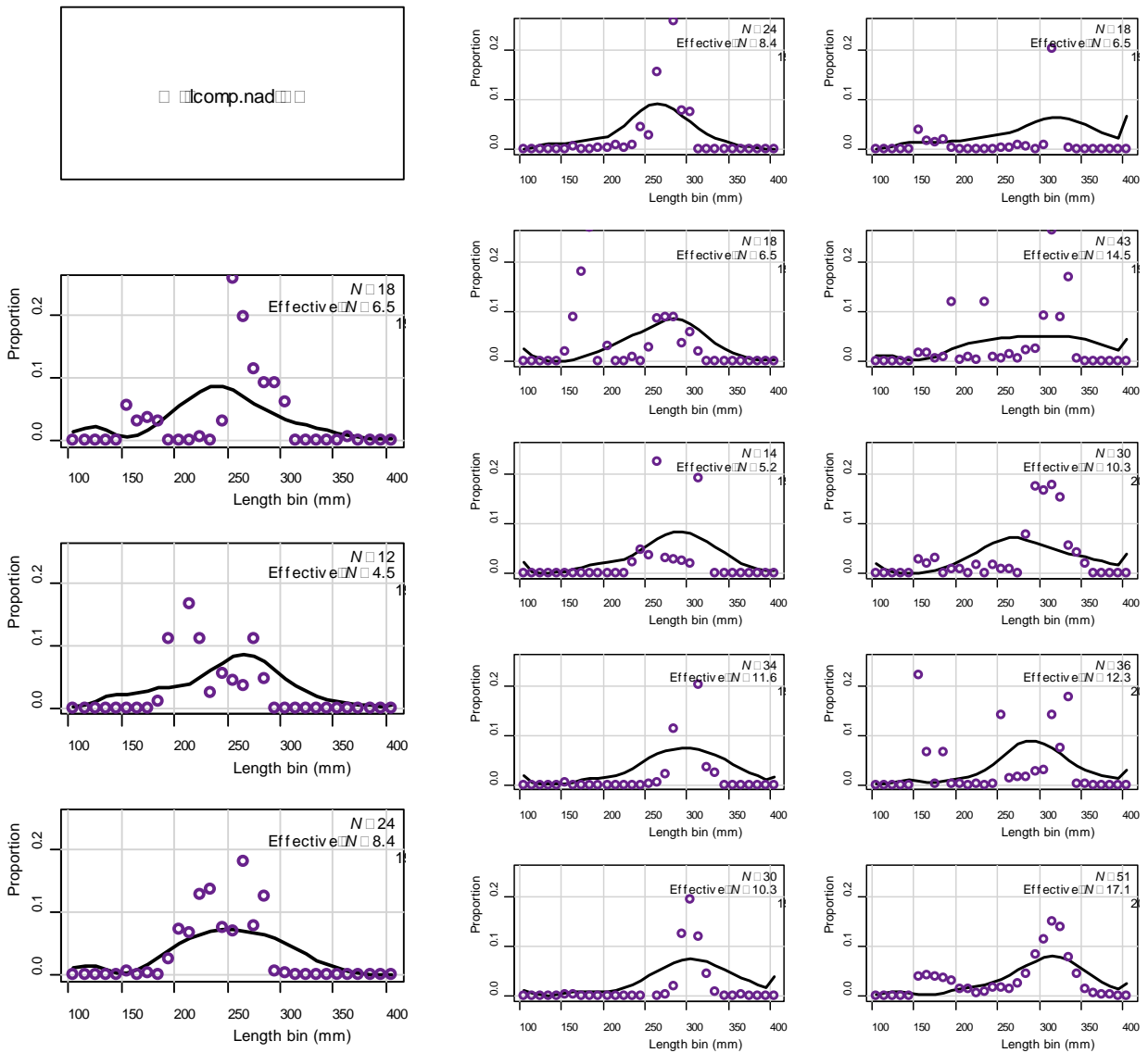




**Figure 132.** The relative abundance index for the southern adult index (SAD) for 1990-2017. The observed values are the open circles with the vertical lines indicating the uncertainty based on the CV values. The filled circles and blue solid line indicate the predicted or fitted values. The bottom panel contains the annual log residuals.



**Figure 133. The relative abundance index for fecundity based on the MARMAP and EcoMon larval data (MARECO) for 1981-1988 and 2000-2017. The observed values are the open circles with the vertical lines indicating the uncertainty based on the CV values. The filled circles and blue solid line indicate the predicted or fitted values. The bottom panel contains the annual log residuals.**



**Figure 134. Annual length composition fits for the NAD index for 1990-2017. Open circles indicate the observed data, while the solid line indicates predicted fits to the data. In the upper right corner of each panel there is the number of trips sampled, the effective sample size, and the year.**

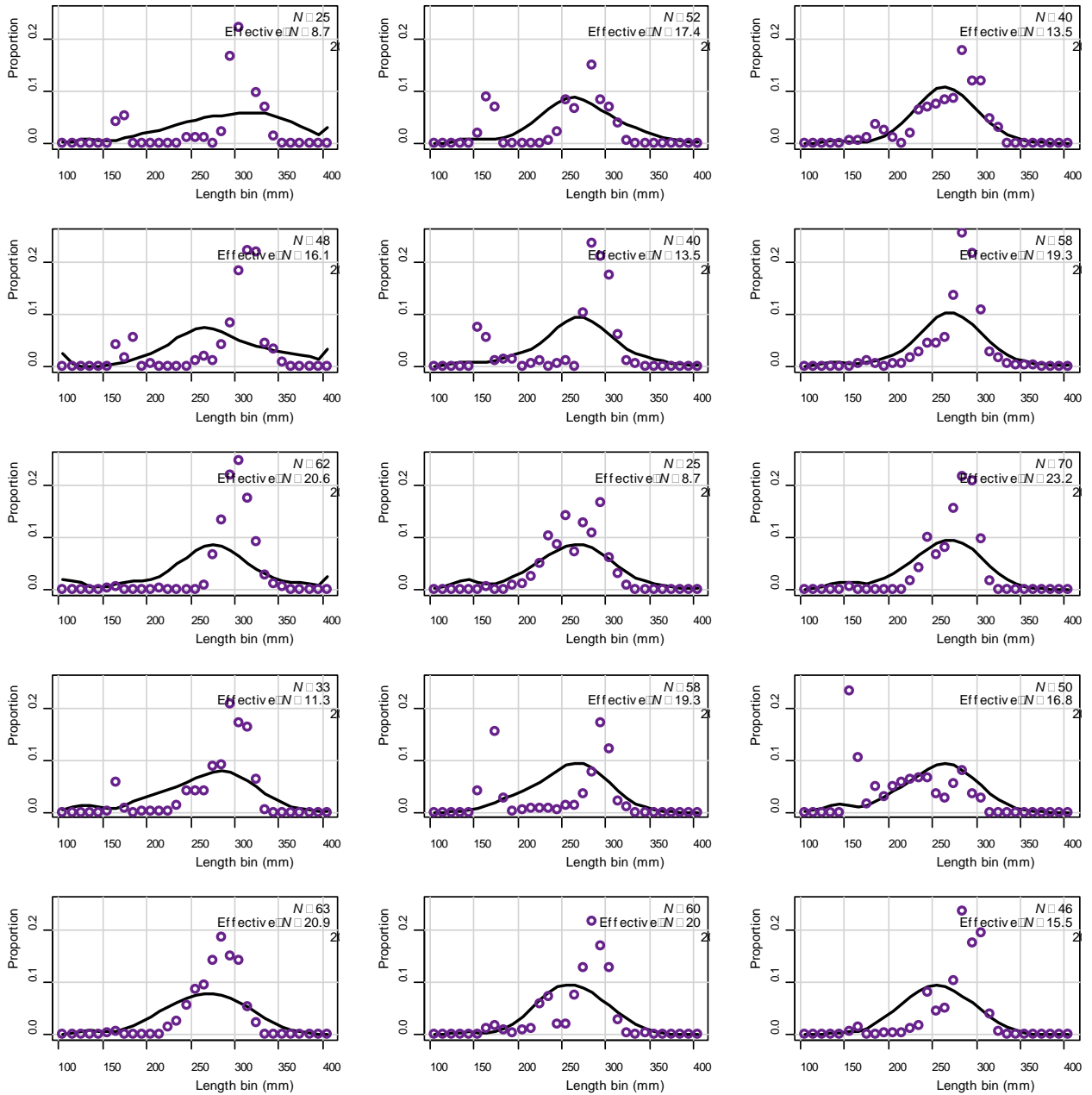
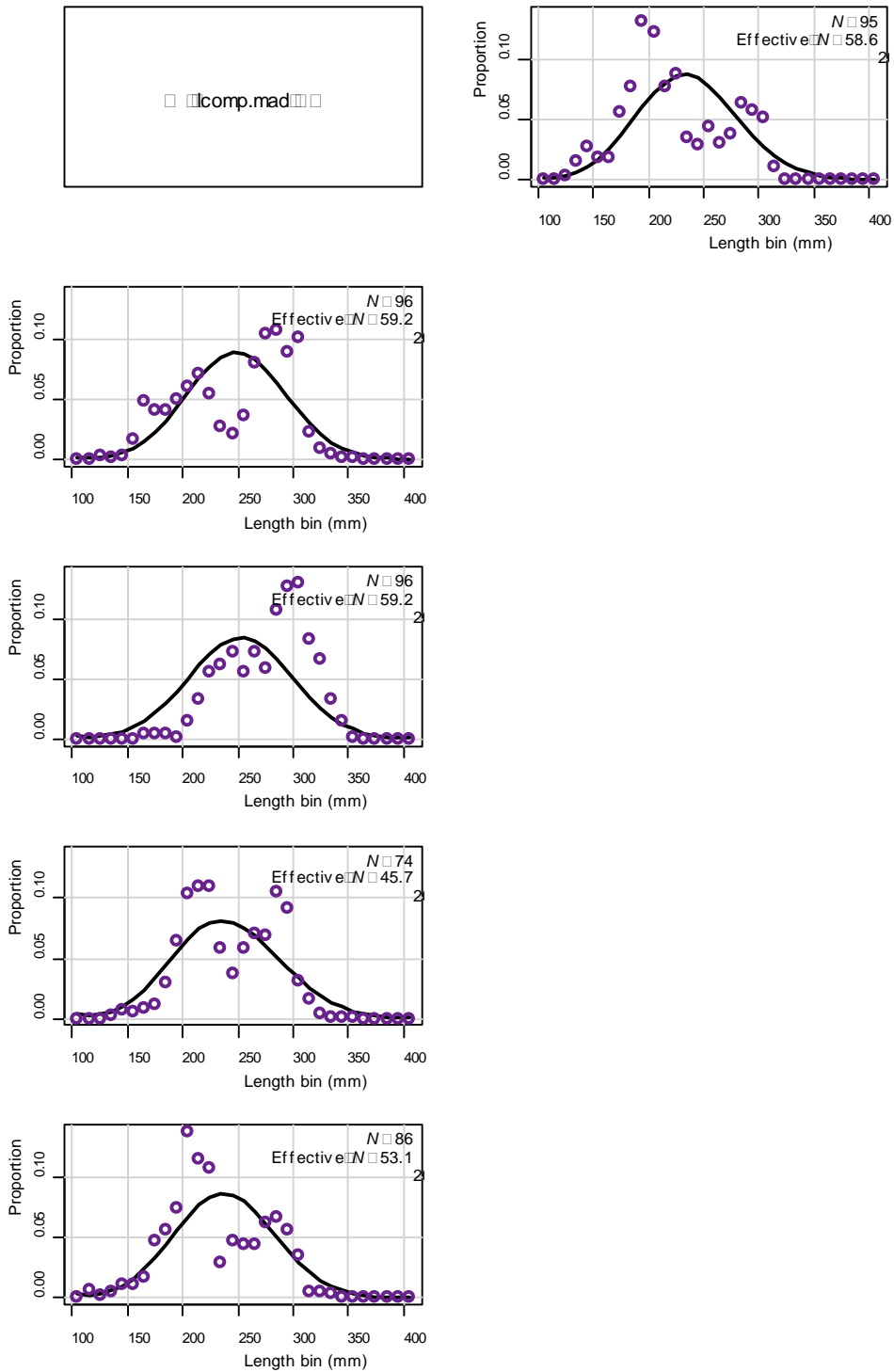
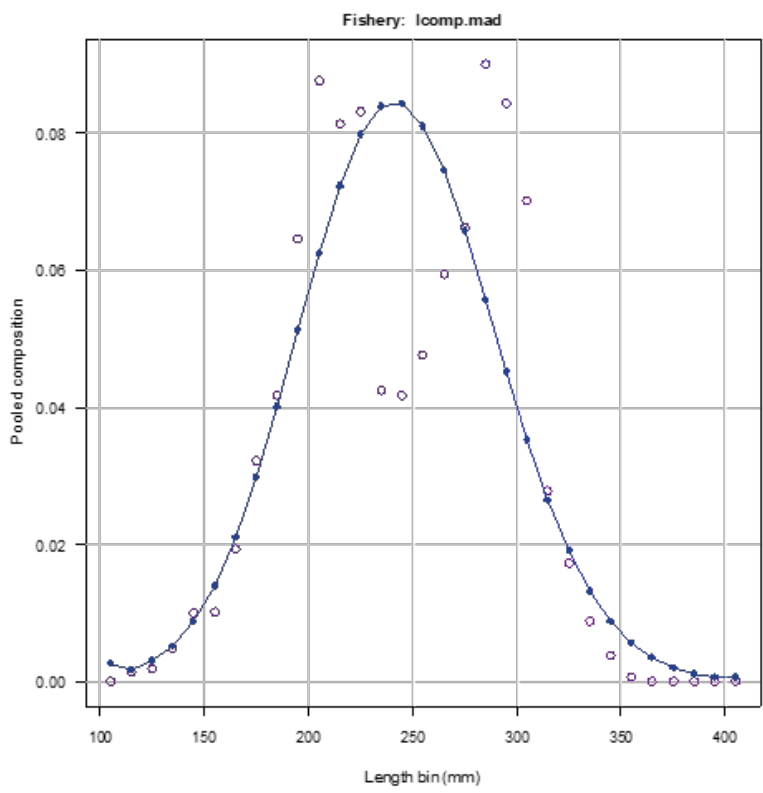
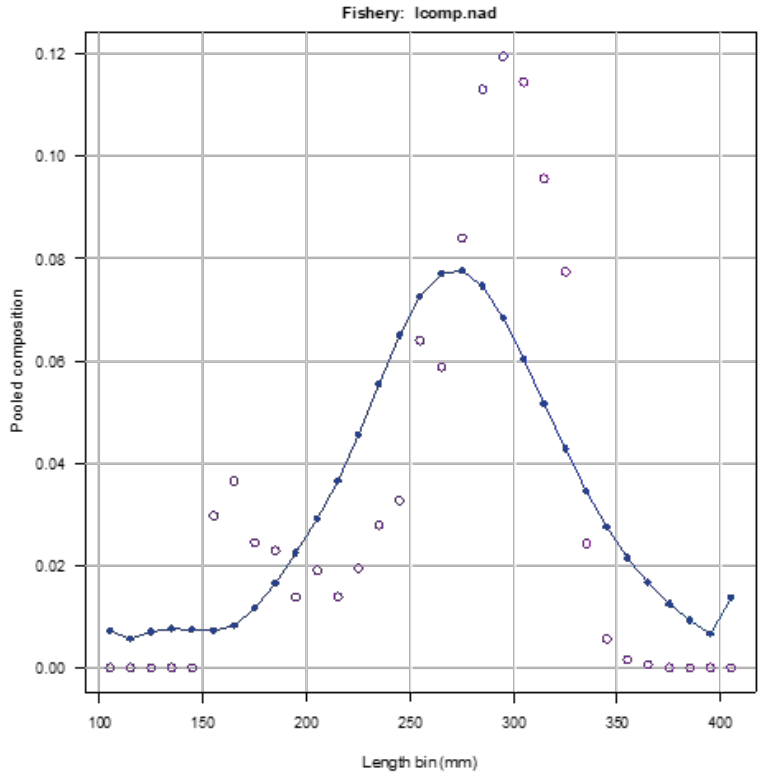


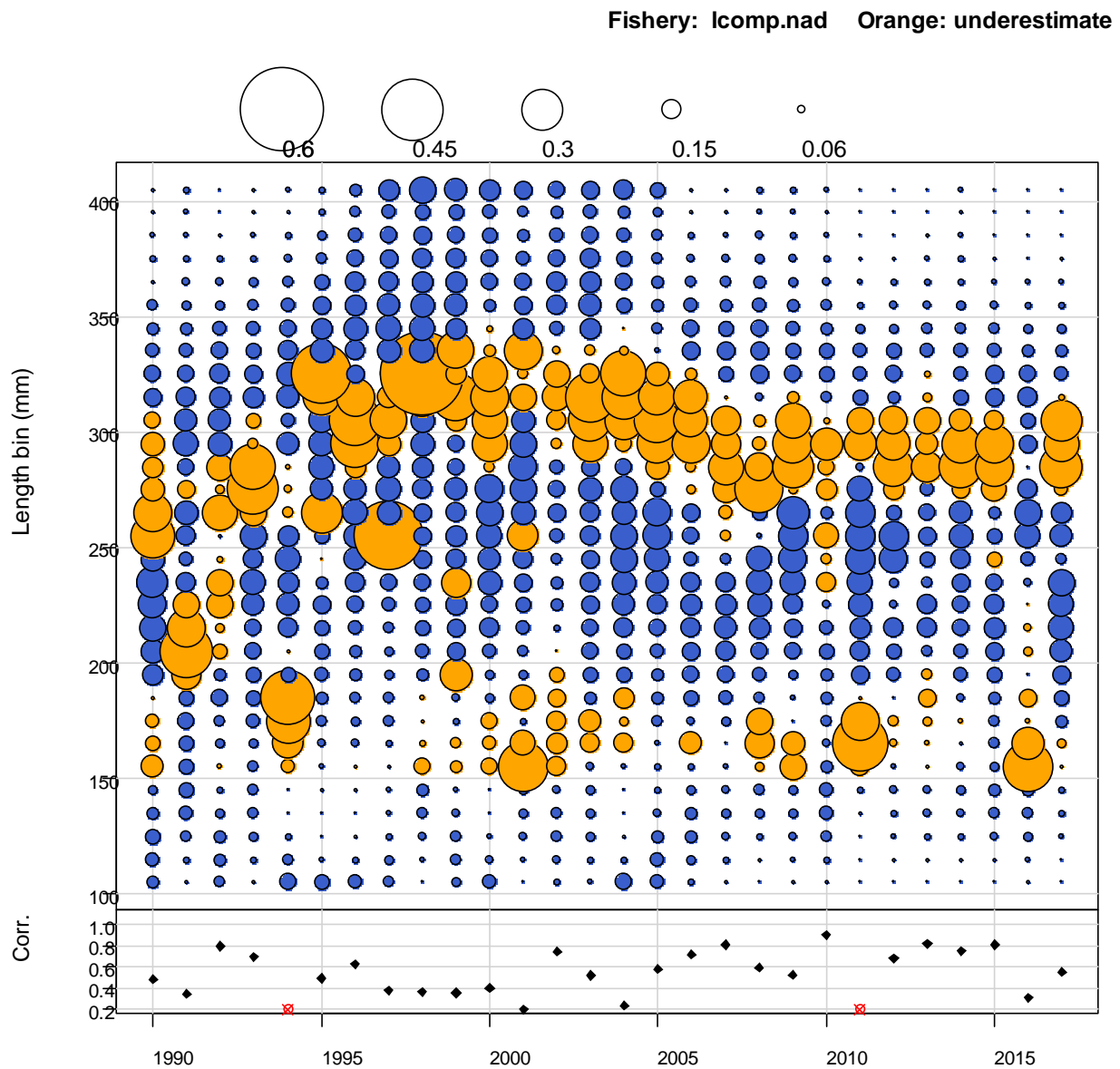
Figure 134 Continued



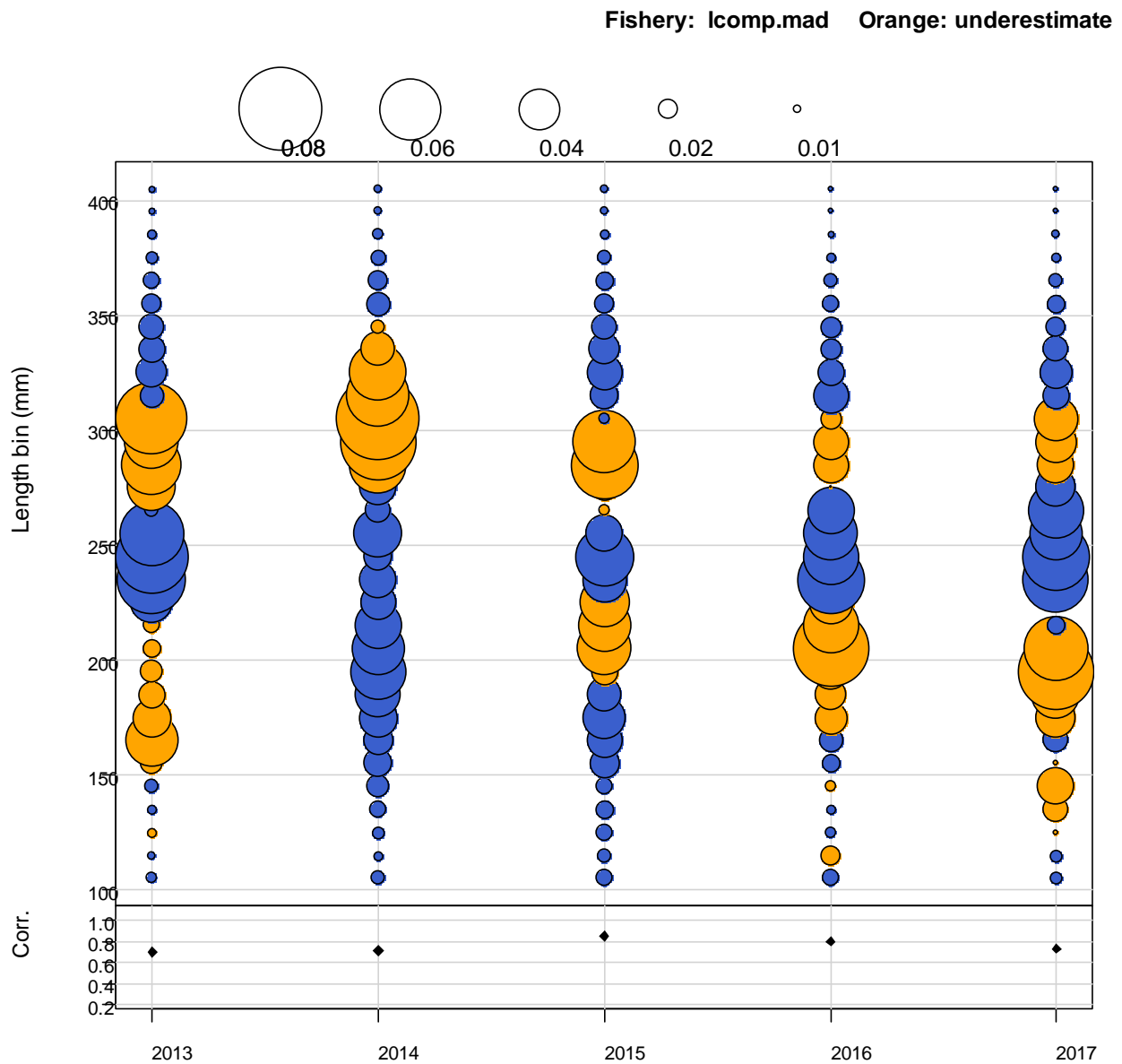
**Figure 135. Annual length composition fits for the MAD index for 2013-2017. Open circles indicate the observed data, while the solid line indicates predicted fits to the data. In the upper right corner of each panel there is the number of trips sampled, the effective sample size, and the year.**



**Figure 136. Pooled length compositions for the NAD (upper) and MAD (lower) indices. Pooling was done with no weighting.**



**Figure 137. Annual length composition fits for the NAD index for 1990-2017. Orange circles indicate an underestimate, while blue circles indicate an overestimate. The bottom panel contains the correlation between the observed and predicted data.**



**Figure 138. Annual length composition fits for the MAD index for 2013-2017. Orange circles indicate an underestimate, while blue circles indicate an overestimate. The bottom panel contains the correlation between the observed and predicted data.**



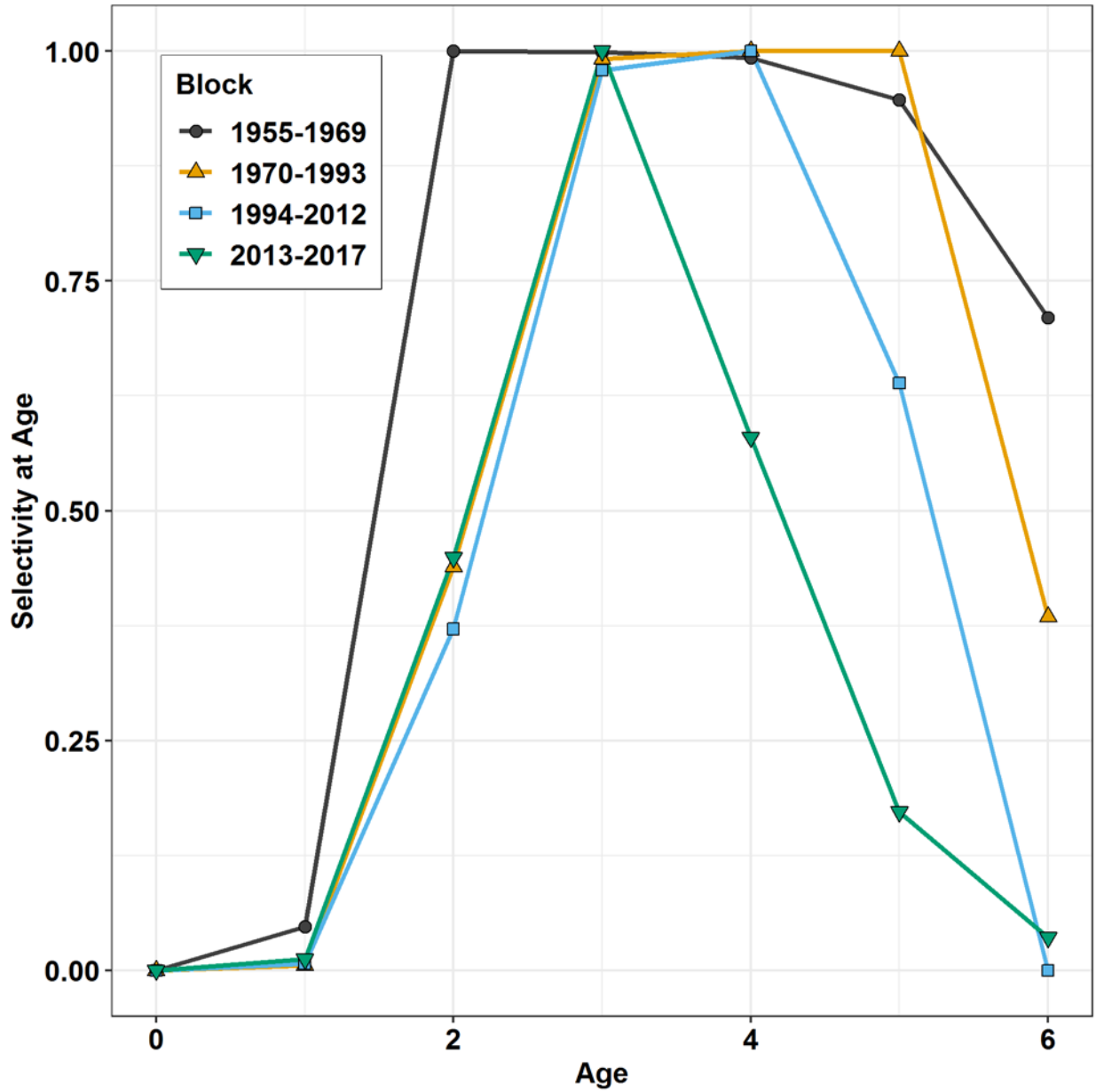


Figure 139. Selectivity-at-age for the commercial reduction fishery in the northern region. Each line indicates a time block (1955-1969, 1970-1993, 1994-2012, and 2013-2017).

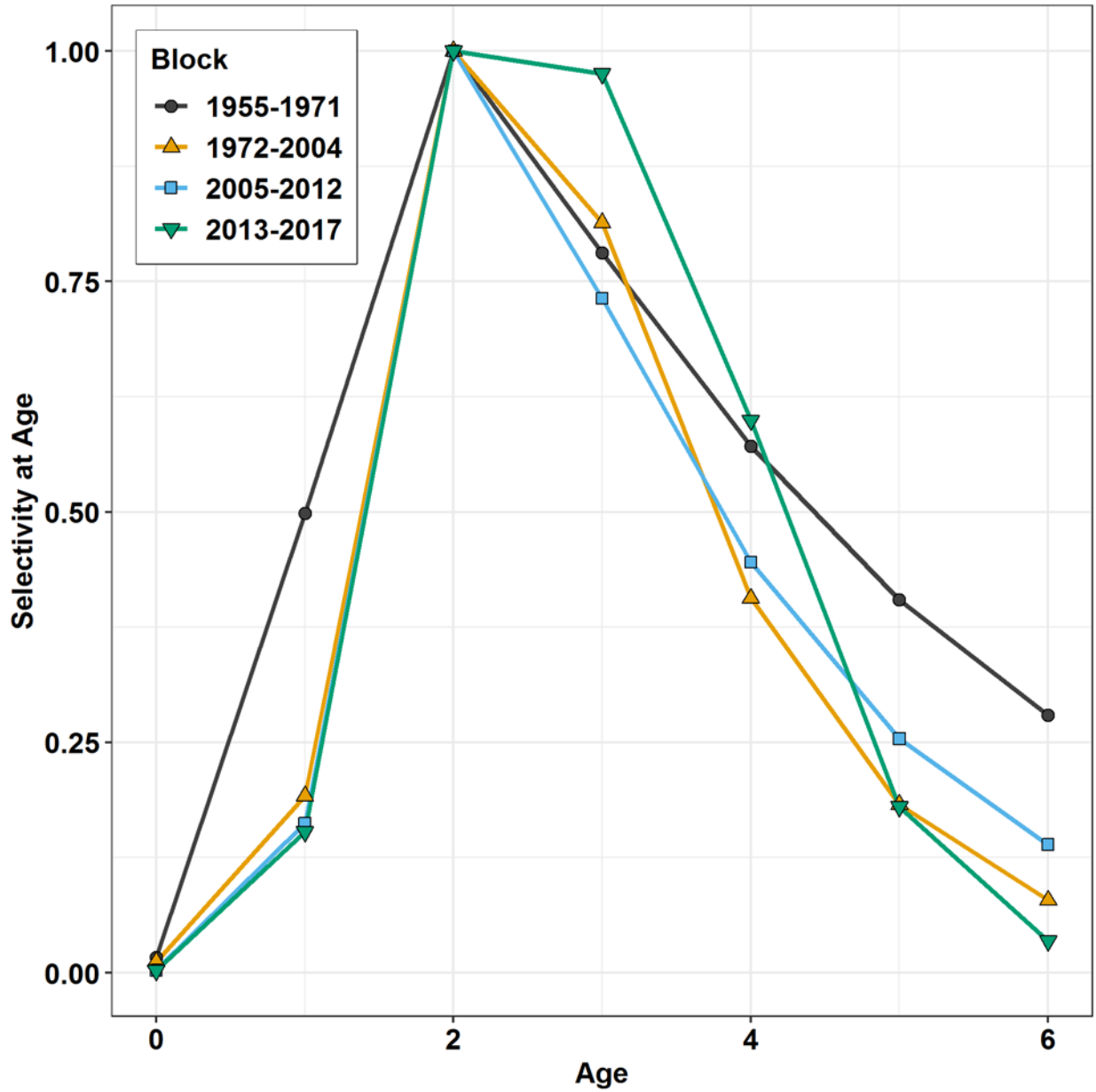


Figure 140. Selectivity-at-age for the commercial reduction fishery in the southern region. Each line indicates a time block (1955-1971, 1972-2004, 2005-2012, and 2013-2017).

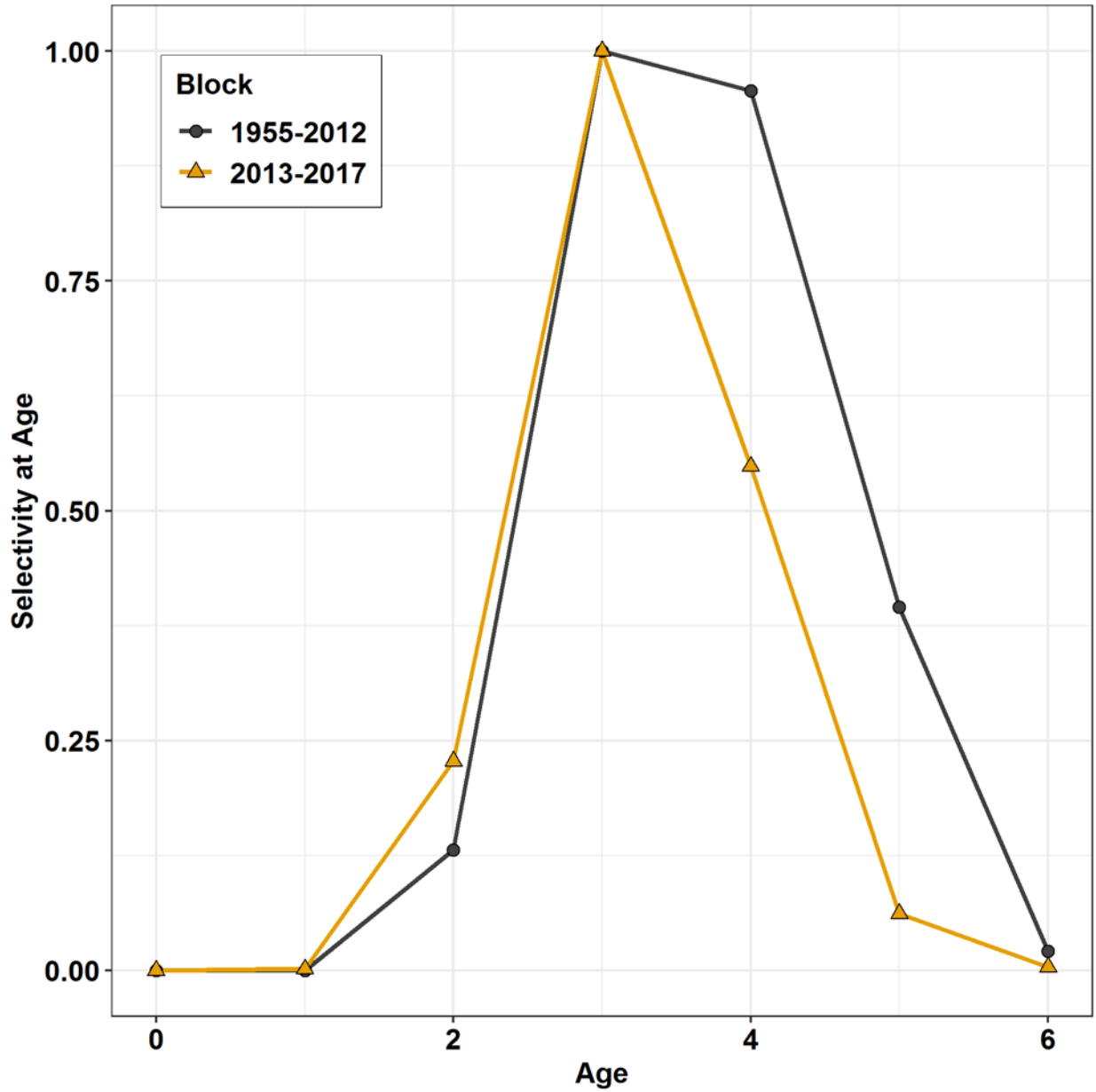


Figure 141. Selectivity-at-age for the commercial bait fishery in the northern region. Each line indicates a time block (1955-2012 and 2013-2017).

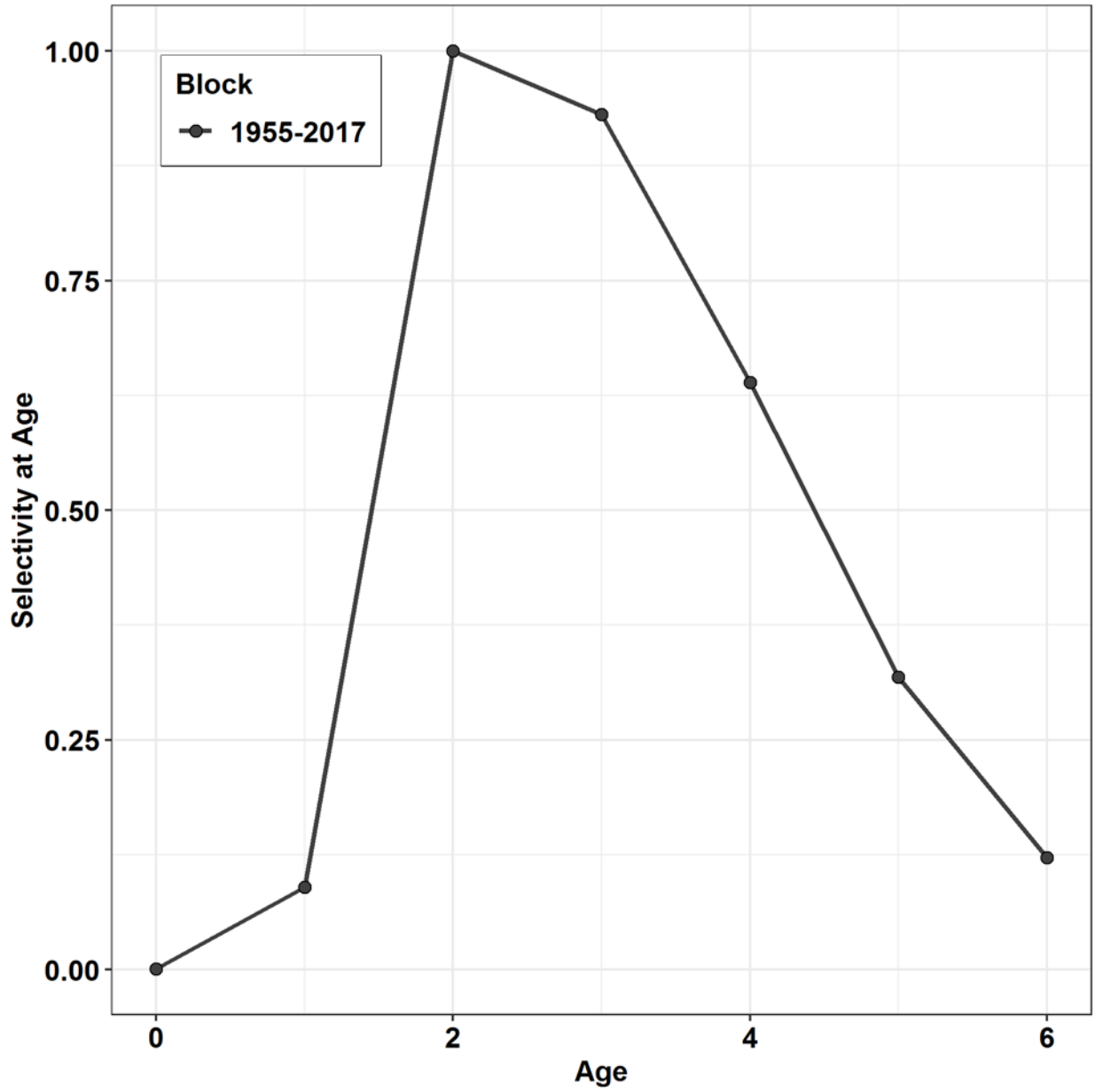
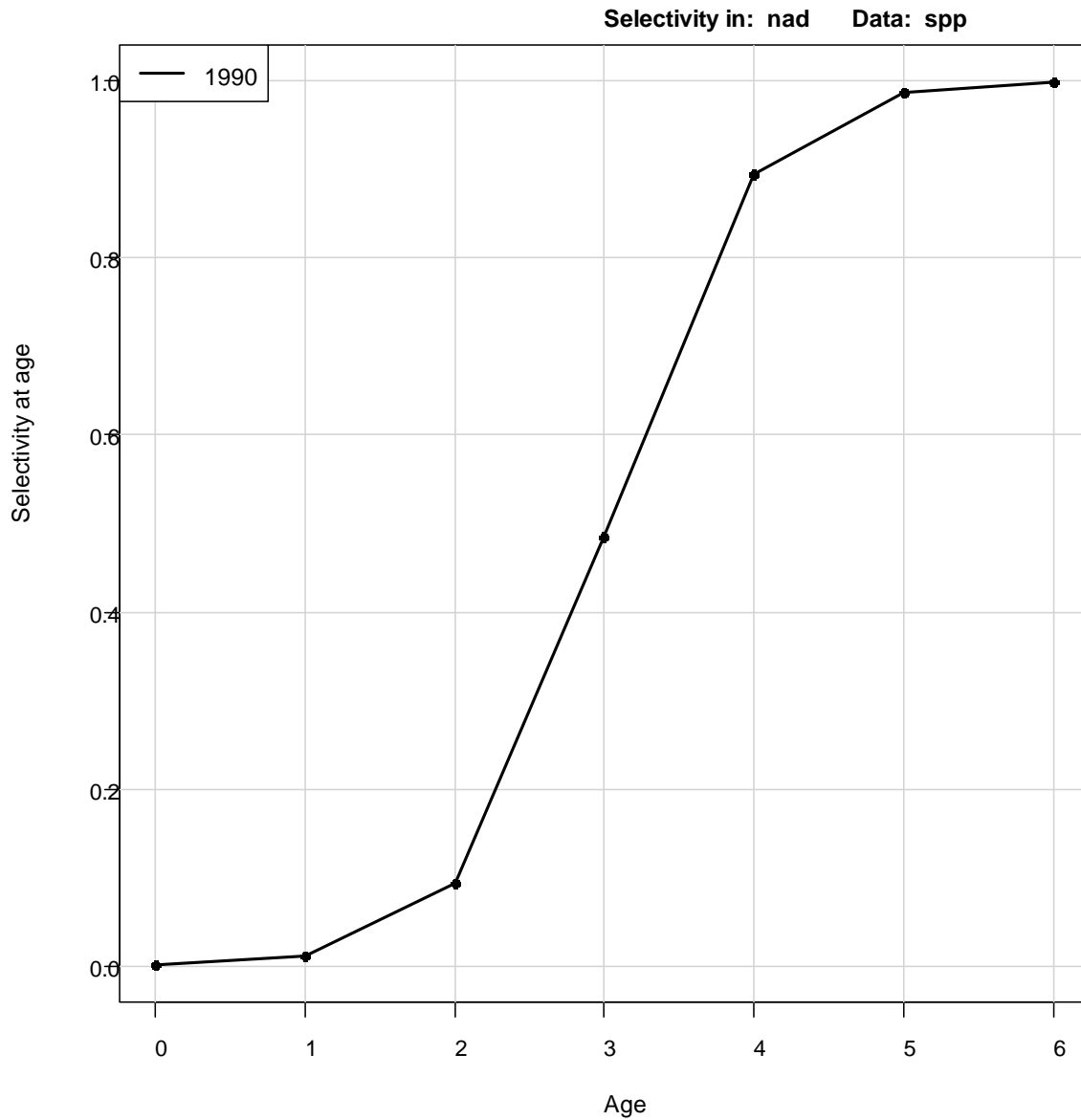
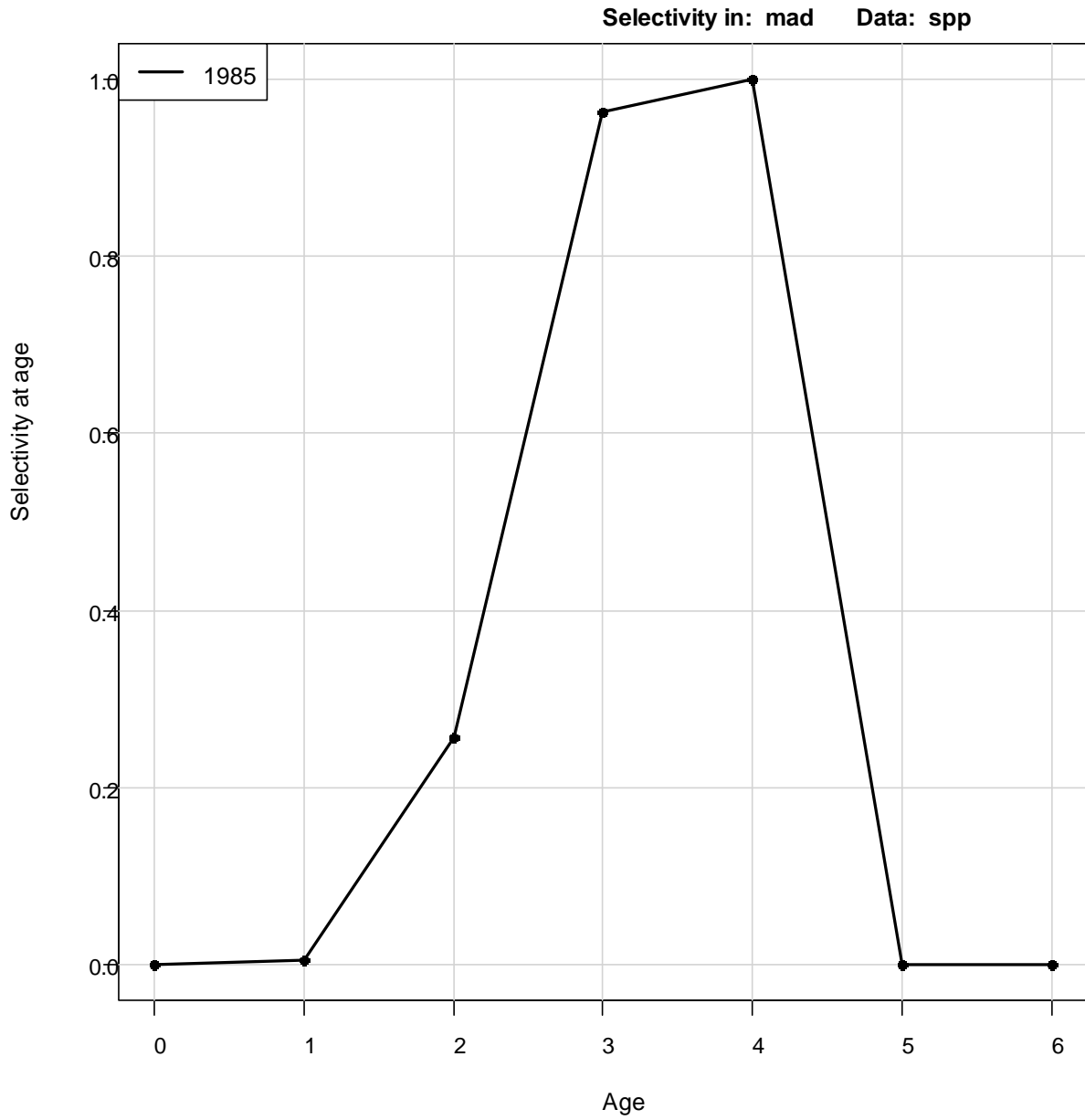


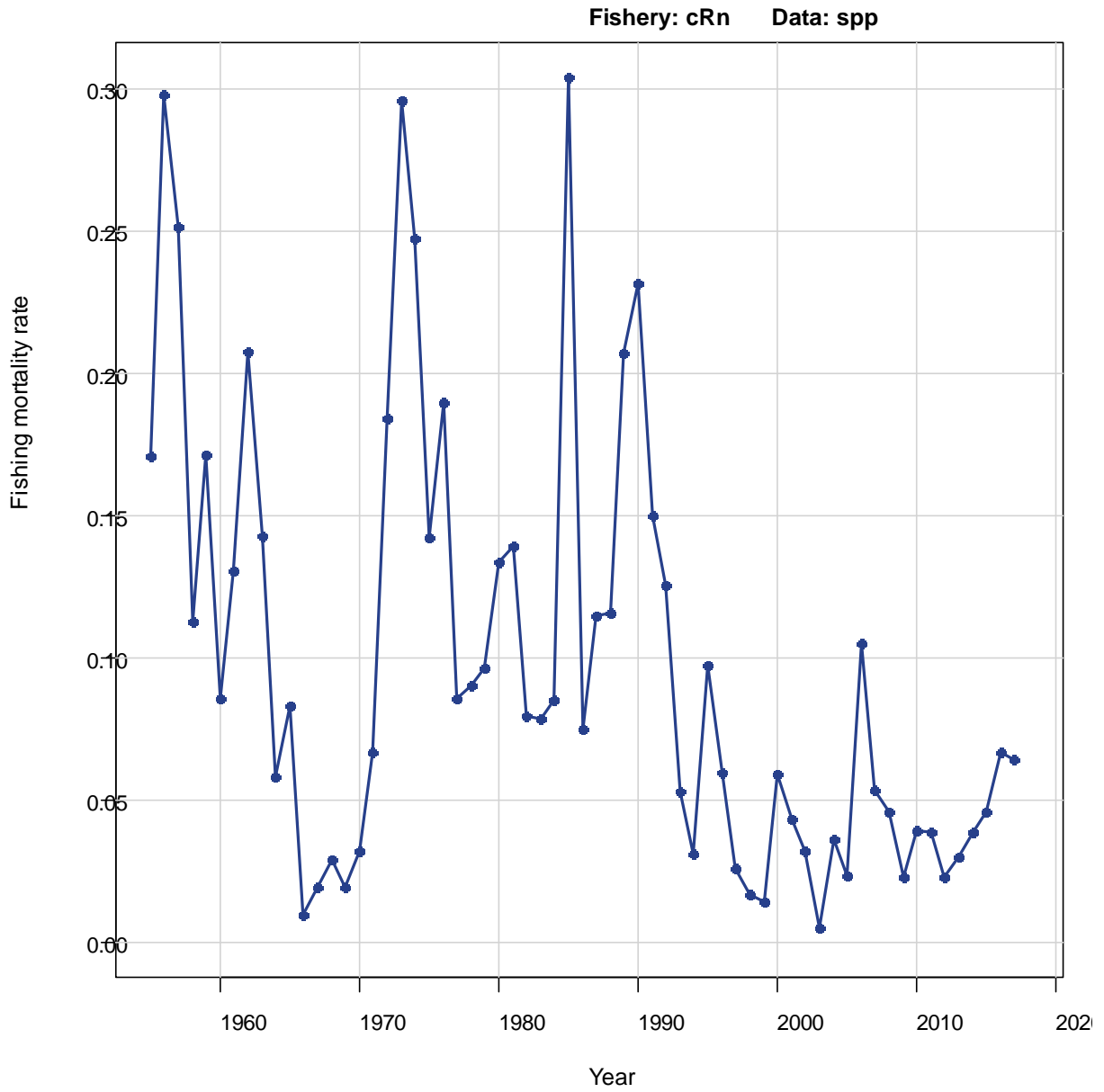
Figure 142. Selectivity-at-age for the commercial bait fishery in the southern region for 1955-2017.



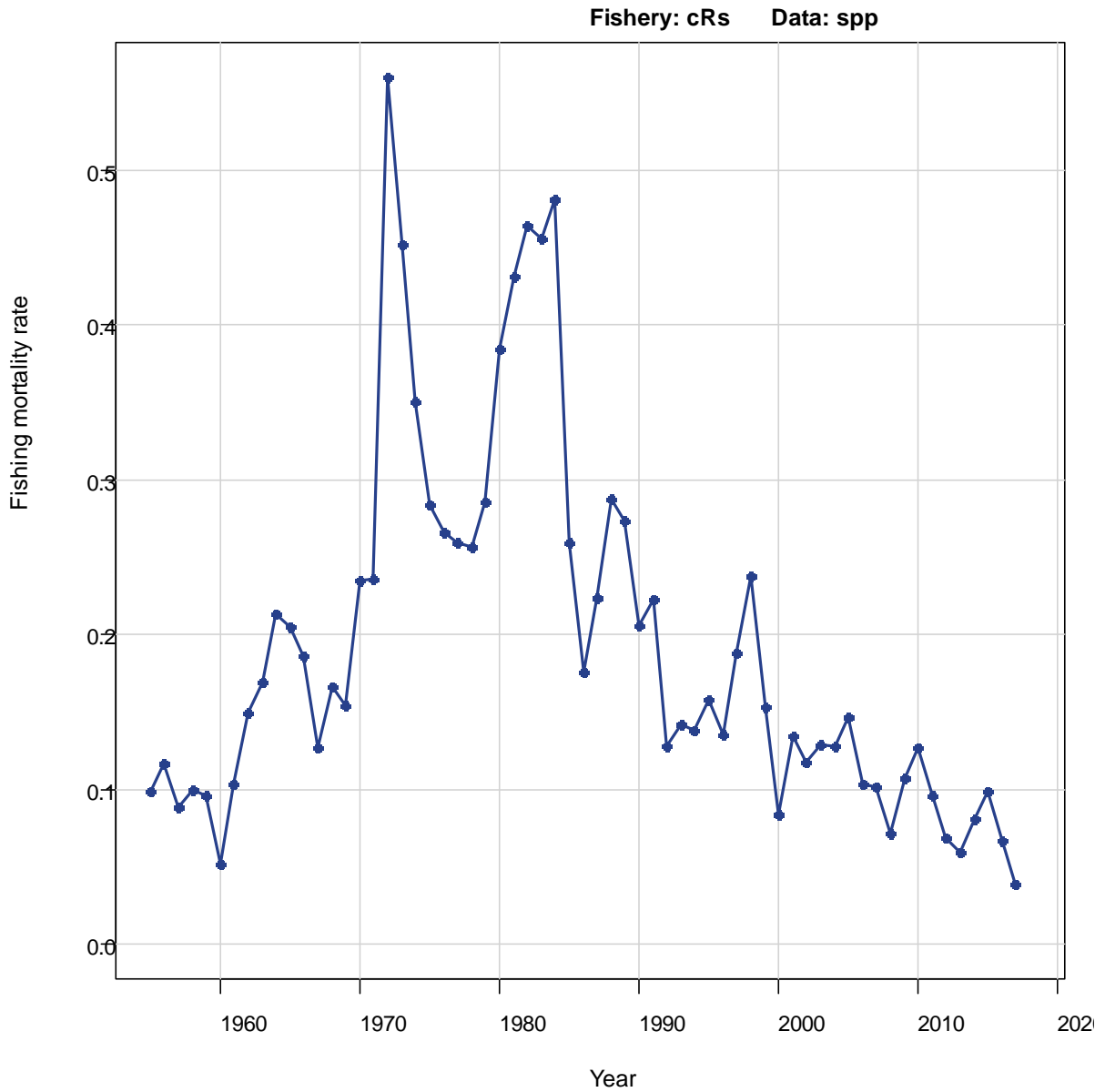
**Figure 143. Selectivity-at-age for the NAD index for 1990-2017.**



**Figure 144. Selectivity-at-age for the MAD index for 1985-2017.**

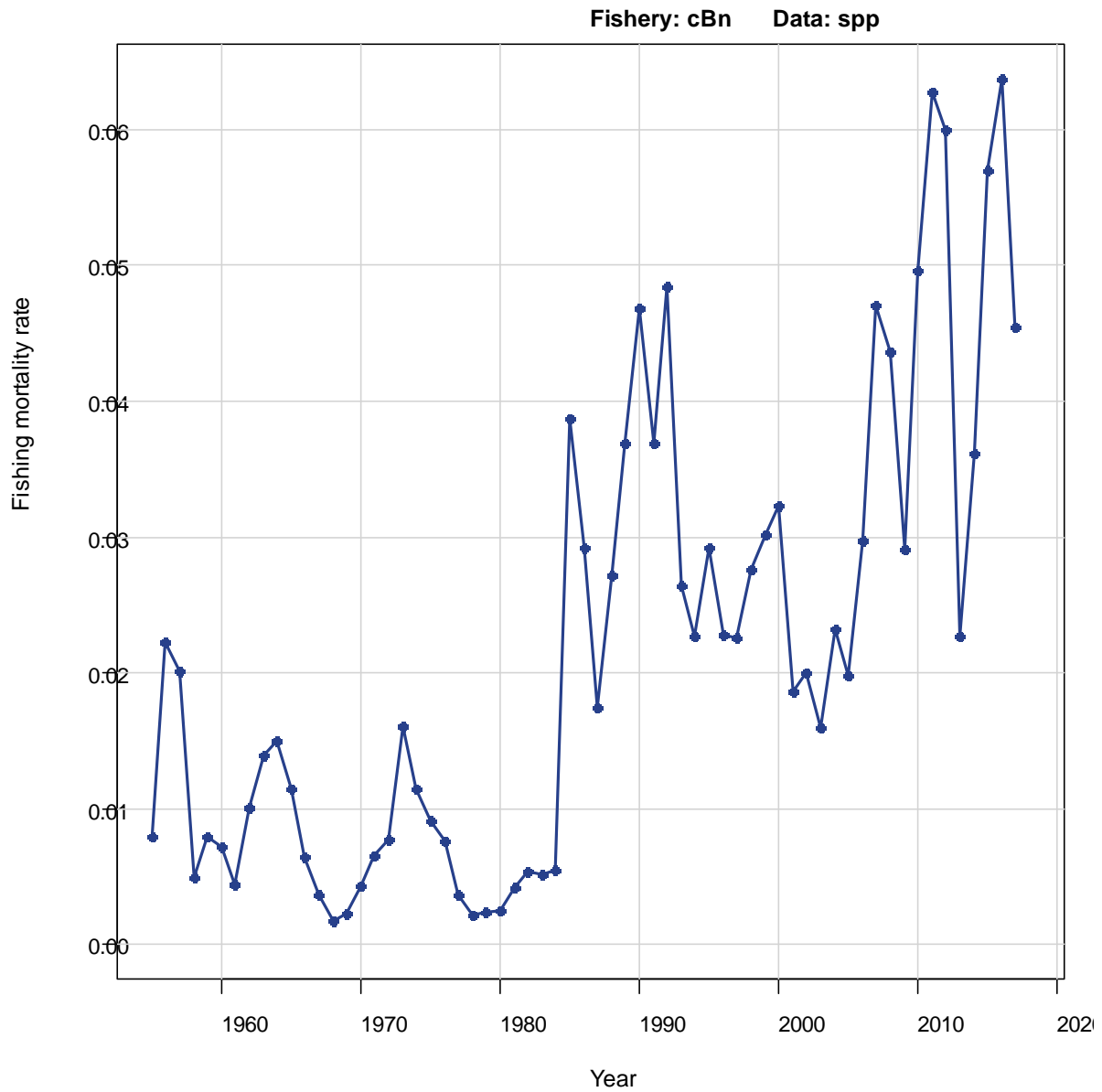


**Figure 145. Full fishing mortality rate for the northern commercial reduction fishery for 1955-2017.**

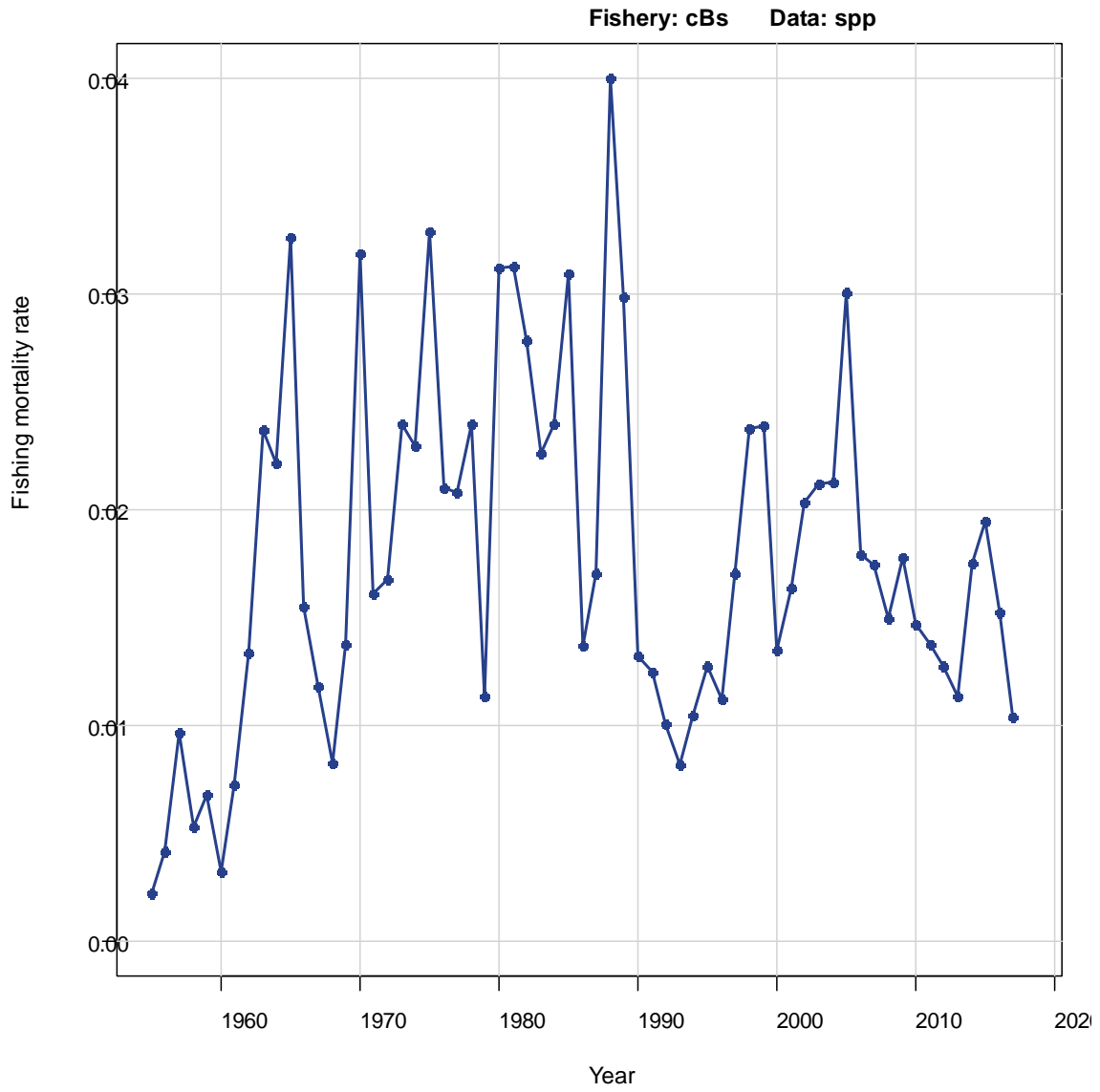


**Figure 146. Full fishing mortality rate for the southern commercial reduction fishery for 1955-2017.**





**Figure 147. Full fishing mortality rate for the northern commercial bait fishery for 1955-2017.**



**Figure 148. Full fishing mortality rate for the southern commercial bait fishery for 1955-2017.**

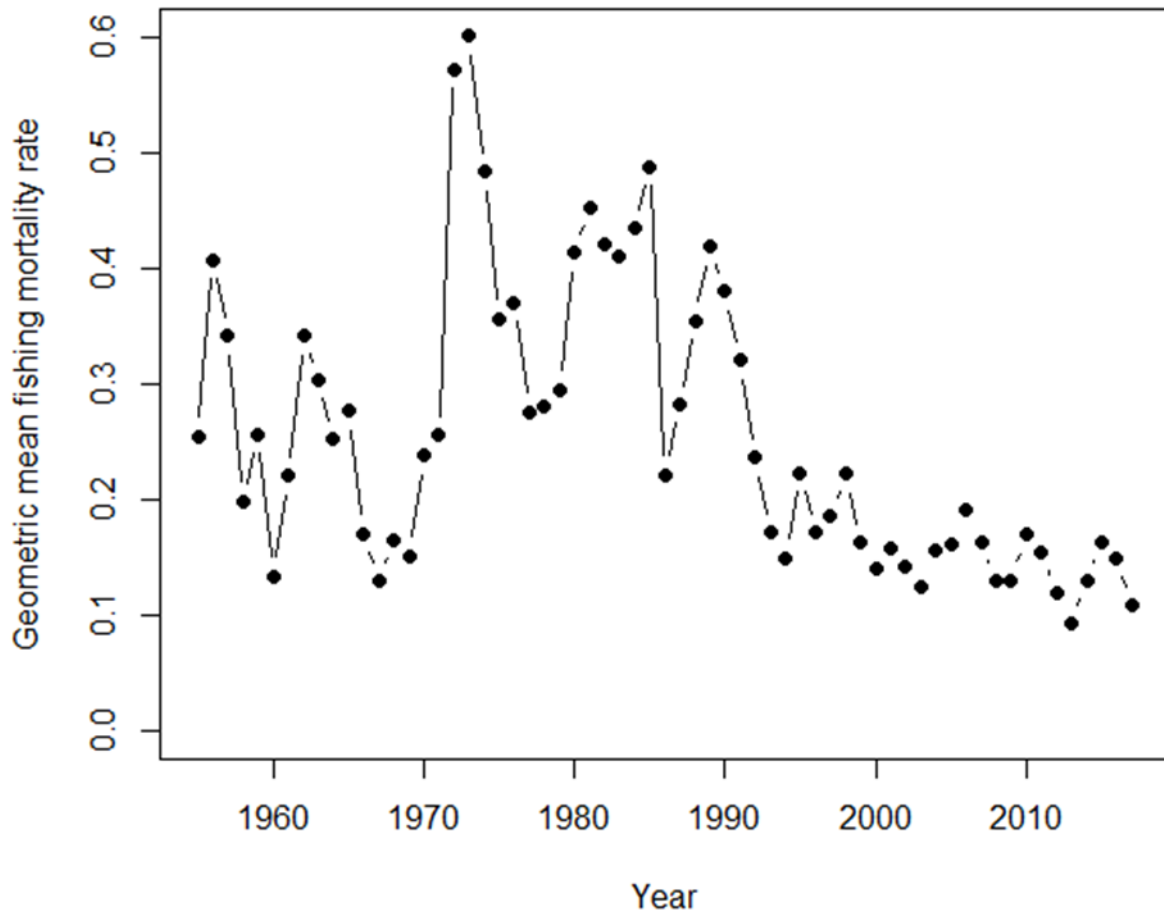
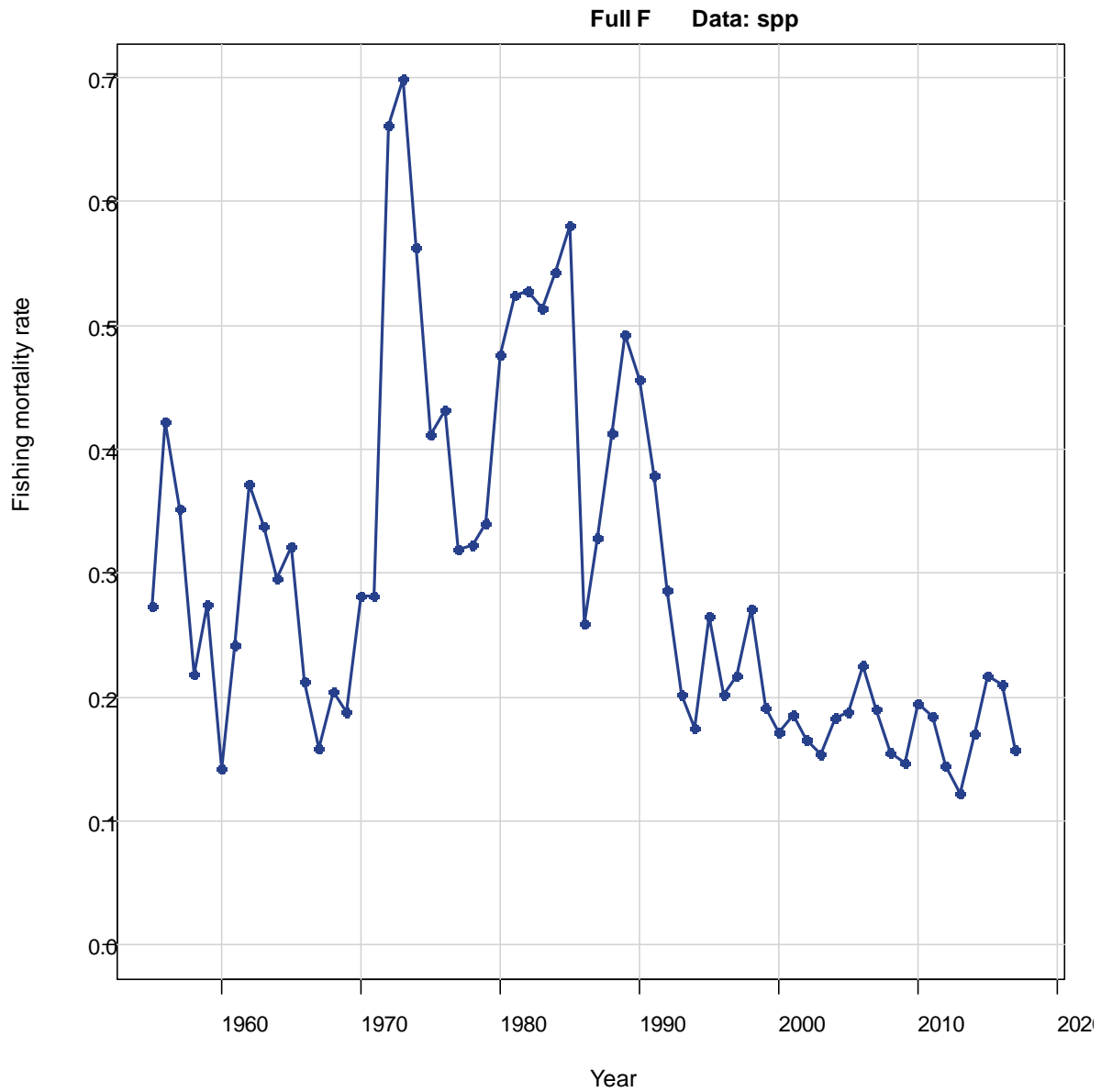
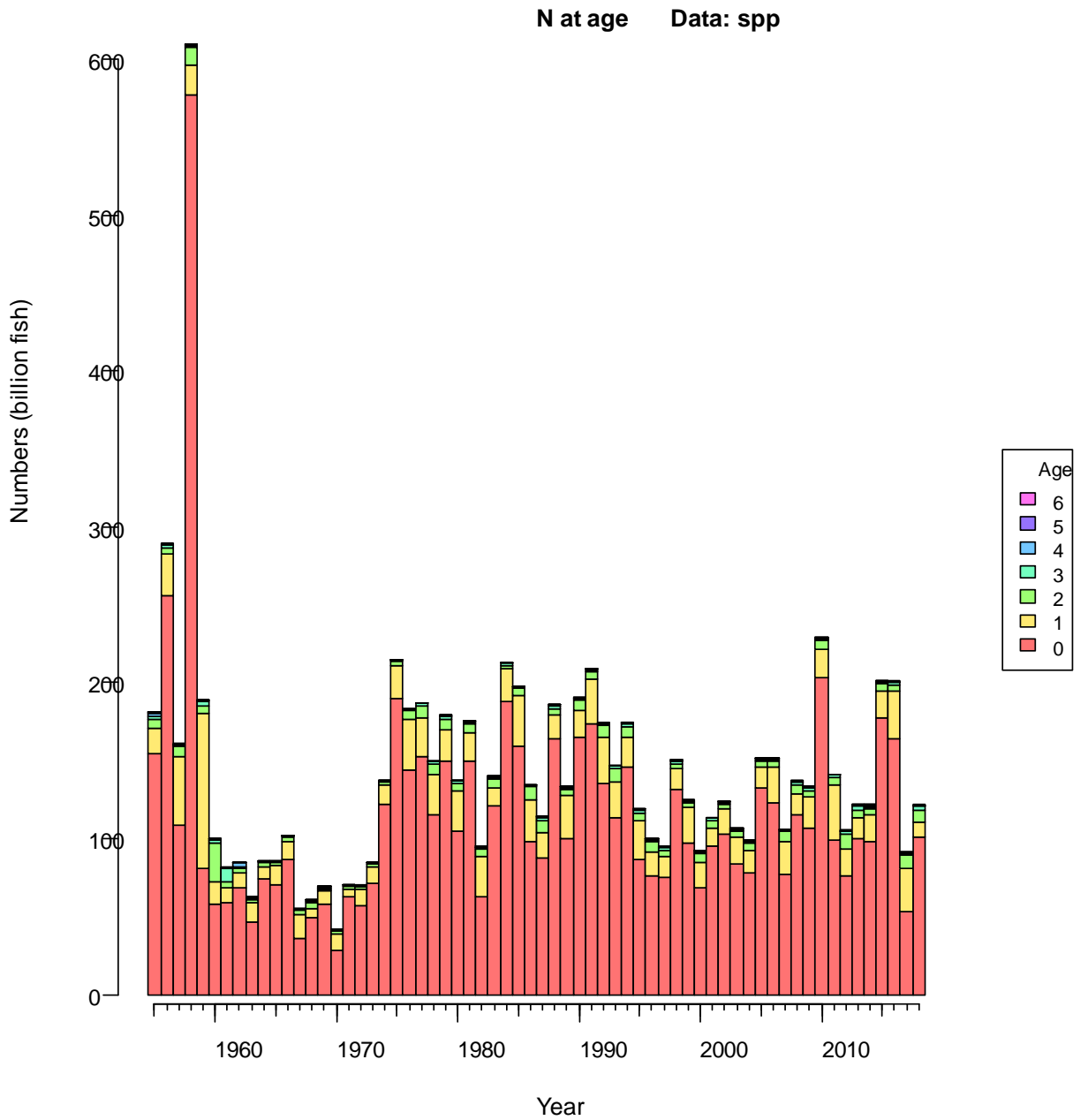


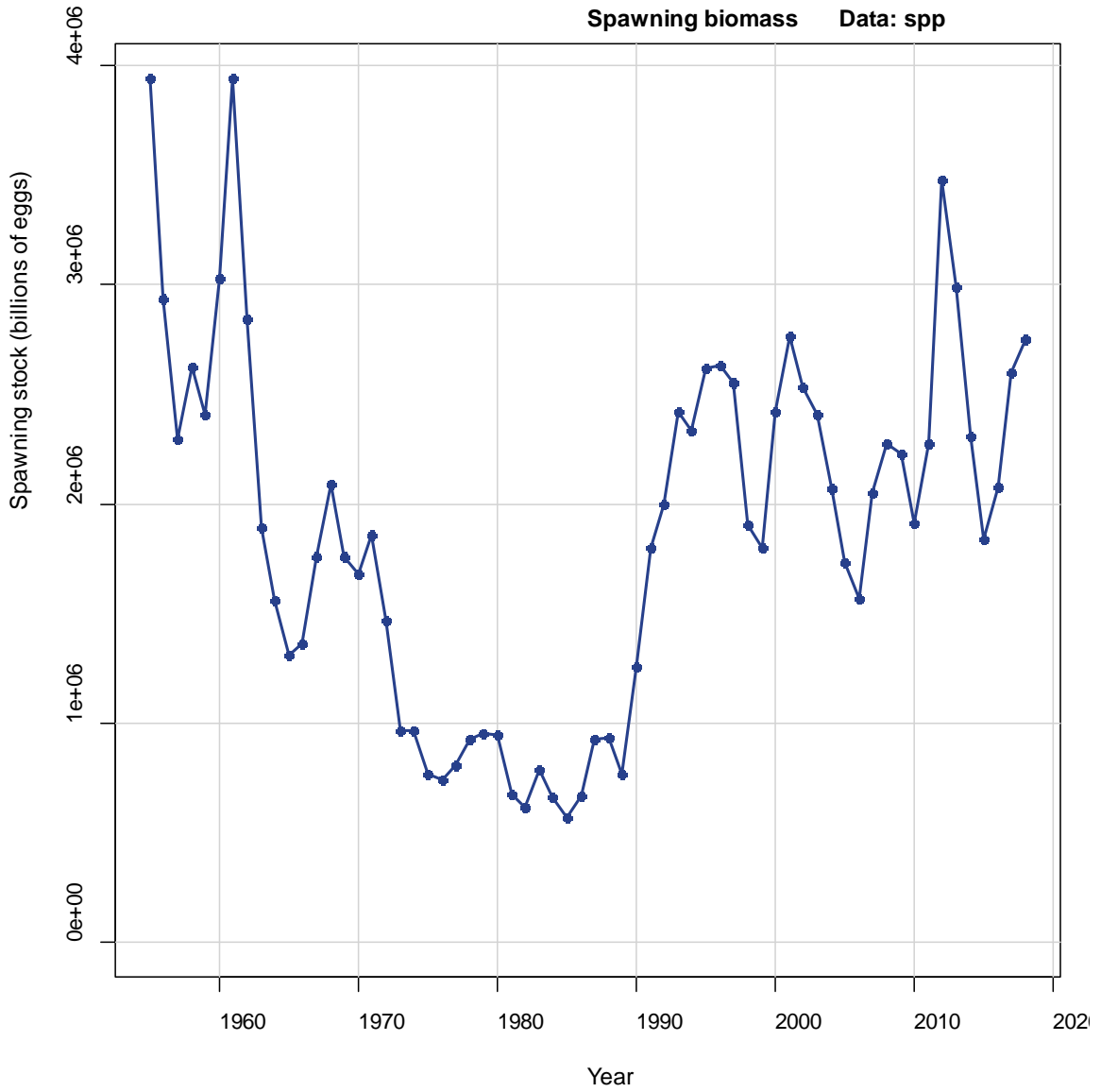
Figure 149. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017.



**Figure 150. Full fishing mortality rate for the Atlantic menhaden population for 1955-2017.**



**Figure 151. Number of fish by age in the population at the start of the year for 1955-2017.**



**Figure 152. Fecundity (billions of eggs) for the Atlantic menhaden population for 1955-2017.**

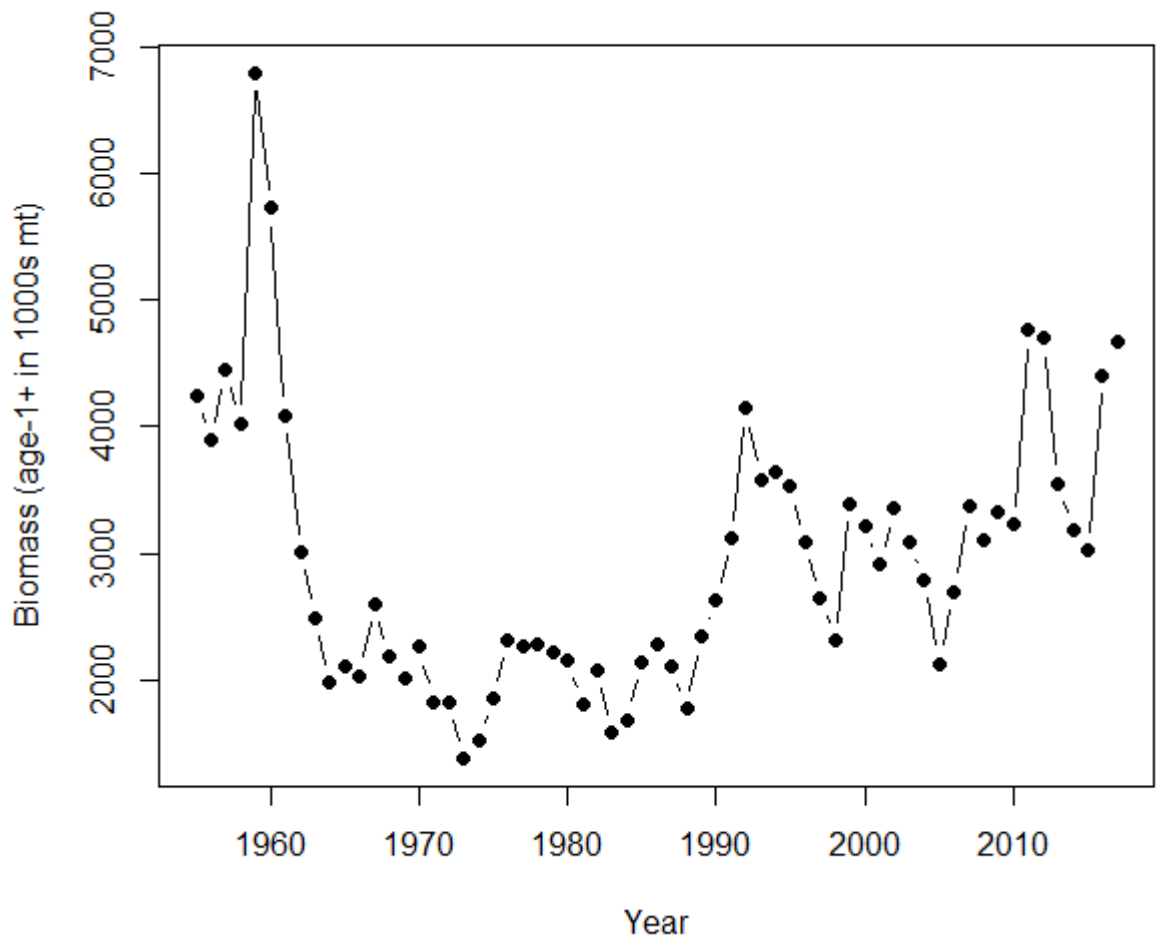
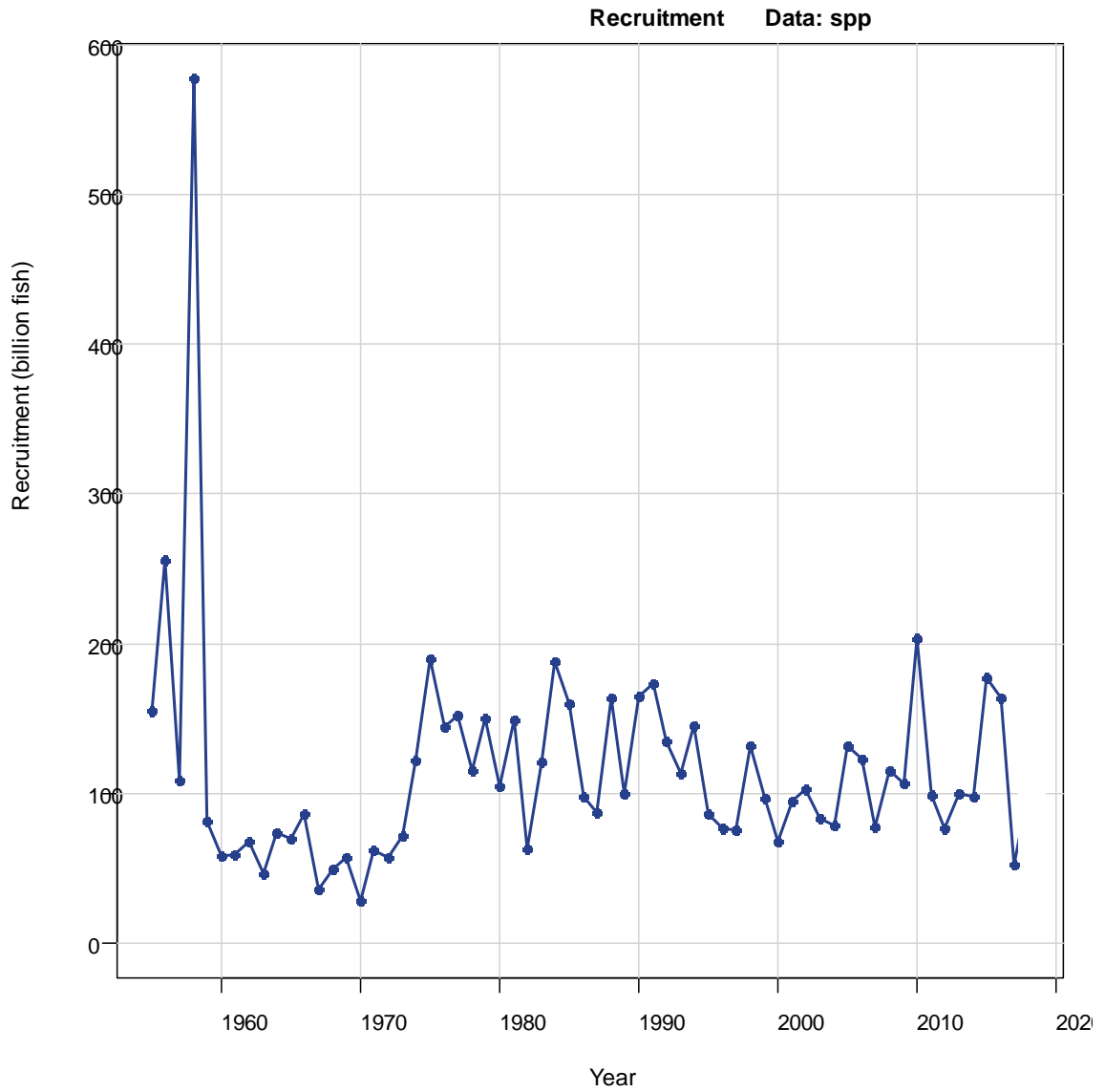
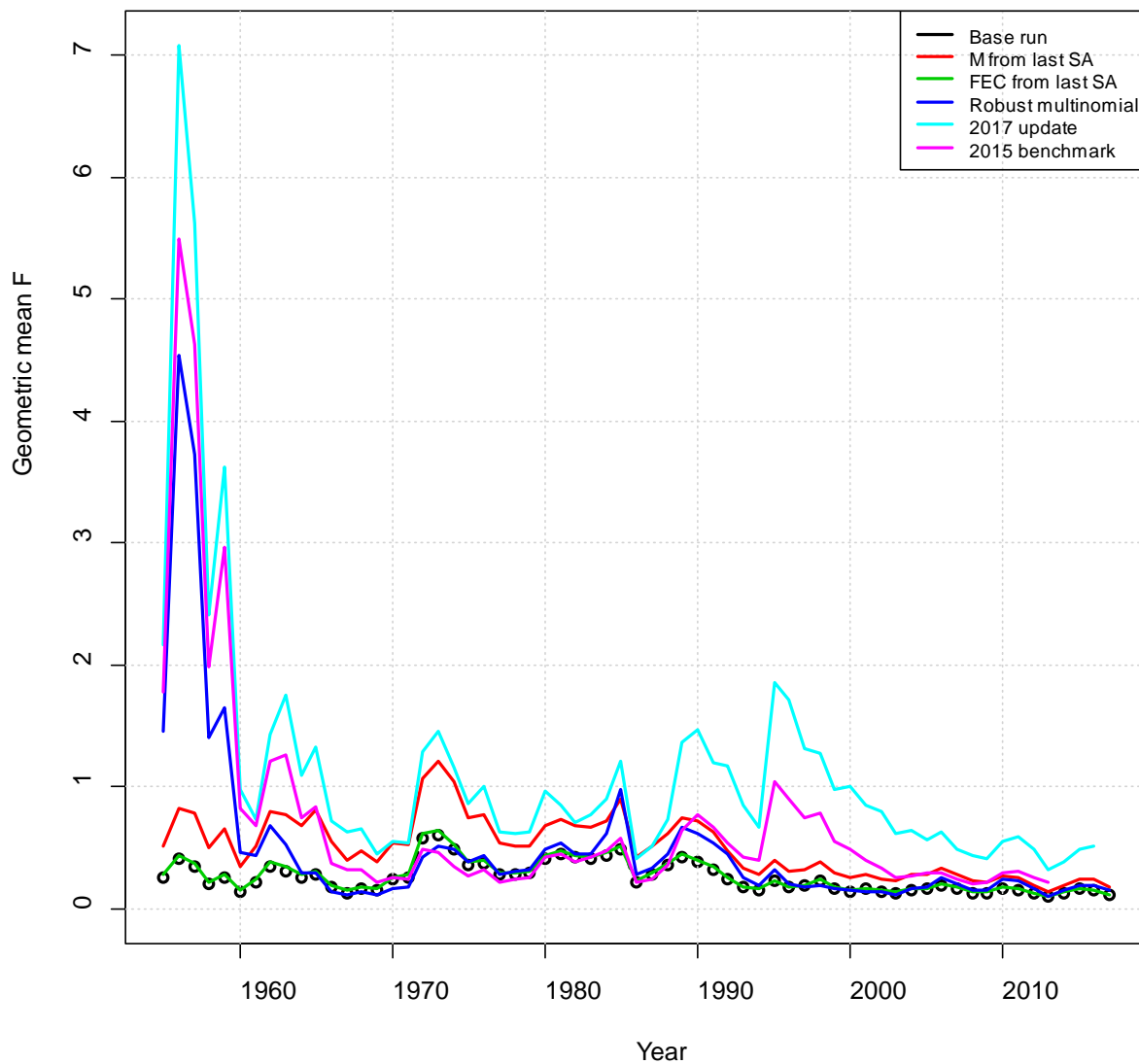


Figure 153. Age-1+ biomass in 1000s of mt for Atlantic menhaden during 1955-2017.

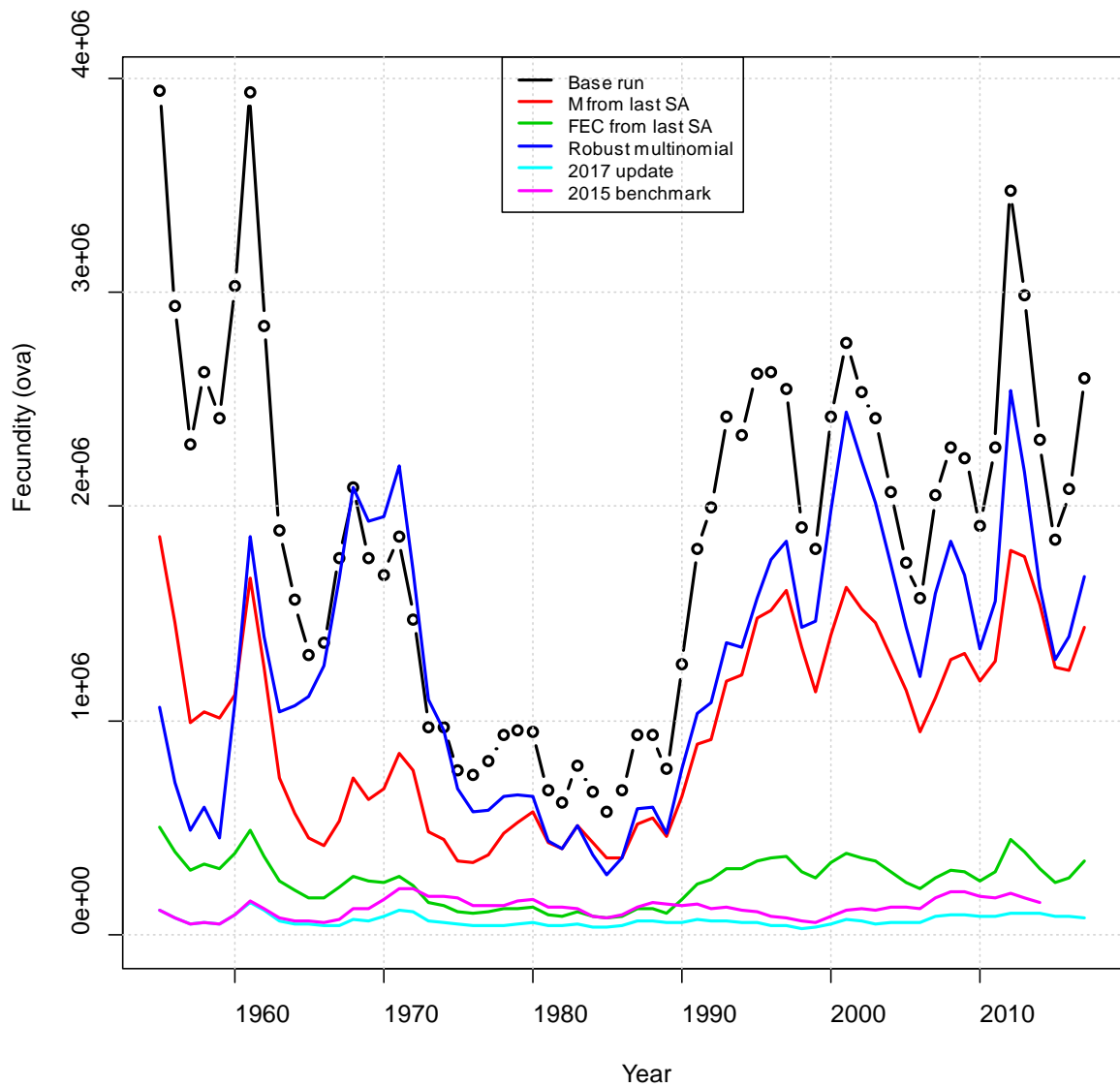


**Figure 154. Recruitment in billions of fish during 1955-2017.**

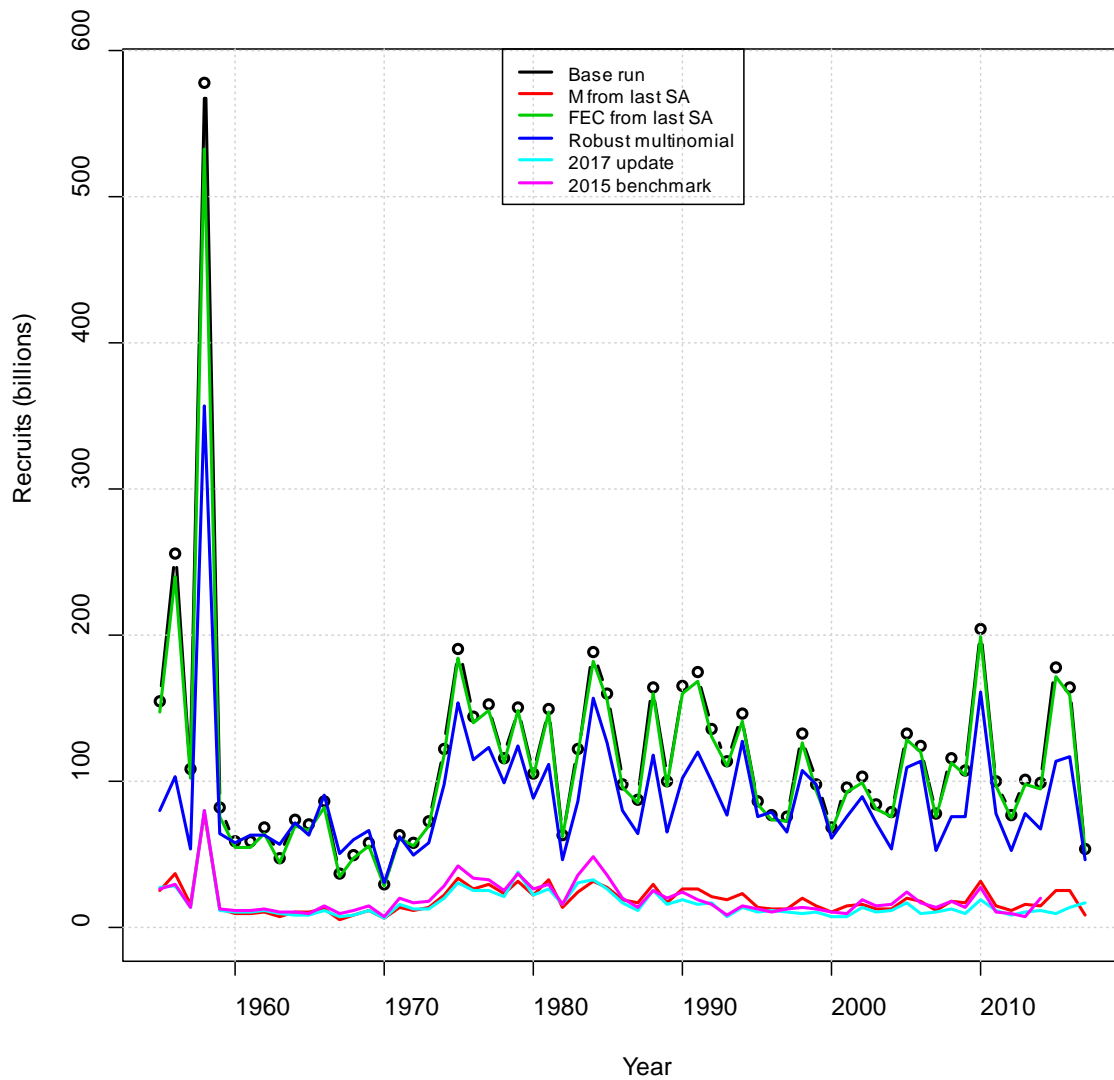




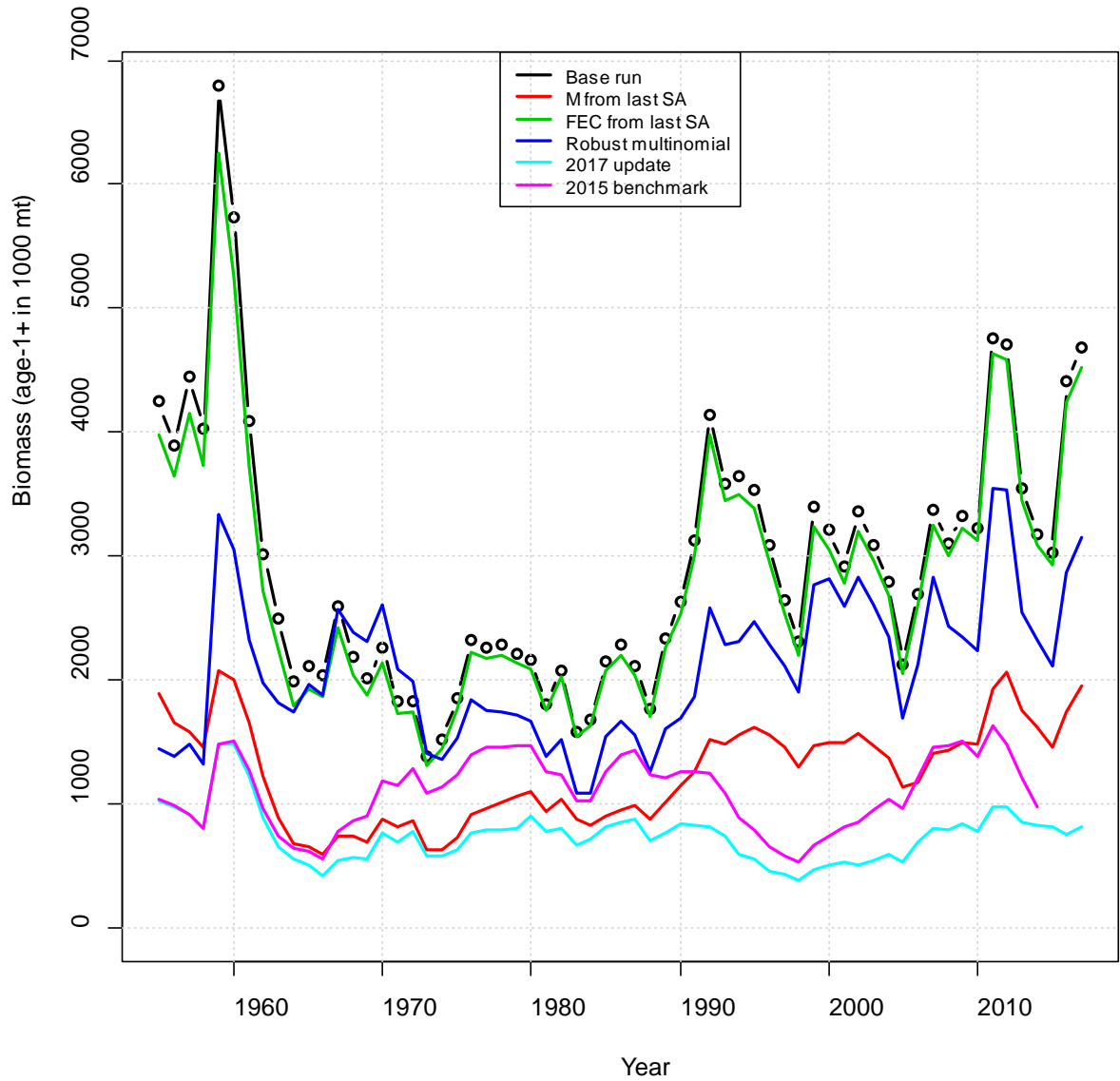
**Figure 155. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015). The previous update and benchmark assessment runs are included in these figures.**



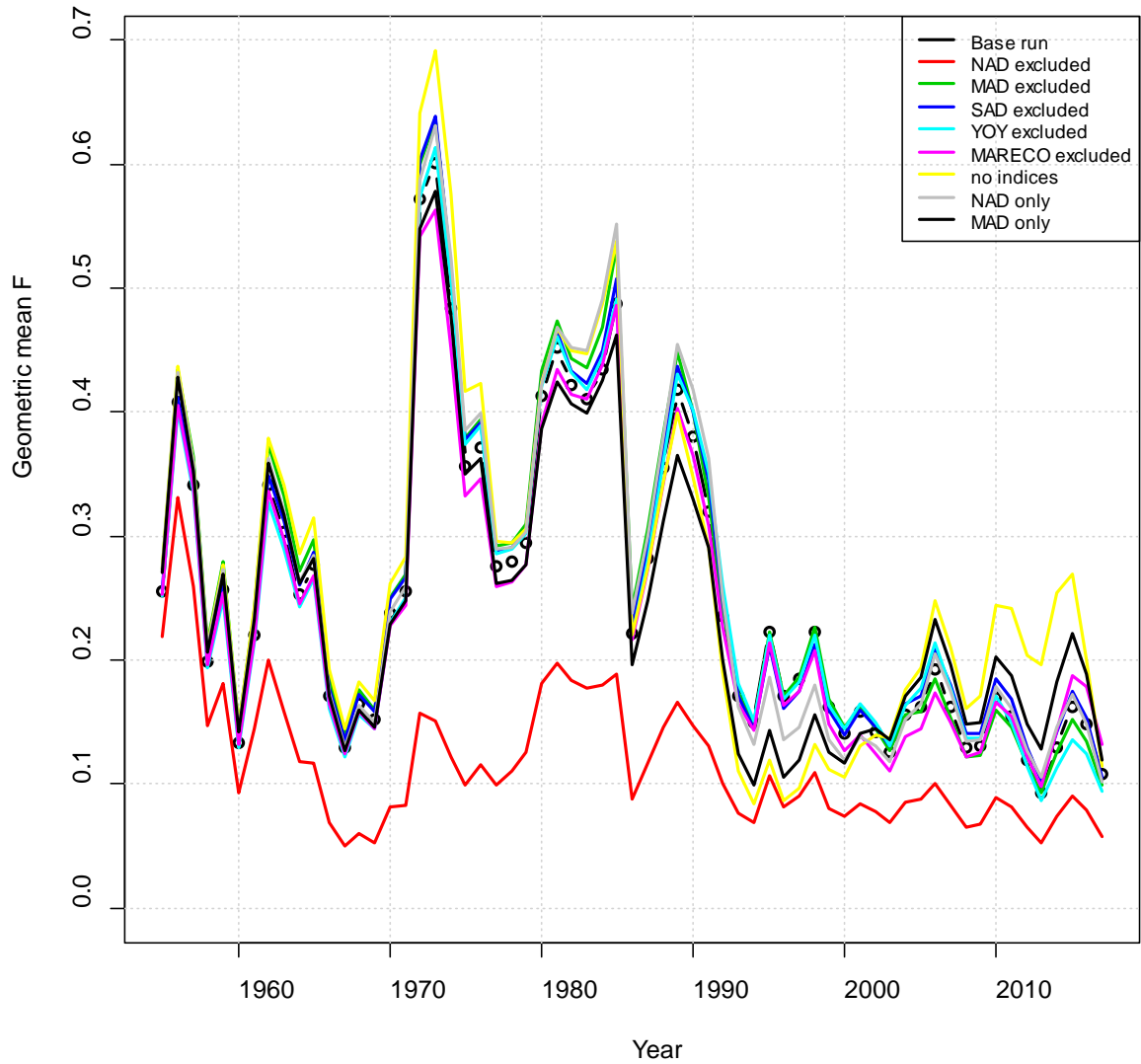
**Figure 156. Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015). The previous update and benchmark assessment runs are included in these figures.**



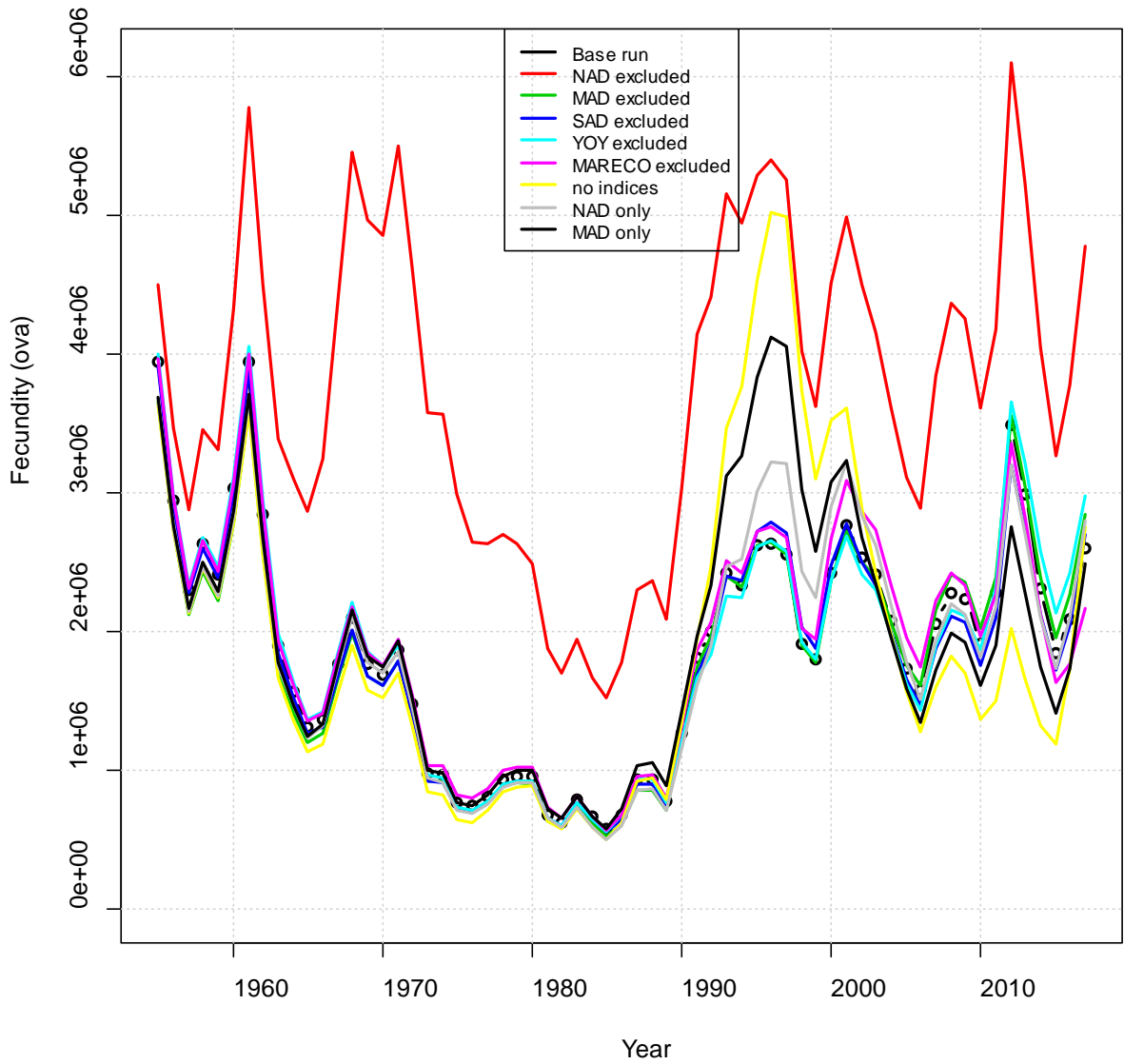
**Figure 157. Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015). The previous update and benchmark assessment runs are included in these figures.**



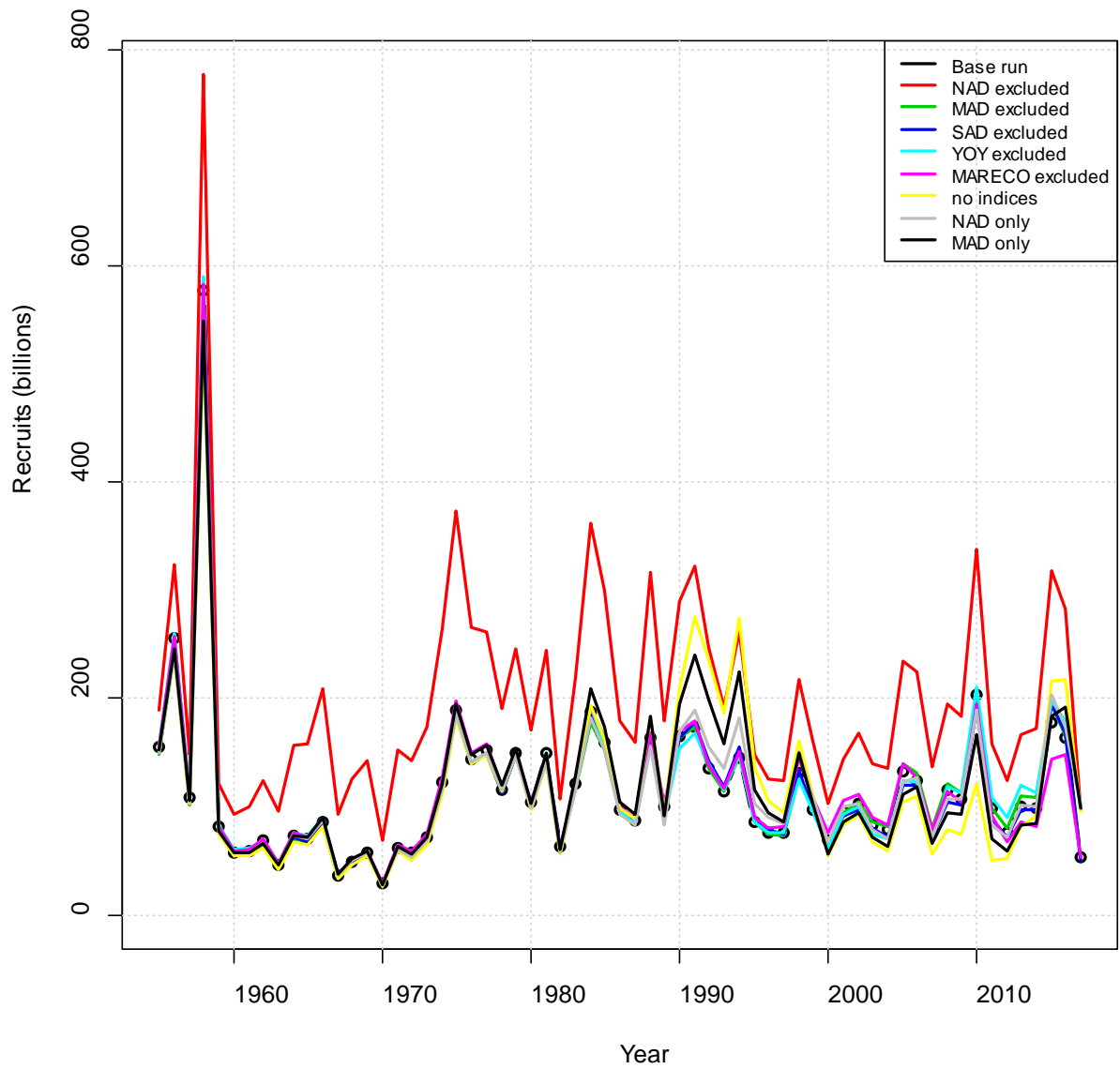
**Figure 158. Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored continuity with the base run for SEDAR 40 (2015). The previous update and benchmark assessment runs are included in these figures.**



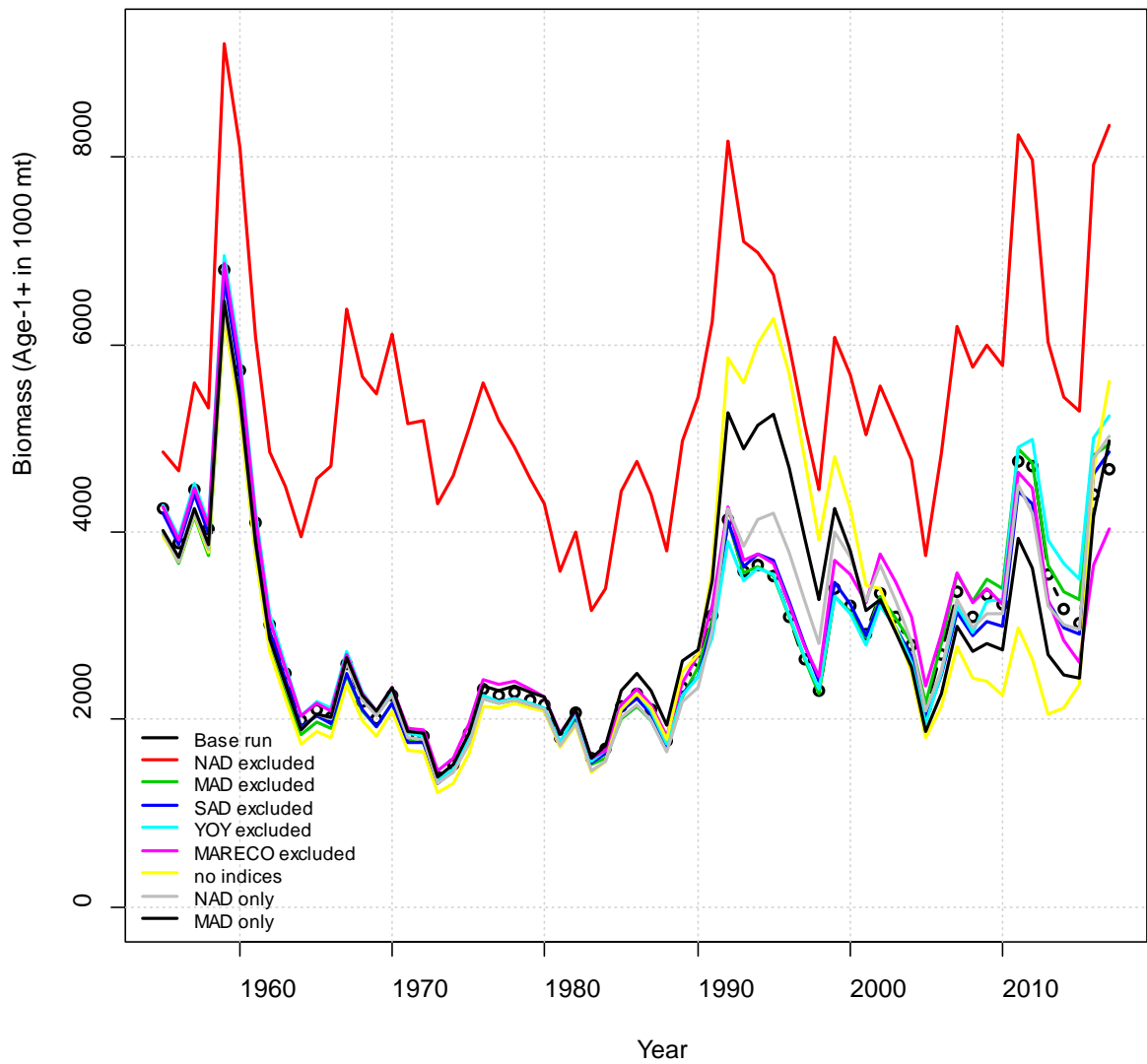
**Figure 159. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices.**



**Figure 160. Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices.**

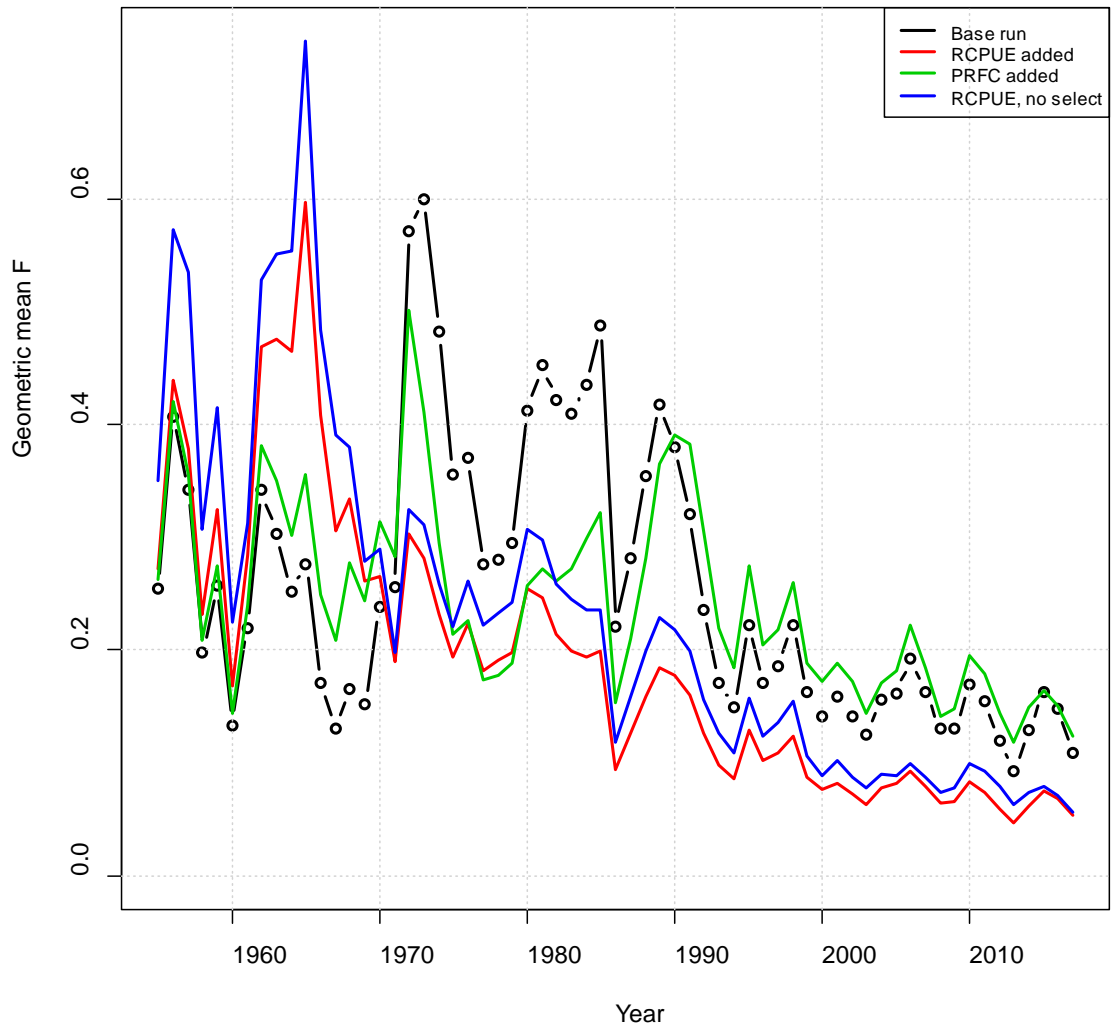


**Figure 161. Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices.**

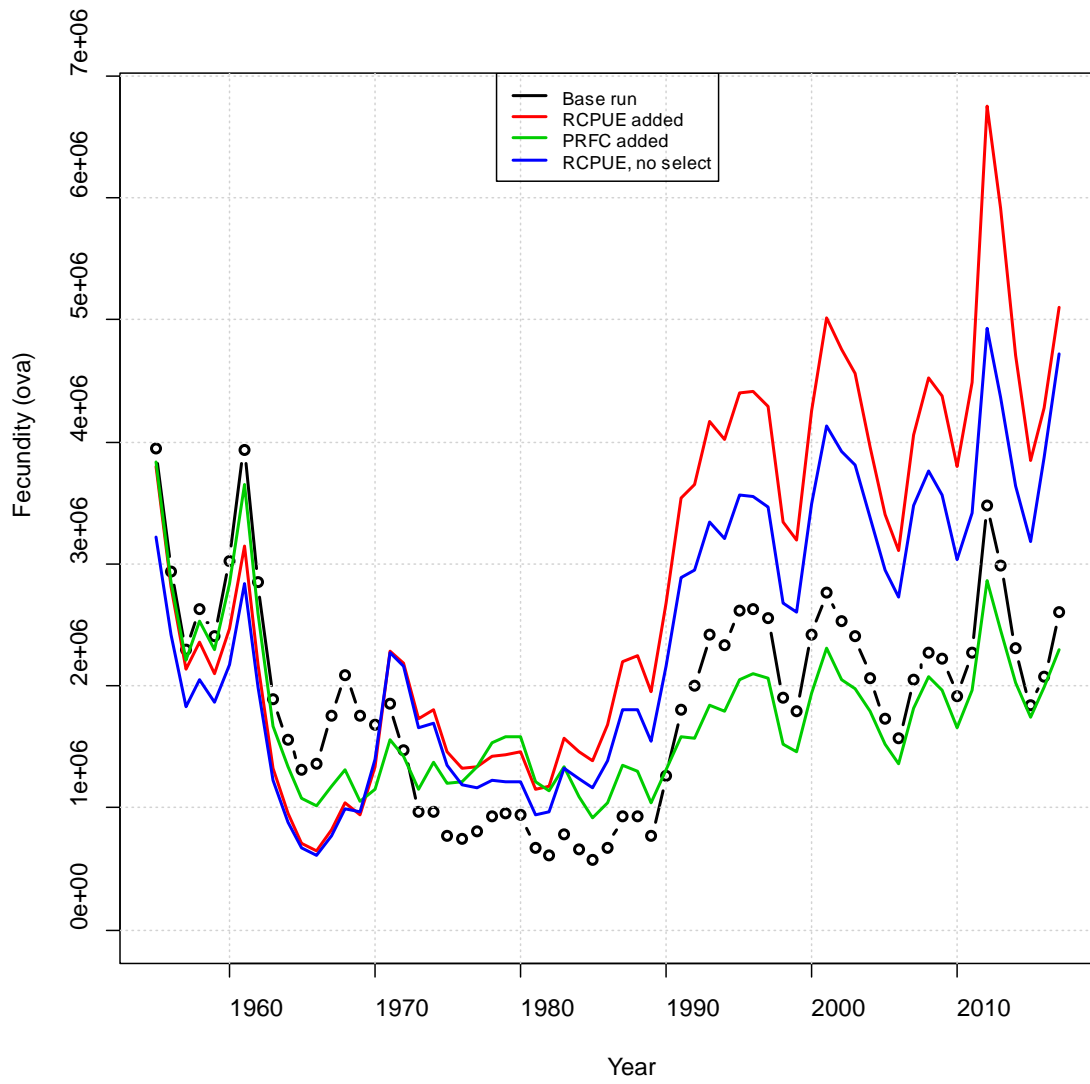


**Figure 162. Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices.**

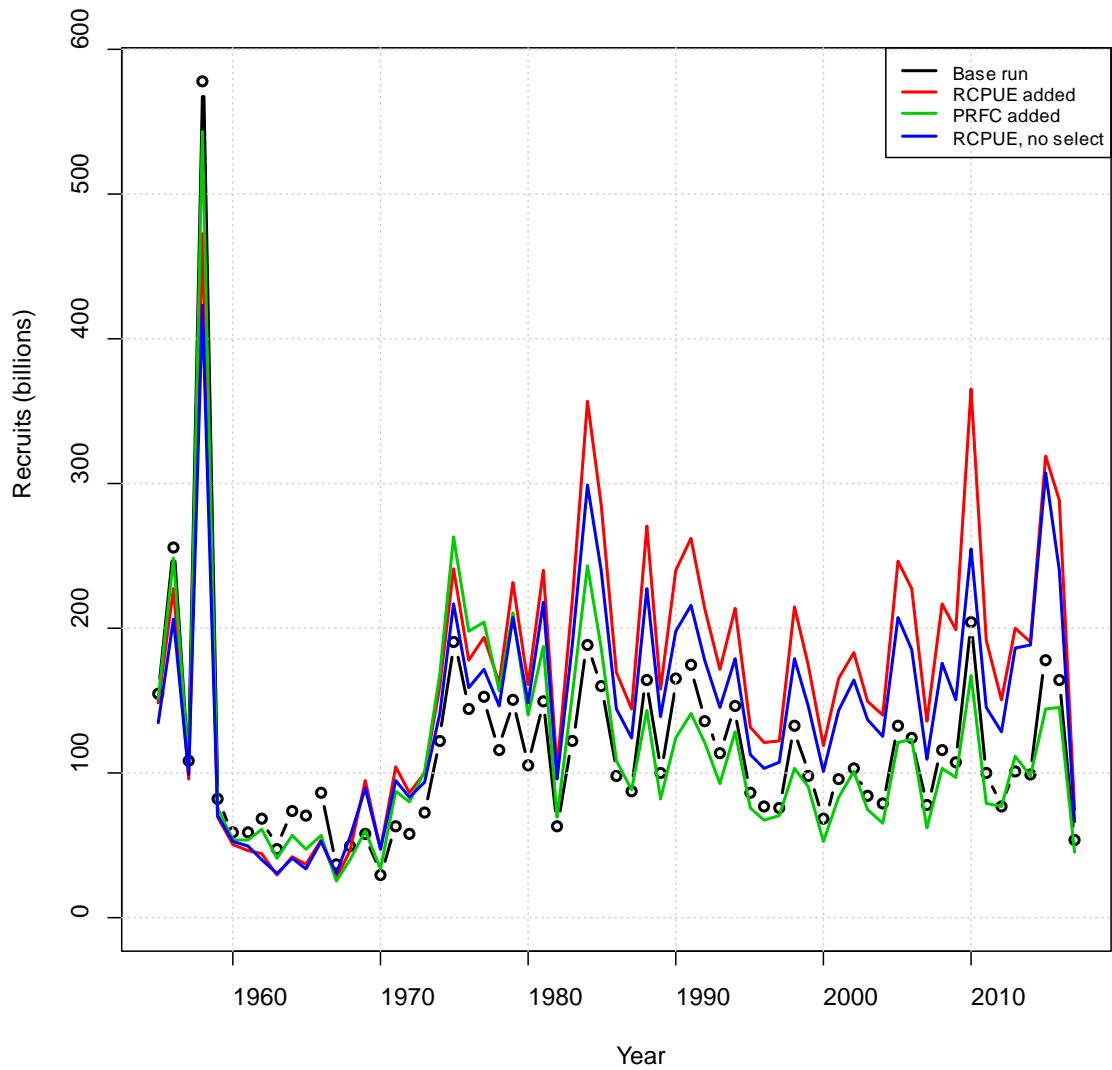




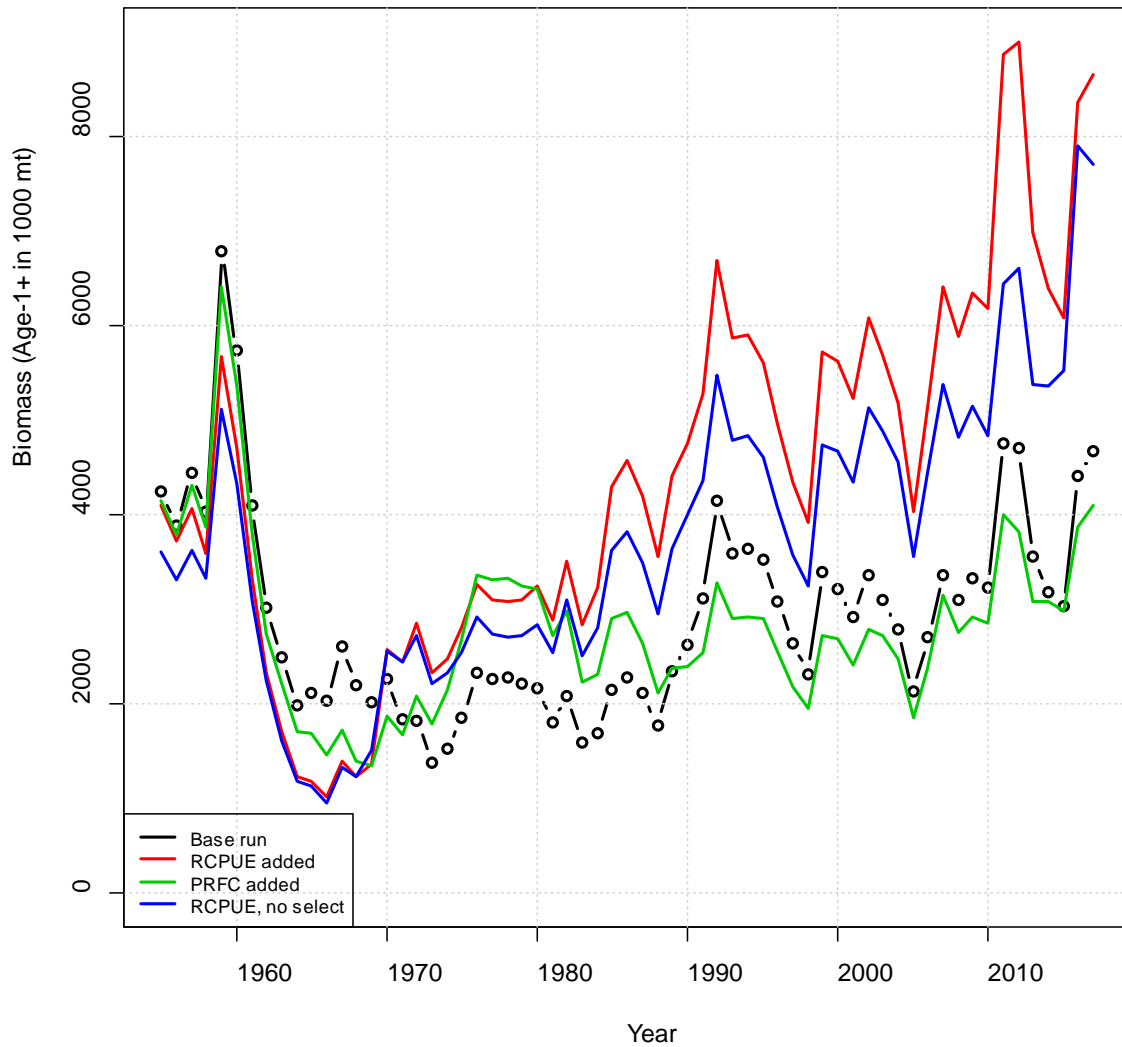
**Figure 163. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019).**



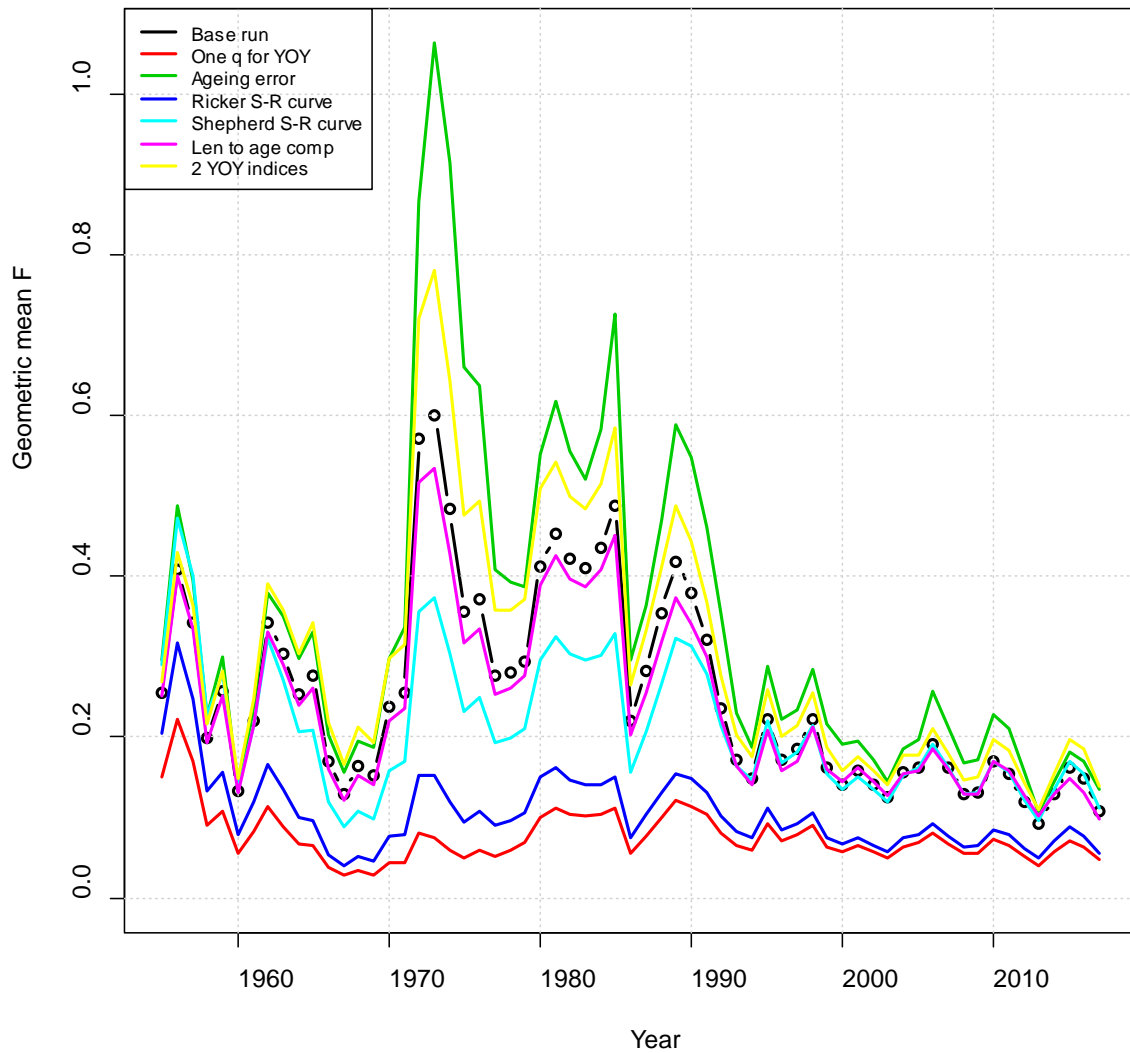
**Figure 164. Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019).**



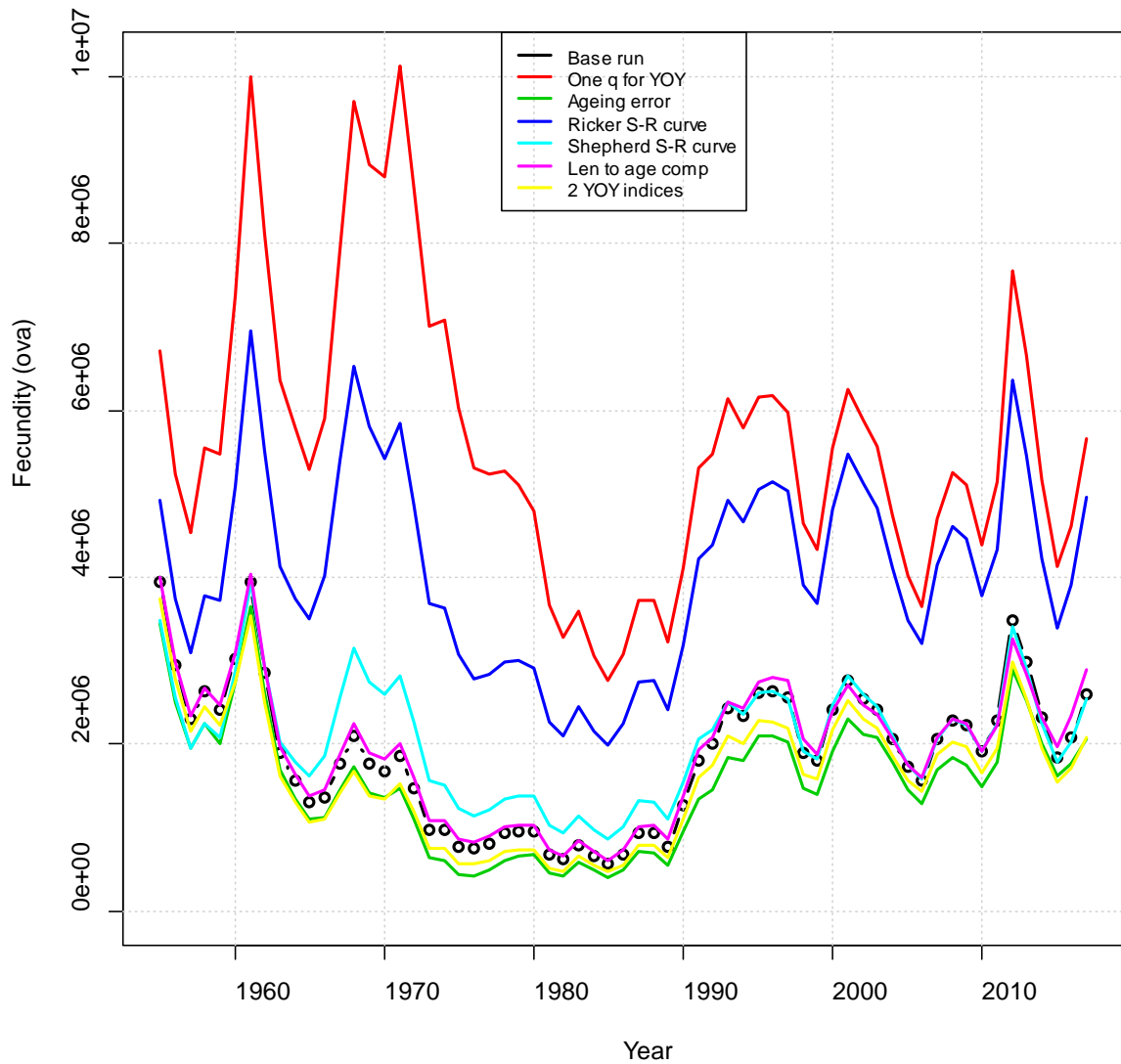
**Figure 165. Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019).**



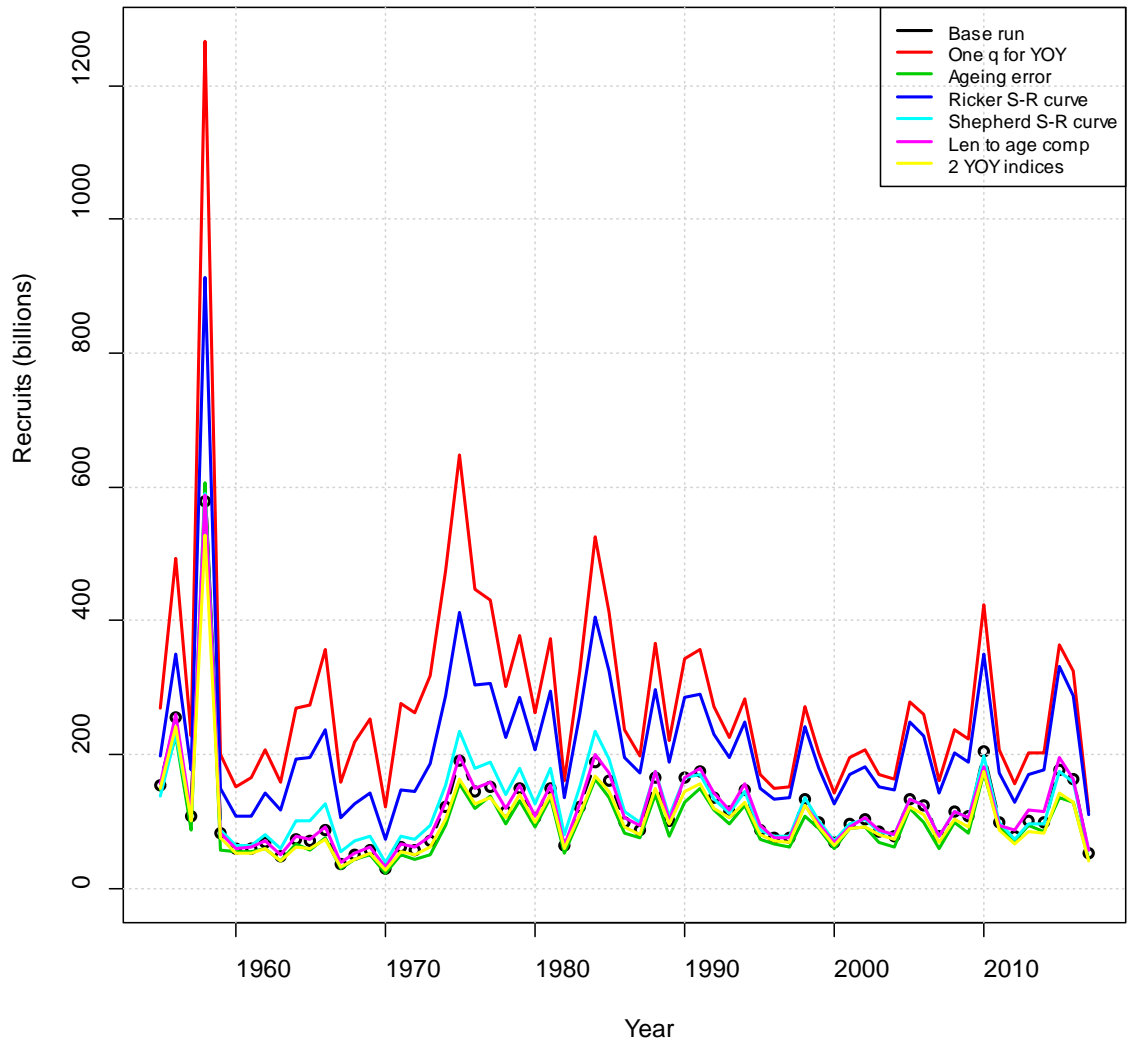
**Figure 166. Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored inclusion and exclusion of indices from the work being completed by the ERP group (ERP Report, SEDAR 2019).**



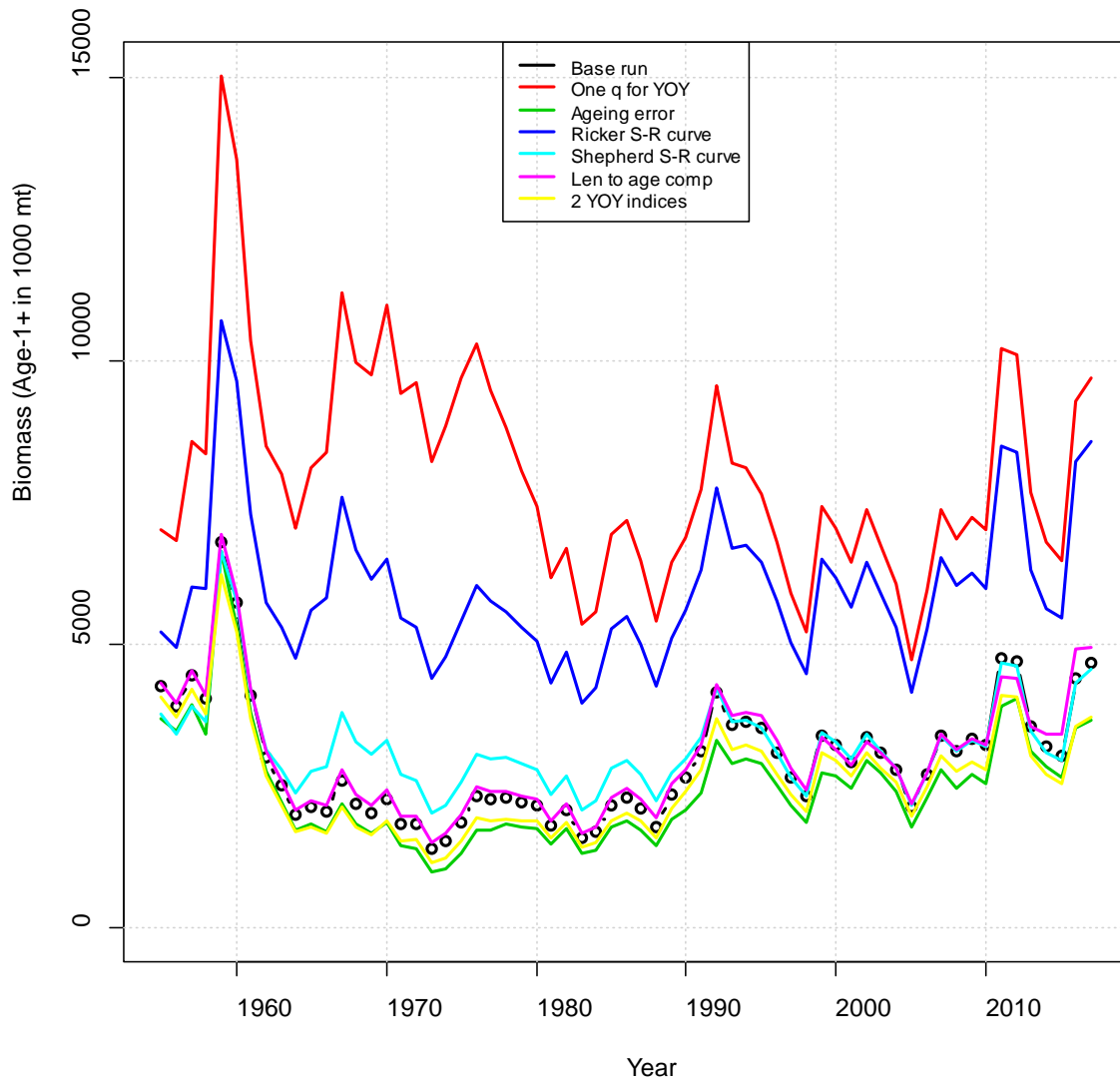
**Figure 167. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type.**



**Figure 168. Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type.**

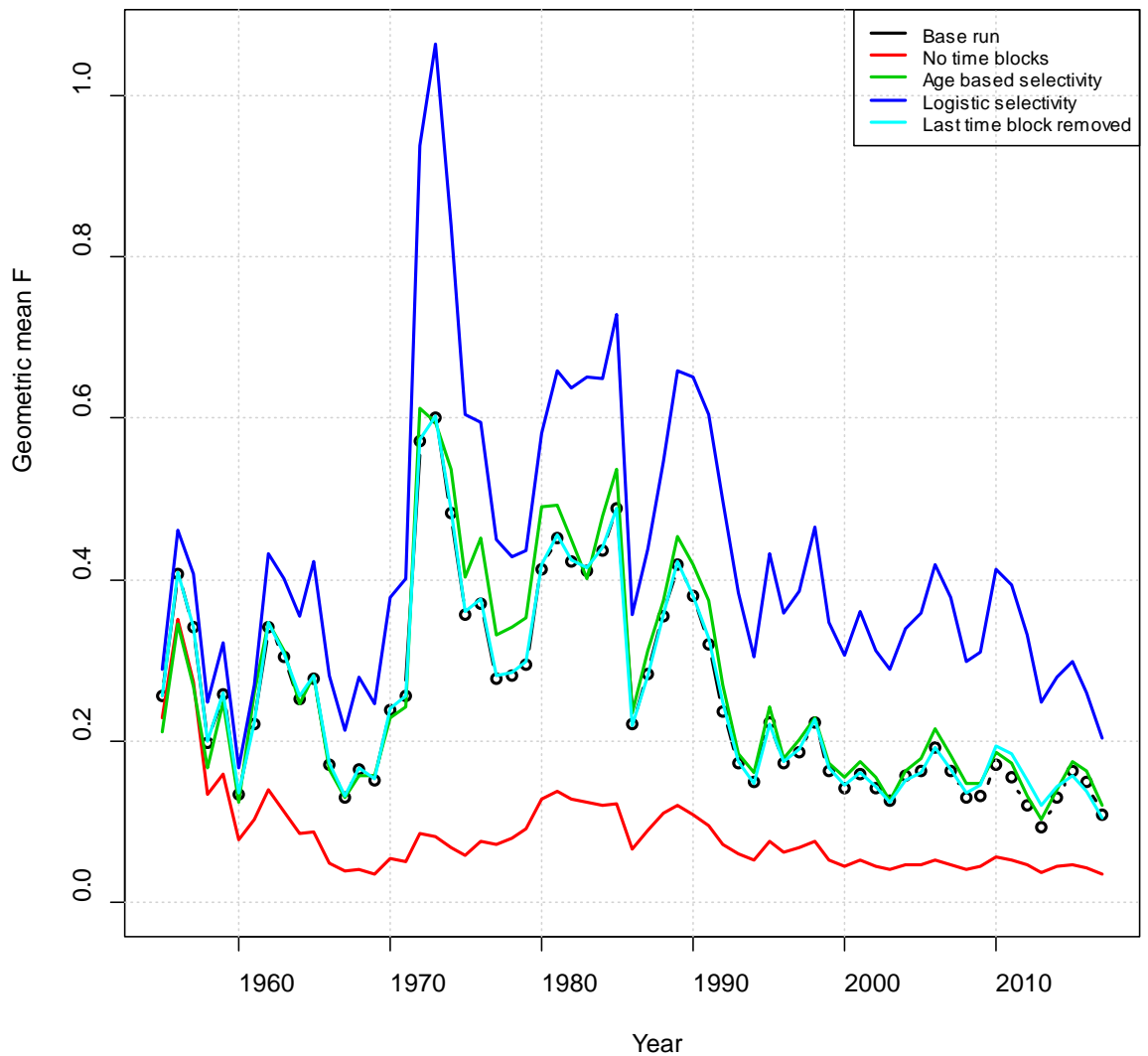


**Figure 169. Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type.**

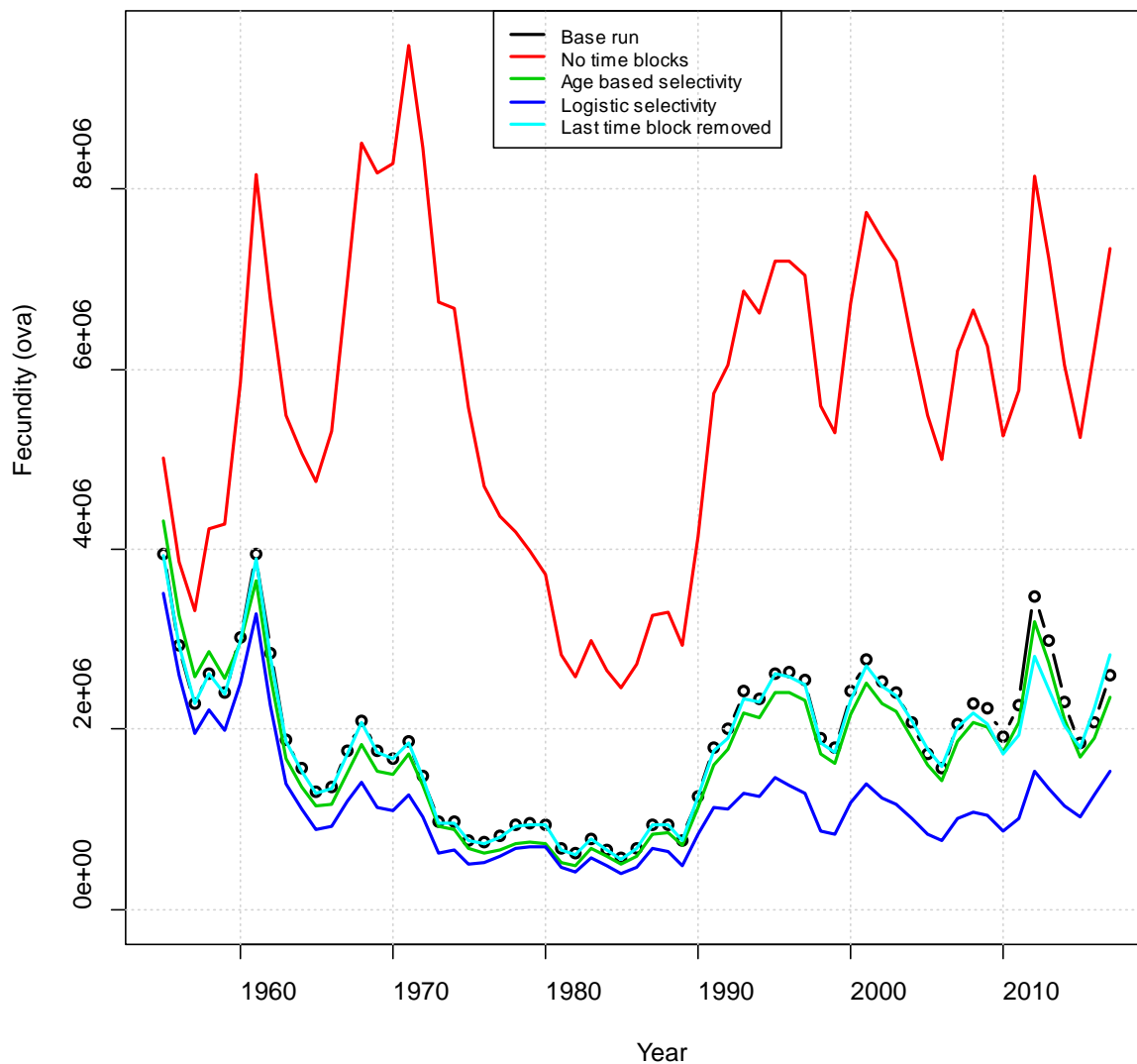


**Figure 170. Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored model structure related to ageing, catchability, the stock-recruitment curve, and data type.**

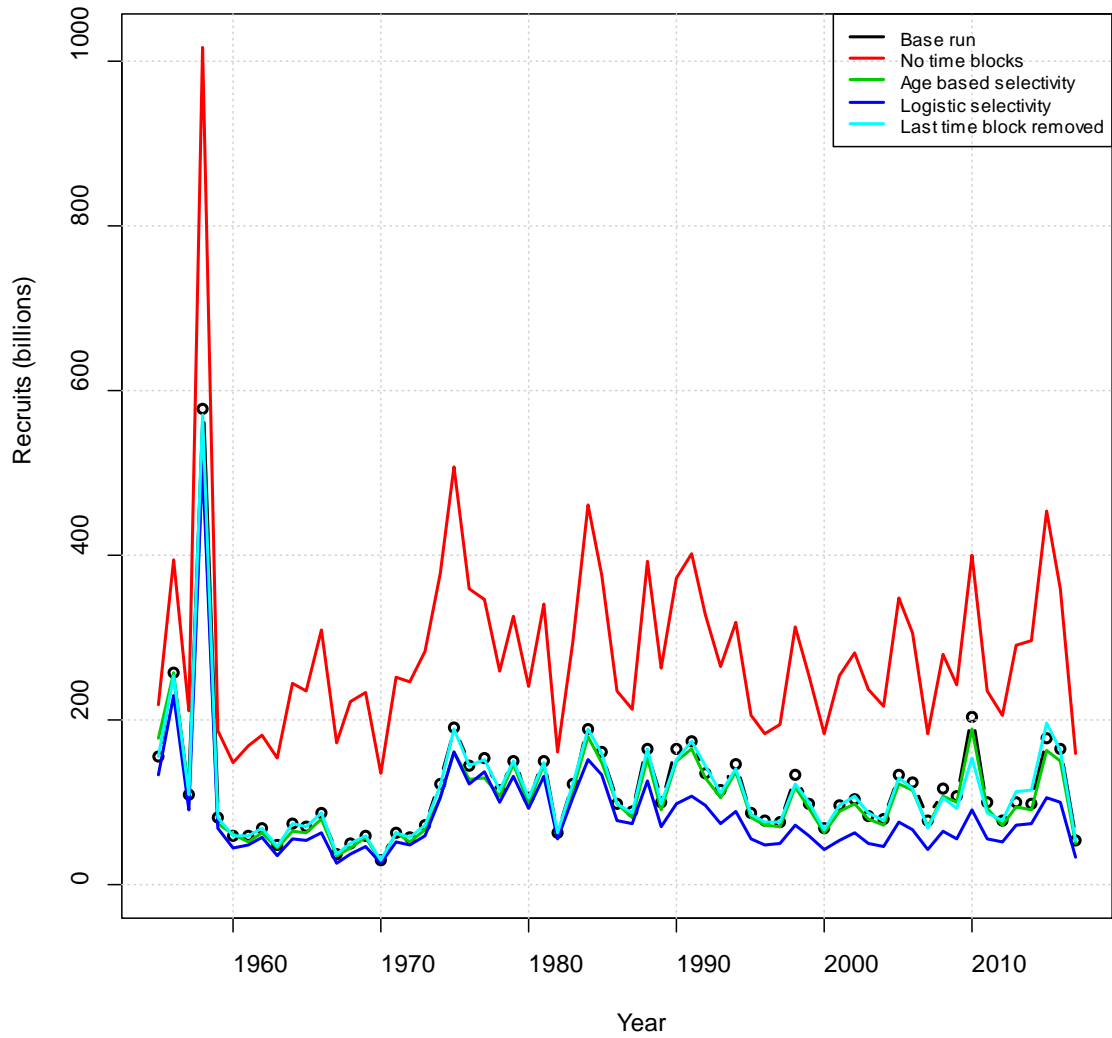




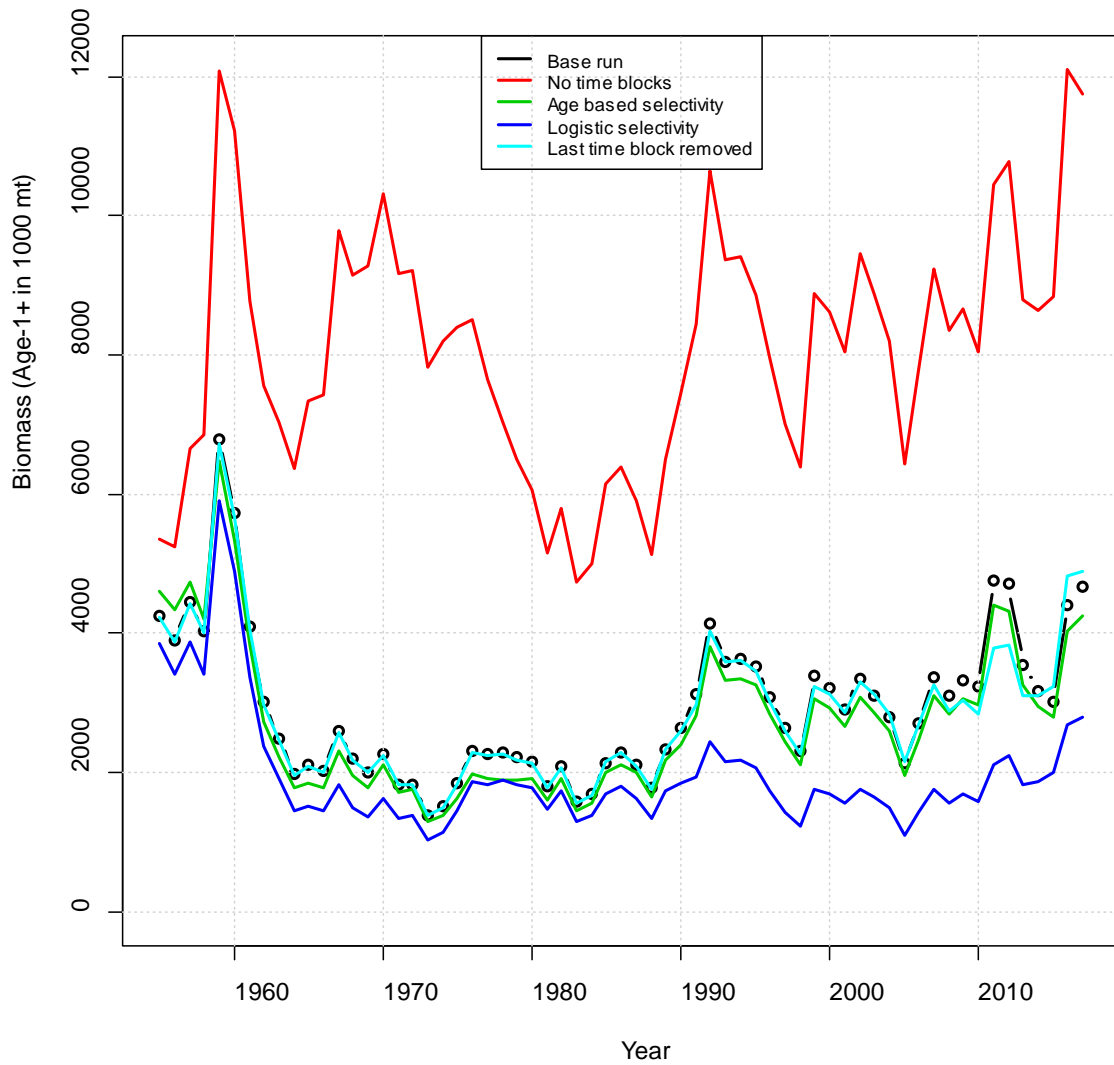
**Figure 171. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery.**



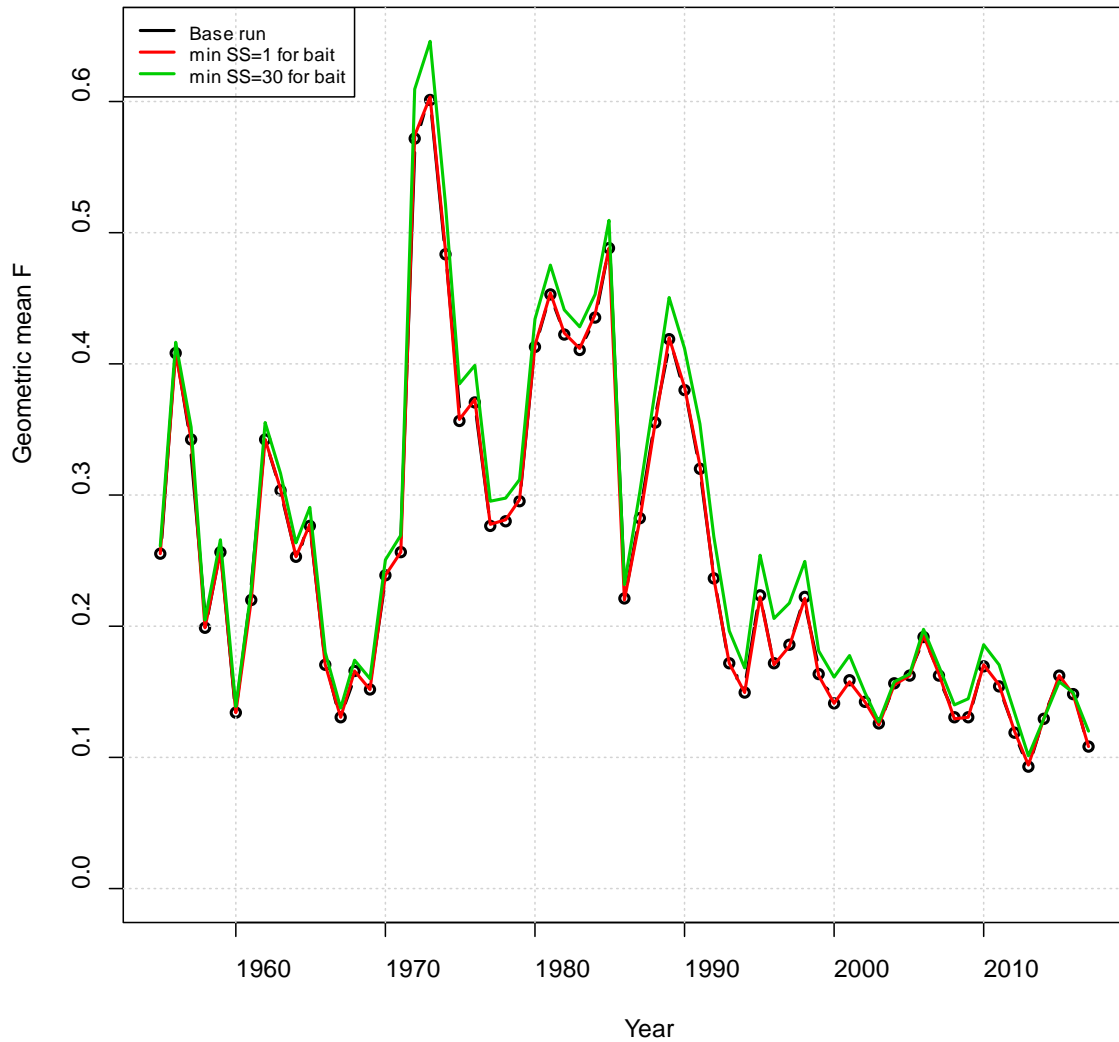
**Figure 172. Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery.**



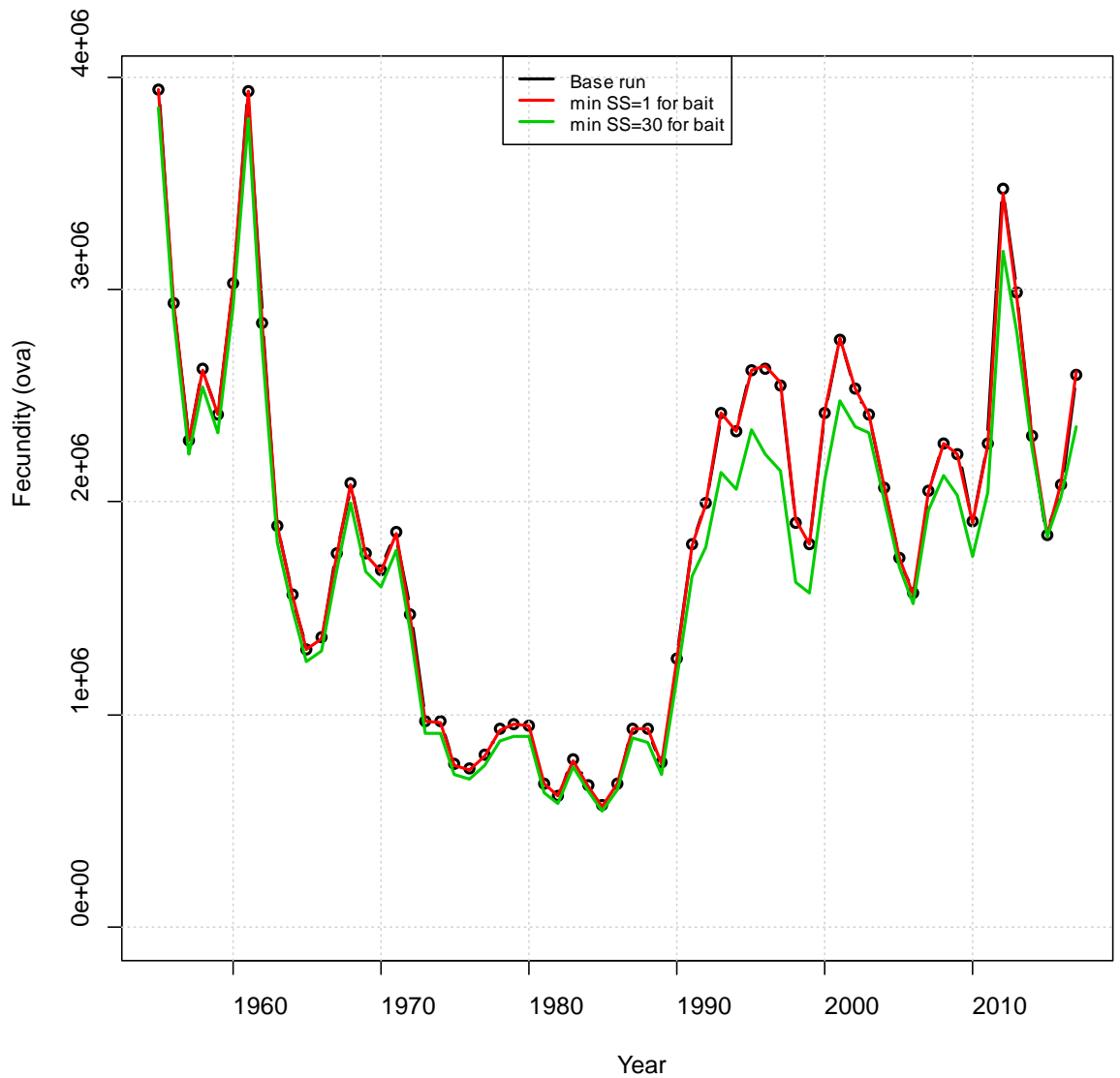
**Figure 173. Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery.**



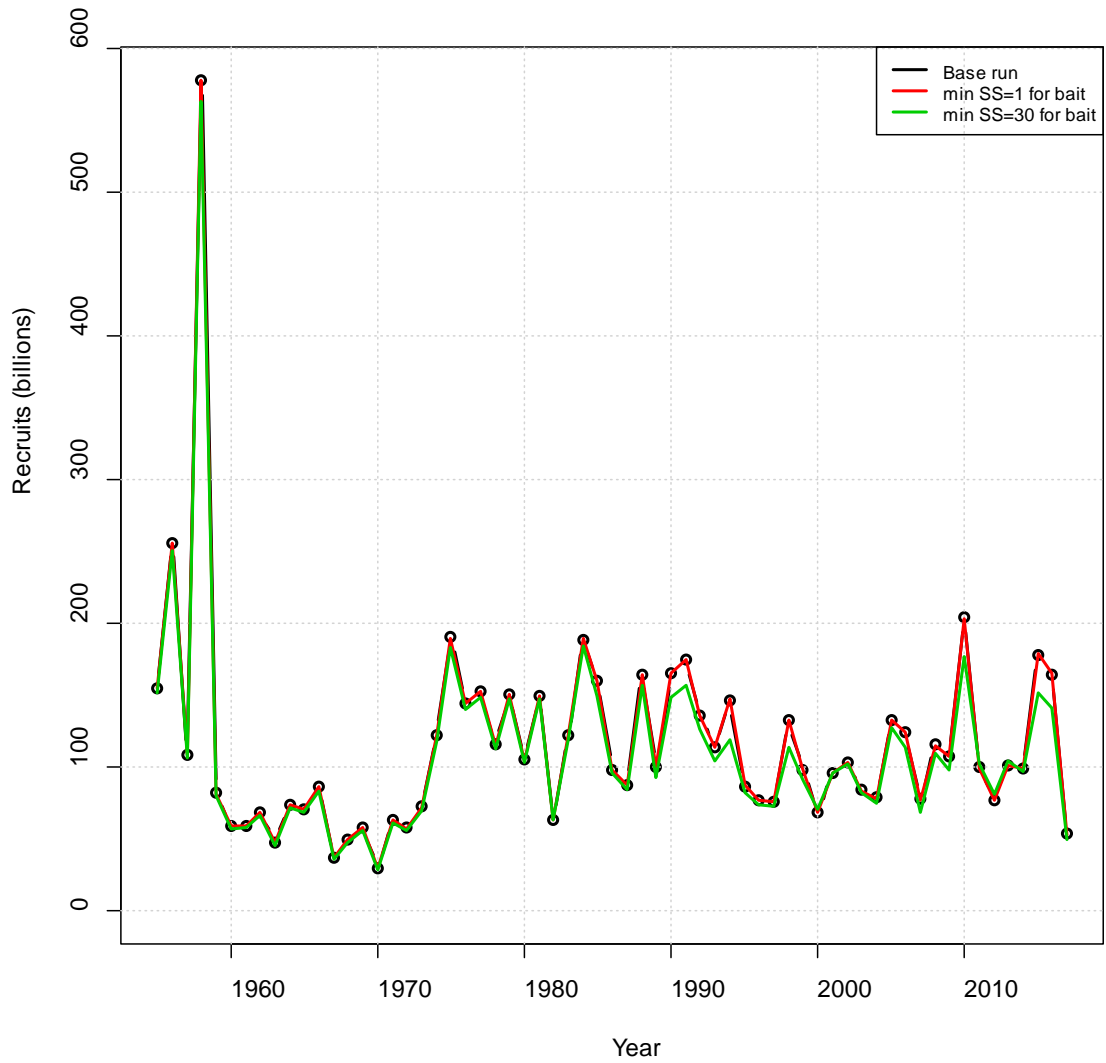
**Figure 174. Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored assumptions about selectivity for the fishery.**



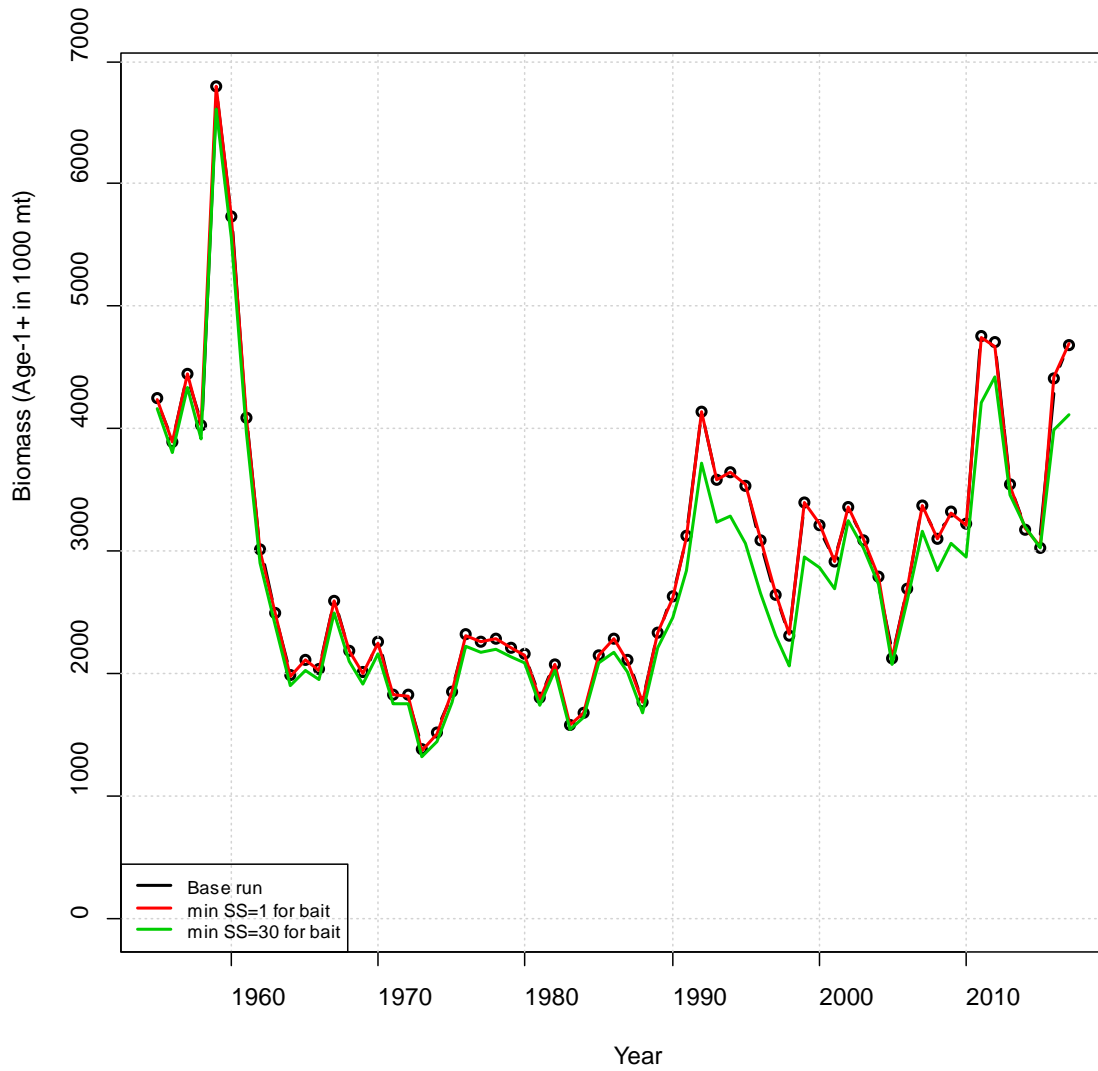
**Figure 175. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored assumptions about required sample sizes for the bait fishery.**



**Figure 176. Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored assumptions about required samples sizes for the bait fishery.**

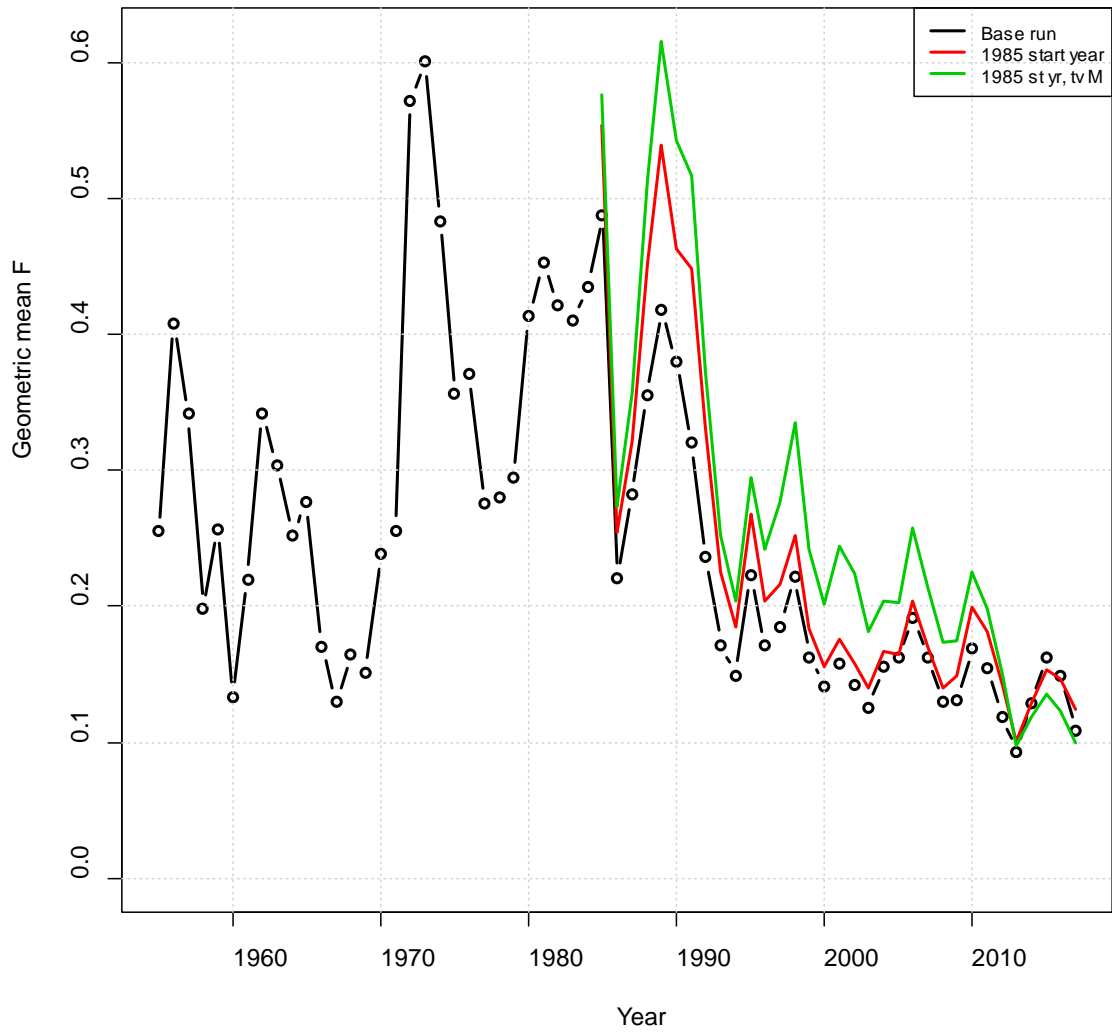


**Figure 177. Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored assumptions about required sample sizes for the bait fishery.**

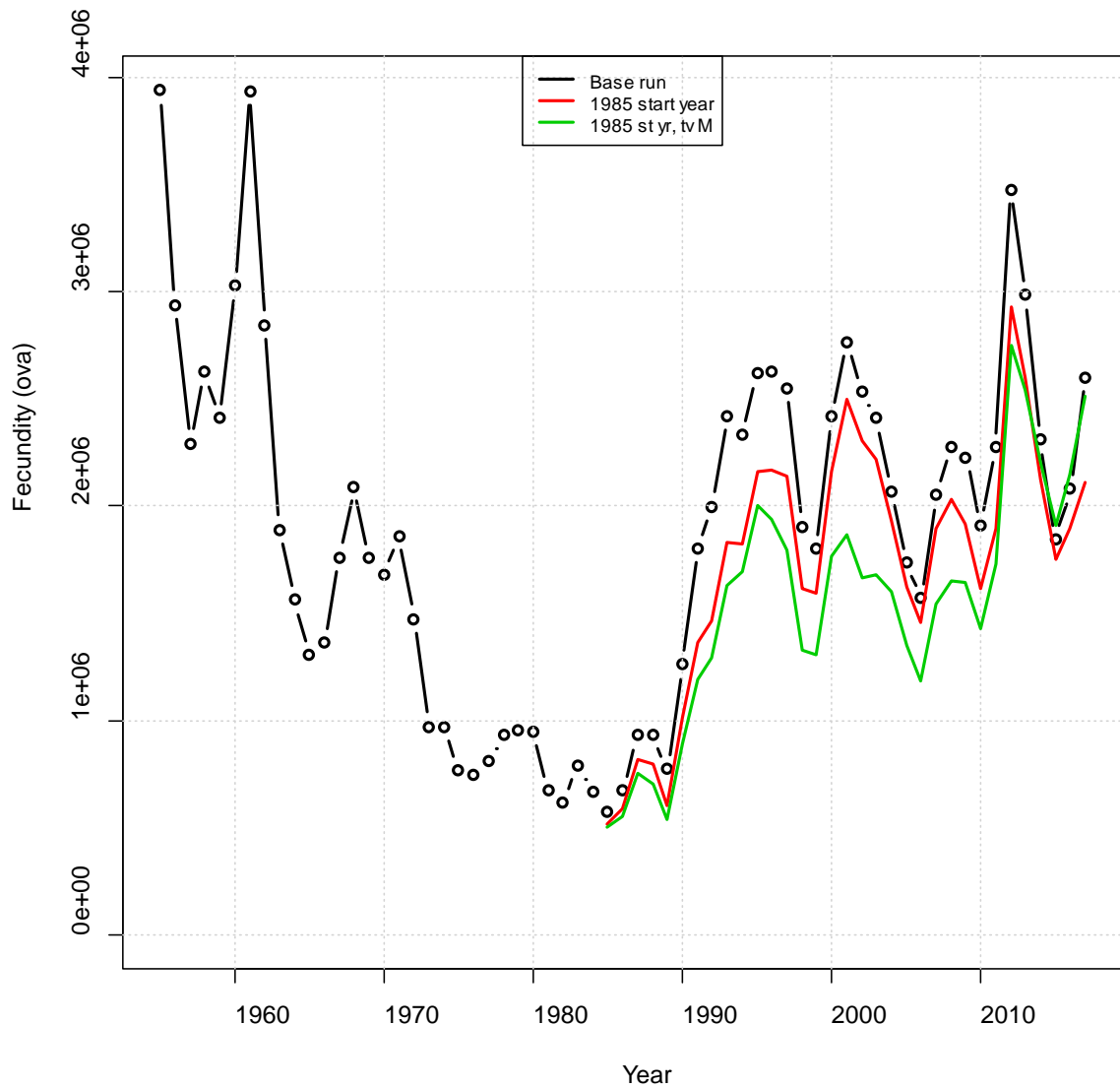


**Figure 178. Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored assumptions about required sample sizes for the bait fishery.**

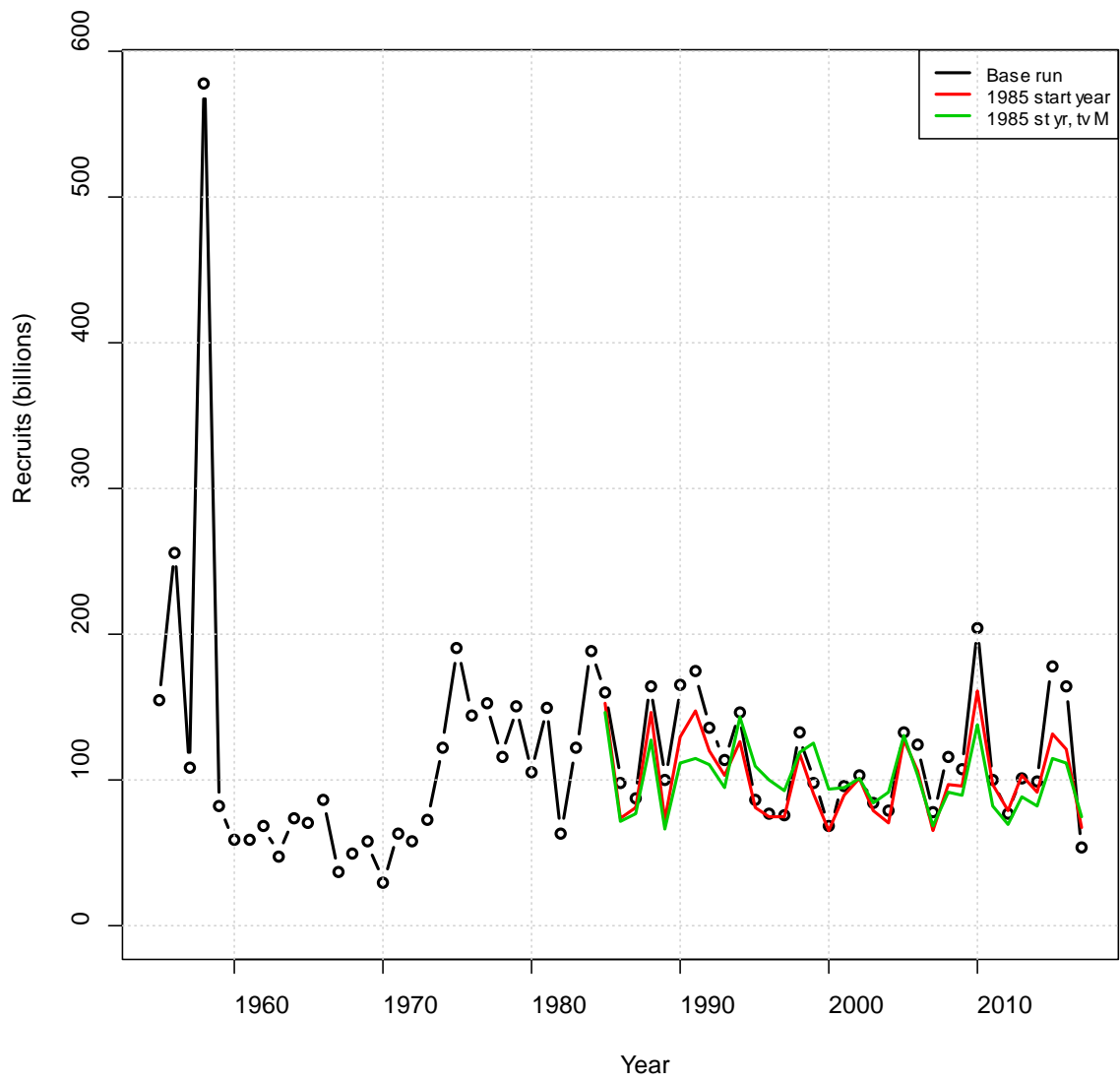




**Figure 179. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality.**



**Figure 180. Fecundity in billions of ova for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality.**



**Figure 181. Recruitment in billions of fish for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality.**

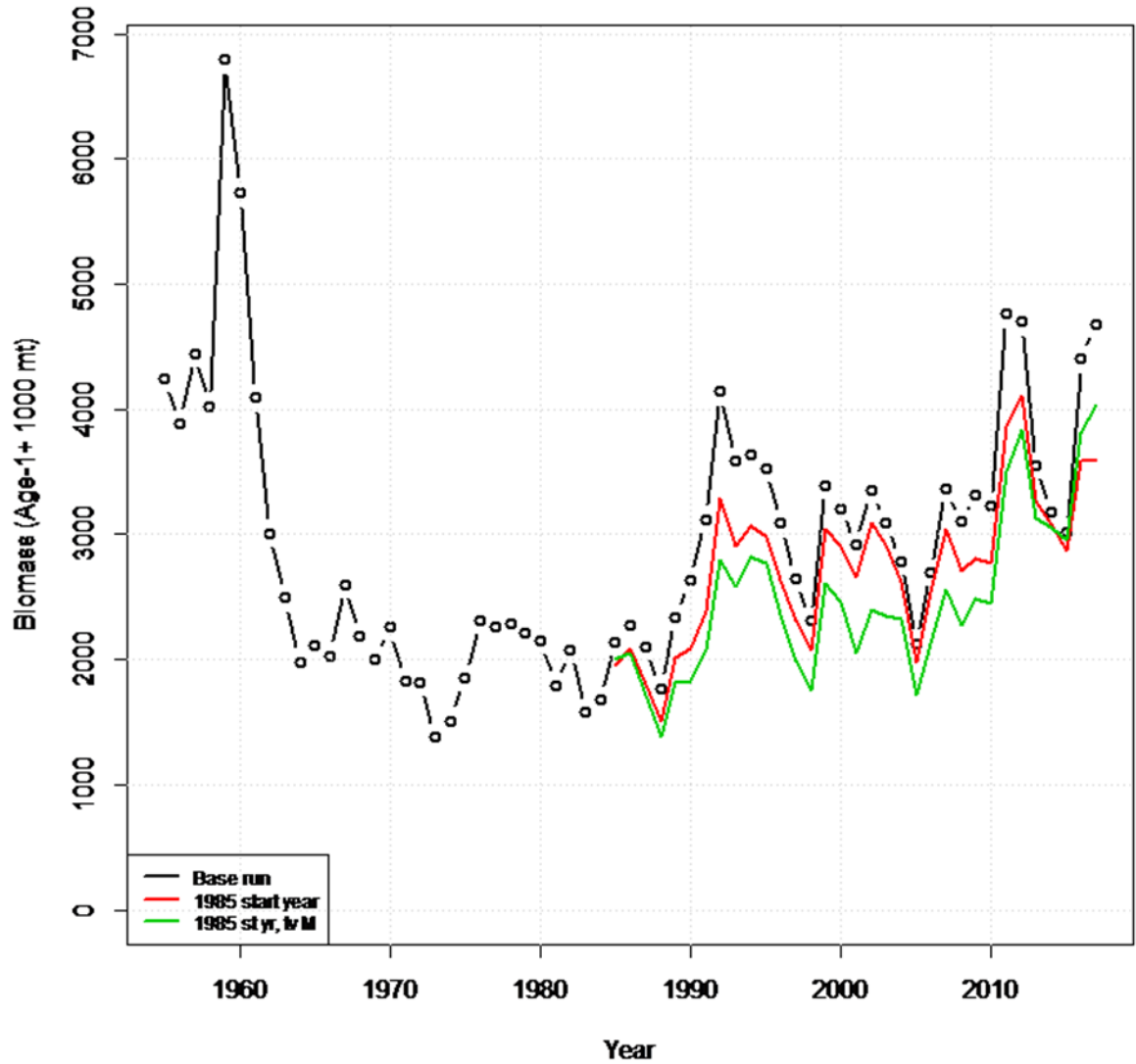
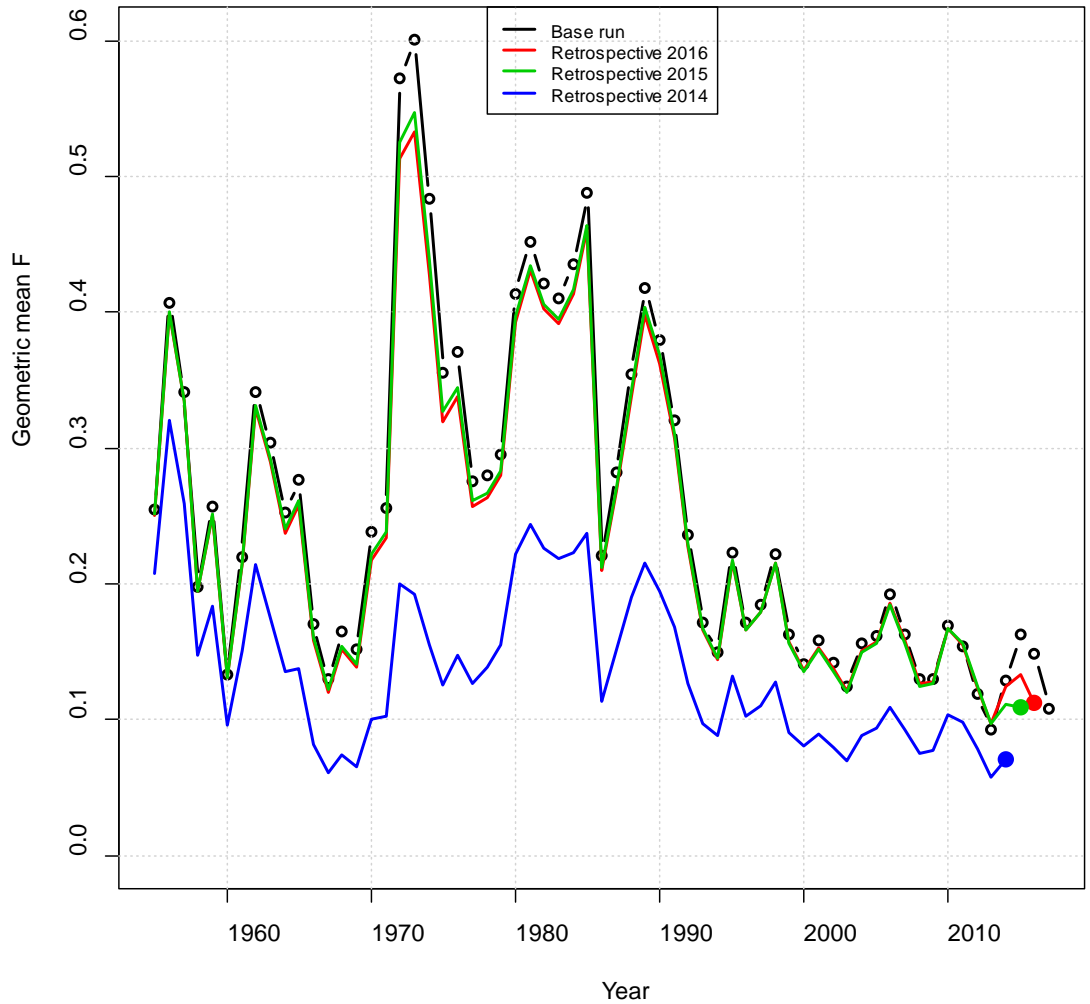
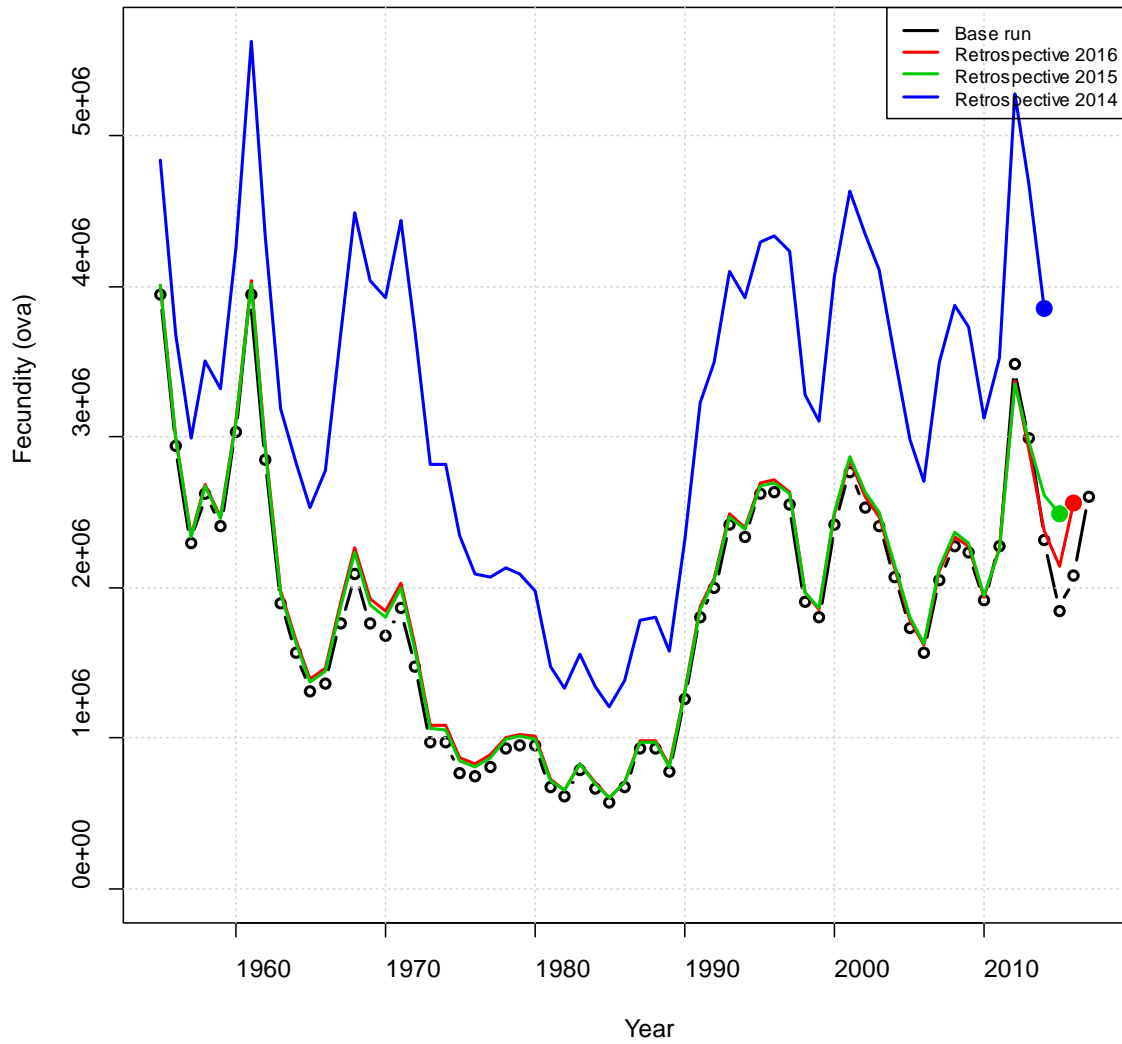


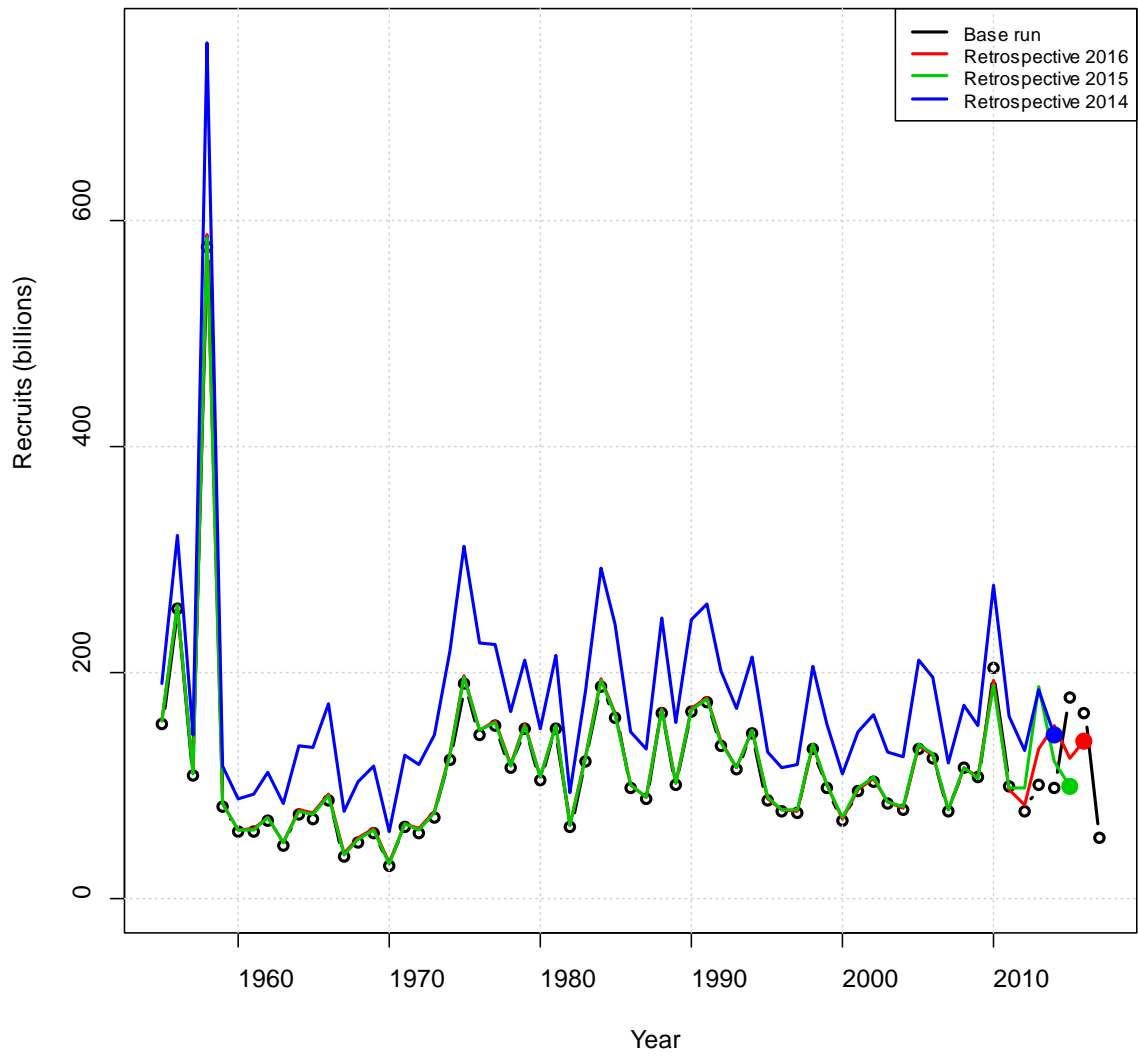
Figure 182. Age-1+ biomass for 1955-2017 for a suite of sensitivity runs that explored assumptions about the start year of the model and the start year of the model in conjunction with time-varying natural mortality.



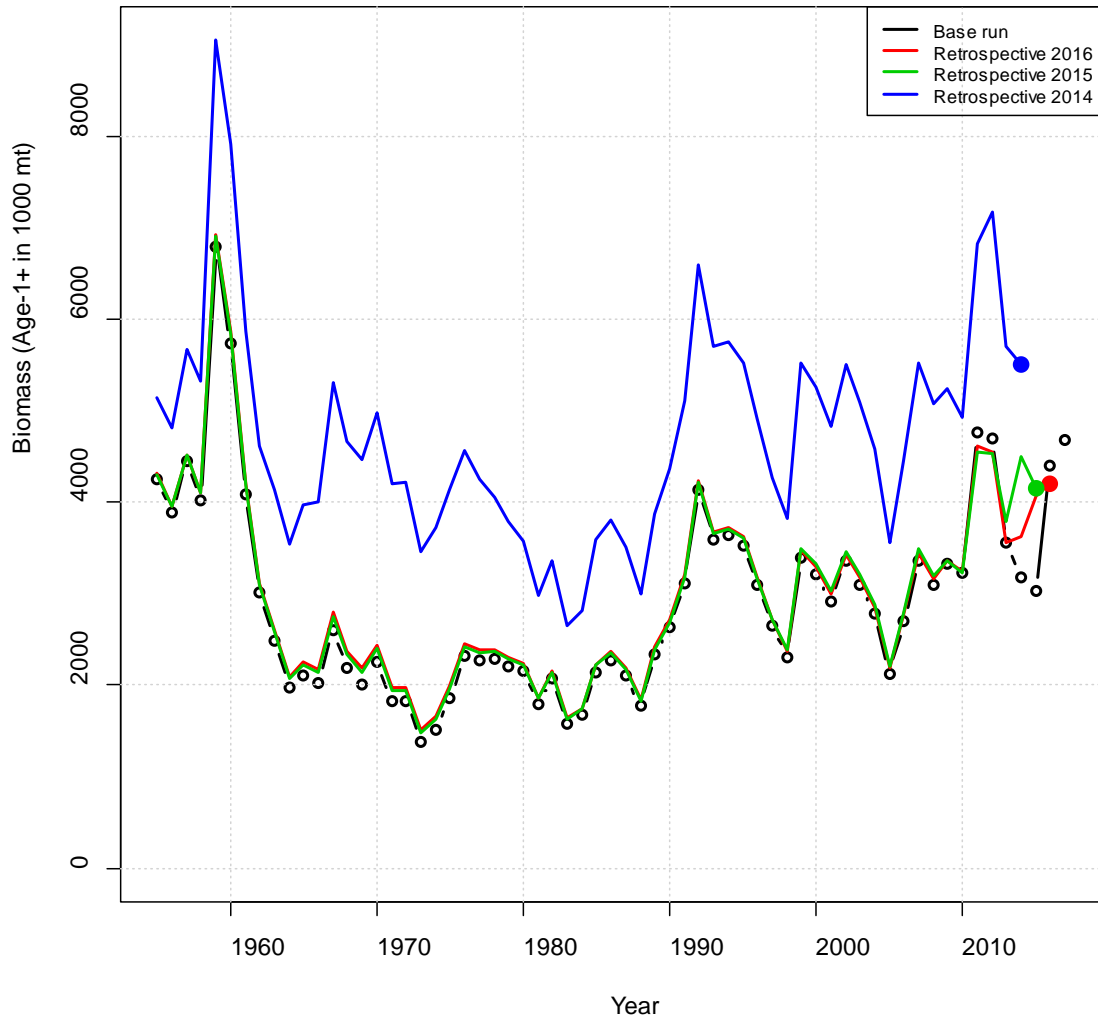
**Figure 183. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the retrospective analysis.**



**Figure 184. Fecundity in billions of ova for 1955-2017 for the retrospective analysis.**

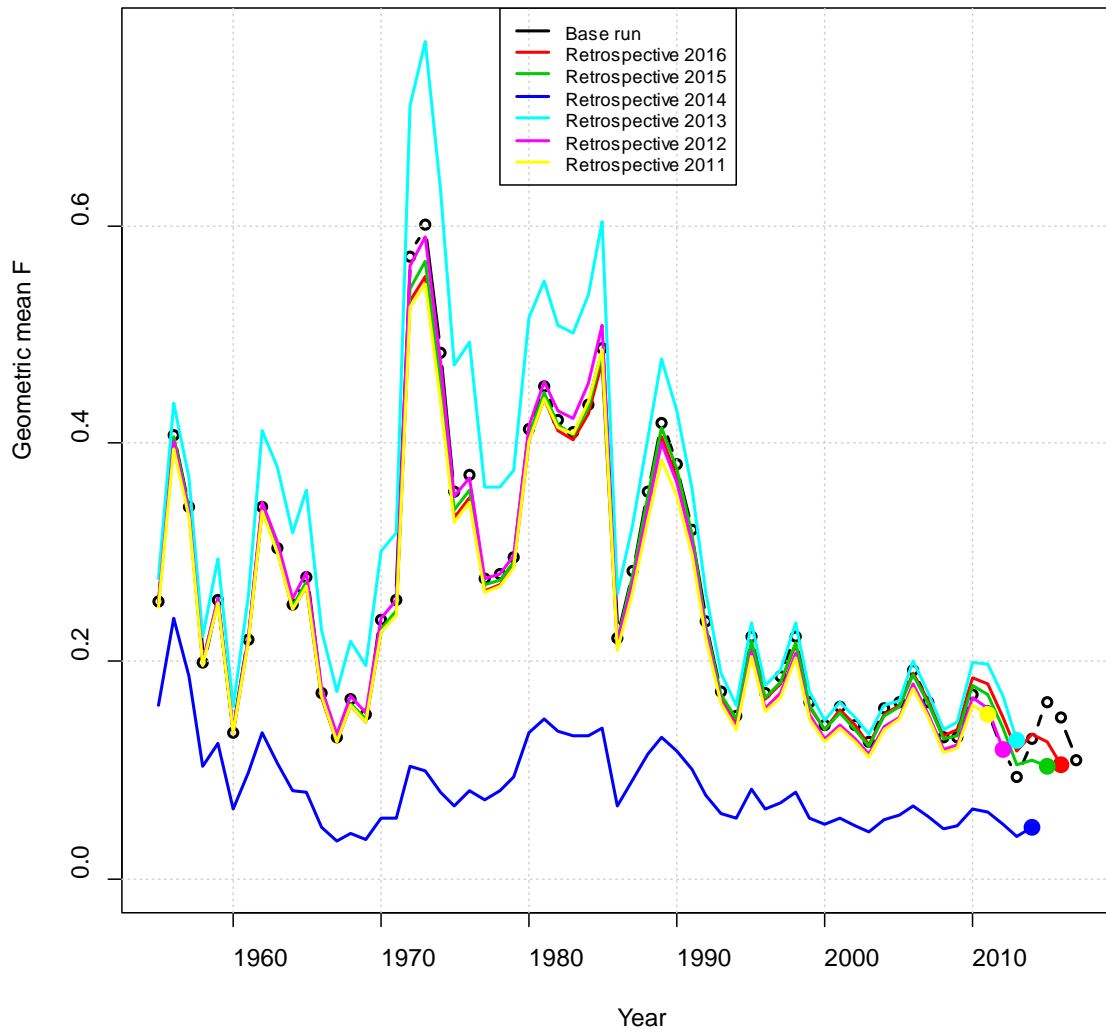


**Figure 185. Recruitment in billions of fish for 1955-2017 for the retrospective analysis.**

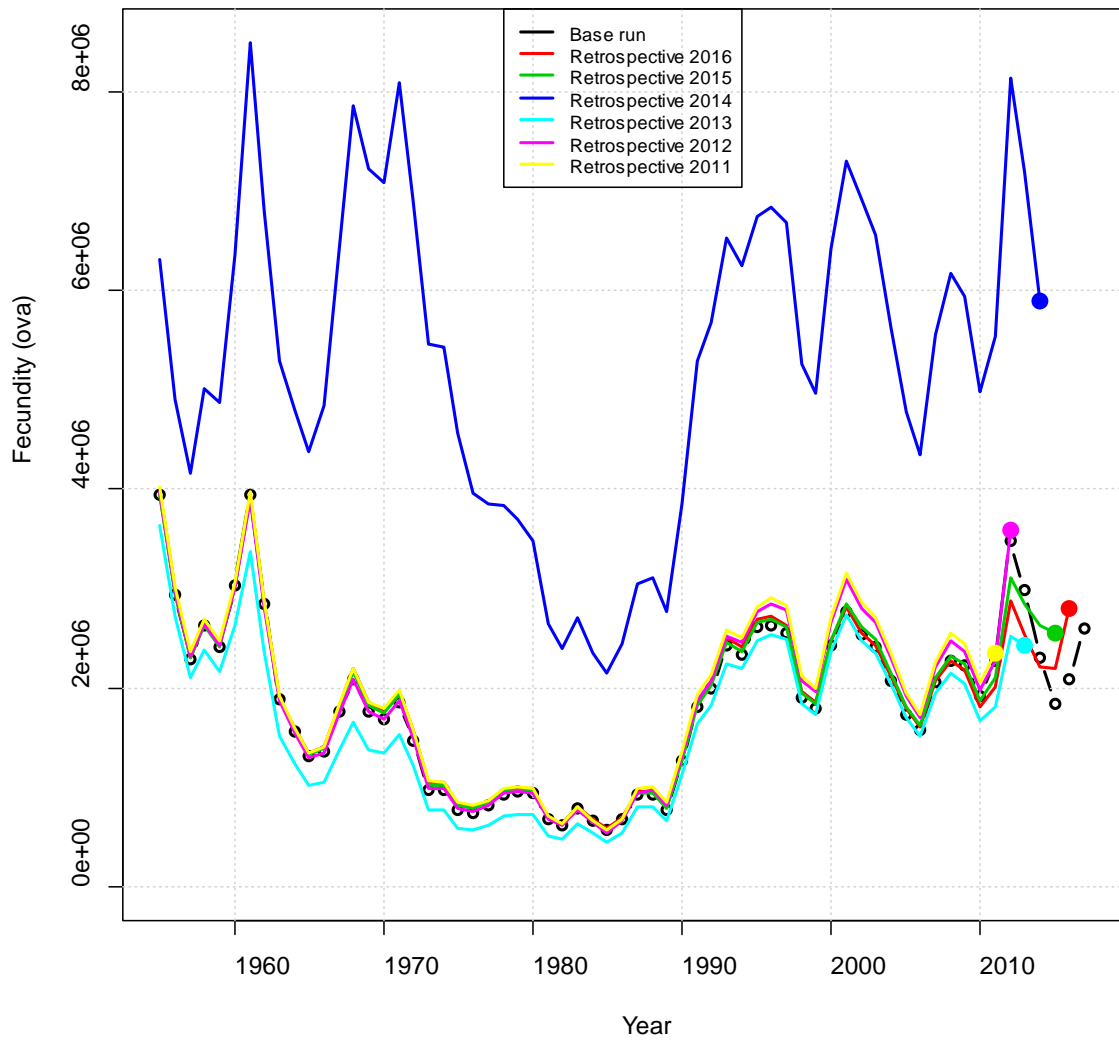


**Figure 186. Age-1+ biomass for 1955-2017 for the retrospective analysis.**

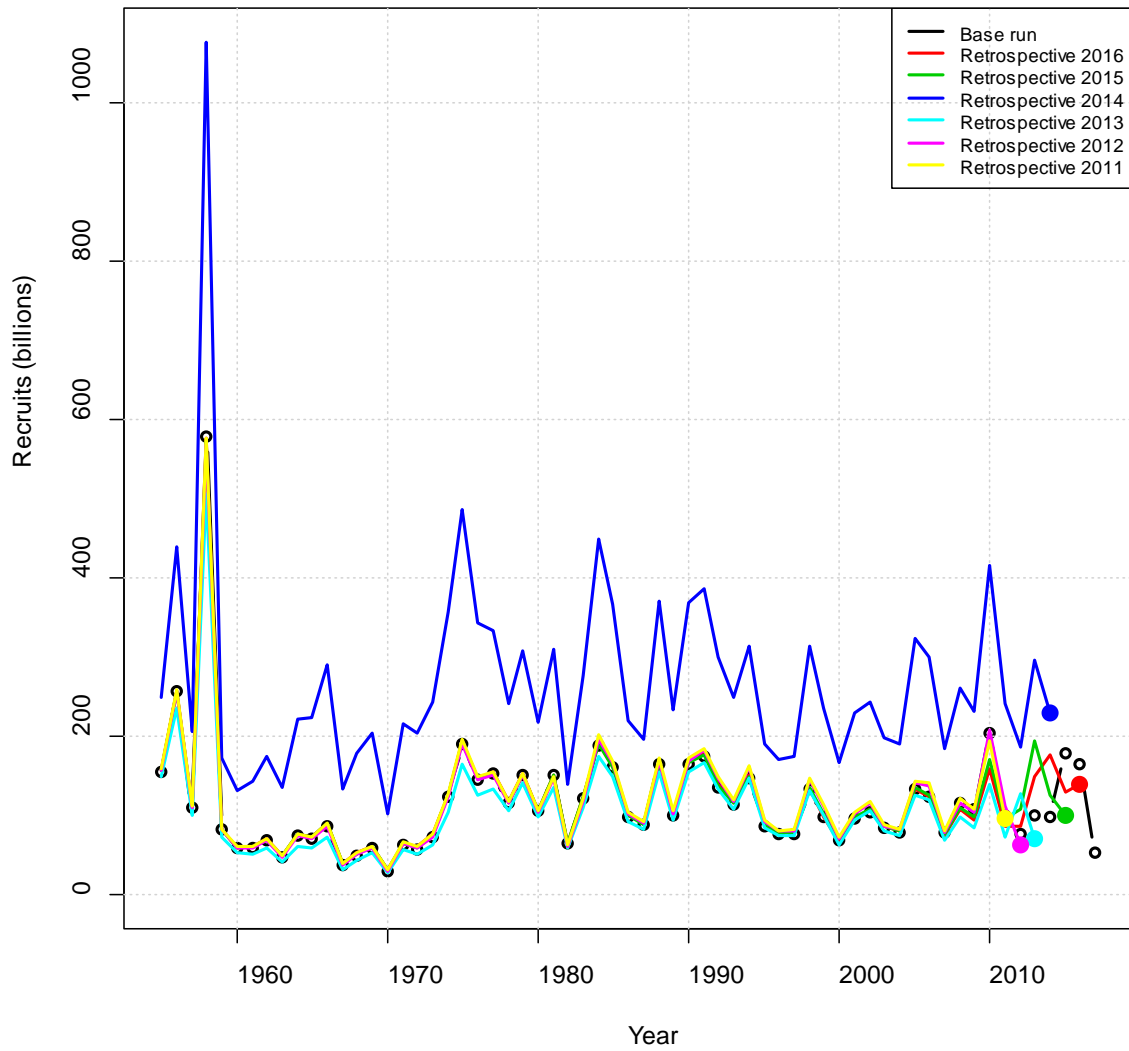




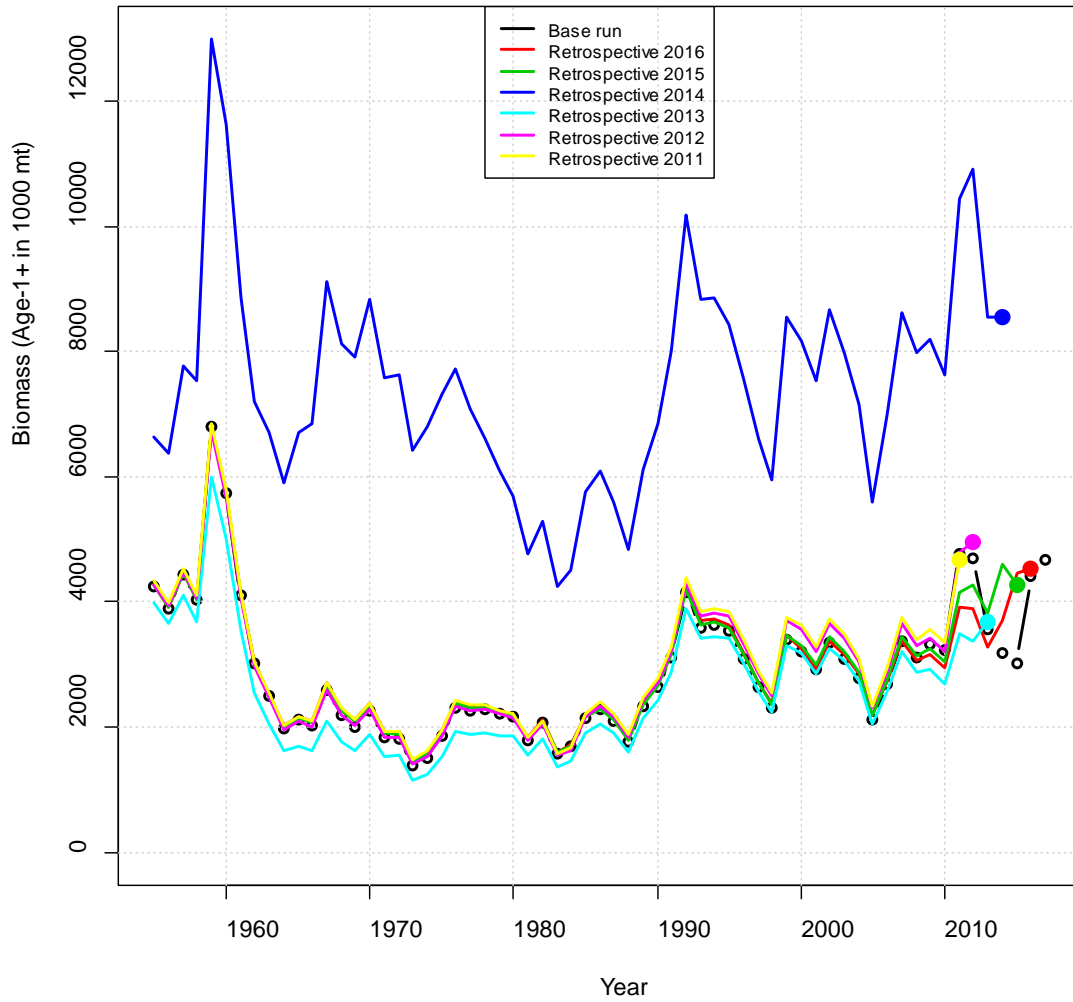
**Figure 187. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the retrospective analysis going back until 2011.**



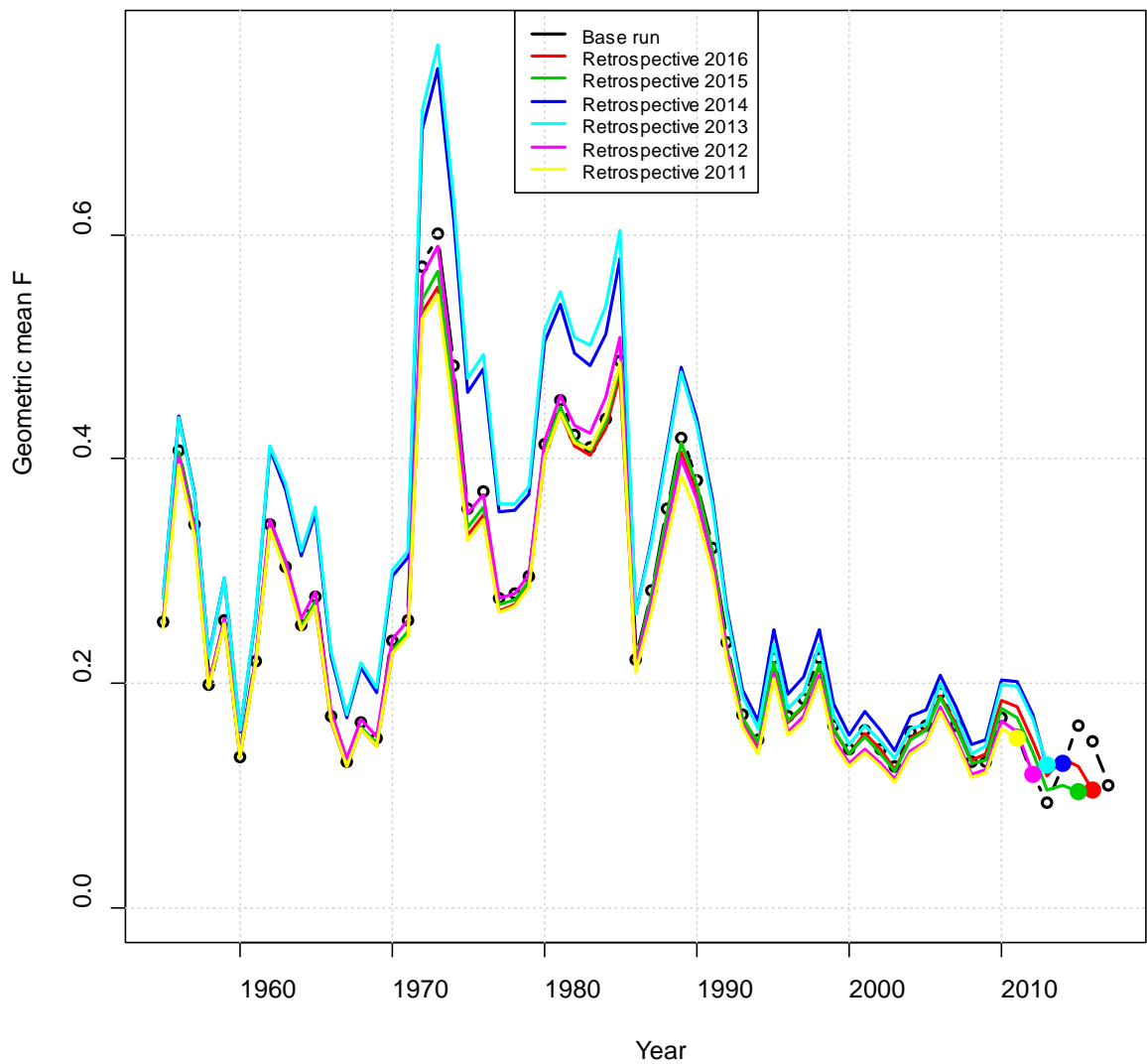
**Figure 188. Fecundity in billions of ova for 1955-2017 for the retrospective analysis going back until 2011.**



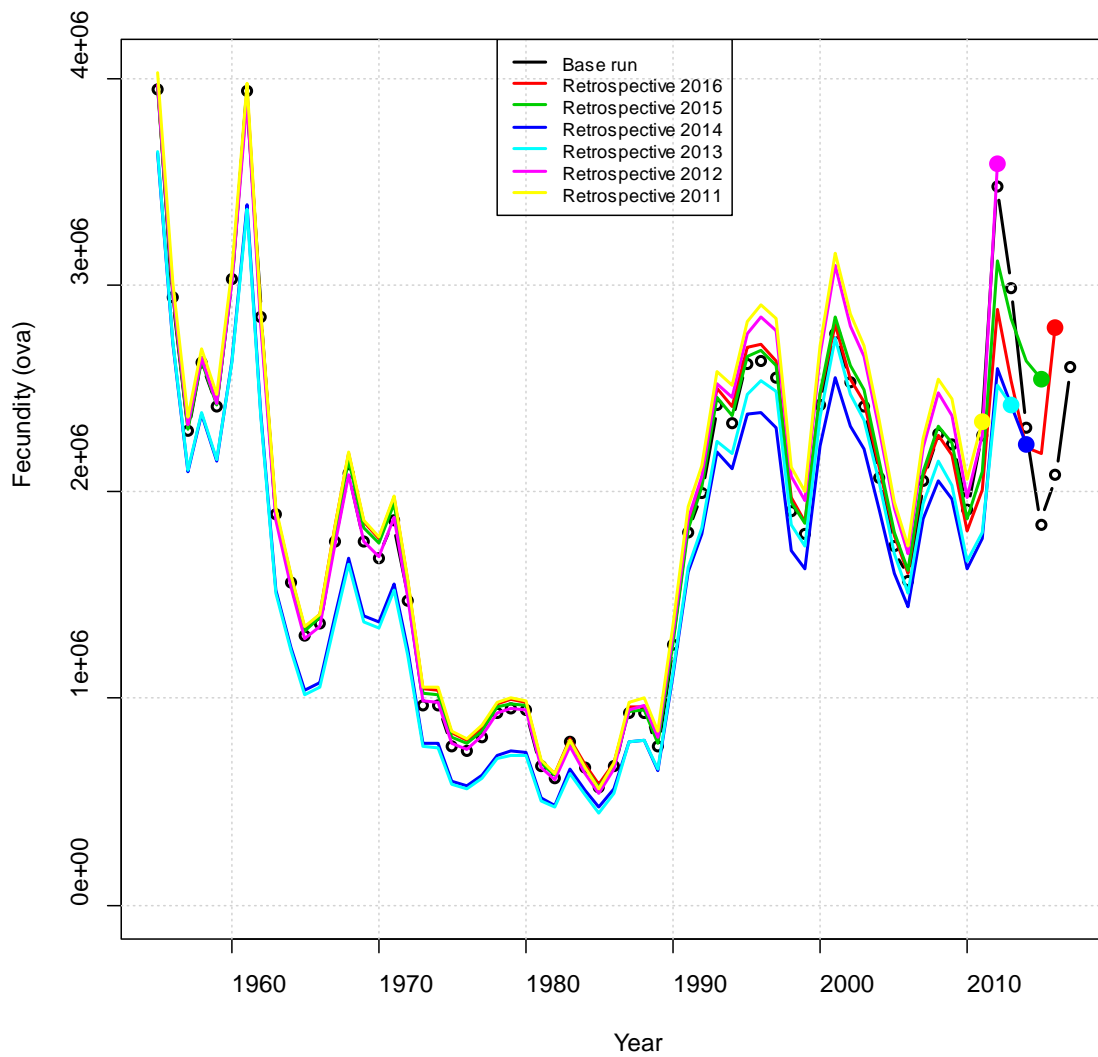
**Figure 189. Recruitment in billions of fish for 1955-2017 for the retrospective analysis going back until 2011.**



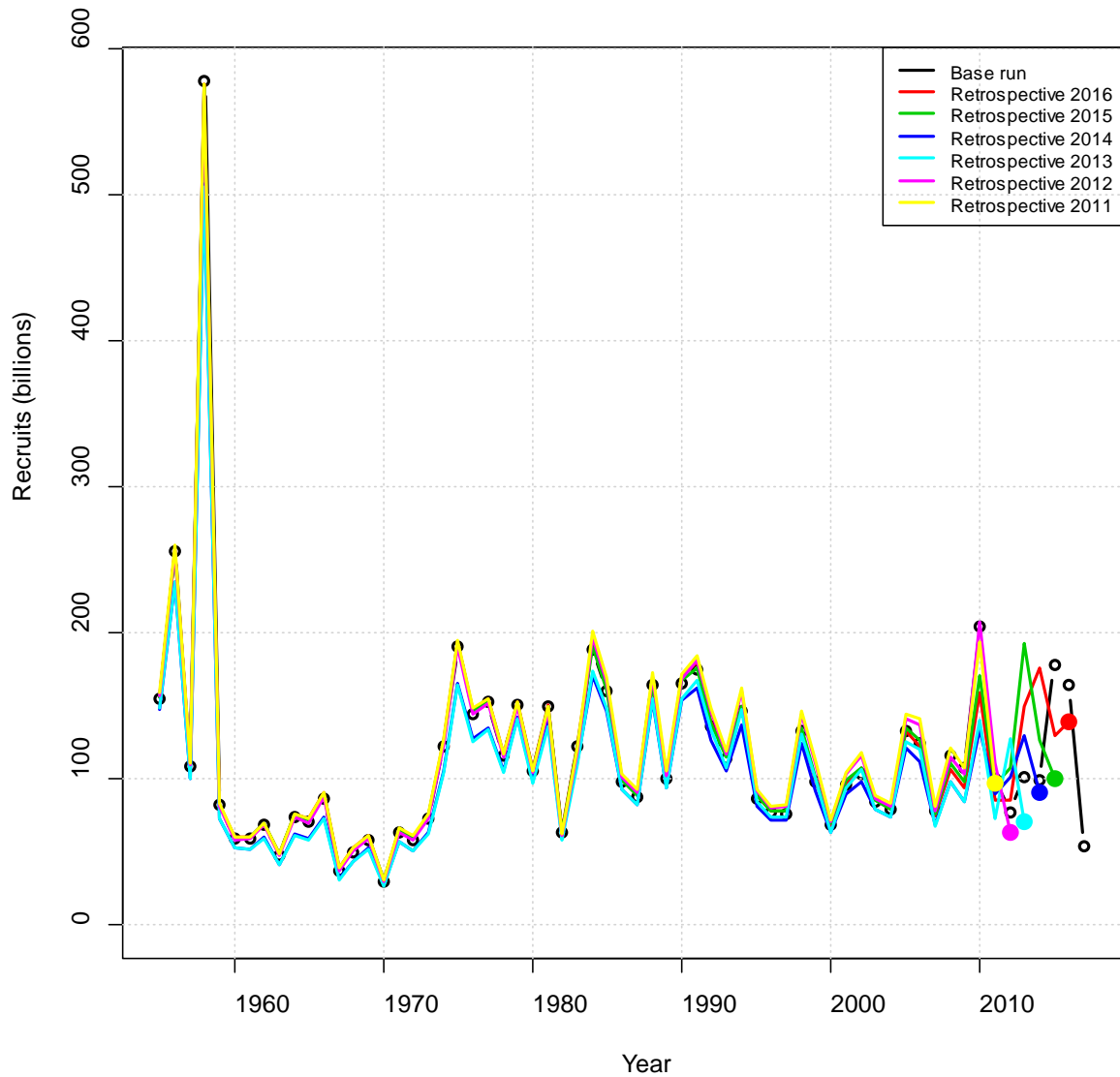
**Figure 190. Age-1+ biomass for 1955-2017 for the retrospective analysis going back until 2011.**



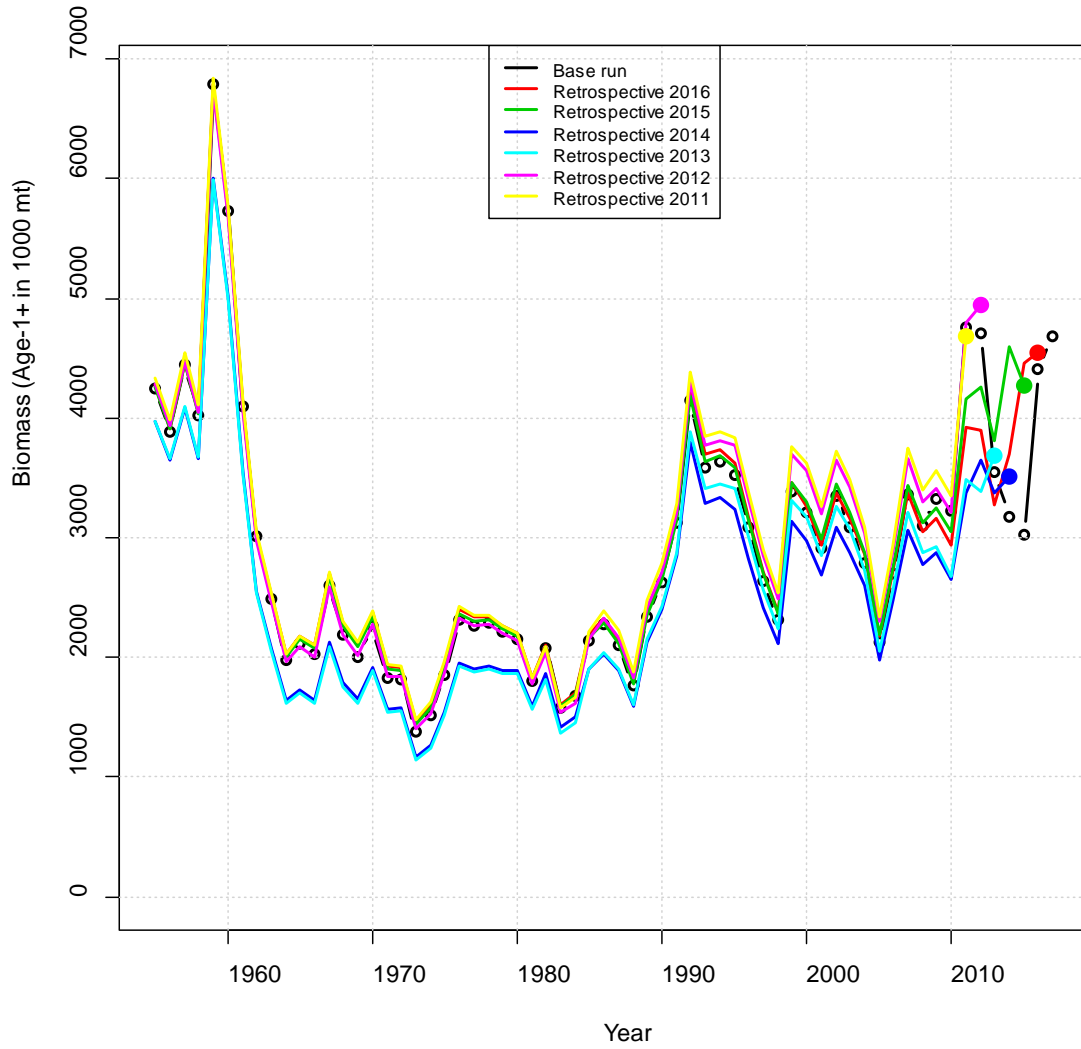
**Figure 191. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period.**



**Figure 192. Fecundity in billions of ova for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period.**

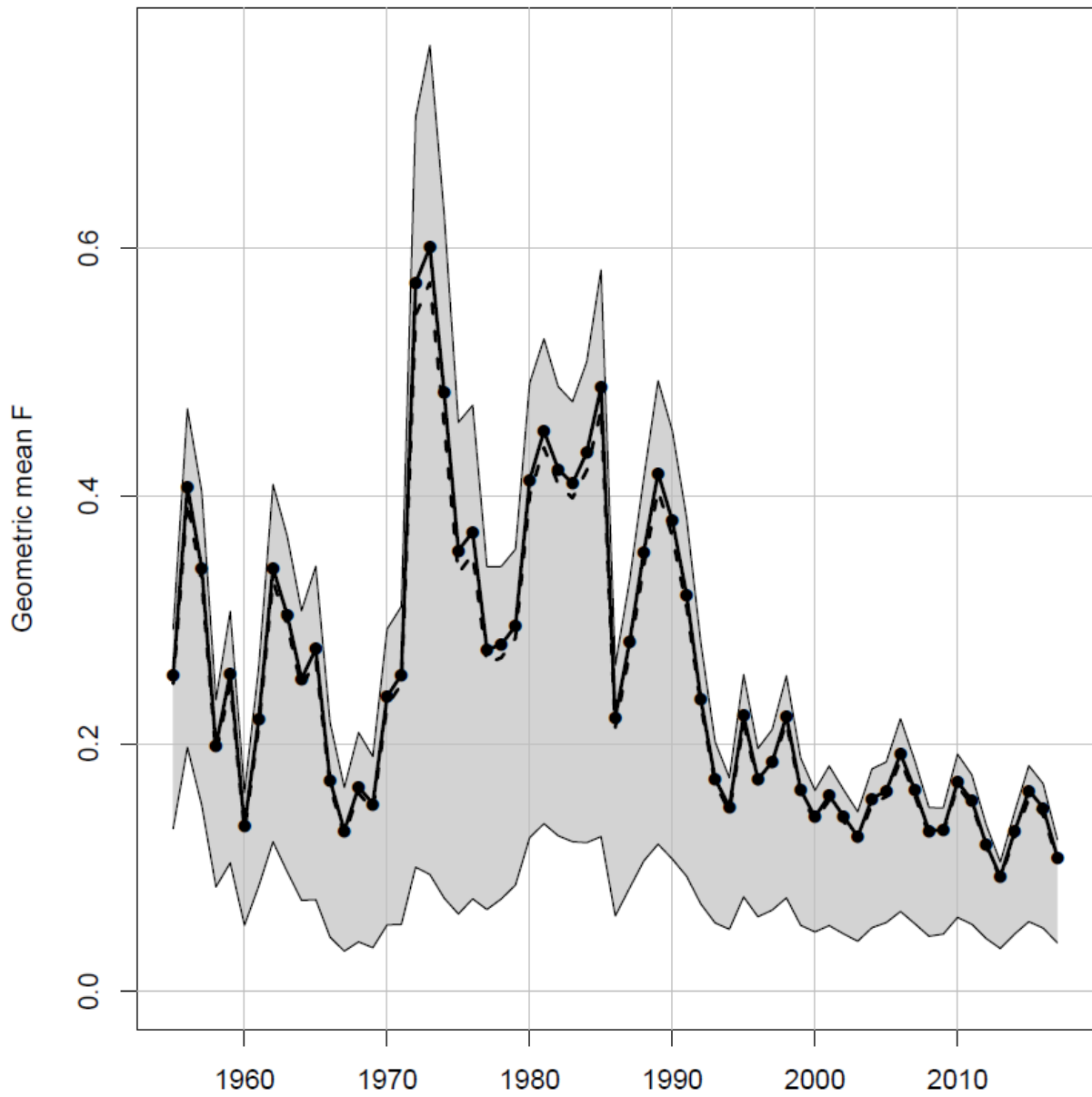


**Figure 193. Recruitment in billions of fish for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period.**



**Figure 194. Age-1+ biomass for 1955-2017 for the retrospective analysis going back until 2011 and the northern age comp fixed at a value similar to the recent time period.**





**Figure 195. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles.**

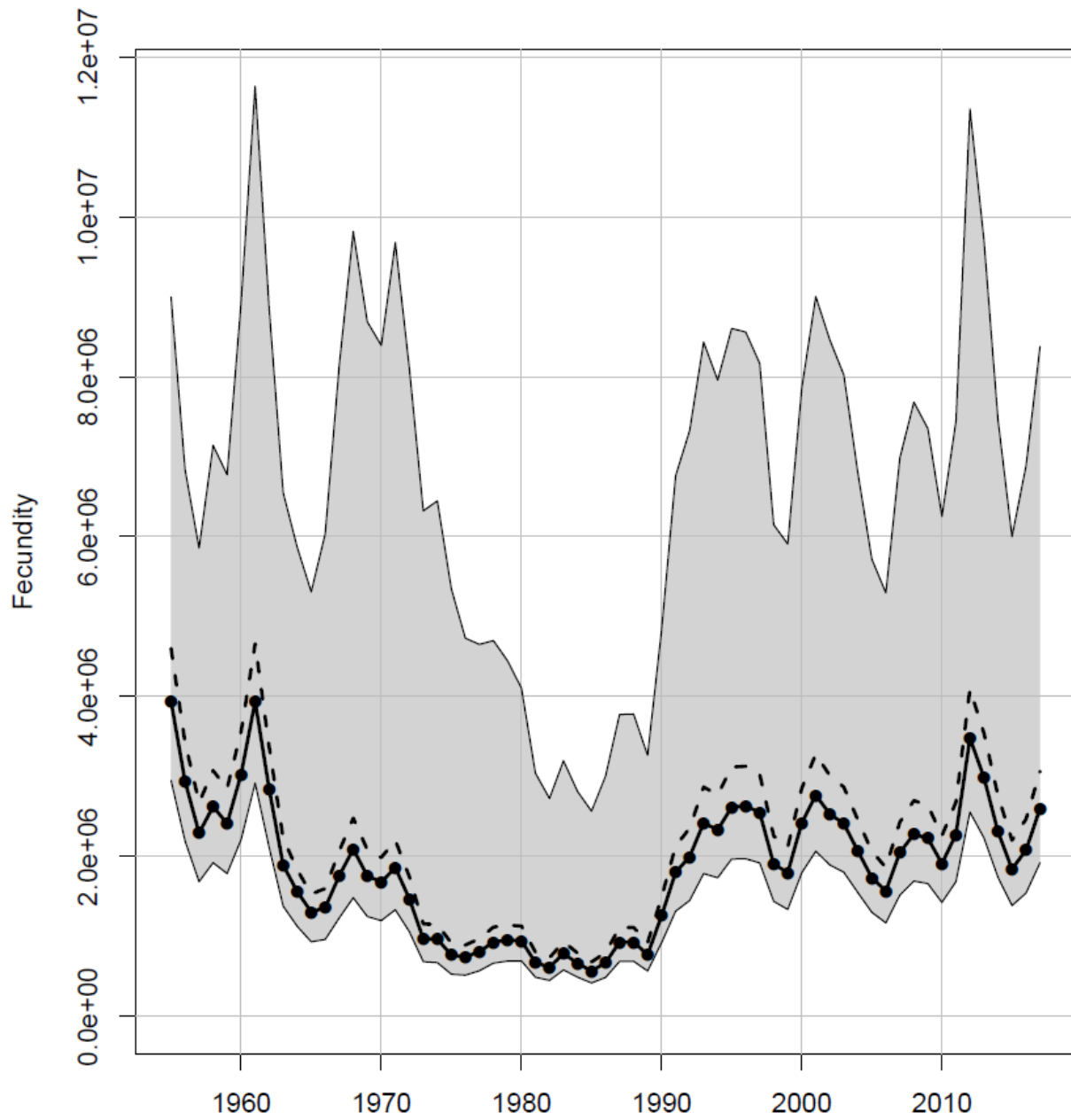
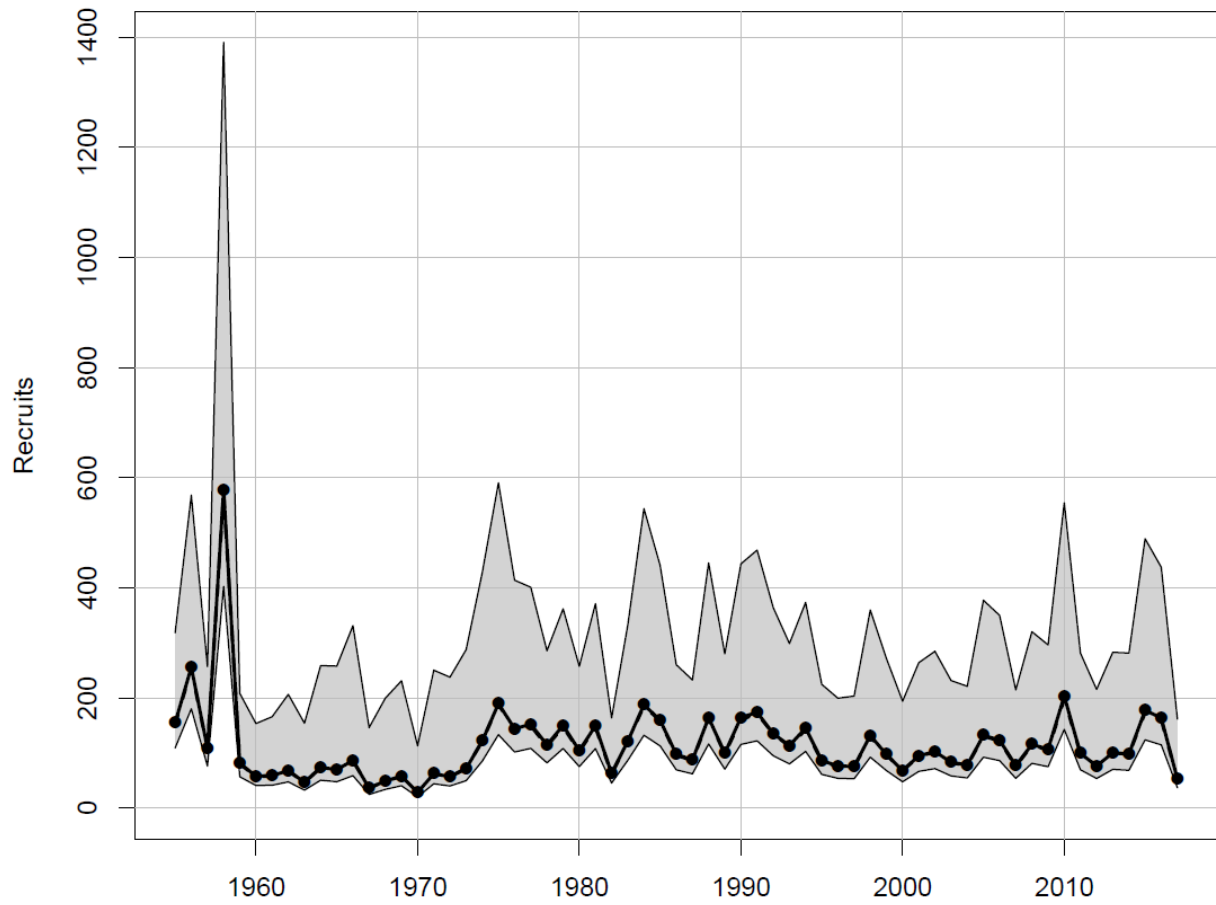


Figure 196. Fecundity in billions of ova for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles.



**Figure 197. Recruitment in billions of fish for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles.**

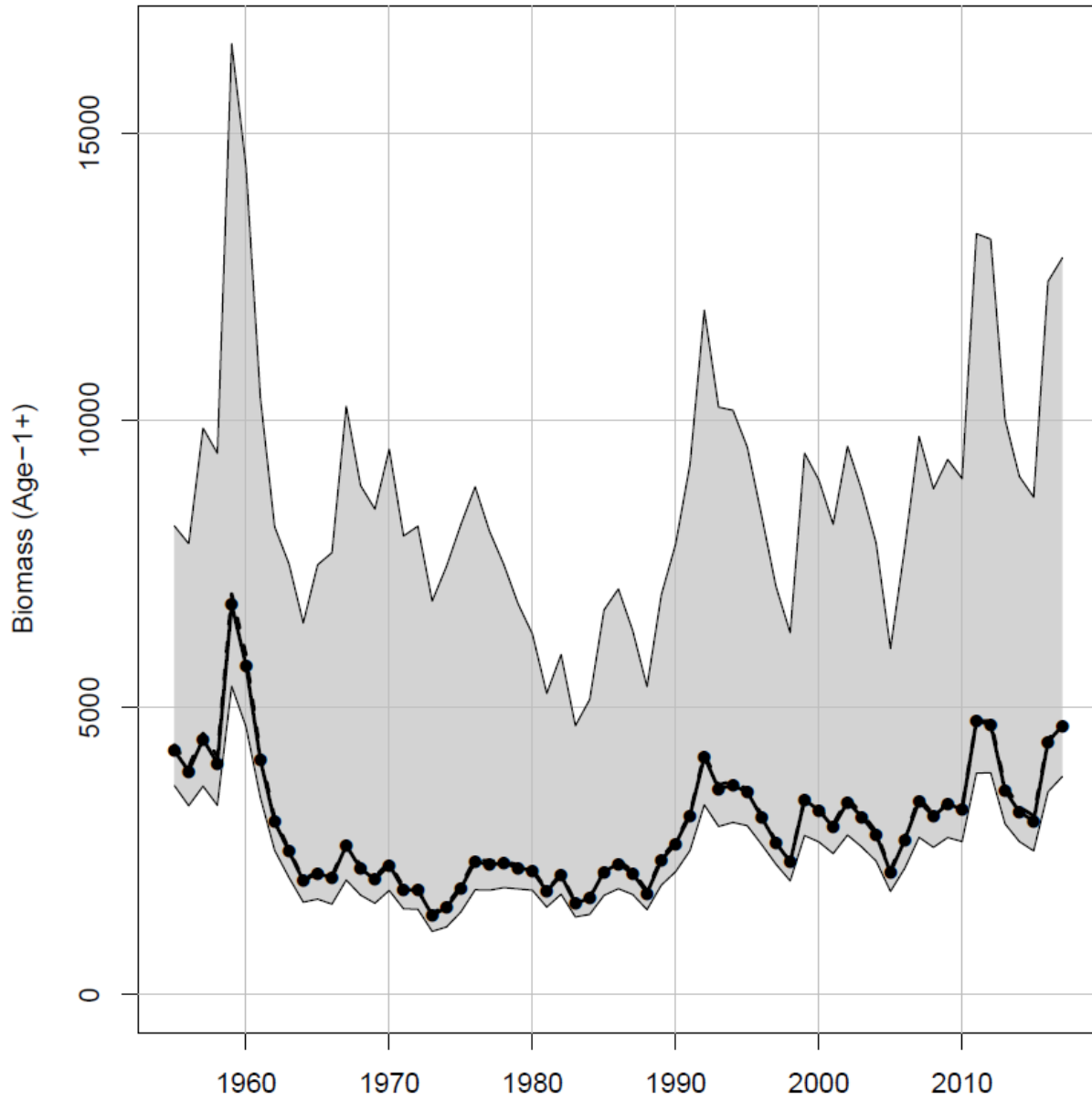


Figure 198. Age-1+ biomass for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles.

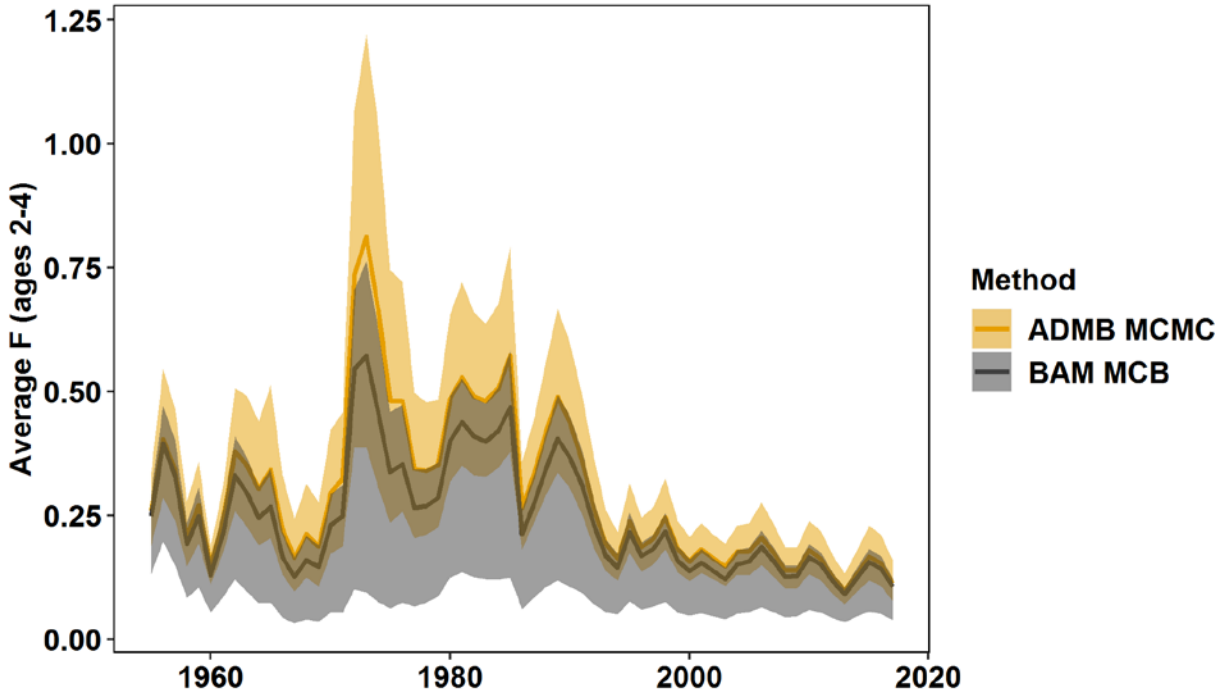


Figure 199. Geometric mean fishing mortality rate for ages-2 to -4 for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles and the MCMC analysis of the base run. The dark gold line for the MCMC analysis is the mean value estimated during the analysis.

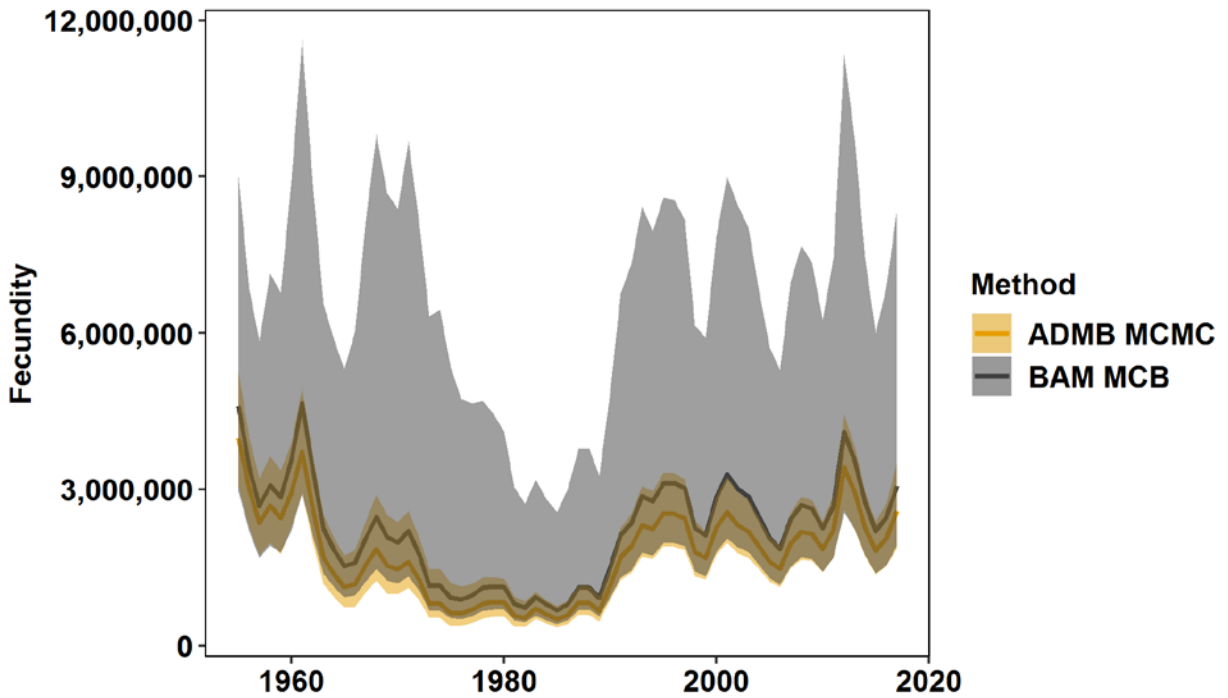


Figure 200. Fecundity in billions of ova for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles and the MCMC analysis of the base run. The dark gold line for the MCMC analysis is the median value estimated during the analysis.

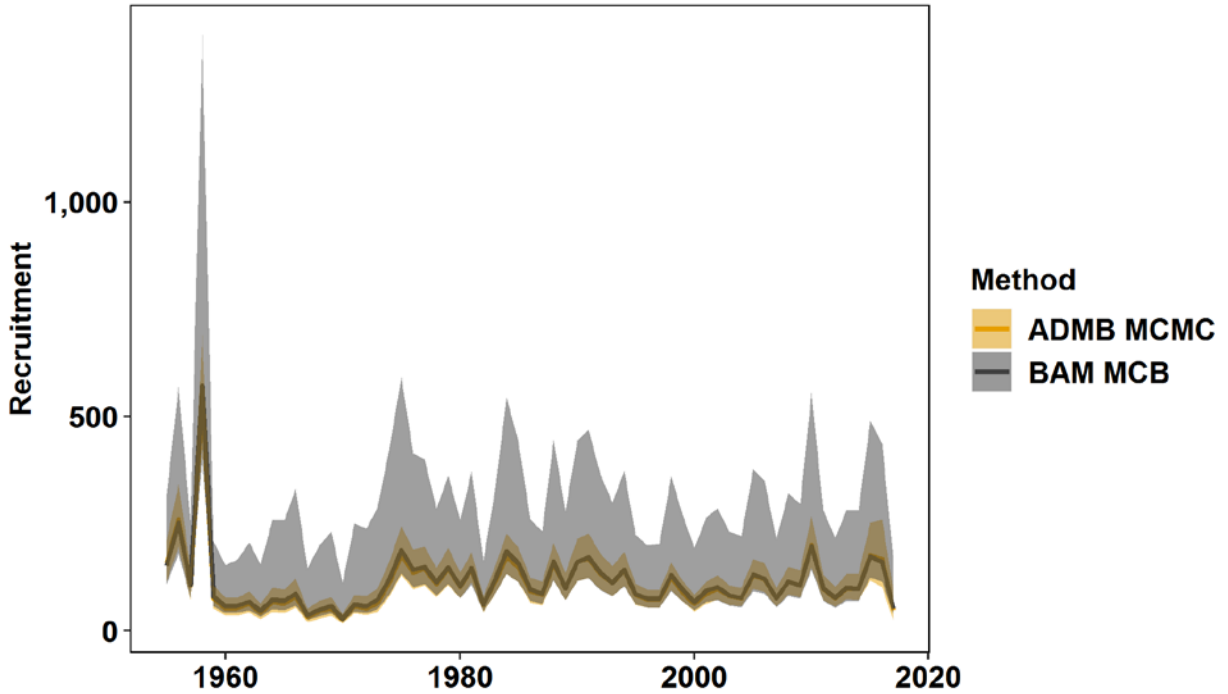


Figure 201. Recruitment in billions of fish for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles and the MCMC analysis of the base run. The dark gold line for the MCMC analysis is the mean value estimated during the analysis.

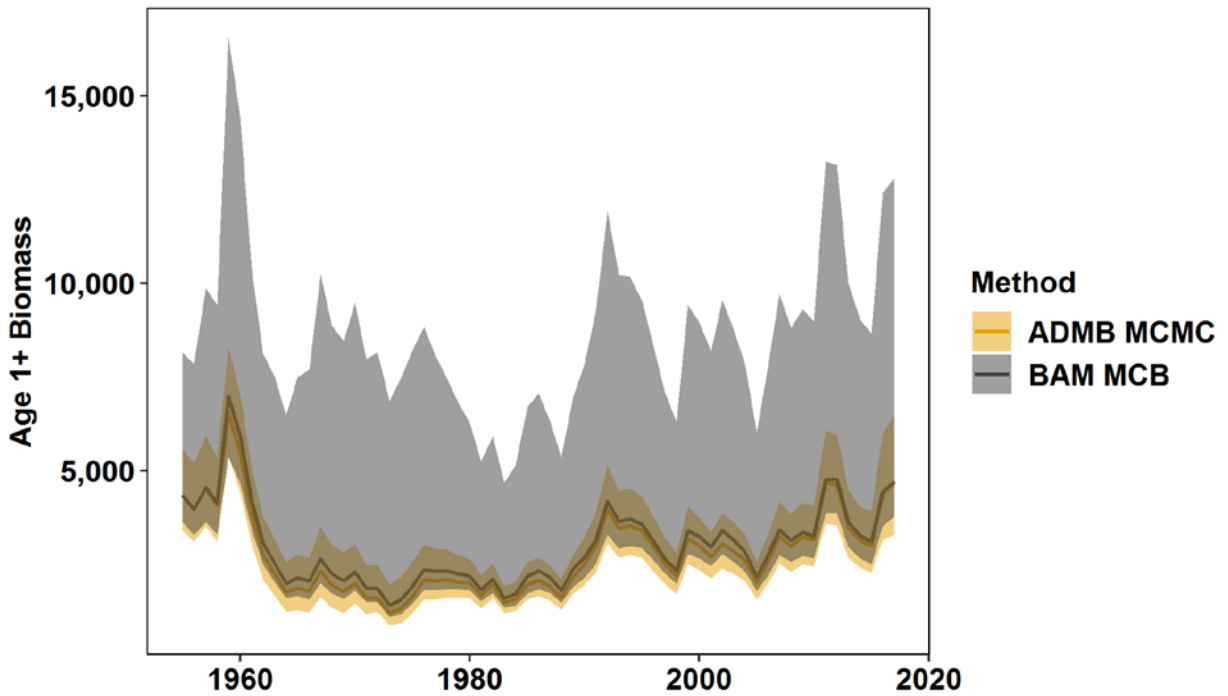


Figure 202. Age-1+ biomass for 1955-2017 for the MCB runs with 95<sup>th</sup> percentiles and the MCMC analysis of the base run. The dark gold line for the MCMC analysis is the mean value estimated during the analysis.

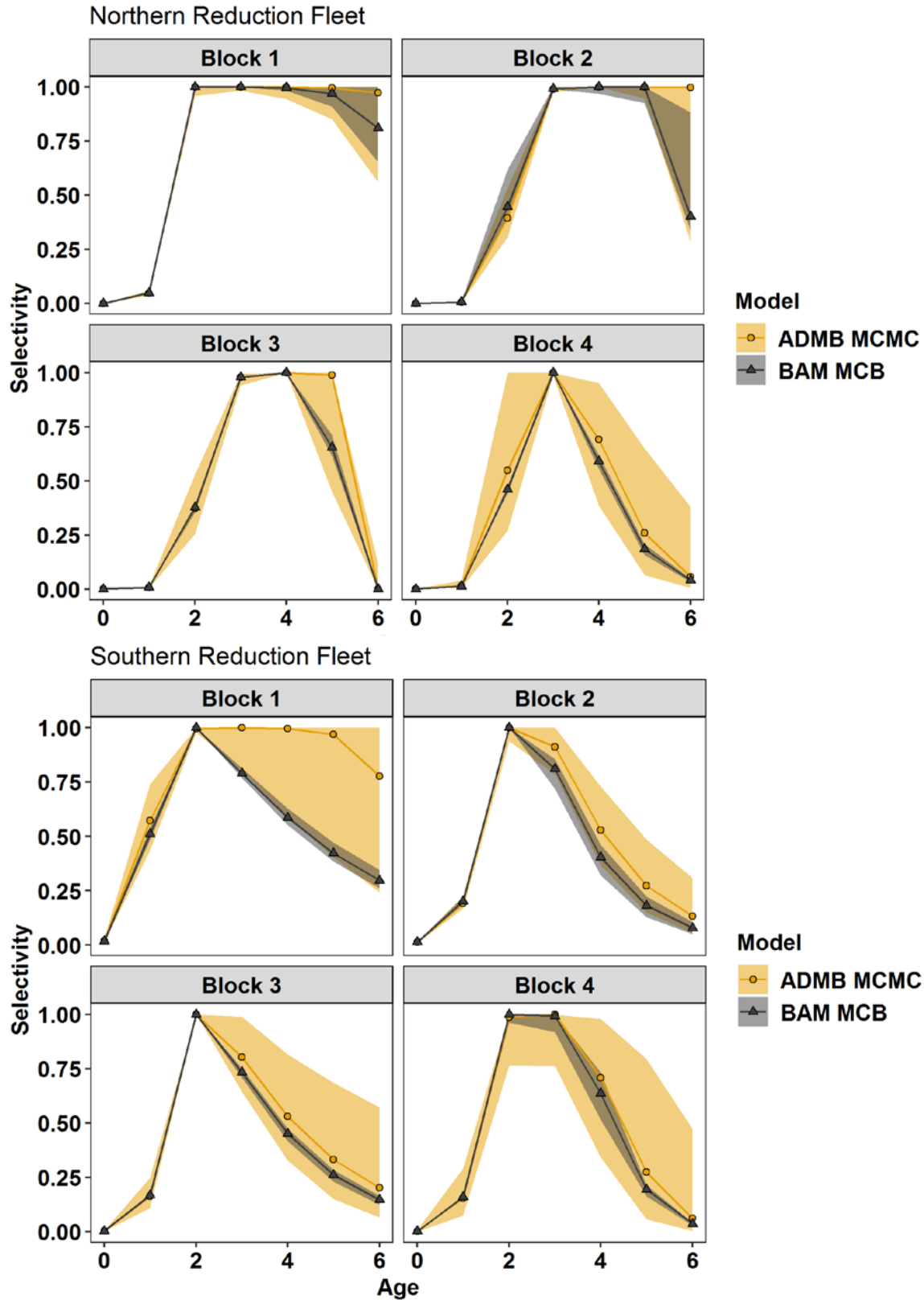


Figure 203. Selectivity estimates with 95% confidence intervals for the reduction fleets from the BAM MCB and MCMC analyses.

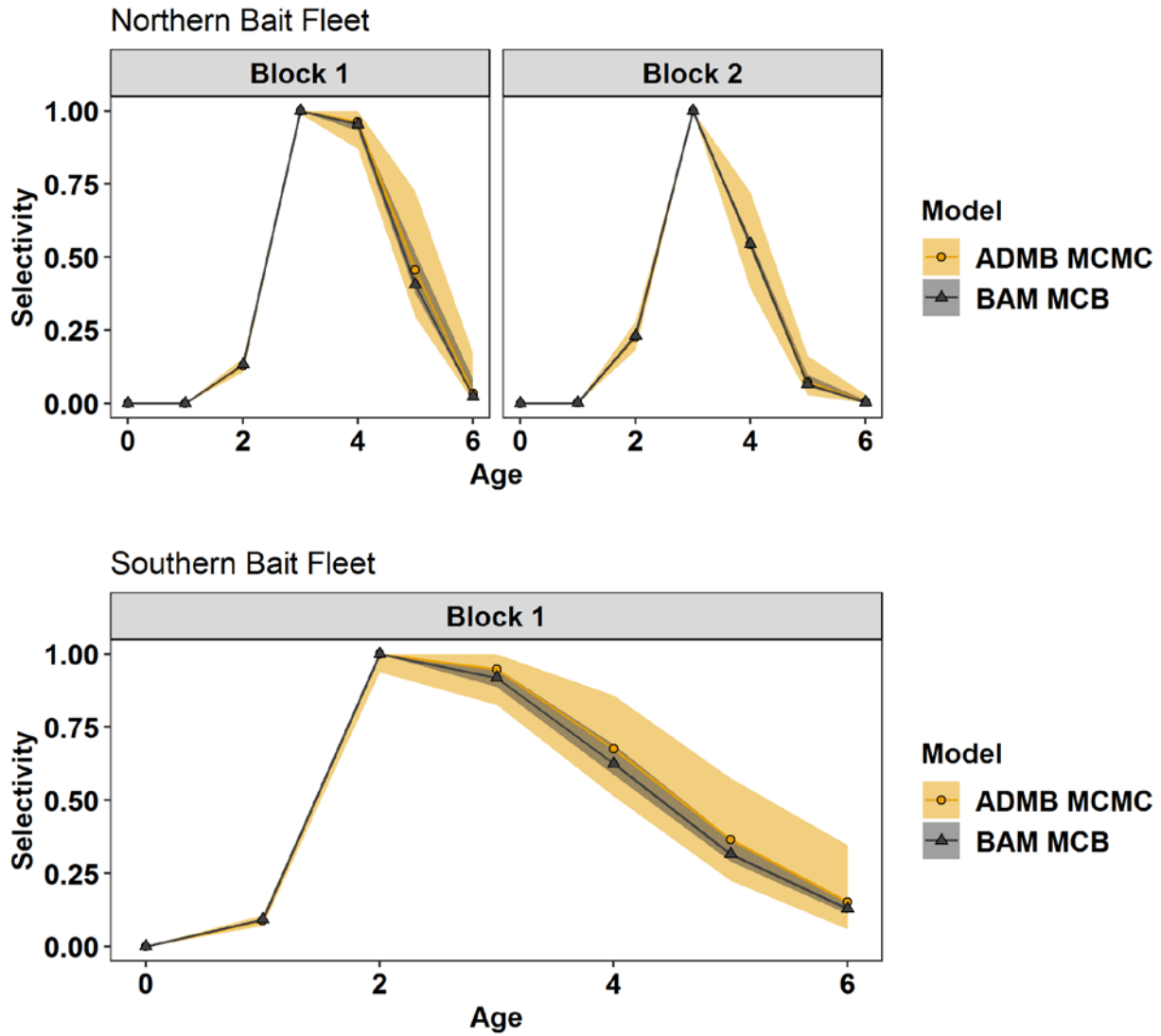
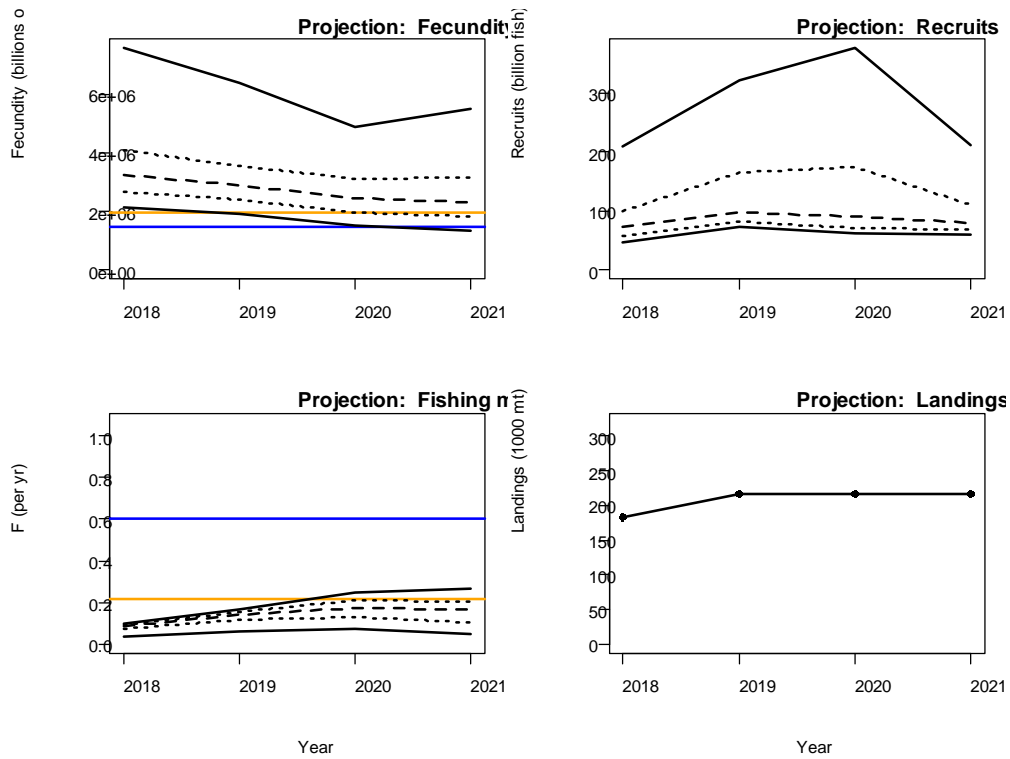
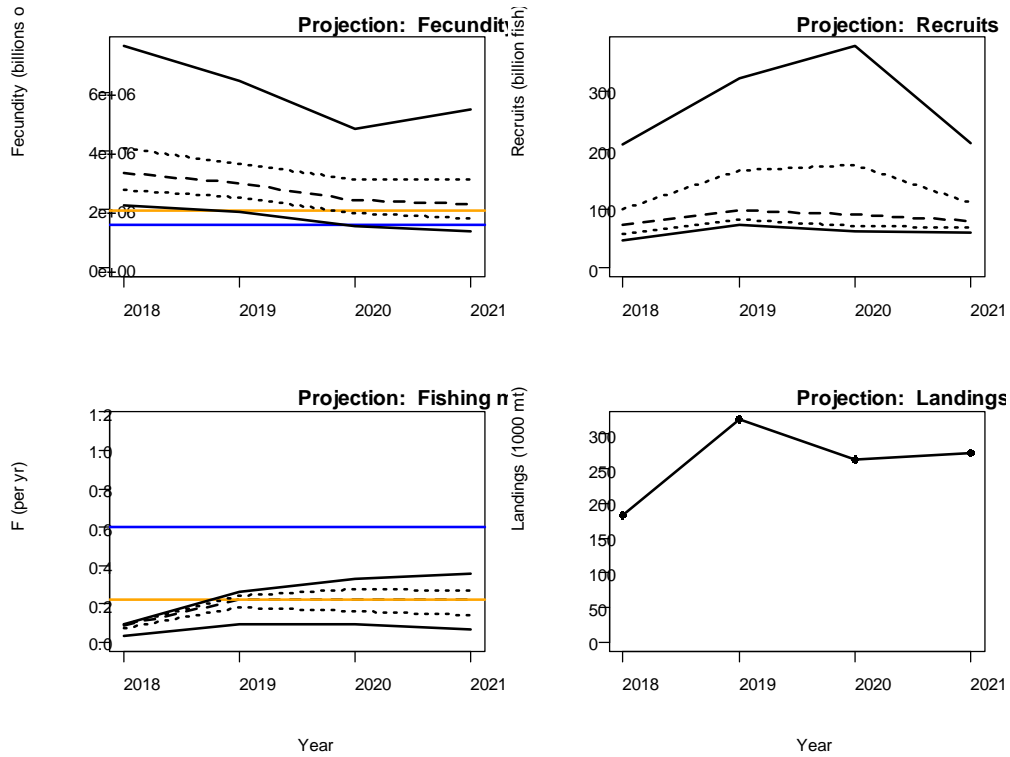


Figure 204. Selectivity estimates with 95% confidence intervals for the bait fleets from the BAM MCB and MCMC analyses.





**Figure 205.** Fecundity, recruits, geometric mean fishing mortality rate, and landings for projections done with a constant TAC of 216,000 mt for 2019-2021. The blue lines indicate the thresholds and the orange lines indicate the targets for the base run. The dashed black line is the 50<sup>th</sup> percentile (median), the dotted black lines are the 25<sup>th</sup> and 75<sup>th</sup> percentiles, and the solid black lines are the 5<sup>th</sup> and 95<sup>th</sup> percentiles.



**Figure 206.** Fecundity, recruits, geometric mean fishing mortality rate, and landings for projections done to reach the  $F_{TARGET}$  during 2019-2021. The blue lines indicate the thresholds and the orange lines indicate the targets for the base run. The dashed black line is the 50<sup>th</sup> percentile (median), the dotted black lines are the 25<sup>th</sup> and 75<sup>th</sup> percentiles, and the solid black lines are the 5<sup>th</sup> and 95<sup>th</sup> percentiles.

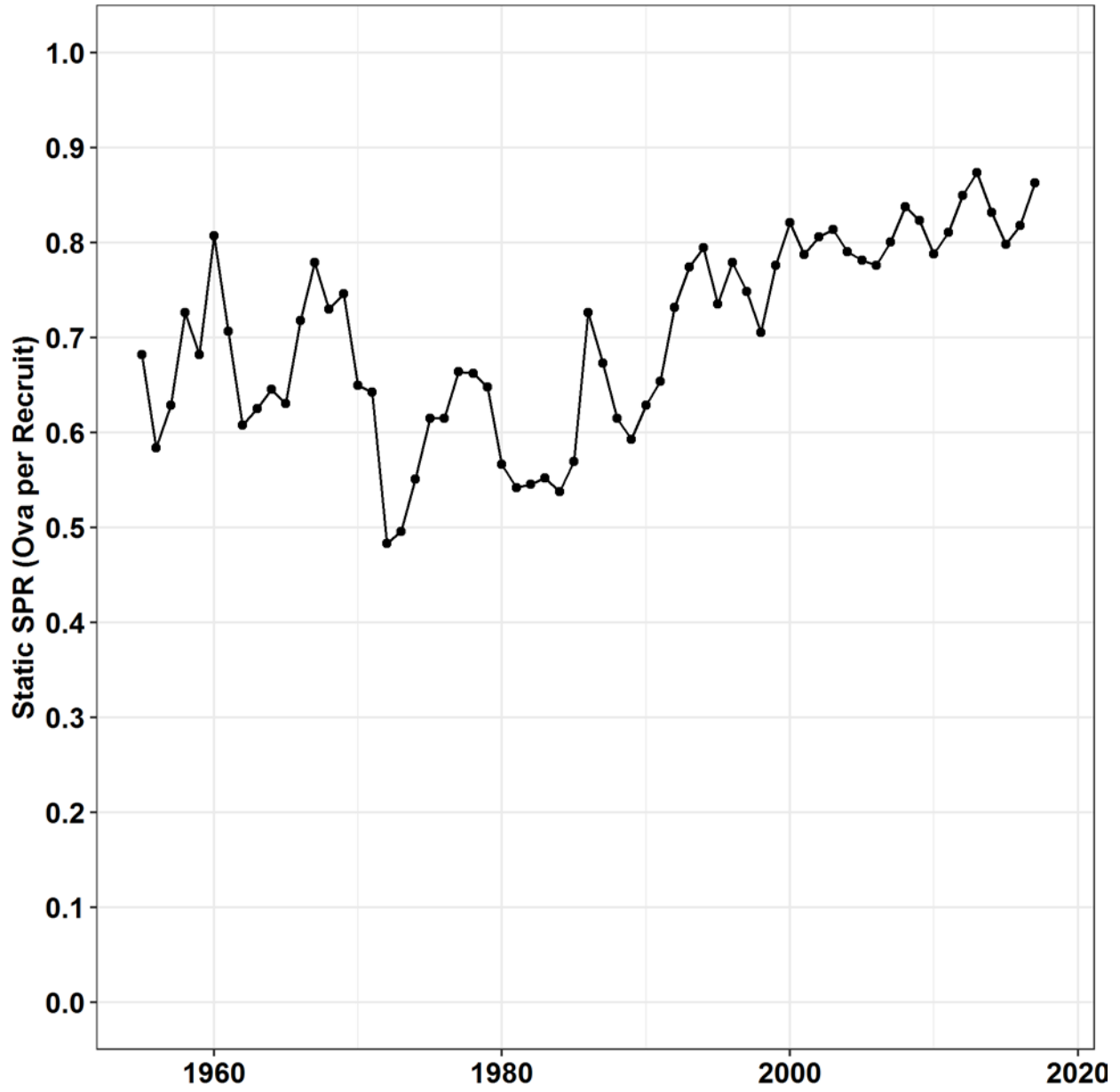
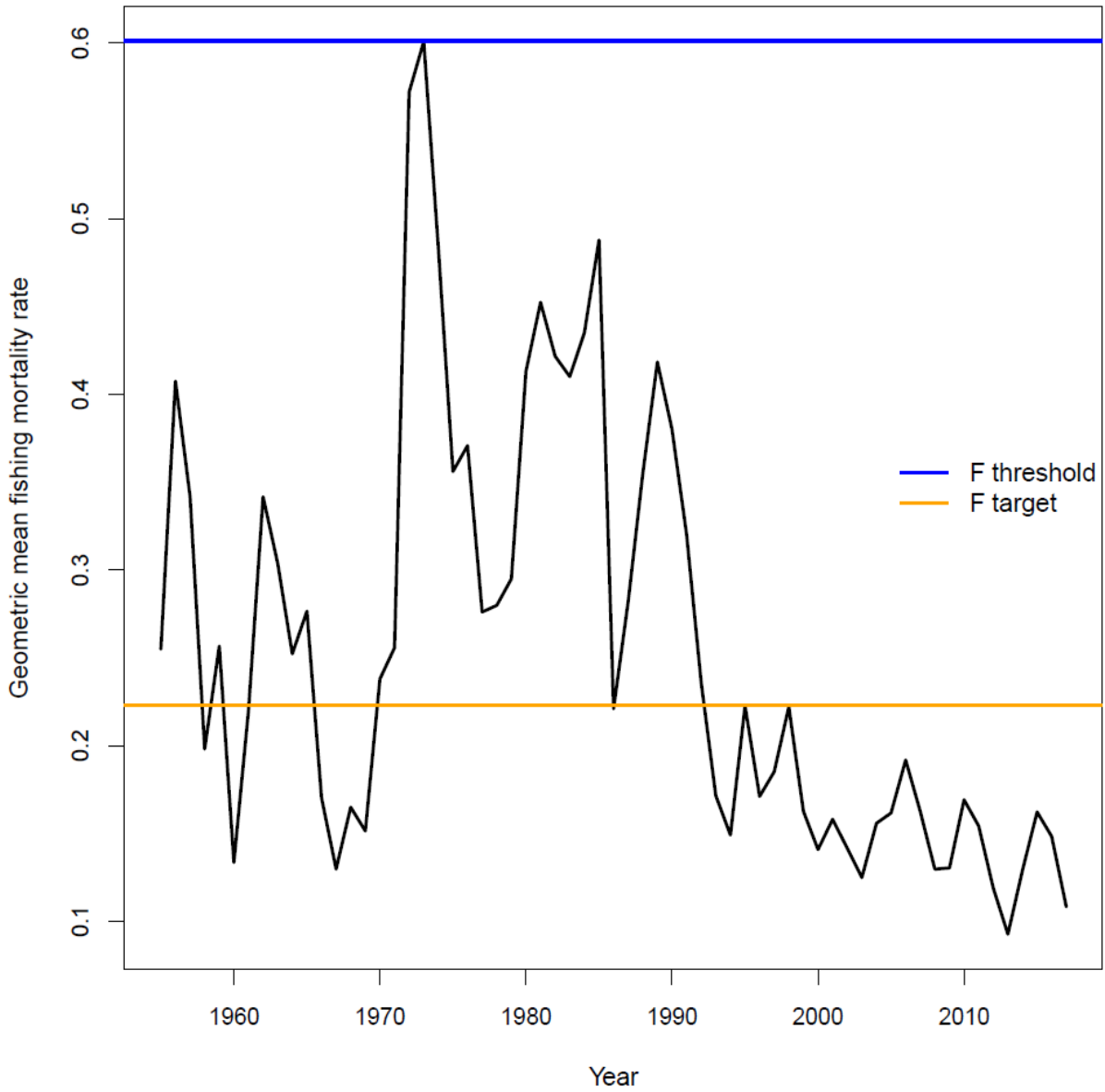
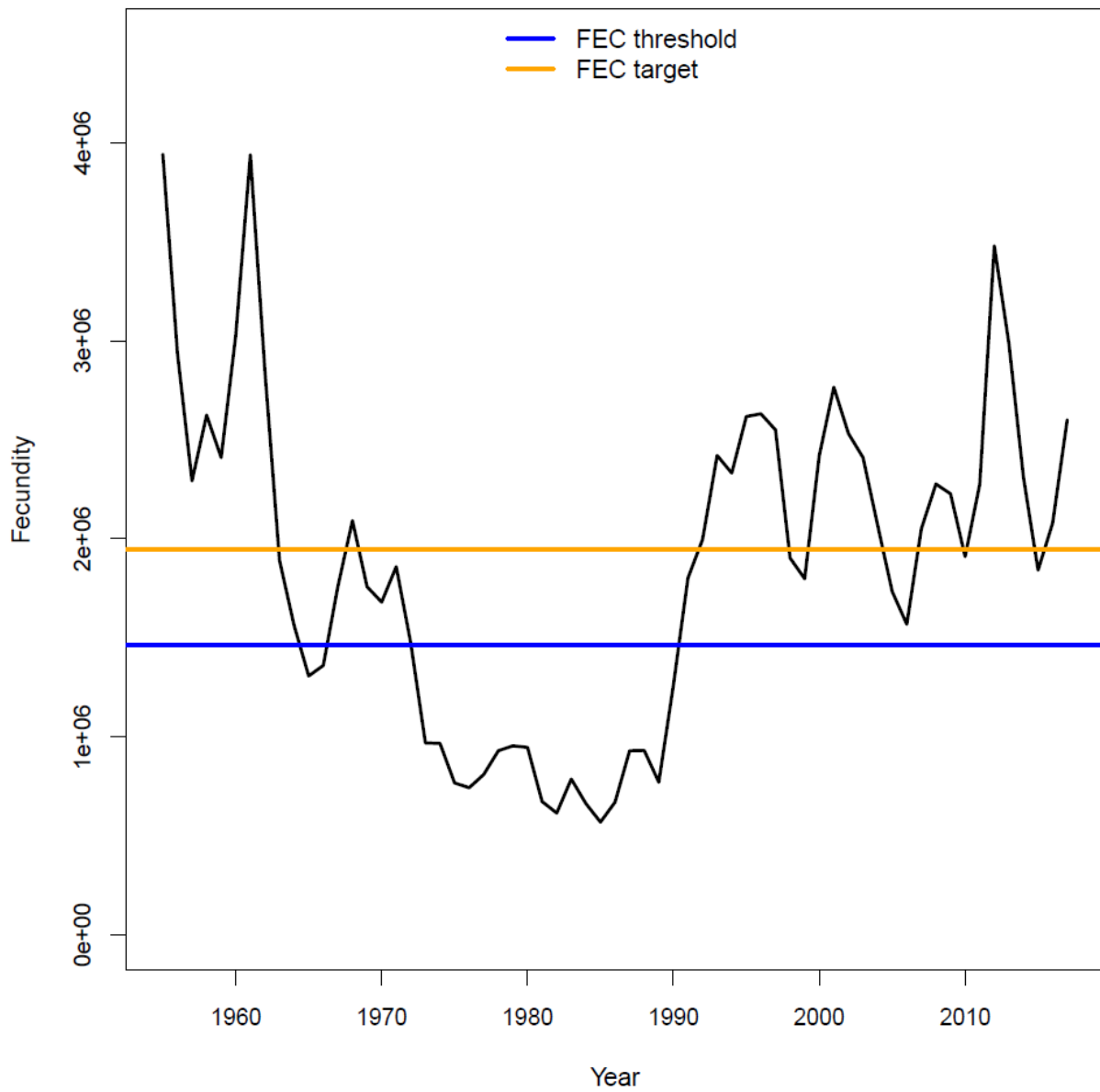


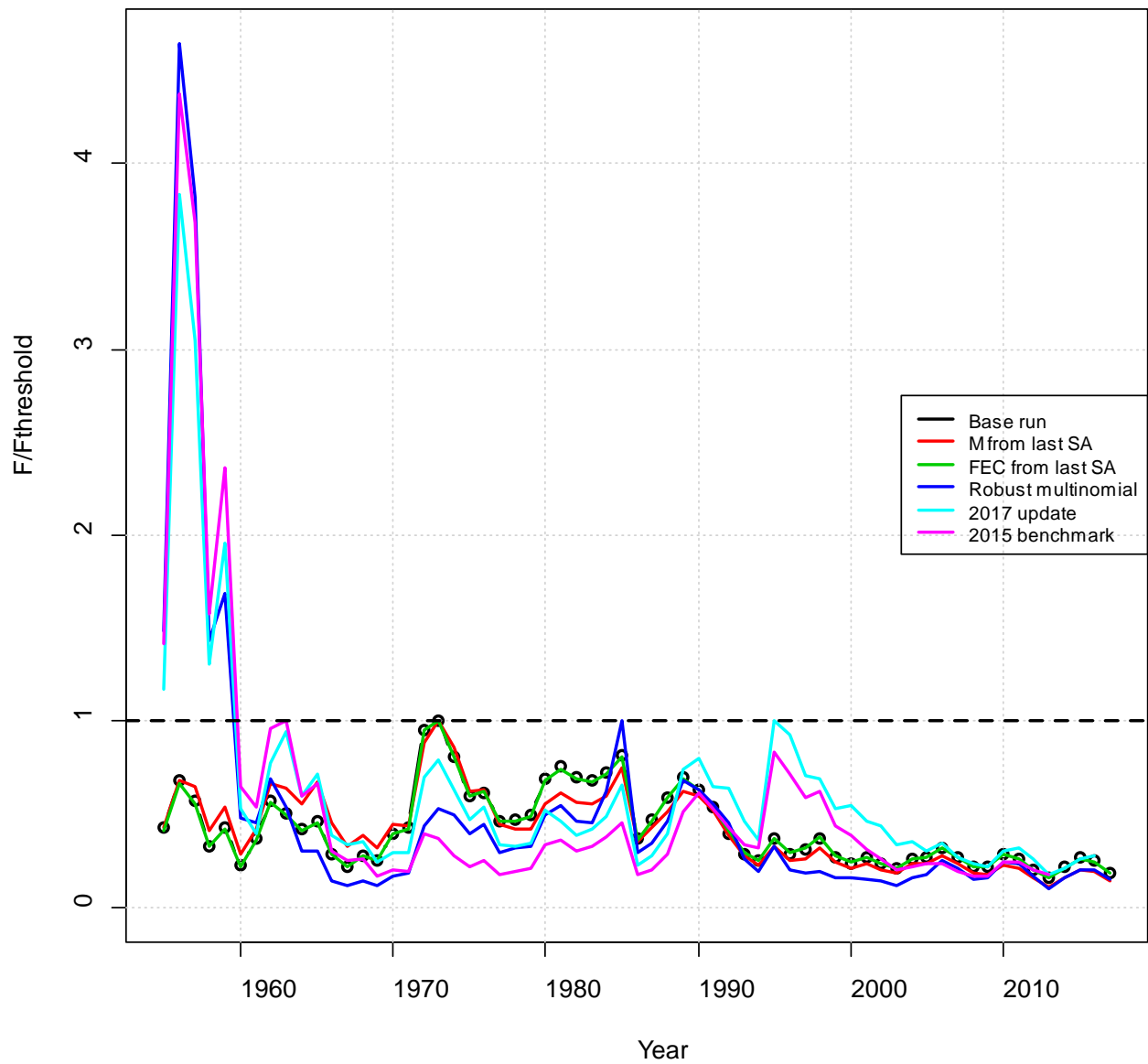
Figure 207. Static spawning potential ratio (SPR) for Atlantic menhaden for 1955-2017.



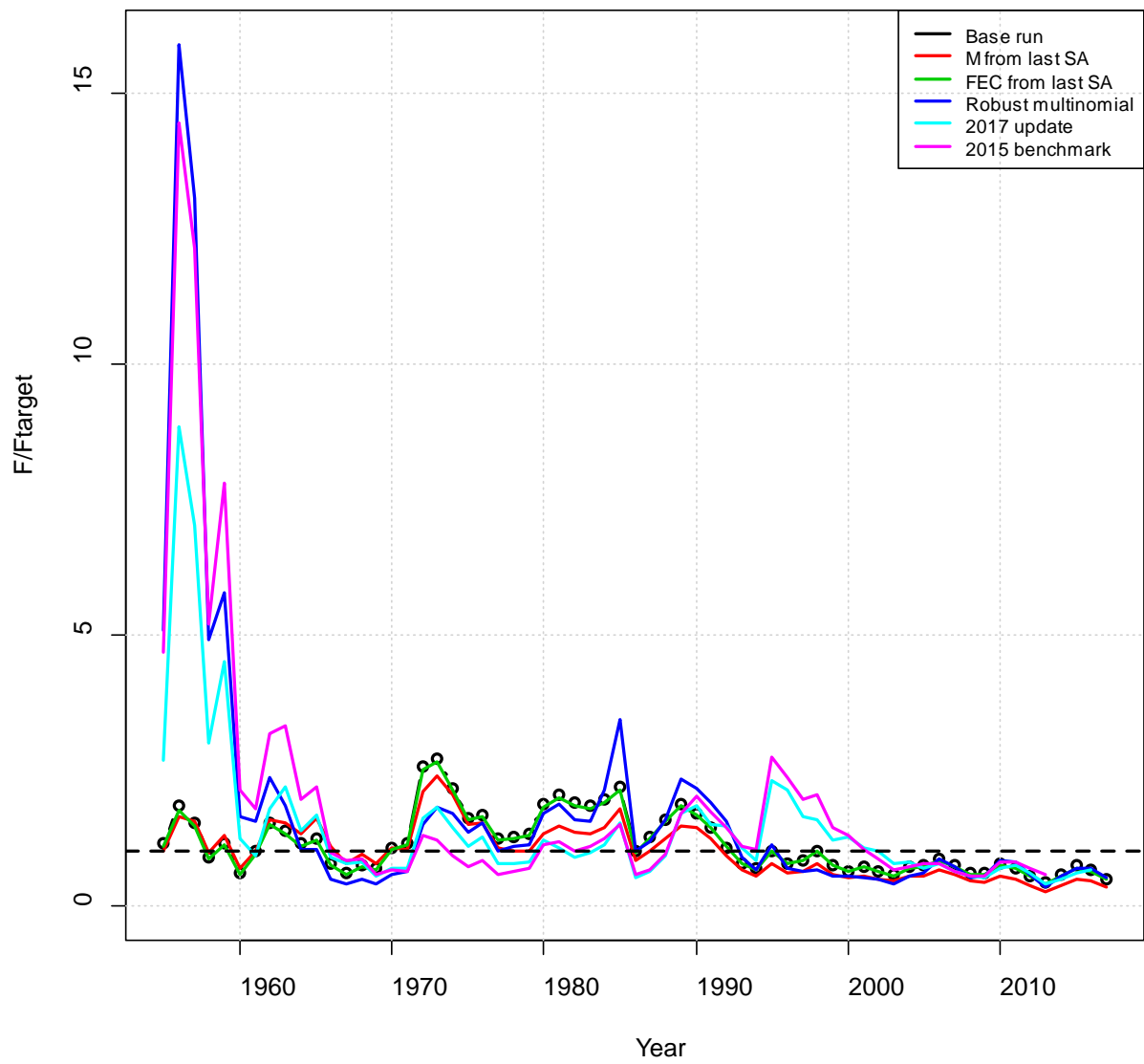
**Figure 208. Geometric mean fishing mortality rate of ages-2 to -4 during 1955-2017. The blue line indicates the threshold and the orange line indicates the targets for the base run.**



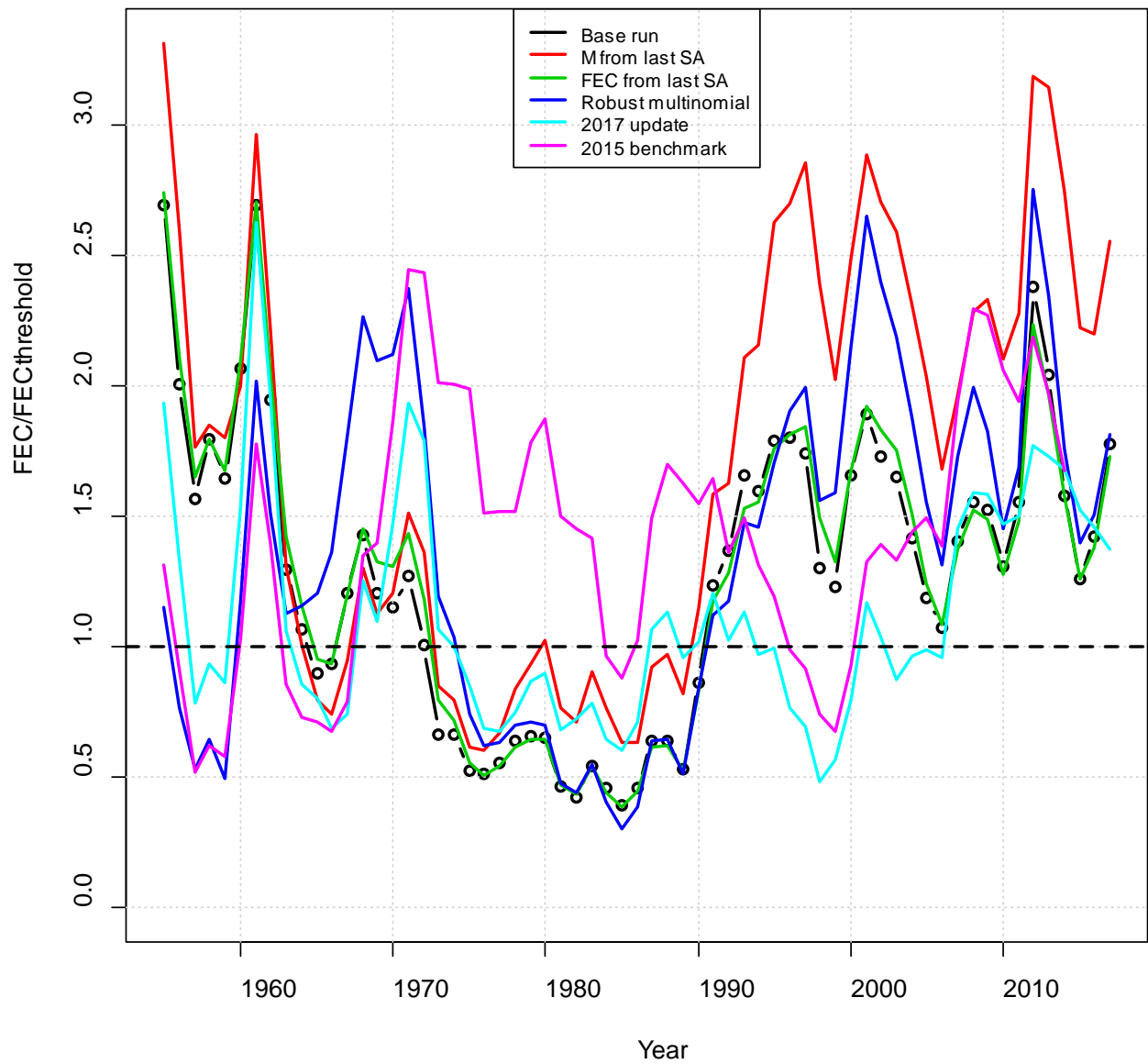
**Figure 209. Fecundity time series for 1955-2017. The blue line indicates the threshold and the orange line indicates the target for the base run.**



**Figure 210. Fishing mortality rate divided by the threshold  $F$  for the suite of sensitivity runs related to continuity with the last update and benchmark assessments.**

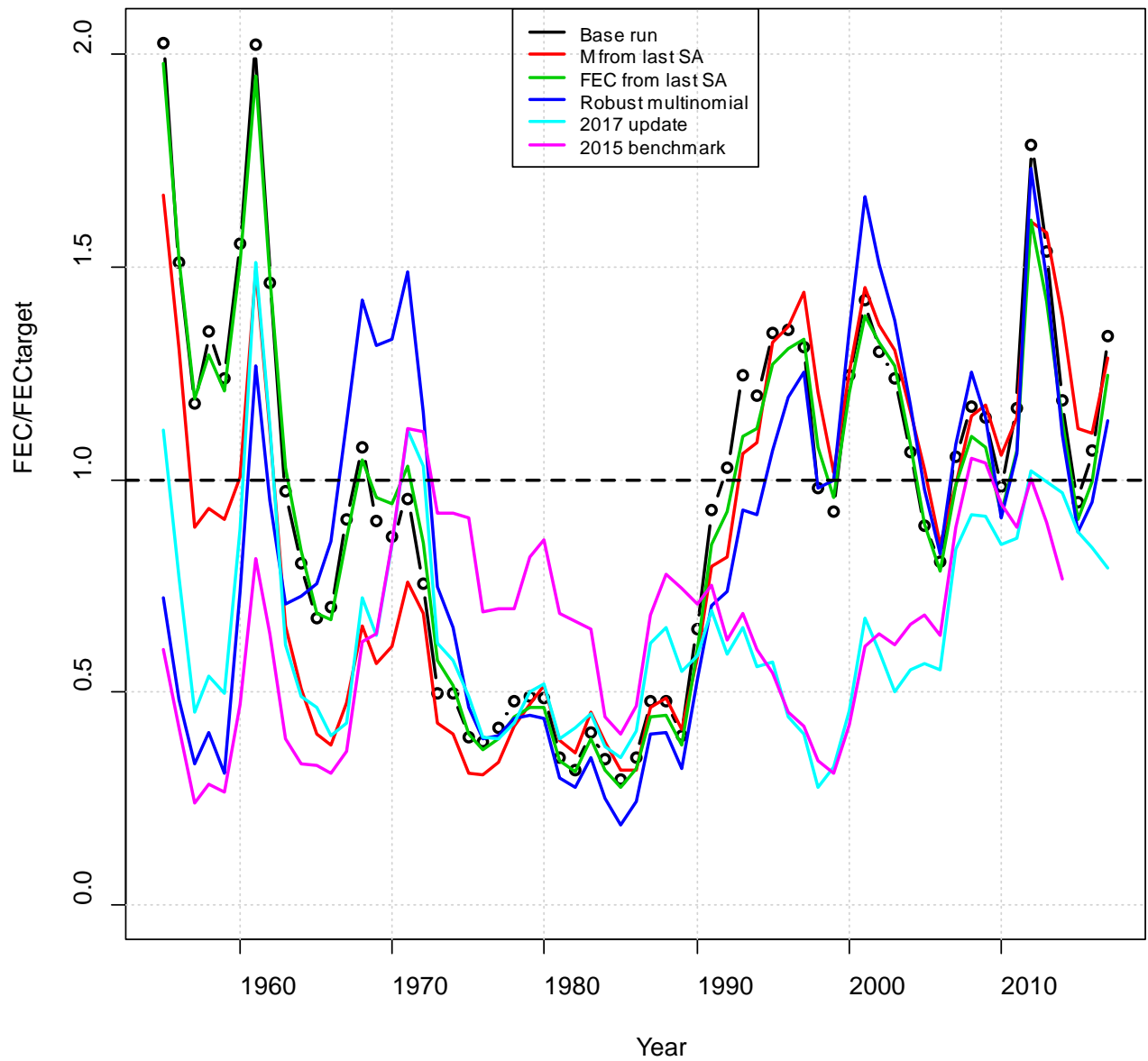


**Figure 211. Fishing mortality rate divided by the target  $F$  for the suite of sensitivity runs related to continuity with the last update and benchmark assessments.**

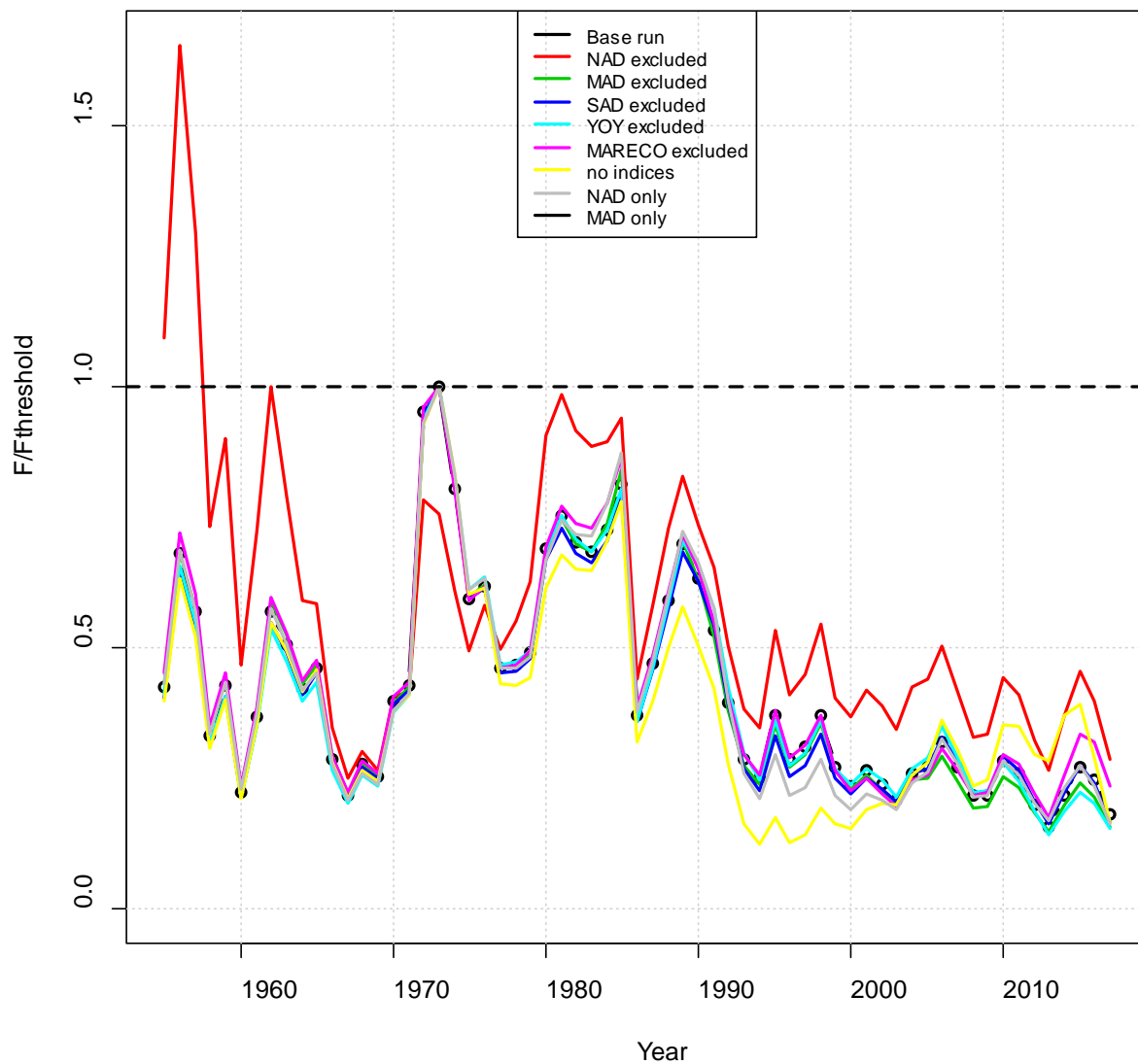


**Figure 212. Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to continuity with the last update and benchmark assessments.**

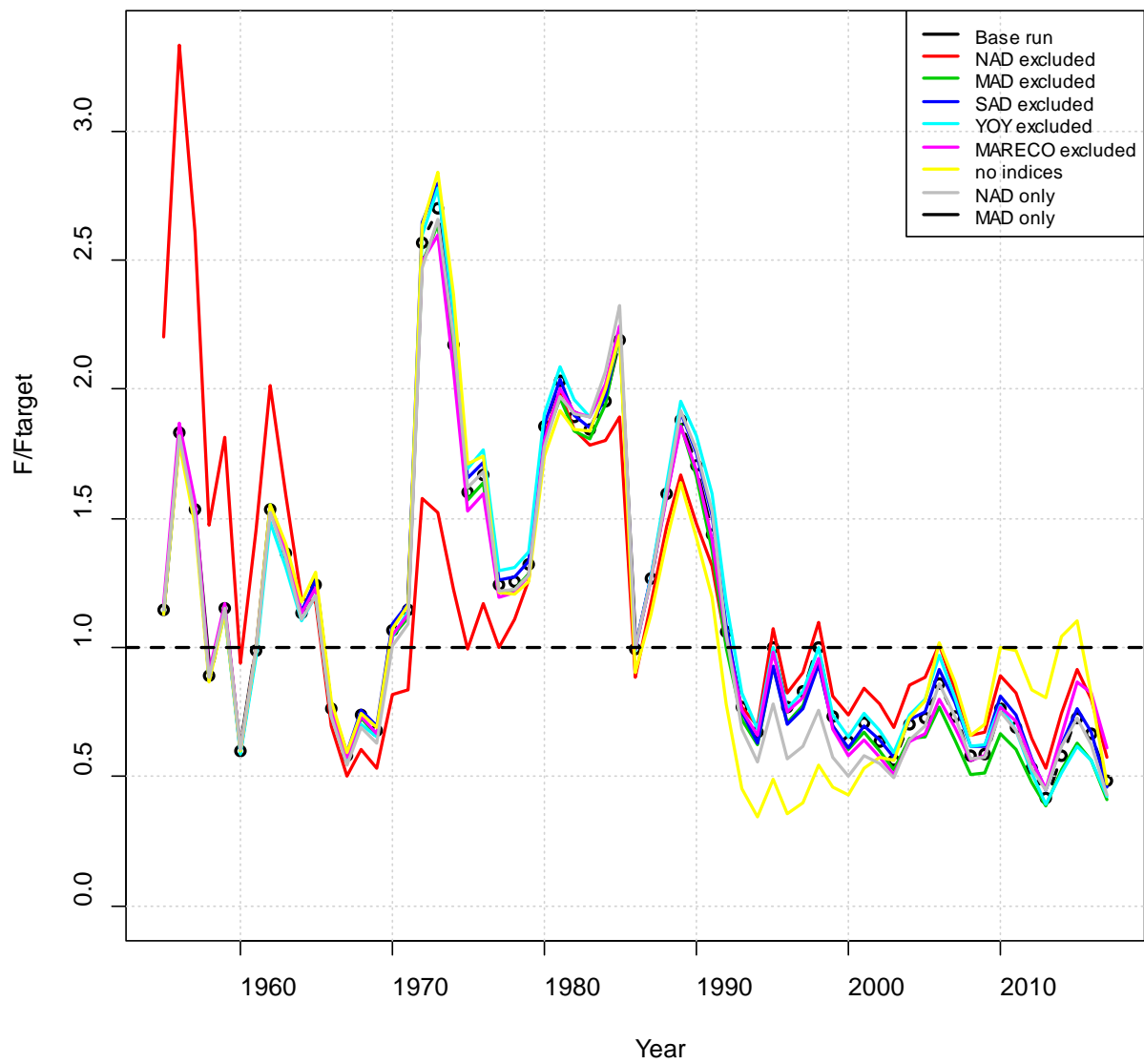




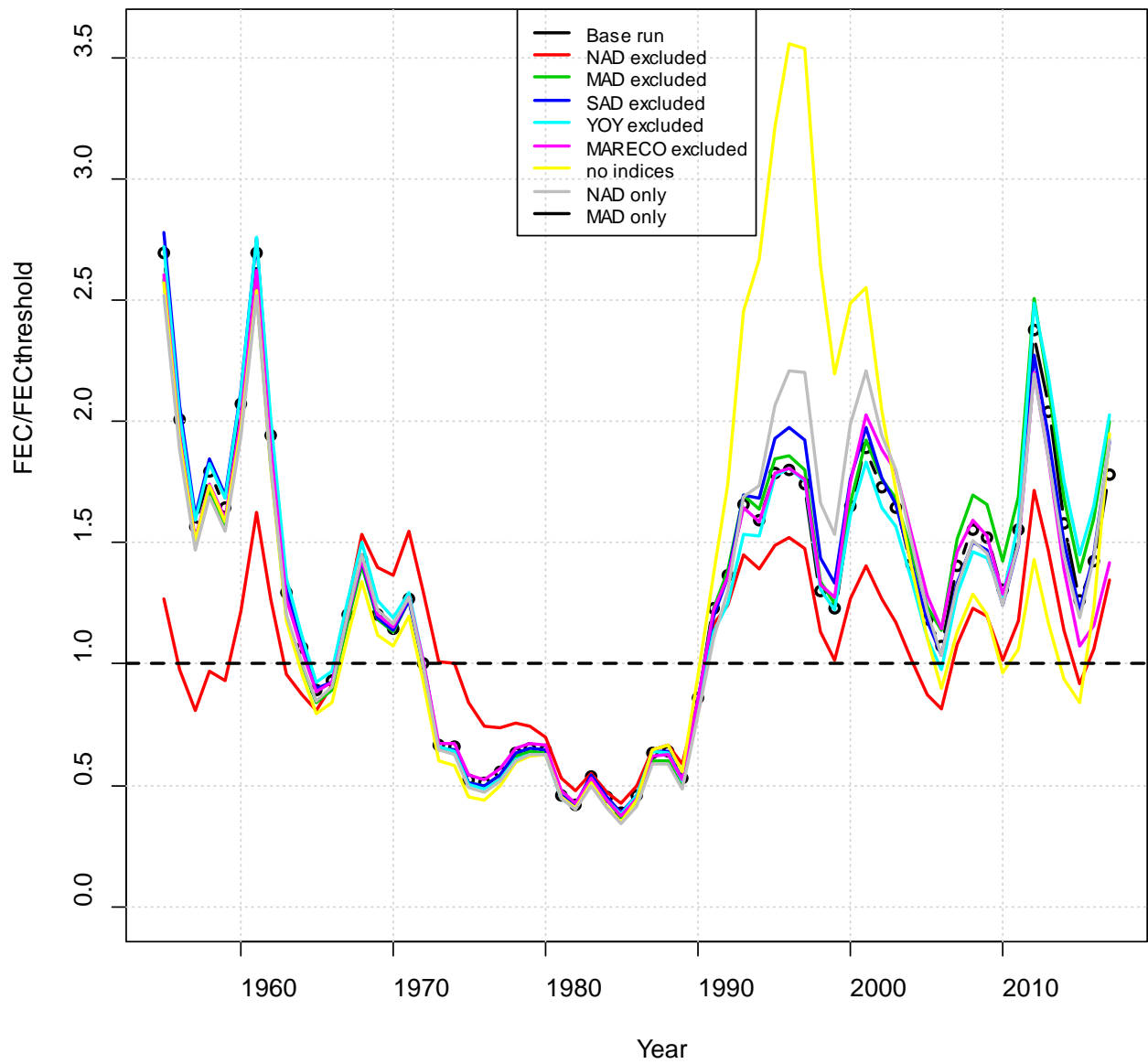
**Figure 213. Fecundity divided by the target fecundity for the suite of sensitivity runs related to continuity with the last update and benchmark assessments.**



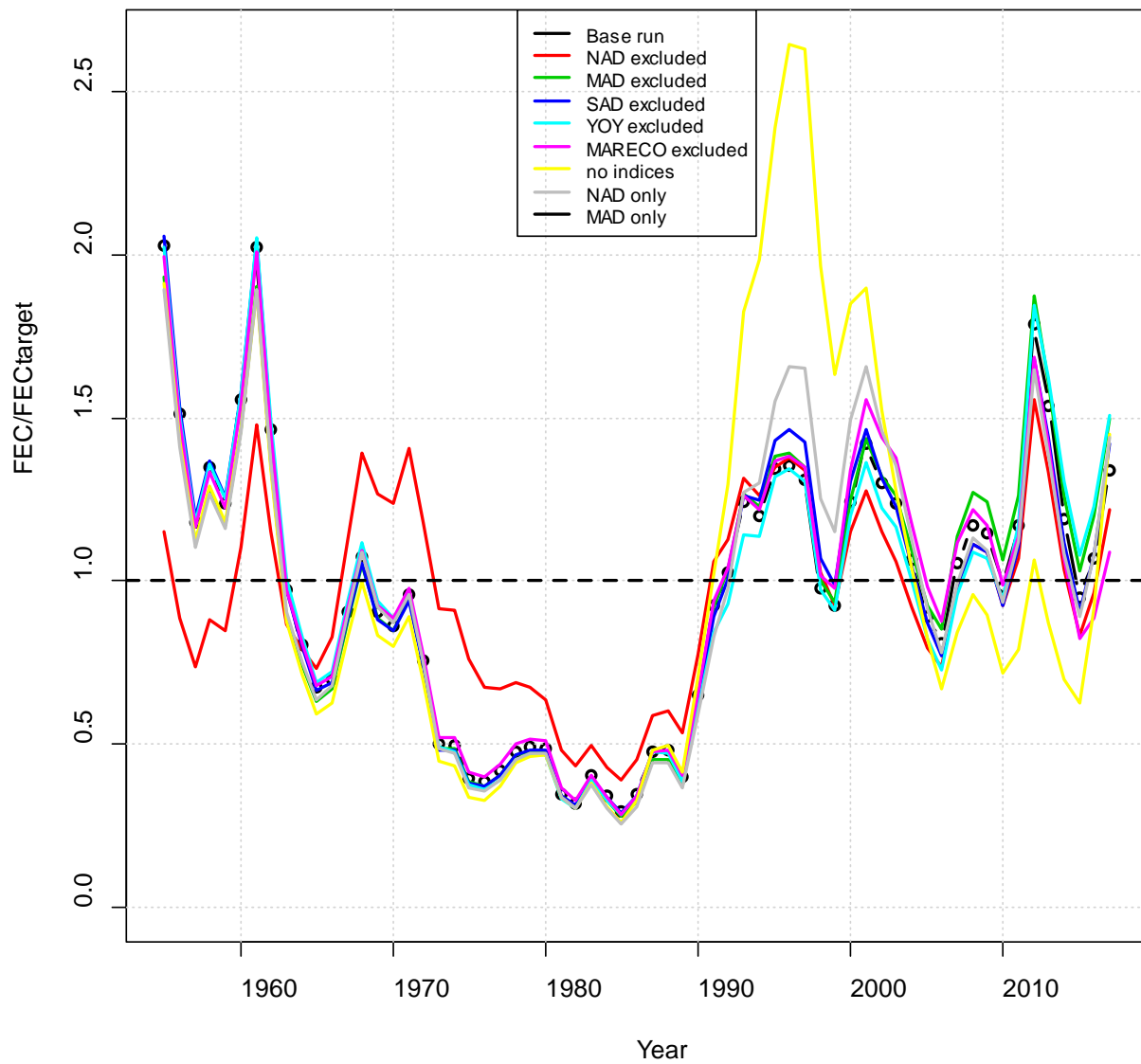
**Figure 214. Fishing mortality rate divided by the threshold  $F$  for the suite of sensitivity runs related to index choice.**



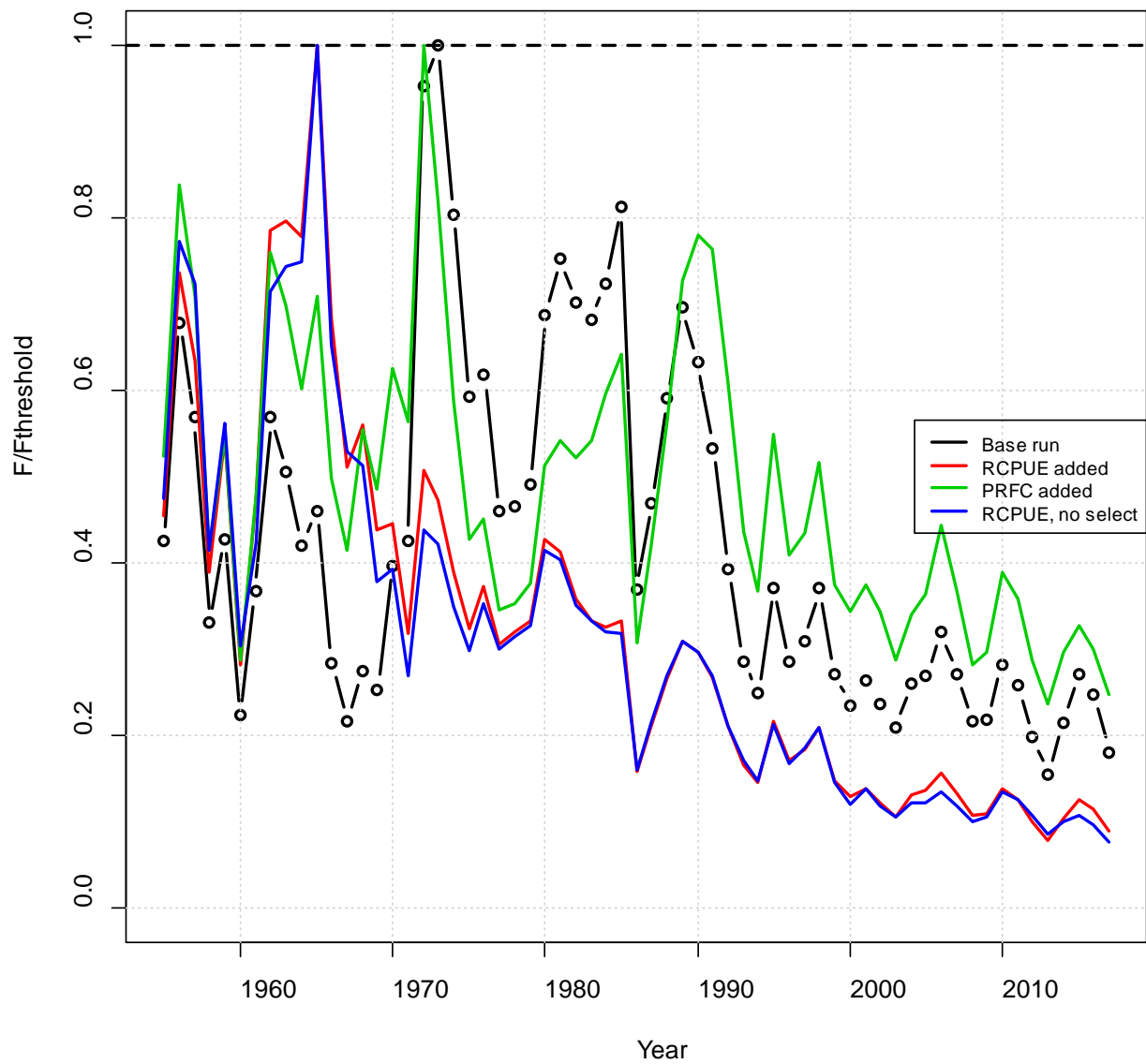
**Figure 215. Fishing mortality rate divided by the target  $F$  for the suite of sensitivity runs related to index choice.**



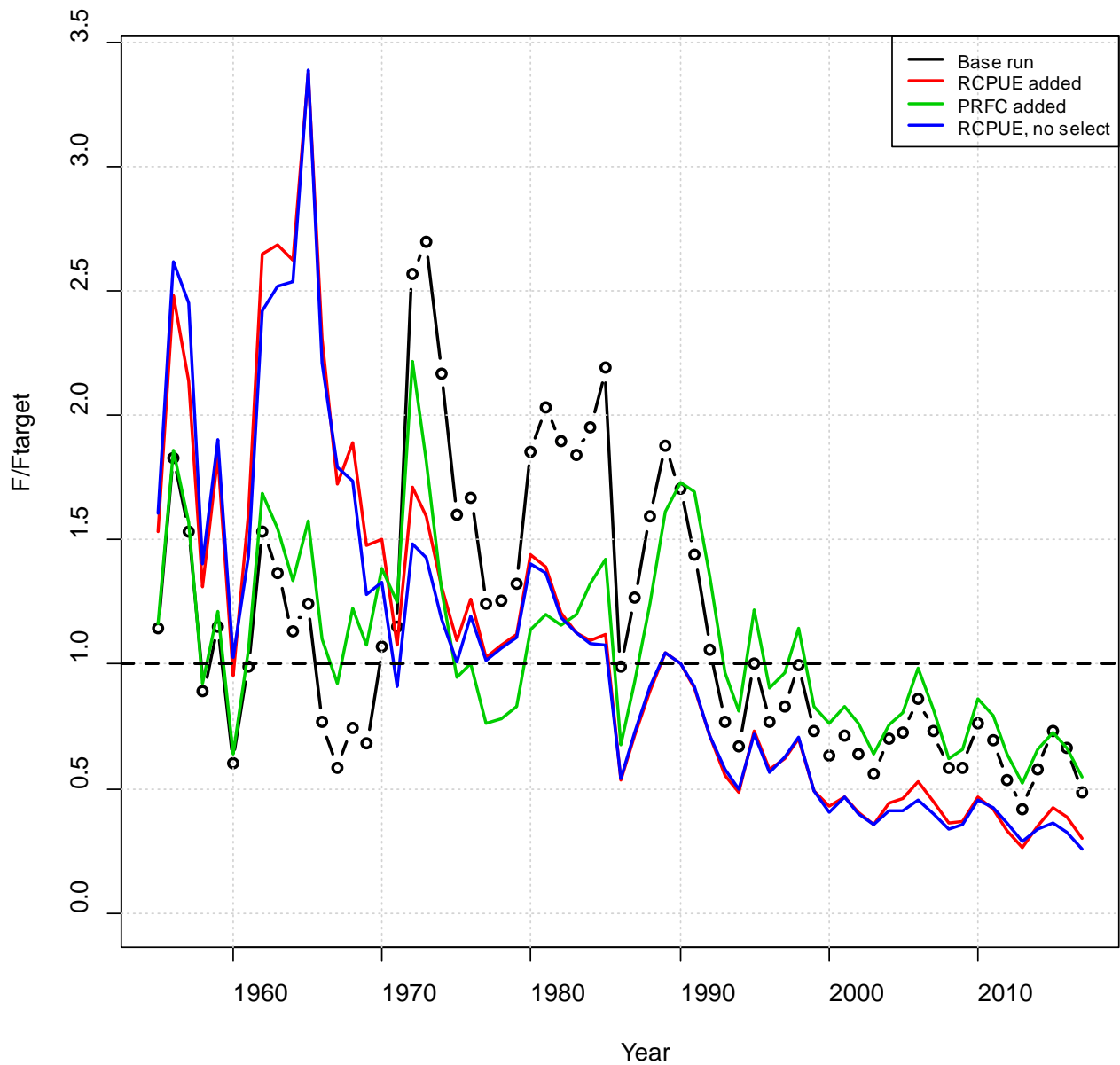
**Figure 216. Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to index choice.**



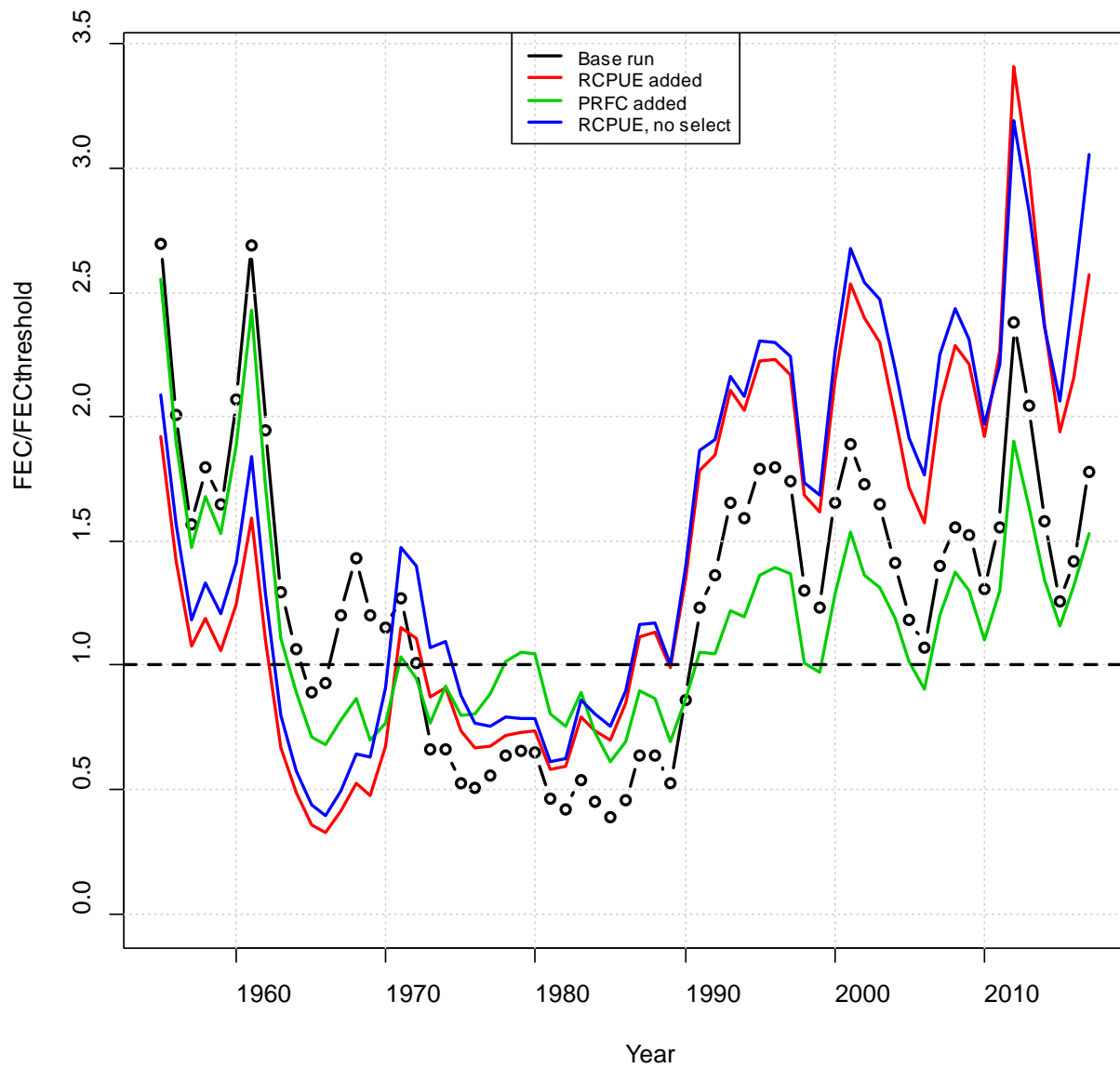
**Figure 217. Fecundity divided by the target fecundity for the suite of sensitivity runs related to index choice.**



**Figure 218. Fishing mortality rate divided by the threshold  $F$  for the suite of sensitivity runs related to index choice and the ERP models.**

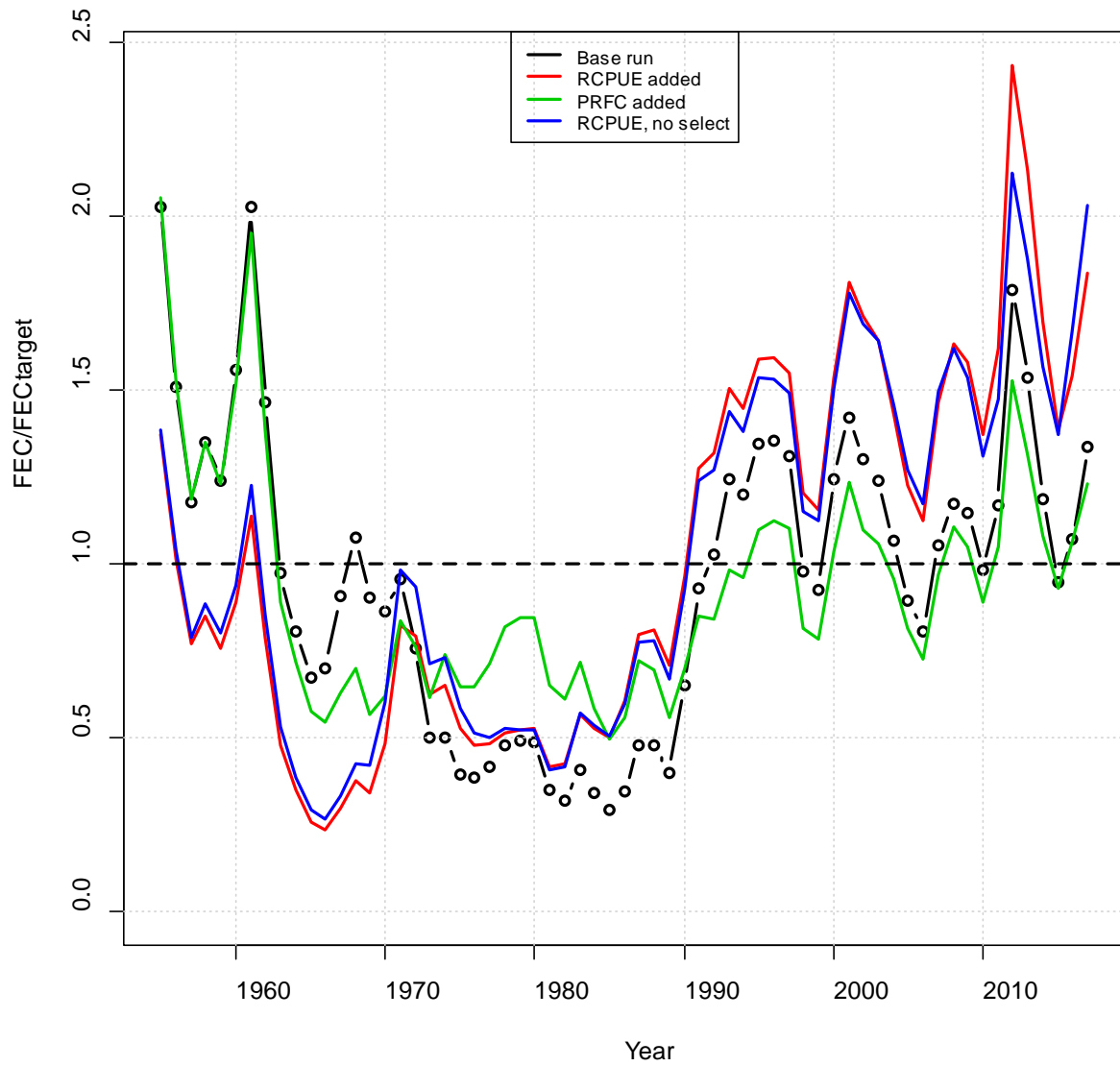


**Figure 219. Fishing mortality rate divided by the target  $F$  for the suite of sensitivity runs related to index choice and the ERP models.**

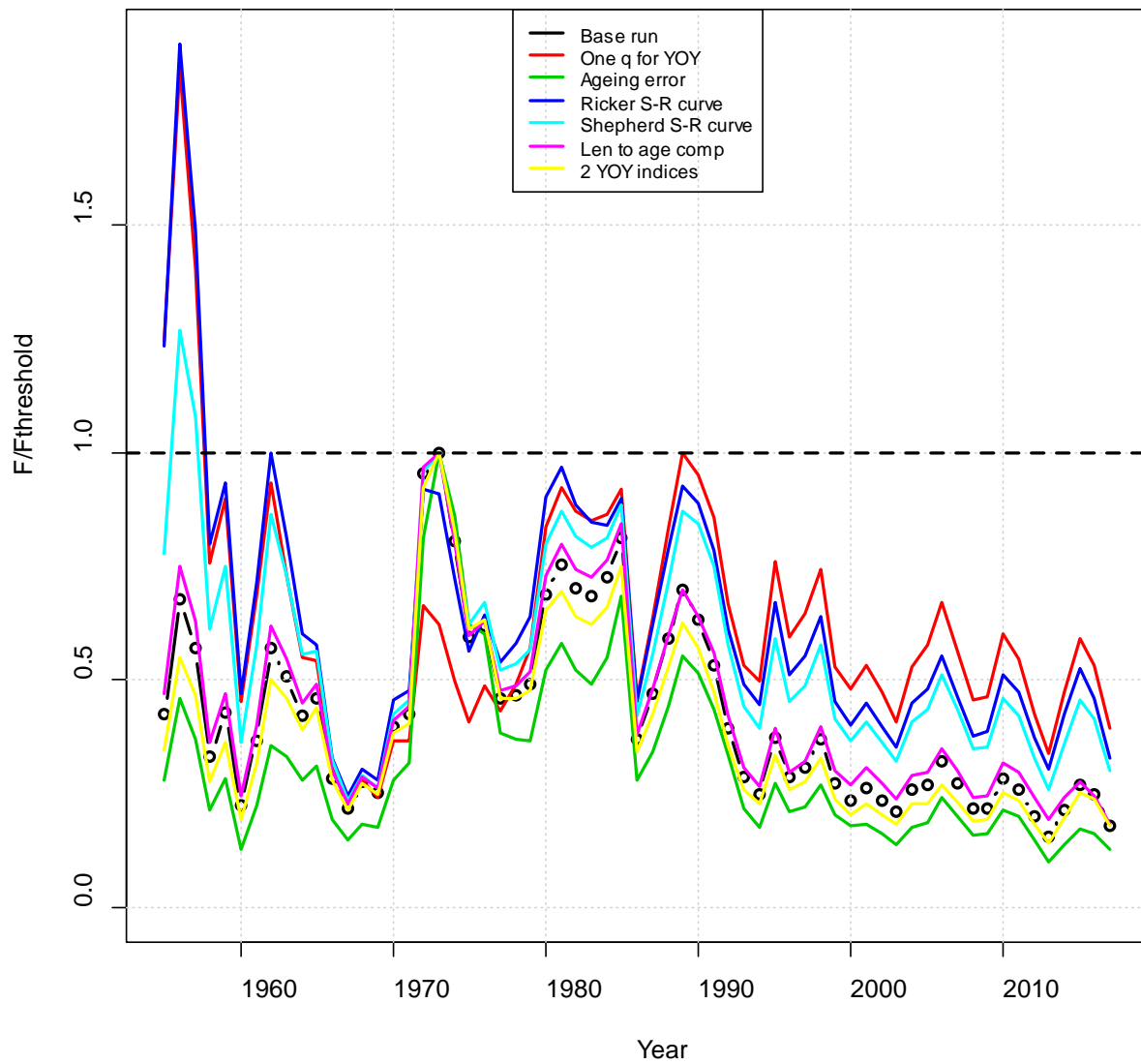


**Figure 220. Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to index choice and the ERP models.**

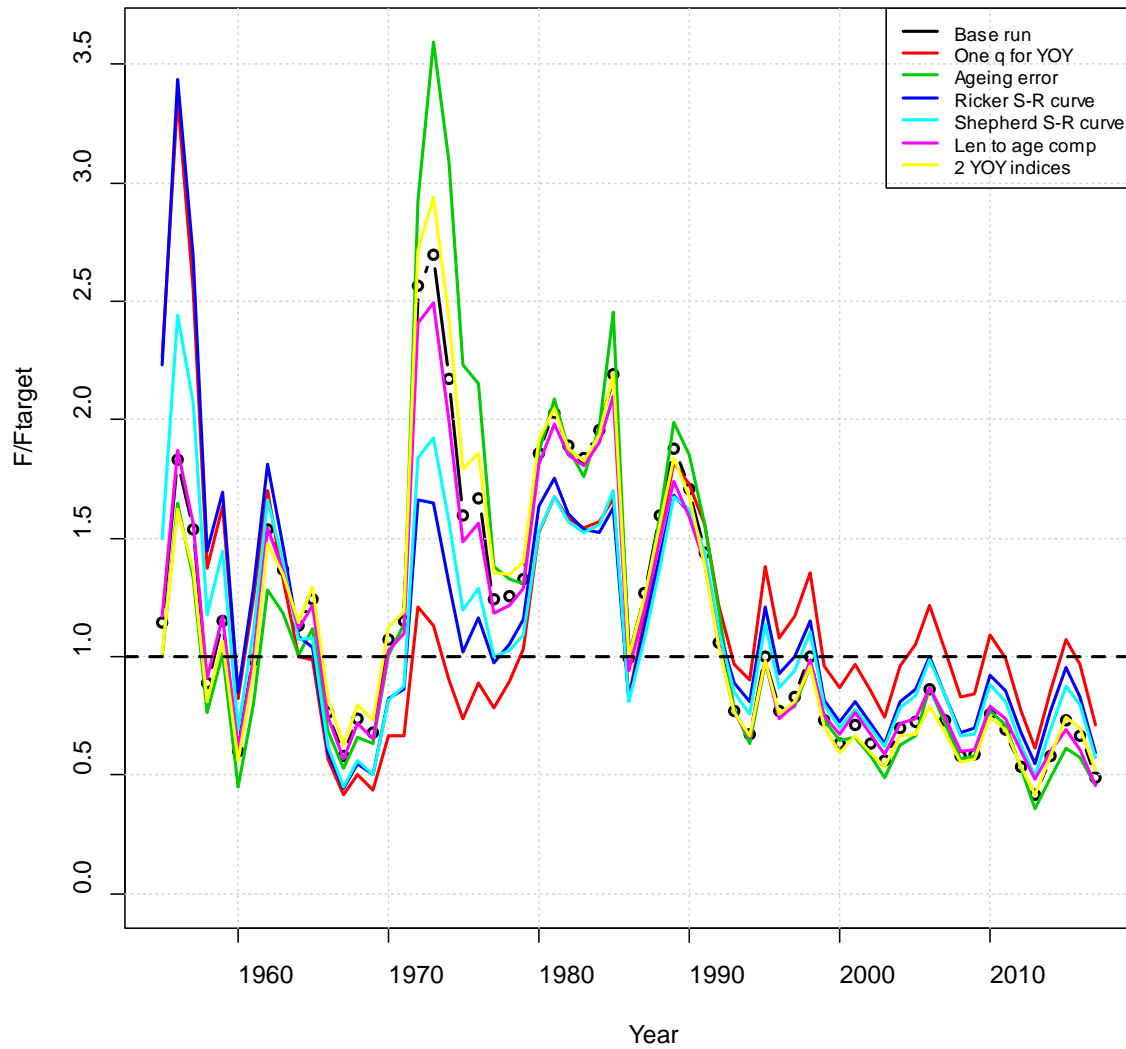




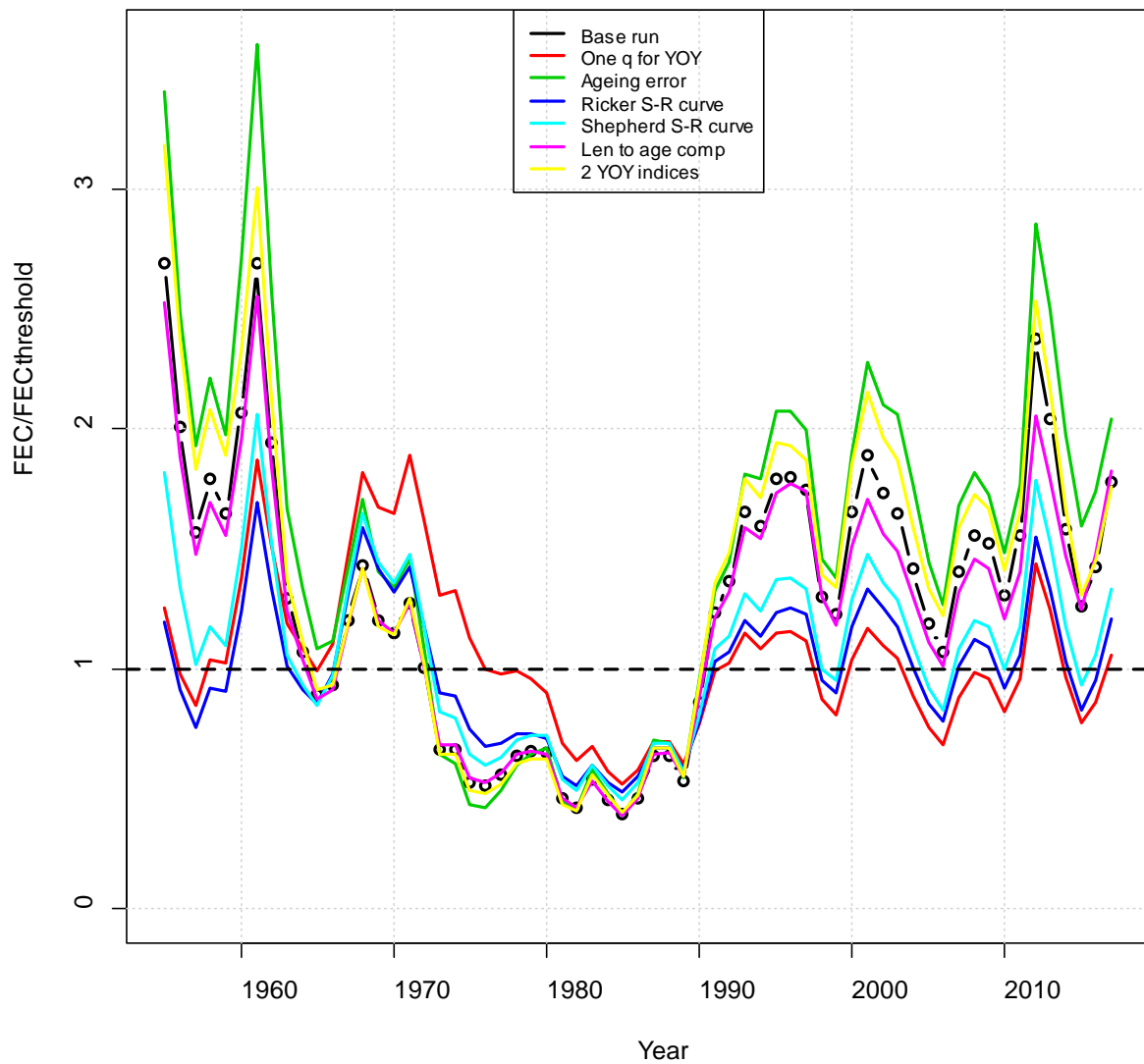
**Figure 221. Fecundity divided by the target fecundity for the suite of sensitivity runs related to index choice and the ERP models.**



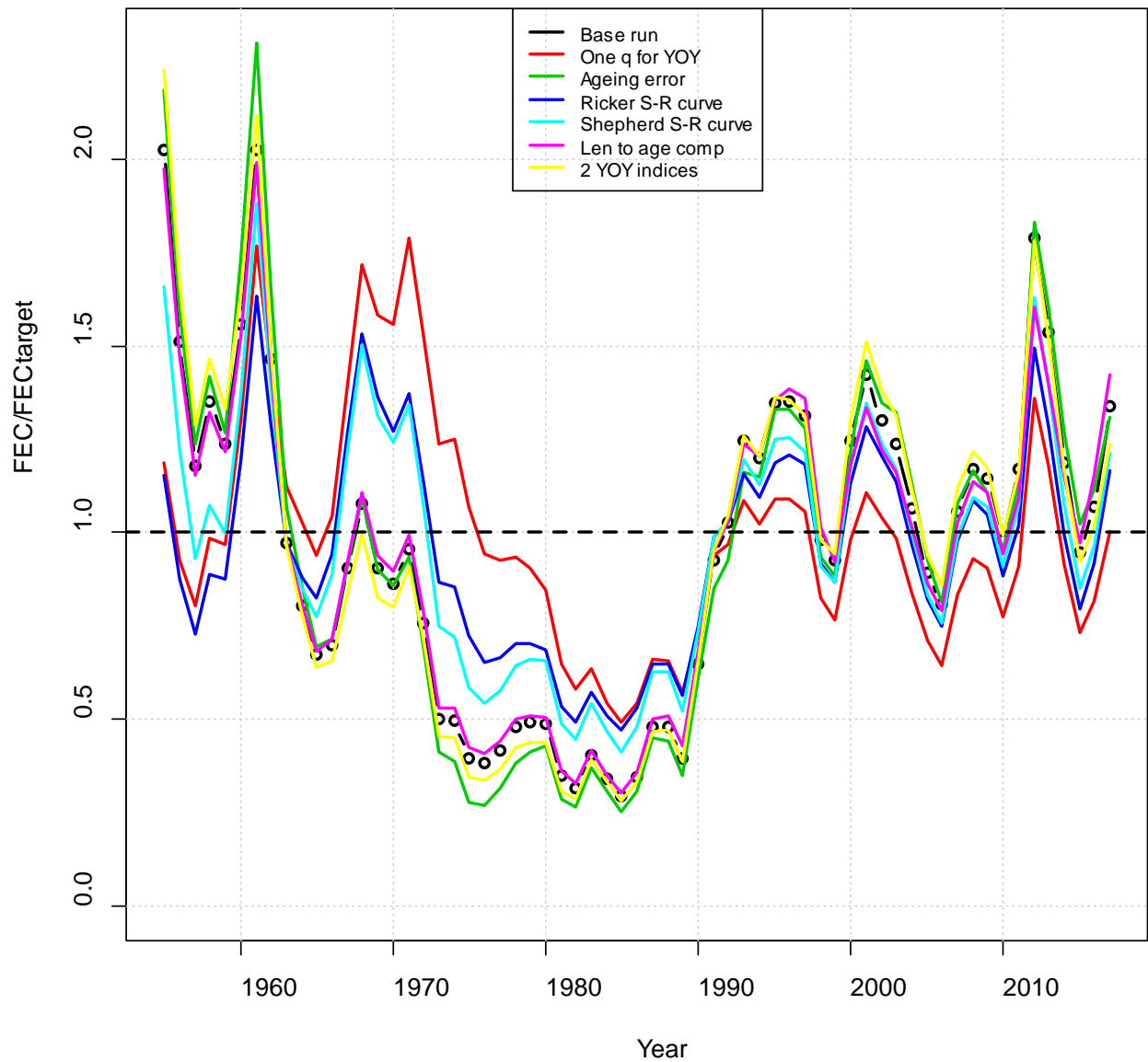
**Figure 222. Fishing mortality rate divided by the threshold  $F$  for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve.**



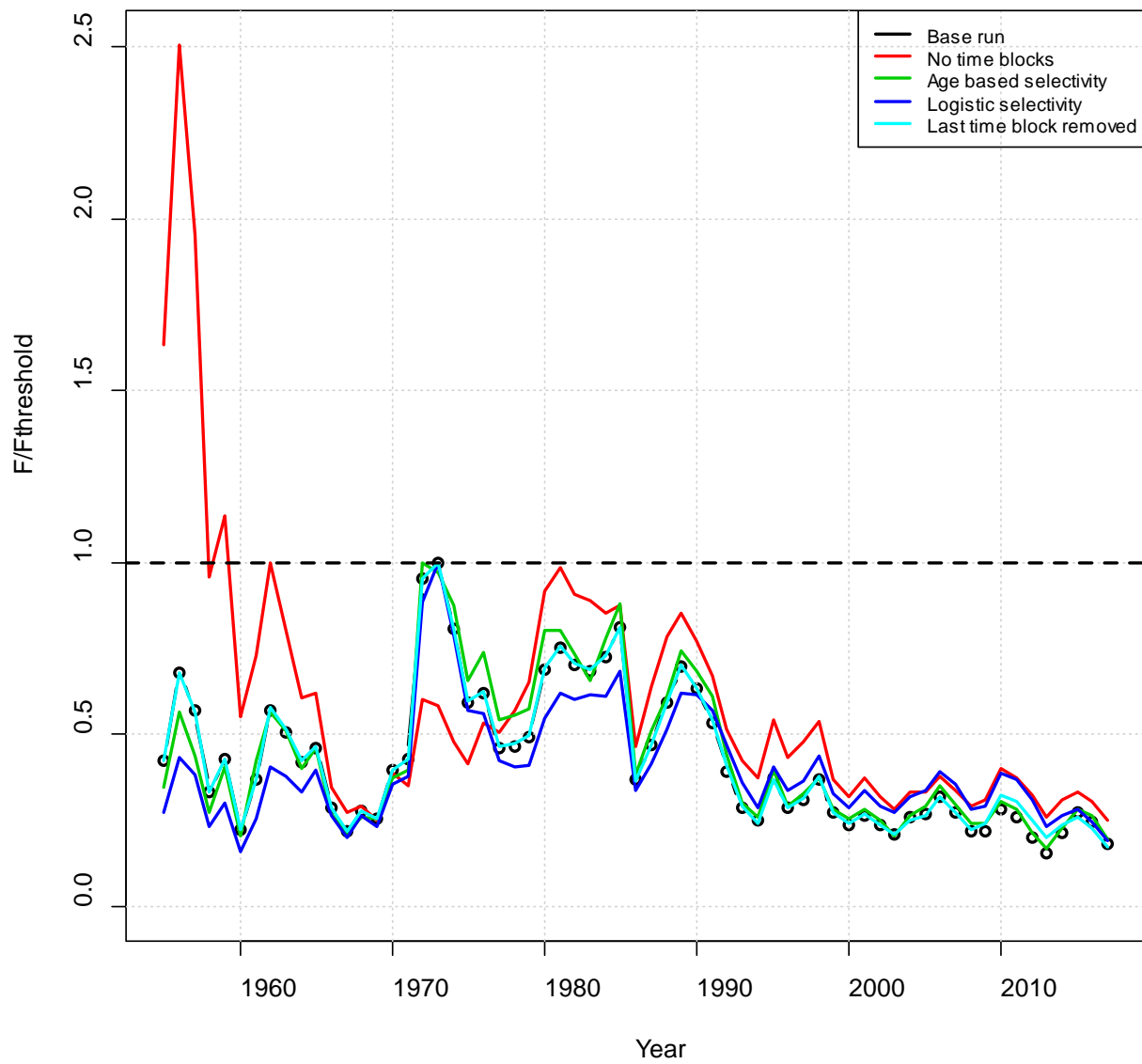
**Figure 223. Fishing mortality rate divided by the target  $F$  for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve.**



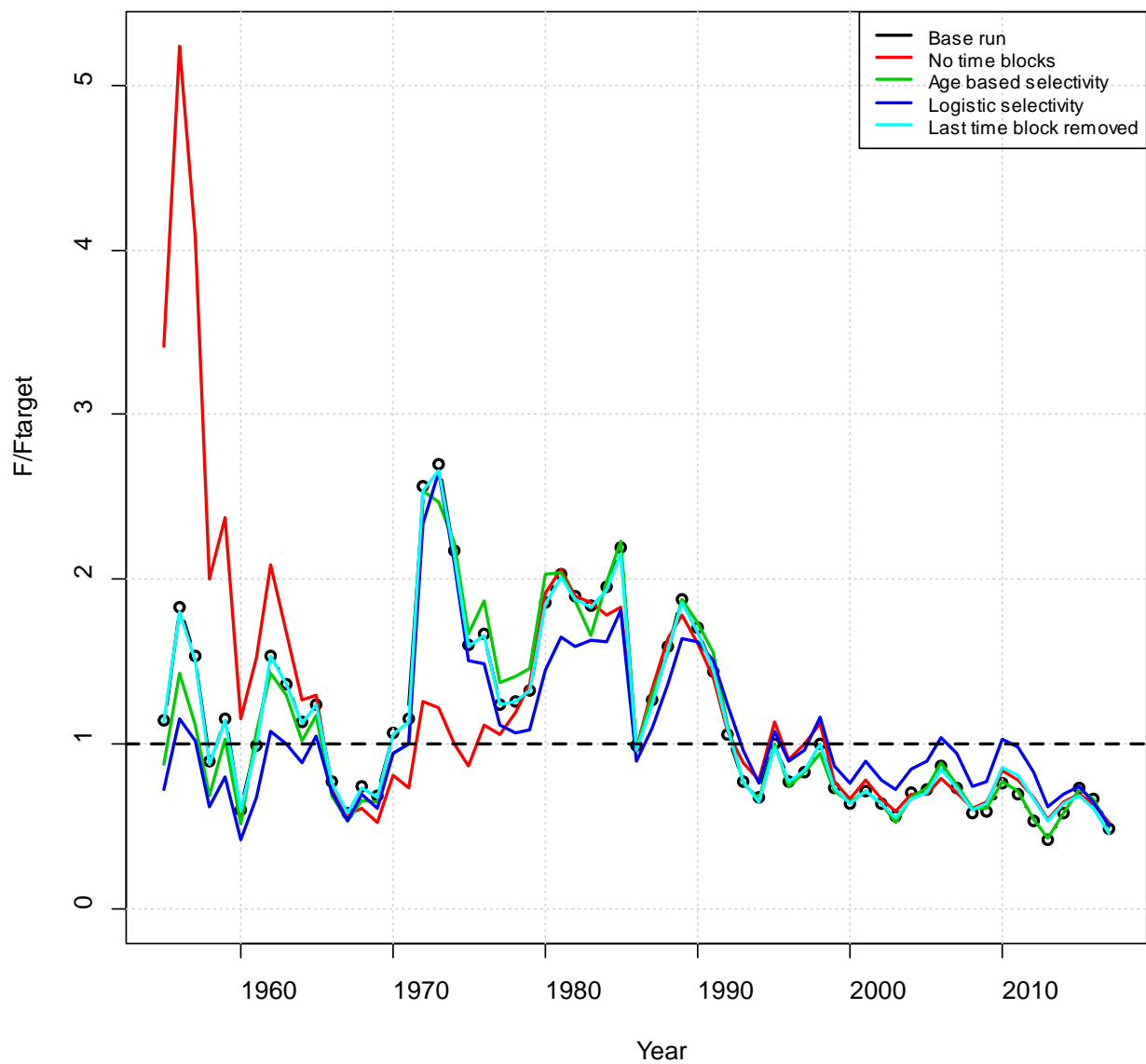
**Figure 224. Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve.**



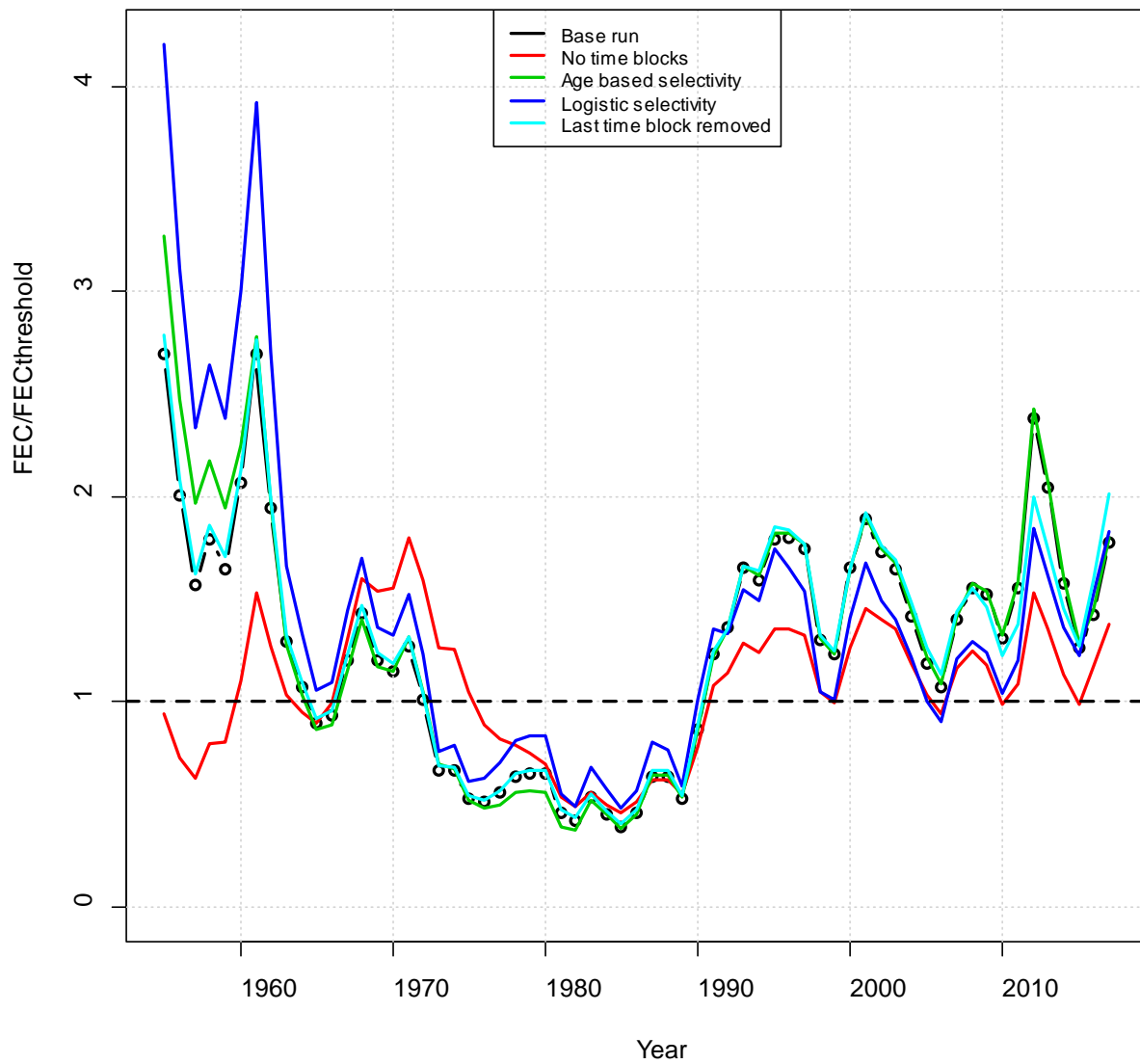
**Figure 225. Fecundity divided by the target fecundity for the suite of sensitivity runs related to catchability, ageing error, and the stock-recruitment curve.**



**Figure 226. Fishing mortality rate divided by the threshold  $F$  for the suite of sensitivity runs related to fishery selectivity.**

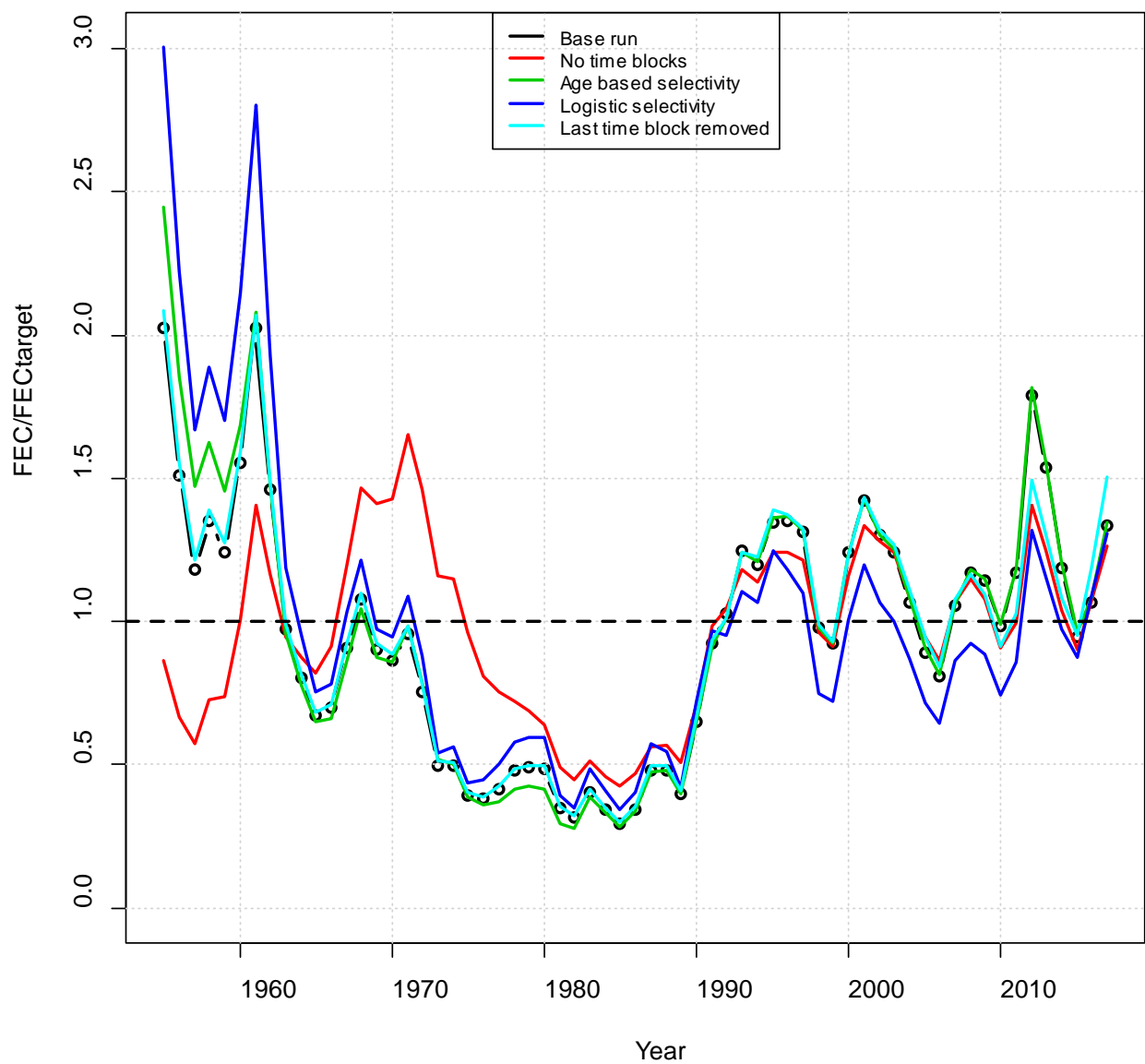


**Figure 227. Fishing mortality rate divided by the target  $F$  for the suite of sensitivity runs related to fishery selectivity.**

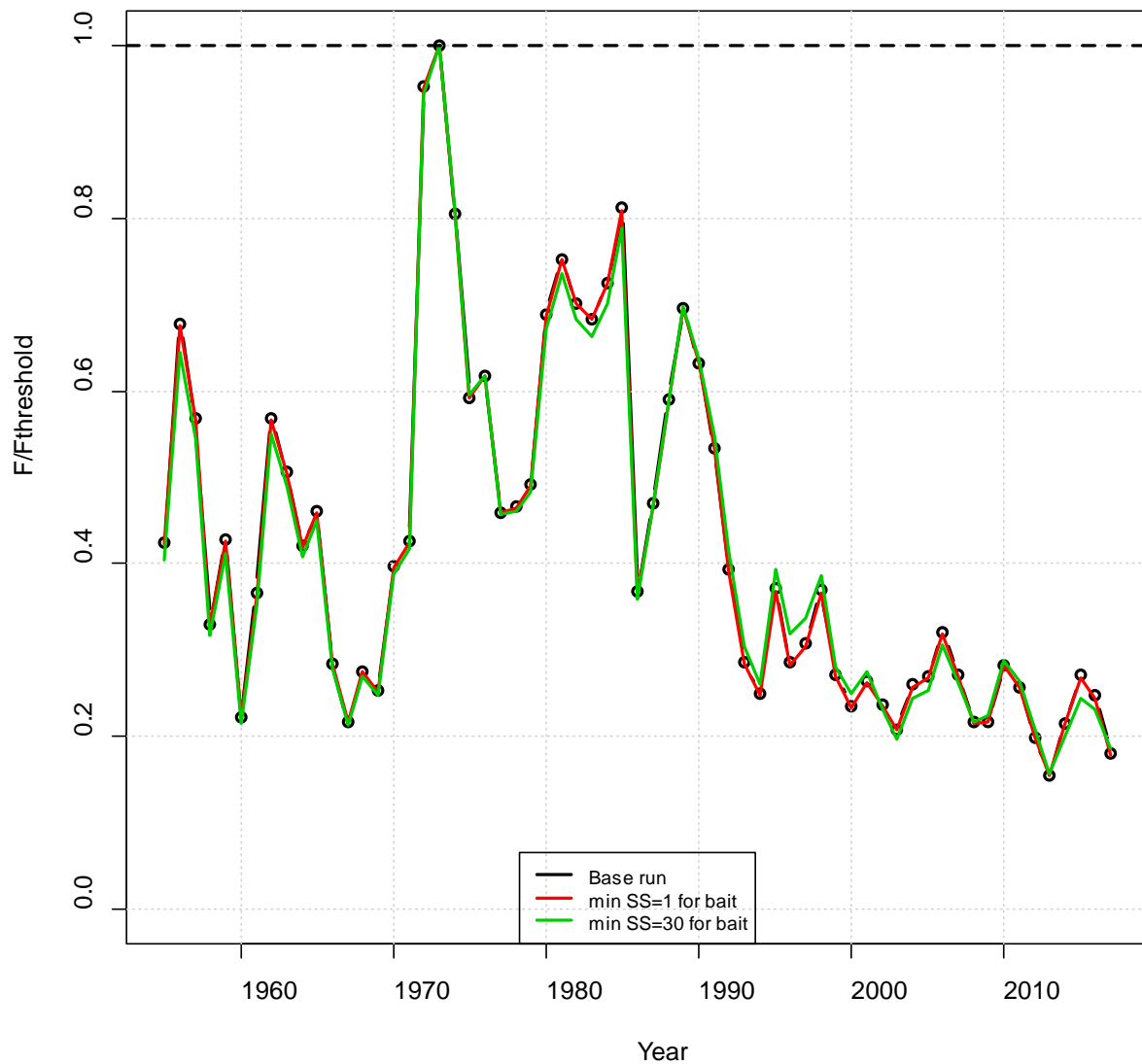


**Figure 228. Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to fishery selectivity.**

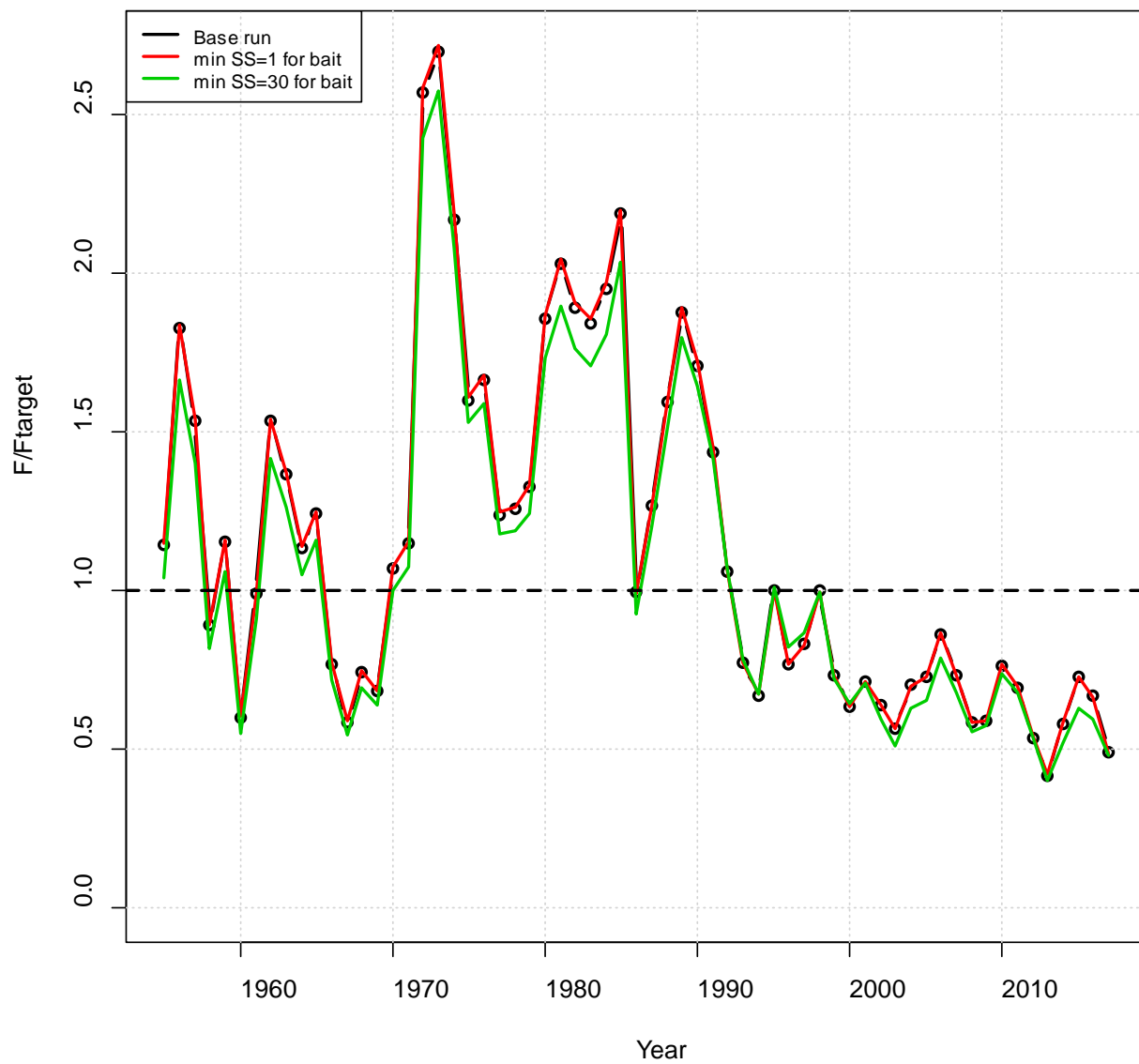




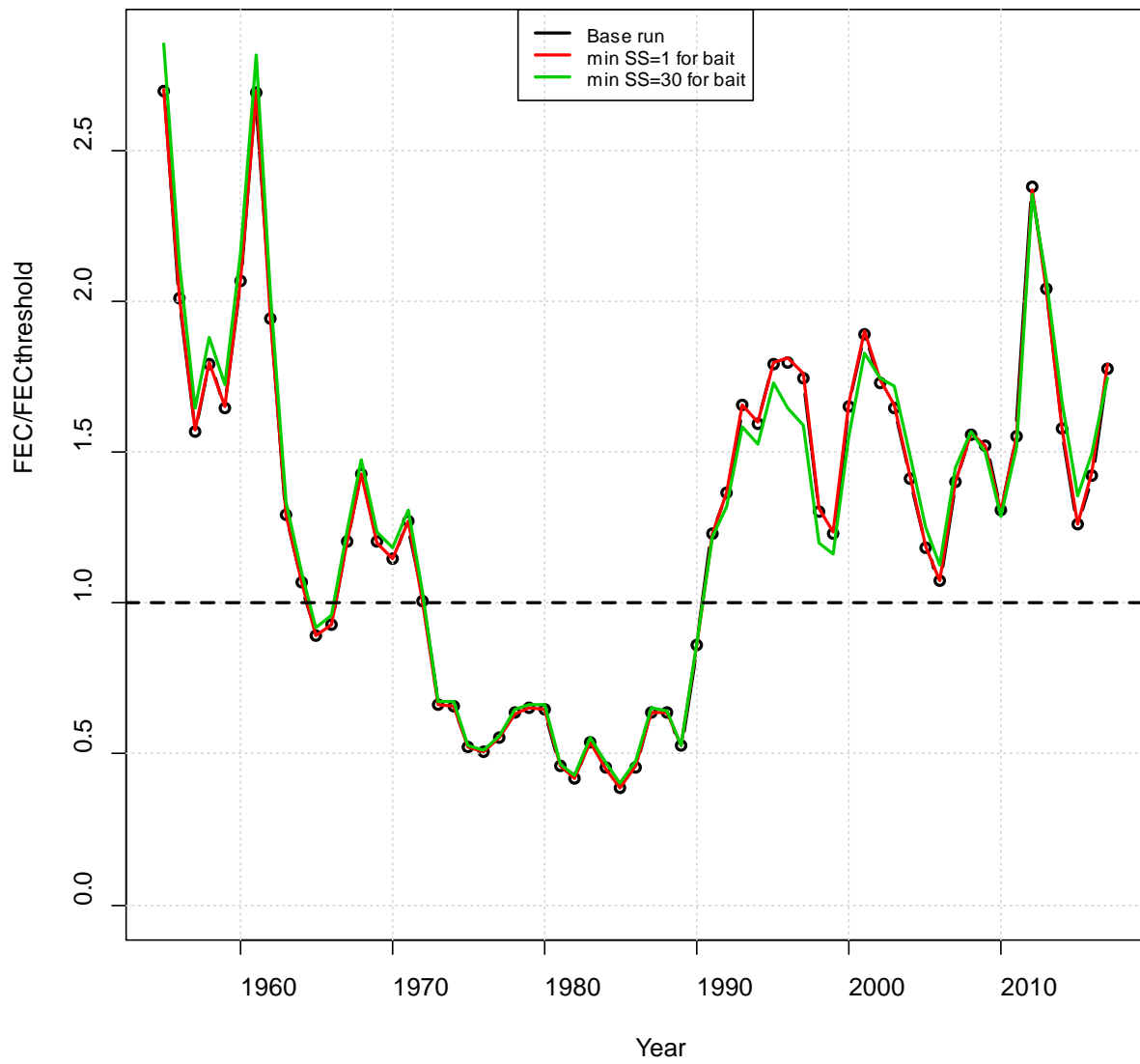
**Figure 229. Fecundity divided by the target fecundity for the suite of sensitivity runs related to fishery selectivity.**



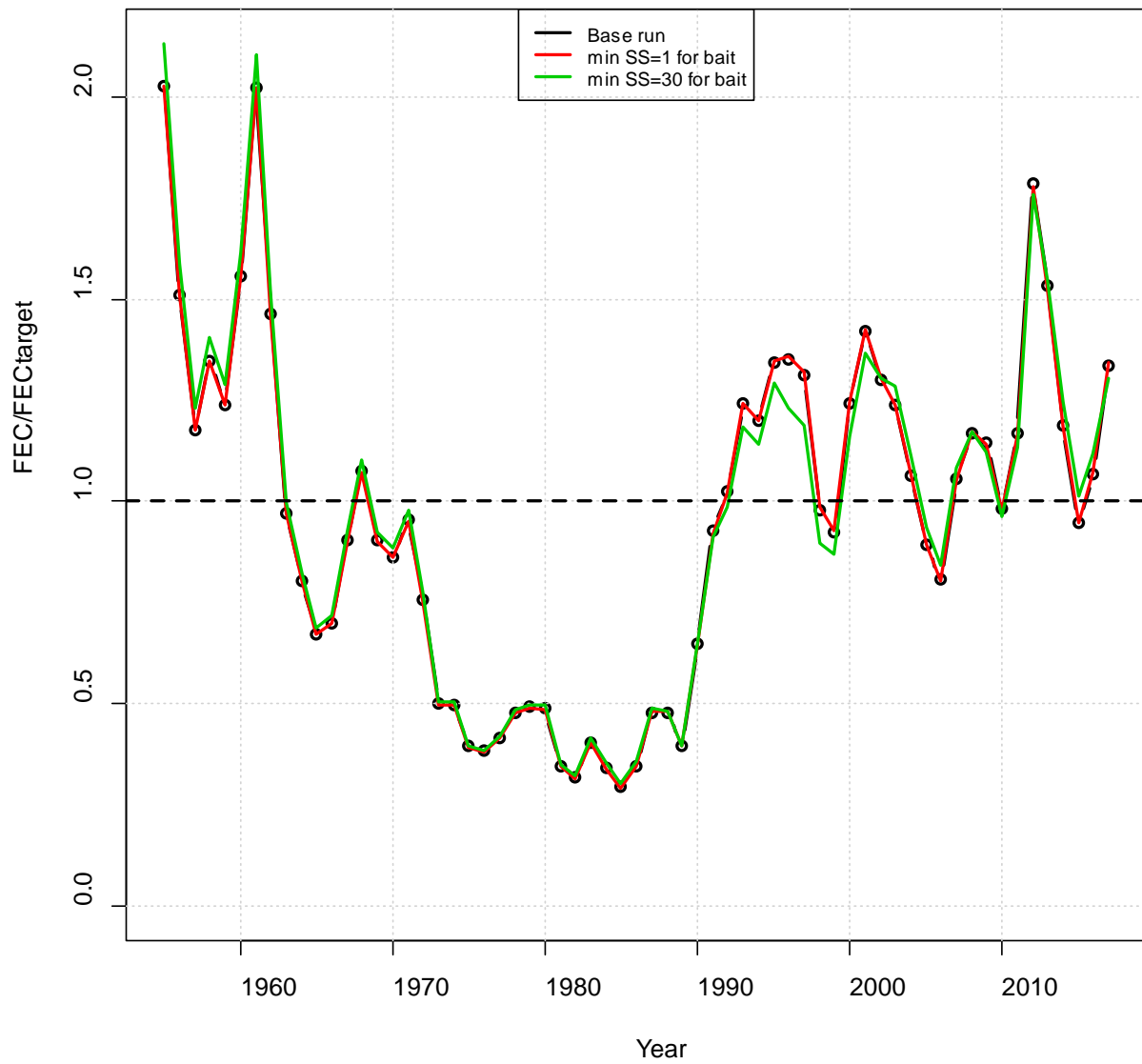
**Figure 230. Fishing mortality rate divided by the threshold  $F$  for the suite of sensitivity runs related to minimum sample size for bait age compositions.**



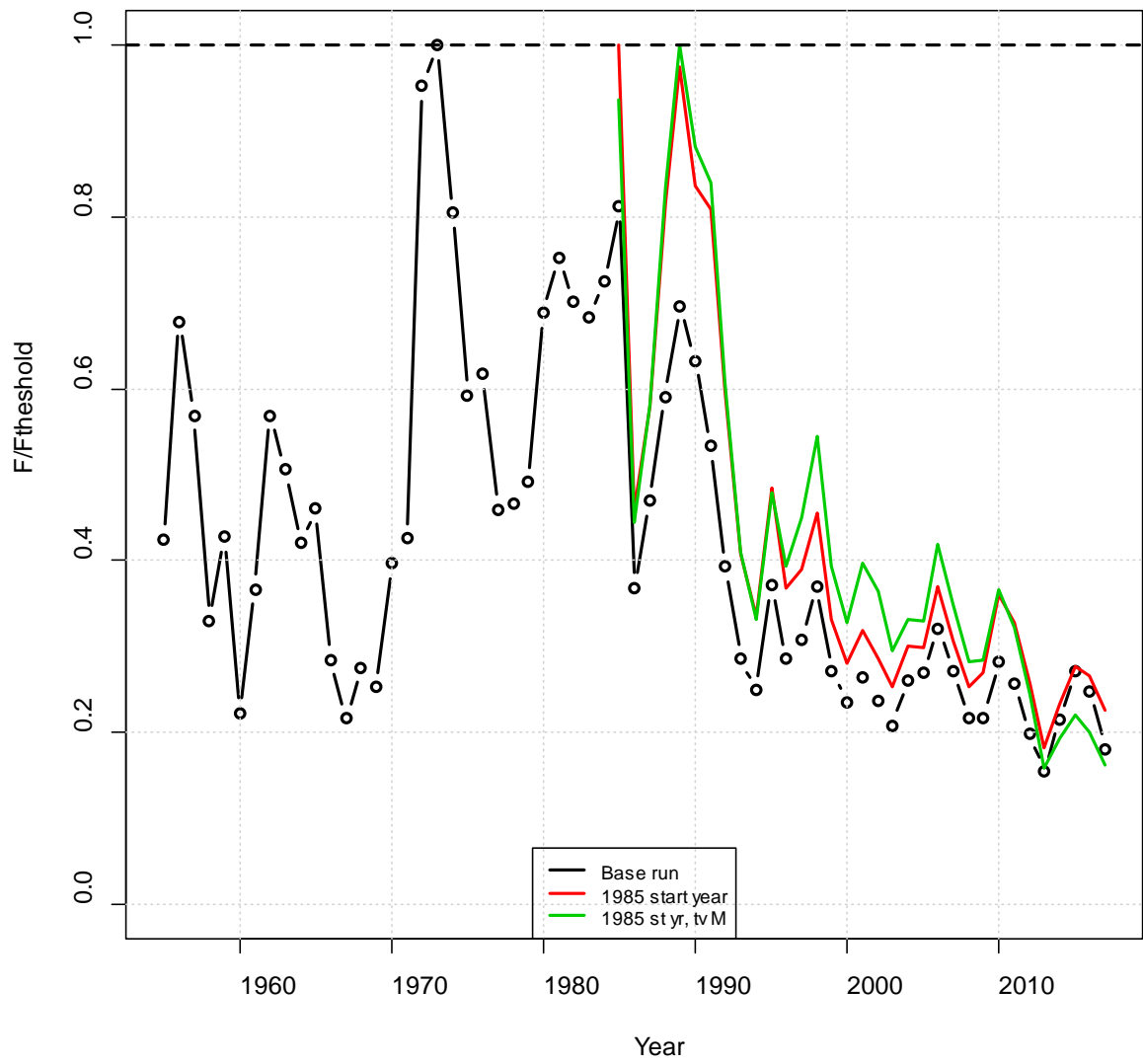
**Figure 231. Fishing mortality rate divided by the target  $F$  for the suite of sensitivity runs related to minimum sample size for bait age compositions.**



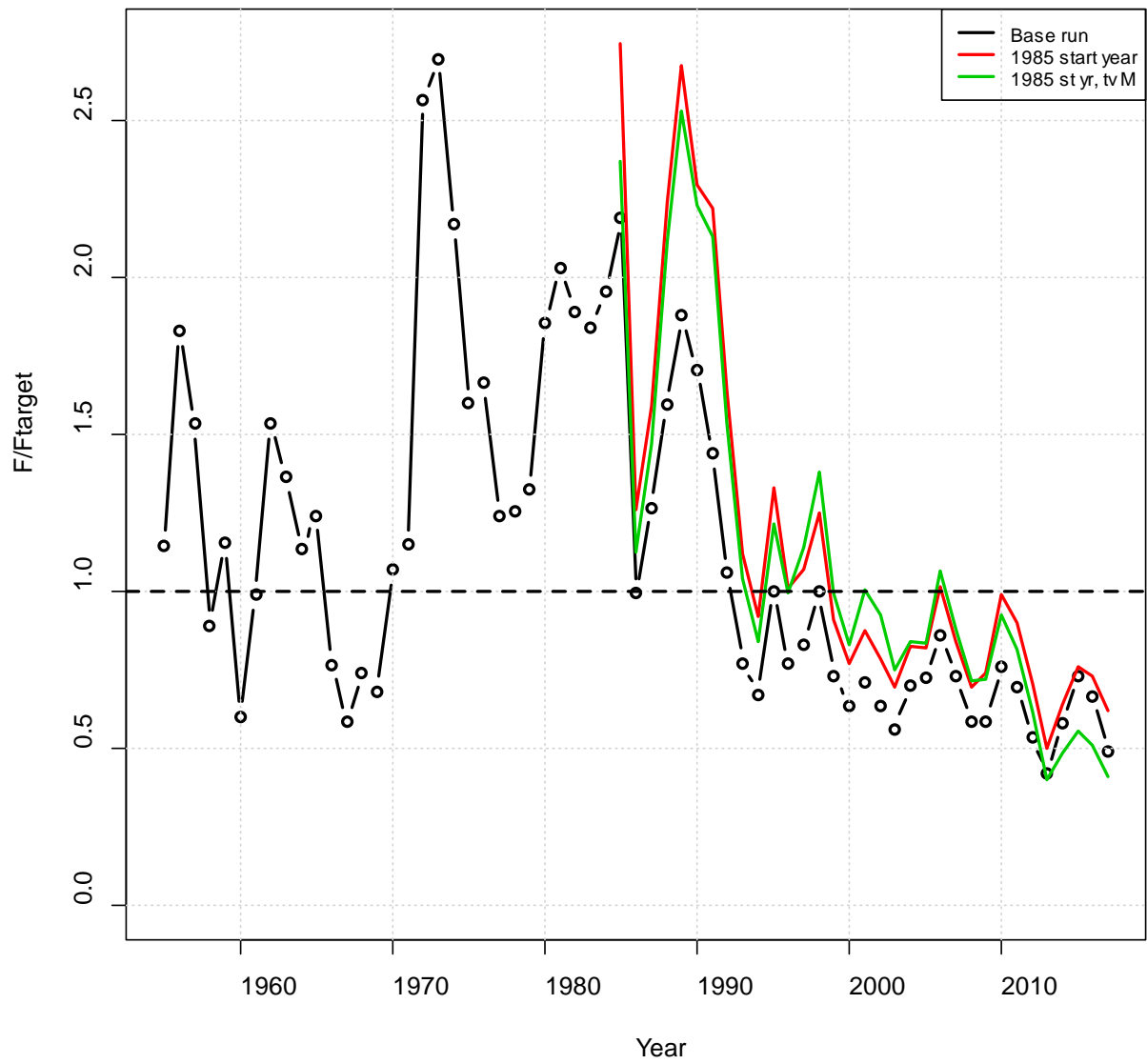
**Figure 232. Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to minimum sample size for bait age compositions.**



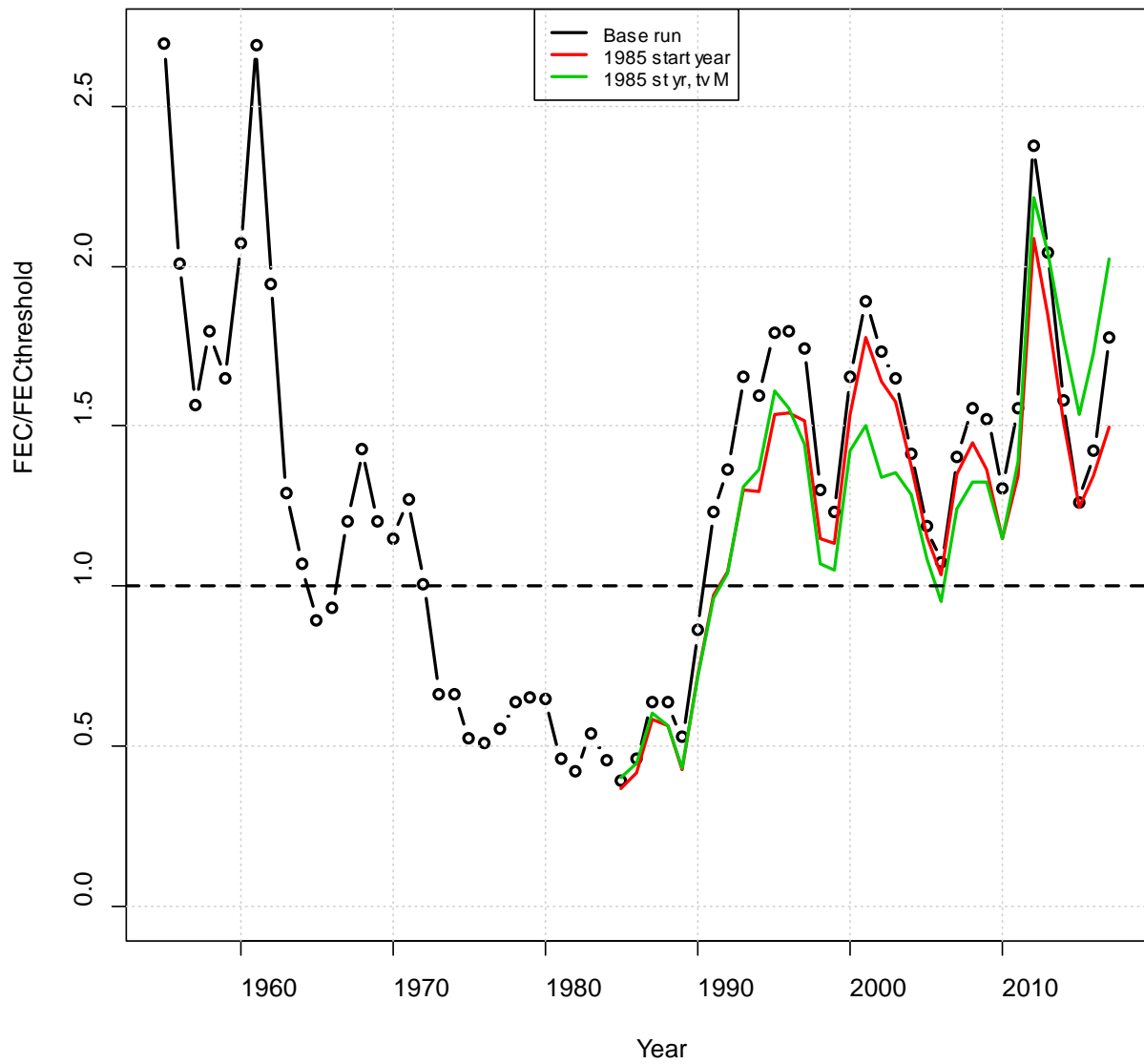
**Figure 233. Fecundity divided by the target fecundity for the suite of sensitivity runs related to minimum sample size for bait age compositions.**



**Figure 234. Fishing mortality rate divided by the threshold  $F$  for the suite of sensitivity runs related to start year and time-varying  $M$ .**

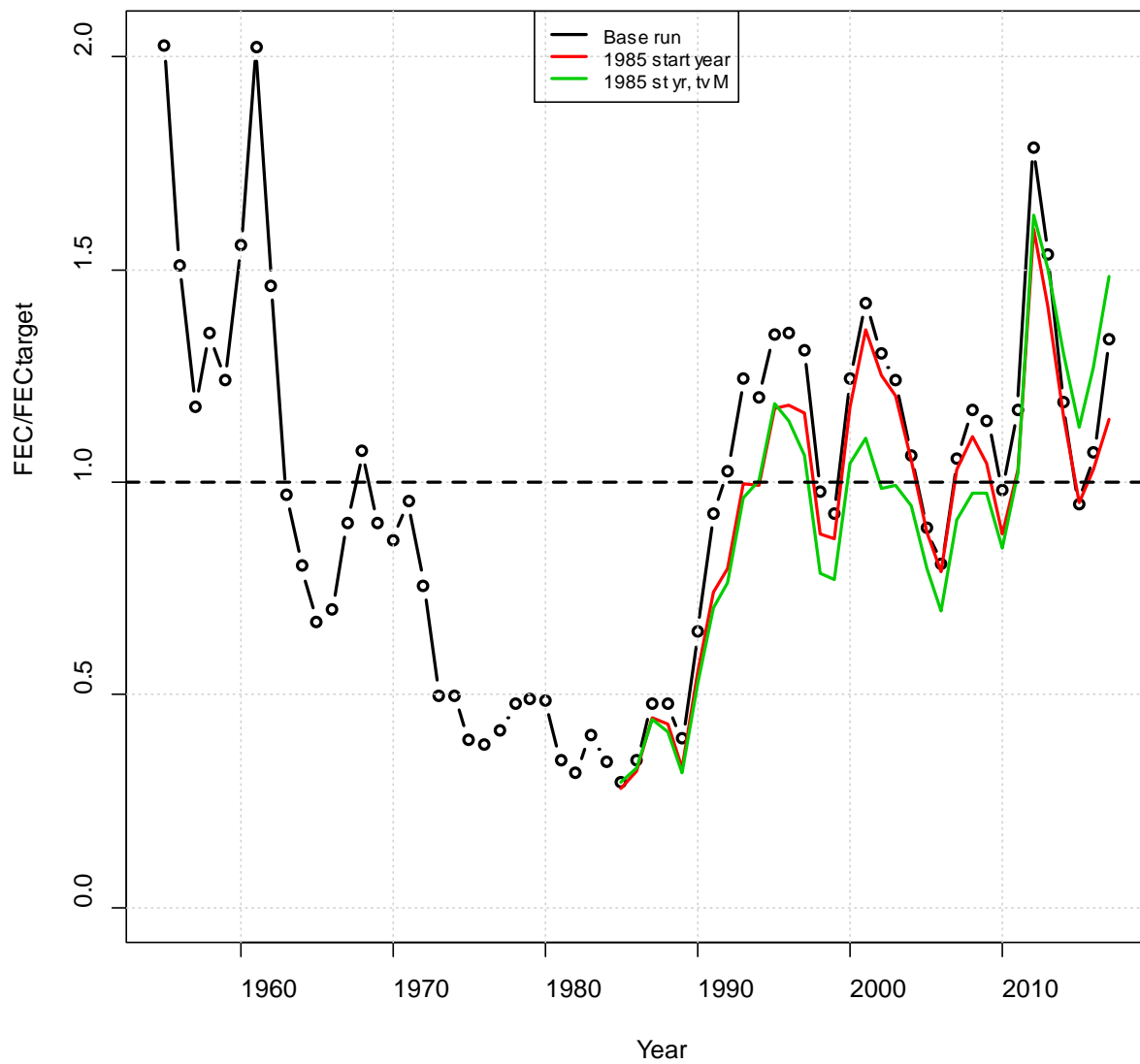


**Figure 235. Fishing mortality rate divided by the target  $F$  for the suite of sensitivity runs related to start year and time-varying  $M$ .**

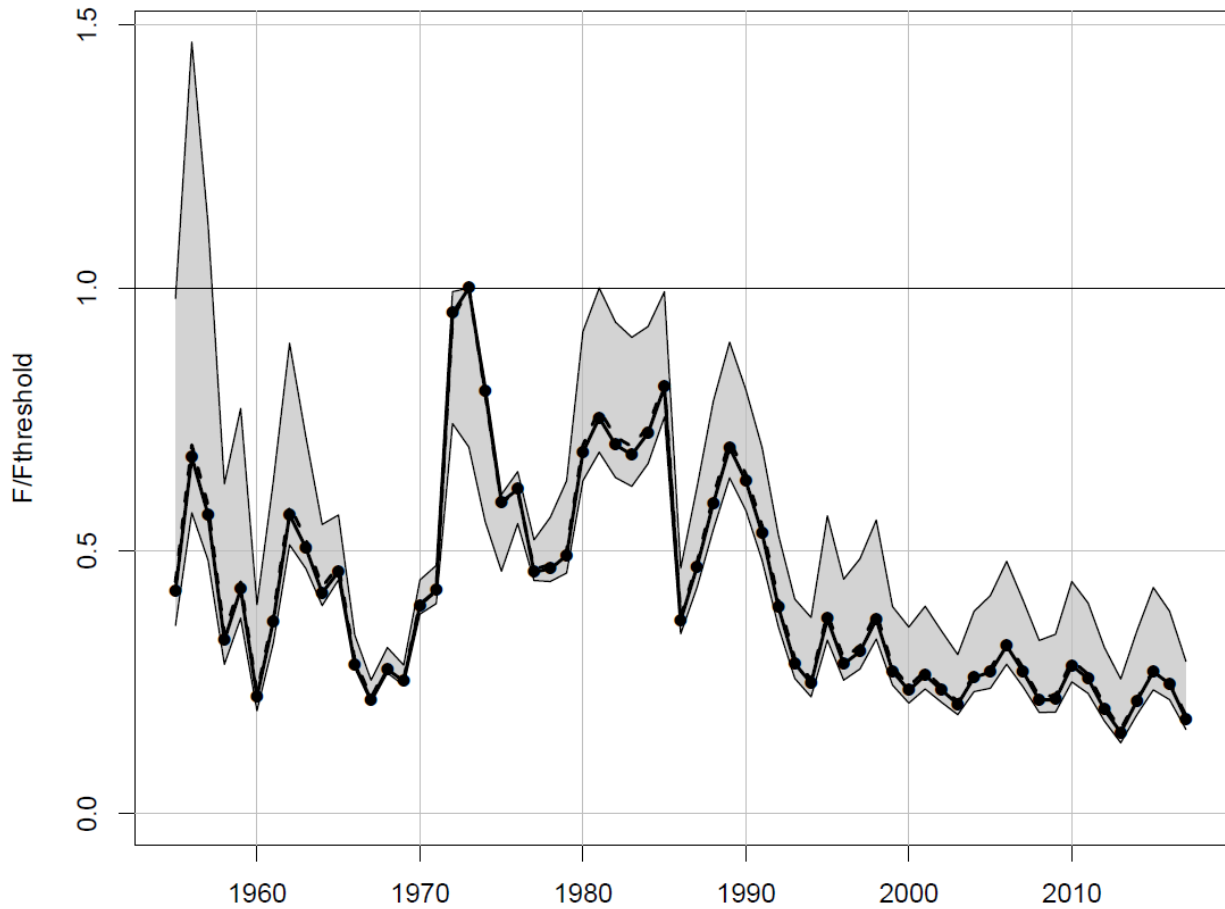


**Figure 236. Fecundity divided by the threshold fecundity for the suite of sensitivity runs related to start year and time-varying  $M$ .**

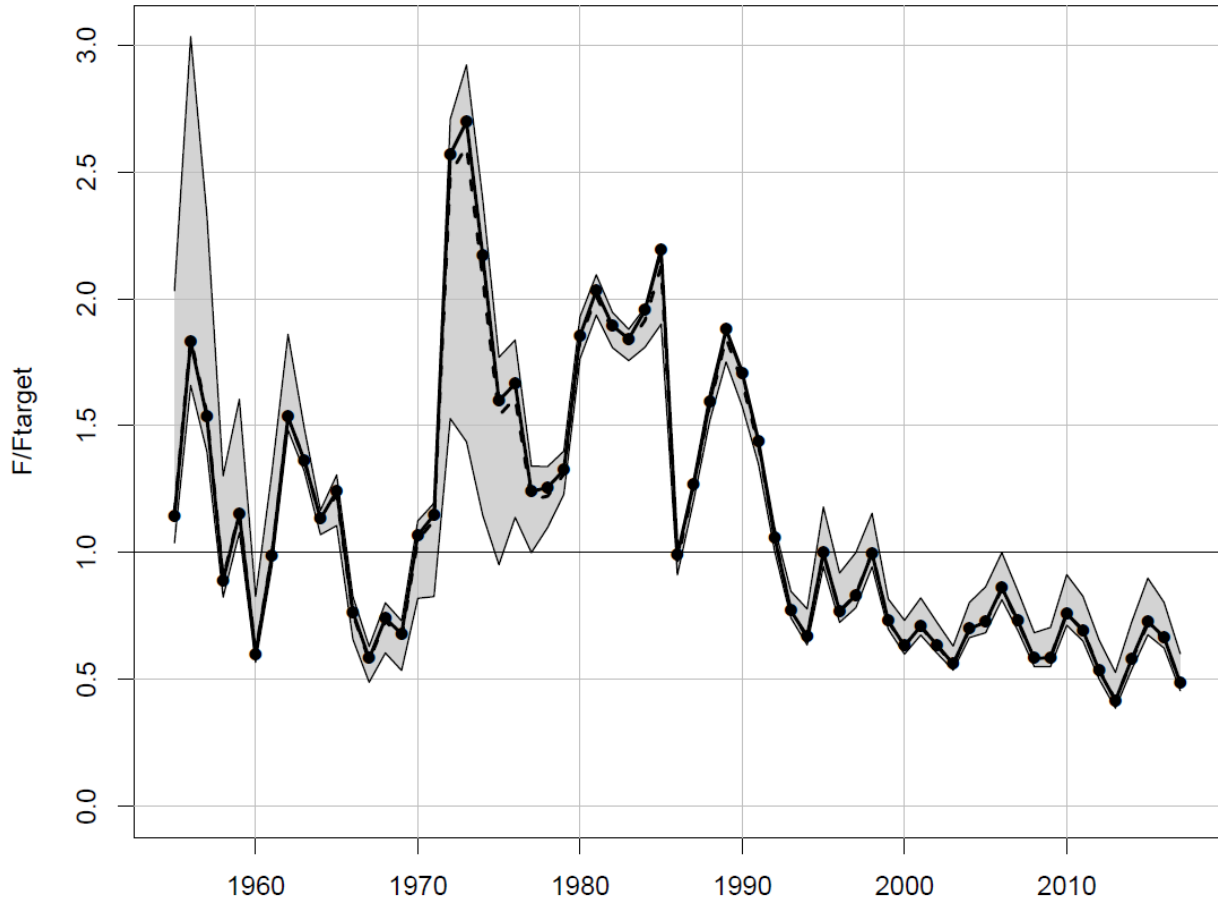




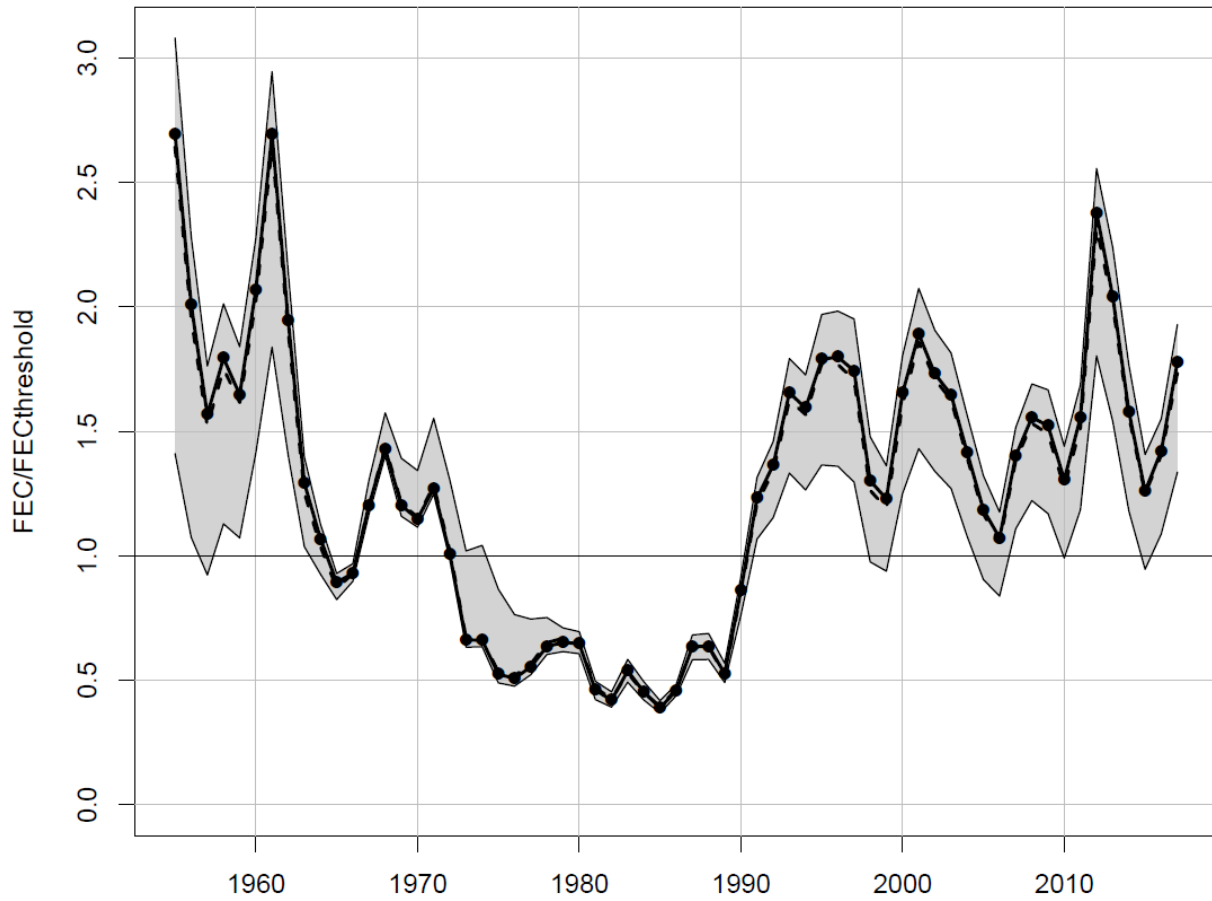
**Figure 237. Fecundity divided by the target fecundity for the suite of sensitivity runs related to start year and time-varying  $M$ .**



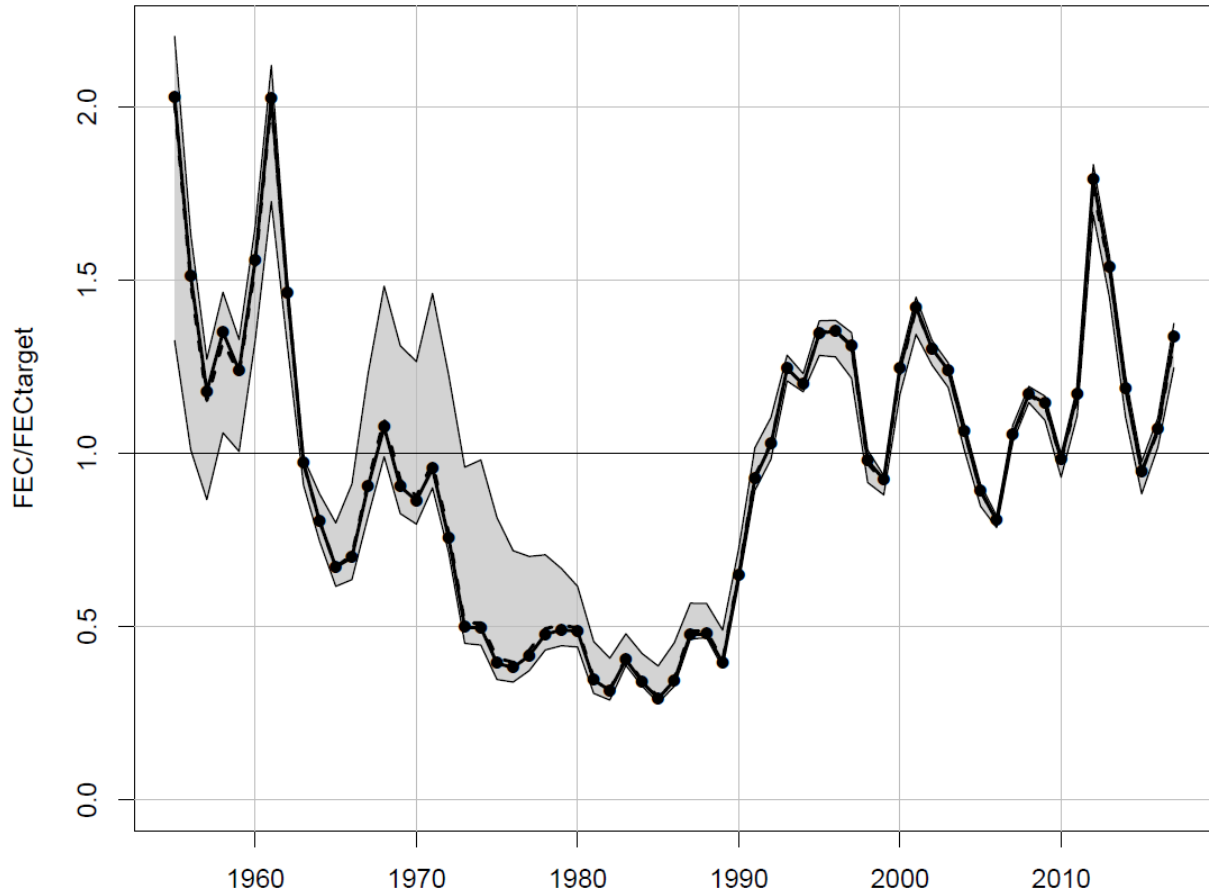
**Figure 238.** Fishing mortality rate divided by the threshold  $F$  for each of the MCB runs. The black solid line is the base run, the dashed back line is the median, and the gray area indicates the 95<sup>th</sup> percentiles.



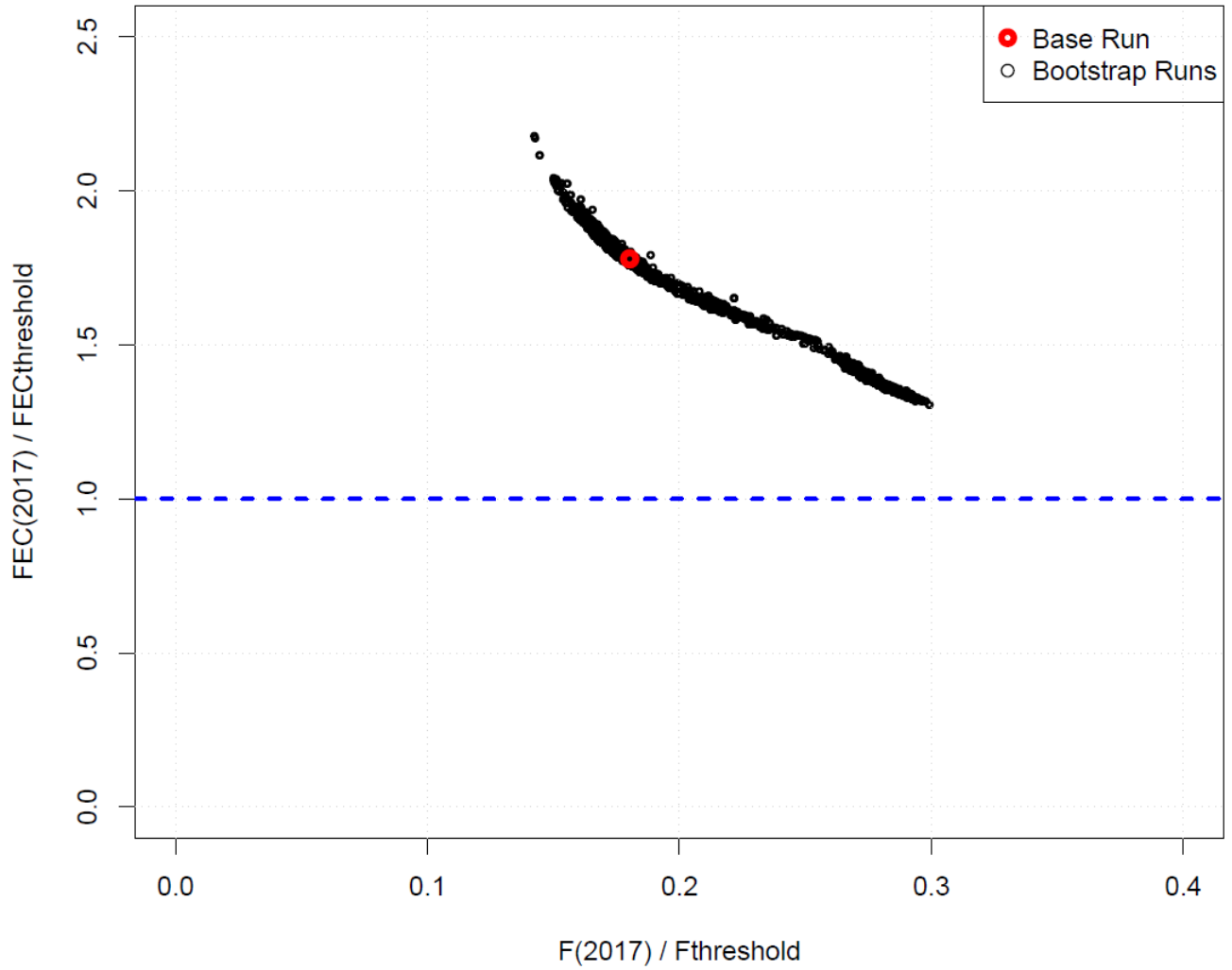
**Figure 239. Fishing mortality rate divided by the target  $F$  for each of the MCB runs. The black solid line is the base run, the dashed back line is the median, and the gray area indicates the 95<sup>th</sup> percentiles.**



**Figure 240. Fecundity divided by the threshold fecundity for each of the MCB runs. The black solid line is the base run, the dashed back line is the median, and the gray area indicates the 95<sup>th</sup> percentiles.**



**Figure 241. Fecundity divided by the target fecundity for each of the MCB runs. The black solid line is the base run, the dashed back line is the median, and the gray area indicates the 95<sup>th</sup> percentiles.**



**Figure 242. Terminal year fishing mortality and fecundity divided by the threshold values for each of the MCB runs. The red circle indicates the base run.**

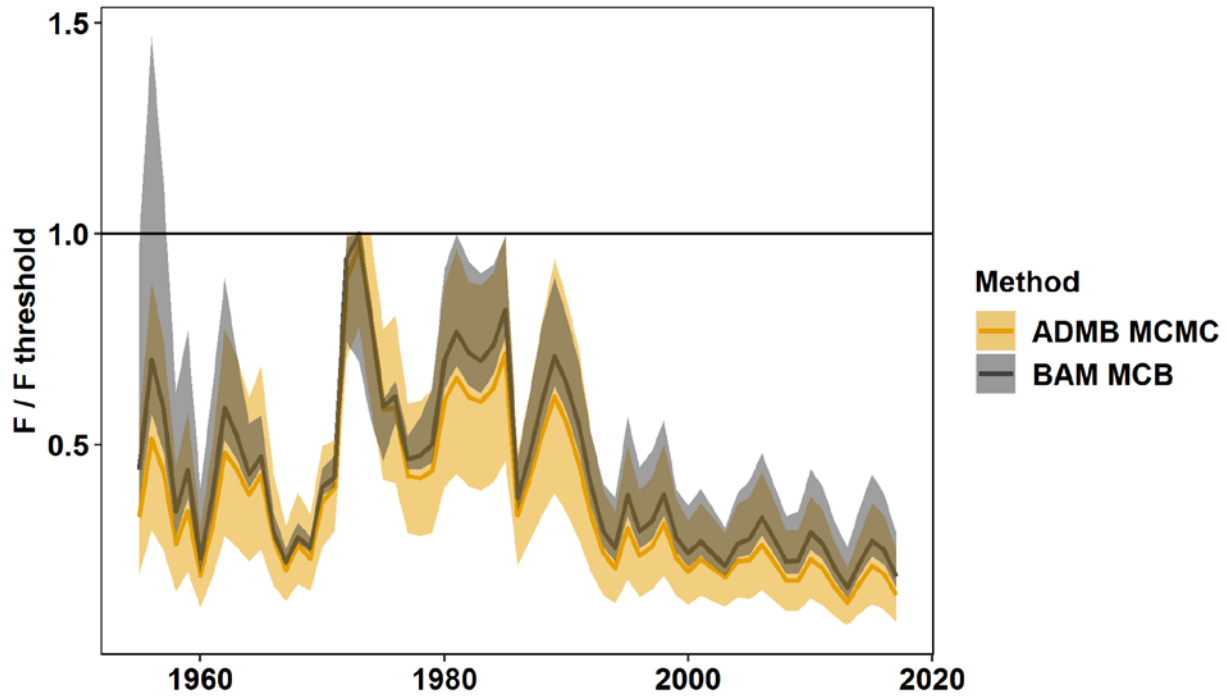


Figure 243. Fishing mortality rate divided by the threshold fishing mortality rate for the MCB analysis and for the MCMC analysis.

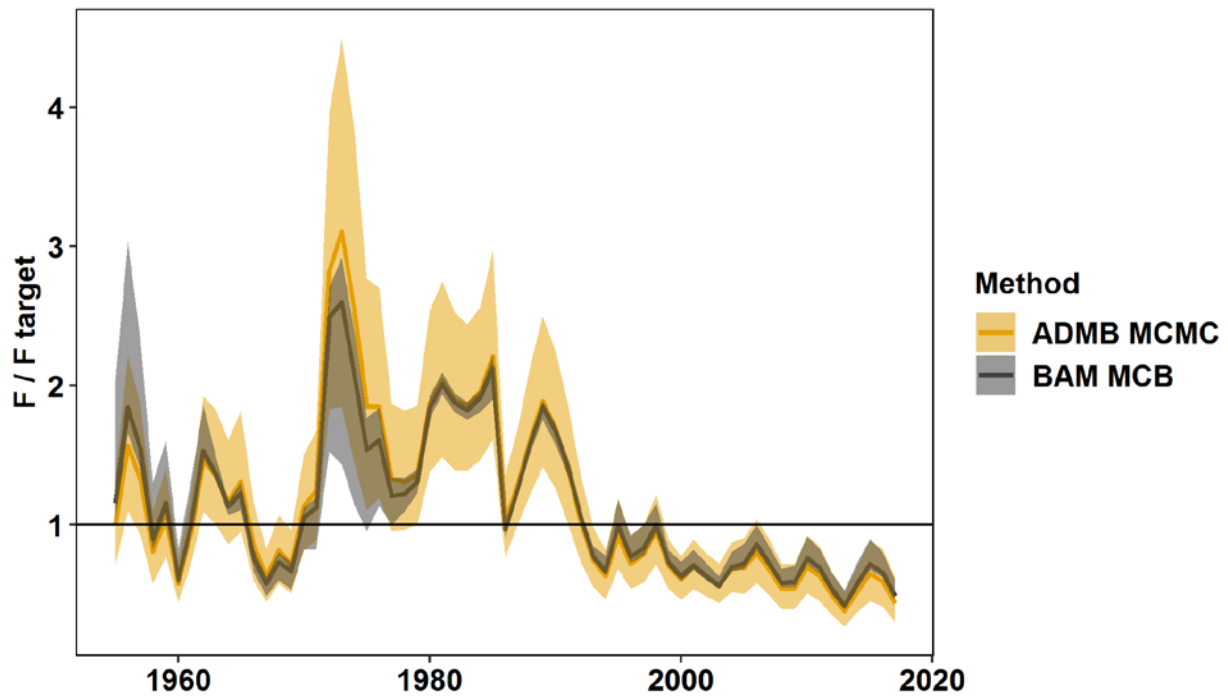


Figure 244. Fishing mortality rate divided by the target fishing mortality rate for the MCB analysis and for the MCMC analysis.

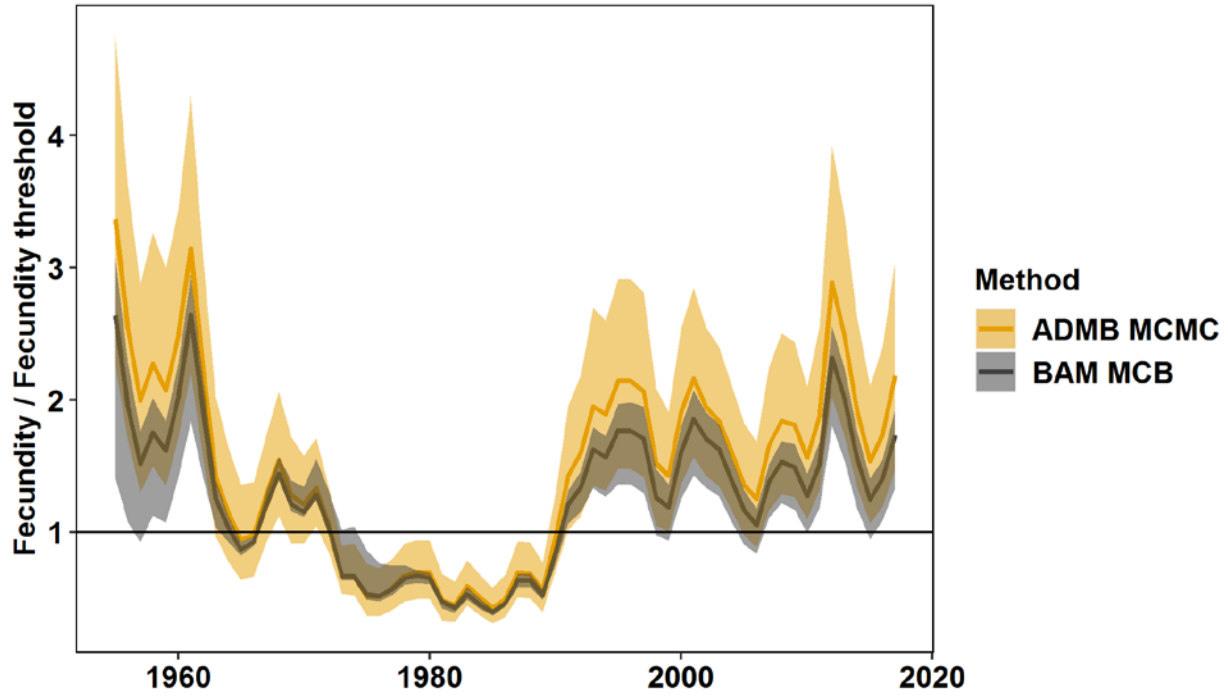


Figure 245. Fecundity divided by the threshold fecundity for the MCB analysis and for the MCMC analysis.

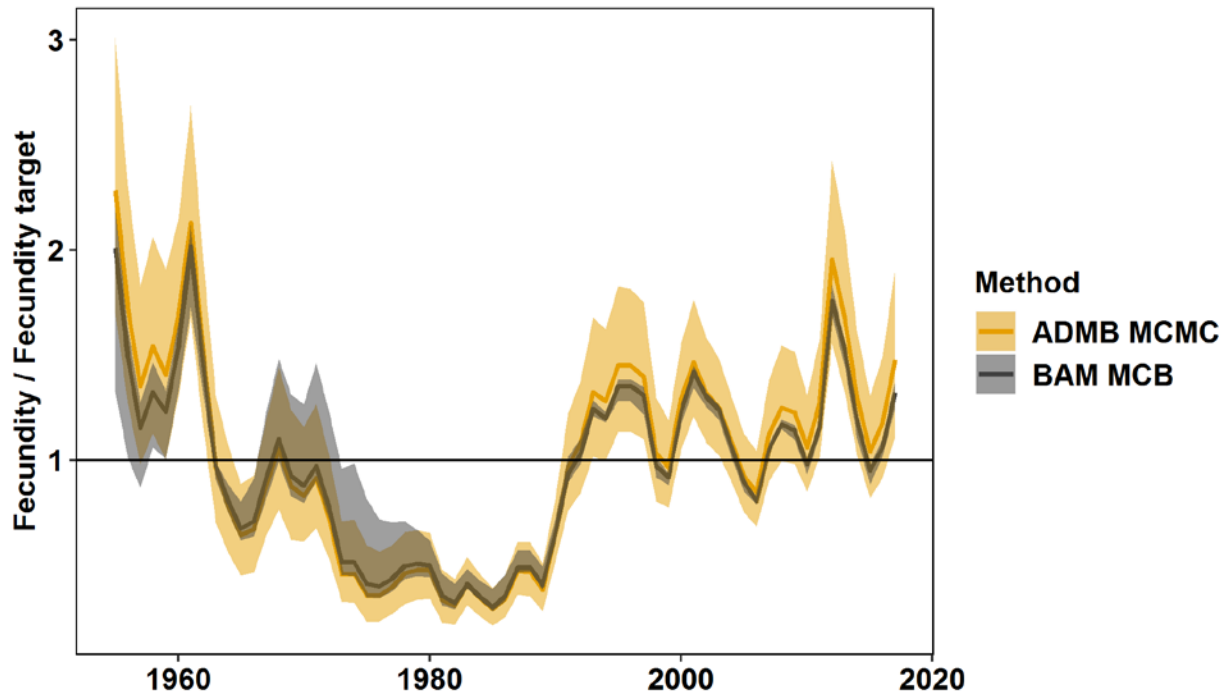


Figure 246. Fecundity divided by the target fecundity for the MCB analysis and for the MCMC analysis.



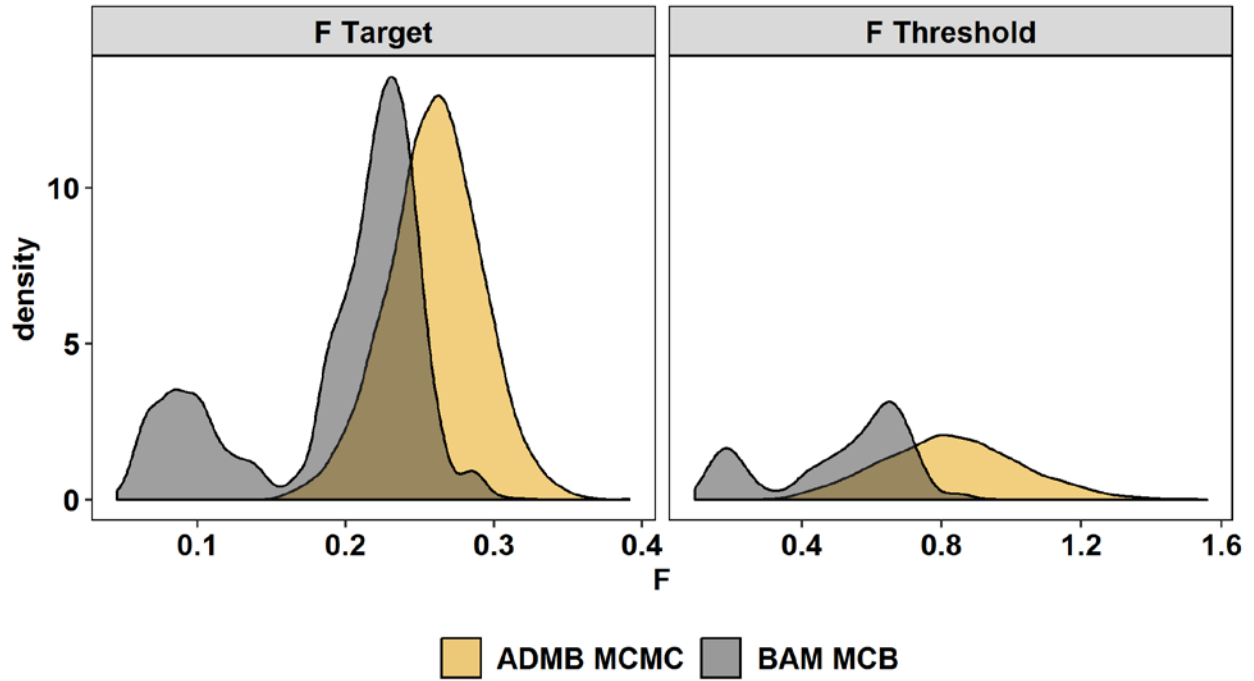


Figure 247. Fishing mortality rate target and threshold distributions for the MCB analysis and for the MCMC analysis.

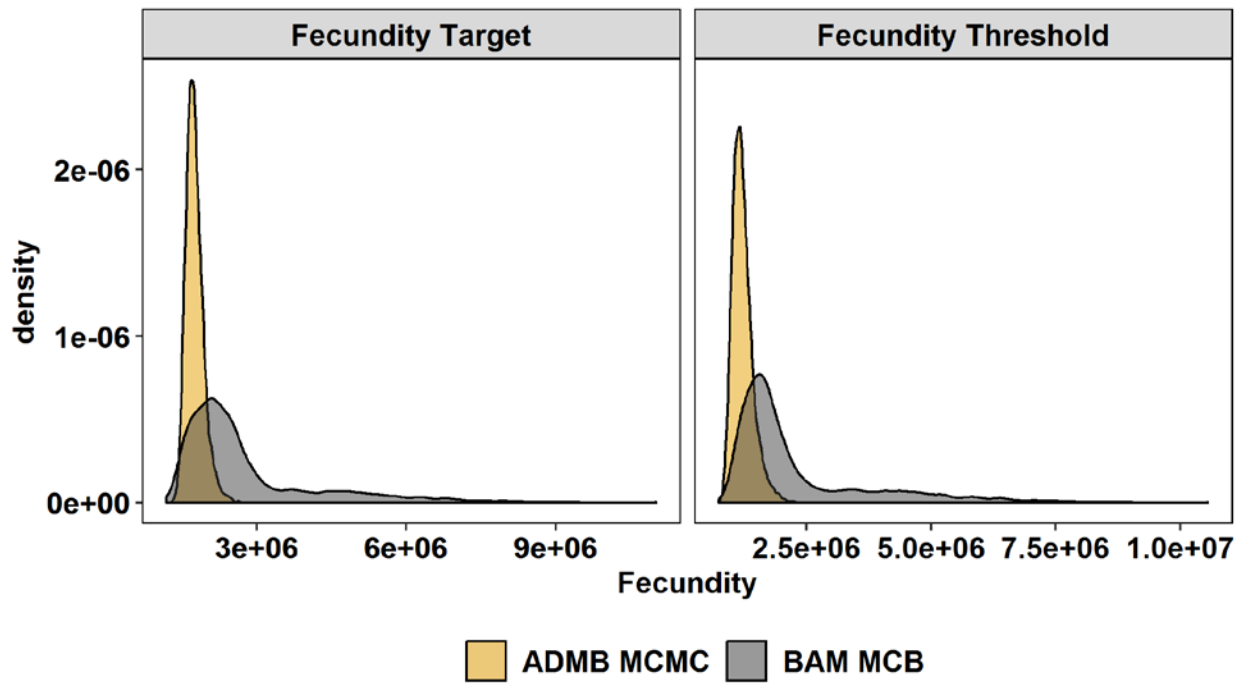


Figure 248. Fecundity target and threshold distributions for the MCB analysis and for the MCMC analysis.

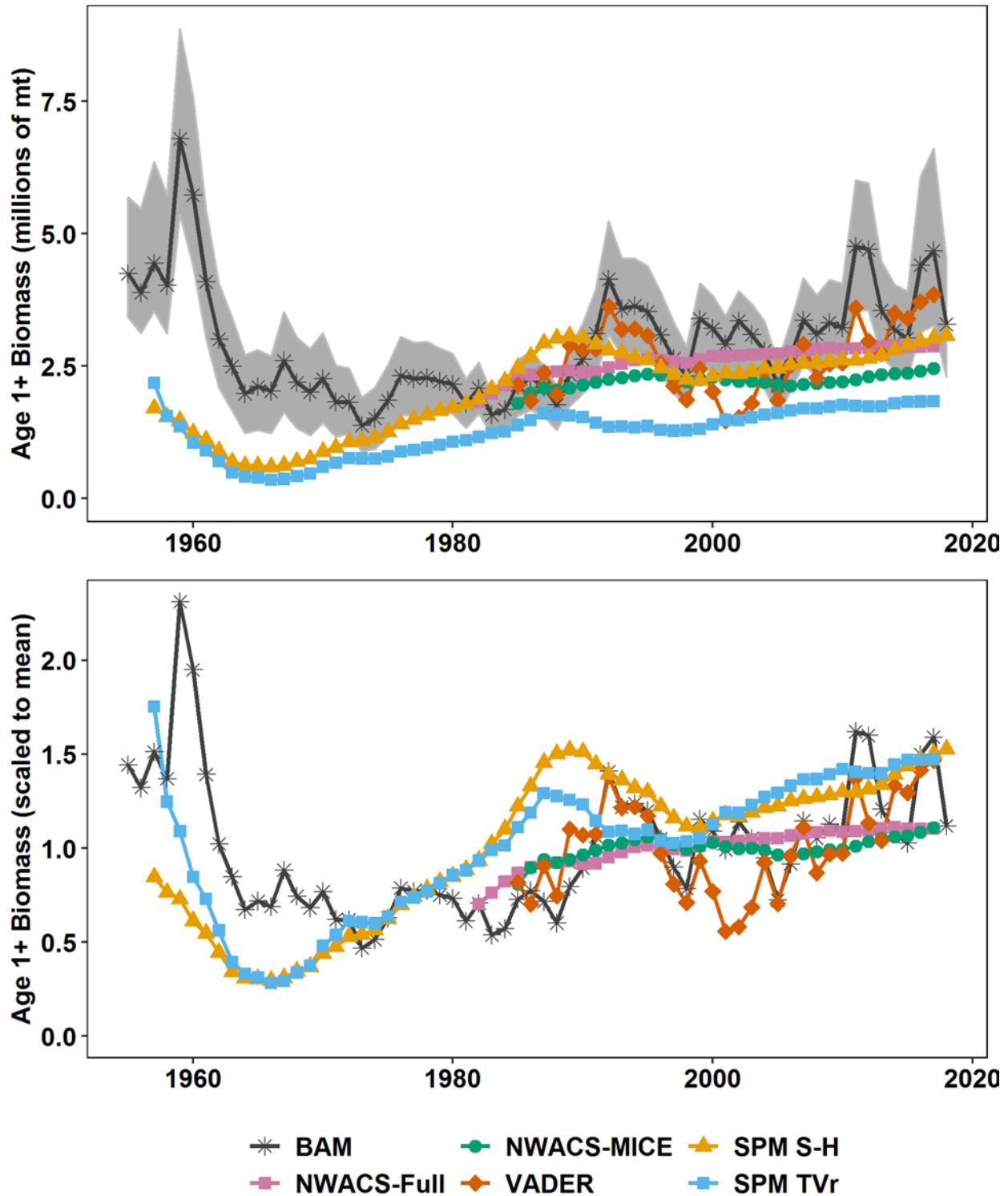


Figure 249. Estimates of age-1+ biomass from the BAM model and the ERP models on an absolute scale (top) and scaled to their time series mean (bottom). Shaded area around BAM estimates indicates 95% confidence interval from MCMC analysis, a minimum estimate of uncertainty.

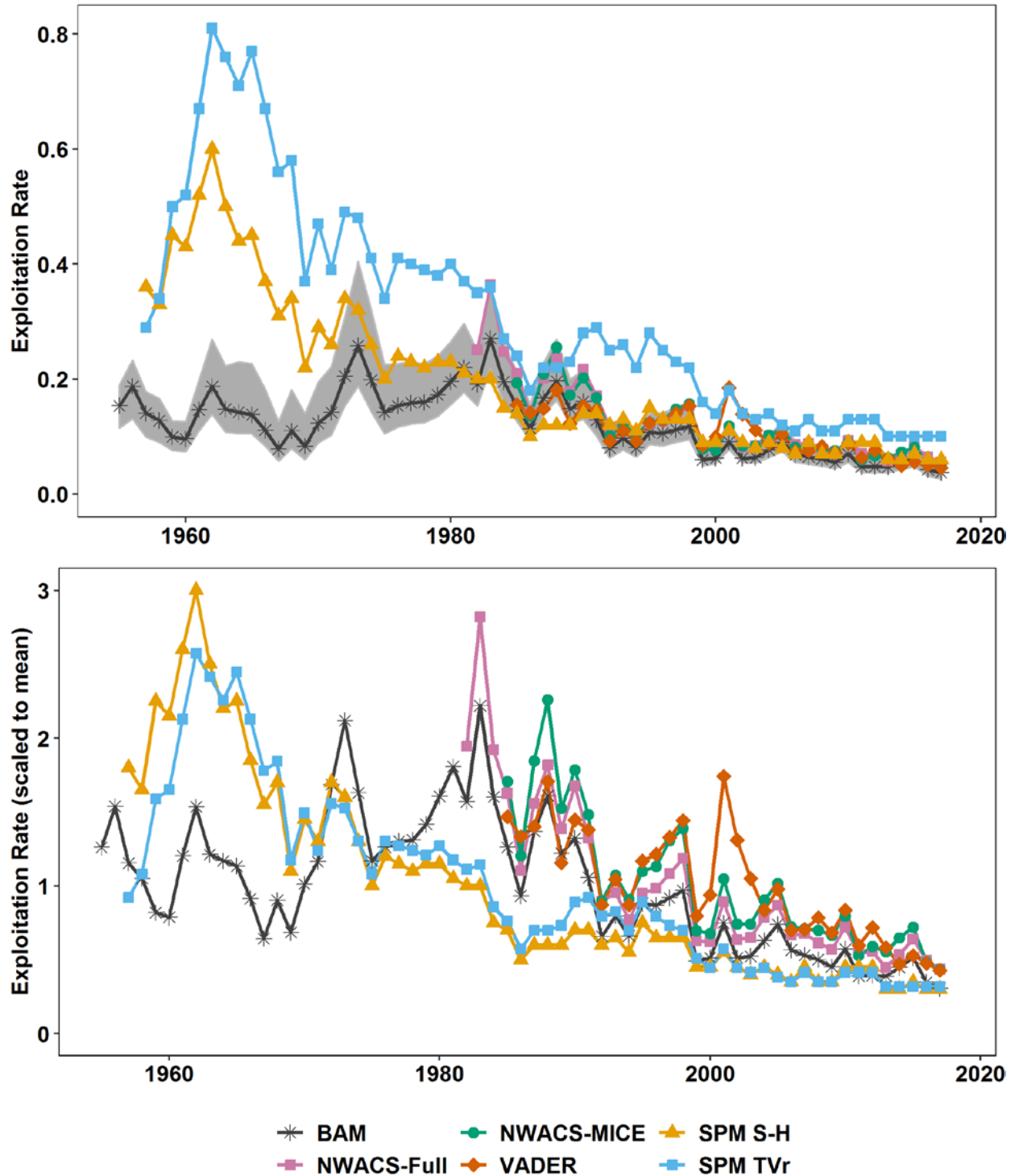
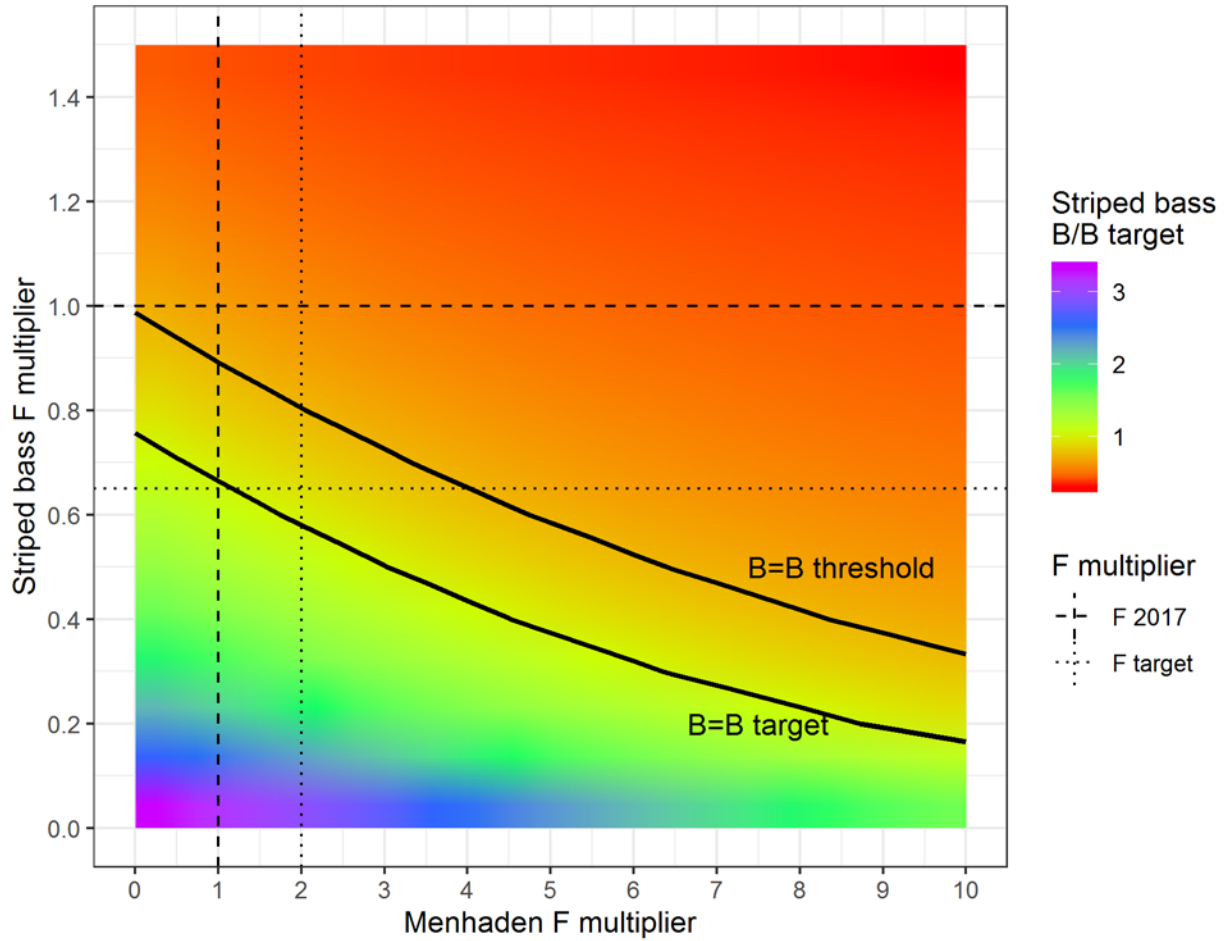


Figure 250. Estimates of age-1+ exploitation rate from the BAM model and the ERP models on an absolute scale (top) and scaled to their time series mean (bottom). Shaded area around BAM estimates indicates 95% confidence interval from MCMC analysis, a minimum estimate of uncertainty.



**Figure 251.** Striped bass age 6+ biomass ratio ( $B/B_{TARGET}$ ) in the terminal year of the EwE projections as a function of fishing mortality on both Atlantic menhaden and striped bass. Fishing mortality for each species is increased or decreased relative to  $F$  in 2017 through the  $F$  multipliers, i.e., an  $F$  multiplier equal to 1 indicates fishing at  $F_{2017}$ . The solid black lines represent the contours where striped bass age 6+ biomass equals the striped bass biomass target or threshold.

## 14 APPENDICES

### 14.1 Reproductive Biology and Fecundity of Atlantic Menhaden

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#### 14.1.1 Introduction

Marine teleost fishes display a wide range of reproductive strategies that have evolved to maximize fitness in response to selective pressures exerted by both biotic and abiotic factors. The majority of exploited marine fishes are gonochoristic, iteroparous, oviparous species (Murua and Saborido-Rey 2003, Lowerre-Barbieri et al. 2011a). Within this framework, however, size- and age-at-maturity, spawning seasonality and location, and spawning mode are species-specific. Spawning mode is typically classified into three distinct categories: namely, determinate total spawning, determinate batch spawning, and indeterminate batch spawning (Hunter and Goldberg 1980, Hunter et al. 1985, Lowerre-Barbieri et al. 2011a). Species inhabiting cold-temperate and boreal environments tend to be determinate spawners, meaning that all gametes destined to be spawned in a given year undergo maturation prior to the onset of the spawning season and are subsequently released in either a single event (i.e., total spawning) or multiple events (i.e., batch spawning) over a short timeframe (Pavlov et al. 2009). Fitness is maximized by releasing all reproductive products in concert with some short-term, favorable environmental condition (e.g., spring bloom). Most temperate and subtropical fishes, however, exhibit indeterminate batch spawning (Hunter et al. 1985, Murua and Saborido-Rey 2003). Spawning seasons are typically protracted, mature ova and sperm are released in several batches, and immature gametes are continually recruited to maturity and spawned throughout the season. Indeterminate batch spawning enables individuals to overcome the limitations of body cavity volume on gamete production and increases the probability that resulting offspring encounter favorable environmental conditions, thereby increasing fitness (Sadvoy 1996).

Quantifying the reproductive potential of an exploited marine species is an essential component of the stock assessment and management process, as this information yields insight into sustainable levels of harvest and the capacity of the stock to recover from overexploitation (Lowerre-Barbieri 2009). Most stock assessments in the US characterize reproductive potential via measures of spawning stock biomass, typically characterized as the total biomass of mature fish or aggregate biomass of mature females only. It is likely, however, that annual fecundity measured as total egg production is a more accurate representation of reproductive potential, given typical nonlinearities in the relationship between fish size and reproductive output (Marshall 2009, Morgan et al. 2009, Lowerre-Barbieri et al. 2011b). Indeed, a number of stock assessments have begun to incorporate estimates of annual egg production as indicators of reproductive potential in lieu of spawning stock biomass (e.g., SEDAR 2015, SEDAR 2018). The

methodology employed to generate these fecundity estimates varies depending on the reproductive biology, and particularly the spawning mode, of the stock of interest. Failure to properly characterize reproductive biology and spawning mode often results in the misapplication of methods meant to quantify fecundity, which in turn can result in the over- or under-estimation of the annual fecundity of a stock (Hunter et al. 1985, Brown-Peterson et al. 2017).

Atlantic menhaden (*Brevoortia tyrannus*) are a gonochoristic, iteroparous, oviparous teleost that comprise a single stock ranging from Nova Scotia to Northern Florida (Higham and Nicholson 1964, Lynch et al. 2010a). This species supports the largest commercial fishery, by volume, on the US East Coast; approximately 76% of the annual harvest is supplied to a reduction facility located in Reedville, Virginia, while the remaining 24% is taken as part of a smaller-scale bait fishery (SEDAR 2015). The status of the Atlantic menhaden stock is assessed using the Beaufort Assessment Model (BAM), and estimates of annual fecundity are used to quantify reproductive potential and develop biological reference points in these assessments. Specifically, population-level egg production is compared with that expected at the threshold fishing mortality rate to determine whether the stock is overfished. A fecundity-at-length relationship is coupled with length-at-age information to yield fecundity-at-age at the beginning of the fishing season. These data are then combined with abundance-at-age and maturity information and summed across ages to estimate annual egg production.

While the assessment approach for Atlantic menhaden has moved beyond the use of spawning stock biomass as a measure of reproductive potential, there are a number of concerns with the fecundity-at-length relationship used to estimate annual fecundity in past assessments, and re-evaluation of the fecundity of this stock was defined as a high-priority research recommendation following the most recent benchmark assessment (SEDAR 2015). Specifically, the fecundity-at-length information used in the past was developed based on sampling that occurred between 1956 and 1981 and was restricted to the coastal ocean in the vicinity of Beaufort, NC during fall (Higham and Nicholson 1964, Dietrich 1979, Lewis et al. 1987). Annual egg production has been shown to exhibit plasticity in response to variability in both biotic and abiotic factors (Brown-Peterson and Warren 2001), and as such a contemporary evaluation of Atlantic menhaden fecundity from throughout a broad range of the stock is warranted. Further, while evaluation of Atlantic menhaden ovary samples collected in the 1950s suggested that this species may exhibit indeterminate batch spawning, the approach used to quantify the aforementioned fecundity-at-length relationship employed methodology associated with determinate total spawning species (Higham and Nicholson 1964, Lewis et al. 1987). Mischaracterization of spawning mode has been shown to impact population-level fecundity estimates on the order of 100-1000 fold (Brown-Peterson et al. 2017). Further, efforts to quantify the reproductive biology and fecundity of two congener species, the Gulf menhaden (*Brevoortia patronus*) and the Brazilian menhaden (*Brevoortia aurea*), found that both exhibit characteristics consistent with indeterminate batch spawning (Macchi and Acha 2000, Brown-Peterson et al. 2017). The designation of Gulf and Brazilian menhaden as indeterminate batch spawners was due, in part, to the use of gonad histology in the respective investigations, a technique that was not widely implemented when the fecundity of Atlantic menhaden was originally assessed.

The objective of this investigation, therefore, was to generate a contemporary evaluation of female Atlantic menhaden reproductive biology that represented a broad spatiotemporal spawning range, and subsequently yield updated estimates of fecundity using methodology that is consistent with the spawning mode of this species. Specifically, we:

- Collected female Atlantic menhaden across all seasons and from throughout the Mid-Atlantic Bight.
- Implemented standard gonad histology techniques to assess ovarian maturity phases, provide insight into spawning mode, and yield information on spawning seasonality, interval, and frequency.
- Counted ova using methodology consistent with the spawning mode of this species.
- Modeled fecundity as a function of fish length and coupled this information with size-at-age, spawning frequency, and maturity data to yield age-specific estimates of annual fecundity.

#### 14.1.2 Methods

##### *Sample Collection*

Female Atlantic menhaden were collected between Cape Cod, MA and Cape Hatteras, NC from 2013-2018 (Figure 1). Samples acquired in April, May, October, and November were provided by the Northeast Area Monitoring and Assessment Program (NEAMAP) Mid-Atlantic/Southern New England Trawl Survey (Bonzek et al. 2008), while those from the summer months (i.e., June, July, and August) were collected in conjunction with port sampling of purse seine boats at the Omega Protein reduction facility in Reedville, Virginia. Female Atlantic menhaden also were acquired from this purse seine fleet in November 2017. Samples collected during the months of December and January were derived from the winter bottom trawl and gillnet fisheries that operate off of the coast of New Jersey.

Atlantic menhaden were processed for biological data at the time of capture on NEAMAP, while those derived from industry sources were held on ice for up to 24h prior to the collection of these data. For each fish, fork length (FL; mm), whole weight (g), macroscopic sex and maturity phase, and total ovary weight (0.001g) were recorded. Maturity phases were classified following Brown-Peterson et al. (2017). Ovaries were preserved in either 10% neutral buffered formalin or Normalin; samples preserved in Normalin were rinsed in tap water and transferred to formalin within one week. Gonadosomatic index (GSI) was calculated for each female fish as:

$$GSI = \left( \frac{OW}{(W-OW)} \right) * 100 \quad (1)$$

where W is whole fish weight and OW is total ovary weight.

##### *Reproductive Biology*

Ovarian tissues from each female Atlantic menhaden were processed using standard histological techniques (Prophet 1992). Specifically, these tissues were fixed for a minimum of one week in 10% neutral buffered formalin prior to histological preparation. The ovaries of a

given fish were removed from formalin, blotted dry with a paper towel, and weighed (0.001g) to yield preserved total ovary weight (PW). Atlantic menhaden ovaries were shown to be homogenous with respect to oocyte abundance and size distribution within each ovary and between left and right ovaries (Higham and Nicholson 1964). As such, a cross section of approximately 5 mm was removed from the central region of either the left or right ovary, placed in a sample cassette, and rinsed for 24h in tap water. These samples were then dehydrated in a series of graded ethanols and embedded in paraffin. Each sample was cross-sectioned at 4  $\mu$ m using a benchtop rotary microtome, and the resulting section was mounted on a glass slide and subsequently stained with hematoxylin and eosin.

Ovarian sections were evaluated at 80x magnification using a dissecting microscope. For a given sample, all egg stages present in the ovary were recorded, and reproductive phase was assigned based on the most advanced egg stage. Reproductive phases were classified as immature, early developing, developing, spawning capable (with an actively spawning subphase), regressing, and regenerating (Brown-Peterson et al. 2011). Further, the presence of oocyte maturation (OM; i.e., germinal vesicle migration and germinal vesicle breakdown) and post ovulatory follicles (POF) was noted for all fish classified as spawning capable or actively spawning. The diversity of egg stages found in the ovary sections of spawning capable fish was used to characterize female Atlantic menhaden as total or batch spawners. Spawning seasonality (SS) was quantified by identifying those months in which spawning capable or actively spawning female Atlantic menhaden were encountered and by evaluating monthly mean GSI (Brown-Peterson et al. 2017).

Two approaches were used to identify whether the reproductive biology of female Atlantic menhaden exhibited characteristics consistent with determinate or indeterminate batch spawning. First, the size-frequency (i.e., diameter-frequency) distribution of ova in a fish collected early in the spawning season was compared with that of a fish collected late in the season. Determinate spawners typically display a notable gap in the size-frequency distribution between immature and mature oocytes, and the relative abundance of mature ova usually declines as the spawning season progresses. In contrast, indeterminate spawners show a more continuous size-frequency distribution and a relatively consistent abundance of mature eggs throughout the spawning period (Brown-Peterson et al. 2017). These size-frequency distributions were obtained by counting and measuring all ova in a 0.02 g – 0.03 g subsample of preserved ovary (PS), and subsequently scaling these data to the whole ovary using the ratio of PW/PS. Atlantic menhaden spawning mode was also evaluated by comparing annual fecundity estimates generated using methodology appropriate for determinate spawning species with those estimates resulting from the approach associated with indeterminate spawning for two spawning capable fish collected at the beginning of the spawning season (Brown-Peterson et al. 2017).

### *Annual Fecundity*

Given that the evaluation of female Atlantic menhaden reproductive biology yielded strong evidence that this species exhibits indeterminate batch spawning (see 'Results & Discussion' section), efforts to quantify annual fecundity followed the methodology associated with this



spawning mode. Specifically, relative batch fecundity (RBF) was estimated and combined with information on spawning frequency, size-at-age, and maturity-at-age to yield estimates of annual fecundity-at-age.

RBF was quantified for each fish in the spawning capable gonad phase and actively spawning sub-phase using the oocyte size-frequency method (Hunter et al. 1985). In this approach, the oocytes in the most advanced stage of maturity, typically third-stage vitellogenic (VTG3), represent the cohort of ova to be released in the proximate batch and batch fecundity (BF) is estimated by counting these ova. Note that while many studies have quantified BF using the hydrated oocyte method (e.g., Macchi and Acha 2000, Brown-Peterson et al. 2017), such an approach was not possible in this investigation, given that no hydrated oocytes were observed. The size-frequency method, albeit more labor-intensive, yields results comparable to those derived from the hydrated oocyte method (Hunter et al. 1985).

The first step in quantifying RBF for Atlantic menhaden involved identifying the size-distribution of VTG3 ova in spawning capable fish, as VTG3 represents the most advanced egg stage in this phase. Four spawning capable fish were selected from throughout the defined spawning season, and the size-frequency distribution of ova was quantified for each using the methods described above. These distributions were then combined into a single size-frequency distribution, and Gaussian mixture models were fitted to this distribution to identify the number of modal groups present, as well as the size range associated with each group. The lower bound on the diameter of VTG3 ova (i.e., minVTG3) was defined as the mean diameter of the largest modal group minus one standard deviation. Batch fecundity (BF) was then quantified for each spawning capable and actively spawning Atlantic menhaden by counting all ova larger than minVTG3 in a 0.02 g – 0.03 g subsample of preserved ovary and scaling these counts to the whole ovary using the ratio of PW/PS. RBF was estimated from BF by:

$$RBF = \frac{BF}{W-OW} \quad (2)$$

This process was repeated so as to yield two estimates of RBF for each fish.

Linear mixed effects (LME) models were applied to evaluate the relationship between RBF and Atlantic menhaden size (Zuur et al. 2009). Specifically, two competing model forms were considered:

$$\begin{aligned} \log(\mathbf{RBF}) &= \beta_1 * \mathbf{L} + \gamma * \mathbf{F} + \boldsymbol{\varepsilon} \quad \text{where } \gamma \sim N(0, \sigma_{fish}^2) \\ \boldsymbol{\varepsilon} &\sim N(0, \sigma^2) \end{aligned} \quad (3)$$

and

$$\begin{aligned} \log(\mathbf{RBF}) &= \gamma * \mathbf{F} + \boldsymbol{\varepsilon} \quad \text{where } \gamma \sim N(0, \sigma_{fish}^2) \\ \boldsymbol{\varepsilon} &\sim N(0, \sigma^2) \end{aligned} \quad (4)$$

where  $\mathbf{RBF}$  was the vector ( $n \times 1$ ) of RBF estimates for the  $n$  individual spawning capable or actively spawning Atlantic menhaden,  $\mathbf{L}$  was the design matrix ( $n \times 1$ ) for the fixed-effect of fork

length,  $\beta_1$  was the coefficient associated with fork length,  $\mathbf{Z}$  was the design matrix ( $n \times 1$ ) for the random effect of fish,  $\gamma$  was the estimate of the random effect (normally distributed with zero mean, variance  $\sigma_{fish}^2$ ), and  $\boldsymbol{\varepsilon}$  ( $n \times 1$ ) was the error vector (distributed normally with zero mean, variance  $\sigma^2$ ). Note that fish was included as a random effect given that there were two estimates of RBF for each individual fish. The most supported model was identified using Akaike information criterion (Akaike 1973, Burnham and Anderson 2002).

Atlantic menhaden spawning interval (SI) was quantified using both the OM and POF methods (Hunter and Macewicz 1985). Spawning interval based on the OM method was calculated as

$$SI_{OM} = \frac{1}{(n_{OM}/n_{SC})} \quad (5)$$

where  $n_{OM}$  was the number of spawning capable fish with oocytes undergoing OM and  $n_{SC}$  was the number of spawning capable fish. Interval based on the POF method was:

$$SI_{POF} = \frac{1}{(n_{POF}/n_{SC})} \quad (6)$$

where  $n_{POF}$  was the number of spawning capable fish containing POFs. Estimates of spawning frequency (SF) for each approach were then generated by:

$$SF_{OM} = \frac{SS}{SI_{OM}} \quad (7)$$

and

$$SF_{POF} = \frac{SS}{SI_{POF}} \quad (8)$$

Annual fecundity-at-age in year  $i$  ( $AF_{ai}$ ) was estimated as:

$$AF_{ai} = RBF * WT_{ai} * SF * PM_{ai} \quad (9)$$

where  $WT_{ai}$  and  $PM_{ai}$  represented weight-at-age and maturity-at-age for female Atlantic menhaden at the beginning of the fishing year  $i$  and were obtained from current efforts related to the 2019 benchmark assessment for this species. Spawning frequency was represented by  $SF_{OM}$ ,  $SF_{POF}$ , and the mean of these two values ( $SF_{\bar{x}}$ ) to characterize the uncertainty in the number of batches of ova spawned by Atlantic menhaden over the course of a spawning season. This approach yielded upper (using  $SF_{OM}$ ), lower (using  $SF_{POF}$ ), and mean (using  $SF_{\bar{x}}$ ) values of  $AF_{ai}$  for this stock.

All statistical analyses were performed using the R software program (v3.3.2, R Core Team 2016). Package 'mixtools' was used to fit Gaussian mixture models to the full egg size-frequency distribution when identifying the minimum egg diameter associated with the proximate batch, while the package 'lme4' was accessed to model RBF.

### 14.1.3 Results & Discussion

#### Sample Collection

A total of 336 female Atlantic menhaden were collected from the nearshore waters of the Mid-Atlantic Bight and Chesapeake Bay from 2013-2018. Of these, 154 fish were derived from the NEAMAP Trawl Survey while 182 were provided by the commercial fishing industry. The sample size in this investigation is comparable with that used to characterize the reproductive biology and fecundity of Gulf menhaden (337 fish; Brown-Peterson et al. 2017) as well as Brazilian menhaden (315 fish; Macchi and Acha 2000). Note that while macroscopic determination of sex has been shown to be problematic for some *Brevoortia* species (Brown-Peterson et al. 2017), only 5 of the 341 fish (1.47%) classified as female macroscopically were found to be male upon histological examination. The relatively low error rate in macroscopic sex determination for Atlantic menhaden is likely due to the larger body and gonad size of this species. Further, while it has been shown that sex determination is more difficult when specimens have been frozen, all fish in this investigation were processed either at the time of capture or after having been held on ice for a short time period.

Atlantic menhaden sampled as part of this investigation ranged in size from 170 mm FL to 330 mm FL (Figure 2). The size range of fish included in the previous investigation of Atlantic menhaden fecundity ranged from 180-360 mm FL (Lewis et al. 1987). The difference in the maximum size between these two studies may be due to differences in the availability of larger fish between the time periods (1950s-1970s v. 2010s) or in sampling methods. Fish were collected from all months of the year with the exception of February, March, and September. Monthly sample sizes ranged from a single fish collected during April to 105 sampled during October (Figure 3). Sample sizes from the remaining months ranged between 19 and 52 female Atlantic menhaden.

### *Reproductive Biology*

Histological preparations of ovarian tissue were evaluated for each of the 336 female Atlantic menhaden collected in this investigation, and this study represents the first to assess the reproductive biology of this species via gonad histology. The ovaries of 42 fish were found to be in the immature phase, 51 were early developing, 64 were developing, 44 were spawning capable, 17 were in the actively spawning sub-phase of the spawning capable phase, 14 were regressing, and 104 were in the regenerating phase. It is worth noting that, of the 17 fish in the actively spawning sub-phase, none of the ovarian tissues were found to contain hydrated oocytes. Eleven of these fish were undergoing OM, with late germinal vesicle migration often as the most advanced stage, and six possessed POFs that were less than 24 h old, indicating that spawning was likely to occur or had occurred within 24 h, respectively (Hunter and Macewicz 1985, Fitzhugh and Hettler 1995). Note that the absence of hydrated oocytes in these Atlantic menhaden was not surprising, given that spawning is thought to occur at night, hydration occurs over an approximate 6h timeframe (Fitzhugh and Hettler 1995), and all collections of fish for this investigation occurred during daylight hours.

For each of the female Atlantic menhaden in the developing, spawning capable, and actively spawning phases (i.e., representing 125 fish), the presence of ova in the most advanced stage of development was accompanied by oocytes in all earlier stages of development. For example, while the ovary of an Atlantic menhaden in the spawning capable phase was characterized by the presence of numerous VTG3 ova, many stage 1 and stage 2 vitellogenic eggs, along with

oocytes in the cortical alveolar stage, were also present (Figure 4). These observations indicated that oocyte development is asynchronous in Atlantic menhaden and confirms that this species exhibits batch spawning (Brown-Peterson et al. 2011). Batch spawning was postulated for this species based on macroscopic assessments of ovaries collected in the late 1950s (Higham and Nicholson 1964), and two congeners of Atlantic menhaden, Gulf menhaden and Brazilian menhaden, were shown to exhibit characteristics associated with batch spawning (Macchi and Acha 2000, Brown-Peterson et al. 2017).

Atlantic menhaden spawning seasonality was assessed by evaluating monthly mean GSI and the percentage of female fish in the spawning capable phase of gonad development throughout the year. Monthly mean GSI showed clear peaks from October to December (Figure 5), and the percentage of spawning capable fish was highest during these months as well (Figure 6). While GSI showed a slight increase in May and spawning capable fish also were present during this time, sample size for this month was small. Specifically, only 22 fish were collected during May and, of those, only one was spawning capable. As such, the estimate of Atlantic menhaden spawning season was restricted to the October – December period (i.e., 92 days) to generate a conservative estimate of season length. The presence of slightly elevated mean GSI in May and the occurrence of a spawning capable fish, along with the observation of Atlantic menhaden larvae along the coast during the spring and early summer in the Mid-Atlantic (Nelson et al. 1977), indicates that the realized spawning season is likely longer than that presented here. Further, the lack of larger Atlantic menhaden from collections during summer months, perhaps due to topping-off in Chesapeake Bay during reduction fleet operations and subsequent sampling from the top of the fish hold during port sampling, may have introduced some bias in this estimate of spawning season duration. Additional collections for these months, as well as those from which samples were not acquired for this investigation (i.e., February, March, and September), are ongoing, and estimates of spawning seasonality will be updated as they become available.

Simpson et al. (2016) documented Atlantic menhaden larval distribution and abundance along Atlantic coast from between Cape Hatteras, NC and Cape Cod, MA, and Keller et al. (1999) showed that Atlantic menhaden larvae occur in Narragansett Bay, RI in June/July and again in October through December. This study did document a single actively spawning Atlantic menhaden in the southern New England area in May, which is consistent with the presence of larvae and juveniles in northern estuaries during summer (Simpson et al. 2016, Keller et al. 1999). However, given the sample size ( $n = 1$ ), spring months were excluded from the spawning season estimate. It is likely that Atlantic menhaden spawn during their spring northerly migration, and additional specimen collections are ongoing to further resolve the spawning seasonality.

The size-frequency distributions of oocytes in the ovaries of spawning capable Atlantic menhaden collected near the beginning (i.e., October) and end (December) of the spawning season were evaluated to characterize the spawning mode of this species (Figure 7). The lack of a distinct gap between immature and mature ova in each of these distributions was consistent with indeterminate spawning. In addition, the relative abundance of mature eggs did not decline late in the spawning season, which serves as evidence of continual recruitment of oocytes into maturity throughout the season and suggests that this species exhibits

indeterminate spawning. Further, annual egg production for two specimens collected early in the spawning season was quantified first using methodology appropriate for determinate batch spawners (i.e., count all mature ova), followed by that associated with indeterminate batch spawning (i.e., combine RBF, fish size, and spawning frequency). For each fish, annual fecundity estimates derived under the assumption of indeterminate batch spawning were nearly double those associated with determinate batch spawning (specimen 1: 1,163,770 eggs v. 538,567 eggs; specimen 2: 937,634 eggs v. 535,096 eggs), indicating that the standing stock of mature ova at the start of the spawning season was insufficient to supply the demand over the course of the spawning period, and that indeterminate spawning is likely. Finally, it is worth noting that mean GSI values remained elevated throughout the duration of the spawning season, a hallmark of indeterminate batch spawning species.

Given the above evidence, it is likely that Atlantic menhaden exhibit indeterminate batch spawning, and this finding is consistent with the determinations of spawning mode for both Gulf menhaden and Brazilian menhaden (Macchi and Acha 2000, Brown-Peterson et al. 2017). Indeed, most warm temperate and subtropical fishes are indeterminate batch spawners (Hunter et al. 1985, Murua and Sabrido-Rey 2003), and Atlantic menhaden appear to be no exception. This investigation represents the first to use empirical information on the reproductive biology of Atlantic menhaden to classify the spawning mode of this species.

#### *Annual Fecundity*

RBF was quantified for 61 Atlantic menhaden, which represented all fish in either the spawning capable phase of maturity or the actively spawning sub-phase, and included individuals ranging from 220 mm FL – 330 mm FL. The oocyte size-frequency method was used to quantify batch fecundity for each of these fish, and analysis of the oocyte size-frequency distribution generated from egg-diameter measurements of four spawning capable Atlantic menhaden supported evidence of five Gaussian curves (Figure 8). The mean diameter of the most advanced stage of ova was 551  $\mu\text{m}$  with a standard deviation of 98  $\mu\text{m}$ . As such, the lower bound of the diameter of the most advanced egg stage in these fish (i.e., minVTG3) was 453  $\mu\text{m}$ , and all ova > 453  $\mu\text{m}$  in diameter were counted to yield estimates of batch fecundity. Note that the previous investigations of Atlantic menhaden fecundity counted all eggs greater than 350  $\mu\text{m}$  in diameter under the assumption that this species exhibits determinate total spawning (Higham and Nicholson 1964, Dietrich 1979, Lewis et al. 1987). Further, alternative approaches to quantifying minVTG3 (e.g., mean – 2\*sd) in this investigation would have altered the resulting batch fecundity and RBF estimates.

Estimates of batch fecundity ranged from 8484 – 363576 eggs/batch, while RBF values varied from 28 – 734 eggs/g ovary-free body weight. RBF was modeled using mixed effects models (3) and (4) above. AIC favored model (4) and the coefficient of the fixed-effect Length was not significant ( $p=0.12$ ) in model (3), indicating no relationship between RBF and Atlantic menhaden size. Indeed, RBF calculations are intended to remove the effect of fish size and facilitate comparisons of batch fecundity for individuals of differing size (Brown-Peterson et al. 2017). The mean, bias-corrected RBF for the Atlantic menhaden stock was 236.92 eggs/g ovary-free body weight (Figure 9). The high variability in both batch fecundity and RBF observed in this investigation was not unexpected, given that batch sizes are influenced by a myriad of both

biotic and abiotic factors (Hunter et al. 1985, Macchi and Acha 2000, Brown-Peterson et al. 2017), and the estimate of mean RBF for Atlantic menhaden fell within the ranges reported for both Gulf menhaden and Brazilian menhaden.

While spawning interval was calculated using the OM and POF methods both monthly and for the full spawning season (Table 1), only those generated using data across the entire season were considered due to relatively low monthly sample sizes of spawning capable and actively spawning fish. The OM method indicated that female Atlantic menhaden spawn once every 5.5 days during the spawning season, while the POF method was used to estimate a 10.2 day spawning interval. The discrepancy in these estimates of spawning interval are typical (Macchi and Acha 2000, Brown-Peterson et al. 2017). It is likely that the OM method underestimates the spawning interval, perhaps due to the aggregation of animals in the actively spawning subphase just prior to a spawning event, while the POF method likely overestimates the interval, since rapid degradation of POFs in warm water environments can make these structures difficult to distinguish from beta-stage atresia. In an effort to ameliorate these biases, a mean spawning interval is usually calculated using the estimates derived from each of these methods. As such, the mean spawning interval for Atlantic menhaden was determined to be 7.86 days. While the mean spawning interval is longer than the 3.2 day interval estimated for Gulf menhaden (Brown-Peterson et al. 2017), it is consistent with the 8.0 day interval of the Brazilian menhaden (Macchi and Acha 2000), a species with a similar life history to that of the Atlantic menhaden.

Given a 92 day spawning season, it is expected that a female Atlantic menhaden would spawn an average of 11.72 times during that season (i.e., mean spawning frequency). Spawning frequency derived using the POF method was 9.02 spawns/season, while that estimated with the OM method was 16.73 spawns/season. These spawning frequency estimates were used to characterize uncertainty in the age-specific annual fecundity for this species.

Estimates of age-specific annual fecundity for Atlantic menhaden spanning age-0 to age-6+ were provided to the 2019 benchmark assessment for this stock. These estimates were generated using Equation (9) where  $RBF$  was 236.92 eggs/g ovary-free body weight,  $SF$  was 11.70 spawns/season, and where  $WT_{ai}$  and  $PM_{ai}$  were the weight-at-age  $a$  and proportion of fish mature at age  $a$  for a given  $i$  at the start of the fishing year (i.e., March 1). Uncertainty in these annual fecundity estimates was characterized by substituting  $SF$  with  $SF_{POF}$  and  $SF_{OM}$  to yield lower and upper bounds on these fecundity estimates. An example of these fecundity estimates for 2015 is provided (Table 2). Note that when compared with the age-specific annual fecundity estimates generated from the fecundity-at-length relationship used previously for this species (Lewis et al. 1987), increases in age-specific annual fecundity range from 554.7% - 680.8%, with a mean increase of 623.5%. Estimates of annual fecundity for Gulf menhaden using methodology consistent with the spawning mode of the species resulted in increases on the order of 1100%-2300% (Brown-Peterson et al. 2017), indicating that the results of this investigation are not unreasonable. The ongoing collections of female Atlantic menhaden during spring, summer, and early fall months will likely increase the annual fecundity estimates of this species further, and perhaps yield results more similar to those observed for the Gulf menhaden. These additional collections may also support the generation of age-specific estimates of  $SF$ . Given that many species exhibit variability in spawning season, spawning

interval, and therefore spawning frequency with age (Lowerre-Barbieri et al. 2011b, Fitzhugh et al. 2012, Brown-Peterson et al. 2017), characterizing these ontogenetic changes for Atlantic menhaden would yield greater insight in to the reproductive biology and annual fecundity for this species.

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### 14.1.6 Tables

**Table 1.** Estimates of spawning interval (SI) in days for female Atlantic menhaden collected from 2013-2018. Monthly estimates of SI using both the oocyte maturation (SI<sub>OM</sub>) and post ovulatory follicle (SI<sub>POF</sub>) methods are given, and estimates aggregated across the spawning season are given in bold font. Sample sizes of spawning capable female Atlantic menhaden by month are provided, and the number of fish undergoing OM or possessing POFs are indicated in parenthesis. Note that, if no fish were observed undergoing OM or containing POFs for a given month, SI was undefined (UND).

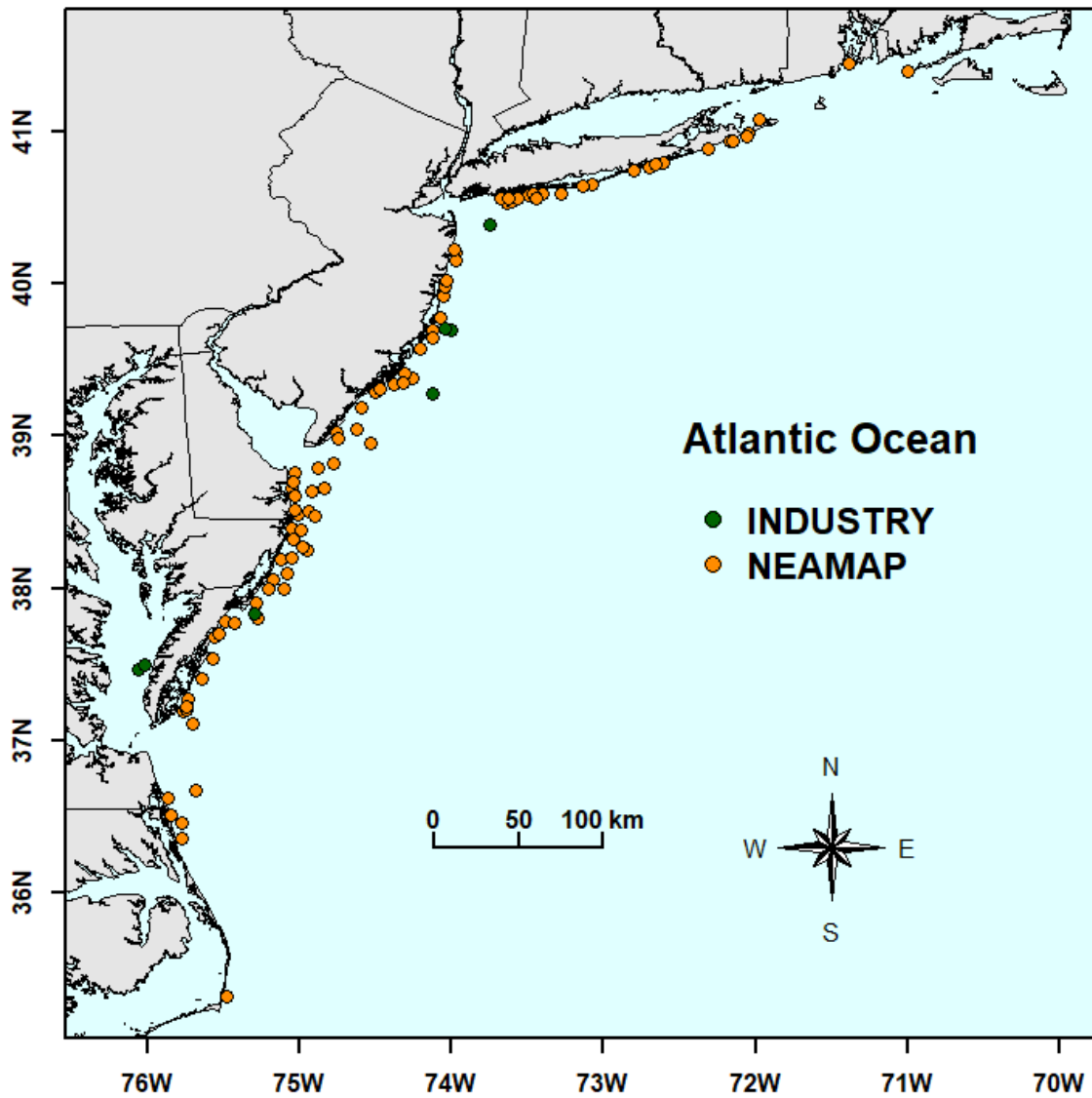
Month	SI <sub>OM</sub>	SI <sub>POF</sub>	Sample Size (OM Count/POF Count)
May	1.00	UND	1(1/0)
Oct	6.60	6.60	33(5/5)
Nov	UND	UND	11(0/0)
Dec	3.20	16.00	16(5/1)
<b>Overall</b>	<b>5.55</b>	<b>10.17</b>	<b>61(11/6)</b>

**Table 2.** Estimates of age-specific annual fecundity for age-1 to age-6 Atlantic menhaden in 2015 using the fecundity-at-length relationship used in past stock assessments (Lewis et al. 1987) and estimates derived from this investigation (Latour & Gartland). Mean, minimum (min.), and maximum (max.) estimates of annual fecundity were derived using mean spawning frequency ( $SF_{\bar{x}}$ ), spawning frequency based on the post ovulatory follicle method ( $SF_{POF}$ ), and spawning frequency based on the oocyte maturation method ( $SF_{OM}$ ). The percent change quantifies the change in estimates of age-specific annual fecundity between Lewis et al. (1987) and this investigation where  $SF_{\bar{x}}$  was used to represent spawning frequency.

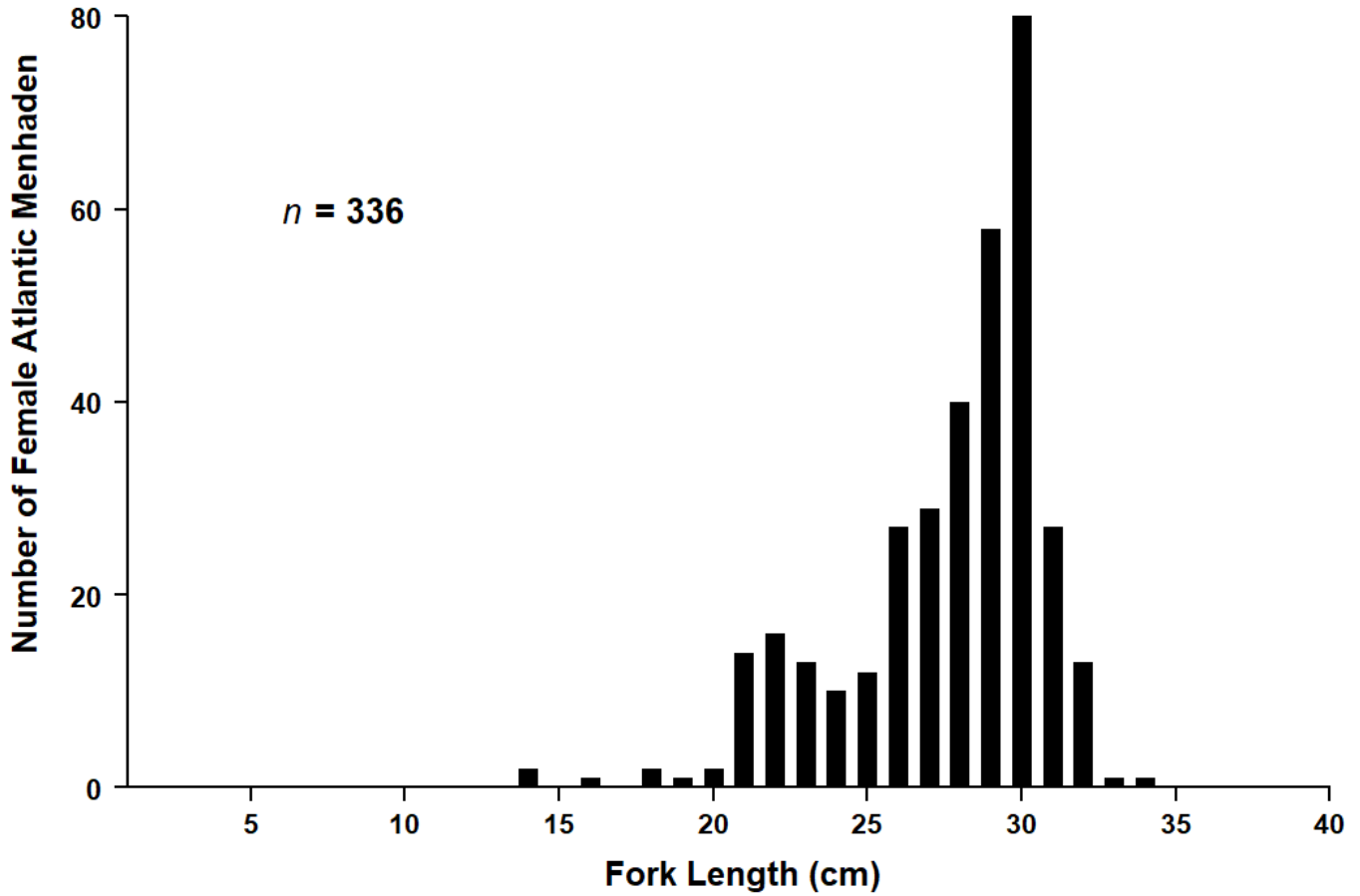
Age	Annual Fecundity			Percent Change	
	Lewis et al. 1987	Latour & Gartland Mean	Latour & Gartland Min.		Latour & Gartland Max.
1	3,770	27,350	21,076	39,086	+625%
2	37,765	270,490	208,437	386,555	+616%
3	98,782	771,287	594,344	1,102,240	+681%
4	137,741	1,044,859	805,156	1,493,198	+659%
5	173,022	1,132,786	872,911	1,618,854	+555%
6+	180,394	1,271,904	980,114	1,817,666	+605%

### 14.1.7 Figures

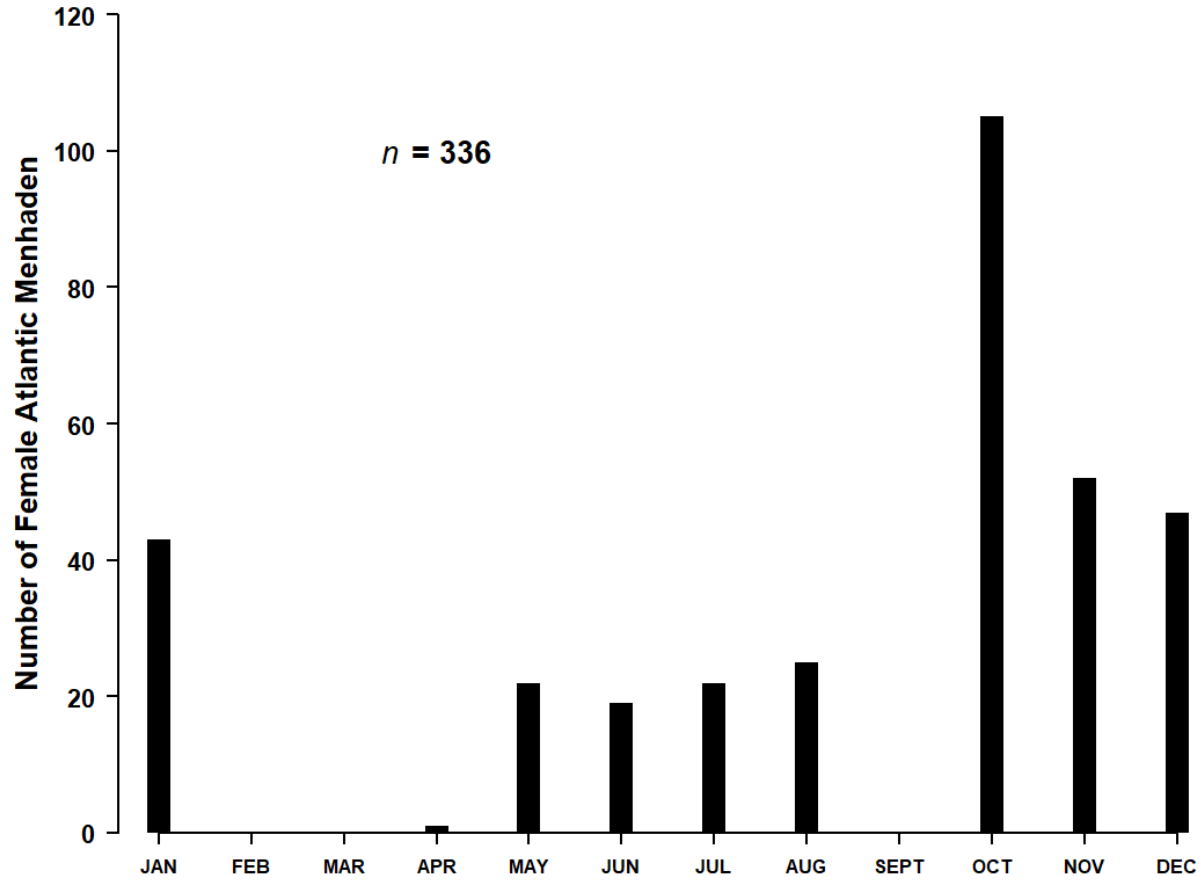
**Figure 1.** Distribution of sites from which female Atlantic menhaden were sampled by the NEAMAP Trawl Survey (orange) and commercial purse seine, trawl, and gillnet fisheries (green) from 2013-2018.



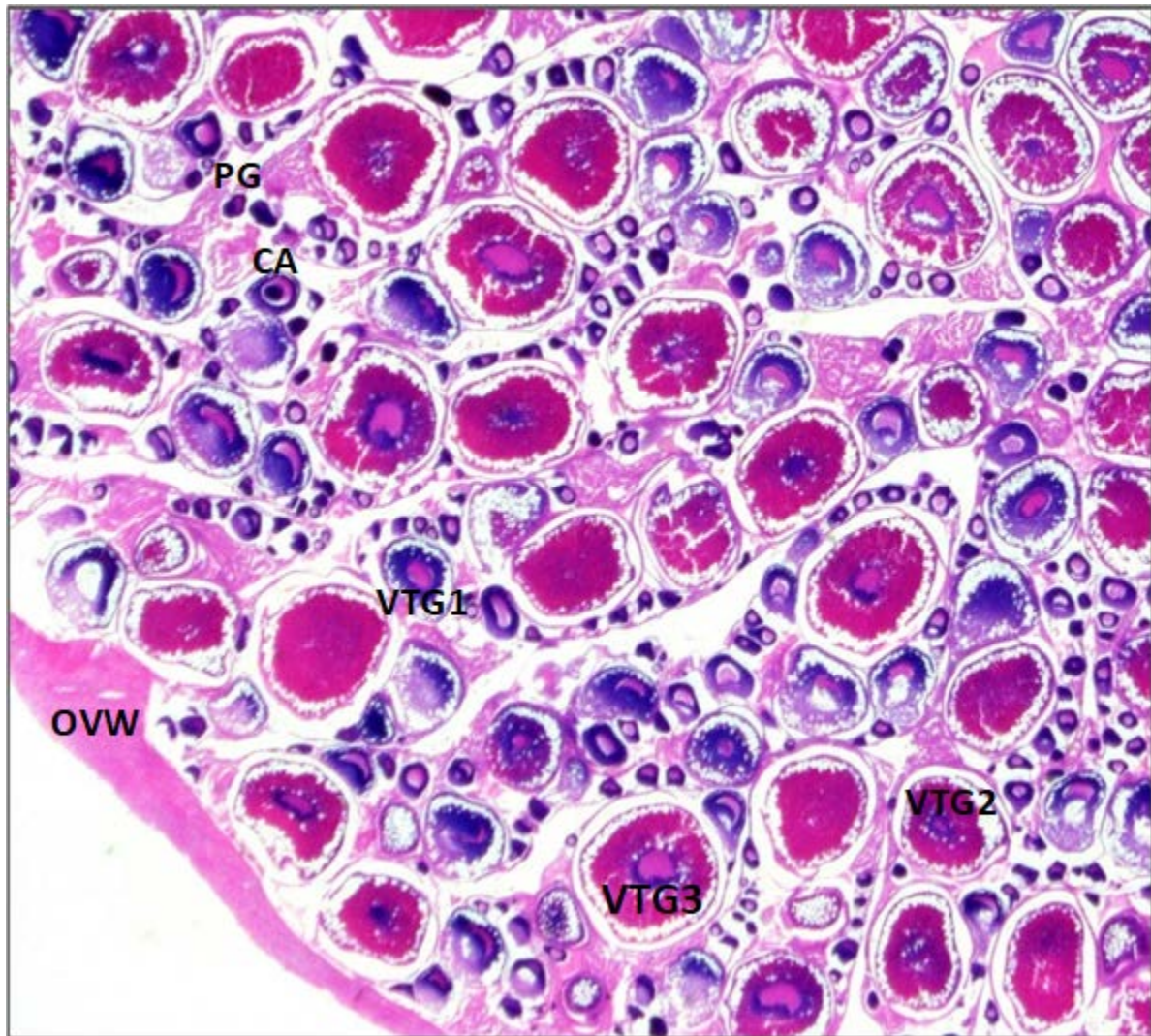
**Figure 2.** Length-frequency distribution of female Atlantic menhaden collected from 2013-2018 to characterize the reproductive biology and fecundity of this species.



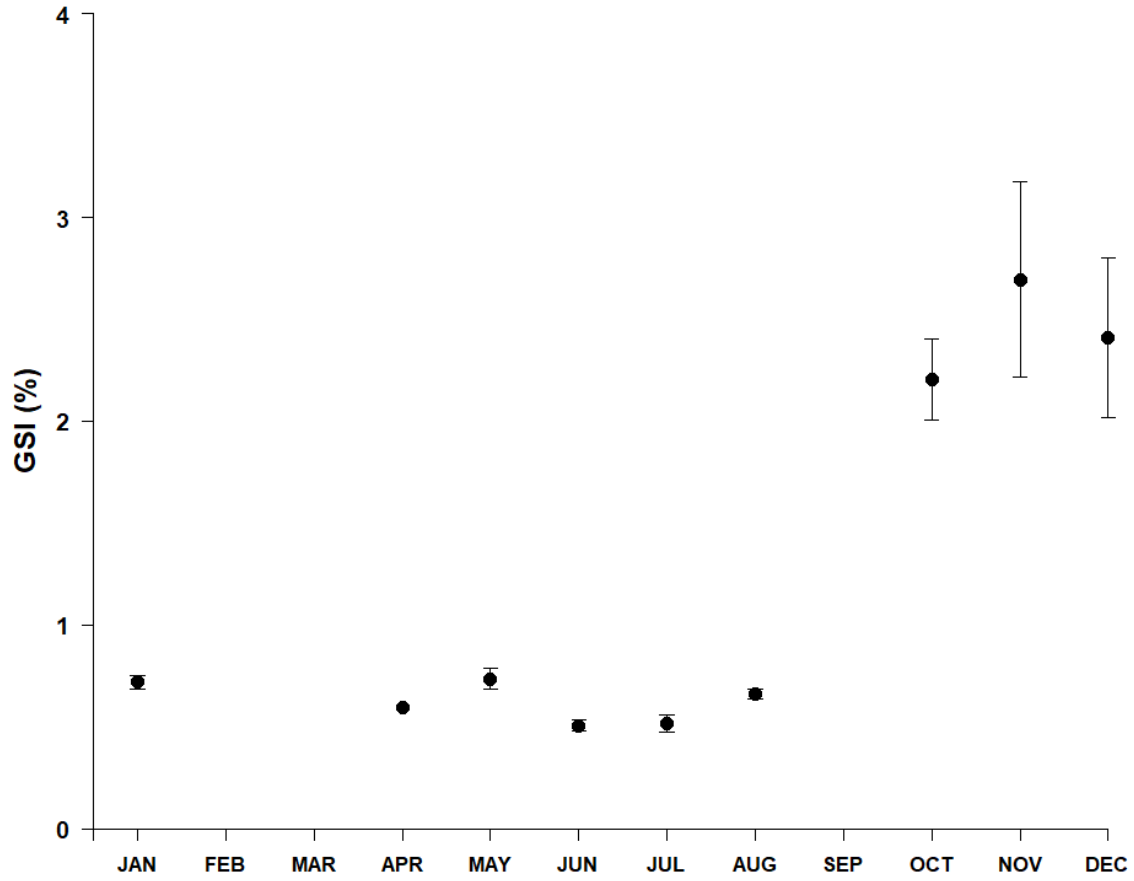
**Figure 3.** Number of female Atlantic menhaden collected monthly from 2013-2018 to characterize the reproductive biology and fecundity of this species.



**Figure 4.** Histological gonad section (80x magnification) of a 295mm fork length, spawning capable Atlantic menhaden collected from the coastal ocean of New Jersey in October 2017. Asynchronous oocyte development characteristic of batch spawning was evident. PG = primary growth, CA = cortical alveolar, VTG1 = first stage vitellogenesis, VTG2 = second stage vitellogenesis, VTG3 = third stage vitellogenesis, OVW = ovarian wall.

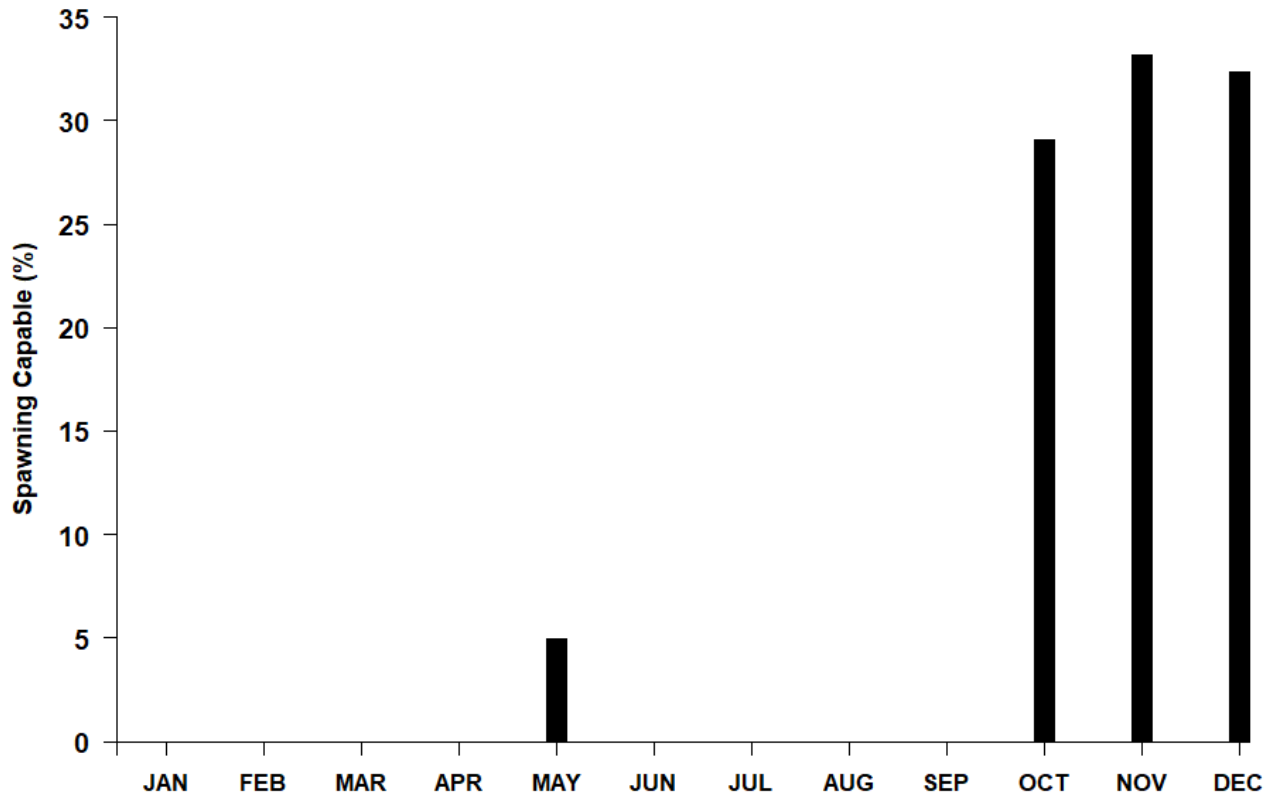


**Figure 5.** Mean monthly gonadosomatic index (GSI) for female Atlantic menhaden collected from 2013-2018. Error bars represent standard errors of the means.

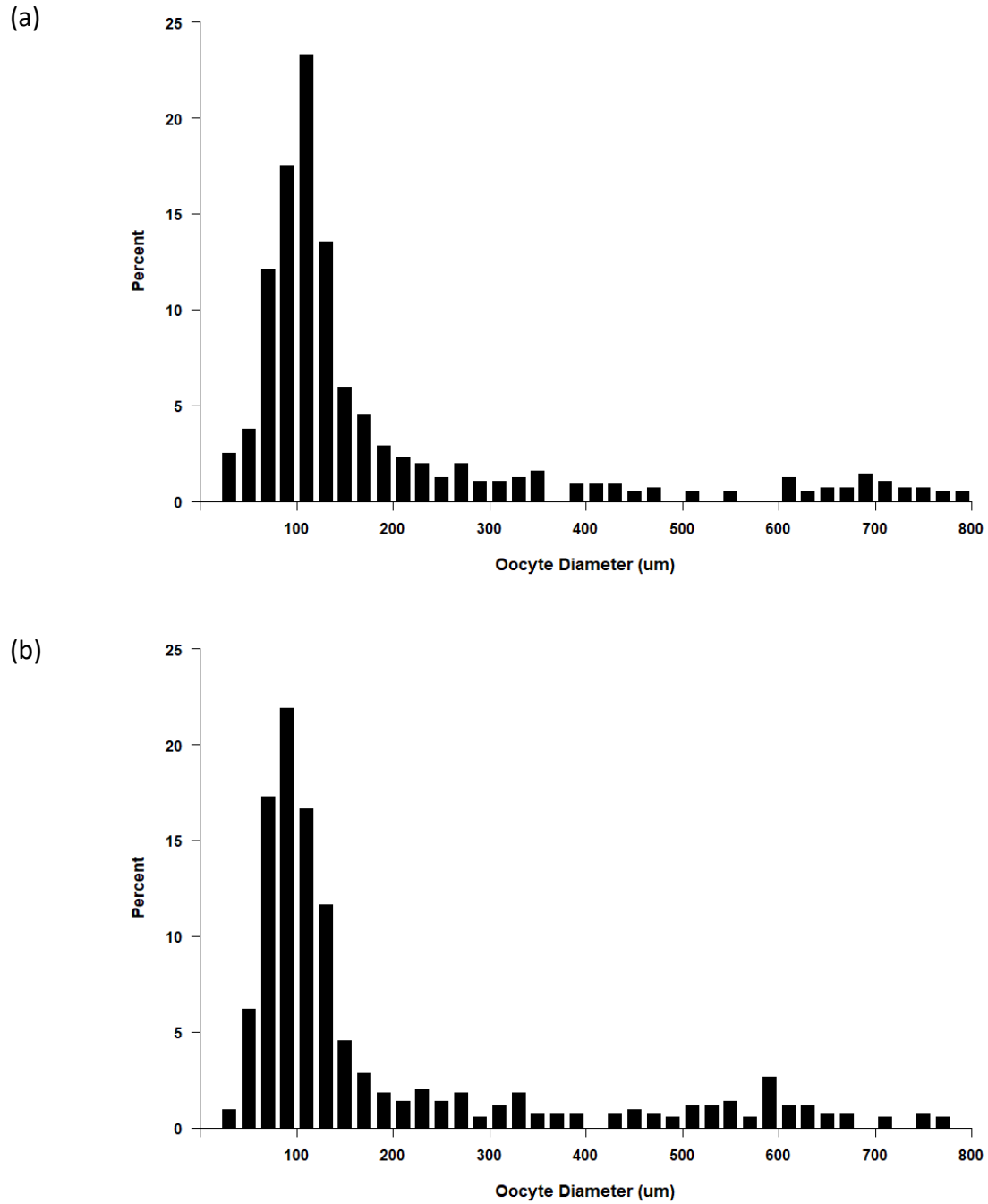




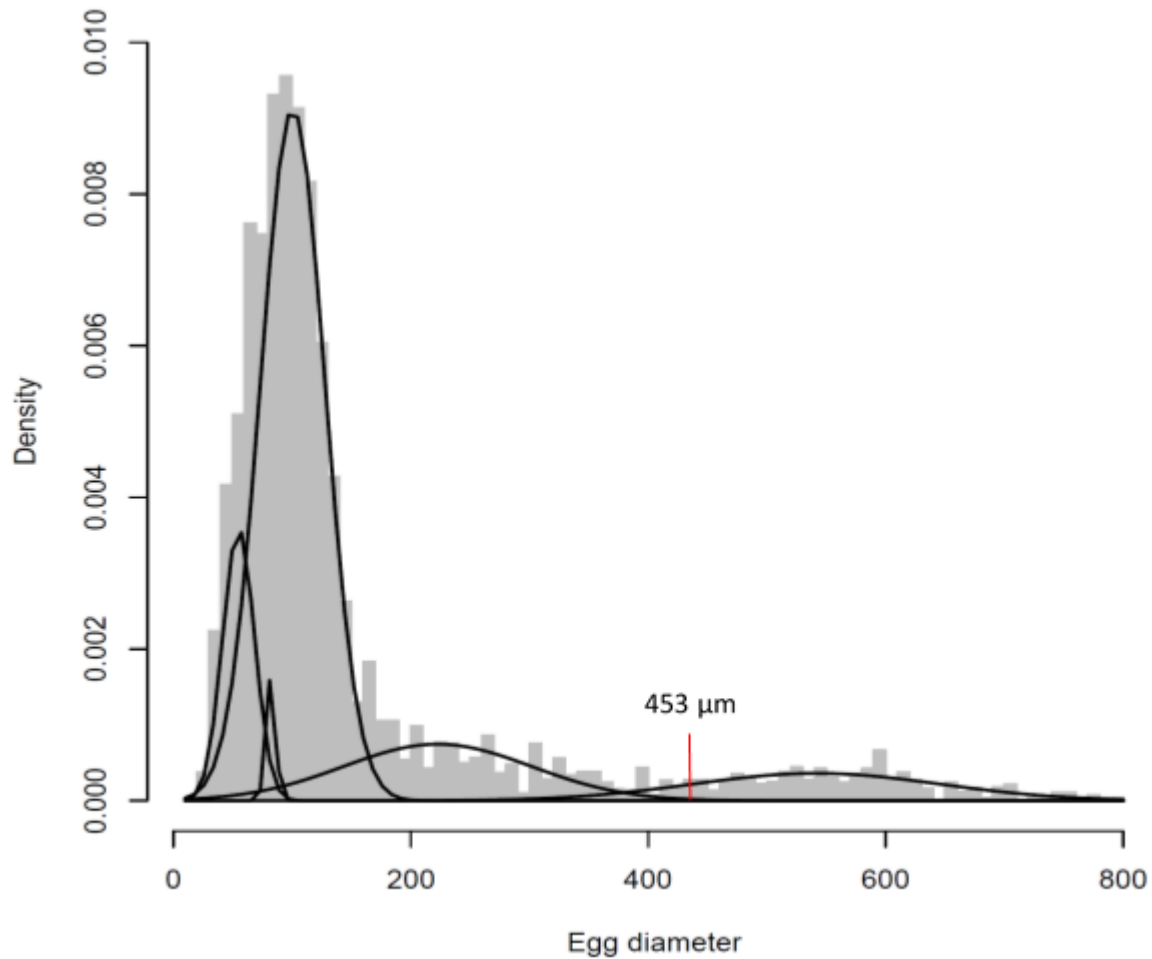
**Figure 6.** Monthly percentage of female Atlantic menhaden in the spawning capable gonad phase (including the actively spawning sub-phase). Fish were collected from 2013-2018 in an effort to characterize the reproductive biology and fecundity for this species.



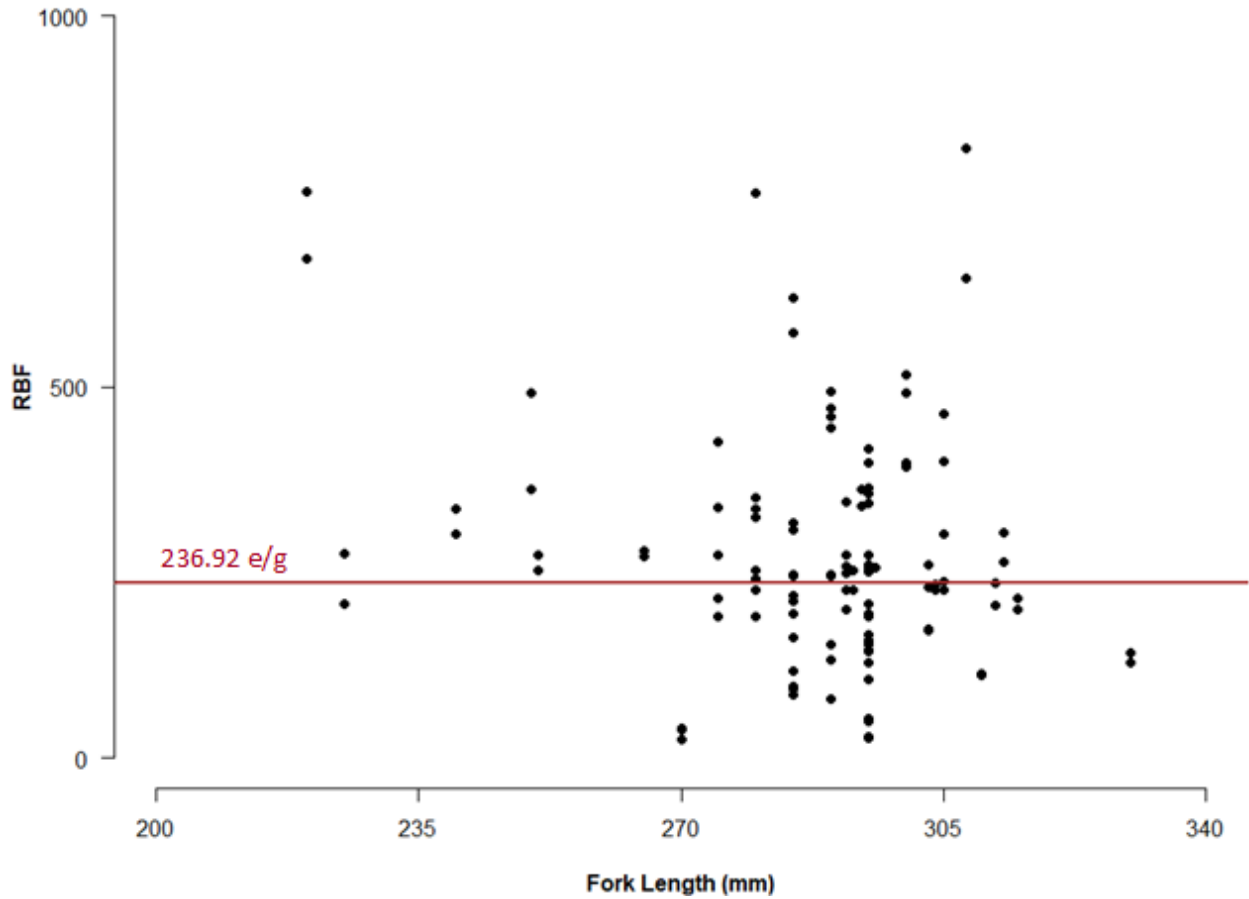
**Figure 7.** Size-frequency distribution of all oocytes present in a spawning capable female Atlantic menhaden collected in (a) October off of the coast of New York and (b) December off of the coast of New Jersey. The fish collected in October was 285 mm fork length (FL), while that sampled in December was 300 mm FL.



**Figure 8.** Size-frequency distribution of all oocytes present in the ovaries of four spawning capable female Atlantic menhaden collected from October – December. Model development supported the presence of five Gaussian curves within this distribution. The mean egg diameter of the largest group was 551  $\mu\text{m}$  with a standard deviation of 98  $\mu\text{m}$ . The lower bound for the size of third stage vitellogenic eggs (minVTG3) was 453  $\mu\text{m}$  (i.e., 551  $\mu\text{m}$  – 98  $\mu\text{m}$ ).

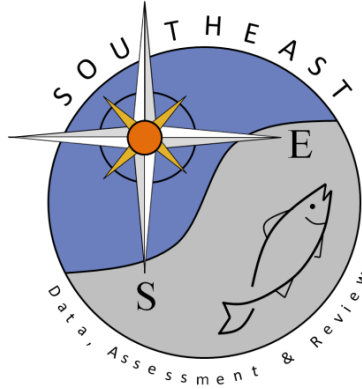


**Figure 9.** Plot of relative batch fecundity (RBF) on female Atlantic menhaden fork length for 61 fish with gonads either in the spawning capable phase or actively spawning sub-phase. Mean bias-corrected RBF for the Atlantic menhaden stock was 236.92 eggs/g ovary-free body weight.



## **14.2 BAM AD Model Builder Code**

[Provided in separate document]



# SEDAR

Southeast Data, Assessment, and Review

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SEDAR 69

Section III: Review Workshop Report

**Atlantic Menhaden**

Benchmark Report

January 2020

SEDAR  
4055 Faber Place Drive, Suite 201 North Charleston, SC 29405

## Table of Contents

1.	Introduction .....	2
1.1	Workshop Time and Place .....	2
1.2	Terms of Reference for the Atlantic Menhaden Single-Species Peer Review .....	2
1.3	List of Participants.....	4
1.4	List of Background Documents and Review workshop working papers.....	5
2.	Review Workshop report .....	6
2.1	Executive Summary.....	6
2.2	Statements addressing each TOR .....	8
2.3	Summary Results of Analytical Requests.....	17
2.4	Submitted Comment.....	17

## 1. Introduction

### 1.1 Workshop Time and Place

The SEDAR 69 Review Workshop for Atlantic menhaden was held November 4-8 , 2019 in Charleston, SC.

### 1.2 Terms of Reference for the Atlantic Menhaden Single-Species Peer Review

1. Evaluate the thoroughness of data collection and the presentation and treatment of fishery-dependent and fishery-independent data in the assessment, including the following but not limited to:
  - a. Presentation of data source variance (e.g., standard errors).
  - b. Justification for inclusion or elimination of available data sources,
  - c. Consideration of data strengths and weaknesses (e.g., temporal and spatial scale, gear selectivities, aging accuracy, sample size),
  - d. Calculation and/or standardization of abundance indices.
2. Evaluate the methods and models used to estimate population parameters (e.g., F, biomass, abundance) and biological reference points, including but not limited to:
  - a. Evaluate the choice and justification of the preferred model(s). Was the most appropriate model (or model averaging approach) chosen given available data and life history of the species?
  - b. If multiple models were considered, evaluate the analysts' explanation of any differences in results.
  - c. Evaluate model parameterization and specification (e.g., choice of CVs, effective sample sizes, likelihood weighting schemes, calculation/specification of M, stock-recruitment relationship, choice of time-varying parameters, plus group treatment).
3. Evaluate the diagnostic analyses performed, including but not limited to:
  - a. Sensitivity analyses to determine model stability and potential consequences of major model assumptions
  - b. Retrospective analysis
4. Evaluate the methods used to characterize uncertainty in estimated parameters. Ensure that the implications of uncertainty in technical conclusions are clearly stated.
5. If a minority report has been filed, review minority opinion and any associated analyses. If possible, make recommendation on current or future use of alternative assessment approach presented in minority report.
6. Recommend best estimates of stock biomass, abundance, and exploitation from the assessment for use in management, if possible, or specify alternative estimation methods.



7. Evaluate the choice of reference points and the methods used to estimate them. Recommend stock status determination from the assessment, or, if appropriate, specify alternative methods/measures.
8. Review the research, data collection, and assessment methodology recommendations provided by the TC and make any additional recommendations warranted. Clearly prioritize the activities needed to inform and maintain the current assessment, and provide recommendations to improve the reliability of future assessments.
9. Recommend timing of the next benchmark assessment and updates, if necessary, relative to the life history and current management of the species.
10. Prepare a peer review panel terms of reference and advisory report summarizing the panel's evaluation of the stock assessment and addressing each peer review term of reference. Develop a list of tasks to be completed following the workshop. Complete and submit the report within 4 weeks of workshop conclusion.

**1.3 List of Participants**

<b>APPOINTEE</b>	<b>FUNCTION</b>	<b>AFFILIATION/LOCATION</b>
<b>Review Panel</b>		
Mike Jones	Review Panel Chair	ASFMC Appointee
Sarah Gaichas	Reviewer	ASMFC Appointee
Kenneth Frank	Reviewer	CIE
Daniel Howell	Reviewer	CIE
Laurence Kell	Reviewer	CIE
<b>Analytical Representatives</b>		
Amy Schueller	Single Species Lead Analyst & Chair	SEFSC – Beaufort, NC
Jason McNamee	Assessment Team	RI DEM – Jamestown, RI
Matt Cieri	ERP Work Group Chair	ME DMR – Boothbay, ME
Katie Drew	Assessment Team	ASMFC – Arlington, VA
Kristen Anstead	Assessment Team	ASMFC – Arlington, VA
Dave Chagaris	ERPLed Analyst	UF – Gainesville, FL
Ray Mroch	Assessment Team	SEFSC- Beaufort, NC
<b>Staff</b>		
Max Appelman	Atlantic Menhaden Coordinator/Rapporteur	ASMFC – Arlington, VA
Sarah Murray	ERP Coordinator/Rapporteur	ASMFC – Arlington, VA
Patrick Campfield	Science Director	ASMFC – Arlington VA
Ciera Graham	Admin	SAFMC
Kathleen Howington	Coordinator	SEDAR
<b>Observers</b>		
Bob Beal	Observer	ASFMC
Julie Neer	Observer	SEDAR
Joseph Ballenger	Observer	SCDNR
Peter Himchak	Observer	Omega Protein
Genny Nesslage	Observer	UMCES
Chris Dollar	Observer	TRCP
Howard Townsend	Observer	NOAA Fisheries
Jeff Kaelin	Observer	Lunds Fisheries

**1.4 List of Background Documents and Review workshop working papers**

Document #	Title	Author
SEDAR 69 – SAR1	Assessment of Atlantic Menhaden Single Species Benchmark Report	To be prepared by SEDAR 69
SEDAR 69 – SAR2	Assessment of Atlantic Menhaden Ecological Reference Point Report	To be prepared by SEDAR 69
<b>Supplementary Materials</b>		
SEDAR 69 – RD01	SEDAR 40 Stock Assessment Report Atlantic Menhaden	SEDAR 2015
SEDAR69 – RD02	Hierarchical analysis of multiple noisy abundance Indices	P. Conn 2010
SEDAR 69 – RD03	Estimation of movement and mortality of Atlantic menhaden during 1966–1969 using a Bayesian multi-state mark-recovery model	Liljestrand et.al. 2019
SEDAR 69 – RD04	Trends in Relative Abundance and Early Life Survival of Atlantic Menhaden during 1977–2013 from Long-Term Ichthyoplankton Programs	Simpson et.al. 2016
SEDAR 69 – RD05	Multi-state dead recovery mark-recovery model performance for estimating movement and mortality rates	Liljestrand et. al. 2019
SEDAR 69 – RD06	A Multispecies Statistical Catch-Atage (Msscaa) Model For A Midatlantic Species Complex	McNamee, 2018
SEDAR 69 – RD07	Evaluating the performance of a multispecies statistical catch-at-age model	Curti, 2013
SEDAR 69 – RD08	Parameter estimation in Stock Assessment Modelling: Caveats with Gradient-based algorithms	Subbey, 2018
SEDAR 69 – RD09	Reconciling single-species TACs in the North Sea demersal fisheries using the Fcube mixed-fisheries advice framework	Ulrich et.al. 2011
SEDAR 69 – RD10	Working Group on Mixed Fisheries Advice (WGMIXFISH-ADVICE)	ICES Advisory Committee, 2016
SEDAR 69 – RD11	Evaluation of Current and Alternative Harvest Control Rules for Blue Whiting Management using Hindcasting	Kell and Levontin, 2019
SEDAR 69 – RD12	Public comment Forum Submissions	SEDAR, 2019
SEDAR 69 – RD13	Cookbook for Using Model Diagnostics in Integrated Stock Assessments	Carvalho, 2019

## 2. Review Workshop report

### 2.1 Executive Summary

The Atlantic States Marine Fisheries Commission (ASMFC) Atlantic Menhaden Stock Assessment Subcommittee (SAS) provided a comprehensive report, complemented by supplementary materials and a series of presentations at the November 4-8, 2019, SEDAR 69 review workshop, held in Charleston, SC. These materials were reviewed and evaluated by a panel of five fishery experts, three from the Center for Independent Experts and two (including a chair) nominated by the ASMFC. The reports and presentations included thorough and extensive documentation of the stock assessment data, methods, and results for Atlantic menhaden, a detailed explanation of how the assessment methods and data sources differed from previous assessments, sensitivity and uncertainty analyses of the stock assessment model, an evaluation of stock status and current reference points, and recommendations for future research and monitoring. Overall the panel was very impressed with both the thoroughness and the clarity of the assessment reports and associated presentations. The panel commends the efforts of the SAS.

This panel report addresses eight Terms of Reference (ToR), which were developed and shared with the panel prior to the SEDAR 69 review workshop. The ToR concerned (1) the data used in the assessment; (2) assessment methods and models; (3 & 4) treatment of uncertainty; (5) any minority opinions (there were none); (6 & 7) assessment results and conclusions related to stock status; and (8) recommendations for research; (9) the timing of future assessments.

The Atlantic menhaden assessment uses both fishery-dependent and fishery-independent data to inform estimates of past and current population status. The panel concluded that the selection of data sets for inclusion in the assessment was defensible and appropriate. We noted that the existing data do not provide good information on the relative abundance of larger, older fish, and recommend that modification of existing data collection efforts or development of a new assessment tool that more effectively samples these fish should be a high priority for the future. The fishery-independent data enter the assessment model as a composite of a large number of surveys, covering the geographic range of Atlantic menhaden, but none of which actually target menhaden. Coherence among these surveys would be desirable, but the panel acknowledged that the observed low level of coherence was not surprising. The panel concluded that the method currently used to aggregate the surveys into a composite was reasonable, but encouraged the SAS to consider other emerging methods, such as the Vector-Autoregressive Spatio-Temporal (VAST) analysis tool.

The panel concluded that the Beaufort Assessment Model (BAM) is a mature assessment tool that has already experienced extensive review and refinement, and thus that it is a highly suitable methodology for the current assessment and for providing advice to managers on stock status. During the review the panel noted evidence that the optimization methods might not be consistently finding the so-called “global optimum” and encouraged more extensive use of jitter analysis to increase confidence in the model fits. Two changes to the assessment model

since SEDAR 40 that had substantial consequences for estimates of stock status values were changes to the methods for calculating fecundity and for quantifying age-dependent natural mortality rates. The panel concluded that both changes were appropriate and defensible. In particular, the panel agreed that the large change to the assumed natural mortality rates was reasonable because it was supported by an empirical analysis for Atlantic menhaden as opposed to previous assumptions which were supported by theory and meta-analyses of other species. Further, the new values did not seem implausible for a short-lived forage species.

The panel appreciated the extensive treatment of model sensitivity, retrospective patterns, and model uncertainty by the SAS. The sensitivity analysis highlighted the importance of having a data source (the NAD) with an asymptotic selectivity pattern. Even though a dome-shaped selectivity might better fit these data, the panel concluded that use of an asymptotic selectivity was better in this case to stabilize estimates of the abundance of older fish. As noted above this points to the importance of finding an assessment method that more effectively samples age 5 and older menhaden. The panel noted that, despite the sensitivity of the model to assumptions about natural mortality, the determination of stock status relative to reference points was robust to this uncertainty. The unusual retrospective pattern revealed by peeling the assessment model back to 2014 further highlighted the importance of increasing confidence that the optimization routines are reliably finding a global solution. The panel endorsed the use of two methods for uncertainty analysis to address different sources of uncertainty, but encouraged the SAS to explore ways to combine the MCB and MCMC simulations into an integrated procedure to ensure that higher-order consequences of uncertainty are captured.

The panel agreed that the estimates of biomass, abundance and exploitation rates presented by the SAS are the best available estimates, and that these estimated provide strong evidence that Atlantic menhaden are neither overfished nor experiencing overfishing. The panel considered the current single species reference points to be appropriate, with the caveat that they should ultimately be replaced by reference points that reflect the role of menhaden as a prey species in the broader ecosystem. The panel encouraged the SAS to explore methods to evaluate the “prediction skill” of their forecasting methods and offered suggestions for possible approaches.

Finally, the panel supported the research, data collection, and assessment methodology recommendations presented by the SAS. We emphasized the importance, as noted earlier, of developing a future survey or fishery dependent dataset that provides more representative samples of larger older fish. We supported the recommendation to conduct a Management Strategy Evaluation (MSE), but suggested that (a) careful thought be given to the approach to avoid progress on management being impeded by a cumbersome process; and (b) that the MSE be framed in the context of Ecosystem Reference Points (ERP), rather than single species management. The panel agreed with the recommendation of an update in 3 years and the next benchmark assessment in 6 years. However, we also noted that this timing could, and probably should, be adapted to complement benchmark assessments for other species that are expected to influence the determination of ERPs for menhaden.

## 2.2 Statements addressing each TOR

**ToR 1 Evaluate the thoroughness of data collection and the presentation and treatment of fishery-dependent and fishery-independent data in the assessment, including the following but not limited to:**

- a. Presentation of data source variance (e.g., standard errors).
- b. Justification for inclusion or elimination of available data sources,
- c. Consideration of data strengths and weaknesses (e.g., temporal and spatial scale, gear selectivities, ageing accuracy, sample size),
- d. Calculation and/or standardization of abundance indices.

The Atlantic menhaden assessment used both fishery-dependent and fishery-independent data. Fishery-dependent data came from the commercial reduction and bait fisheries. Consideration of six fishery-dependent indices was dismissed as in SEDAR 40 (2015) because of the lack of age/length data. Two additional indices based on CPUE, used to support ecosystem reference point (ERP) modeling, were not used in the current assessment as well. A few concerns were raised regarding the collection, assembly and treatment of the fishery-dependent data from the commercial reduction and bait fisheries. Expanded sampling was recommended in the bait fishery given the deficiency of age-5+ fish and the top of hold sampling in the reduction fishery should be examined further to ensure accurate characterization of the total trip catch, not just from the last tow which is current procedure. The panel considered the estimation of fishery-dependent data source variances to be appropriate.

A total of 49 fishery independent surveys were considered for inclusion in the assessment as indices of young-of-year (YOY) or adult (age-1+) abundance. These were initially screened using a standard set of criteria and reduced to a total of sixteen. The surveys do not specifically target menhaden and many use a small-mesh trawl as opposed to purse seining which is the dominant component of the fishery. Length frequencies are collected from each survey to separate YOY from older fish (age-1+) but there are no ageing data, consequently none of the surveys had a time series of numbers or biomass at age. The lack of such data limits the utility of the surveys to track the temporal development of cohorts. However, the Connecticut Long Island Sound trawl survey, where 0-group vs 1+ were regressed on one another suggested some level of internal consistency in the survey. In this case the YOY index was reasonably well correlated with the age-1+ index the following year, suggesting both indices were picking up on a coherent population trend. Given the availability of length frequency data it may be possible to assess cohort tracking through a modal analysis which forms the basis for a future research recommendation.

Cross-correlation analysis was used to assess the degree of coherence among the fishery-independent surveys. One would expect a high degree of correspondence in the index time trends given the unit stock assumption underlying the assessment. All pairs of correlation coefficients among the 16 YOY series (120 in total) were positive, with 14 being statistically significant at the  $p < 0.05$  level. As might be expected, the significant correlations tended to occur among those surveys in close geographic proximity (on the order of 100 km or less). A

similar result was evident in the analysis of the age-1+ indices (5 out of 28 correlations with  $p < 0.05$ ). Given the life history characteristics of the species, the schooling nature of menhaden, and the large geographical scale of the surveyed population, the panel acknowledged that it was unrealistic to expect time trends in the indices to exhibit uniformly high correlation across the entire geographic domain of the surveys.

The multiple fishery-independent indices were combined into regional composite indices using a hierarchical modeling method developed by Conn (2009). This method was also used (and reviewed) in the previous assessment (SEDAR 40 - 2015) for Atlantic menhaden. Four composite indices were developed: a northern adult index (NAD), a mid-Atlantic adult index (MAD), a southern adult index (SAD), and a young-of-year abundance index (YOY). As in past menhaden assessments the use of the Conn (2009) method was discussed, specifically in terms of the mechanics of the procedure to combine surveys and exploration of the use of alternative weighting schemes. During the current review the use of the VAST (Vector-Autoregressive Spatio-Temporal) package as an alternative to the index standardized methodology by Conn (2009) was recommended. It is available in the R statistical environment and may be a superior choice as to how best to combine multiple indices of menhaden abundance.

Many large-scale commercial fisheries targeting small pelagic fish species (e.g, Atlantic and Pacific herring, capelin stocks in the Barents Sea and Iceland) employ acoustic technology to survey the population. While this method alone has limitations, when used in conjunction with other survey methods it can provide useful data on biomass trends and distributional patterns. Despite these potential advantages it appears acoustics may have limited application to menhaden given their occupancy of relatively shallow, highly turbid waters associated with nearshore and estuarine habitats. Additional survey strategies were discussed including the use of acoustic surveys during winter in deeper, offshore waters and the use of aerial surveys given the ease with which highly concentrated menhaden schools can be detected by aircraft.

The panel briefly discussed the information on habitat conditions included in the single species assessment report, but did not devote much time to this because it does not currently play a significant role in the assessment. They noted that the NEFSC Ecosystem Context Assessment data are of limited value because menhaden are so rarely found in this trawl survey, and encouraged the SAS to consider offering recommendations on how this survey might be made more relevant to menhaden. For both single species and ecosystem based assessments in the future, relevant information on environmental covariates that could affect menhaden productivity would be extremely valuable.

**ToR 2. Evaluate the methods and models used to estimate population parameters (e.g., F, biomass, abundance) and biological reference points, including but not limited to:**

- a. Evaluate the choice and justification of the preferred model(s). Was the most appropriate model (or model averaging approach) chosen given available data and life history of the species?

The panel agreed that the BAM single-species statistical catch-at-age (SCAA) model was an appropriate tool for assessing this stock. The model results were well presented, with fits to the

data presented both as direct fits to the data (with error bars where appropriate) and bubble plots, selectivities were shown and overall modeled populations and  $F$  presented. This provided a basis for evaluating the model fit and performance. Although surplus production models were presented in the context of the ERP work, they were not considered as representing a viable alternative to the BAM model. The review panel concurs with this conclusion.

The main concern with the BAM model not covered in ToR 2.c (below) was with the optimization of the solution. Some evidence was presented and investigated further during the meeting that there were occasions where the optimizer failed to converge to the appropriate solution. While recognizing that absolute convergence to the global optimum cannot be guaranteed, the panel recommended the use of a jitter analysis to increase confidence in the final optimized solution. The panel considered that such an analysis was necessary and sufficient to address the concerns, and that the optimizer (with a jitter analysis) was suitable to support the stock assessment.

A second concern was over the lack of data on the large fish, which is problematic for a SCAA. Collecting better data on the larger fish is discussed further in section 8, where it is identified as the most pressing data collection recommendation for this stock.

- b. If multiple models were considered, evaluate the analysts' explanation of any differences in results.

Three different models were presented, the BAM single species SCAA model and two variants of surplus production models. Although the surplus production models were presented in the context of the ERP work, they could represent a potential stock assessment model. The team's choice of the BAM over the surplus production models was both appropriate and well justified, and the deficiencies of the available CPUE time series, as noted by the SAS, would indicate that adequate data do not exist to use surplus production models to assess this stock.

- c. Evaluate model parameterization and specification (e.g., choice of CVs, effective sample sizes, likelihood weighting schemes, calculation/specification of  $M$ , stock-recruitment relationship, choice of time-varying parameters, plus group treatment).

There were a number of changes in the model since the previous review in SEDAR 40 (2015). The biggest of these were the change in fecundity estimation and the change in estimation of  $M$ .

The rationale for the change in fecundity was clearly presented – the panel agreed that the new methodology better represented the biology of menhaden spawning and was therefore a better reflection of reality than the previous approach. The panel noted that while this change obviously scales the estimates of population-level fecundity – the metric being reported as an



alternative to spawning stock biomass - it has little impact on the management outputs of the model because the management targets are similarly scaled upward.

The change in  $M$  had a larger impact on the model results. The new methodology was directly based on data. The panel noted that the data used was from the 1960s, but accepted that the conditions to repeat the experiment (processing plants spread out along the coast) no longer existed. Comparing the  $M$ -at-age estimates with other similar fish gave a “sanity check” on the values, and led the SAS to conclude the higher estimates were not unreasonable for this species. Noting that estimating  $M$  is notoriously difficult in stock assessments, the panel therefore accepted this revised methodology as providing the best available estimates of  $M$ . As a side point, the panel noted that with the higher  $M$ , there are relatively few modelled fish in the plus group, and there are therefore not any plus-group related issues with this assessment.

Time varying blocks of selectivity were chosen, and the justification was clearly explained and appeared valid. There is a possibility that the choice of blocks could be simplified slightly, but the panel concluded that the current scheme represents a viable basis for advice. The choice of two blocks for catchability ( $q$ ) in the YOY survey was clearly explained and shown to be justified.

The choice of selectivity form (logistic rather than dome shaped) for the NAD index was highlighted as an area of concern. The misfit data suggested that a dome-shaped selectivity performed better for that survey, however this would leave the model with no asymptotic selectivity tuning dataset and hence no direct data constraint on the modeled number of larger fish. The panel concluded that the logistic selection for the NAD was the appropriate choice at present, but recommended a re-evaluation of the available data aimed at identifying an index series that provided better coverage of the larger fish, and in the longer term gave a recommendation to survey these larger fish directly.

Related to the issue of large fish, the panel noted a trend in the length-weight relationship for the larger fish. However, given the data available the SAS argued this could simply be due to a change in sampling for the larger fish – after some discussion, the panel accepted this position. The panel therefore does not recommend that this trend be accounted for in the model; ultimately this issue should be addressed through improved data collection of larger fish.

The panel noted that a modified (Dirichlet) likelihood scheme was used for this assessment, and that the change in methodology for computing the likelihoods had an impact on the final solution. The new likelihood weighting scheme was considered appropriate by the panel, although time constraints prevented a more in-depth analysis of the weighting scheme. In addition to the effects of the weighting scheme, the change in methodology for computing likelihoods produced an appreciable change in the model solution. In principle the new scheme is an improvement, as the Dirichlet is designed to be self-weighting and to perform better with correlated data. The Dirichlet was also presented as being increasingly used in other US fisheries assessments. There was not time to address this further at the review, and the panel therefore recommends that the technical team compare the changes they obtained for menhaden with changes in other stocks where this change in likelihood calculation has occurred.

In summary, this is clearly a mature assessment model, and while noting that further research to improve the model is warranted (see ToR 8), the panel concluded that this represents a suitable and viable basis for giving advice for this stock.

**ToR 3. Evaluate the diagnostic analyses performed, including but not limited to:**

- a. Sensitivity analyses to determine model stability and potential consequences of major model assumptions

Sensitivity analyses were presented on including or excluding surveys, both as a “leave one out” analysis and with surveys excluded in combination. Mostly this showed little sensitivity to choice of tuning series, which might be expected given the lack of signal in the different surveys. The exception was the NAD, where leaving this out had large impacts on the model results. This is because this is the one series with a logistic function. The sensitivity runs did serve to highlight this feature of model tuning, and further sensitivity runs involving giving the NAD a dome shaped selectivity confirmed that the selectivity was the driving factor here, rather than the inclusion or exclusion of the NAD data. This is discussed in more detail under ToR 2c.

Further sensitivity tests on the choice of  $M$  showed that the absolute model estimates were sensitive to choice of  $M$ , as would be expected, but that the trends and status determination were robust to the different  $M$  values examined.

A sensitivity test on the method used to compute misfit scores for the likelihood components was presented, and demonstrated quite a large change in modelled population. A recommendation for research would be to identify other stocks where similar changes have been made in the likelihood methodology, and compare the changes encountered here with those obtained in other assessments.

There is an issue over the level of detail to be provided on the outcomes of the sensitivity runs in future reviews. It is suggested that the diagnostics in the current report be retained, but that in addition a full suite of diagnostics (including the parameter estimates and likelihood components) be made available on line for examination prior to and during the review.

In general, the panel concluded that reasonable range of modeling assumptions and dataset choices were examined in the sensitivity tests, and that that these served their purpose in identifying issues around model stability that would need to be monitored during further use of the assessment model.

- b. Retrospective analysis

A retrospective analysis was presented for the BAM model, and showed little systematic pattern. The analysis did highlight an instability, where the 2014 retrospective was markedly

different from the 2013 and 2015 values. In this context the retrospective runs were useful for validating that such an outlier is not occurring in the terminal year of the assessment.

Given the issue with fitting highlighted under ToR 2, it is important that the convergence of the retrospective runs also be validated using a jitter analysis to avoid potential issues of reaching erroneous conclusions on the basis of unconverged solutions.

**ToR 4. Evaluate the methods used to characterize uncertainty in estimated parameters. Ensure that the implications of uncertainty in technical conclusions are clearly stated.**

Uncertainty for the BAM was assessed using two methods: a Monte Carlo Bootstrap (MCB) that focused on uncertainty in two key life history parameters (natural mortality and fecundity), and an MCMC analysis that evaluated uncertainty in the model estimated parameters. The MCB analysis revealed greater uncertainty in estimated population and fishery outputs (biomass, fishing mortality, recruitment). Uncertainty in the model estimated parameters (MCMC outputs) had a substantially smaller effect on these outputs. Evaluation of stock status with respect to reference points was robust to the uncertainty scenarios presented.

The panel concluded that the methods used to characterize uncertainty in estimated parameters were appropriate and reasonable. We appreciated the use of two methods for propagating uncertainty that addressed distinct sources of uncertainty, and do not recommend using only one method, since they address different sources of uncertainty. While the methods were judged sufficient and appropriate for the current assessment, the panel had a few suggestions for future work on model uncertainty:

- Examine the relative contributions of uncertainty in  $M$  and uncertainty in fecundity on the MCB outputs, particularly with respect to their influence on stock status relative to reference points. If one source dominates, the concern about potential covariation among these two life history parameters will be alleviated.
- Consider ways to combine the two methods into a single uncertainty analysis. While computationally cumbersome, running the MCMC analysis across a range of plausible  $M$  and fecundity parameter values (perhaps using a grid approach) selected from the joint distribution of these parameters generated for the MCB analysis, would be a viable strategy, even if only conducted for a small number of  $M$ /fecundity parameter cases.
- Try to determine the cause of the bimodal distribution of outcomes depicted for  $F$  target and  $F$  threshold in Figure 247 from the MCB simulations. The lower mode suggests some simulations produced very low estimated  $F$  values. This is not a major concern but it would be useful to understand why this pattern arose from the MCB runs.

**ToR 5. If a minority report has been filed, review minority opinion and any associated analyses.**

No minority report was filed.

**ToR 6. Recommend best estimates of stock biomass, abundance, and exploitation from the assessment for use in management, if possible, or specify alternative estimation methods.**

The panel concluded that the estimates of biomass, abundance, and exploitation rates presented for the base run of the BAM model reported in the single species report are the best available estimates of these quantities. See ToR 2, 3, and 4 for more details on the panel's assessment of the methods used to obtain these estimates, and to evaluate their sensitivity to key modeling assumptions and to important uncertainties.

**ToR 7. Evaluate the choice of reference points and the methods used to estimate them. Recommend stock status determination from the assessment, or, if appropriate, specify alternative methods/measures.**

The panel discussed the choice of single species reference points and the methods used to estimate them. Current target and threshold fishing mortality reference points are based on the median and maximum geometric mean fishing mortality rates respectively for ages-2 to -4 during the period 1960-2012. Reference points for reproductive output are the fecundity (number of maturing or ripe eggs) estimates associated with the fishing mortality target and threshold estimated from the BAM. Calculations were based upon the estimated selection pattern of landings across all fleets and areas, and the assumed time invariant  $M$ -at-age and 1:1 sex ratio. Uncertainty in the derived reference point was estimated by two approaches namely a parametric Monte Carlo bootstrap (MCB) procedure in which the input values of  $M$  and fecundity were resampled (MCB) and a MCMC analysis to estimate parameter uncertainty (see ToR 4).

The panel agreed that the methods applied were sound, as the reference points were based on past fishing levels, during the 1960-2012 period, which had not caused stock collapse when the fishery was without management constraints. The panel also agreed with the SAS decision not to base reference points on  $F_{MSY}$  calculations for this species. Finally the panel noted that while these single species reference points were appropriate in the context of a single species assessment, ultimately they should be replaced by Ecological Reference Points (ERPs) informed by multi-species analyses, as discussed at length in the ERP report.

An evaluation of methods used for projections of future stock status was not explicitly included in the ToR; however, a main reason for conducting stock assessments and estimating reference points is to inform determination of future total allowable catches (TACs). The capacity of the stock assessment model to forecast the future state of the resource is therefore important. Due to the assumed high level of natural mortality, future stock biomass is largely driven by year-class strength and hence recruitment. There does not, however, appear to be a stock recruitment relationship although recruitment has been relatively stable, with no signs of recruitment failure

events. Variability in recruitment is relatively low (with a CV of 30%); the SAS used a non-linear time series (NLTS) approach for projections, which in the absence of a stock recruitment relationship, the panel considered appropriate.

There is a relatively long lag between the last year in the assessment and the years for which TACs are being set, e.g., the last year in the current assessment is 2017 which will be projected for reported landings in 2018 and preliminary estimates for 2019. The TAC will then be set for 2020 to 2022. Given the high level of natural mortality, the stock in 2020 through 2022 is likely to be dominated by year-classes not estimated by the current assessment. Therefore, an evaluation of prediction skill is important. The panel suggests that the SAS consider doing this using a hindcasting approach. This is similar to a retrospective analysis where most recent years in the assessment are removed and the stock is projected forward. The performance of this retrospective forecast can then be compared with the historical outcomes.

The panel also suggests that the SAS examines estimates of surplus production (SP) obtained from BAM to provide a check on whether predictions of changes in biomass ( $B_{t+1} - B_t$ ) can reliably be made based on catch and  $B_t$ . Answering whether similar B levels exhibited similar SP at different historical times is a check on whether there has been non-stationarity in production processes (Walters et al. 2008).

Finally, the panel encourages the SAS to explore use of empirical indicators to monitor stock status and performance. These could be used to examine spatial and temporal trends in stock demography, e.g., the relative abundance of large individuals that may make a major contribution to spawning potential. This is especially important since changes in growth have been seen in the past and natural mortality is substantially greater than fishing mortality.

Walters, C.J., R. Hilborn, and V. Christensen. 2008. Surplus production dynamics in declining and recovering fish populations. *Canadian Journal of Fisheries and Aquatic Sciences* 65(11): 2536-2551.

**ToR 8. Review the research, data collection, and assessment methodology recommendations provided by the TC and make any additional recommendations warranted. Clearly prioritize the activities needed to inform and maintain the current assessment, and provide recommendations to improve the reliability of future assessments.**

A number of short and longer term recommendations were made for research, data collection, modelling and management by the TC. The panel was in general agreement with these recommendations. The panel offered the following supplementary comments.

In the short term, the panel strongly encourages a thorough exploration of options for adding a survey or fishery-dependent dataset that more representatively samples the larger, older fish in the population. One option might be expansion of sampling from the bait fishery. The panel also suggested further exploration of the size frequency data from the existing fishery independent surveys to assess the internal consistency of the surveys (i.e., cohort tracking) as a further screening tool for inclusion/deletion of surveys in future assessments (see ToR 1). Collection of age data for the existing fishery independent surveys is also considered a priority,

and has been recommended in the past (SEDAR 40 - 2015). The panel also supported the TC's recommendations for the development of a coast-wide fishery-independent index of abundance-at-age given that none of the existing fishery-independent surveys are specifically directed towards menhaden.

One of the recommendations under assessment methods was to conduct a Management Strategy Evaluation (MSE). The panel agrees that an MSE would be valuable for evaluating the robustness to uncertainty of reference points and control rules informed by the single species assessment. Another potential benefit would be to evaluate the benefits of improved data collection and biological sampling. However, there are "devils in the details": decisions about how to structure the MSE will require careful thought to avoid progress on management being impeded by a process that could take several years and require a large commitment of resources. Finally, if an MSE is to be undertaken, the panel recommends that the effort be framed in the context of Ecosystem Reference Points rather than single species management, as discussed in the review of the ERP report.

With respect to research recommendations regarding assessment methods, the panel noted that while the automatic differentiation optimizer in ADMB is fast and therefore efficient, it is vulnerable to false convergence problems. It is therefore important the performance of the optimization be examined carefully before presenting model solutions. There were instances with the single species BAM model (see ToR 2) where diagnostics suggested an optimization failure. The panel therefore strongly recommends that a so-called jitter analysis be performed on any model solution. This involves running a large number of optimizations, each one with slightly different starting parameters, to increase confidence that the final solution represents solution global optimum.

**ToR 9. Recommend timing of the next benchmark assessment and updates, if necessary, relative to the life history and current management of the species.**

The SAS recommended continuing the timing of benchmark assessments and updates for the single species assessment, with an update in 3 years and the next benchmark in 6 years. The panel supports this recommendation. The single species assessment model is "mature" and does not appear to require any substantial modifications that would warrant a benchmark sooner than 2025. Given the relatively short lifespan of Atlantic menhaden, and the unpredictability of future recruitment trends, it does not seem appropriate to extend the time between benchmarks beyond 6 years. Even if recommendations from this review regarding fishery-independent assessment of larger, older menhaden are successfully addressed soon, it will take several years for a new index time series to be highly informative in the assessment model.

The panel notes, however, that with movement towards ecosystem-based reference points for Atlantic menhaden and consequently linkages between management strategies for several species of ASMFC concern, there will be large benefits in the future for synchronization of assessment updates and benchmarks among the key species in the models that inform

ecosystem-based reference points. This may have implications for the timing of future Atlantic menhaden assessment updates.

### **2.3 Summary Results of Analytical Requests**

During the single species assessment review, the panel requested and viewed the results of the following additional BAM runs or output evaluations:

- Jitter analysis (repeat the optimization many times with slightly varying starting values) to convince us that the optimization is robust.
- Jitter analysis to examine whether the unusual retrospective pattern for 2014 is an optimization issue (false convergence).
- Examine the parameter values associated with the sensitivity test when the NAD composite index was excluded.
- A run with a single  $q$  parameter estimated for the age-0 index, as opposed the base run with 2  $q$  time blocks.
- A run where the selectivity for the NAD can be dome shaped (double logistic).
- Plot the range of uncertainty in  $M$  and fecundity used for the MCB runs.

### **2.4 Submitted Comment**

The panel reviewed comments provided by the public and considered them during their deliberations. The panel appreciated the public interest and transparency in the process.







###Northern Adult Index (NAD)

#Starting and ending years of the index

1990

2017

#Observed index (numbers) and CVs (1.5 multiplier, 0.5 multiplier, 0.8 multiplier, and from Cohn)

1.14	0.43	1.10	0.90	0.69	1.17	0.75	0.40	0.33	1.98	0.91	0.65	1.56
	0.48	0.52	1.15	0.80	1.20	0.95	0.41	0.88	0.92	1.78	0.62	1.62
	2.33	1.56	0.75									
#1.12	1.13	1.14	1.09	1.15	1.10	0.88	0.88	1.31	0.91	0.99	1.25	0.89
	1.02	1.10	0.89	1.00	0.88	0.95	0.91	1.19	0.97	0.89	0.93	0.93
	1.08	0.90	0.96									
#0.37	0.38	0.38	0.36	0.38	0.37	0.29	0.29	0.44	0.30	0.33	0.42	0.30
	0.34	0.37	0.30	0.33	0.29	0.32	0.30	0.40	0.32	0.30	0.31	0.31
	0.36	0.30	0.32									
#0.60	0.60	0.61	0.58	0.61	0.59	0.47	0.47	0.70	0.49	0.53	0.67	0.47
	0.54	0.59	0.47	0.53	0.47	0.51	0.49	0.64	0.52	0.47	0.50	0.49
	0.58	0.48	0.51									
0.74	0.75	0.76	0.73	0.77	0.74	0.58	0.59	0.88	0.61	0.66	0.83	0.59
	0.68	0.73	0.59	0.67	0.59	0.63	0.61	0.80	0.65	0.59	0.62	0.62
	0.72	0.60	0.64									

#Number and vector of years of length composition data

28

1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005
2006	2007	2008	2009		2010	2011	2012	2013	2014	2015	2016	2017			

#sample sizes of length comps by year (first row number of trip, second row number of fish)

18	12	24	24	18	14	34	30	18	43	30	36	51
	25	48	62	33	63	52	40	25	58	60	40	58
	70	50	46									
118	40	122	119	53	261	192	110	176	495	464	268	602
	56	294	740	335	553	344	149	172	889	464	164	688
	1134	410	163									

#length composition by year (year,lengthbin 10mm)

0.000	0.000	0.000	0.000	0.000	0.054	0.030	0.036	0.030	0.000	0.000	0.000	0.006
	0.000	0.030	0.257	0.198	0.114	0.090	0.090	0.060	0.000	0.000	0.000	0.000
	0.000	0.006	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.111	0.287	0.166	0.111
	0.023	0.055	0.044	0.034	0.111	0.045	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.005	0.002	0.025	0.073	0.068	0.129
	0.137	0.076	0.071	0.183	0.078	0.127	0.007	0.005	0.002	0.000	0.000	0.000
	0.002	0.000	0.000	0.000	0.000	0.000						

0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.003	0.003	0.008	0.003
	0.008	0.046	0.028	0.156	0.327	0.260	0.079	0.077	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.019	0.090	0.180	0.270	0.000	0.030	0.000	0.000
	0.009	0.000	0.028	0.086	0.088	0.088	0.037	0.058	0.019	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.001	0.000
	0.022	0.048	0.036	0.224	0.030	0.027	0.025	0.019	0.190	0.376	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.002	0.005	0.021	0.112	0.287	0.305	0.202	0.036	0.025	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.004	0.004	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.464	0.000	0.004	0.022	0.125	0.195	0.122	0.046	0.010	0.000
	0.000	0.004	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.040	0.018	0.016	0.019	0.003	0.001	0.001	0.001
	0.000	0.001	0.003	0.003	0.008	0.005	0.001	0.008	0.203	0.662	0.004	0.001
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.017	0.017	0.005	0.009	0.120	0.003	0.008	0.002
	0.120	0.008	0.005	0.014	0.005	0.023	0.025	0.092	0.263	0.089	0.170	0.005
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.028	0.020	0.030	0.000	0.008	0.008	0.000	0.016
	0.000	0.016	0.008	0.008	0.000	0.078	0.174	0.165	0.177	0.152	0.055	0.040
	0.018	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.222	0.066	0.001	0.066	0.001	0.001	0.000	0.001
	0.000	0.003	0.142	0.014	0.015	0.017	0.026	0.029	0.142	0.074	0.178	0.001
	0.001	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.040	0.042	0.039	0.037	0.033	0.016	0.014	0.007
	0.011	0.017	0.018	0.015	0.027	0.046	0.084	0.115	0.150	0.141	0.079	0.045
	0.014	0.006	0.003	0.003	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.000	0.042	0.054	0.000	0.000	0.000	0.000	0.000
	0.000	0.012	0.012	0.012	0.000	0.024	0.167	0.222	0.275	0.097	0.070	0.014
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.018	0.055	0.000	0.006	0.000	0.000
	0.000	0.000	0.010	0.020	0.010	0.041	0.084	0.184	0.222	0.220	0.045	0.033
	0.008	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.002	0.006	0.001	0.000	0.001	0.001	0.002	0.000
	0.000	0.001	0.001	0.009	0.065	0.132	0.220	0.248	0.174	0.092	0.027	0.012
	0.004	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.002	0.057	0.008	0.000	0.003	0.003	0.001	0.002
	0.014	0.040	0.040	0.041	0.087	0.091	0.206	0.172	0.164	0.064	0.005	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.003	0.006	0.002	0.000	0.000	0.000	0.001	0.015
	0.026	0.057	0.088	0.095	0.143	0.187	0.152	0.144	0.055	0.023	0.002	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						

0.000	0.000	0.000	0.000	0.000	0.019	0.089	0.070	0.000	0.000	0.001	0.000	0.001
	0.007	0.024	0.084	0.067	0.289	0.151	0.084	0.069	0.040	0.006	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.075	0.057	0.010	0.013	0.013	0.000	0.005	0.010
	0.000	0.005	0.010	0.000	0.103	0.236	0.211	0.174	0.062	0.010	0.005	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.008	0.011	0.026	0.049
	0.103	0.087	0.141	0.072	0.126	0.107	0.165	0.062	0.031	0.008	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.042	0.282	0.154	0.027	0.001	0.006	0.007	0.007
	0.008	0.004	0.012	0.013	0.034	0.078	0.170	0.122	0.021	0.010	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.002	0.012	0.018	0.011	0.003	0.011	0.013	0.059
	0.073	0.021	0.021	0.076	0.129	0.217	0.170	0.128	0.029	0.004	0.000	0.004
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.007	0.007	0.012	0.037	0.025	0.012	0.002	0.019
	0.064	0.070	0.075	0.083	0.086	0.177	0.120	0.121	0.049	0.032	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.001	0.005	0.011	0.005	0.000	0.006	0.006	0.018
	0.029	0.045	0.044	0.057	0.136	0.255	0.216	0.108	0.027	0.016	0.005	0.004
	0.002	0.002	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.001	0.017
	0.042	0.099	0.067	0.079	0.154	0.215	0.208	0.096	0.017	0.001	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.231	0.105	0.017	0.050	0.029	0.050	0.057	0.062
	0.066	0.067	0.036	0.028	0.056	0.079	0.036	0.028	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.008	0.016	0.000	0.000	0.003	0.003	0.003	0.013
	0.019	0.081	0.046	0.051	0.103	0.237	0.176	0.195	0.039	0.006	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						

### ###Middle Adult Index (MAD)

#Starting and ending years of the index

1985

2017

#Observed index (numbers) and CVs

1.80	1.77	1.94	1.86	1.20	0.94	0.78	1.32	0.58	1.39	1.35	0.58	0.58
	0.72	0.51	1.44	0.85	0.46	1.01	0.52	1.35	0.40	0.86	0.39	0.90
	0.85	0.63	0.56	0.91	1.53	1.98	0.57	0.46				
1.15	1.14	1.18	1.14	1.18	1.15	1.16	1.16	1.19	1.14	1.13	1.20	1.22
	0.40	0.43	0.36	0.38	0.43	0.36	0.38	0.39	0.42	0.42	0.45	0.41
	0.39	0.38	0.44	0.40	0.38	0.45	0.43	0.41				

#Number and vector of years of length composition data

5

2013 2014 2015 2016 2017

#sample sizes of length comps by year (first row number of trip, second row number of fish)

96 96 74 86 95

1352 1266 1213 1634 727

#length composition by year (year,lengthbin 10mm)

0.000	0.000	0.003	0.002	0.003	0.016	0.049	0.041	0.041	0.050	0.060	0.071	0.055
	0.028	0.022	0.036	0.080	0.104	0.107	0.089	0.102	0.023	0.009	0.005	0.001
	0.001	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.004	0.004	0.002	0.015	0.033	0.055
	0.062	0.073	0.055	0.073	0.058	0.107	0.127	0.129	0.083	0.066	0.033	0.015
	0.001	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.000	0.002	0.007	0.005	0.009	0.012	0.030	0.065	0.103	0.110	0.110
	0.058	0.038	0.059	0.070	0.069	0.106	0.092	0.032	0.016	0.004	0.001	0.001
	0.001	0.000	0.000	0.000	0.000	0.000						
0.000	0.007	0.002	0.005	0.012	0.012	0.017	0.047	0.057	0.074	0.138	0.116	0.108
	0.030	0.047	0.044	0.044	0.062	0.067	0.056	0.036	0.006	0.006	0.004	0.001
	0.000	0.000	0.000	0.000	0.000	0.000						
0.000	0.000	0.004	0.015	0.028	0.018	0.018	0.057	0.077	0.132	0.123	0.077	0.088
	0.035	0.029	0.044	0.030	0.038	0.064	0.058	0.052	0.011	0.001	0.001	0.001
	0.000	0.000	0.000	0.000	0.000	0.000						

###Southern Adult Index (SAD)

#Starting and ending years of the index

1990

2017

#Observed index (numbers) and CVs (multiplier of 0.5, Conn values)

3.69	1.16	0.86	0.47	0.36	0.17	0.27	0.22	0.75	0.25	0.85	0.81	0.89
	1.08	0.45	1.20	3.19	0.41	0.63	2.34	0.80	1.45	1.22	0.86	0.80
	1.16	0.33	1.33									
#0.32	0.30	0.31	0.34	0.37	0.41	0.37	0.37	0.32	0.37	0.41	0.37	0.32
	0.25	0.25	0.23	0.20	0.24	0.20	0.22	0.20	0.20	0.18	0.20	0.22
	0.20	0.27	0.21									
0.63	0.59	0.63	0.68	0.75	0.82	0.73	0.74	0.64	0.74	0.81	0.74	0.65
	0.50	0.51	0.46	0.41	0.47	0.39	0.44	0.39	0.39	0.36	0.40	0.44
	0.41	0.54	0.41									

#Number and vector of years of length composition data

#28

#1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005  
2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017

#sample sizes of length comps by year (first row number of trip, second row number of fish)

#22	29	23	26	10	15	21	25	29	13	12	30	32
	108	47	112	134	51	527	565	554	613	610	590	621
	645	527	619									
#3640	1116	994	433	117	51	144	194	931	136	468	880	896
	1206	642	4044	6216	364	1060	19851	1134	2048	1693	2921	2668
	1746	1416	2525									

#length composition by year (year,lengthbin 10mm)

#0.000	0.000	0.090	0.387	0.289	0.163	0.049	0.016	0.002	0.000	0.001	0.002	0.000
	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.013	0.063	0.367	0.307	0.108	0.058	0.027	0.028	0.025	0.004	0.001	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.162	0.216	0.263	0.173	0.064	0.027	0.030	0.031	0.017	0.014	0.000	0.000
	0.000	0.000	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.085	0.247	0.279	0.115	0.039	0.030	0.143	0.044	0.007	0.009	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.137	0.231	0.094	0.222	0.145	0.051	0.060	0.043	0.017	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.000	0.157	0.039	0.039	0.059	0.059	0.255	0.314	0.078	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.278	0.118	0.069	0.049	0.049	0.028	0.035	0.111	0.222	0.035	0.007	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.046	0.155	0.093	0.113	0.119	0.088	0.093	0.216	0.036	0.021	0.010	0.000
	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.005	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.086	0.277	0.195	0.147	0.088	0.084	0.047	0.042	0.028	0.004	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.000	0.022	0.074	0.228	0.228	0.184	0.074	0.081	0.059	0.044	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.006	0.026	0.075	0.135	0.122	0.154	0.182	0.269	0.032	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						

#0.000	0.031	0.360	0.249	0.181	0.122	0.025	0.007	0.008	0.009	0.008	0.000	0.000
	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.001	0.063	0.363	0.296	0.134	0.067	0.030	0.027	0.017	0.003	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.096	0.145	0.183	0.291	0.152	0.050	0.027	0.041	0.011	0.002	0.000	0.000
	0.001	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.071	0.036	0.132	0.188	0.107	0.214	0.161	0.060	0.026	0.005	0.000	0.001
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.237	0.388	0.142	0.068	0.063	0.025	0.028	0.022	0.015	0.010	0.003	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.055	0.384	0.239	0.162	0.082	0.030	0.016	0.008	0.008	0.014	0.001	0.002
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.010	0.011	0.137	0.302	0.367	0.098	0.035	0.032	0.005	0.000	0.000	0.000
	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.011	0.106	0.361	0.159	0.078	0.139	0.041	0.039	0.044	0.013	0.003	0.001
	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.102	0.360	0.277	0.127	0.036	0.028	0.023	0.017	0.012	0.009	0.003	0.002
	0.002	0.002	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.149	0.182	0.118	0.115	0.086	0.157	0.122	0.058	0.004	0.005	0.002	0.001
	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.143	0.294	0.129	0.124	0.108	0.067	0.069	0.039	0.016	0.003	0.001	0.001
	0.001	0.002	0.002	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.027	0.139	0.163	0.128	0.081	0.127	0.140	0.134	0.019	0.035	0.003	0.002
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.011	0.110	0.200	0.191	0.171	0.154	0.079	0.050	0.011	0.011	0.006	0.001
	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.064	0.046	0.080	0.137	0.168	0.159	0.139	0.127	0.028	0.018	0.010	0.007
	0.007	0.003	0.002	0.001	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						
#0.000	0.104	0.241	0.224	0.175	0.062	0.071	0.053	0.034	0.016	0.009	0.003	0.002
	0.003	0.002	0.002	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.000	0.000	0.000	0.000	0.000	0.000						





#####Commercial reduction fishery - north  
#####

###Starting and ending years for landings time series

1955

2017

##commercial reduction landings vector (1,000s mt) and assumed CVs

402.7	478.9	389.8	248.3	318.4	323.9	334.8	321.4	147.5	50.6	58.0	7.9	17.2
	33.1	15.4	15.8	33.4	69.1	90.7	77.9	48.4	86.8	53.3	63.5	70.2
	83.0	68.1	35.1	39.4	35.0	111.3	42.6	83.0	73.6	98.8	144.1	104.6
	99.1	58.4	33.4	96.3	61.6	25.2	12.3	8.4	43.2	39.6	27.2	4.1
	25.9	15.4	60.1	36.6	39.3	18.7	28.7	29.6	23.9	32.7	29.9	28.8
	45.0	58.5										
0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04										

#Number and vector of years of age compositions for commercial reduction fleet

63

1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967
	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979
	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991
	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003
	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
	2016	2017										

#Sample size of age comp data (first row observed Nsets, second row Nfish)

422	560	564	450	531	475	403	481	303	232	330	93	92
	285	181	35	38	76	73	128	185	201	220	190	169
	175	222	84	84	311	149	53	94	165	136	166	146
	118	64	30	71	50	13	10	12	49	38	29	9
	29	24	104	52	55	24	38	41	33	37	29	39
	70	107										
8408	11050	11247	8777	10470	9346	8059	9598	6058	4619	6564	1859	1840
	5701	3621	700	760	759	729	1280	1850	2010	2200	1861	1688
	1744	2220	840	840	3110	1490	530	940	1650	1360	1660	1460
	1180	640	300	710	500	130	100	120	490	380	290	90
	290	240	1040	520	550	240	380	410	330	370	290	390
	700	1070										

##commercial reduction age comps

0.000	0.015	0.471	0.217	0.253	0.032	0.012						
0.000	0.133	0.555	0.195	0.025	0.072	0.020						
0.000	0.270	0.610	0.051	0.033	0.017	0.020						

0.000	0.025	0.908	0.042	0.010	0.008	0.009
0.000	0.531	0.291	0.159	0.009	0.004	0.007
0.000	0.009	0.892	0.037	0.049	0.009	0.004
0.000	0.003	0.160	0.803	0.012	0.018	0.003
0.000	0.015	0.245	0.218	0.457	0.033	0.032
0.000	0.296	0.438	0.095	0.068	0.080	0.023
0.000	0.034	0.357	0.345	0.128	0.065	0.072
0.000	0.160	0.370	0.373	0.071	0.013	0.014
0.000	0.201	0.467	0.212	0.100	0.009	0.012
0.000	0.055	0.296	0.567	0.072	0.009	0.000
0.000	0.007	0.479	0.388	0.116	0.009	0.001
0.000	0.001	0.251	0.594	0.149	0.005	0.000
0.000	0.150	0.793	0.050	0.007	0.000	0.000
0.000	0.126	0.288	0.433	0.137	0.017	0.000
0.000	0.169	0.286	0.452	0.085	0.008	0.000
0.000	0.021	0.821	0.133	0.024	0.001	0.000
0.000	0.028	0.844	0.117	0.006	0.004	0.000
0.000	0.000	0.798	0.175	0.025	0.001	0.000
0.000	0.092	0.823	0.071	0.013	0.000	0.000
0.000	0.022	0.567	0.326	0.079	0.006	0.001
0.000	0.000	0.298	0.567	0.120	0.015	0.000
0.000	0.007	0.579	0.332	0.076	0.006	0.000
0.000	0.002	0.237	0.462	0.243	0.051	0.004
0.000	0.001	0.357	0.357	0.210	0.070	0.006
0.000	0.042	0.393	0.473	0.063	0.025	0.004
0.000	0.012	0.826	0.120	0.037	0.005	0.000
0.000	0.024	0.343	0.506	0.097	0.029	0.001
0.000	0.020	0.760	0.089	0.111	0.017	0.003
0.000	0.010	0.795	0.107	0.050	0.031	0.006
0.000	0.005	0.652	0.277	0.058	0.006	0.002
0.000	0.000	0.225	0.486	0.260	0.026	0.003
0.000	0.081	0.623	0.173	0.097	0.025	0.000
0.000	0.011	0.788	0.134	0.049	0.018	0.001
0.000	0.085	0.430	0.385	0.072	0.023	0.005
0.000	0.058	0.687	0.107	0.118	0.026	0.004

0.000	0.045	0.675	0.226	0.036	0.017	0.002
0.000	0.017	0.420	0.333	0.183	0.047	0.000
0.000	0.020	0.567	0.329	0.079	0.006	0.000
0.000	0.000	0.579	0.320	0.092	0.008	0.000
0.000	0.000	0.495	0.293	0.158	0.055	0.000
0.000	0.000	0.657	0.281	0.062	0.000	0.000
0.000	0.000	0.389	0.428	0.168	0.015	0.000
0.000	0.005	0.559	0.406	0.019	0.011	0.000
0.000	0.000	0.150	0.796	0.055	0.000	0.000
0.000	0.040	0.347	0.491	0.120	0.002	0.000
0.000	0.000	0.474	0.378	0.139	0.010	0.000
0.000	0.004	0.615	0.320	0.061	0.000	0.000
0.000	0.000	0.219	0.605	0.174	0.002	0.000
0.000	0.022	0.456	0.422	0.099	0.001	0.000
0.000	0.022	0.761	0.174	0.041	0.002	0.000
0.000	0.002	0.216	0.668	0.106	0.008	0.000
0.000	0.123	0.299	0.463	0.102	0.013	0.000
0.000	0.000	0.456	0.348	0.193	0.003	0.000
0.000	0.058	0.726	0.190	0.023	0.003	0.000
0.000	0.001	0.778	0.192	0.029	0.000	0.000
0.000	0.028	0.724	0.233	0.015	0.000	0.000
0.000	0.085	0.518	0.274	0.119	0.004	0.000
0.000	0.006	0.593	0.362	0.038	0.000	0.000
0.000	0.075	0.413	0.481	0.031	0.000	0.000
0.000	0.017	0.572	0.393	0.015	0.003	0.000

#####Commercial reduction fishery - south  
#####

###Starting and ending years for landings time series

1955

2017

##commercial reduction landings vector (1,000s mt) and assumed CVs

241.7	236.4	215.8	264.0	343.7	208.4	243.9	219.3	200.9	219.8	216.6	212.8	177.2
	202.8	146.9	243.6	216.9	296.8	256.2	214.3	201.8	253.7	287.8	280.5	305.6
	318.5	313.2	347.4	379.3	291.3	195.4	195.4	243.9	235.6	223.2	257.1	276.9
	198.5	262.2	226.6	243.6	231.4	234.0	233.6	162.8	124.1	193.9	146.9	162.0

	152.6	137.5	97.2	137.8	101.8	125.1	154.4	144.5	136.7	98.3	101.2	114.7
	92.4	70.5										
0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
	0.04	0.04										

#Number and vector of years of age compositions for commercial reduction fleet

63

1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967
	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979
	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991
	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003
	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
	2016	2017										

#Sample size of age comp data (first row observed Nsets, second row Nfish)

384	442	424	377	386	215	258	310	349	293	651	692	690
	1061	576	390	379	580	564	433	545	472	508	525	469
	556	700	823	434	858	623	488	646	572	553	518	623
	443	468	441	390	372	397	374	350	255	354	331	340
	387	329	253	327	222	259	289	282	230	176	179	217
	180	128										
7742	8831	8467	7008	7490	4167	5158	6197	6977	5824	13017	13848	13648
	21168	11511	7761	7510	5800	5640	4330	5450	4720	5080	5250	4680
	5548	7000	8230	4340	8580	6230	4880	6460	5708	5530	5180	6230
	4430	4680	4410	3900	3720	3970	3740	3500	2550	3540	3310	3400
	3880	3290	2530	3270	2220	2590	2890	2820	2300	1760	1790	2170
	1800	1280										

##commercial reduction age comps

0.374	0.323	0.269	0.016	0.016	0.002	0.000
0.017	0.885	0.049	0.018	0.004	0.022	0.004
0.151	0.598	0.217	0.010	0.011	0.007	0.006
0.059	0.466	0.443	0.018	0.005	0.005	0.004
0.003	0.855	0.099	0.034	0.005	0.002	0.002
0.052	0.192	0.701	0.018	0.025	0.008	0.004
0.000	0.538	0.217	0.234	0.004	0.007	0.000
0.040	0.387	0.491	0.033	0.044	0.003	0.002
0.079	0.460	0.386	0.059	0.007	0.008	0.002
0.187	0.433	0.349	0.028	0.002	0.000	0.000
0.184	0.528	0.269	0.018	0.001	0.000	0.000

0.265	0.414	0.299	0.020	0.001	0.000	0.000
0.007	0.663	0.269	0.057	0.003	0.000	0.000
0.143	0.349	0.468	0.037	0.003	0.000	0.000
0.188	0.442	0.330	0.038	0.002	0.000	0.000
0.016	0.650	0.309	0.022	0.003	0.000	0.000
0.083	0.288	0.569	0.054	0.005	0.001	0.000
0.033	0.618	0.285	0.061	0.003	0.000	0.000
0.036	0.372	0.591	0.001	0.000	0.000	0.000
0.196	0.388	0.413	0.003	0.000	0.000	0.000
0.154	0.371	0.469	0.006	0.001	0.000	0.000
0.101	0.572	0.324	0.003	0.000	0.000	0.000
0.140	0.289	0.567	0.003	0.000	0.000	0.000
0.158	0.230	0.558	0.050	0.003	0.000	0.000
0.413	0.172	0.403	0.012	0.001	0.000	0.000
0.028	0.476	0.452	0.038	0.004	0.001	0.000
0.316	0.186	0.460	0.038	0.000	0.000	0.000
0.038	0.306	0.558	0.096	0.001	0.000	0.000
0.279	0.148	0.547	0.016	0.008	0.001	0.000
0.396	0.311	0.244	0.040	0.007	0.002	0.000
0.235	0.394	0.364	0.006	0.000	0.000	0.000
0.056	0.126	0.797	0.019	0.002	0.001	0.000
0.022	0.253	0.691	0.031	0.003	0.000	0.000
0.175	0.146	0.573	0.099	0.006	0.001	0.000
0.069	0.514	0.402	0.014	0.001	0.000	0.000
0.190	0.078	0.697	0.023	0.010	0.002	0.000
0.317	0.360	0.281	0.038	0.004	0.001	0.000
0.243	0.428	0.313	0.014	0.002	0.000	0.000
0.049	0.266	0.608	0.074	0.003	0.000	0.000
0.064	0.197	0.609	0.094	0.035	0.002	0.000
0.044	0.408	0.366	0.150	0.031	0.002	0.000
0.036	0.226	0.630	0.092	0.015	0.001	0.000
0.027	0.260	0.423	0.236	0.047	0.007	0.001
0.073	0.187	0.535	0.123	0.073	0.009	0.001
0.188	0.292	0.428	0.069	0.020	0.003	0.000
0.140	0.205	0.510	0.127	0.016	0.002	0.000

0.039	0.073	0.604	0.265	0.018	0.001	0.000
0.242	0.284	0.321	0.140	0.012	0.000	0.000
0.088	0.185	0.643	0.073	0.010	0.001	0.000
0.020	0.234	0.670	0.060	0.015	0.001	0.000
0.020	0.131	0.618	0.210	0.018	0.003	0.000
0.016	0.525	0.378	0.072	0.008	0.000	0.000
0.001	0.306	0.631	0.054	0.008	0.000	0.000
0.017	0.115	0.812	0.053	0.003	0.000	0.000
0.007	0.515	0.311	0.147	0.019	0.001	0.000
0.017	0.447	0.494	0.034	0.008	0.000	0.000
0.000	0.477	0.467	0.048	0.007	0.002	0.000
0.007	0.183	0.789	0.020	0.001	0.000	0.000
0.043	0.457	0.388	0.095	0.016	0.000	0.000
0.007	0.482	0.377	0.106	0.026	0.002	0.000
0.000	0.141	0.759	0.092	0.009	0.000	0.000
0.022	0.303	0.509	0.160	0.006	0.000	0.000
0.000	0.249	0.581	0.144	0.026	0.000	0.000

#####Commercial bait fishery (includes rec) - north  
#####

###Starting and ending years for landings time series

1955

2017

##commercial bait landings vector (1,000s mt) and assumed CVs

10.1	17.5	10.6	3.5	8.0	7.6	8.4	10.6	6.1	4.3	3.3	1.8	1.4
	0.8	1.1	1.4	1.9	2.1	2.6	2.1	1.9	2.0	1.4	1.1	1.2
	1.1	1.3	1.5	1.5	1.7	8.2	9.0	8.9	13.0	11.8	14.6	17.8
	23.6	18.0	19.4	22.5	16.4	18.3	16.3	13.2	15.4	13.3	13.8	8.9
	12.2	10.3	13.2	21.1	27.2	19.4	26.2	34.7	40.8	20.2	22.2	25.9
	31.1	28.4										
0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15
	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15
	0.15	0.15	0.15	0.15	0.15	0.10	0.10	0.10	0.10	0.10	0.10	0.10
	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.05	0.05	0.05
	0.05	0.05										

#Number and vector of years of age compositions for commercial bait fleet

1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997
	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
	2010	2011	2012	2013	2014	2015	2016	2017				

#Sample size of age comp data (first row observed Nsets, second row Nfish)

0	0	0	0	3	0	0	0	3	41	21	25	12
	28	25	31	75	59	11	3	0	36	98	123	51
	62	51	63	27	88	156	159	175				
0	0	0	0	30	0	0	0	29	401	190	203	111
	225	201	266	678	524	101	29	0	259	729	973	435
	466	449	547	236	806	1291	1018	1487				

##commercial bait age comps

0.000	0.021	0.792	0.096	0.071	0.016	0.004
0.000	0.001	0.294	0.499	0.105	0.080	0.020
0.000	0.002	0.277	0.500	0.198	0.014	0.009
0.000	0.001	0.086	0.522	0.348	0.039	0.004
0.000	0.008	0.219	0.377	0.306	0.088	0.001
0.000	0.002	0.565	0.248	0.132	0.049	0.004
0.000	0.014	0.290	0.527	0.119	0.041	0.010
0.000	0.026	0.408	0.209	0.277	0.065	0.016
0.000	0.010	0.440	0.412	0.092	0.043	0.003
0.000	0.000	0.109	0.496	0.342	0.049	0.003
0.000	0.000	0.088	0.475	0.435	0.001	0.000
0.000	0.000	0.435	0.439	0.120	0.006	0.000
0.000	0.000	0.153	0.319	0.392	0.118	0.018
0.000	0.000	0.108	0.386	0.410	0.082	0.013
0.000	0.000	0.149	0.478	0.319	0.043	0.011
0.000	0.004	0.415	0.315	0.230	0.030	0.007
0.000	0.000	0.111	0.734	0.136	0.014	0.004
0.000	0.000	0.053	0.550	0.338	0.058	0.001
0.000	0.000	0.127	0.661	0.202	0.011	0.000
0.000	0.000	0.249	0.606	0.144	0.000	0.000
0.000	0.001	0.183	0.631	0.164	0.022	0.000
0.000	0.004	0.289	0.587	0.116	0.000	0.004
0.000	0.000	0.383	0.482	0.126	0.008	0.002
0.000	0.000	0.262	0.585	0.139	0.013	0.000
0.000	0.000	0.204	0.608	0.175	0.013	0.000

0.000	0.000	0.365	0.380	0.227	0.025	0.002
0.000	0.000	0.142	0.486	0.327	0.045	0.000
0.000	0.000	0.392	0.468	0.130	0.008	0.002
0.000	0.000	0.257	0.555	0.159	0.029	0.000
0.000	0.000	0.065	0.524	0.388	0.020	0.003
0.000	0.002	0.376	0.522	0.101	0.000	0.000
0.000	0.021	0.406	0.521	0.046	0.006	0.000
0.000	0.020	0.605	0.347	0.027	0.001	0.000

#####Commercial bait fishery (includes rec) - south  
#####

###Starting and ending years for landings time series

1955

2017

##commercial bait landings vector (1,000s mt) and assumed CVs

4.5	5.7	14.1	11.2	12.6	11.8	16.6	16.0	18.3	16.0	20.3	12.0	10.2
	8.7	9.5	20.2	11.6	8.2	12.2	12.4	19.8	17.7	21.7	24.8	11.8
	25.0	21.5	18.7	18.2	13.0	19.7	14.0	18.2	32.3	20.6	15.0	13.7
	13.8	14.5	16.7	18.8	19.2	21.9	22.9	22.3	18.8	23.2	24.3	25.4
	24.6	29.2	16.1	22.7	21.6	21.0	17.5	19.0	25.1	17.7	20.8	21.2
	18.8	17.7										
0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15
	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15
	0.15	0.15	0.15	0.15	0.15	0.10	0.10	0.10	0.10	0.10	0.10	0.10
	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.05	0.05	0.05
	0.05	0.05										

#Number and vector of years of age compositions for commercial bait fleet

33

1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997
	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
	2010	2011	2012	2013	2014	2015	2016	2017				

#Sample size of age comp data (first row observed Nsets, second row Nfish)

80	42	22	1	0	1	8	7	13	14	18	16	32
	47	41	31	34	20	42	40	41	28	55	45	68
	53	60	44	49	60	30	22	19				
800	420	220	10	0	10	78	70	121	139	174	156	293
	411	338	270	286	180	328	327	316	220	434	366	573
	435	508	408	434	559	251	205	137				



##commercial bait age comps

0.005	0.363	0.616	0.011	0.004	0.001	0.000
0.001	0.067	0.862	0.059	0.007	0.004	0.001
0.001	0.102	0.829	0.063	0.005	0.000	0.000
0.004	0.071	0.667	0.221	0.034	0.003	0.000
0.004	0.385	0.547	0.052	0.010	0.002	0.000
0.005	0.073	0.897	0.022	0.003	0.001	0.000
0.013	0.323	0.583	0.076	0.004	0.001	0.000
0.000	0.552	0.448	0.000	0.000	0.000	0.000
0.008	0.385	0.511	0.088	0.005	0.003	0.000
0.001	0.151	0.648	0.145	0.049	0.005	0.000
0.000	0.392	0.374	0.218	0.017	0.000	0.000
0.000	0.008	0.757	0.198	0.036	0.000	0.000
0.000	0.055	0.531	0.346	0.056	0.008	0.004
0.036	0.066	0.540	0.237	0.108	0.012	0.003
0.000	0.106	0.662	0.174	0.052	0.006	0.000
0.008	0.222	0.658	0.112	0.000	0.000	0.000
0.004	0.043	0.659	0.274	0.017	0.004	0.000
0.000	0.046	0.264	0.495	0.173	0.020	0.002
0.007	0.098	0.740	0.140	0.015	0.000	0.000
0.000	0.068	0.732	0.166	0.031	0.003	0.000
0.000	0.009	0.515	0.446	0.026	0.003	0.000
0.000	0.335	0.448	0.193	0.023	0.000	0.000
0.000	0.246	0.669	0.066	0.019	0.000	0.000
0.006	0.045	0.809	0.111	0.017	0.013	0.000
0.004	0.246	0.365	0.338	0.047	0.000	0.000
0.003	0.311	0.525	0.101	0.059	0.002	0.000
0.000	0.344	0.467	0.119	0.050	0.020	0.000
0.000	0.068	0.825	0.084	0.017	0.002	0.002
0.007	0.452	0.288	0.172	0.054	0.027	0.000
0.000	0.440	0.364	0.136	0.055	0.005	0.000
0.010	0.309	0.589	0.089	0.002	0.000	0.000
0.000	0.228	0.423	0.321	0.021	0.007	0.000
0.002	0.275	0.469	0.241	0.013	0.000	0.000



0.0 -5.0 7.0 7 0.0 -1.0 1 # Dirichlet-multinomial overdispersion parameter (log-space): cBn age comps

0.0 -5.0 5.0 7 0.0 -1.0 1 # Dirichlet-multinomial overdispersion parameter (log-space): cBs age comps

##### Selectivity parameters #####

##### Commercial reduction and bait fisheries

2.0 0.1 10.0 5 2.0 -0.5 1 #cRn age at 50% selectivity

3.0 0.1 25.0 5 3.0 -0.5 1 #cRn slope of ascending limb

3.5 0.01 10.0 5 4.5 -0.5 1 #cRn age at 50% selectivity descending limb

3.0 0.1 25.0 5 3.0 -0.5 1 #cRn slope of descending limb

2.0 0.1 10.0 5 2.0 -0.5 1 #cRn2 age at 50% selectivity

3.0 0.1 10.0 5 3.0 -0.5 1 #cRn2 slope of ascending limb

3.5 0.01 10.0 5 4.5 -0.5 1 #cRn2 age at 50% selectivity descending limb

3.0 0.1 25.0 5 3.0 -0.5 1 #cRn2 slope of descending limb

2.0 0.1 10.0 5 2.0 -0.5 1 #cRn3 age at 50% selectivity

3.0 0.1 10.0 5 3.0 -0.5 1 #cRn3 slope of ascending limb

3.5 0.01 10.0 5 4.5 -0.5 1 #cRn3 age at 50% selectivity descending limb

3.0 0.1 25.0 5 3.0 -0.5 1 #cRn3 slope of descending limb

2.0 0.1 10.0 5 2.0 -0.5 1 #cRn4 age at 50% selectivity

3.0 0.1 10.0 5 3.0 -0.5 1 #cRn4 slope of ascending limb

3.5 0.01 10.0 5 4.5 -0.5 1 #cRn4 age at 50% selectivity descending limb

3.0 0.1 10.0 5 3.0 -0.5 1 #cRn4 slope of descending limb

1.0 0.1 10.0 5 2.0 -0.5 1 #cRs age at 50% selectivity

3.0 0.1 10.0 5 3.0 -0.5 1 #cRs slope of ascending limb

6.5 0.01 10.0 5 4.5 -0.5 1 #cRs age at 50% selectivity descending limb

2.0 0.1 25.0 5 3.0 -0.5 1 #cRs slope of descending limb

1.0 0.1 10.0 5 2.0 -0.5 1 #cRs2 age at 50% selectivity

3.0 0.1 10.0 5 3.0 -0.5 1 #cRs2 slope of ascending limb

6.5 0.01 10.0 5 4.5 -0.5 1 #cRs2 age at 50% selectivity descending limb

2.0 0.1 25.0 5 3.0 -0.5 1 #cRs2 slope of descending limb

1.0	0.1	10.0	5	2.0	-0.5	1	#cRs3 age at 50% selectivity
3.0	0.1	10.0	5		3.0	-0.5	1 #cRs3 slope of ascending limb
6.5	0.01	10.0	5		4.5	-0.5	1 #cRs3 age at 50% selectivity descending limb
2.0	0.1	10.0	5		3.0	-0.5	1 #cRs3 slope of descending limb
1.0	0.1	10.0	5	2.0	-0.5	1	#cRs4 age at 50% selectivity
3.0	0.1	10.0	5		3.0	-0.5	1 #cRs4 slope of ascending limb
6.5	0.01	10.0	5		4.5	-0.5	1 #cRs4 age at 50% selectivity descending limb
2.0	0.1	10.0	5		3.0	-0.5	1 #cRs4 slope of descending limb
2.0	0.1	10.0	5	2.0	-0.5	1	#cBn age at 50% selectivity
3.0	0.1	10.0	5		3.0	-0.5	1 #cBn slope of ascending limb
3.5	0.01	10.0	5		4.5	-0.5	1 #cBn age at 50% selectivity descending limb
3.0	0.1	10.0	5		3.0	-0.5	1 #cBn slope of descending limb
2.0	0.1	10.0	5	2.0	-0.5	1	#cBn2 age at 50% selectivity
3.0	0.1	10.0	5		3.0	-0.5	1 #cBn2 slope of ascending limb
3.5	0.01	10.0	5		4.5	-0.5	1 #cBn2 age at 50% selectivity descending limb
3.0	0.1	10.0	5		3.0	-0.5	1 #cBn2 slope of descending limb
1.0	0.1	10.0	5	2.0	-0.5	1	#cBs age at 50% selectivity
3.0	0.1	10.0	5		3.0	-0.5	1 #cBs slope of ascending limb
6.5	0.01	10.0	5		4.5	-0.5	1 #cBs age at 50% selectivity descending limb
2.0	0.1	10.0	5		3.0	-0.5	1 #cBs slope of descending limb
1.0	0.1	10.0	-5	2.0	-0.5	1	#cBs2 age at 50% selectivity
3.0	0.1	10.0	-5		3.0	-0.5	1 #cBs2 slope of ascending limb
6.5	0.01	10.0	-5		4.5	-0.5	1 #cBs2 age at 50% selectivity descending limb
2.0	0.1	10.0	-5		3.0	-0.5	1 #cBs2 slope of descending limb
-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRn selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRn selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRn selectivity in logit space
-0.6	-15.0	0.50	-5	0.0	-0.5	1	#age-3 cRn selectivity in logit space

0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-4 cRn selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-5 cRn selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-6+ cRn selectivity in logit space
-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRn2 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRn2 selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRn2 selectivity in logit space
9.0	-15.0	0.50	-5	0.0	-0.5	1	#age-3 cRn2 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-4 cRn2 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-5 cRn2 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-6+ cRn2 selectivity in logit space
-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRn3 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRn3 selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRn3 selectivity in logit space
9.0	-15.0	0.50	-5	0.0	-0.5	1	#age-3 cRn3 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-4 cRn3 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-5 cRn3 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-6+ cRn3 selectivity in logit space
-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRn4 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRn4 selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRn4 selectivity in logit space
9.0	-15.0	0.50	-5	0.0	-0.5	1	#age-3 cRn4 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-4 cRn4 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-5 cRn4 selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-6+ cRn4 selectivity in logit space
-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRs selectivity in logit space
2.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRs selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRs selectivity in logit space
0.0	-15.0	10.0	-5	0.0	-0.5	1	#age-3 cRs selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-4 cRs selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-5 cRs selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-6+ cRs selectivity in logit space

-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRs2 selectivity in logit space
2.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRs2 selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRs2 selectivity in logit space
0.0	-15.0	10.0	-5	0.0	-0.5	1	#age-3 cRs2 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-4 cRs2 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-5 cRs2 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-6+ cRs2 selectivity in logit space

-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRs3 selectivity in logit space
2.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRs3 selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRs3 selectivity in logit space
0.0	-15.0	10.0	-5	0.0	-0.5	1	#age-3 cRs3 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-4 cRs3 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-5 cRs3 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-6+ cRs3 selectivity in logit space

-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cRs4 selectivity in logit space
2.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cRs4 selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cRs4 selectivity in logit space
0.0	-15.0	10.0	-5	0.0	-0.5	1	#age-3 cRs4 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-4 cRs4 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-5 cRs4 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-6+ cRs4 selectivity in logit space

-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cBn selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cBn selectivity in logit space
9.0	-10.0	10.0	-5	5.0	-0.5	1	#age-2 cBn selectivity in logit space
9.0	-15.0	0.50	-5	0.0	-0.5	1	#age-3 cBn selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-4 cBn selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-5 cBn selectivity in logit space
0.0	-10.0	2.75	-5	0.0	-0.5	1	#age-6+ cBn selectivity in logit space

-9.0	-10.0	10.0	-5	-5.0	-0.5	1	#age-0 cBn2 selectivity in logit space
0.0	-10.0	10.0	-5	0.0	-0.5	1	#age-1 cBn2 selectivity in logit space

9.0 -10.0 10.0 -5 5.0 -0.5 1 #age-2 cBn2 selectivity in logit space  
 9.0 -15.0 0.50 -5 0.0 -0.5 1 #age-3 cBn2 selectivity in logit space  
 0.0 -10.0 2.75 -5 0.0 -0.5 1 #age-4 cBn2 selectivity in logit space  
 0.0 -10.0 2.75 -5 0.0 -0.5 1 #age-5 cBn2 selectivity in logit space  
 0.0 -10.0 2.75 -5 0.0 -0.5 1 #age-6+ cBn2 selectivity in logit space

-9.0 -10.0 10.0 -5 -5.0 -0.5 1 #age-0 cBs selectivity in logit space  
 2.0 -10.0 10.0 -5 0.0 -0.5 1 #age-1 cBs selectivity in logit space  
 9.0 -10.0 10.0 -5 5.0 -0.5 1 #age-2 cBs selectivity in logit space  
 0.0 -15.0 10.0 -5 0.0 -0.5 1 #age-3 cBs selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-4 cBs selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-5 cBs selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-6+ cBs selectivity in logit space

-9.0 -10.0 10.0 -5 -5.0 -0.5 1 #age-0 cBs2 selectivity in logit space  
 2.0 -10.0 10.0 -5 0.0 -0.5 1 #age-1 cBs2 selectivity in logit space  
 9.0 -10.0 10.0 -5 5.0 -0.5 1 #age-2 cBs2 selectivity in logit space  
 0.0 -15.0 10.0 -5 0.0 -0.5 1 #age-3 cBs2 selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-4 cBs2 selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-5 cBs2 selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-6+ cBs2 selectivity in logit space

##### Indices - NAD, MAD, and SAD

3.0 0.1 10.0 5 2.0 -0.5 1 #NAD age at 50% selectivity  
 6.0 0.1 10.0 5 3.0 -0.5 1 #NAD slope of ascending limb  
 3.5 0.01 10.0 -5 4.5 -0.5 1 #NAD age at 50% selectivity descending limb  
 3.0 0.1 10.0 -5 3.0 -0.5 1 #NAD slope of descending limb

2.0 0.1 10.0 5 2.0 -0.5 1 #MAD age at 50% selectivity  
 3.0 0.1 10.0 5 3.0 -0.5 1 #MAD slope of ascending limb  
 3.5 0.01 10.0 5 4.5 -0.5 1 #MAD age at 50% selectivity descending limb  
 3.0 0.1 35.0 5 3.0 -0.5 1 #MAD slope of descending limb

0.3 0.01 10.0 -5 2.0 -0.5 1 #SAD age at 50% selectivity  
 7.0 0.1 25.0 -5 3.0 -0.5 1 #SAD slope of ascending limb

2.0 0.01 10.0 -5 4.5 -0.5 1 #SAD age at 50% selectivity descending limb  
 7.0 0.1 25.0 -5 3.0 -0.5 1 #SAD slope of descending limb

-9.0 -10.0 10.0 -5 -5.0 -0.5 1 #age-0 NAD selectivity in logit space  
 2.0 -10.0 10.0 -5 0.0 -0.5 1 #age-1 NAD selectivity in logit space  
 9.0 -10.0 10.0 -5 5.0 -0.5 1 #age-2 NAD selectivity in logit space  
 0.0 -15.0 10.0 -5 0.0 -0.5 1 #age-3 NAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-4 NAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-5 NAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-6+ NAD selectivity in logit space

-9.0 -10.0 10.0 -5 -5.0 -0.5 1 #age-0 MAD selectivity in logit space  
 2.0 -10.0 10.0 -5 0.0 -0.5 1 #age-1 MAD selectivity in logit space  
 9.0 -10.0 10.0 -5 5.0 -0.5 1 #age-2 MAD selectivity in logit space  
 0.0 -15.0 10.0 -5 0.0 -0.5 1 #age-3 MAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-4 MAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-5 MAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-6+ MAD selectivity in logit space

-9.0 -10.0 10.0 -5 -5.0 -0.5 1 #age-0 SAD selectivity in logit space  
 2.0 -10.0 10.0 -5 0.0 -0.5 1 #age-1 SAD selectivity in logit space  
 9.0 -10.0 10.0 -5 5.0 -0.5 1 #age-2 SAD selectivity in logit space  
 0.0 -15.0 10.0 -5 0.0 -0.5 1 #age-3 SAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-4 SAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-5 SAD selectivity in logit space  
 0.0 -10.0 10.0 -5 0.0 -0.5 1 #age-6+ SAD selectivity in logit space

##### Index catchability parameters #####

-6.0 -9 -0.1 3 -8.0 -0.5 1 #NAD index (log q)  
 -6.0 -9 -0.1 3 -8.0 -0.5 1 #MAD index (log q)  
 -6.0 -9 -0.1 3 -8.0 -0.5 1 #SAD index (log q)  
 -6.0 -9 -1 3 -5.3 -0.5 1 #JAI index (log q) - period 1  
 -6.0 -9 -1 3 -5.3 -0.5 1 #JAI index (log q) - period 2  
 -6.0 -19 -1 3 -5.3 -0.5 1 #MARMAP index (log q)  
 -6.0 -19 -1 3 -5.3 -0.5 1 #ECOMON index (log q)



##### Fishing mortality parameters #####

-9.0 -10.0 1.0 1 -3.0 -0.5 1 #commercial reduction north log mean F  
-7.0 -10.0 1.0 1 -3.0 -0.5 1 #commercial reduction south log mean F  
-8.0 -10.0 1.0 1 -3.0 -0.5 1 #commercial bait north log mean F  
-6.0 -10.0 1.0 1 -3.0 -0.5 1 #commercial bait south log mean F

##### Dev vectors

#####

#####

# lower # upper # #

# bound # bound # phase #

#-----#-----#-----#

-5.0 5.0 2 # comm reduction F devs - north  
-5.0 5.0 2 # comm reduction F devs - south  
-5.0 5.0 2 # comm bait F devs - north  
-5.0 5.0 2 # comm bait F devs - south  
-3.0 3.0 -4 # Random walk on q  
-5.0 5.0 2 # recruitment devs  
-25.0 25.0 3 # Nage devs

#commercial reduction F dev initial guesses (1955-2017)-north and south

0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0

#commercial bait F dev initial guesses (1955-2017)-north and south

0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0  
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0





0.0	0.1	0.7	0.9	1.0	1.0	1.0
0.0	0.2	0.7	1.0	1.0	1.0	1.0
0.0	0.1	0.8	1.0	1.0	1.0	1.0
0.0	0.2	0.7	1.0	1.0	1.0	1.0
0.0	0.2	0.7	1.0	1.0	1.0	1.0
0.0	0.2	0.9	1.0	1.0	1.0	1.0
0.0	0.1	0.9	1.0	1.0	1.0	1.0
0.0	0.1	0.6	1.0	1.0	1.0	1.0
0.0	0.1	0.7	0.9	1.0	1.0	1.0
0.0	0.0	0.5	0.9	1.0	1.0	1.0
0.0	0.0	0.3	0.9	1.0	1.0	1.0
0.0	0.0	0.2	0.8	1.0	1.0	1.0
0.0	0.0	0.2	0.7	1.0	1.0	1.0
0.0	0.0	0.2	0.7	0.9	1.0	1.0
0.0	0.0	0.2	0.7	0.9	1.0	1.0
0.0	0.0	0.1	0.6	0.9	1.0	1.0
0.0	0.0	0.2	0.5	0.9	1.0	1.0
0.0	0.0	0.3	0.7	0.9	1.0	1.0
0.0	0.0	0.3	0.7	0.9	1.0	1.0
0.0	0.0	0.2	0.8	0.9	1.0	1.0
0.0	0.0	0.2	0.7	1.0	1.0	1.0
0.0	0.0	0.2	0.7	0.9	1.0	1.0
0.0	0.0	0.2	0.7	0.9	1.0	1.0
0.0	0.0	0.2	0.7	0.9	1.0	1.0
0.0	0.0	0.2	0.7	0.9	1.0	1.0
0.0	0.1	0.4	0.7	0.9	1.0	1.0
0.0	0.1	0.6	0.9	0.9	1.0	1.0
0.0	0.1	0.5	0.9	1.0	1.0	1.0
0.0	0.0	0.6	0.9	1.0	1.0	1.0
0.0	0.1	0.4	0.9	1.0	1.0	1.0
0.0	0.0	0.7	0.9	1.0	1.0	1.0
0.0	0.0	0.6	0.9	1.0	1.0	1.0
0.0	0.0	0.6	1.0	1.0	1.0	1.0
0.0	0.0	0.4	1.0	1.0	1.0	1.0
0.0	0.1	0.5	0.9	1.0	1.0	1.0
0.0	0.1	0.7	0.9	1.0	1.0	1.0

0.0	0.1	0.8	0.9	1.0	1.0	1.0
0.0	0.1	0.7	1.0	1.0	1.0	1.0
0.0	0.1	0.7	1.0	1.0	1.0	1.0
0.0	0.1	0.6	0.9	1.0	1.0	1.0
0.0	0.0	0.6	0.9	1.0	1.0	1.0
0.0	0.1	0.5	0.9	1.0	1.0	1.0
0.0	0.1	0.6	0.9	1.0	1.0	1.0
0.0	0.1	0.6	0.9	1.0	1.0	1.0
0.0	0.1	0.7	0.9	1.0	1.0	1.0
0.0	0.1	0.5	0.9	1.0	1.0	1.0
0.0	0.1	0.6	0.9	1.0	1.0	1.0
0.0	0.3	0.6	0.9	1.0	1.0	1.0
0.0	0.2	0.7	0.9	1.0	1.0	1.0
0.0	0.1	0.7	0.9	0.9	1.0	1.0
0.0	0.1	0.5	0.9	1.0	1.0	1.0
0.0	0.1	0.6	0.9	0.9	1.0	1.0
0.0	0.1	0.6	0.9	0.9	1.0	1.0

#Proportion female by age

0.5	0.5	0.5	0.5	0.5	0.5	0.5
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#time-invariant fecundity at age (number of maturing ova per individual)

80747	183091	497566	891030	1304177	1708351	2094744
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#time-varying fecundity at age (nummber of maturity ova per individual)

81192	182063	602603	980332	1187126	1450397	1820860
61942	168971	572897	1034736	1322951	11509886	1680235
102034	154602	456669	1038222	1424756	1611806	1752104
54512	191372	456744	882606	1471317	1739473	1842124
130249	127640	459554	855192	1416972	1827608	1977659
74444	242879	377241	829416	1280044	2023995	2100932
98695	186857	565242	743208	1270896	1683611	2669826
115552	219314	535896	980127	1185259	1753115	2040925
124061	239431	546781	962528	1440723	1663112	2249479
118326	251296	572627	898280	1382616	1908530	2144360

100982 247933 598449 939736 120866917515402356725  
114960 209108 645259 994374 127763114561132054318  
127715 268483 567573 1174597137392615596941642033  
143456 237501 743696 1109294176708317043131781802  
138700 263529 581313 1346324180497723665761975456  
93254 315294 629948 1089882197170226146962935271  
108917 288346 874708 1154730174622725531213497556  
34190 207193 896671 1620812181081525235553058594  
67050 154449 509420 1564069244166325640063391664  
67764 163173 569925 938230 213193732520523379898  
49389 134450 474060 1007139146399825595213999748  
44840 109463 351314 885051 134602020532392860798  
45800 98172 307751 677987 132665915756892674974  
59980 101611 283305 593398 110062517501641721188  
52500 115499 299610 573356 936251 15986172128977  
45957 99333 289657 617664 955331 13063672149662  
57728 106590 249550 542497 104658214088381679554  
42441 120918 306846 477664 859276 15676091911701  
58759 109232 327114 587854 779179 12217052158300  
49244 116086 346231 629157 912565 11443951611803  
48649 107637 302297 694521 100319512486131561135  
51200 102273 299497 583029 110785214222381573008  
42361 113876 284193 576276 946963 15433781861813  
49584 104116 316298 566336 910059 13768781969451  
71042 132508 318285 597870 937546 12725801853933  
67347 181212 413377 630785 923255 13797051640554  
112090 156462 503422 790234 100240912612871872657  
62896 215568 438603 860708 119391913962601589433  
92452 141190 522897 809811 117823615771861784466  
36020 209556 418675 933667 121054514304231915535  
24674 139966 571757 860555 140473715980911618336  
34418 115121 549098 1038609144923718974381948223  
45268 108876 510328 1107146153449921546632382517  
122245 136532 403842 1081544167854120074222943113  
52555 243073 463052 857324 168660421863732429363

28645 193563 593901 906823 139992122376462602856  
99822 164099 697749 1038071137804219679432698468  
75858 247457 643896 1313332151505718180322516230  
87327 187832 601990 1114185188125519804842198796  
29855 193356 527762 901120 144564523390932407690  
46636 114419 507417 932731 110450416496102681776  
72060 169241 439499 892044 132213512298971767323  
84020 202714 526633 871144 128135916566241303513  
127262 220678 553295 854692 130208016360881925496  
91901 223366 566379 878367 108340316761061939180  
106092 225889 485138 871479 111590912250221976098  
198907 236375 559629 809025 108621912715381307802  
109020 326955 549328 858022 115928112225391367961  
105598 264324 609880 829262 107317315081181304674  
101516 213521 605906 875100 103484312134581837125  
124599 228374 494000 862490 109328511721251300292  
110267 252679 537491 791739 101877912601301259294  
110267 231143 532503 818381 105691111057851382238

#time-invariant weight (in grams) at age at spawning

29.1 66.0 179.4 321.3 470.3 616.0 755.4

#time-varying weight (in grams) at age at spawning

29.3 65.7 217.3 353.5 428.1 523.0 656.6  
22.3 60.9 206.6 373.1 477.1 544.5 605.9  
36.8 55.8 164.7 374.4 513.8 581.2 631.8  
19.7 69.0 164.7 318.3 530.6 627.3 664.3  
47.0 46.0 165.7 308.4 511.0 659.0 713.2  
26.8 87.6 136.0 299.1 461.6 729.9 757.6  
35.6 67.4 203.8 268.0 458.3 607.1 962.8  
41.7 79.1 193.2 353.4 427.4 632.2 736.0  
44.7 86.3 197.2 347.1 519.5 599.7 811.2  
42.7 90.6 206.5 323.9 498.6 688.2 773.3  
36.4 89.4 215.8 338.9 435.9 631.6 849.8  
41.5 75.4 232.7 358.6 460.7 525.1 740.8

46.1	96.8	204.7	423.6	495.4	562.4	592.1
51.7	85.6	268.2	400.0	637.2	614.6	642.5
50.0	95.0	209.6	485.5	650.9	853.4	712.4
33.6	113.7	227.2	393.0	711.0	942.9	1058.5
39.3	104.0	315.4	416.4	629.7	920.7	1261.2
12.3	74.7	323.3	584.5	653.0	910.0	1102.9
24.2	55.7	183.7	564.0	880.5	924.6	1223.1
24.4	58.8	205.5	338.3	768.8	1172.7	1218.8
17.8	48.5	170.9	363.2	527.9	923.0	1442.3
16.2	39.5	126.7	319.2	485.4	740.4	1031.6
16.5	35.4	111.0	244.5	478.4	568.2	964.6
21.6	36.6	102.2	214.0	396.9	631.1	620.7
18.9	41.6	108.0	206.8	337.6	576.5	767.7
16.6	35.8	104.5	222.7	344.5	471.1	775.2
20.8	38.4	90.0	195.6	377.4	508.0	605.7
15.3	43.6	110.7	172.2	309.9	565.3	689.4
21.2	39.4	118.0	212.0	281.0	440.6	778.3
17.8	41.9	124.9	226.9	329.1	412.7	581.2
17.5	38.8	109.0	250.4	361.8	450.3	563.0
18.5	36.9	108.0	210.2	399.5	512.9	567.2
15.3	41.1	102.5	207.8	341.5	556.6	671.4
17.9	37.5	114.1	204.2	328.2	496.5	710.2
25.6	47.8	114.8	215.6	338.1	458.9	668.5
24.3	65.3	149.1	227.5	332.9	497.5	591.6
40.4	56.4	181.5	285.0	361.5	454.8	675.3
22.7	77.7	158.2	310.4	430.5	503.5	573.2
33.3	50.9	188.6	292.0	424.9	568.7	643.5
13.0	75.6	151.0	336.7	436.5	515.8	690.8
8.9	50.5	206.2	310.3	506.6	576.3	583.6
12.4	41.5	198.0	374.5	522.6	684.2	702.5
16.3	39.3	184.0	399.2	553.3	777.0	859.1
44.1	49.2	145.6	390.0	605.3	723.9	1061.3
19.0	87.7	167.0	309.2	608.2	788.4	876.0
10.3	69.8	214.2	327.0	504.8	806.9	938.6
36.0	59.2	251.6	374.3	496.9	709.7	973.1



27.4	89.2	232.2	473.6	546.3	655.6	907.4
31.5	67.7	217.1	401.8	678.4	714.2	792.9
10.8	69.7	190.3	324.9	521.3	843.5	868.2
16.8	41.3	183.0	336.3	398.3	594.9	967.1
26.0	61.0	158.5	321.7	476.8	443.5	637.3
30.3	73.1	189.9	314.1	462.1	597.4	470.1
45.9	79.6	199.5	308.2	469.5	590.0	694.3
33.1	80.5	204.2	316.7	390.7	604.4	699.3
38.3	81.5	174.9	314.3	402.4	441.8	712.6
71.7	85.2	201.8	291.7	391.7	458.5	471.6
39.3	117.9	198.1	309.4	418.0	440.9	493.3
38.1	95.3	219.9	299.0	387.0	543.8	470.5
36.6	77.0	218.5	315.6	373.2	437.6	662.5
44.9	82.4	178.1	311.0	394.2	422.7	468.9
39.8	91.1	193.8	285.5	367.4	454.4	454.1
39.8	83.4	192.0	295.1	381.1	398.8	498.4

#time-invariant weight (in grams) at age at start of fishing year

44.9	117.2	239.7	363.7	473.3	565.6	643.9
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#time-varying weight (in grams) at age at middle of fishing year

38.5	132.7	294.0	418.9	484.9	562.5	656.9
26.5	111.2	283.4	454.9	529.6	594.3	640.1
45.3	98.8	244.8	432.9	575.4	618.6	669.6
25.1	115.8	239.0	388.7	559.1	657.0	687.2
65.9	81.4	242.8	386.7	521.1	656.7	709.4
37.0	139.1	199.8	382.7	515.5	632.3	728.5
54.2	125.0	268.4	345.6	516.4	617.1	720.9
60.3	134.6	280.0	417.8	497.0	633.8	692.8
65.0	148.2	261.3	429.2	571.9	639.7	731.8
66.9	150.0	280.6	379.6	549.4	720.1	766.2
55.4	151.2	284.3	397.8	475.4	637.6	856.1
68.9	127.2	295.0	413.9	488.0	547.2	699.1
66.9	166.6	264.3	449.7	523.5	552.3	598.6
76.6	131.2	324.2	434.0	596.3	609.6	596.3

79.4	145.6	256.4	477.3	619.9	725.3	674.1
58.4	186.9	272.5	426.0	607.0	808.5	833.4
50.8	176.1	363.1	433.7	636.2	708.6	990.4
26.0	131.9	358.2	539.8	621.2	881.4	784.6
42.4	124.0	277.8	512.7	694.9	826.7	1155.3
30.0	109.3	280.2	437.0	624.0	820.9	1042.3
28.4	88.5	225.0	397.8	587.1	697.8	918.6
18.9	70.7	195.9	345.5	470.1	717.3	744.6
22.2	67.4	152.7	310.6	454.2	510.7	824.5
30.3	71.4	165.5	252.9	414.8	544.3	532.5
26.5	71.1	169.8	276.4	359.9	501.3	615.4
23.1	58.5	148.5	283.4	380.5	465.2	569.2
21.7	72.4	123.5	242.5	393.9	468.9	563.3
26.1	75.5	167.6	212.7	343.1	491.6	539.7
32.1	73.4	180.5	273.8	322.3	442.8	573.0
24.9	71.1	166.0	294.8	373.9	448.0	536.4
23.0	70.9	146.0	275.9	398.5	459.8	584.9
26.7	69.2	158.1	241.0	387.6	483.8	529.5
27.1	77.3	157.7	256.5	348.2	491.5	550.0
28.6	72.4	169.0	256.6	351.7	460.8	582.8
43.2	97.9	158.7	265.6	350.4	435.8	573.1
39.4	120.6	218.6	259.0	352.3	431.5	506.0
55.1	98.7	240.2	332.8	359.9	423.5	497.8
31.6	134.9	203.0	344.6	422.9	452.9	479.0
53.6	100.1	260.3	314.7	422.4	487.9	534.1
26.4	129.1	230.0	377.9	418.7	476.0	532.3
24.7	124.7	255.9	370.8	473.7	508.0	511.3
19.0	103.5	301.9	386.2	499.4	546.0	580.7
31.1	92.8	256.0	458.8	502.9	606.4	598.1
64.1	99.5	238.9	409.4	571.3	599.7	690.6
42.3	141.6	231.0	382.8	535.5	644.5	676.1
29.5	143.2	275.2	376.2	497.1	629.2	689.7
58.1	134.6	307.1	421.8	511.1	578.8	695.0
39.7	153.4	304.7	449.2	564.4	625.1	633.9
50.5	122.9	276.8	437.2	552.3	693.0	716.2

26.0	120.2	254.9	364.5	521.5	620.8	803.7
37.0	92.7	235.8	369.7	418.4	570.5	664.3
45.7	120.1	209.6	352.7	454.0	449.3	597.8
56.4	136.3	245.3	319.3	456.1	510.9	466.5
62.7	141.7	265.9	345.7	404.8	540.8	547.6
56.3	123.6	258.6	366.0	413.4	465.6	606.8
60.4	140.3	226.4	349.4	431.6	455.5	506.6
97.1	141.1	253.7	341.4	410.7	471.5	480.6
71.0	168.2	251.6	340.5	457.2	449.2	494.8
56.7	162.5	266.4	339.7	398.1	566.5	472.4
58.3	124.4	268.7	355.0	401.1	433.8	665.2
71.5	138.1	230.0	338.0	427.9	441.1	455.2
61.9	145.6	247.6	332.0	377.7	484.8	466.2
61.9	135.8	231.1	334.7	418.9	399.3	527.7

#Time varying length at age for April 15

95.5	165.5	232.7	267.7	283.6	300.7	320.9
79.6	159.3	229.7	272.7	292.8	304.6	314.1
106.7	156.1	214.0	273.4	299.8	310.6	318.3
79.8	164.6	214.0	260.9	303.1	318.1	323.3
115.0	146.7	213.7	257.7	301.2	323.3	330.5
83.3	177.3	201.8	255.3	290.8	335.8	337.0
95.8	165.6	227.7	247.2	290.6	315.7	365.4
104.5	172.9	224.7	268.6	284.5	320.5	334.6
108.3	177.2	225.1	267.0	301.8	315.3	345.9
106.4	179.8	228.3	260.5	297.4	328.7	340.7
102.7	179.6	231.6	264.3	284.4	319.2	350.5
99.7	170.3	238.1	269.2	289.6	300.6	334.9
115.4	185.1	229.3	284.8	296.5	307.4	311.6
120.1	176.2	249.1	280.6	322.1	316.3	319.9
107.7	181.9	230.4	297.0	325.3	351.8	330.7
77.3	194.6	236.1	278.7	332.9	364.2	375.6
108.5	191.4	262.4	283.6	321.8	359.8	398.1
39.5	169.0	264.2	315.3	325.2	360.2	380.0
82.7	159.5	220.9	310.6	356.6	361.7	394.4

92.2	158.6	229.4	265.6	340.2	388.8	393.7
79.2	147.8	216.5	270.2	304.1	359.0	413.9
77.8	139.3	196.9	260.5	294.0	337.1	371.1
78.0	134.7	189.0	240.2	294.1	307.8	365.5
89.6	136.3	184.5	230.1	278.3	319.7	315.9
86.7	140.6	187.9	228.1	264.1	311.9	339.1
75.6	134.0	185.0	233.7	266.4	292.2	341.6
85.5	138.4	176.7	223.6	274.3	299.9	315.4
70.3	143.4	188.8	215.1	257.2	310.3	329.3
88.3	140.3	192.6	229.3	249.7	286.3	342.3
79.7	141.1	196.7	234.4	261.7	280.9	311.7
81.2	138.5	187.8	242.0	270.0	287.8	309.0
79.8	136.1	187.4	229.0	278.5	300.3	308.7
71.9	141.0	184.5	228.0	265.4	307.9	326.1
71.6	137.9	190.5	227.1	261.7	297.6	331.5
80.4	149.2	191.4	230.4	264.8	289.8	326.0
84.7	164.0	207.6	234.7	262.7	297.9	313.1
108.6	156.2	219.9	251.5	269.8	288.7	327.1
85.7	171.1	211.1	257.3	284.5	298.3	309.7
94.6	151.2	222.5	253.3	282.3	309.3	321.4
50.3	171.0	208.8	264.8	285.7	299.0	328.0
38.3	154.4	229.3	259.4	299.7	310.7	310.2
58.8	146.3	227.9	273.8	303.9	328.3	329.8
64.9	141.6	223.3	279.9	307.8	343.0	351.9
109.6	151.5	207.1	278.2	316.7	333.7	377.3
57.7	177.9	215.5	259.0	317.4	342.6	353.5
25.2	170.3	231.5	262.8	300.0	345.4	361.0
87.7	163.7	245.1	273.5	297.7	332.5	365.3
84.2	180.1	238.4	294.7	306.5	323.5	358.1
93.5	165.7	231.3	278.6	327.6	332.3	342.5
47.7	166.4	223.4	259.7	300.3	349.4	352.6
52.4	144.7	220.5	264.2	275.5	312.0	363.9
73.9	162.5	212.3	260.6	293.1	284.2	318.3
80.6	170.2	222.8	259.4	290.4	313.6	289.1
116.7	174.2	225.9	255.9	292.1	312.6	328.0

86.6	172.0	227.2	258.1	274.1	314.9	329.0
96.0	175.0	216.6	257.2	276.7	284.0	330.8
135.8	176.7	226.3	252.6	274.2	287.5	289.5
90.0	192.8	224.7	256.0	281.6	283.8	293.7
102.4	183.4	231.3	253.2	273.2	305.0	289.2
94.3	170.6	231.2	257.4	270.1	283.2	323.8
105.2	174.9	217.7	255.7	275.0	280.1	289.0
100.7	179.5	223.2	250.2	268.2	286.8	286.1
100.7	175.0	221.9	252.2	272.6	274.6	294.9

#Time varying length at age for June 1

103.7	174.6	238.4	271.2	286.6	302.6	321.1
89.9	166.3	235.9	276.5	295.2	306.5	315.4
114.2	164.0	220.0	277.6	302.4	312.3	319.6
88.5	170.9	219.9	266.1	305.9	319.9	324.5
123.2	153.9	219.0	262.2	305.6	325.2	331.7
94.7	183.9	207.7	259.8	294.1	339.6	338.3
106.7	173.8	233.1	252.0	294.4	318.3	368.7
114.6	180.3	230.5	273.0	288.6	323.8	336.5
118.2	184.3	230.1	271.2	305.3	318.6	348.6
116.1	186.9	233.4	263.9	300.4	331.5	343.4
111.3	187.4	236.8	267.8	286.7	321.4	352.8
111.3	177.8	244.3	273.0	292.1	302.2	336.4
123.1	193.8	235.8	289.7	299.2	309.1	312.7
127.9	183.1	255.6	286.3	326.0	318.3	321.1
119.3	188.8	236.5	301.9	330.2	355.0	332.1
93.9	203.6	242.2	284.2	336.6	368.5	378.1
116.2	202.0	269.5	288.9	326.7	362.6	401.9
57.5	175.6	270.9	320.8	329.9	364.5	382.0
92.9	170.0	226.7	314.9	360.9	365.8	398.3
99.2	166.4	235.6	270.5	342.9	392.2	397.2
87.1	154.1	222.4	273.8	308.3	360.8	416.6
85.0	145.8	202.4	265.0	296.0	340.7	372.2
85.4	141.0	194.4	245.0	297.5	309.0	368.6
96.1	142.8	190.0	234.5	282.6	322.3	316.6

92.7	146.3	193.7	233.0	267.7	315.7	341.1
83.9	139.4	190.0	238.8	270.6	295.2	344.9
92.9	145.1	181.5	227.9	278.9	303.6	317.9
79.6	149.7	194.2	219.4	260.9	314.4	332.5
95.0	147.7	198.0	233.6	253.6	289.6	345.9
87.3	147.0	202.6	239.0	265.2	284.4	314.5
88.2	144.8	193.0	246.8	273.9	290.6	312.2
87.8	142.2	192.6	233.6	282.4	303.6	310.9
80.6	147.6	189.9	232.4	269.5	311.0	328.9
82.1	144.9	195.8	231.9	265.4	301.2	334.0
92.3	157.1	197.1	234.7	269.0	292.8	329.2
94.3	171.9	213.6	239.3	266.1	301.6	315.6
116.7	163.5	225.2	256.0	273.6	291.5	330.4
94.0	177.8	216.7	260.8	287.9	301.3	312.0
104.9	158.5	228.0	257.6	284.7	311.9	323.9
64.8	178.8	215.2	269.4	289.1	300.6	329.9
53.3	164.6	235.3	265.1	303.4	313.2	311.3
69.8	157.0	235.2	278.4	308.8	331.4	331.8
76.7	150.3	230.9	285.0	311.3	347.3	354.4
118.7	160.3	214.0	283.7	320.3	336.4	381.2
73.8	185.1	222.0	264.4	321.3	345.2	355.5
46.6	181.0	237.1	267.5	304.3	348.1	362.8
101.9	175.3	252.1	277.9	301.2	335.9	367.2
95.6	187.9	244.6	299.4	309.9	326.1	360.8
103.5	173.8	235.6	282.0	330.7	335.0	344.4
61.2	173.8	229.1	262.1	302.1	351.5	354.7
69.3	154.2	226.0	268.3	276.8	313.0	365.3
88.5	171.8	218.9	264.7	296.0	285.0	318.8
94.9	178.6	227.9	264.0	293.5	315.6	289.5
124.0	182.3	230.8	258.7	295.3	314.8	329.4
100.0	177.9	231.8	260.9	275.6	317.2	330.7
108.0	182.7	221.3	259.8	278.3	284.8	332.4
143.9	183.9	230.7	256.4	275.6	288.4	289.9
104.7	198.3	228.9	258.6	284.6	284.6	294.2
112.0	191.0	235.0	255.7	274.7	307.4	289.7

106.3	177.3	235.1	259.9	271.6	284.1	325.8
116.5	182.1	222.3	257.7	276.6	281.0	289.5
111.6	185.9	227.5	253.3	269.2	288.0	286.6
111.6	181.8	225.6	254.8	274.8	275.2	295.6

#Time varying length at age for October 15

128.6	200.7	254.7	281.3	295.2	308.1	321.5
120.5	187.7	253.7	287.6	302.4	312.1	319.1
136.8	187.1	238.4	289.7	309.8	317.5	323.3
114.9	190.2	237.4	281.8	314.2	324.9	328.2
147.8	175.6	235.3	275.4	319.2	330.8	335.1
127.9	203.8	225.6	273.7	304.1	351.2	342.1
138.1	197.6	249.3	266.8	306.2	325.8	378.7
144.0	201.6	247.6	286.1	300.7	333.7	342.2
146.9	205.0	244.5	283.5	315.9	328.6	357.1
145.1	207.8	247.9	273.6	309.2	340.1	351.6
137.7	210.5	251.9	278.1	293.3	327.7	359.7
145.5	200.8	262.7	284.0	299.3	306.7	341.0
146.7	219.4	255.8	304.5	307.2	314.2	315.7
152.0	204.1	274.8	303.7	337.8	324.1	324.7
153.8	209.9	255.3	316.3	345.4	364.4	336.3
140.8	230.6	260.7	300.9	347.4	381.8	385.6
139.9	231.9	290.5	305.1	341.6	370.6	413.4
107.5	195.9	290.0	337.2	344.1	377.8	388.1
123.2	199.2	244.1	327.1	373.7	378.2	410.1
120.9	189.5	252.6	285.6	350.7	402.2	408.2
110.7	173.1	240.0	283.7	321.2	365.7	424.4
107.2	165.3	219.2	278.4	301.8	351.8	375.3
108.0	160.4	210.5	259.8	307.7	312.4	378.2
116.0	162.9	207.0	247.9	295.7	330.1	318.5
111.0	163.6	211.5	247.9	278.8	327.2	347.1
108.8	155.9	205.0	254.6	283.7	304.3	355.1
115.6	165.0	196.4	241.0	292.9	315.1	325.5
107.2	169.0	210.2	232.8	272.3	326.8	342.6
115.5	170.0	214.4	246.4	265.7	299.5	356.9

110.4	165.2	220.6	253.0	275.5	295.3	323.1
109.5	164.1	209.0	261.2	285.8	298.8	322.0
112.1	161.1	208.6	247.8	294.0	313.7	317.5
106.6	167.1	206.5	245.6	282.0	320.3	337.5
113.2	166.0	211.5	246.5	276.4	312.3	341.6
126.4	180.5	214.2	247.4	281.9	302.0	339.0
122.8	194.7	231.1	253.2	276.4	313.0	323.3
141.4	185.4	240.4	269.2	284.8	299.8	340.4
119.5	198.1	233.5	271.0	297.8	310.5	318.7
135.4	180.9	244.7	270.6	291.5	319.3	331.2
106.8	202.1	234.9	283.1	299.0	305.2	335.5
96.9	194.3	253.0	282.4	314.7	320.9	314.3
102.6	188.1	256.2	291.9	324.1	340.7	337.7
111.5	176.3	253.1	299.9	321.6	360.7	362.1
145.8	185.9	234.6	299.5	330.8	344.3	392.9
119.8	206.3	240.9	280.7	332.6	352.6	361.6
105.0	211.5	253.8	281.5	317.2	356.2	368.0
140.7	206.8	272.4	291.0	311.5	346.0	373.0
128.5	209.4	261.6	312.8	320.2	333.7	368.9
132.7	197.1	247.6	291.1	339.6	343.1	350.1
100.6	195.5	245.6	268.8	307.1	357.4	361.0
115.6	181.6	242.1	279.9	280.5	315.6	369.2
128.6	197.1	238.0	276.7	304.2	287.0	320.3
134.0	201.9	241.8	277.2	302.3	321.4	290.6
145.8	204.5	244.2	266.3	304.6	321.4	333.6
136.8	195.5	244.3	268.7	279.8	323.6	335.5
141.6	204.1	235.5	266.9	282.8	287.1	336.9
167.1	203.8	243.1	267.8	279.7	291.0	291.2
144.4	214.0	240.8	265.7	293.9	286.9	295.7
139.7	211.3	245.6	262.7	278.9	314.9	291.0
139.8	196.4	245.5	267.0	275.8	286.5	331.8
147.5	202.2	235.5	263.0	281.5	283.5	290.9
142.3	203.6	239.6	262.4	272.0	291.3	288.1
142.3	200.7	235.7	262.0	281.1	276.5	297.9



#time of year (as fraction) for spawning: Mar 1=0d/365d

0.000

#age-dependent natural mortality at age (ages 0-4+)

1.76 1.31 1.03 0.90 0.81 0.76 0.72

#time-varying natural mortality at age (ages 0-6+)

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72

1.76 1.31 1.03 0.90 0.81 0.76 0.72



#Spawner-recruit parameters

# SR function switch (integer 1=Beverton-Holt, 2=Ricker)

1

#switch for rate increase in q: Integer value (choose estimation phase, negative value turns it off)

-1

#annual positive rate of increase on all fishery dependent q's due to technology creep

0.0

# DD q switch: Integer value (choose estimation phase, negative value turns it off)

-1

#density dependent catchability exponent, value of zero is density independent, est range is (0.1,0.9)

0.0

#SE of density dependent catchability exponent (0.128 provides 95% CI in range 0.5)

0.128

#Age to begin counting D-D q (should be age near full exploitation)

2.0

#Variance ( $sd^2$ ) of fishery dependent random walk catchabilities (0.03 is near the  $sd=0.17$  of Wilberg and Bence)

0.03

#Tuning F (not applied in last phase of optimization, or not applied at all if penalty weight=0)

0.15

#Year for tuning F

2015

#threshold sample sizes ntrips ( $\geq$ ) for length comps (set to 99999.0 if sel is fixed):

1.0 #NAD len comps

1.0 #MAD len comps

#35.0 #SAD len comps

#threshold sample sizes ntrips ( $\geq$ ) for age comps (set to 99999.0 if sel is fixed)

3.0 #cRn age comps

3.0 #cRs age comps

3.0 #cBn age comps

3.0 #cBs age comps

# Projection input

2022 #Projection end year, must be later than assessment endyr

2019 #New management start year, must be later than assessment endyr

1 #Switching indicating value to use for defining projection F: 1=Fcurrent, 2=Fmsy, 3=F30, 4=F40

1.0 #Multiplier "c" applied to compute projection F, for example Fproj=cFmsy

#Ageing error matrix (columns are true age 0-6+, rows are ages as read for age comps: columns should sum to one)

1.0	0.0	0.0	0.0	0.0	0.0	0.0
0.0	1.0	0.0	0.0	0.0	0.0	0.0
0.0	0.0	1.0	0.0	0.0	0.0	0.0
0.0	0.0	0.0	1.0	0.0	0.0	0.0
0.0	0.0	0.0	0.0	1.0	0.0	0.0
0.0	0.0	0.0	0.0	0.0	1.0	0.0
0.0	0.0	0.0	0.0	0.0	0.0	1.0

999 #end of data file flag

### 14.2.2 BAM AD Model Builder Code (.tpl file)

///~~#####~~

///~~###~~

///~~### SEDAR 69 Atlantic menhaden assessment model, 2019~~

///~~### NMFS, Beaufort Lab, Sustainable Fisheries Branch~~

///~~###~~

///~~#####~~

DATA\_SECTION

!!cout << "Starting Beaufort Assessment Model" << endl;

!!cout << endl;

!!cout << "        BAM!" << endl;

!!cout << endl;

//~~----->~~

//-- BAM DATA\_SECTION: set-up section

//~~----->~~

// Starting and ending year of the model (year data starts)

init\_int styr;

```
init_int endyr;

//Starting year to estimate recruitment deviation from S-R curve
init_int styr_rec_dev;
//Ending year to estimate recruitment deviation from S-R curve
init_int endyr_rec_dev;
//possible 3 phases of constraints on recruitment deviations
init_int endyr_rec_phase1;
init_int endyr_rec_phase2;

// ending years for selectivity blocks
init_int endyr_selex_phase1;
init_int endyr_selex_phase2;
init_int endyr_selex_phase3;
init_int endyr_selex_phase4;
init_int endyr_selex_phase5;
init_int endyr_selex_phase6;
init_int endyr_selex_phase7;

//number assessment years
number nyrs;
number nyrs_rec;

//this section MUST BE INDENTED!!!
LOCAL_CALCS
  nyrs=endyr-styr+1.;
  nyrs_rec=endyr_rec_dev-styr_rec_dev+1.;
END_CALCS

//Total number of ages in population model
init_int nages;
// Vector of ages for age bins in population model
init_vector agebins(1,nages);

//Total number of ages used to match age comps: plus group may differ from popn, first age must not
```

```

init_int nages_agec;

//Vector of ages for age bins in age comps
init_vector agebins_agec(1,nages_agec);

//Total number of length bins for each matrix and width of bins
init_int nlenbins;    //used to match data
init_number lenbins_width; //width of length bins (mm)

//Vector of lengths for length bins (mm)(midpoint)
init_vector lenbins(1,nlenbins);

//Max F used in spr and msy calcs
init_number max_F_spr_msy;
//Total number of iterations for spr calcs
init_int n_iter_spr;
//Total number of iterations for msy calcs
int n_iter_msy;
LOCAL_CALCS
    n_iter_msy=n_iter_spr;
END_CALCS

//Starting year to compute arithmetic average recruitment for SPR-related values
init_int styr_rec_spr;
//Ending year to compute arithmetic average recruitment for SPR-related values
init_int endyr_rec_spr;
number nyrs_rec_spr;
LOCAL_CALCS
    nyrs_rec_spr=endyr_rec_spr-styr_rec_spr+1.;
END_CALCS

//Number years at end of time series over which to average sector F's, for weighted selectivities
init_int selpar_n_yrs_wgtd;
//bias correction (set to 1.0 for no bias correction or a negative value to compute from rec variance)
init_number set_BiasCor;

```



```

init_int styr_sad_cpue;
init_int endyr_sad_cpue;
init_vector obs_sad_cpue(styr_sad_cpue, endyr_sad_cpue); //Observed CPUE
init_vector sad_cpue_cv(styr_sad_cpue, endyr_sad_cpue); //CV of cpue

// Length Compositions
//init_int nyr_sad_lenc;
//init_ivector yrs_sad_lenc(1, nyr_sad_lenc);
//init_vector nsamp_sad_lenc(1, nyr_sad_lenc);
//init_vector nfish_sad_lenc(1, nyr_sad_lenc);
//init_matrix obs_sad_lenc(1, nyr_sad_lenc, 1, nlenbins);

#####Young of the year (YOY)#####
//CPUE
init_int styr_jai_cpue;
init_int endyr_jai_cpue;
init_vector obs_jai_cpue(styr_jai_cpue, endyr_jai_cpue); //Observed CPUE
init_vector jai_cpue_cv(styr_jai_cpue, endyr_jai_cpue); //CV of cpue
init_int yr_q_change;

#####MARMAP AND ECOMON
INDEX#####
//CPUE
init_int nyr_mareco_cpue;
init_ivector yrs_mareco_cpue(1, nyr_mareco_cpue);
init_vector obs_mareco_cpue(1, nyr_mareco_cpue); //Observed CPUE
init_vector mareco_cpue_cv(1, nyr_mareco_cpue); //CV of cpue

#####Commercial reduction fishery fleet - north #####
// Comm reduction landings (1000 mt)
init_int styr_cRn_L;
init_int endyr_cRn_L;
init_vector obs_cRn_L(styr_cRn_L, endyr_cRn_L);
init_vector cRn_L_cv(styr_cRn_L, endyr_cRn_L);

// Comm reduction age compositions

```



```

init_int nyr_cRn_agec;
init_ivector yrs_cRn_agec(1,nyr_cRn_agec);
init_vector nsamp_cRn_agec(1,nyr_cRn_agec);
init_vector nfish_cRn_agec(1,nyr_cRn_agec);
init_matrix obs_cRn_agec(1,nyr_cRn_agec,1,nages_agec);

//#####Commercial reduction fishery fleet - south #####
// Comm reduction landings (1000 mt)
init_int styr_cRs_L;
init_int endyr_cRs_L;
init_vector obs_cRs_L(styr_cRs_L,ender_cRs_L);
init_vector cRs_L_cv(styr_cRs_L,ender_cRs_L);

// Comm reduction age compositions
init_int nyr_cRs_agec;
init_ivector yrs_cRs_agec(1,nyr_cRs_agec);
init_vector nsamp_cRs_agec(1,nyr_cRs_agec);
init_vector nfish_cRs_agec(1,nyr_cRs_agec);
init_matrix obs_cRs_agec(1,nyr_cRs_agec,1,nages_agec);

//#####Commercial bait fishery fleet - north #####
// Comm bait landings (1000 mt) - includes rec
init_int styr_cBn_L;
init_int endyr_cBn_L;
init_vector obs_cBn_L(styr_cBn_L,ender_cBn_L);
init_vector cBn_L_cv(styr_cBn_L,ender_cBn_L);

// Comm reduction age compositions
init_int nyr_cBn_agec;
init_ivector yrs_cBn_agec(1,nyr_cBn_agec);
init_vector nsamp_cBn_agec(1,nyr_cBn_agec);
init_vector nfish_cBn_agec(1,nyr_cBn_agec);
init_matrix obs_cBn_agec(1,nyr_cBn_agec,1,nages_agec);

//#####Commercial bait fishery fleet - south #####

```



```
//init_vector set_log_dm_sad_lc(1,7); //Dirichlet-multinomial overdispersion parameter-SAD
```

```
init_vector set_log_dm_cRn_ac(1,7); //Dirichlet-multinomial overdispersion parameter-Comm reduction north
```

```
init_vector set_log_dm_cRs_ac(1,7); //Dirichlet-multinomial overdispersion parameter-Comm reduction south
```

```
init_vector set_log_dm_cBn_ac(1,7); //Dirichlet-multinomial overdispersion parameter-Comm bait north
```

```
init_vector set_log_dm_cBs_ac(1,7); //Dirichlet-multinomial overdispersion parameter-Comm bait south
```

```
//Initial guesses or fixed values of estimated selectivity parameters
```

```
init_vector set_selpar_A50_cRn(1,7); //paramaters for comm reduction double logistic
```

```
init_vector set_selpar_slope_cRn(1,7); //north - block 1
```

```
init_vector set_selpar_A502_cRn(1,7);
```

```
init_vector set_selpar_slope2_cRn(1,7);
```

```
init_vector set_selpar_A50_cRn2(1,7); //paramaters for comm reduction double logistic
```

```
init_vector set_selpar_slope_cRn2(1,7); //north - block 2
```

```
init_vector set_selpar_A502_cRn2(1,7);
```

```
init_vector set_selpar_slope2_cRn2(1,7);
```

```
init_vector set_selpar_A50_cRn3(1,7); //paramaters for comm reduction double logistic
```

```
init_vector set_selpar_slope_cRn3(1,7); //north - block 3
```

```
init_vector set_selpar_A502_cRn3(1,7);
```

```
init_vector set_selpar_slope2_cRn3(1,7);
```

```
init_vector set_selpar_A50_cRn4(1,7); //paramaters for comm reduction double logistic
```

```
init_vector set_selpar_slope_cRn4(1,7); //north - block 4
```

```
init_vector set_selpar_A502_cRn4(1,7);
```

```
init_vector set_selpar_slope2_cRn4(1,7);
```

```
init_vector set_selpar_A50_cRs(1,7); //paramaters for comm reduction double logistic
```

```
init_vector set_selpar_slope_cRs(1,7); //south - block 1
```

```
init_vector set_selpar_A502_cRs(1,7);
```

```
init_vector set_selpar_slope2_cRs(1,7);
```

```
init_vector set_selpar_A50_cRs2(1,7); //paramaters for comm reduction double logistic
```

```
init_vector set_selpar_slope_cRs2(1,7); //south - block 2
```

```
init_vector set_selpar_A502_cRs2(1,7);
init_vector set_selpar_slope2_cRs2(1,7);

init_vector set_selpar_A50_cRs3(1,7); //paramaters for comm reduction double logistic
init_vector set_selpar_slope_cRs3(1,7); //south - block 3
init_vector set_selpar_A502_cRs3(1,7);
init_vector set_selpar_slope2_cRs3(1,7);

init_vector set_selpar_A50_cRs4(1,7); //paramaters for comm reduction double logistic
init_vector set_selpar_slope_cRs4(1,7); //south - block 4
init_vector set_selpar_A502_cRs4(1,7);
init_vector set_selpar_slope2_cRs4(1,7);

init_vector set_selpar_A50_cBn(1,7); //paramaters for comm bait double logistic
init_vector set_selpar_slope_cBn(1,7); //north - block 1
init_vector set_selpar_A502_cBn(1,7);
init_vector set_selpar_slope2_cBn(1,7);

init_vector set_selpar_A50_cBn2(1,7); //paramaters for comm bait double logistic
init_vector set_selpar_slope_cBn2(1,7); //north - block 2
init_vector set_selpar_A502_cBn2(1,7);
init_vector set_selpar_slope2_cBn2(1,7);

init_vector set_selpar_A50_cBs(1,7); //paramaters for comm bait double logistic
init_vector set_selpar_slope_cBs(1,7); //south - block 1
init_vector set_selpar_A502_cBs(1,7);
init_vector set_selpar_slope2_cBs(1,7);

init_vector set_selpar_A50_cBs2(1,7); //paramaters for comm bait double logistic
init_vector set_selpar_slope_cBs2(1,7); //south - block 2
init_vector set_selpar_A502_cBs2(1,7);
init_vector set_selpar_slope2_cBs2(1,7);

init_vector set_sel_age0_cRn(1,7); //input in logit space by age
init_vector set_sel_age1_cRn(1,7); //Commerical reduction fishery - north - block 1
```

init\_vector set\_sel\_age2\_cRn(1,7);

init\_vector set\_sel\_age3\_cRn(1,7);

init\_vector set\_sel\_age4\_cRn(1,7);

init\_vector set\_sel\_age5\_cRn(1,7);

init\_vector set\_sel\_age6\_cRn(1,7);

init\_vector set\_sel\_age0\_cRn2(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cRn2(1,7); //Commerical reduction fishery - north - block 2

init\_vector set\_sel\_age2\_cRn2(1,7);

init\_vector set\_sel\_age3\_cRn2(1,7);

init\_vector set\_sel\_age4\_cRn2(1,7);

init\_vector set\_sel\_age5\_cRn2(1,7);

init\_vector set\_sel\_age6\_cRn2(1,7);

init\_vector set\_sel\_age0\_cRn3(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cRn3(1,7); //Commerical reduction fishery - north - block 3

init\_vector set\_sel\_age2\_cRn3(1,7);

init\_vector set\_sel\_age3\_cRn3(1,7);

init\_vector set\_sel\_age4\_cRn3(1,7);

init\_vector set\_sel\_age5\_cRn3(1,7);

init\_vector set\_sel\_age6\_cRn3(1,7);

init\_vector set\_sel\_age0\_cRn4(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cRn4(1,7); //Commerical reduction fishery - north - block 4

init\_vector set\_sel\_age2\_cRn4(1,7);

init\_vector set\_sel\_age3\_cRn4(1,7);

init\_vector set\_sel\_age4\_cRn4(1,7);

init\_vector set\_sel\_age5\_cRn4(1,7);

init\_vector set\_sel\_age6\_cRn4(1,7);

init\_vector set\_sel\_age0\_cRs(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cRs(1,7); //Commerical reduction fishery - south - block 1

init\_vector set\_sel\_age2\_cRs(1,7);

init\_vector set\_sel\_age3\_cRs(1,7);

init\_vector set\_sel\_age4\_cRs(1,7);

init\_vector set\_sel\_age5\_cRs(1,7);

init\_vector set\_sel\_age6\_cRs(1,7);

init\_vector set\_sel\_age0\_cRs2(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cRs2(1,7); //Commerical reduction fishery - south - block 2

init\_vector set\_sel\_age2\_cRs2(1,7);

init\_vector set\_sel\_age3\_cRs2(1,7);

init\_vector set\_sel\_age4\_cRs2(1,7);

init\_vector set\_sel\_age5\_cRs2(1,7);

init\_vector set\_sel\_age6\_cRs2(1,7);

init\_vector set\_sel\_age0\_cRs3(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cRs3(1,7); //Commerical reduction fishery - south - block 3

init\_vector set\_sel\_age2\_cRs3(1,7);

init\_vector set\_sel\_age3\_cRs3(1,7);

init\_vector set\_sel\_age4\_cRs3(1,7);

init\_vector set\_sel\_age5\_cRs3(1,7);

init\_vector set\_sel\_age6\_cRs3(1,7);

init\_vector set\_sel\_age0\_cRs4(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cRs4(1,7); //Commerical reduction fishery - south - block 4

init\_vector set\_sel\_age2\_cRs4(1,7);

init\_vector set\_sel\_age3\_cRs4(1,7);

init\_vector set\_sel\_age4\_cRs4(1,7);

init\_vector set\_sel\_age5\_cRs4(1,7);

init\_vector set\_sel\_age6\_cRs4(1,7);

init\_vector set\_sel\_age0\_cBn(1,7); //input in logit space by age

init\_vector set\_sel\_age1\_cBn(1,7); //Commerical bait fishery - north - block 1

init\_vector set\_sel\_age2\_cBn(1,7);

init\_vector set\_sel\_age3\_cBn(1,7);

init\_vector set\_sel\_age4\_cBn(1,7);

init\_vector set\_sel\_age5\_cBn(1,7);

init\_vector set\_sel\_age6\_cBn(1,7);

```
init_vector set_sel_age0_cBn2(1,7); //input in logit space by age
init_vector set_sel_age1_cBn2(1,7); //Commerical bait fishery - north - block 2
init_vector set_sel_age2_cBn2(1,7);
init_vector set_sel_age3_cBn2(1,7);
init_vector set_sel_age4_cBn2(1,7);
init_vector set_sel_age5_cBn2(1,7);
init_vector set_sel_age6_cBn2(1,7);
```

```
init_vector set_sel_age0_cBs(1,7); //input in logit space by age
init_vector set_sel_age1_cBs(1,7); //Commerical bait fishery - south - block 1
init_vector set_sel_age2_cBs(1,7);
init_vector set_sel_age3_cBs(1,7);
init_vector set_sel_age4_cBs(1,7);
init_vector set_sel_age5_cBs(1,7);
init_vector set_sel_age6_cBs(1,7);
```

```
init_vector set_sel_age0_cBs2(1,7); //input in logit space by age
init_vector set_sel_age1_cBs2(1,7); //Commerical bait fishery - south - block 2
init_vector set_sel_age2_cBs2(1,7);
init_vector set_sel_age3_cBs2(1,7);
init_vector set_sel_age4_cBs2(1,7);
init_vector set_sel_age5_cBs2(1,7);
init_vector set_sel_age6_cBs2(1,7);
```

```
init_vector set_selpar_A50_nad(1,7); //parameters for northern adult index (NAD)
init_vector set_selpar_slope_nad(1,7); //double logistic or logistic
init_vector set_selpar_A502_nad(1,7);
init_vector set_selpar_slope2_nad(1,7);
```

```
init_vector set_selpar_A50_mad(1,7); //parameters for middle adult index (MAD)
init_vector set_selpar_slope_mad(1,7); //double logistic or logistic
init_vector set_selpar_A502_mad(1,7);
init_vector set_selpar_slope2_mad(1,7);
```

```
init_vector set_selpar_A50_sad(1,7); //parameters for southern adult index (SAD)
init_vector set_selpar_slope_sad(1,7); //double logistic or logistic
init_vector set_selpar_A502_sad(1,7);
init_vector set_selpar_slope2_sad(1,7);
```

```
init_vector set_sel_age0_nad(1,7); //input in logit space by age
init_vector set_sel_age1_nad(1,7); //NAD index
init_vector set_sel_age2_nad(1,7);
init_vector set_sel_age3_nad(1,7);
init_vector set_sel_age4_nad(1,7);
init_vector set_sel_age5_nad(1,7);
init_vector set_sel_age6_nad(1,7);
```

```
init_vector set_sel_age0_mad(1,7); //input in logit space by age
init_vector set_sel_age1_mad(1,7); //MAD index
init_vector set_sel_age2_mad(1,7);
init_vector set_sel_age3_mad(1,7);
init_vector set_sel_age4_mad(1,7);
init_vector set_sel_age5_mad(1,7);
init_vector set_sel_age6_mad(1,7);
```

```
init_vector set_sel_age0_sad(1,7); //input in logit space by age
init_vector set_sel_age1_sad(1,7); //SAD index
init_vector set_sel_age2_sad(1,7);
init_vector set_sel_age3_sad(1,7);
init_vector set_sel_age4_sad(1,7);
init_vector set_sel_age5_sad(1,7);
init_vector set_sel_age6_sad(1,7);
```

```
//--index catchability-----
```

```
init_vector set_log_q_nad(1,7); //catchability coefficient (log) for NAD index
init_vector set_log_q_mad(1,7); //catchability coefficient (log) for MAD index
init_vector set_log_q_sad(1,7); //catchability coefficient (log) for SAD index
init_vector set_log_q_jai(1,7); //catchability coefficient (log) for JAI index
init_vector set_log_q2_jai(1,7); //catchability coefficient (log) for JAI index
```







```

init_matrix tv_fecundity(styr,endyr,1,nages); //time-varying fecundity at age
init_vector wgt_spawn(1,nages); //weight at age at spawning
init_matrix tv_wgt_spawn(styr,endyr,1,nages); //time-varying weight at age at spawning
init_vector wgt_middle(1,nages); //weight at age at middle of year
init_matrix tv_wgt_middle(styr,endyr,1,nages); //time-varying weight at age at the middle of fishing year
init_matrix tv_len_apr15(styr,endyr,1,nages); //time-varying length at age on May 15
init_matrix tv_len_jun1(styr,endyr,1,nages); //time-varying length at age on June 1
init_matrix tv_len_oct15(styr,endyr,1,nages); //time-varying length at age on Oct 15
init_number spawn_time_frac; //time of year of peak spawning, as a fraction of the year

// Natural mortality
init_vector set_M(1,nages); //age-dependent: used in model
init_matrix set_tv_M(styr,endyr,1,nages); //time-varying and age-varying natural mortality

//Spawner-recruit parameters (Initial guesses or fixed values)
init_int SR_switch;

//rate of increase on q
init_int set_q_rate_phase; //value sets estimation phase of rate increase, negative value turns it off
init_number set_q_rate;

//density dependence on fishery q's
init_int set_q_DD_phase; //value sets estimation phase of random walk, negative value turns it off
init_number set_q_DD_beta; //value of 0.0 is density independent
init_number set_q_DD_beta_se;
init_int set_q_DD_stage; //age to begin counting biomass, should be near full exploitation

//random walk on fishery q's
init_number set_RWq_var; //assumed variance of RW q

//Tune Fapex (tuning removed in final year of optimization)
init_number set_Ftune;
init_int set_Ftune_yr;

//threshold sample sizes for length comps

```

```

init_number minSS_nad_lenc;
init_number minSS_mad_lenc;
//init_number minSS_sad_lenc;

//threshold sample sizes for age comps
init_number minSS_cRn_agec;
init_number minSS_cRs_agec;
init_number minSS_cBn_agec;
init_number minSS_cBs_agec;

//input for deterministic F-based projections
init_int endyr_proj; //last year of projections, by default, first year is endyr+1
init_int styr_regs; //apply current F until styr_regs, then the projection F
init_int Fproj_switch; //Value to use for Fproj: 1=current F, 2=Fmsy, 3=F30, 4=F40
init_number Fproj_mult; //multiplier to the Fproj
int styr_proj;
LOCAL_CALCS
  styr_proj=endyr+1;
END_CALCS

//ageing error matrix (columns are true ages, rows are ages as read for age comps: columns should sum to one)
init_matrix age_error(1,nages,1,nages);

// #####Indexing integers for year(iyear), age(iage),length(ilen) #####
int iyear;
int iage;
int ilen;
int ff;

number sqrt2pi;
number g2mt;          //conversion of grams to metric tons
number g2kg;          //conversion of grams to kg
number g2klb;         //conversion of grams to 1000 lb
number mt2klb;        //conversion of metric tons to 1000 lb
number mt2lb;         //conversion of metric tons to lb

```

```
number dzero;          //small additive constant to prevent division by zero
number huge_number;    //huge number, to avoid irregular parameter space
```

```
init_number end_of_data_file;
```

```
//!cout << "start year of reduction landings " << styr_cRn_L << endl;
```

```
//!cout << "Start year of JAI " << styr_jai_cpue << endl;
```

```
//!cout << "Linf set up " << set_Linf << endl;
```

```
//!cout << "start year of cBs " << styr_cBs_L << endl;
```

```
//!cout << "start year of cRs " << styr_cRs_L << endl;
```

```
//!cout << "start year of cBn " << styr_cBn_L << endl;
```

```
//this section MUST BE INDENTED!!!
```

```
LOCAL_CALCS
```

```
if(end_of_data_file!=999)
```

```
{
```

```
    cout << "*** WARNING: Data File NOT READ CORRECTLY ***" << endl;
```

```
    exit(0);
```

```
}
```

```
else
```

```
{cout << "Data File read correctly" << endl;}
```

```
END_CALCS
```

```
PARAMETER_SECTION
```

```
LOCAL_CALCS
```

```
const double Linf_LO=set_Linf(2); const double Linf_HI=set_Linf(3); const double Linf_PH=set_Linf(4);
```

```
const double K_LO=set_K(2); const double K_HI=set_K(3); const double K_PH=set_K(4);
```

```
const double t0_LO=set_t0(2); const double t0_HI=set_t0(3); const double t0_PH=set_t0(4);
```

```
const double len_cv_nad_LO=set_len_cv_nad(2); const double len_cv_nad_HI=set_len_cv_nad(3); const double len_cv_nad_PH=set_len_cv_nad(4);
```

```
const double len_cv_mad_LO=set_len_cv_mad(2); const double len_cv_mad_HI=set_len_cv_mad(3); const double len_cv_mad_PH=set_len_cv_mad(4);
```

```
//const double len_cv_sad_LO=set_len_cv_sad(2); const double len_cv_sad_HI=set_len_cv_sad(3); const double len_cv_sad_PH=set_len_cv_sad(4);
```

const double steep\_LO=set\_steep(2); const double steep\_HI=set\_steep(3); const double steep\_PH=set\_steep(4);  
const double log\_R0\_LO=set\_log\_R0(2); const double log\_R0\_HI=set\_log\_R0(3); const double  
log\_R0\_PH=set\_log\_R0(4);

const double R\_autocorr\_LO=set\_R\_autocorr(2); const double R\_autocorr\_HI=set\_R\_autocorr(3); const double  
R\_autocorr\_PH=set\_R\_autocorr(4);

const double rec\_sigma\_LO=set\_rec\_sigma(2); const double rec\_sigma\_HI=set\_rec\_sigma(3); const double  
rec\_sigma\_PH=set\_rec\_sigma(4);

const double log\_dm\_cRn\_ac\_LO=set\_log\_dm\_cRn\_ac(2); const double  
log\_dm\_cRn\_ac\_HI=set\_log\_dm\_cRn\_ac(3); const double log\_dm\_cRn\_ac\_PH=set\_log\_dm\_cRn\_ac(4);

const double log\_dm\_cRs\_ac\_LO=set\_log\_dm\_cRs\_ac(2); const double  
log\_dm\_cRs\_ac\_HI=set\_log\_dm\_cRs\_ac(3); const double log\_dm\_cRs\_ac\_PH=set\_log\_dm\_cRs\_ac(4);

const double log\_dm\_cBn\_ac\_LO=set\_log\_dm\_cBn\_ac(2); const double  
log\_dm\_cBn\_ac\_HI=set\_log\_dm\_cBn\_ac(3); const double log\_dm\_cBn\_ac\_PH=set\_log\_dm\_cBn\_ac(4);

const double log\_dm\_cBs\_ac\_LO=set\_log\_dm\_cBs\_ac(2); const double  
log\_dm\_cBs\_ac\_HI=set\_log\_dm\_cBs\_ac(3); const double log\_dm\_cBs\_ac\_PH=set\_log\_dm\_cBs\_ac(4);

const double log\_dm\_nad\_lc\_LO=set\_log\_dm\_nad\_lc(2); const double log\_dm\_nad\_lc\_HI=set\_log\_dm\_nad\_lc(3);  
const double log\_dm\_nad\_lc\_PH=set\_log\_dm\_nad\_lc(4);

const double log\_dm\_mad\_lc\_LO=set\_log\_dm\_mad\_lc(2); const double  
log\_dm\_mad\_lc\_HI=set\_log\_dm\_mad\_lc(3); const double log\_dm\_mad\_lc\_PH=set\_log\_dm\_mad\_lc(4);

//const double log\_dm\_sad\_lc\_LO=set\_log\_dm\_sad\_lc(2); const double  
log\_dm\_sad\_lc\_HI=set\_log\_dm\_sad\_lc(3); const double log\_dm\_sad\_lc\_PH=set\_log\_dm\_sad\_lc(4);

const double selpar\_A50\_cRn\_LO=set\_selpar\_A50\_cRn(2); const double  
selpar\_A50\_cRn\_HI=set\_selpar\_A50\_cRn(3); const double selpar\_A50\_cRn\_PH=set\_selpar\_A50\_cRn(4);

const double selpar\_slope\_cRn\_LO=set\_selpar\_slope\_cRn(2); const double  
selpar\_slope\_cRn\_HI=set\_selpar\_slope\_cRn(3); const double selpar\_slope\_cRn\_PH=set\_selpar\_slope\_cRn(4);

const double selpar\_A502\_cRn\_LO=set\_selpar\_A502\_cRn(2); const double  
selpar\_A502\_cRn\_HI=set\_selpar\_A502\_cRn(3); const double selpar\_A502\_cRn\_PH=set\_selpar\_A502\_cRn(4);

const double selpar\_slope2\_cRn\_LO=set\_selpar\_slope2\_cRn(2); const double  
selpar\_slope2\_cRn\_HI=set\_selpar\_slope2\_cRn(3); const double selpar\_slope2\_cRn\_PH=set\_selpar\_slope2\_cRn(4);

const double selpar\_A50\_cRn2\_LO=set\_selpar\_A50\_cRn2(2); const double  
selpar\_A50\_cRn2\_HI=set\_selpar\_A50\_cRn2(3); const double selpar\_A50\_cRn2\_PH=set\_selpar\_A50\_cRn2(4);

const double selpar\_slope\_cRn2\_LO=set\_selpar\_slope\_cRn2(2); const double  
selpar\_slope\_cRn2\_HI=set\_selpar\_slope\_cRn2(3); const double selpar\_slope\_cRn2\_PH=set\_selpar\_slope\_cRn2(4);

const double selpar\_A502\_cRn2\_LO=set\_selpar\_A502\_cRn2(2); const double  
selpar\_A502\_cRn2\_HI=set\_selpar\_A502\_cRn2(3); const double selpar\_A502\_cRn2\_PH=set\_selpar\_A502\_cRn2(4);

const double selpar\_slope2\_cRn2\_LO=set\_selpar\_slope2\_cRn2(2); const double  
selpar\_slope2\_cRn2\_HI=set\_selpar\_slope2\_cRn2(3); const double  
selpar\_slope2\_cRn2\_PH=set\_selpar\_slope2\_cRn2(4);

const double selpar\_A50\_cRn3\_LO=set\_selpar\_A50\_cRn3(2); const double  
selpar\_A50\_cRn3\_HI=set\_selpar\_A50\_cRn3(3); const double selpar\_A50\_cRn3\_PH=set\_selpar\_A50\_cRn3(4);

const double selpar\_slope\_cRn3\_LO=set\_selpar\_slope\_cRn3(2); const double  
selpar\_slope\_cRn3\_HI=set\_selpar\_slope\_cRn3(3); const double selpar\_slope\_cRn3\_PH=set\_selpar\_slope\_cRn3(4);

const double selpar\_A502\_cRn3\_LO=set\_selpar\_A502\_cRn3(2); const double  
selpar\_A502\_cRn3\_HI=set\_selpar\_A502\_cRn3(3); const double selpar\_A502\_cRn3\_PH=set\_selpar\_A502\_cRn3(4);

const double selpar\_slope2\_cRn3\_LO=set\_selpar\_slope2\_cRn3(2); const double  
selpar\_slope2\_cRn3\_HI=set\_selpar\_slope2\_cRn3(3); const double  
selpar\_slope2\_cRn3\_PH=set\_selpar\_slope2\_cRn3(4);

const double selpar\_A50\_cRn4\_LO=set\_selpar\_A50\_cRn4(2); const double  
selpar\_A50\_cRn4\_HI=set\_selpar\_A50\_cRn4(3); const double selpar\_A50\_cRn4\_PH=set\_selpar\_A50\_cRn4(4);

const double selpar\_slope\_cRn4\_LO=set\_selpar\_slope\_cRn4(2); const double  
selpar\_slope\_cRn4\_HI=set\_selpar\_slope\_cRn4(3); const double selpar\_slope\_cRn4\_PH=set\_selpar\_slope\_cRn4(4);

const double selpar\_A502\_cRn4\_LO=set\_selpar\_A502\_cRn4(2); const double  
selpar\_A502\_cRn4\_HI=set\_selpar\_A502\_cRn4(3); const double selpar\_A502\_cRn4\_PH=set\_selpar\_A502\_cRn4(4);

const double selpar\_slope2\_cRn4\_LO=set\_selpar\_slope2\_cRn4(2); const double  
selpar\_slope2\_cRn4\_HI=set\_selpar\_slope2\_cRn4(3); const double  
selpar\_slope2\_cRn4\_PH=set\_selpar\_slope2\_cRn4(4);

const double selpar\_A50\_cRs\_LO=set\_selpar\_A50\_cRs(2); const double  
selpar\_A50\_cRs\_HI=set\_selpar\_A50\_cRs(3); const double selpar\_A50\_cRs\_PH=set\_selpar\_A50\_cRs(4);

const double selpar\_slope\_cRs\_LO=set\_selpar\_slope\_cRs(2); const double  
selpar\_slope\_cRs\_HI=set\_selpar\_slope\_cRs(3); const double selpar\_slope\_cRs\_PH=set\_selpar\_slope\_cRs(4);

const double selpar\_A502\_cRs\_LO=set\_selpar\_A502\_cRs(2); const double  
selpar\_A502\_cRs\_HI=set\_selpar\_A502\_cRs(3); const double selpar\_A502\_cRs\_PH=set\_selpar\_A502\_cRs(4);

const double selpar\_slope2\_cRs\_LO=set\_selpar\_slope2\_cRs(2); const double  
selpar\_slope2\_cRs\_HI=set\_selpar\_slope2\_cRs(3); const double selpar\_slope2\_cRs\_PH=set\_selpar\_slope2\_cRs(4);

const double selpar\_A50\_cRs2\_LO=set\_selpar\_A50\_cRs2(2); const double  
selpar\_A50\_cRs2\_HI=set\_selpar\_A50\_cRs2(3); const double selpar\_A50\_cRs2\_PH=set\_selpar\_A50\_cRs2(4);

const double selpar\_slope\_cRs2\_LO=set\_selpar\_slope\_cRs2(2); const double  
selpar\_slope\_cRs2\_HI=set\_selpar\_slope\_cRs2(3); const double selpar\_slope\_cRs2\_PH=set\_selpar\_slope\_cRs2(4);

const double selpar\_A502\_cRs2\_LO=set\_selpar\_A502\_cRs2(2); const double  
selpar\_A502\_cRs2\_HI=set\_selpar\_A502\_cRs2(3); const double selpar\_A502\_cRs2\_PH=set\_selpar\_A502\_cRs2(4);

const double selpar\_slope2\_cRs2\_LO=set\_selpar\_slope2\_cRs2(2); const double  
selpar\_slope2\_cRs2\_HI=set\_selpar\_slope2\_cRs2(3); const double  
selpar\_slope2\_cRs2\_PH=set\_selpar\_slope2\_cRs2(4);

const double selpar\_A50\_cRs3\_LO=set\_selpar\_A50\_cRs3(2); const double  
selpar\_A50\_cRs3\_HI=set\_selpar\_A50\_cRs3(3); const double selpar\_A50\_cRs3\_PH=set\_selpar\_A50\_cRs3(4);

const double selpar\_slope\_cRs3\_LO=set\_selpar\_slope\_cRs3(2); const double  
selpar\_slope\_cRs3\_HI=set\_selpar\_slope\_cRs3(3); const double selpar\_slope\_cRs3\_PH=set\_selpar\_slope\_cRs3(4);

const double selpar\_A502\_cRs3\_LO=set\_selpar\_A502\_cRs3(2); const double  
selpar\_A502\_cRs3\_HI=set\_selpar\_A502\_cRs3(3); const double selpar\_A502\_cRs3\_PH=set\_selpar\_A502\_cRs3(4);

const double selpar\_slope2\_cRs3\_LO=set\_selpar\_slope2\_cRs3(2); const double  
selpar\_slope2\_cRs3\_HI=set\_selpar\_slope2\_cRs3(3); const double  
selpar\_slope2\_cRs3\_PH=set\_selpar\_slope2\_cRs3(4);

const double selpar\_A50\_cRs4\_LO=set\_selpar\_A50\_cRs4(2); const double  
selpar\_A50\_cRs4\_HI=set\_selpar\_A50\_cRs4(3); const double selpar\_A50\_cRs4\_PH=set\_selpar\_A50\_cRs4(4);

const double selpar\_slope\_cRs4\_LO=set\_selpar\_slope\_cRs4(2); const double  
selpar\_slope\_cRs4\_HI=set\_selpar\_slope\_cRs4(3); const double selpar\_slope\_cRs4\_PH=set\_selpar\_slope\_cRs4(4);

const double selpar\_A502\_cRs4\_LO=set\_selpar\_A502\_cRs4(2); const double  
selpar\_A502\_cRs4\_HI=set\_selpar\_A502\_cRs4(3); const double selpar\_A502\_cRs4\_PH=set\_selpar\_A502\_cRs4(4);

const double selpar\_slope2\_cRs4\_LO=set\_selpar\_slope2\_cRs4(2); const double  
selpar\_slope2\_cRs4\_HI=set\_selpar\_slope2\_cRs4(3); const double  
selpar\_slope2\_cRs4\_PH=set\_selpar\_slope2\_cRs4(4);

const double selpar\_A50\_cBn\_LO=set\_selpar\_A50\_cBn(2); const double  
selpar\_A50\_cBn\_HI=set\_selpar\_A50\_cBn(3); const double selpar\_A50\_cBn\_PH=set\_selpar\_A50\_cBn(4);

const double selpar\_slope\_cBn\_LO=set\_selpar\_slope\_cBn(2); const double  
selpar\_slope\_cBn\_HI=set\_selpar\_slope\_cBn(3); const double selpar\_slope\_cBn\_PH=set\_selpar\_slope\_cBn(4);

const double selpar\_A502\_cBn\_LO=set\_selpar\_A502\_cBn(2); const double  
selpar\_A502\_cBn\_HI=set\_selpar\_A502\_cBn(3); const double selpar\_A502\_cBn\_PH=set\_selpar\_A502\_cBn(4);

const double selpar\_slope2\_cBn\_LO=set\_selpar\_slope2\_cBn(2); const double  
selpar\_slope2\_cBn\_HI=set\_selpar\_slope2\_cBn(3); const double selpar\_slope2\_cBn\_PH=set\_selpar\_slope2\_cBn(4);

const double selpar\_A50\_cBn2\_LO=set\_selpar\_A50\_cBn2(2); const double  
selpar\_A50\_cBn2\_HI=set\_selpar\_A50\_cBn2(3); const double selpar\_A50\_cBn2\_PH=set\_selpar\_A50\_cBn2(4);

const double selpar\_slope\_cBn2\_LO=set\_selpar\_slope\_cBn2(2); const double  
selpar\_slope\_cBn2\_HI=set\_selpar\_slope\_cBn2(3); const double selpar\_slope\_cBn2\_PH=set\_selpar\_slope\_cBn2(4);

const double selpar\_A502\_cBn2\_LO=set\_selpar\_A502\_cBn2(2); const double  
selpar\_A502\_cBn2\_HI=set\_selpar\_A502\_cBn2(3); const double selpar\_A502\_cBn2\_PH=set\_selpar\_A502\_cBn2(4);

const double selpar\_slope2\_cBn2\_LO=set\_selpar\_slope2\_cBn2(2); const double  
selpar\_slope2\_cBn2\_HI=set\_selpar\_slope2\_cBn2(3); const double  
selpar\_slope2\_cBn2\_PH=set\_selpar\_slope2\_cBn2(4);

const double selpar\_A50\_cBs\_LO=set\_selpar\_A50\_cBs(2); const double  
selpar\_A50\_cBs\_HI=set\_selpar\_A50\_cBs(3); const double selpar\_A50\_cBs\_PH=set\_selpar\_A50\_cBs(4);



const double selpar\_slope\_cBs\_LO=set\_selpar\_slope\_cBs(2); const double  
selpar\_slope\_cBs\_HI=set\_selpar\_slope\_cBs(3); const double selpar\_slope\_cBs\_PH=set\_selpar\_slope\_cBs(4);

const double selpar\_A502\_cBs\_LO=set\_selpar\_A502\_cBs(2); const double  
selpar\_A502\_cBs\_HI=set\_selpar\_A502\_cBs(3); const double selpar\_A502\_cBs\_PH=set\_selpar\_A502\_cBs(4);

const double selpar\_slope2\_cBs\_LO=set\_selpar\_slope2\_cBs(2); const double  
selpar\_slope2\_cBs\_HI=set\_selpar\_slope2\_cBs(3); const double selpar\_slope2\_cBs\_PH=set\_selpar\_slope2\_cBs(4);

const double selpar\_A50\_cBs2\_LO=set\_selpar\_A50\_cBs2(2); const double  
selpar\_A50\_cBs2\_HI=set\_selpar\_A50\_cBs2(3); const double selpar\_A50\_cBs2\_PH=set\_selpar\_A50\_cBs2(4);

const double selpar\_slope\_cBs2\_LO=set\_selpar\_slope\_cBs2(2); const double  
selpar\_slope\_cBs2\_HI=set\_selpar\_slope\_cBs2(3); const double selpar\_slope\_cBs2\_PH=set\_selpar\_slope\_cBs2(4);

const double selpar\_A502\_cBs2\_LO=set\_selpar\_A502\_cBs2(2); const double  
selpar\_A502\_cBs2\_HI=set\_selpar\_A502\_cBs2(3); const double selpar\_A502\_cBs2\_PH=set\_selpar\_A502\_cBs2(4);

const double selpar\_slope2\_cBs2\_LO=set\_selpar\_slope2\_cBs2(2); const double  
selpar\_slope2\_cBs2\_HI=set\_selpar\_slope2\_cBs2(3); const double  
selpar\_slope2\_cBs2\_PH=set\_selpar\_slope2\_cBs2(4);

const double selpar\_age0\_cRn\_LO=set\_sel\_age0\_cRn(2); const double selpar\_age0\_cRn\_HI=set\_sel\_age0\_cRn(3);  
const double selpar\_age0\_cRn\_PH=set\_sel\_age0\_cRn(4);

const double selpar\_age1\_cRn\_LO=set\_sel\_age1\_cRn(2); const double selpar\_age1\_cRn\_HI=set\_sel\_age1\_cRn(3);  
const double selpar\_age1\_cRn\_PH=set\_sel\_age1\_cRn(4);

const double selpar\_age2\_cRn\_LO=set\_sel\_age2\_cRn(2); const double selpar\_age2\_cRn\_HI=set\_sel\_age2\_cRn(3);  
const double selpar\_age2\_cRn\_PH=set\_sel\_age2\_cRn(4);

const double selpar\_age3\_cRn\_LO=set\_sel\_age3\_cRn(2); const double selpar\_age3\_cRn\_HI=set\_sel\_age3\_cRn(3);  
const double selpar\_age3\_cRn\_PH=set\_sel\_age3\_cRn(4);

const double selpar\_age4\_cRn\_LO=set\_sel\_age4\_cRn(2); const double selpar\_age4\_cRn\_HI=set\_sel\_age4\_cRn(3);  
const double selpar\_age4\_cRn\_PH=set\_sel\_age4\_cRn(4);

const double selpar\_age5\_cRn\_LO=set\_sel\_age5\_cRn(2); const double selpar\_age5\_cRn\_HI=set\_sel\_age5\_cRn(3);  
const double selpar\_age5\_cRn\_PH=set\_sel\_age5\_cRn(4);

const double selpar\_age6\_cRn\_LO=set\_sel\_age6\_cRn(2); const double selpar\_age6\_cRn\_HI=set\_sel\_age6\_cRn(3);  
const double selpar\_age6\_cRn\_PH=set\_sel\_age6\_cRn(4);

const double selpar\_age0\_cRn2\_LO=set\_sel\_age0\_cRn2(2); const double  
selpar\_age0\_cRn2\_HI=set\_sel\_age0\_cRn2(3); const double selpar\_age0\_cRn2\_PH=set\_sel\_age0\_cRn2(4);

const double selpar\_age1\_cRn2\_LO=set\_sel\_age1\_cRn2(2); const double  
selpar\_age1\_cRn2\_HI=set\_sel\_age1\_cRn2(3); const double selpar\_age1\_cRn2\_PH=set\_sel\_age1\_cRn2(4);

const double selpar\_age2\_cRn2\_LO=set\_sel\_age2\_cRn2(2); const double  
selpar\_age2\_cRn2\_HI=set\_sel\_age2\_cRn2(3); const double selpar\_age2\_cRn2\_PH=set\_sel\_age2\_cRn2(4);

const double selpar\_age3\_cRn2\_LO=set\_sel\_age3\_cRn2(2); const double  
selpar\_age3\_cRn2\_HI=set\_sel\_age3\_cRn2(3); const double selpar\_age3\_cRn2\_PH=set\_sel\_age3\_cRn2(4);

const double selpar\_age4\_cRn2\_LO=set\_sel\_age4\_cRn2(2); const double  
selpar\_age4\_cRn2\_HI=set\_sel\_age4\_cRn2(3); const double selpar\_age4\_cRn2\_PH=set\_sel\_age4\_cRn2(4);

const double selpar\_age5\_cRn2\_LO=set\_sel\_age5\_cRn2(2); const double  
selpar\_age5\_cRn2\_HI=set\_sel\_age5\_cRn2(3); const double selpar\_age5\_cRn2\_PH=set\_sel\_age5\_cRn2(4);

const double selpar\_age6\_cRn2\_LO=set\_sel\_age6\_cRn2(2); const double  
selpar\_age6\_cRn2\_HI=set\_sel\_age6\_cRn2(3); const double selpar\_age6\_cRn2\_PH=set\_sel\_age6\_cRn2(4);

const double selpar\_age0\_cRn3\_LO=set\_sel\_age0\_cRn3(2); const double  
selpar\_age0\_cRn3\_HI=set\_sel\_age0\_cRn3(3); const double selpar\_age0\_cRn3\_PH=set\_sel\_age0\_cRn3(4);

const double selpar\_age1\_cRn3\_LO=set\_sel\_age1\_cRn3(2); const double  
selpar\_age1\_cRn3\_HI=set\_sel\_age1\_cRn3(3); const double selpar\_age1\_cRn3\_PH=set\_sel\_age1\_cRn3(4);

const double selpar\_age2\_cRn3\_LO=set\_sel\_age2\_cRn3(2); const double  
selpar\_age2\_cRn3\_HI=set\_sel\_age2\_cRn3(3); const double selpar\_age2\_cRn3\_PH=set\_sel\_age2\_cRn3(4);

const double selpar\_age3\_cRn3\_LO=set\_sel\_age3\_cRn3(2); const double  
selpar\_age3\_cRn3\_HI=set\_sel\_age3\_cRn3(3); const double selpar\_age3\_cRn3\_PH=set\_sel\_age3\_cRn3(4);

const double selpar\_age4\_cRn3\_LO=set\_sel\_age4\_cRn3(2); const double  
selpar\_age4\_cRn3\_HI=set\_sel\_age4\_cRn3(3); const double selpar\_age4\_cRn3\_PH=set\_sel\_age4\_cRn3(4);

const double selpar\_age5\_cRn3\_LO=set\_sel\_age5\_cRn3(2); const double  
selpar\_age5\_cRn3\_HI=set\_sel\_age5\_cRn3(3); const double selpar\_age5\_cRn3\_PH=set\_sel\_age5\_cRn3(4);

const double selpar\_age6\_cRn3\_LO=set\_sel\_age6\_cRn3(2); const double  
selpar\_age6\_cRn3\_HI=set\_sel\_age6\_cRn3(3); const double selpar\_age6\_cRn3\_PH=set\_sel\_age6\_cRn3(4);

const double selpar\_age0\_cRn4\_LO=set\_sel\_age0\_cRn4(2); const double  
selpar\_age0\_cRn4\_HI=set\_sel\_age0\_cRn4(3); const double selpar\_age0\_cRn4\_PH=set\_sel\_age0\_cRn4(4);

const double selpar\_age1\_cRn4\_LO=set\_sel\_age1\_cRn4(2); const double  
selpar\_age1\_cRn4\_HI=set\_sel\_age1\_cRn4(3); const double selpar\_age1\_cRn4\_PH=set\_sel\_age1\_cRn4(4);

const double selpar\_age2\_cRn4\_LO=set\_sel\_age2\_cRn4(2); const double  
selpar\_age2\_cRn4\_HI=set\_sel\_age2\_cRn4(3); const double selpar\_age2\_cRn4\_PH=set\_sel\_age2\_cRn4(4);

const double selpar\_age3\_cRn4\_LO=set\_sel\_age3\_cRn4(2); const double  
selpar\_age3\_cRn4\_HI=set\_sel\_age3\_cRn4(3); const double selpar\_age3\_cRn4\_PH=set\_sel\_age3\_cRn4(4);

const double selpar\_age4\_cRn4\_LO=set\_sel\_age4\_cRn4(2); const double  
selpar\_age4\_cRn4\_HI=set\_sel\_age4\_cRn4(3); const double selpar\_age4\_cRn4\_PH=set\_sel\_age4\_cRn4(4);

const double selpar\_age5\_cRn4\_LO=set\_sel\_age5\_cRn4(2); const double  
selpar\_age5\_cRn4\_HI=set\_sel\_age5\_cRn4(3); const double selpar\_age5\_cRn4\_PH=set\_sel\_age5\_cRn4(4);

const double selpar\_age6\_cRn4\_LO=set\_sel\_age6\_cRn4(2); const double  
selpar\_age6\_cRn4\_HI=set\_sel\_age6\_cRn4(3); const double selpar\_age6\_cRn4\_PH=set\_sel\_age6\_cRn4(4);

const double selpar\_age0\_cRs\_LO=set\_sel\_age0\_cRs(2); const double selpar\_age0\_cRs\_HI=set\_sel\_age0\_cRs(3);  
const double selpar\_age0\_cRs\_PH=set\_sel\_age0\_cRs(4);

const double selpar\_age1\_cRs\_LO=set\_sel\_age1\_cRs(2); const double selpar\_age1\_cRs\_HI=set\_sel\_age1\_cRs(3);  
const double selpar\_age1\_cRs\_PH=set\_sel\_age1\_cRs(4);

const double selpar\_age2\_cRs\_LO=set\_sel\_age2\_cRs(2); const double selpar\_age2\_cRs\_HI=set\_sel\_age2\_cRs(3);  
const double selpar\_age2\_cRs\_PH=set\_sel\_age2\_cRs(4);



const double selpar\_age1\_cRs4\_LO=set\_sel\_age1\_cRs4(2); const double  
selpar\_age1\_cRs4\_HI=set\_sel\_age1\_cRs4(3); const double selpar\_age1\_cRs4\_PH=set\_sel\_age1\_cRs4(4);

const double selpar\_age2\_cRs4\_LO=set\_sel\_age2\_cRs4(2); const double  
selpar\_age2\_cRs4\_HI=set\_sel\_age2\_cRs4(3); const double selpar\_age2\_cRs4\_PH=set\_sel\_age2\_cRs4(4);

const double selpar\_age3\_cRs4\_LO=set\_sel\_age3\_cRs4(2); const double  
selpar\_age3\_cRs4\_HI=set\_sel\_age3\_cRs4(3); const double selpar\_age3\_cRs4\_PH=set\_sel\_age3\_cRs4(4);

const double selpar\_age4\_cRs4\_LO=set\_sel\_age4\_cRs4(2); const double  
selpar\_age4\_cRs4\_HI=set\_sel\_age4\_cRs4(3); const double selpar\_age4\_cRs4\_PH=set\_sel\_age4\_cRs4(4);

const double selpar\_age5\_cRs4\_LO=set\_sel\_age5\_cRs4(2); const double  
selpar\_age5\_cRs4\_HI=set\_sel\_age5\_cRs4(3); const double selpar\_age5\_cRs4\_PH=set\_sel\_age5\_cRs4(4);

const double selpar\_age6\_cRs4\_LO=set\_sel\_age6\_cRs4(2); const double  
selpar\_age6\_cRs4\_HI=set\_sel\_age6\_cRs4(3); const double selpar\_age6\_cRs4\_PH=set\_sel\_age6\_cRs4(4);

const double selpar\_age0\_cBn\_LO=set\_sel\_age0\_cBn(2); const double selpar\_age0\_cBn\_HI=set\_sel\_age0\_cBn(3);  
const double selpar\_age0\_cBn\_PH=set\_sel\_age0\_cBn(4);

const double selpar\_age1\_cBn\_LO=set\_sel\_age1\_cBn(2); const double selpar\_age1\_cBn\_HI=set\_sel\_age1\_cBn(3);  
const double selpar\_age1\_cBn\_PH=set\_sel\_age1\_cBn(4);

const double selpar\_age2\_cBn\_LO=set\_sel\_age2\_cBn(2); const double selpar\_age2\_cBn\_HI=set\_sel\_age2\_cBn(3);  
const double selpar\_age2\_cBn\_PH=set\_sel\_age2\_cBn(4);

const double selpar\_age3\_cBn\_LO=set\_sel\_age3\_cBn(2); const double selpar\_age3\_cBn\_HI=set\_sel\_age3\_cBn(3);  
const double selpar\_age3\_cBn\_PH=set\_sel\_age3\_cBn(4);

const double selpar\_age4\_cBn\_LO=set\_sel\_age4\_cBn(2); const double selpar\_age4\_cBn\_HI=set\_sel\_age4\_cBn(3);  
const double selpar\_age4\_cBn\_PH=set\_sel\_age4\_cBn(4);

const double selpar\_age5\_cBn\_LO=set\_sel\_age5\_cBn(2); const double selpar\_age5\_cBn\_HI=set\_sel\_age5\_cBn(3);  
const double selpar\_age5\_cBn\_PH=set\_sel\_age5\_cBn(4);

const double selpar\_age6\_cBn\_LO=set\_sel\_age6\_cBn(2); const double selpar\_age6\_cBn\_HI=set\_sel\_age6\_cBn(3);  
const double selpar\_age6\_cBn\_PH=set\_sel\_age6\_cBn(4);

const double selpar\_age0\_cBn2\_LO=set\_sel\_age0\_cBn2(2); const double  
selpar\_age0\_cBn2\_HI=set\_sel\_age0\_cBn2(3); const double selpar\_age0\_cBn2\_PH=set\_sel\_age0\_cBn2(4);

const double selpar\_age1\_cBn2\_LO=set\_sel\_age1\_cBn2(2); const double  
selpar\_age1\_cBn2\_HI=set\_sel\_age1\_cBn2(3); const double selpar\_age1\_cBn2\_PH=set\_sel\_age1\_cBn2(4);

const double selpar\_age2\_cBn2\_LO=set\_sel\_age2\_cBn2(2); const double  
selpar\_age2\_cBn2\_HI=set\_sel\_age2\_cBn2(3); const double selpar\_age2\_cBn2\_PH=set\_sel\_age2\_cBn2(4);

const double selpar\_age3\_cBn2\_LO=set\_sel\_age3\_cBn2(2); const double  
selpar\_age3\_cBn2\_HI=set\_sel\_age3\_cBn2(3); const double selpar\_age3\_cBn2\_PH=set\_sel\_age3\_cBn2(4);

const double selpar\_age4\_cBn2\_LO=set\_sel\_age4\_cBn2(2); const double  
selpar\_age4\_cBn2\_HI=set\_sel\_age4\_cBn2(3); const double selpar\_age4\_cBn2\_PH=set\_sel\_age4\_cBn2(4);

const double selpar\_age5\_cBn2\_LO=set\_sel\_age5\_cBn2(2); const double  
selpar\_age5\_cBn2\_HI=set\_sel\_age5\_cBn2(3); const double selpar\_age5\_cBn2\_PH=set\_sel\_age5\_cBn2(4);

const double selpar\_age6\_cBn2\_LO=set\_sel\_age6\_cBn2(2); const double  
selpar\_age6\_cBn2\_HI=set\_sel\_age6\_cBn2(3); const double selpar\_age6\_cBn2\_PH=set\_sel\_age6\_cBn2(4);

const double selpar\_age0\_cBs\_LO=set\_sel\_age0\_cBs(2); const double selpar\_age0\_cBs\_HI=set\_sel\_age0\_cBs(3);  
const double selpar\_age0\_cBs\_PH=set\_sel\_age0\_cBs(4);

const double selpar\_age1\_cBs\_LO=set\_sel\_age1\_cBs(2); const double selpar\_age1\_cBs\_HI=set\_sel\_age1\_cBs(3);  
const double selpar\_age1\_cBs\_PH=set\_sel\_age1\_cBs(4);

const double selpar\_age2\_cBs\_LO=set\_sel\_age2\_cBs(2); const double selpar\_age2\_cBs\_HI=set\_sel\_age2\_cBs(3);  
const double selpar\_age2\_cBs\_PH=set\_sel\_age2\_cBs(4);

const double selpar\_age3\_cBs\_LO=set\_sel\_age3\_cBs(2); const double selpar\_age3\_cBs\_HI=set\_sel\_age3\_cBs(3);  
const double selpar\_age3\_cBs\_PH=set\_sel\_age3\_cBs(4);

const double selpar\_age4\_cBs\_LO=set\_sel\_age4\_cBs(2); const double selpar\_age4\_cBs\_HI=set\_sel\_age4\_cBs(3);  
const double selpar\_age4\_cBs\_PH=set\_sel\_age4\_cBs(4);

const double selpar\_age5\_cBs\_LO=set\_sel\_age5\_cBs(2); const double selpar\_age5\_cBs\_HI=set\_sel\_age5\_cBs(3);  
const double selpar\_age5\_cBs\_PH=set\_sel\_age5\_cBs(4);

const double selpar\_age6\_cBs\_LO=set\_sel\_age6\_cBs(2); const double selpar\_age6\_cBs\_HI=set\_sel\_age6\_cBs(3);  
const double selpar\_age6\_cBs\_PH=set\_sel\_age6\_cBs(4);

const double selpar\_age0\_cBs2\_LO=set\_sel\_age0\_cBs2(2); const double  
selpar\_age0\_cBs2\_HI=set\_sel\_age0\_cBs2(3); const double selpar\_age0\_cBs2\_PH=set\_sel\_age0\_cBs2(4);

const double selpar\_age1\_cBs2\_LO=set\_sel\_age1\_cBs2(2); const double  
selpar\_age1\_cBs2\_HI=set\_sel\_age1\_cBs2(3); const double selpar\_age1\_cBs2\_PH=set\_sel\_age1\_cBs2(4);

const double selpar\_age2\_cBs2\_LO=set\_sel\_age2\_cBs2(2); const double  
selpar\_age2\_cBs2\_HI=set\_sel\_age2\_cBs2(3); const double selpar\_age2\_cBs2\_PH=set\_sel\_age2\_cBs2(4);

const double selpar\_age3\_cBs2\_LO=set\_sel\_age3\_cBs2(2); const double  
selpar\_age3\_cBs2\_HI=set\_sel\_age3\_cBs2(3); const double selpar\_age3\_cBs2\_PH=set\_sel\_age3\_cBs2(4);

const double selpar\_age4\_cBs2\_LO=set\_sel\_age4\_cBs2(2); const double  
selpar\_age4\_cBs2\_HI=set\_sel\_age4\_cBs2(3); const double selpar\_age4\_cBs2\_PH=set\_sel\_age4\_cBs2(4);

const double selpar\_age5\_cBs2\_LO=set\_sel\_age5\_cBs2(2); const double  
selpar\_age5\_cBs2\_HI=set\_sel\_age5\_cBs2(3); const double selpar\_age5\_cBs2\_PH=set\_sel\_age5\_cBs2(4);

const double selpar\_age6\_cBs2\_LO=set\_sel\_age6\_cBs2(2); const double  
selpar\_age6\_cBs2\_HI=set\_sel\_age6\_cBs2(3); const double selpar\_age6\_cBs2\_PH=set\_sel\_age6\_cBs2(4);

const double selpar\_A50\_nad\_LO=set\_selpar\_A50\_nad(2); const double  
selpar\_A50\_nad\_HI=set\_selpar\_A50\_nad(3); const double selpar\_A50\_nad\_PH=set\_selpar\_A50\_nad(4);

const double selpar\_slope\_nad\_LO=set\_selpar\_slope\_nad(2); const double  
selpar\_slope\_nad\_HI=set\_selpar\_slope\_nad(3); const double selpar\_slope\_nad\_PH=set\_selpar\_slope\_nad(4);

const double selpar\_A502\_nad\_LO=set\_selpar\_A502\_nad(2); const double  
selpar\_A502\_nad\_HI=set\_selpar\_A502\_nad(3); const double selpar\_A502\_nad\_PH=set\_selpar\_A502\_nad(4);

const double selpar\_slope2\_nad\_LO=set\_selpar\_slope2\_nad(2); const double  
selpar\_slope2\_nad\_HI=set\_selpar\_slope2\_nad(3); const double selpar\_slope2\_nad\_PH=set\_selpar\_slope2\_nad(4);

const double selpar\_A50\_mad\_LO=set\_selpar\_A50\_mad(2); const double  
selpar\_A50\_mad\_HI=set\_selpar\_A50\_mad(3); const double selpar\_A50\_mad\_PH=set\_selpar\_A50\_mad(4);

const double selpar\_slope\_mad\_LO=set\_selpar\_slope\_mad(2); const double  
selpar\_slope\_mad\_HI=set\_selpar\_slope\_mad(3); const double selpar\_slope\_mad\_PH=set\_selpar\_slope\_mad(4);

const double selpar\_A502\_mad\_LO=set\_selpar\_A502\_mad(2); const double  
selpar\_A502\_mad\_HI=set\_selpar\_A502\_mad(3); const double selpar\_A502\_mad\_PH=set\_selpar\_A502\_mad(4);

const double selpar\_slope2\_mad\_LO=set\_selpar\_slope2\_mad(2); const double  
selpar\_slope2\_mad\_HI=set\_selpar\_slope2\_mad(3); const double  
selpar\_slope2\_mad\_PH=set\_selpar\_slope2\_mad(4);

const double selpar\_A50\_sad\_LO=set\_selpar\_A50\_sad(2); const double  
selpar\_A50\_sad\_HI=set\_selpar\_A50\_sad(3); const double selpar\_A50\_sad\_PH=set\_selpar\_A50\_sad(4);

const double selpar\_slope\_sad\_LO=set\_selpar\_slope\_sad(2); const double  
selpar\_slope\_sad\_HI=set\_selpar\_slope\_sad(3); const double selpar\_slope\_sad\_PH=set\_selpar\_slope\_sad(4);

const double selpar\_A502\_sad\_LO=set\_selpar\_A502\_sad(2); const double  
selpar\_A502\_sad\_HI=set\_selpar\_A502\_sad(3); const double selpar\_A502\_sad\_PH=set\_selpar\_A502\_sad(4);

const double selpar\_slope2\_sad\_LO=set\_selpar\_slope2\_sad(2); const double  
selpar\_slope2\_sad\_HI=set\_selpar\_slope2\_sad(3); const double selpar\_slope2\_sad\_PH=set\_selpar\_slope2\_sad(4);

const double selpar\_age0\_nad\_LO=set\_sel\_age0\_nad(2); const double  
selpar\_age0\_nad\_HI=set\_sel\_age0\_nad(3); const double selpar\_age0\_nad\_PH=set\_sel\_age0\_nad(4);

const double selpar\_age1\_nad\_LO=set\_sel\_age1\_nad(2); const double  
selpar\_age1\_nad\_HI=set\_sel\_age1\_nad(3); const double selpar\_age1\_nad\_PH=set\_sel\_age1\_nad(4);

const double selpar\_age2\_nad\_LO=set\_sel\_age2\_nad(2); const double  
selpar\_age2\_nad\_HI=set\_sel\_age2\_nad(3); const double selpar\_age2\_nad\_PH=set\_sel\_age2\_nad(4);

const double selpar\_age3\_nad\_LO=set\_sel\_age3\_nad(2); const double  
selpar\_age3\_nad\_HI=set\_sel\_age3\_nad(3); const double selpar\_age3\_nad\_PH=set\_sel\_age3\_nad(4);

const double selpar\_age4\_nad\_LO=set\_sel\_age4\_nad(2); const double  
selpar\_age4\_nad\_HI=set\_sel\_age4\_nad(3); const double selpar\_age4\_nad\_PH=set\_sel\_age4\_nad(4);

const double selpar\_age5\_nad\_LO=set\_sel\_age5\_nad(2); const double  
selpar\_age5\_nad\_HI=set\_sel\_age5\_nad(3); const double selpar\_age5\_nad\_PH=set\_sel\_age5\_nad(4);

const double selpar\_age6\_nad\_LO=set\_sel\_age6\_nad(2); const double  
selpar\_age6\_nad\_HI=set\_sel\_age6\_nad(3); const double selpar\_age6\_nad\_PH=set\_sel\_age6\_nad(4);

const double selpar\_age0\_mad\_LO=set\_sel\_age0\_mad(2); const double  
selpar\_age0\_mad\_HI=set\_sel\_age0\_mad(3); const double selpar\_age0\_mad\_PH=set\_sel\_age0\_mad(4);

const double selpar\_age1\_mad\_LO=set\_sel\_age1\_mad(2); const double  
selpar\_age1\_mad\_HI=set\_sel\_age1\_mad(3); const double selpar\_age1\_mad\_PH=set\_sel\_age1\_mad(4);

const double selpar\_age2\_mad\_LO=set\_sel\_age2\_mad(2); const double  
selpar\_age2\_mad\_HI=set\_sel\_age2\_mad(3); const double selpar\_age2\_mad\_PH=set\_sel\_age2\_mad(4);

const double selpar\_age3\_mad\_LO=set\_sel\_age3\_mad(2); const double  
selpar\_age3\_mad\_HI=set\_sel\_age3\_mad(3); const double selpar\_age3\_mad\_PH=set\_sel\_age3\_mad(4);

const double selpar\_age4\_mad\_LO=set\_sel\_age4\_mad(2); const double  
selpar\_age4\_mad\_HI=set\_sel\_age4\_mad(3); const double selpar\_age4\_mad\_PH=set\_sel\_age4\_mad(4);

const double selpar\_age5\_mad\_LO=set\_sel\_age5\_mad(2); const double  
selpar\_age5\_mad\_HI=set\_sel\_age5\_mad(3); const double selpar\_age5\_mad\_PH=set\_sel\_age5\_mad(4);

const double selpar\_age6\_mad\_LO=set\_sel\_age6\_mad(2); const double  
selpar\_age6\_mad\_HI=set\_sel\_age6\_mad(3); const double selpar\_age6\_mad\_PH=set\_sel\_age6\_mad(4);

const double selpar\_age0\_sad\_LO=set\_sel\_age0\_sad(2); const double selpar\_age0\_sad\_HI=set\_sel\_age0\_sad(3);  
const double selpar\_age0\_sad\_PH=set\_sel\_age0\_sad(4);

const double selpar\_age1\_sad\_LO=set\_sel\_age1\_sad(2); const double selpar\_age1\_sad\_HI=set\_sel\_age1\_sad(3);  
const double selpar\_age1\_sad\_PH=set\_sel\_age1\_sad(4);

const double selpar\_age2\_sad\_LO=set\_sel\_age2\_sad(2); const double selpar\_age2\_sad\_HI=set\_sel\_age2\_sad(3);  
const double selpar\_age2\_sad\_PH=set\_sel\_age2\_sad(4);

const double selpar\_age3\_sad\_LO=set\_sel\_age3\_sad(2); const double selpar\_age3\_sad\_HI=set\_sel\_age3\_sad(3);  
const double selpar\_age3\_sad\_PH=set\_sel\_age3\_sad(4);

const double selpar\_age4\_sad\_LO=set\_sel\_age4\_sad(2); const double selpar\_age4\_sad\_HI=set\_sel\_age4\_sad(3);  
const double selpar\_age4\_sad\_PH=set\_sel\_age4\_sad(4);

const double selpar\_age5\_sad\_LO=set\_sel\_age5\_sad(2); const double selpar\_age5\_sad\_HI=set\_sel\_age5\_sad(3);  
const double selpar\_age5\_sad\_PH=set\_sel\_age5\_sad(4);

const double selpar\_age6\_sad\_LO=set\_sel\_age6\_sad(2); const double selpar\_age6\_sad\_HI=set\_sel\_age6\_sad(3);  
const double selpar\_age6\_sad\_PH=set\_sel\_age6\_sad(4);

const double log\_q\_nad\_LO=set\_log\_q\_nad(2); const double log\_q\_nad\_HI=set\_log\_q\_nad(3); const double  
log\_q\_nad\_PH=set\_log\_q\_nad(4);

const double log\_q\_mad\_LO=set\_log\_q\_mad(2); const double log\_q\_mad\_HI=set\_log\_q\_mad(3); const double  
log\_q\_mad\_PH=set\_log\_q\_mad(4);

const double log\_q\_sad\_LO=set\_log\_q\_sad(2); const double log\_q\_sad\_HI=set\_log\_q\_sad(3); const double  
log\_q\_sad\_PH=set\_log\_q\_sad(4);

const double log\_q\_jai\_LO=set\_log\_q\_jai(2); const double log\_q\_jai\_HI=set\_log\_q\_jai(3); const double  
log\_q\_jai\_PH=set\_log\_q\_jai(4);

const double log\_q2\_jai\_LO=set\_log\_q2\_jai(2); const double log\_q2\_jai\_HI=set\_log\_q2\_jai(3); const double  
log\_q2\_jai\_PH=set\_log\_q2\_jai(4);

const double log\_q\_mar\_LO=set\_log\_q\_mar(2); const double log\_q\_mar\_HI=set\_log\_q\_mar(3); const double  
log\_q\_mar\_PH=set\_log\_q\_mar(4);

const double log\_q\_eco\_LO=set\_log\_q\_eco(2); const double log\_q\_eco\_HI=set\_log\_q\_eco(3); const double  
log\_q\_eco\_PH=set\_log\_q\_eco(4);

const double log\_avg\_F\_cRn\_LO=set\_log\_avg\_F\_cRn(2); const double log\_avg\_F\_cRn\_HI=set\_log\_avg\_F\_cRn(3);  
const double log\_avg\_F\_cRn\_PH=set\_log\_avg\_F\_cRn(4);

const double log\_avg\_F\_cRs\_LO=set\_log\_avg\_F\_cRs(2); const double log\_avg\_F\_cRs\_HI=set\_log\_avg\_F\_cRs(3);  
const double log\_avg\_F\_cRs\_PH=set\_log\_avg\_F\_cRs(4);

const double log\_avg\_F\_cBn\_LO=set\_log\_avg\_F\_cBn(2); const double log\_avg\_F\_cBn\_HI=set\_log\_avg\_F\_cBn(3);  
const double log\_avg\_F\_cBn\_PH=set\_log\_avg\_F\_cBn(4);

```
const double log_avg_F_cBs_LO=set_log_avg_F_cBs(2); const double log_avg_F_cBs_HI=set_log_avg_F_cBs(3);
const double log_avg_F_cBs_PH=set_log_avg_F_cBs(4);
```

```
//-dev vectors-----
```

```
const double log_F_dev_cRn_LO=set_log_F_dev_cRn(1); const double log_F_dev_cRn_HI=set_log_F_dev_cRn(2);
const double log_F_dev_cRn_PH=set_log_F_dev_cRn(3);
```

```
const double log_F_dev_cRs_LO=set_log_F_dev_cRs(1); const double log_F_dev_cRs_HI=set_log_F_dev_cRs(2);
const double log_F_dev_cRs_PH=set_log_F_dev_cRs(3);
```

```
const double log_F_dev_cBn_LO=set_log_F_dev_cBn(1); const double log_F_dev_cBn_HI=set_log_F_dev_cBn(2);
const double log_F_dev_cBn_PH=set_log_F_dev_cBn(3);
```

```
const double log_F_dev_cBs_LO=set_log_F_dev_cBs(1); const double log_F_dev_cBs_HI=set_log_F_dev_cBs(2);
const double log_F_dev_cBs_PH=set_log_F_dev_cBs(3);
```

```
const double log_RWq_LO=set_log_RWq_dev(1); const double log_RWq_HI=set_log_RWq_dev(2); const double
log_RWq_PH=set_log_RWq_dev(3);
```

```
const double log_rec_dev_LO=set_log_rec_dev(1); const double log_rec_dev_HI=set_log_rec_dev(2); const
double log_rec_dev_PH=set_log_rec_dev(3);
```

```
const double log_Nage_dev_LO=set_log_Nage_dev(1); const double log_Nage_dev_HI=set_log_Nage_dev(2);
const double log_Nage_dev_PH=set_log_Nage_dev(3);
```

```
END_CALC
```

```
////-----Growth-----
```

```
//Population growth parms and conversions
```

```
init_bounded_number Linf(Linf_LO,Linf_HI,Linf_PH);
```

```
init_bounded_number K(K_LO,K_HI,K_PH);
```

```
init_bounded_number t0(t0_LO,t0_HI,t0_PH);
```

```
init_bounded_number len_cv_nad_val(len_cv_nad_LO,len_cv_nad_HI,len_cv_nad_PH);
```

```
init_bounded_number len_cv_mad_val(len_cv_mad_LO,len_cv_mad_HI,len_cv_mad_PH);
```

```
//init_bounded_number len_cv_sad_val(len_cv_sad_LO,len_cv_sad_HI,len_cv_sad_PH);
```

```
vector Linf_out(1,8);
```

```
vector K_out(1,8);
```

```
vector t0_out(1,8);
```

```
vector len_cv_nad_val_out(1,8);
```

```
vector len_cv_mad_val_out(1,8);
```

```
//vector len_cv_sad_val_out(1,8);
```

```
vector meanlen_FL(1,nages); //mean fork length (mm) at age all fish
```



```

matrix meanlen_FL_apr15(styr,endyr,1,nages); //mean fork length April 15
matrix meanlen_FL_jun1(styr,endyr,1,nages); //mean fork length June 1
matrix meanlen_FL_oct15(styr,endyr,1,nages); //mean fork length October 15
vector wgt_fish_mt(1,nages);
vector wgt_spawn_mt(1,nages);
matrix wgt_spawn_mt_tv(styr,endyr,1,nages); //time varying weight at spawn
matrix tv_wgt_middle_mt(styr,endyr,1,nages);
matrix tv_wgt_spawn_mt(styr,endyr,1,nages);

matrix len_cR_mm(styr,endyr,1,nages); //mean length at age of commercial reduction landings in mm
matrix wholewgt_cR_mt(styr,endyr,1,nages); //whole wgt of commercial reduction landings in 1000 mt

3darray lenprob_apr15(styr,endyr,1,nages,1,nlenbins); //distn of size at age (age-length key, 10 mm bins) in
population
3darray lenprob_jun1(styr,endyr,1,nages,1,nlenbins); //distn of size at age (age-length key, 10 mm bins) in
population
3darray lenprob_oct15(styr,endyr,1,nages,1,nlenbins); //distn of size at age (age-length key, 10 mm bins) in
population
matrix lenprob(1,nages,1,nlenbins); //distn of size at age (age-length key, 10 mm bins) in population
number zscore_len; //standardized normal values used for computing lenprob
vector cprob_lenvec(1,nlenbins); //cumulative probabilities used for computing lenprob
number zscore_lzero; //standardized normal values for length = 0
number cprob_lzero; //length probability mass below zero, used for computing lenprob

//matrices below are used to match length comps
3darray lenprob_nad(styr,endyr,1,nages,1,nlenbins);
3darray lenprob_mad(styr,endyr,1,nages,1,nlenbins);
//3darray lenprob_sad(styr,endyr,1,nages,1,nlenbins);

//init_bounded_dev_vector log_len_cv_dev(1,nages,-2,2,3)
matrix len_sd_nad(styr,endyr,1,nages);
matrix len_sd_mad(styr,endyr,1,nages);
//matrix len_sd_sad(styr,endyr,1,nages);
vector len_cv_nad(1,nages); //for fishgraph
vector len_cv_mad(1,nages); //for fishgraph
//vector len_cv_sad(1,nages); //for fishgraph

```

```

vector len_cv_apr15(1,nages);
vector len_cv_jun1(1,nages);
vector len_cv_oct15(1,nages);

//----Predicted length and age compositions
matrix pred_nad_lenc(1,nyr_nad_lenc,1,nlenbins);
matrix pred_mad_lenc(1,nyr_mad_lenc,1,nlenbins);
//matrix pred_sad_lenc(1,nyr_sad_lenc,1,nlenbins);

matrix pred_cRn_agec(1,nyr_cRn_agec,1,nages_agec);
matrix pred_cRn_agec_allages(1,nyr_cRn_agec,1,nages);
matrix ErrorFree_cRn_agec(1,nyr_cRn_agec,1,nages);

matrix pred_cRs_agec(1,nyr_cRs_agec,1,nages_agec);
matrix pred_cRs_agec_allages(1,nyr_cRs_agec,1,nages);
matrix ErrorFree_cRs_agec(1,nyr_cRs_agec,1,nages);

matrix pred_cBn_agec(1,nyr_cBn_agec,1,nages_agec);
matrix pred_cBn_agec_allages(1,nyr_cBn_agec,1,nages);
matrix ErrorFree_cBn_agec(1,nyr_cBn_agec,1,nages);

matrix pred_cBs_agec(1,nyr_cBs_agec,1,nages_agec);
matrix pred_cBs_agec_allages(1,nyr_cBs_agec,1,nages);
matrix ErrorFree_cBs_agec(1,nyr_cBs_agec,1,nages);

//Sample size (perhaps adjusted herein) used in fitting comp data
vector nsamp_nad_lenc_allyr(styr,endyr);
vector nsamp_mad_lenc_allyr(styr,endyr);
//vector nsamp_sad_lenc_allyr(styr,endyr);

vector nsamp_cRn_agec_allyr(styr,endyr);
vector nsamp_cRs_agec_allyr(styr,endyr);
vector nsamp_cBn_agec_allyr(styr,endyr);
vector nsamp_cBs_agec_allyr(styr,endyr);

```

```

//Nfish used in MCB analysis (not used in fitting)
vector nfish_nad_lenc_allyr(styr,endyr);
vector nfish_mad_lenc_allyr(styr,endyr);
//vector nfish_sad_lenc_allyr(styr,endyr);

vector nfish_cRs_agec_allyr(styr,endyr);
vector nfish_cRn_agec_allyr(styr,endyr);
vector nfish_cBn_agec_allyr(styr,endyr);
vector nfish_cBs_agec_allyr(styr,endyr);

//Computed effective sample size for output (not used in fitting)
vector neff_nad_lenc_allyr(styr,endyr);
vector neff_mad_lenc_allyr(styr,endyr);
//vector neff_sad_lenc_allyr(styr,endyr);

vector neff_cRn_agec_allyr(styr,endyr);
vector neff_cRs_agec_allyr(styr,endyr);
vector neff_cBn_agec_allyr(styr,endyr);
vector neff_cBs_agec_allyr(styr,endyr);

//-----Population-----
matrix N(styr,endyr+1,1,nages); //Population numbers by year and age at start of yr
matrix N_mdyr(styr,endyr,1,nages); //Population numbers by year and age at mdpt of yr: used for comps and
cpue
matrix N_spawn(styr,endyr,1,nages); //Population numbers by year and age at peaking spawning: used for SSB
matrix N_nad(styr,endyr,1,nages);
matrix N_mad(styr,endyr,1,nages);
matrix N_sad(styr,endyr,1,nages);
init_bounded_vector log_Nage_dev(2,nages,log_Nage_dev_LO,log_Nage_dev_HI,log_Nage_dev_PH);
vector log_Nage_dev_output(1,nages); //used in output. equals zero for first age
matrix B(styr,endyr+1,1,nages); //Population biomass by year and age at start of yr
matrix B_mdyr(styr,endyr+1,1,nages); //population biomass at the middle of the yr
vector totB(styr,endyr+1); //Total biomass by year
vector totN(styr,endyr+1); //Total abundance by year
vector SSB(styr,endyr+1); //Total spawning biomass by year (female + male mature biomass)
vector rec(styr,endyr+1); //Recruits by year

```

```

vector prop_f(1,nages);
vector prop_m(1,nages);
vector maturity_f(1,nages);
vector maturity_m(1,nages);
matrix tv_maturity(styr,endyr,1,nages);
vector reprod(1,nages);
matrix reprod_tv(styr,endyr,1,nages);
matrix SSBatage(styr,endyr,1,nages);

/--Stock-Recruit Function (Beverton-Holt, steepness parameterization)-----
init_bounded_number log_R0(log_R0_LO,log_R0_HI,log_R0_PH); //log(virgin Recruitment)
vector log_R0_out(1,8);
number R0; //virgin recruitment
init_bounded_number steep(steep_LO,steep_HI,steep_PH); //steepness
vector steep_out(1,8);
init_bounded_number rec_sigma(rec_sigma_LO,rec_sigma_HI,rec_sigma_PH); //sd recruitment residuals
vector rec_sigma_out(1,8);
init_bounded_number R_autocorr(R_autocorr_LO,R_autocorr_HI,R_autocorr_PH); //autocorrelation in SR
vector R_autocorr_out(1,8);

number rec_sigma_sq; //square of rec_sigma
number rec_logL_add; //additive term in -logL term

init_bounded_dev_vector
log_rec_dev(styr_rec_dev,endyr_rec_dev,log_rec_dev_LO,log_rec_dev_HI,log_rec_dev_PH);
vector log_rec_dev_output(styr,endyr+1); //used in t.series output. equals zero except for yrs in
log_rec_dev
vector log_rec_dev_out(styr_rec_dev,endyr_rec_dev); //used in output for bound checking

number var_rec_dev; //variance of log recruitment deviations, from yrs with unconstrained S-
R(XXXX-XXXX)
number sigma_rec_dev; //sample SD of log residuals (may not equal rec_sigma
number BiasCor; //Bias correction in equilibrium recruits
number S0; //equal to spr_F0*R0 = virgin SSB
number B0; //equal to bpr_F0*R0 = virgin B
number R1; //Recruits in styr

```

```

number R_virgin;           //unfished recruitment with bias correction
vector SdS0(styr,endyr+1); //Spawners relative to the unfished level

init_bounded_number log_dm_nad_lc(log_dm_nad_lc_LO,log_dm_nad_lc_HI,log_dm_nad_lc_PH);
init_bounded_number log_dm_mad_lc(log_dm_mad_lc_LO,log_dm_mad_lc_HI,log_dm_mad_lc_PH);
//init_bounded_number log_dm_sad_lc(log_dm_sad_lc_LO,log_dm_sad_lc_HI,log_dm_sad_lc_PH);

init_bounded_number log_dm_cRn_ac(log_dm_cRn_ac_LO,log_dm_cRn_ac_HI,log_dm_cRn_ac_PH);
init_bounded_number log_dm_cRs_ac(log_dm_cRs_ac_LO,log_dm_cRs_ac_HI,log_dm_cRs_ac_PH);
init_bounded_number log_dm_cBn_ac(log_dm_cBn_ac_LO,log_dm_cBn_ac_HI,log_dm_cBn_ac_PH);
init_bounded_number log_dm_cBs_ac(log_dm_cBs_ac_LO,log_dm_cBs_ac_HI,log_dm_cBs_ac_PH);

vector log_dm_nad_lc_out(1,8);
vector log_dm_mad_lc_out(1,8);
//vector log_dm_sad_lc_out(1,8);

vector log_dm_cRn_ac_out(1,8);
vector log_dm_cRs_ac_out(1,8);
vector log_dm_cBn_ac_out(1,8);
vector log_dm_cBs_ac_out(1,8);

//-----
///---Selectivity-----

//Commercial reduction-----
matrix sel_cRn(styr,endyr,1,nages);
matrix sel_cRs(styr,endyr,1,nages);
vector sel_cRn_block1(1,nages);
vector sel_cRn_block2(1,nages);
vector sel_cRn_block3(1,nages);
vector sel_cRn_block4(1,nages);
vector sel_cRs_block1(1,nages);
vector sel_cRs_block2(1,nages);
vector sel_cRs_block3(1,nages);
vector sel_cRs_block4(1,nages);

```

//north - block 1

```
init_bounded_number selpar_A50_cRn(selpar_A50_cRn_LO,selpar_A50_cRn_HI,selpar_A50_cRn_PH);
init_bounded_number selpar_slope_cRn(selpar_slope_cRn_LO,selpar_slope_cRn_HI,selpar_slope_cRn_PH);
init_bounded_number selpar_A502_cRn(selpar_A502_cRn_LO,selpar_A502_cRn_HI,selpar_A502_cRn_PH);
init_bounded_number selpar_slope2_cRn(selpar_slope2_cRn_LO,selpar_slope2_cRn_HI,selpar_slope2_cRn_PH);
vector selpar_A50_cRn_out(1,8);
vector selpar_slope_cRn_out(1,8);
vector selpar_A502_cRn_out(1,8);
vector selpar_slope2_cRn_out(1,8);
```

//north - block 2

```
init_bounded_number selpar_A50_cRn2(selpar_A50_cRn2_LO,selpar_A50_cRn2_HI,selpar_A50_cRn2_PH);
init_bounded_number selpar_slope_cRn2(selpar_slope_cRn2_LO,selpar_slope_cRn2_HI,selpar_slope_cRn2_PH);
init_bounded_number selpar_A502_cRn2(selpar_A502_cRn2_LO,selpar_A502_cRn2_HI,selpar_A502_cRn2_PH);
init_bounded_number
selpar_slope2_cRn2(selpar_slope2_cRn2_LO,selpar_slope2_cRn2_HI,selpar_slope2_cRn2_PH);
vector selpar_A50_cRn2_out(1,8);
vector selpar_slope_cRn2_out(1,8);
vector selpar_A502_cRn2_out(1,8);
vector selpar_slope2_cRn2_out(1,8);
```

//north - block 3

```
init_bounded_number selpar_A50_cRn3(selpar_A50_cRn3_LO,selpar_A50_cRn3_HI,selpar_A50_cRn3_PH);
init_bounded_number selpar_slope_cRn3(selpar_slope_cRn3_LO,selpar_slope_cRn3_HI,selpar_slope_cRn3_PH);
init_bounded_number selpar_A502_cRn3(selpar_A502_cRn3_LO,selpar_A502_cRn3_HI,selpar_A502_cRn3_PH);
init_bounded_number
selpar_slope2_cRn3(selpar_slope2_cRn3_LO,selpar_slope2_cRn3_HI,selpar_slope2_cRn3_PH);
vector selpar_A50_cRn3_out(1,8);
vector selpar_slope_cRn3_out(1,8);
vector selpar_A502_cRn3_out(1,8);
vector selpar_slope2_cRn3_out(1,8);
```

//north - block 4

```
init_bounded_number selpar_A50_cRn4(selpar_A50_cRn4_LO,selpar_A50_cRn4_HI,selpar_A50_cRn4_PH);
init_bounded_number selpar_slope_cRn4(selpar_slope_cRn4_LO,selpar_slope_cRn4_HI,selpar_slope_cRn4_PH);
```

```
init_bounded_number selpar_A502_cRn4(selpar_A502_cRn4_LO,selpar_A502_cRn4_HI,selpar_A502_cRn4_PH);
init_bounded_number
selpar_slope2_cRn4(selpar_slope2_cRn4_LO,selpar_slope2_cRn4_HI,selpar_slope2_cRn4_PH);
vector selpar_A50_cRn4_out(1,8);
vector selpar_slope_cRn4_out(1,8);
vector selpar_A502_cRn4_out(1,8);
vector selpar_slope2_cRn4_out(1,8);

//south - block 1
init_bounded_number selpar_A50_cRs(selpar_A50_cRs_LO,selpar_A50_cRs_HI,selpar_A50_cRs_PH);
init_bounded_number selpar_slope_cRs(selpar_slope_cRs_LO,selpar_slope_cRs_HI,selpar_slope_cRs_PH);
init_bounded_number selpar_A502_cRs(selpar_A502_cRs_LO,selpar_A502_cRs_HI,selpar_A502_cRs_PH);
init_bounded_number selpar_slope2_cRs(selpar_slope2_cRs_LO,selpar_slope2_cRs_HI,selpar_slope2_cRs_PH);
vector selpar_A50_cRs_out(1,8);
vector selpar_slope_cRs_out(1,8);
vector selpar_A502_cRs_out(1,8);
vector selpar_slope2_cRs_out(1,8);

//south - block 2
init_bounded_number selpar_A50_cRs2(selpar_A50_cRs2_LO,selpar_A50_cRs2_HI,selpar_A50_cRs2_PH);
init_bounded_number selpar_slope_cRs2(selpar_slope_cRs2_LO,selpar_slope_cRs2_HI,selpar_slope_cRs2_PH);
init_bounded_number selpar_A502_cRs2(selpar_A502_cRs2_LO,selpar_A502_cRs2_HI,selpar_A502_cRs2_PH);
init_bounded_number
selpar_slope2_cRs2(selpar_slope2_cRs2_LO,selpar_slope2_cRs2_HI,selpar_slope2_cRs2_PH);
vector selpar_A50_cRs2_out(1,8);
vector selpar_slope_cRs2_out(1,8);
vector selpar_A502_cRs2_out(1,8);
vector selpar_slope2_cRs2_out(1,8);

//south - block 3
init_bounded_number selpar_A50_cRs3(selpar_A50_cRs3_LO,selpar_A50_cRs3_HI,selpar_A50_cRs3_PH);
init_bounded_number selpar_slope_cRs3(selpar_slope_cRs3_LO,selpar_slope_cRs3_HI,selpar_slope_cRs3_PH);
init_bounded_number selpar_A502_cRs3(selpar_A502_cRs3_LO,selpar_A502_cRs3_HI,selpar_A502_cRs3_PH);
init_bounded_number
selpar_slope2_cRs3(selpar_slope2_cRs3_LO,selpar_slope2_cRs3_HI,selpar_slope2_cRs3_PH);
vector selpar_A50_cRs3_out(1,8);
```

```
vector selpar_slope_cRs3_out(1,8);
vector selpar_A502_cRs3_out(1,8);
vector selpar_slope2_cRs3_out(1,8);
```

```
//south - block 4
```

```
init_bounded_number selpar_A50_cRs4(selpar_A50_cRs4_LO,selpar_A50_cRs4_HI,selpar_A50_cRs4_PH);
init_bounded_number selpar_slope_cRs4(selpar_slope_cRs4_LO,selpar_slope_cRs4_HI,selpar_slope_cRs4_PH);
init_bounded_number selpar_A502_cRs4(selpar_A502_cRs4_LO,selpar_A502_cRs4_HI,selpar_A502_cRs4_PH);
init_bounded_number
selpar_slope2_cRs4(selpar_slope2_cRs4_LO,selpar_slope2_cRs4_HI,selpar_slope2_cRs4_PH);
vector selpar_A50_cRs4_out(1,8);
vector selpar_slope_cRs4_out(1,8);
vector selpar_A502_cRs4_out(1,8);
vector selpar_slope2_cRs4_out(1,8);
```

```
//logit based selectivity cR north - block 1
```

```
init_bounded_number sel_age0_cRn_logit(selpar_age0_cRn_LO,selpar_age0_cRn_HI,selpar_age0_cRn_PH);
init_bounded_number sel_age1_cRn_logit(selpar_age1_cRn_LO,selpar_age1_cRn_HI,selpar_age1_cRn_PH);
init_bounded_number sel_age2_cRn_logit(selpar_age2_cRn_LO,selpar_age2_cRn_HI,selpar_age2_cRn_PH);
init_bounded_number sel_age3_cRn_logit(selpar_age3_cRn_LO,selpar_age3_cRn_HI,selpar_age3_cRn_PH);
init_bounded_number sel_age4_cRn_logit(selpar_age4_cRn_LO,selpar_age4_cRn_HI,selpar_age4_cRn_PH);
init_bounded_number sel_age5_cRn_logit(selpar_age5_cRn_LO,selpar_age5_cRn_HI,selpar_age5_cRn_PH);
init_bounded_number sel_age6_cRn_logit(selpar_age6_cRn_LO,selpar_age6_cRn_HI,selpar_age6_cRn_PH);
vector sel_age_cRn_vec(1,nages);
number selpar_age0_cRn;
number selpar_age1_cRn;
number selpar_age2_cRn;
number selpar_age3_cRn;
number selpar_age4_cRn;
number selpar_age5_cRn;
number selpar_age6_cRn;
vector selpar_age0_cRn_out(1,8);
vector selpar_age1_cRn_out(1,8);
vector selpar_age2_cRn_out(1,8);
vector selpar_age3_cRn_out(1,8);
vector selpar_age4_cRn_out(1,8);
```



```
vector selpar_age5_cRn_out(1,8);  
vector selpar_age6_cRn_out(1,8);
```

```
//logit based selectivity cR north - block 2
```

```
init_bounded_number sel_age0_cRn2_logit(selpar_age0_cRn2_LO,selpar_age0_cRn2_HI,selpar_age0_cRn2_PH);  
init_bounded_number sel_age1_cRn2_logit(selpar_age1_cRn2_LO,selpar_age1_cRn2_HI,selpar_age1_cRn2_PH);  
init_bounded_number sel_age2_cRn2_logit(selpar_age2_cRn2_LO,selpar_age2_cRn2_HI,selpar_age2_cRn2_PH);  
init_bounded_number sel_age3_cRn2_logit(selpar_age3_cRn2_LO,selpar_age3_cRn2_HI,selpar_age3_cRn2_PH);  
init_bounded_number sel_age4_cRn2_logit(selpar_age4_cRn2_LO,selpar_age4_cRn2_HI,selpar_age4_cRn2_PH);  
init_bounded_number sel_age5_cRn2_logit(selpar_age5_cRn2_LO,selpar_age5_cRn2_HI,selpar_age5_cRn2_PH);  
init_bounded_number sel_age6_cRn2_logit(selpar_age6_cRn2_LO,selpar_age6_cRn2_HI,selpar_age6_cRn2_PH);  
vector sel_age_cRn2_vec(1,nages);  
number selpar_age0_cRn2;  
number selpar_age1_cRn2;  
number selpar_age2_cRn2;  
number selpar_age3_cRn2;  
number selpar_age4_cRn2;  
number selpar_age5_cRn2;  
number selpar_age6_cRn2;  
vector selpar_age0_cRn2_out(1,8);  
vector selpar_age1_cRn2_out(1,8);  
vector selpar_age2_cRn2_out(1,8);  
vector selpar_age3_cRn2_out(1,8);  
vector selpar_age4_cRn2_out(1,8);  
vector selpar_age5_cRn2_out(1,8);  
vector selpar_age6_cRn2_out(1,8);
```

```
//logit based selectivity cR north - block 3
```

```
init_bounded_number sel_age0_cRn3_logit(selpar_age0_cRn3_LO,selpar_age0_cRn3_HI,selpar_age0_cRn3_PH);  
init_bounded_number sel_age1_cRn3_logit(selpar_age1_cRn3_LO,selpar_age1_cRn3_HI,selpar_age1_cRn3_PH);  
init_bounded_number sel_age2_cRn3_logit(selpar_age2_cRn3_LO,selpar_age2_cRn3_HI,selpar_age2_cRn3_PH);  
init_bounded_number sel_age3_cRn3_logit(selpar_age3_cRn3_LO,selpar_age3_cRn3_HI,selpar_age3_cRn3_PH);  
init_bounded_number sel_age4_cRn3_logit(selpar_age4_cRn3_LO,selpar_age4_cRn3_HI,selpar_age4_cRn3_PH);  
init_bounded_number sel_age5_cRn3_logit(selpar_age5_cRn3_LO,selpar_age5_cRn3_HI,selpar_age5_cRn3_PH);  
init_bounded_number sel_age6_cRn3_logit(selpar_age6_cRn3_LO,selpar_age6_cRn3_HI,selpar_age6_cRn3_PH);
```

```
vector sel_age_cRn3_vec(1,nages);
number selpar_age0_cRn3;
number selpar_age1_cRn3;
number selpar_age2_cRn3;
number selpar_age3_cRn3;
number selpar_age4_cRn3;
number selpar_age5_cRn3;
number selpar_age6_cRn3;
vector selpar_age0_cRn3_out(1,8);
vector selpar_age1_cRn3_out(1,8);
vector selpar_age2_cRn3_out(1,8);
vector selpar_age3_cRn3_out(1,8);
vector selpar_age4_cRn3_out(1,8);
vector selpar_age5_cRn3_out(1,8);
vector selpar_age6_cRn3_out(1,8);

//logit based selectivity cR north - block 4
init_bounded_number sel_age0_cRn4_logit(selpar_age0_cRn4_LO,selpar_age0_cRn4_HI,selpar_age0_cRn4_PH);
init_bounded_number sel_age1_cRn4_logit(selpar_age1_cRn4_LO,selpar_age1_cRn4_HI,selpar_age1_cRn4_PH);
init_bounded_number sel_age2_cRn4_logit(selpar_age2_cRn4_LO,selpar_age2_cRn4_HI,selpar_age2_cRn4_PH);
init_bounded_number sel_age3_cRn4_logit(selpar_age3_cRn4_LO,selpar_age3_cRn4_HI,selpar_age3_cRn4_PH);
init_bounded_number sel_age4_cRn4_logit(selpar_age4_cRn4_LO,selpar_age4_cRn4_HI,selpar_age4_cRn4_PH);
init_bounded_number sel_age5_cRn4_logit(selpar_age5_cRn4_LO,selpar_age5_cRn4_HI,selpar_age5_cRn4_PH);
init_bounded_number sel_age6_cRn4_logit(selpar_age6_cRn4_LO,selpar_age6_cRn4_HI,selpar_age6_cRn4_PH);
vector sel_age_cRn4_vec(1,nages);
number selpar_age0_cRn4;
number selpar_age1_cRn4;
number selpar_age2_cRn4;
number selpar_age3_cRn4;
number selpar_age4_cRn4;
number selpar_age5_cRn4;
number selpar_age6_cRn4;
vector selpar_age0_cRn4_out(1,8);
vector selpar_age1_cRn4_out(1,8);
vector selpar_age2_cRn4_out(1,8);
```

```
vector selpar_age3_cRn4_out(1,8);
vector selpar_age4_cRn4_out(1,8);
vector selpar_age5_cRn4_out(1,8);
vector selpar_age6_cRn4_out(1,8);
```

```
//logit based selectivity cR south - block 1
```

```
init_bounded_number sel_age0_cRs_logit(selpar_age0_cRs_LO,selpar_age0_cRs_HI,selpar_age0_cRs_PH);
init_bounded_number sel_age1_cRs_logit(selpar_age1_cRs_LO,selpar_age1_cRs_HI,selpar_age1_cRs_PH);
init_bounded_number sel_age2_cRs_logit(selpar_age2_cRs_LO,selpar_age2_cRs_HI,selpar_age2_cRs_PH);
init_bounded_number sel_age3_cRs_logit(selpar_age3_cRs_LO,selpar_age3_cRs_HI,selpar_age3_cRs_PH);
init_bounded_number sel_age4_cRs_logit(selpar_age4_cRs_LO,selpar_age4_cRs_HI,selpar_age4_cRs_PH);
init_bounded_number sel_age5_cRs_logit(selpar_age5_cRs_LO,selpar_age5_cRs_HI,selpar_age5_cRs_PH);
init_bounded_number sel_age6_cRs_logit(selpar_age6_cRs_LO,selpar_age6_cRs_HI,selpar_age6_cRs_PH);
vector sel_age_cRs_vec(1,nages);
number selpar_age0_cRs;
number selpar_age1_cRs;
number selpar_age2_cRs;
number selpar_age3_cRs;
number selpar_age4_cRs;
number selpar_age5_cRs;
number selpar_age6_cRs;
vector selpar_age0_cRs_out(1,8);
vector selpar_age1_cRs_out(1,8);
vector selpar_age2_cRs_out(1,8);
vector selpar_age3_cRs_out(1,8);
vector selpar_age4_cRs_out(1,8);
vector selpar_age5_cRs_out(1,8);
vector selpar_age6_cRs_out(1,8);
```

```
//logit based selectivity cR south - block 2
```

```
init_bounded_number sel_age0_cRs2_logit(selpar_age0_cRs2_LO,selpar_age0_cRs2_HI,selpar_age0_cRs2_PH);
init_bounded_number sel_age1_cRs2_logit(selpar_age1_cRs2_LO,selpar_age1_cRs2_HI,selpar_age1_cRs2_PH);
init_bounded_number sel_age2_cRs2_logit(selpar_age2_cRs2_LO,selpar_age2_cRs2_HI,selpar_age2_cRs2_PH);
init_bounded_number sel_age3_cRs2_logit(selpar_age3_cRs2_LO,selpar_age3_cRs2_HI,selpar_age3_cRs2_PH);
init_bounded_number sel_age4_cRs2_logit(selpar_age4_cRs2_LO,selpar_age4_cRs2_HI,selpar_age4_cRs2_PH);
```

```
init_bounded_number sel_age5_cRs2_logit(selpar_age5_cRs2_LO,selpar_age5_cRs2_HI,selpar_age5_cRs2_PH);
init_bounded_number sel_age6_cRs2_logit(selpar_age6_cRs2_LO,selpar_age6_cRs2_HI,selpar_age6_cRs2_PH);
vector sel_age_cRs2_vec(1,nages);
number selpar_age0_cRs2;
number selpar_age1_cRs2;
number selpar_age2_cRs2;
number selpar_age3_cRs2;
number selpar_age4_cRs2;
number selpar_age5_cRs2;
number selpar_age6_cRs2;
vector selpar_age0_cRs2_out(1,8);
vector selpar_age1_cRs2_out(1,8);
vector selpar_age2_cRs2_out(1,8);
vector selpar_age3_cRs2_out(1,8);
vector selpar_age4_cRs2_out(1,8);
vector selpar_age5_cRs2_out(1,8);
vector selpar_age6_cRs2_out(1,8);
```

//logit based selectivity cR south - block 3

```
init_bounded_number sel_age0_cRs3_logit(selpar_age0_cRs3_LO,selpar_age0_cRs3_HI,selpar_age0_cRs3_PH);
init_bounded_number sel_age1_cRs3_logit(selpar_age1_cRs3_LO,selpar_age1_cRs3_HI,selpar_age1_cRs3_PH);
init_bounded_number sel_age2_cRs3_logit(selpar_age2_cRs3_LO,selpar_age2_cRs3_HI,selpar_age2_cRs3_PH);
init_bounded_number sel_age3_cRs3_logit(selpar_age3_cRs3_LO,selpar_age3_cRs3_HI,selpar_age3_cRs3_PH);
init_bounded_number sel_age4_cRs3_logit(selpar_age4_cRs3_LO,selpar_age4_cRs3_HI,selpar_age4_cRs3_PH);
init_bounded_number sel_age5_cRs3_logit(selpar_age5_cRs3_LO,selpar_age5_cRs3_HI,selpar_age5_cRs3_PH);
init_bounded_number sel_age6_cRs3_logit(selpar_age6_cRs3_LO,selpar_age6_cRs3_HI,selpar_age6_cRs3_PH);
vector sel_age_cRs3_vec(1,nages);
number selpar_age0_cRs3;
number selpar_age1_cRs3;
number selpar_age2_cRs3;
number selpar_age3_cRs3;
number selpar_age4_cRs3;
number selpar_age5_cRs3;
number selpar_age6_cRs3;
vector selpar_age0_cRs3_out(1,8);
```

```
vector selpar_age1_cRs3_out(1,8);
vector selpar_age2_cRs3_out(1,8);
vector selpar_age3_cRs3_out(1,8);
vector selpar_age4_cRs3_out(1,8);
vector selpar_age5_cRs3_out(1,8);
vector selpar_age6_cRs3_out(1,8);
```

```
//logit based selectivity cR south - block 4
```

```
init_bounded_number sel_age0_cRs4_logit(selpar_age0_cRs4_LO,selpar_age0_cRs4_HI,selpar_age0_cRs4_PH);
init_bounded_number sel_age1_cRs4_logit(selpar_age1_cRs4_LO,selpar_age1_cRs4_HI,selpar_age1_cRs4_PH);
init_bounded_number sel_age2_cRs4_logit(selpar_age2_cRs4_LO,selpar_age2_cRs4_HI,selpar_age2_cRs4_PH);
init_bounded_number sel_age3_cRs4_logit(selpar_age3_cRs4_LO,selpar_age3_cRs4_HI,selpar_age3_cRs4_PH);
init_bounded_number sel_age4_cRs4_logit(selpar_age4_cRs4_LO,selpar_age4_cRs4_HI,selpar_age4_cRs4_PH);
init_bounded_number sel_age5_cRs4_logit(selpar_age5_cRs4_LO,selpar_age5_cRs4_HI,selpar_age5_cRs4_PH);
init_bounded_number sel_age6_cRs4_logit(selpar_age6_cRs4_LO,selpar_age6_cRs4_HI,selpar_age6_cRs4_PH);
vector sel_age_cRs4_vec(1,nages);
number selpar_age0_cRs4;
number selpar_age1_cRs4;
number selpar_age2_cRs4;
number selpar_age3_cRs4;
number selpar_age4_cRs4;
number selpar_age5_cRs4;
number selpar_age6_cRs4;
vector selpar_age0_cRs4_out(1,8);
vector selpar_age1_cRs4_out(1,8);
vector selpar_age2_cRs4_out(1,8);
vector selpar_age3_cRs4_out(1,8);
vector selpar_age4_cRs4_out(1,8);
vector selpar_age5_cRs4_out(1,8);
vector selpar_age6_cRs4_out(1,8);
```

```
//Commercial bait-----
```

```
matrix sel_cBn(styr,endyr,1,nages);
matrix sel_cBs(styr,endyr,1,nages);
vector sel_cBn_block1(1,nages);
```

```
vector sel_cBn_block2(1,nages);  
vector sel_cBs_block1(1,nages);  
vector sel_cBs_block2(1,nages);
```

```
//north - block 1
```

```
init_bounded_number selpar_A50_cBn(selpar_A50_cBn_LO,selpar_A50_cBn_HI,selpar_A50_cBn_PH);  
init_bounded_number selpar_slope_cBn(selpar_slope_cBn_LO,selpar_slope_cBn_HI,selpar_slope_cBn_PH);  
init_bounded_number selpar_A502_cBn(selpar_A502_cBn_LO,selpar_A502_cBn_HI,selpar_A502_cBn_PH);  
init_bounded_number selpar_slope2_cBn(selpar_slope2_cBn_LO,selpar_slope2_cBn_HI,selpar_slope2_cBn_PH);  
vector selpar_A50_cBn_out(1,8);  
vector selpar_slope_cBn_out(1,8);  
vector selpar_A502_cBn_out(1,8);  
vector selpar_slope2_cBn_out(1,8);
```

```
//north - block 2
```

```
init_bounded_number selpar_A50_cBn2(selpar_A50_cBn2_LO,selpar_A50_cBn2_HI,selpar_A50_cBn2_PH);  
init_bounded_number selpar_slope_cBn2(selpar_slope_cBn2_LO,selpar_slope_cBn2_HI,selpar_slope_cBn2_PH);  
init_bounded_number selpar_A502_cBn2(selpar_A502_cBn2_LO,selpar_A502_cBn2_HI,selpar_A502_cBn2_PH);  
init_bounded_number  
selpar_slope2_cBn2(selpar_slope2_cBn2_LO,selpar_slope2_cBn2_HI,selpar_slope2_cBn2_PH);  
vector selpar_A50_cBn2_out(1,8);  
vector selpar_slope_cBn2_out(1,8);  
vector selpar_A502_cBn2_out(1,8);  
vector selpar_slope2_cBn2_out(1,8);
```

```
//south - block 1
```

```
init_bounded_number selpar_A50_cBs(selpar_A50_cBs_LO,selpar_A50_cBs_HI,selpar_A50_cBs_PH);  
init_bounded_number selpar_slope_cBs(selpar_slope_cBs_LO,selpar_slope_cBs_HI,selpar_slope_cBs_PH);  
init_bounded_number selpar_A502_cBs(selpar_A502_cBs_LO,selpar_A502_cBs_HI,selpar_A502_cBs_PH);  
init_bounded_number selpar_slope2_cBs(selpar_slope2_cBs_LO,selpar_slope2_cBs_HI,selpar_slope2_cBs_PH);  
vector selpar_A50_cBs_out(1,8);  
vector selpar_slope_cBs_out(1,8);  
vector selpar_A502_cBs_out(1,8);  
vector selpar_slope2_cBs_out(1,8);
```

```
//south - block 2
```

```
init_bounded_number selpar_A50_cBs2(selpar_A50_cBs2_LO,selpar_A50_cBs2_HI,selpar_A50_cBs2_PH);
init_bounded_number selpar_slope_cBs2(selpar_slope_cBs2_LO,selpar_slope_cBs2_HI,selpar_slope_cBs2_PH);
init_bounded_number selpar_A502_cBs2(selpar_A502_cBs2_LO,selpar_A502_cBs2_HI,selpar_A502_cBs2_PH);
init_bounded_number
selpar_slope2_cBs2(selpar_slope2_cBs2_LO,selpar_slope2_cBs2_HI,selpar_slope2_cBs2_PH);
vector selpar_A50_cBs2_out(1,8);
vector selpar_slope_cBs2_out(1,8);
vector selpar_A502_cBs2_out(1,8);
vector selpar_slope2_cBs2_out(1,8);
```

```
//logit based selectivity cB north - block 1
```

```
init_bounded_number sel_age0_cBn_logit(selpar_age0_cBn_LO,selpar_age0_cBn_HI,selpar_age0_cBn_PH);
init_bounded_number sel_age1_cBn_logit(selpar_age1_cBn_LO,selpar_age1_cBn_HI,selpar_age1_cBn_PH);
init_bounded_number sel_age2_cBn_logit(selpar_age2_cBn_LO,selpar_age2_cBn_HI,selpar_age2_cBn_PH);
init_bounded_number sel_age3_cBn_logit(selpar_age3_cBn_LO,selpar_age3_cBn_HI,selpar_age3_cBn_PH);
init_bounded_number sel_age4_cBn_logit(selpar_age4_cBn_LO,selpar_age4_cBn_HI,selpar_age4_cBn_PH);
init_bounded_number sel_age5_cBn_logit(selpar_age5_cBn_LO,selpar_age5_cBn_HI,selpar_age5_cBn_PH);
init_bounded_number sel_age6_cBn_logit(selpar_age6_cBn_LO,selpar_age6_cBn_HI,selpar_age6_cBn_PH);
vector sel_age_cBn_vec(1,nages);
number selpar_age0_cBn;
number selpar_age1_cBn;
number selpar_age2_cBn;
number selpar_age3_cBn;
number selpar_age4_cBn;
number selpar_age5_cBn;
number selpar_age6_cBn;
vector selpar_age0_cBn_out(1,8);
vector selpar_age1_cBn_out(1,8);
vector selpar_age2_cBn_out(1,8);
vector selpar_age3_cBn_out(1,8);
vector selpar_age4_cBn_out(1,8);
vector selpar_age5_cBn_out(1,8);
vector selpar_age6_cBn_out(1,8);
```

```
//logit based selectivity cB north - block 2
```

```
init_bounded_number sel_age0_cBn2_logit(selpar_age0_cBn2_LO,selpar_age0_cBn2_HI,selpar_age0_cBn2_PH);
```

```
init_bounded_number sel_age1_cBn2_logit(selpar_age1_cBn2_LO,selpar_age1_cBn2_HI,selpar_age1_cBn2_PH);
init_bounded_number sel_age2_cBn2_logit(selpar_age2_cBn2_LO,selpar_age2_cBn2_HI,selpar_age2_cBn2_PH);
init_bounded_number sel_age3_cBn2_logit(selpar_age3_cBn2_LO,selpar_age3_cBn2_HI,selpar_age3_cBn2_PH);
init_bounded_number sel_age4_cBn2_logit(selpar_age4_cBn2_LO,selpar_age4_cBn2_HI,selpar_age4_cBn2_PH);
init_bounded_number sel_age5_cBn2_logit(selpar_age5_cBn2_LO,selpar_age5_cBn2_HI,selpar_age5_cBn2_PH);
init_bounded_number sel_age6_cBn2_logit(selpar_age6_cBn2_LO,selpar_age6_cBn2_HI,selpar_age6_cBn2_PH);
vector sel_age_cBn2_vec(1,nages);
number selpar_age0_cBn2;
number selpar_age1_cBn2;
number selpar_age2_cBn2;
number selpar_age3_cBn2;
number selpar_age4_cBn2;
number selpar_age5_cBn2;
number selpar_age6_cBn2;
vector selpar_age0_cBn2_out(1,8);
vector selpar_age1_cBn2_out(1,8);
vector selpar_age2_cBn2_out(1,8);
vector selpar_age3_cBn2_out(1,8);
vector selpar_age4_cBn2_out(1,8);
vector selpar_age5_cBn2_out(1,8);
vector selpar_age6_cBn2_out(1,8);
```

```
//logit based selectivity cB south - block 1
```

```
init_bounded_number sel_age0_cBs_logit(selpar_age0_cBs_LO,selpar_age0_cBs_HI,selpar_age0_cBs_PH);
init_bounded_number sel_age1_cBs_logit(selpar_age1_cBs_LO,selpar_age1_cBs_HI,selpar_age1_cBs_PH);
init_bounded_number sel_age2_cBs_logit(selpar_age2_cBs_LO,selpar_age2_cBs_HI,selpar_age2_cBs_PH);
init_bounded_number sel_age3_cBs_logit(selpar_age3_cBs_LO,selpar_age3_cBs_HI,selpar_age3_cBs_PH);
init_bounded_number sel_age4_cBs_logit(selpar_age4_cBs_LO,selpar_age4_cBs_HI,selpar_age4_cBs_PH);
init_bounded_number sel_age5_cBs_logit(selpar_age5_cBs_LO,selpar_age5_cBs_HI,selpar_age5_cBs_PH);
init_bounded_number sel_age6_cBs_logit(selpar_age6_cBs_LO,selpar_age6_cBs_HI,selpar_age6_cBs_PH);
vector sel_age_cBs_vec(1,nages);
number selpar_age0_cBs;
number selpar_age1_cBs;
number selpar_age2_cBs;
number selpar_age3_cBs;
```



```
number selpar_age4_cBs;  
number selpar_age5_cBs;  
number selpar_age6_cBs;  
vector selpar_age0_cBs_out(1,8);  
vector selpar_age1_cBs_out(1,8);  
vector selpar_age2_cBs_out(1,8);  
vector selpar_age3_cBs_out(1,8);  
vector selpar_age4_cBs_out(1,8);  
vector selpar_age5_cBs_out(1,8);  
vector selpar_age6_cBs_out(1,8);
```

```
//logit based selectivity cB south - block 2
```

```
init_bounded_number sel_age0_cBs2_logit(selpar_age0_cBs2_LO,selpar_age0_cBs2_HI,selpar_age0_cBs2_PH);  
init_bounded_number sel_age1_cBs2_logit(selpar_age1_cBs2_LO,selpar_age1_cBs2_HI,selpar_age1_cBs2_PH);  
init_bounded_number sel_age2_cBs2_logit(selpar_age2_cBs2_LO,selpar_age2_cBs2_HI,selpar_age2_cBs2_PH);  
init_bounded_number sel_age3_cBs2_logit(selpar_age3_cBs2_LO,selpar_age3_cBs2_HI,selpar_age3_cBs2_PH);  
init_bounded_number sel_age4_cBs2_logit(selpar_age4_cBs2_LO,selpar_age4_cBs2_HI,selpar_age4_cBs2_PH);  
init_bounded_number sel_age5_cBs2_logit(selpar_age5_cBs2_LO,selpar_age5_cBs2_HI,selpar_age5_cBs2_PH);  
init_bounded_number sel_age6_cBs2_logit(selpar_age6_cBs2_LO,selpar_age6_cBs2_HI,selpar_age6_cBs2_PH);  
vector sel_age_cBs2_vec(1,nages);  
number selpar_age0_cBs2;  
number selpar_age1_cBs2;  
number selpar_age2_cBs2;  
number selpar_age3_cBs2;  
number selpar_age4_cBs2;  
number selpar_age5_cBs2;  
number selpar_age6_cBs2;  
vector selpar_age0_cBs2_out(1,8);  
vector selpar_age1_cBs2_out(1,8);  
vector selpar_age2_cBs2_out(1,8);  
vector selpar_age3_cBs2_out(1,8);  
vector selpar_age4_cBs2_out(1,8);  
vector selpar_age5_cBs2_out(1,8);  
vector selpar_age6_cBs2_out(1,8);
```

```

//Northern adult index selectivity-----
matrix sel_nad(styr_nad_cpue,endyr_nad_cpue,1,nages);
vector sel_nad_block1(1,nages);

init_bounded_number selpar_A50_nad(selpar_A50_nad_LO,selpar_A50_nad_HI,selpar_A50_nad_PH);
init_bounded_number selpar_slope_nad(selpar_slope_nad_LO,selpar_slope_nad_HI,selpar_slope_nad_PH);
init_bounded_number selpar_A502_nad(selpar_A502_nad_LO,selpar_A502_nad_HI,selpar_A502_nad_PH);
init_bounded_number selpar_slope2_nad(selpar_slope2_nad_LO,selpar_slope2_nad_HI,selpar_slope2_nad_PH);
vector selpar_A50_nad_out(1,8);
vector selpar_slope_nad_out(1,8);
vector selpar_A502_nad_out(1,8);
vector selpar_slope2_nad_out(1,8);

//logit based selectivity for NAD index
init_bounded_number sel_age0_nad_logit(selpar_age0_nad_LO,selpar_age0_nad_HI,selpar_age0_nad_PH);
init_bounded_number sel_age1_nad_logit(selpar_age1_nad_LO,selpar_age1_nad_HI,selpar_age1_nad_PH);
init_bounded_number sel_age2_nad_logit(selpar_age2_nad_LO,selpar_age2_nad_HI,selpar_age2_nad_PH);
init_bounded_number sel_age3_nad_logit(selpar_age3_nad_LO,selpar_age3_nad_HI,selpar_age3_nad_PH);
init_bounded_number sel_age4_nad_logit(selpar_age4_nad_LO,selpar_age4_nad_HI,selpar_age4_nad_PH);
init_bounded_number sel_age5_nad_logit(selpar_age5_nad_LO,selpar_age5_nad_HI,selpar_age5_nad_PH);
init_bounded_number sel_age6_nad_logit(selpar_age6_nad_LO,selpar_age6_nad_HI,selpar_age6_nad_PH);
vector sel_age_nad_vec(1,nages);
number selpar_age0_nad;
number selpar_age1_nad;
number selpar_age2_nad;
number selpar_age3_nad;
number selpar_age4_nad;
number selpar_age5_nad;
number selpar_age6_nad;
vector selpar_age0_nad_out(1,8);
vector selpar_age1_nad_out(1,8);
vector selpar_age2_nad_out(1,8);
vector selpar_age3_nad_out(1,8);
vector selpar_age4_nad_out(1,8);
vector selpar_age5_nad_out(1,8);

```

```
vector selpar_age6_nad_out(1,8);
```

```
//Middle adult index selectivity-----
```

```
matrix sel_mad(styr_mad_cpue,endyr_mad_cpue,1,nages);
```

```
vector sel_mad_block1(1,nages);
```

```
init_bounded_number selpar_A50_mad(selpar_A50_mad_LO,selpar_A50_mad_HI,selpar_A50_mad_PH);
```

```
init_bounded_number selpar_slope_mad(selpar_slope_mad_LO,selpar_slope_mad_HI,selpar_slope_mad_PH);
```

```
init_bounded_number selpar_A502_mad(selpar_A502_mad_LO,selpar_A502_mad_HI,selpar_A502_mad_PH);
```

```
init_bounded_number
```

```
selpar_slope2_mad(selpar_slope2_mad_LO,selpar_slope2_mad_HI,selpar_slope2_mad_PH);
```

```
vector selpar_A50_mad_out(1,8);
```

```
vector selpar_slope_mad_out(1,8);
```

```
vector selpar_A502_mad_out(1,8);
```

```
vector selpar_slope2_mad_out(1,8);
```

```
//logit based selectivity for MAD index
```

```
init_bounded_number sel_age0_mad_logit(selpar_age0_mad_LO,selpar_age0_mad_HI,selpar_age0_mad_PH);
```

```
init_bounded_number sel_age1_mad_logit(selpar_age1_mad_LO,selpar_age1_mad_HI,selpar_age1_mad_PH);
```

```
init_bounded_number sel_age2_mad_logit(selpar_age2_mad_LO,selpar_age2_mad_HI,selpar_age2_mad_PH);
```

```
init_bounded_number sel_age3_mad_logit(selpar_age3_mad_LO,selpar_age3_mad_HI,selpar_age3_mad_PH);
```

```
init_bounded_number sel_age4_mad_logit(selpar_age4_mad_LO,selpar_age4_mad_HI,selpar_age4_mad_PH);
```

```
init_bounded_number sel_age5_mad_logit(selpar_age5_mad_LO,selpar_age5_mad_HI,selpar_age5_mad_PH);
```

```
init_bounded_number sel_age6_mad_logit(selpar_age6_mad_LO,selpar_age6_mad_HI,selpar_age6_mad_PH);
```

```
vector sel_age_mad_vec(1,nages);
```

```
number selpar_age0_mad;
```

```
number selpar_age1_mad;
```

```
number selpar_age2_mad;
```

```
number selpar_age3_mad;
```

```
number selpar_age4_mad;
```

```
number selpar_age5_mad;
```

```
number selpar_age6_mad;
```

```
vector selpar_age0_mad_out(1,8);
```

```
vector selpar_age1_mad_out(1,8);
```

```
vector selpar_age2_mad_out(1,8);
```

```
vector selpar_age3_mad_out(1,8);
```

```
vector selpar_age4_mad_out(1,8);
vector selpar_age5_mad_out(1,8);
vector selpar_age6_mad_out(1,8);
```

```
//Southern adult index selectivity-----
```

```
matrix sel_sad(styr_sad_cpue,endyr_sad_cpue,1,nages);
vector sel_sad_block1(1,nages);
```

```
init_bounded_number selpar_A50_sad(selpar_A50_sad_LO,selpar_A50_sad_HI,selpar_A50_sad_PH);
init_bounded_number selpar_slope_sad(selpar_slope_sad_LO,selpar_slope_sad_HI,selpar_slope_sad_PH);
init_bounded_number selpar_A502_sad(selpar_A502_sad_LO,selpar_A502_sad_HI,selpar_A502_sad_PH);
init_bounded_number selpar_slope2_sad(selpar_slope2_sad_LO,selpar_slope2_sad_HI,selpar_slope2_sad_PH);
vector selpar_A50_sad_out(1,8);
vector selpar_slope_sad_out(1,8);
vector selpar_A502_sad_out(1,8);
vector selpar_slope2_sad_out(1,8);
```

```
//logit based selectivity for SAD index
```

```
init_bounded_number sel_age0_sad_logit(selpar_age0_sad_LO,selpar_age0_sad_HI,selpar_age0_sad_PH);
init_bounded_number sel_age1_sad_logit(selpar_age1_sad_LO,selpar_age1_sad_HI,selpar_age1_sad_PH);
init_bounded_number sel_age2_sad_logit(selpar_age2_sad_LO,selpar_age2_sad_HI,selpar_age2_sad_PH);
init_bounded_number sel_age3_sad_logit(selpar_age3_sad_LO,selpar_age3_sad_HI,selpar_age3_sad_PH);
init_bounded_number sel_age4_sad_logit(selpar_age4_sad_LO,selpar_age4_sad_HI,selpar_age4_sad_PH);
init_bounded_number sel_age5_sad_logit(selpar_age5_sad_LO,selpar_age5_sad_HI,selpar_age5_sad_PH);
init_bounded_number sel_age6_sad_logit(selpar_age6_sad_LO,selpar_age6_sad_HI,selpar_age6_sad_PH);
vector sel_age_sad_vec(1,nages);
number selpar_age0_sad;
number selpar_age1_sad;
number selpar_age2_sad;
number selpar_age3_sad;
number selpar_age4_sad;
number selpar_age5_sad;
number selpar_age6_sad;
vector selpar_age0_sad_out(1,8);
vector selpar_age1_sad_out(1,8);
```

```
vector selpar_age2_sad_out(1,8);
vector selpar_age3_sad_out(1,8);
vector selpar_age4_sad_out(1,8);
vector selpar_age5_sad_out(1,8);
vector selpar_age6_sad_out(1,8);
```

```
//Weighted total selectivity-----
```

```
//effort-weighted, recent selectivities
```

```
vector sel_wgtd_L(1,nages); //toward landings
```

```
vector sel_wgtd_tot(1,nages); //toward Z, landings plus deads discards
```

```
//-----
```

```
//-----CPUE Predictions-----
```

```
//Northern adult index
```

```
vector pred_nad_cpue(styr_nad_cpue, endyr_nad_cpue); //predicted NAD index (number fish per effort)
```

```
matrix N_nad_cpue(styr_nad_cpue, endyr_nad_cpue, 1, nages); //used to compute NAD index
```

```
//Middle adult index
```

```
vector pred_mad_cpue(styr_mad_cpue, endyr_mad_cpue); //predicted MAD index (number fish per effort)
```

```
matrix N_mad_cpue(styr_mad_cpue, endyr_mad_cpue, 1, nages); //used to compute MAD index
```

```
//Southern adult index
```

```
vector pred_sad_cpue(styr_sad_cpue, endyr_sad_cpue); //predicted SAD index (number fish per effort)
```

```
vector N_sad_cpue(styr_sad_cpue, endyr_sad_cpue); //used to compute SAD index
```

```
//Juvenile abundance index
```

```
vector pred_jai_cpue(styr_jai_cpue, endyr_jai_cpue); //predicted JAI index (number fish per effort)
```

```
vector N_jai_cpue(styr_jai_cpue, endyr_jai_cpue); //used to compute JAI index
```

```
//MARMAP and ECOMON index
```

```
vector pred_mareco_cpue(1, nyr_mareco_cpue);
```

```
vector SSB_mareco_cpue(1, nyr_mareco_cpue);
```

```
//---Catchability (CPUE q's)-----
```

```

init_bounded_number log_q_nad(log_q_nad_LO,log_q_nad_HI,log_q_nad_PH);
init_bounded_number log_q_mad(log_q_mad_LO,log_q_mad_HI,log_q_mad_PH);
init_bounded_number log_q_sad(log_q_sad_LO,log_q_sad_HI,log_q_sad_PH);
init_bounded_number log_q_jai(log_q_jai_LO,log_q_jai_HI,log_q_jai_PH);
init_bounded_number log_q2_jai(log_q2_jai_LO,log_q2_jai_HI,log_q2_jai_PH);
init_bounded_number log_q_mar(log_q_mar_LO,log_q_mar_HI,log_q_mar_PH);
init_bounded_number log_q_eco(log_q_eco_LO,log_q_eco_HI,log_q_eco_PH);
vector log_q_nad_out(1,8);
vector log_q_mad_out(1,8);
vector log_q_sad_out(1,8);
vector log_q_jai_out(1,8);
vector log_q2_jai_out(1,8);
vector log_q_mar_out(1,8);
vector log_q_eco_out(1,8);

number q_rate;

vector q_rate_fcn_nad(styr_nad_cpue,endyr_nad_cpue); //increase due to technology creep (saturates in
2003)-shouldn't really be used since fishery-independent

vector q_rate_fcn_mad(styr_mad_cpue,endyr_mad_cpue); //increase due to technology creep (saturates in
2003)-shouldn't really be used since fishery-independent

vector q_rate_fcn_sad(styr_sad_cpue,endyr_sad_cpue); //increase due to technology creep (saturates in 2003)-
shouldn't really be used since fishery-independent

vector q_rate_fcn_jai(styr_jai_cpue,endyr_jai_cpue); //increase due to technology creep (saturates in 2003)-
shouldn't really be used since fishery-independent

//vector q_rate_fcn_mar(styr_mar_cpue,endyr_mar_cpue); //increase due to technology creep (saturates in
2003)-shouldn't really be used since fishery-independent

//vector q_rate_fcn_eco(styr_eco_cpue,endyr_eco_cpue); //increase due to technology creep (saturates in
2003)-shouldn't really be used since fishery-independent

//init_bounded_number q_DD_beta(0.1,0.9,set_q_DD_phase); //not estimated so commented out and
declared as number (below)

number q_DD_beta;

vector q_DD_fcn(styr,endyr); //density dependent function as a multiple of q (scaled a la Katsukawa and
Matsuda. 2003)

number B0_q_DD; //B0 of ages q_DD_age plus

vector B_q_DD(styr,endyr); //annual biomass of ages q_DD_age plus

//Random walk catchability - not using

```

```

init_bounded_vector q_RW_log_dev_nad(styr_nad_cpue, endyr_nad_cpue-
1, log_RWq_LO, log_RWq_HI, log_RWq_PH);

init_bounded_vector q_RW_log_dev_mad(styr_mad_cpue, endyr_mad_cpue-
1, log_RWq_LO, log_RWq_HI, log_RWq_PH);

init_bounded_vector q_RW_log_dev_sad(styr_sad_cpue, endyr_sad_cpue-
1, log_RWq_LO, log_RWq_HI, log_RWq_PH);

init_bounded_vector q_RW_log_dev_jai(styr_jai_cpue, endyr_jai_cpue-
1, log_RWq_LO, log_RWq_HI, log_RWq_PH);

//init_bounded_vector q_RW_log_dev_mar(styr_mar_cpue, endyr_mar_cpue-
1, log_RWq_LO, log_RWq_HI, log_RWq_PH);

//init_bounded_vector q_RW_log_dev_eco(styr_eco_cpue, endyr_eco_cpue-
1, log_RWq_LO, log_RWq_HI, log_RWq_PH);

//Fishery independent catchability over time, may be constant
vector q_nad(styr_nad_cpue, endyr_nad_cpue);
vector q_mad(styr_mad_cpue, endyr_mad_cpue);
vector q_sad(styr_sad_cpue, endyr_sad_cpue);
vector q_jai(styr_jai_cpue, endyr_jai_cpue);
vector q2_jai(styr_jai_cpue, endyr_jai_cpue);
vector q_mar(1,8);
vector q_eco(9,26);

//-----
//---Landings in numbers (total or 1000 fish) and in wgt (1000s mt)-----
matrix L_cRn_num(styr, endyr, 1, nages); //landings (numbers) at age
matrix L_cRn_mt(styr, endyr, 1, nages); //landings (1000 mt whole weight) at age
vector pred_cRn_L_mt(styr, endyr); //yearly landings in 1000 mt whole summed over ages

matrix L_cRs_num(styr, endyr, 1, nages); //landings (numbers) at age
matrix L_cRs_mt(styr, endyr, 1, nages); //landings (1000 mt whole weight) at age
vector pred_cRs_L_mt(styr, endyr); //yearly landings in 1000 mt whole summed over ages

matrix L_cBn_num(styr, endyr, 1, nages); //landings (numbers) at age
matrix L_cBn_mt(styr, endyr, 1, nages); //landings (1000 mt whole weight) at age
vector pred_cBn_L_mt(styr, endyr); //yearly landings in 1000 mt whole summed over ages

matrix L_cBs_num(styr, endyr, 1, nages); //landings (numbers) at age

```

```

matrix L_cBs_mt(styr,endyr,1,nages); //landings (1000 mt whole weight) at age
vector pred_cBs_L_mt(styr,endyr); //yearly landings in 1000 mt whole summed over ages

matrix L_total_num(styr,endyr,1,nages); //total landings in number at age
matrix L_total_mt(styr,endyr,1,nages); //landings in 1000 mt whole wgt at age
vector L_total_mt_yr(styr,endyr); //total landings (1000 mt whole wgt) by yr summed over ages

////---MSY calcs-----
number F_cRn_prop; //proportion of F_sum attributable to cRn, last X=selpar_n_yrs_wgtd yrs
number F_cRs_prop; //proportion of F_sum attributable to cRs, last X=selpar_n_yrs_wgtd yrs
number F_cBn_prop; //proportion of F_sum attributable to cBn, last X=selpar_n_yrs_wgtd yrs
number F_cBs_prop; //proportion of F_sum attributable to cBs, last X=selpar_n_yrs_wgtd yrs
number F_temp_sum; //sum of geom mean Fsum's in last X yrs, used to compute F_fishery_prop

vector F_end(1,nages);
vector F_end_L(1,nages);
number F_end_apex;

number SSB_msy_out; //SSB (total mature biomass) at msy
number F_msy_out; //F at msy
number msy_mt_out; //max sustainable yield (1000 mt whole wgt)
number B_msy_out; //total biomass at MSY
number R_msy_out; //equilibrium recruitment at F=Fmsy
number spr_msy_out; //spr at F=Fmsy

number F35_dum; //intermediate calculation for F35
number F30_dum; //intermediate calculation for F30
number F40_dum; //intermediate calculation for F40
number F35_out; //F35
number F30_out; //F30
number F40_out; //F40
number SSB_F30_out;
number B_F30_out;
number R_F30_out;

```



```

number L_F30_knum_out;
number L_F30_mt_out;
number rec_mean;    //arithmetic average recruitment used in SPR-related quantities

vector N_age_msy(1,nages);    //numbers at age for MSY calculations: beginning of yr
vector N_age_msy_spawn(1,nages); //numbers at age for MSY calculations: time of peak spawning
vector L_age_msy(1,nages);    //landings at age for MSY calculations
vector Z_age_msy(1,nages);    //total mortality at age for MSY calculations
vector F_L_age_msy(1,nages);  //fishing mortality landings (not discards) at age for MSY calculations
vector F_msy(1,n_iter_msy);  //values of full F to be used in equilibrium calculations
vector spr_msy(1,n_iter_msy); //reproductive capacity-per-recruit values corresponding to F values in F_msy
vector R_eq(1,n_iter_msy);    //equilibrium recruitment values corresponding to F values in F_msy
vector L_eq_mt(1,n_iter_msy); //equilibrium landings(1000 mt whole wgt) values corresponding to F values in
F_msy
vector SSB_eq(1,n_iter_msy);  //equilibrium reproductive capacity values corresponding to F values in F_msy
vector B_eq(1,n_iter_msy);    //equilibrium biomass values corresponding to F values in F_msy

vector FdF_msy(styr,endyr);
vector FdF30(styr,endyr);
vector SdSSB_msy(styr,endyr+1);
number SdSSB_msy_end;
number FdF_msy_end;
number FdF_msy_end_mean;    //geometric mean of last X yrs
vector SdSSB_F30(styr,endyr+1);
number SdSSB_F30_end;
number FdF30_end_mean;    //geometric mean of last selpar_n_yrs_wgted yrs
number Fend_mean_temp;    //intermediate calc for geometric mean of last selpar_n_yrs_wgted yrs
number Fend_mean;    //geometric mean of last selpar_n_yrs_wgted yrs
vector L_age_F30(1,nages);  //landings at age for F30 calculations

vector wgt_wgted_L_mt(1,nages); //fishery-weighted average weight at age of landings in whole weight
number wgt_wgted_L_denom;    //used in intermediate calculations

number iter_inc_msy;    //increments used to compute msy, equals 1/(n_iter_msy-1)

////-----Mortality-----

```

```

vector M(1,nages);          //age-dependent natural mortality
matrix tv_M(styr,endyr,1,nages);    //age and time varying natural mortality

matrix F(styr,endyr,1,nages);
vector Fsum(styr,endyr);      //Full fishing mortality rate by year
vector Fapex(styr,endyr);    //Max across ages, fishing mortality rate by year (may differ from Fsum bc of
dome-shaped sel
matrix Z(styr,endyr,1,nages);

init_bounded_number log_avg_F_cRn(log_avg_F_cRn_LO,log_avg_F_cRn_HI,log_avg_F_cRn_PH);
vector log_avg_F_cRn_out(1,8);
init_bounded_dev_vector
log_F_dev_cRn(styr_cRn_L,endyr_cRn_L,log_F_dev_cRn_LO,log_F_dev_cRn_HI,log_F_dev_cRn_PH);
vector log_F_dev_cRn_out(styr_cRn_L,endyr_cRn_L);
matrix F_cRn(styr,endyr,1,nages);
vector F_cRn_out(styr,endyr);    //used for intermediate calculations in fcn get_mortality
number log_F_dev_init_cRn;
number log_F_dev_end_cRn;

init_bounded_number log_avg_F_cRs(log_avg_F_cRs_LO,log_avg_F_cRs_HI,log_avg_F_cRs_PH);
vector log_avg_F_cRs_out(1,8);
init_bounded_dev_vector
log_F_dev_cRs(styr_cRs_L,endyr_cRs_L,log_F_dev_cRs_LO,log_F_dev_cRs_HI,log_F_dev_cRs_PH);
vector log_F_dev_cRs_out(styr_cRs_L,endyr_cRs_L);
matrix F_cRs(styr,endyr,1,nages);
vector F_cRs_out(styr,endyr);    //used for intermediate calculations in fcn get_mortality
number log_F_dev_init_cRs;
number log_F_dev_end_cRs;

init_bounded_number log_avg_F_cBn(log_avg_F_cBn_LO,log_avg_F_cBn_HI,log_avg_F_cBn_PH);
vector log_avg_F_cBn_out(1,8);
init_bounded_dev_vector
log_F_dev_cBn(styr_cBn_L,endyr_cBn_L,log_F_dev_cBn_LO,log_F_dev_cBn_HI,log_F_dev_cBn_PH);
vector log_F_dev_cBn_out(styr_cBn_L,endyr_cBn_L);
matrix F_cBn(styr,endyr,1,nages);
vector F_cBn_out(styr,endyr);    //used for intermediate calculations in fcn get_mortality

```

```

number log_F_dev_init_cBn;
number log_F_dev_end_cBn;

init_bounded_number log_avg_F_cBs(log_avg_F_cBs_LO,log_avg_F_cBs_HI,log_avg_F_cBs_PH);
vector log_avg_F_cBs_out(1,8);
init_bounded_dev_vector
log_F_dev_cBs(styr_cBs_L,endyr_cBs_L,log_F_dev_cBs_LO,log_F_dev_cBs_HI,log_F_dev_cBs_PH);
vector log_F_dev_cBs_out(styr_cBs_L,endyr_cBs_L);
matrix F_cBs(styr,endyr,1,nages);
vector F_cBs_out(styr,endyr); //used for intermediate calculations in fcn get_mortality
number log_F_dev_init_cBs;
number log_F_dev_end_cBs;

//---Per-recruit stuff-----
vector N_age_spr(1,nages); //numbers at age for SPR calculations: beginning of year
vector N_age_spr_spawn(1,nages); //numbers at age for SPR calculations: time of peak spawning
vector L_age_spr(1,nages); //catch at age for SPR calculations
vector Z_age_spr(1,nages); //total mortality at age for SPR calculations
vector spr_static(styr,endyr); //vector of static SPR values by year
vector F_L_age_spr(1,nages); //fishing mortality of landings (not discards) at age for SPR calculations
vector F_spr(1,n_iter_spr); //values of full F to be used in per-recruit calculations
vector spr_spr(1,n_iter_spr); //reproductive capacity-per-recruit values corresponding to F values in F_spr
vector spr_ratio(1,n_iter_spr); //reproductive capacity-per-recruit relative to spr_F0 values corresponding to F
values in F_spr
vector L_spr(1,n_iter_spr); //landings(lb)-per-recruit (ypr) values corresponding to F values in F_spr

vector N_spr_F0(1,nages); //Used to compute spr at F=0: at time of peak spawning
vector N_bpr_F0(1,nages); //Used to compute bpr at F=0: at start of year
vector N_spr_initial(1,nages); //Initial spawners per recruit at age given initial F
vector N_initial_eq(1,nages); //Initial equilibrium abundance at age
vector F_initial(1,nages); //initial F at age
vector Z_initial(1,nages); //initial Z at age
number spr_initial; //initial spawners per recruit
number spr_F0; //Spawning biomass per recruit at F=0
number bpr_F0; //Biomass per recruit at F=0

```

```
number iter_inc_spr; //increments used to compute msy, equals max_F_spr_msy/(n_iter_spr-1)
```

```
////-----SDNR output-----
```

```
number sdnr_lc_nad;  
number sdnr_lc_mad;  
//number sdnr_lc_sad;
```

```
number sdnr_ac_cRn;  
number sdnr_ac_cRs;  
number sdnr_ac_cBn;  
number sdnr_ac_cBs;
```

```
number sdnr_l_nad;  
number sdnr_l_mad;  
number sdnr_l_sad;  
number sdnr_l_jai;  
number sdnr_l_mareco;
```

```
////-----Objective function components-----
```

```
number w_L;
```

```
number w_l_nad;  
number w_l_mad;  
number w_l_sad;  
number w_l_jai;  
number w_l_mareco;
```

```
number w_lc_nad;  
number w_lc_mad;  
//number w_lc_sad;
```

```
number w_ac_cRn;  
number w_ac_cRs;  
number w_ac_cBn;
```

number w\_ac\_cBs;

number w\_Nage\_init;

number w\_rec;

number w\_rec\_early;

number w\_rec\_end;

number w\_fullF;

number w\_Ftune;

number f\_cRn\_L;

number f\_cRs\_L;

number f\_cBn\_L;

number f\_cBs\_L;

number f\_nad\_cpue;

number f\_mad\_cpue;

number f\_sad\_cpue;

number f\_jai\_cpue;

number f\_mareco\_cpue;

number f\_nad\_lenc;

number f\_mad\_lenc;

//number f\_sad\_lenc;

number f\_cRn\_agec;

number f\_cRs\_agec;

number f\_cBn\_agec;

number f\_cBs\_agec;

// Penalties and constraints. Not all are used.

number f\_Nage\_init; //weight on log devs to estimate initial abundance (excluding first age)

number f\_rec\_dev; //weight on recruitment deviations to fit S-R curve

number f\_rec\_dev\_early; //extra weight on deviations in first recruitment stanza

number f\_rec\_dev\_end; //extra weight on deviations in ending recruitment stanza

number f\_fullF\_constraint; //penalty for Fapex>X





```

log_dm_mad_lc=set_log_dm_mad_lc(1);
//log_dm_sad_lc=set_log_dm_sad_lc(1);

log_dm_cRn_ac=set_log_dm_cRn_ac(1);
log_dm_cRs_ac=set_log_dm_cRs_ac(1);
log_dm_cBn_ac=set_log_dm_cBn_ac(1);
log_dm_cBs_ac=set_log_dm_cBs_ac(1);

log_q_nad=set_log_q_nad(1);
log_q_mad=set_log_q_mad(1);
log_q_sad=set_log_q_sad(1);
log_q_jai=set_log_q_jai(1);
log_q2_jai=set_log_q2_jai(1);
log_q_mar=set_log_q_mar(1);
log_q_eco=set_log_q_eco(1);

q_rate=set_q_rate;
q_rate_fcn_nad=1.0;
q_rate_fcn_mad=1.0;
q_rate_fcn_sad=1.0;
q_rate_fcn_jai=1.0;
//q_rate_fcn_mar=1.0;
//q_rate_fcn_eco=1.0;
q_DD_beta=set_q_DD_beta;
q_DD_fcn=1.0;
q_RW_log_dev_nad.initialize();
q_RW_log_dev_mad.initialize();
q_RW_log_dev_sad.initialize();
q_RW_log_dev_jai.initialize();
//q_RW_log_dev_mar.initialize();
//q_RW_log_dev_eco.initialize();

if (set_q_rate_phase<0 & q_rate!=0.0)
{
for (iyear=styr_nad_cpue; iyear<=endyr_nad_cpue; iyear++)

```



```

{ if (iyear>styr_nad_cpue & iyear <=2003)
  //q_rate_fcn_nad(iyear)=(1.0+q_rate)*q_rate_fcn_nad(iyear-1); //compound
  q_rate_fcn_nad(iyear)=(1.0+(iyear-styr_nad_cpue)*q_rate)*q_rate_fcn_nad(styr_nad_cpue); //linear
}
if (iyear>2003) {q_rate_fcn_nad(iyear)=q_rate_fcn_nad(iyear-1);}
}
for (iyear=styr_mad_cpue; iyear<=endyr_mad_cpue; iyear++)
{ if (iyear>styr_mad_cpue & iyear <=2003)
  //q_rate_fcn_mad(iyear)=(1.0+q_rate)*q_rate_fcn_mad(iyear-1); //compound
  q_rate_fcn_mad(iyear)=(1.0+(iyear-styr_mad_cpue)*q_rate)*q_rate_fcn_mad(styr_mad_cpue); //linear
}
if (iyear>2003) {q_rate_fcn_mad(iyear)=q_rate_fcn_mad(iyear-1);}
}
for (iyear=styr_sad_cpue; iyear<=endyr_sad_cpue; iyear++)
{ if (iyear>styr_sad_cpue & iyear <=2003)
  //q_rate_fcn_sad(iyear)=(1.0+q_rate)*q_rate_fcn_sad(iyear-1); //compound
  q_rate_fcn_sad(iyear)=(1.0+(iyear-styr_sad_cpue)*q_rate)*q_rate_fcn_sad(styr_sad_cpue); //linear
}
if (iyear>2003) {q_rate_fcn_sad(iyear)=q_rate_fcn_sad(iyear-1);}
}
for (iyear=styr_jai_cpue; iyear<=endyr_jai_cpue; iyear++)
{ if (iyear>styr_jai_cpue & iyear <=2003)
  //q_rate_fcn_jai(iyear)=(1.0+q_rate)*q_rate_fcn_jai(iyear-1); //compound
  q_rate_fcn_jai(iyear)=(1.0+(iyear-styr_jai_cpue)*q_rate)*q_rate_fcn_jai(styr_jai_cpue); //linear
}
if (iyear>2003) {q_rate_fcn_jai(iyear)=q_rate_fcn_jai(iyear-1);}
}
//for (iyear=styr_mar_cpue; iyear<=endyr_mar_cpue; iyear++)
//{ if (iyear>styr_mar_cpue & iyear <=2003)
//  //q_rate_fcn_mar(iyear)=(1.0+q_rate)*q_rate_fcn_mar(iyear-1); //compound
//  q_rate_fcn_mar(iyear)=(1.0+(iyear-styr_mar_cpue)*q_rate)*q_rate_fcn_mar(styr_mar_cpue); //linear
// }
// if (iyear>2003) {q_rate_fcn_mar(iyear)=q_rate_fcn_mar(iyear-1);}
// }
//for (iyear=styr_eco_cpue; iyear<=endyr_eco_cpue; iyear++)

```

```
// { if (iyear>styr_eco_cpue & iyear <=2003)
//   {/q_rate_fcn_eco(iyear)=(1.0+q_rate)*q_rate_fcn_eco(iyear-1); //compound
//     q_rate_fcn_eco(iyear)=(1.0+(iyear-styr_eco_cpue)*q_rate)*q_rate_fcn_eco(styr_eco_cpue); //linear
//   }
//   if (iyear>2003) {q_rate_fcn_eco(iyear)=q_rate_fcn_eco(iyear-1);}
// }
} //end q_rate conditional
```

```
w_l=set_w_l;
```

```
w_l_nad=set_w_l_nad;
```

```
w_l_mad=set_w_l_mad;
```

```
w_l_sad=set_w_l_sad;
```

```
w_l_jai=set_w_l_jai;
```

```
w_l_mareco=set_w_l_mareco;
```

```
w_lc_nad=set_w_lc_nad;
```

```
w_lc_mad=set_w_lc_mad;
```

```
//w_lc_sad=set_w_lc_sad;
```

```
w_ac_cRn=set_w_ac_cRn;
```

```
w_ac_cRs=set_w_ac_cRs;
```

```
w_ac_cBn=set_w_ac_cBn;
```

```
w_ac_cBs=set_w_ac_cBs;
```

```
w_Nage_init=set_w_Nage_init;
```

```
w_rec=set_w_rec;
```

```
w_rec_early=set_w_rec_early;
```

```
w_rec_end=set_w_rec_end;
```

```
w_fullF=set_w_fullF;
```

```
w_Ftune=set_w_Ftune;
```

```
log_avg_F_cRn=set_log_avg_F_cRn(1);
```

```
log_avg_F_cRs=set_log_avg_F_cRs(1);
```

```
log_avg_F_cBn=set_log_avg_F_cBn(1);
```

log\_avg\_F\_cBs=set\_log\_avg\_F\_cBs(1);

log\_F\_dev\_cRn=set\_log\_F\_dev\_cRn\_vals;

log\_F\_dev\_cRs=set\_log\_F\_dev\_cRs\_vals;

log\_F\_dev\_cBn=set\_log\_F\_dev\_cBn\_vals;

log\_F\_dev\_cBs=set\_log\_F\_dev\_cBs\_vals;

selpar\_A50\_cRn=set\_selpar\_A50\_cRn(1); //Block 1

selpar\_slope\_cRn=set\_selpar\_slope\_cRn(1);

selpar\_A502\_cRn=set\_selpar\_A502\_cRn(1);

selpar\_slope2\_cRn=set\_selpar\_slope2\_cRn(1);

selpar\_A50\_cRn2=set\_selpar\_A50\_cRn2(1); //Block 2

selpar\_slope\_cRn2=set\_selpar\_slope\_cRn2(1);

selpar\_A502\_cRn2=set\_selpar\_A502\_cRn2(1);

selpar\_slope2\_cRn2=set\_selpar\_slope2\_cRn2(1);

selpar\_A50\_cRn3=set\_selpar\_A50\_cRn3(1); //Block 3

selpar\_slope\_cRn3=set\_selpar\_slope\_cRn3(1);

selpar\_A502\_cRn3=set\_selpar\_A502\_cRn3(1);

selpar\_slope2\_cRn3=set\_selpar\_slope2\_cRn3(1);

selpar\_A50\_cRn4=set\_selpar\_A50\_cRn4(1); //Block 4

selpar\_slope\_cRn4=set\_selpar\_slope\_cRn4(1);

selpar\_A502\_cRn4=set\_selpar\_A502\_cRn4(1);

selpar\_slope2\_cRn4=set\_selpar\_slope2\_cRn4(1);

selpar\_A50\_cRs=set\_selpar\_A50\_cRs(1); //Block 1

selpar\_slope\_cRs=set\_selpar\_slope\_cRs(1);

selpar\_A502\_cRs=set\_selpar\_A502\_cRs(1);

selpar\_slope2\_cRs=set\_selpar\_slope2\_cRs(1);

selpar\_A50\_cRs2=set\_selpar\_A50\_cRs2(1); //Block 2

selpar\_slope\_cRs2=set\_selpar\_slope\_cRs2(1);

selpar\_A502\_cRs2=set\_selpar\_A502\_cRs2(1);

selpar\_slope2\_cRs2=set\_selpar\_slope2\_cRs2(1);

selpar\_A50\_cRs3=set\_selpar\_A50\_cRs3(1); //Block 3

selpar\_slope\_cRs3=set\_selpar\_slope\_cRs3(1);

selpar\_A502\_cRs3=set\_selpar\_A502\_cRs3(1);

selpar\_slope2\_cRs3=set\_selpar\_slope2\_cRs3(1);

selpar\_A50\_cRs4=set\_selpar\_A50\_cRs4(1); //Block 4

selpar\_slope\_cRs4=set\_selpar\_slope\_cRs4(1);

selpar\_A502\_cRs4=set\_selpar\_A502\_cRs4(1);

selpar\_slope2\_cRs4=set\_selpar\_slope2\_cRs4(1);

sel\_age0\_cRn\_logit=set\_sel\_age0\_cRn(1); //setting cR selectivity at age in logit space - block 1

sel\_age1\_cRn\_logit=set\_sel\_age1\_cRn(1);

sel\_age2\_cRn\_logit=set\_sel\_age2\_cRn(1);

sel\_age3\_cRn\_logit=set\_sel\_age3\_cRn(1);

sel\_age4\_cRn\_logit=set\_sel\_age4\_cRn(1);

sel\_age5\_cRn\_logit=set\_sel\_age5\_cRn(1);

sel\_age6\_cRn\_logit=set\_sel\_age6\_cRn(1);

sel\_age0\_cRn2\_logit=set\_sel\_age0\_cRn2(1); //setting cR selectivity at age in logit space - block 2

sel\_age1\_cRn2\_logit=set\_sel\_age1\_cRn2(1);

sel\_age2\_cRn2\_logit=set\_sel\_age2\_cRn2(1);

sel\_age3\_cRn2\_logit=set\_sel\_age3\_cRn2(1);

sel\_age4\_cRn2\_logit=set\_sel\_age4\_cRn2(1);

sel\_age5\_cRn2\_logit=set\_sel\_age5\_cRn2(1);

sel\_age6\_cRn2\_logit=set\_sel\_age6\_cRn2(1);

sel\_age0\_cRn3\_logit=set\_sel\_age0\_cRn3(1); //setting cR selectivity at age in logit space - block 3

sel\_age1\_cRn3\_logit=set\_sel\_age1\_cRn3(1);

sel\_age2\_cRn3\_logit=set\_sel\_age2\_cRn3(1);

sel\_age3\_cRn3\_logit=set\_sel\_age3\_cRn3(1);

sel\_age4\_cRn3\_logit=set\_sel\_age4\_cRn3(1);

sel\_age5\_cRn3\_logit=set\_sel\_age5\_cRn3(1);

sel\_age6\_cRn3\_logit=set\_sel\_age6\_cRn3(1);

```
sel_age0_cRn4_logit=set_sel_age0_cRn4(1); //setting cR selectivity at age in logit space - block 4
sel_age1_cRn4_logit=set_sel_age1_cRn4(1);
sel_age2_cRn4_logit=set_sel_age2_cRn4(1);
sel_age3_cRn4_logit=set_sel_age3_cRn4(1);
sel_age4_cRn4_logit=set_sel_age4_cRn4(1);
sel_age5_cRn4_logit=set_sel_age5_cRn4(1);
sel_age6_cRn4_logit=set_sel_age6_cRn4(1);
```

```
sel_age0_cRs_logit=set_sel_age0_cRs(1); //setting cR selectivity at age in logit space - block 1
sel_age1_cRs_logit=set_sel_age1_cRs(1);
sel_age2_cRs_logit=set_sel_age2_cRs(1);
sel_age3_cRs_logit=set_sel_age3_cRs(1);
sel_age4_cRs_logit=set_sel_age4_cRs(1);
sel_age5_cRs_logit=set_sel_age5_cRs(1);
sel_age6_cRs_logit=set_sel_age6_cRs(1);
```

```
sel_age0_cRs2_logit=set_sel_age0_cRs2(1); //setting cR selectivity at age in logit space - block 2
sel_age1_cRs2_logit=set_sel_age1_cRs2(1);
sel_age2_cRs2_logit=set_sel_age2_cRs2(1);
sel_age3_cRs2_logit=set_sel_age3_cRs2(1);
sel_age4_cRs2_logit=set_sel_age4_cRs2(1);
sel_age5_cRs2_logit=set_sel_age5_cRs2(1);
sel_age6_cRs2_logit=set_sel_age6_cRs2(1);
```

```
sel_age0_cRs3_logit=set_sel_age0_cRs3(1); //setting cR selectivity at age in logit space - block 3
sel_age1_cRs3_logit=set_sel_age1_cRs3(1);
sel_age2_cRs3_logit=set_sel_age2_cRs3(1);
sel_age3_cRs3_logit=set_sel_age3_cRs3(1);
sel_age4_cRs3_logit=set_sel_age4_cRs3(1);
sel_age5_cRs3_logit=set_sel_age5_cRs3(1);
sel_age6_cRs3_logit=set_sel_age6_cRs3(1);
```

```
sel_age0_cRs4_logit=set_sel_age0_cRs4(1); //setting cR selectivity at age in logit space - block 4
sel_age1_cRs4_logit=set_sel_age1_cRs4(1);
```

```
sel_age2_cRs4_logit=set_sel_age2_cRs4(1);
sel_age3_cRs4_logit=set_sel_age3_cRs4(1);
sel_age4_cRs4_logit=set_sel_age4_cRs4(1);
sel_age5_cRs4_logit=set_sel_age5_cRs4(1);
sel_age6_cRs4_logit=set_sel_age6_cRs4(1);
```

```
selpar_A50_cBn=set_selpar_A50_cBn(1);          //Block 1
selpar_slope_cBn=set_selpar_slope_cBn(1);
selpar_A502_cBn=set_selpar_A502_cBn(1);
selpar_slope2_cBn=set_selpar_slope2_cBn(1);
```

```
selpar_A50_cBn2=set_selpar_A50_cBn2(1);       //Block 2
selpar_slope_cBn2=set_selpar_slope_cBn2(1);
selpar_A502_cBn2=set_selpar_A502_cBn2(1);
selpar_slope2_cBn2=set_selpar_slope2_cBn2(1);
```

```
selpar_A50_cBs=set_selpar_A50_cBs(1);         //Block 1
selpar_slope_cBs=set_selpar_slope_cBs(1);
selpar_A502_cBs=set_selpar_A502_cBs(1);
selpar_slope2_cBs=set_selpar_slope2_cBs(1);
```

```
selpar_A50_cBs2=set_selpar_A50_cBs2(1);      //Block 2
selpar_slope_cBs2=set_selpar_slope_cBs2(1);
selpar_A502_cBs2=set_selpar_A502_cBs2(1);
selpar_slope2_cBs2=set_selpar_slope2_cBs2(1);
```

```
sel_age0_cBn_logit=set_sel_age0_cBn(1); //setting cB selectivity at age in logit space - block 1
sel_age1_cBn_logit=set_sel_age1_cBn(1);
sel_age2_cBn_logit=set_sel_age2_cBn(1);
sel_age3_cBn_logit=set_sel_age3_cBn(1);
sel_age4_cBn_logit=set_sel_age4_cBn(1);
sel_age5_cBn_logit=set_sel_age5_cBn(1);
sel_age6_cBn_logit=set_sel_age6_cBn(1);
```

```
sel_age0_cBn2_logit=set_sel_age0_cBn2(1); //setting cB selectivity at age in logit space - block 2
```

```
sel_age1_cBn2_logit=set_sel_age1_cBn2(1);
sel_age2_cBn2_logit=set_sel_age2_cBn2(1);
sel_age3_cBn2_logit=set_sel_age3_cBn2(1);
sel_age4_cBn2_logit=set_sel_age4_cBn2(1);
sel_age5_cBn2_logit=set_sel_age5_cBn2(1);
sel_age6_cBn2_logit=set_sel_age6_cBn2(1);
```

```
sel_age0_cBs_logit=set_sel_age0_cBs(1); //setting cB selectivity at age in logit space - block 1
sel_age1_cBs_logit=set_sel_age1_cBs(1);
sel_age2_cBs_logit=set_sel_age2_cBs(1);
sel_age3_cBs_logit=set_sel_age3_cBs(1);
sel_age4_cBs_logit=set_sel_age4_cBs(1);
sel_age5_cBs_logit=set_sel_age5_cBs(1);
sel_age6_cBs_logit=set_sel_age6_cBs(1);
```

```
sel_age0_cBs2_logit=set_sel_age0_cBs2(1); //setting cB selectivity at age in logit space - block 2
sel_age1_cBs2_logit=set_sel_age1_cBs2(1);
sel_age2_cBs2_logit=set_sel_age2_cBs2(1);
sel_age3_cBs2_logit=set_sel_age3_cBs2(1);
sel_age4_cBs2_logit=set_sel_age4_cBs2(1);
sel_age5_cBs2_logit=set_sel_age5_cBs2(1);
sel_age6_cBs2_logit=set_sel_age6_cBs2(1);
```

```
selpar_A50_nad=set_selpar_A50_nad(1);
selpar_slope_nad=set_selpar_slope_nad(1);
selpar_A502_nad=set_selpar_A502_nad(1);
selpar_slope2_nad=set_selpar_slope2_nad(1);
```

```
sel_age0_nad_logit=set_sel_age0_nad(1); //setting NAD selectivity at age in logit space
sel_age1_nad_logit=set_sel_age1_nad(1);
sel_age2_nad_logit=set_sel_age2_nad(1);
sel_age3_nad_logit=set_sel_age3_nad(1);
sel_age4_nad_logit=set_sel_age4_nad(1);
sel_age5_nad_logit=set_sel_age5_nad(1);
sel_age6_nad_logit=set_sel_age6_nad(1);
```

```
selpar_A50_mad=set_selpar_A50_mad(1);
selpar_slope_mad=set_selpar_slope_mad(1);
selpar_A502_mad=set_selpar_A502_mad(1);
selpar_slope2_mad=set_selpar_slope2_mad(1);
```

```
sel_age0_mad_logit=set_sel_age0_mad(1); //setting MAD selectivity at age in logit space
sel_age1_mad_logit=set_sel_age1_mad(1);
sel_age2_mad_logit=set_sel_age2_mad(1);
sel_age3_mad_logit=set_sel_age3_mad(1);
sel_age4_mad_logit=set_sel_age4_mad(1);
sel_age5_mad_logit=set_sel_age5_mad(1);
sel_age6_mad_logit=set_sel_age6_mad(1);
```

```
selpar_A50_sad=set_selpar_A50_sad(1);
selpar_slope_sad=set_selpar_slope_sad(1);
selpar_A502_sad=set_selpar_A502_sad(1);
selpar_slope2_sad=set_selpar_slope2_sad(1);
```

```
sel_age0_sad_logit=set_sel_age0_sad(1); //setting SAD selectivity at age in logit space
sel_age1_sad_logit=set_sel_age1_sad(1);
sel_age2_sad_logit=set_sel_age2_sad(1);
sel_age3_sad_logit=set_sel_age3_sad(1);
sel_age4_sad_logit=set_sel_age4_sad(1);
sel_age5_sad_logit=set_sel_age5_sad(1);
sel_age6_sad_logit=set_sel_age6_sad(1);
```

```
sqrt2pi=sqrt(2.*3.14159265);
g2mt=0.000001; //conversion of grams to metric tons
g2kg=0.001; //conversion of grams to kg
mt2klb=2.20462; //conversion of metric tons to 1000 lb
mt2lb=mt2klb*1000.0; //conversion of metric tons to lb
g2klb=g2mt*mt2klb; //conversion of grams to 1000 lb
dzero=0.00001;
huge_number=1.0e+10;
```



```

SSB_msy_out=0.0;

iter_inc_msy=max_F_spr_msy/(n_iter_msy-1);
iter_inc_spr=max_F_spr_msy/(n_iter_spr-1);

maturity_f=maturity_f_obs;
maturity_m=maturity_m_obs;
tv_maturity=tv_maturity_obs;
prop_f=prop_f_obs;
prop_m=1.0-prop_f_obs;

//Fill in sample sizes of comps, possibly sampled in nonconsec yrs
//Used primarily for output in R object

nsamp_nad_lenc_allyr=missing;
nsamp_mad_lenc_allyr=missing;
//nsamp_sad_lenc_allyr=missing;

nsamp_cRn_agec_allyr=missing;
nsamp_cRs_agec_allyr=missing;
nsamp_cBn_agec_allyr=missing;
nsamp_cBs_agec_allyr=missing;

nfish_nad_lenc_allyr=missing;
nfish_mad_lenc_allyr=missing;
//nfish_sad_lenc_allyr=missing;

nfish_cRn_agec_allyr=missing;
nfish_cRs_agec_allyr=missing;
nfish_cBn_agec_allyr=missing;
nfish_cBs_agec_allyr=missing;

for (iyear=1; iyear<=nyr_nad_lenc; iyear++)
  {if (nsamp_nad_lenc(iyear)>=minSS_nad_lenc)

```

```

    {nsamp_nad_lenc_allyr(yrs_nad_lenc(iyear))=nsamp_nad_lenc(iyear);
    nfish_nad_lenc_allyr(yrs_nad_lenc(iyear))=nfish_nad_lenc(iyear);}}

for (iyear=1; iyear<=nyr_mad_lenc; iyear++)
  {if (nsamp_mad_lenc(iyear)>=minSS_mad_lenc)
    {nsamp_mad_lenc_allyr(yrs_mad_lenc(iyear))=nsamp_mad_lenc(iyear);
    nfish_mad_lenc_allyr(yrs_mad_lenc(iyear))=nfish_mad_lenc(iyear);}}

//for (iyear=1; iyear<=nyr_sad_lenc; iyear++)
// {if (nsamp_sad_lenc(iyear)>=minSS_sad_lenc)
// {nsamp_sad_lenc_allyr(yrs_sad_lenc(iyear))=nsamp_sad_lenc(iyear);
// nfish_sad_lenc_allyr(yrs_sad_lenc(iyear))=nfish_sad_lenc(iyear);}}

for (iyear=1; iyear<=nyr_cRn_agec; iyear++)
  {if (nsamp_cRn_agec(iyear)>=minSS_cRn_agec)
    {nsamp_cRn_agec_allyr(yrs_cRn_agec(iyear))=nsamp_cRn_agec(iyear);
    nfish_cRn_agec_allyr(yrs_cRn_agec(iyear))=nfish_cRn_agec(iyear);}}

for (iyear=1; iyear<=nyr_cRs_agec; iyear++)
  {if (nsamp_cRs_agec(iyear)>=minSS_cRs_agec)
    {nsamp_cRs_agec_allyr(yrs_cRs_agec(iyear))=nsamp_cRs_agec(iyear);
    nfish_cRs_agec_allyr(yrs_cRs_agec(iyear))=nfish_cRs_agec(iyear);}}

for (iyear=1; iyear<=nyr_cBn_agec; iyear++)
  {if (nsamp_cBn_agec(iyear)>=minSS_cBn_agec)
    {nsamp_cBn_agec_allyr(yrs_cBn_agec(iyear))=nsamp_cBn_agec(iyear);
    nfish_cBn_agec_allyr(yrs_cBn_agec(iyear))=nfish_cBn_agec(iyear);}}

for (iyear=1; iyear<=nyr_cBs_agec; iyear++)
  {if (nsamp_cBs_agec(iyear)>=minSS_cBs_agec)
    {nsamp_cBs_agec_allyr(yrs_cBs_agec(iyear))=nsamp_cBs_agec(iyear);
    nfish_cBs_agec_allyr(yrs_cBs_agec(iyear))=nfish_cBs_agec(iyear);}}

//fill in Fs for msy and per-recruit analyses

```

```
F_msy(1)=0.0;
for (ff=2;ff<=n_iter_msy;ff++) {F_msy(ff)=F_msy(ff-1)+iter_inc_msy;}
F_spr(1)=0.0;
for (ff=2;ff<=n_iter_spr;ff++) {F_spr(ff)=F_spr(ff-1)+iter_inc_spr;}
```

```
//fill in F's, Catch matrices, and log rec dev with zero's
```

```
F_cRn.initialize(); L_cRn_num.initialize();
F_cRs.initialize(); L_cRs_num.initialize();
F_cBn.initialize(); L_cBn_num.initialize();
F_cBs.initialize(); L_cBs_num.initialize();
```

```
F_cRn_out.initialize();
F_cRs_out.initialize();
F_cBn_out.initialize();
F_cBs_out.initialize();
```

```
sel_cRn.initialize();
sel_cRs.initialize();
sel_cBn.initialize();
sel_cBs.initialize();
```

```
sel_nad.initialize();
sel_mad.initialize();
sel_sad.initialize();
```

```
sel_cRn_block1.initialize();
sel_cRn_block2.initialize();
sel_cRn_block3.initialize();
sel_cRn_block4.initialize();
sel_cRs_block1.initialize();
sel_cRs_block2.initialize();
sel_cRs_block3.initialize();
sel_cRs_block4.initialize();
sel_cBn_block1.initialize();
```



```

//cout << "got reprod" << endl;
get_length_at_age_dist();
//cout<< "got predicted length at age distribution"<<endl;
get_weight_at_age_landings();
//cout<< "got weight at age of landings"<<endl;
get_spr_F0();
//cout << "got F0 spr" << endl;
get_selectivity();
//cout << "got selectivity" << endl;
get_mortality();
//cout << "got mortalities" << endl;
get_bias_corr();
//cout<< "got recruitment bias correction" << endl;
get_numbers_at_age();
//cout << "got numbers at age" << endl;
get_landings_numbers();
//cout << "got landings in numbers" << endl;
get_landings_wgt();
//cout << "got landings in wgt" << endl;
get_catchability_fcns();
//cout << "got catchability_fcns" << endl;
get_indices();
//cout << "got indices" << endl;
get_length_comps();
//cout<< "got length comps"<< endl;
get_age_comps();
//cout<< "got age comps"<< endl;
evaluate_objective_function();
//cout << "objective function calculations complete" << endl;

```

FUNCTION get\_length\_weight\_at\_age

```

    //population fork length in mm
    //compute mean length (mm FL) and weight (whole) at age
    meanlen_FL=Linf*(1.0-mfexp(-K*(agebins-t0)));

```

```

meanlen_FL_apr15=tv_len_apr15;
meanlen_FL_jun1=tv_len_jun1;
meanlen_FL_oct15=tv_len_oct15;
wgt_fish_mt=g2mt*wgt_middle; //wgt in mt - middle of year
wgt_spawn_mt=g2mt*wgt_spawn; //wgt in mt - spawning (Mar 1)
tv_wgt_middle_mt=g2mt*tv_wgt_middle;
tv_wgt_spawn_mt=g2mt*tv_wgt_spawn;

```

FUNCTION get\_reprod

```

reprod=elem_prod(elem_prod(prop_f,maturity_f),fecundity);

for (iyear=styr; iyear<=endyr; iyear++)
{
  reprod_tv(iyear)=elem_prod(elem_prod(prop_f,tv_maturity(iyear)),tv_fecundity(iyear));
}

```

FUNCTION get\_length\_at\_age\_dist

```

//compute matrix of length at age, based on the normal distribution
//population
for (iyear=styr; iyear<=endyr; iyear++)
{
  for (iage=1;iage<=nages;iage++)
  {
    len_cv_mad(iage)=len_cv_mad_val;
    len_sd_mad(iyear,iage)=meanlen_FL_apr15(iyear,iage)*len_cv_mad(iage);
    zscore_lzero=(0.0-meanlen_FL_apr15(iyear,iage))/len_sd_mad(iyear,iage);
    cprob_lzero=cumd_norm(zscore_lzero);

    //first length bin
    //population
    zscore_len=((lenbins(1)+0.5*lenbins_width)-meanlen_FL_apr15(iyear,iage)) / len_sd_mad(iyear,iage);
    cprob_lenvec(1)=cumd_norm(zscore_len); //includes any probability mass below zero
    lenprob_apr15(iyear,iage,1)=cprob_lenvec(1)-cprob_lzero; //removes any probability mass below zero

```

```

//most other length bins
//population
for (ilen=2;ilen<nlenbins;ilen++)
{
  zscore_len=((lenbins(ilen)+0.5*lenbins_width)-meanlen_FL_apr15(iyear,iage)) / len_sd_mad(iyear,iage);
  cprob_lenvec(ilen)=cumd_norm(zscore_len);
  lenprob_apr15(iyear,iage,ilen)=cprob_lenvec(ilen)-cprob_lenvec(ilen-1);
}

//last length bin is a plus group
//population
zscore_len=((lenbins(nlenbins)-0.5*lenbins_width)-meanlen_FL_apr15(iyear,iage)) / len_sd_mad(iyear,iage);
lenprob_apr15(iyear,iage,nlenbins)=1.0-cumd_norm(zscore_len);
lenprob_apr15(iyear,iage)=lenprob_apr15(iyear,iage)/(1.0-cprob_lzero); //renormalize to account for any prob
mass below size=0
}

//fleet and survey specific length probs
//lenprob_mad(iyear)=lenprob_apr15(iyear);
lenprob_mad=lenprob_apr15;
}
//cout << "lenprob mad " << lenprob_mad << endl;

//for (iyear=styr; iyear<=endyr; iyear++)
//{
//for (iage=1;iage<=nages;iage++)
//{
// len_cv_sad(iage)=len_cv_sad_val;
// len_sd_sad(iyear,iage)=meanlen_FL_apr15(iyear,iage)*len_cv_sad(iage);
// zscore_lzero=(0.0-meanlen_FL_apr15(iyear,iage))/len_sd_sad(iyear,iage);
// cprob_lzero=cumd_norm(zscore_lzero);

//first length bin
//population
// zscore_len=((lenbins(1)+0.5*lenbins_width)-meanlen_FL_apr15(iyear,iage)) / len_sd_sad(iyear,iage);

```

```

// cprob_lenvec(1)=cumd_norm(zscore_len);    //includes any probability mass below zero
// lenprob_apr15(iyear,iage,1)=cprob_lenvec(1)-cprob_lzero; //removes any probability mass below zero

//most other length bins
//population
// for (ilen=2;ilen<nlenbins;ilen++)
// {
//   zscore_len=((lenbins(ilen)+0.5*lenbins_width)-meanlen_FL_apr15(iyear,iage)) / len_sd_sad(iyear,iage);
//   cprob_lenvec(ilen)=cumd_norm(zscore_len);
//   lenprob_apr15(iyear,iage,ilen)=cprob_lenvec(ilen)-cprob_lenvec(ilen-1);
// }

//last length bin is a plus group
//population
// zscore_len=((lenbins(nlenbins)-0.5*lenbins_width)-meanlen_FL_apr15(iyear,iage)) / len_sd_sad(iyear,iage);
//   lenprob_apr15(iyear,iage,nlenbins)=1.0-cumd_norm(zscore_len);
//   lenprob_apr15(iyear,iage)=lenprob_apr15(iyear,iage)/(1.0-cprob_lzero); //renormalize to account for any
//   prob mass below size=0
// }

//fleet and survey specific length probs
//lenprob_sad(iyear)=lenprob_jun1(iyear);
//lenprob_sad=lenprob_apr15;
//}

for (iyear=styr; iyear<=endyr; iyear++)
{
for (iage=1;iage<=nages;iage++)
{
len_cv_nad(iage)=len_cv_nad_val;
len_sd_nad(iyear,iage)=meanlen_FL_oct15(iyear,iage)*len_cv_nad(iage);
zscore_lzero=(0.0-meanlen_FL_oct15(iyear,iage))/len_sd_nad(iyear,iage);
cprob_lzero=cumd_norm(zscore_lzero);

//first length bin

```



```

        //population
zscore_len=((lenbins(1)+0.5*lenbins_width)-meanlen_FL_oct15(iyear,iage)) / len_sd_nad(iyear,iage);
cprob_lenvec(1)=cumd_norm(zscore_len);    //includes any probability mass below zero
lenprob_oct15(iyear,iage,1)=cprob_lenvec(1)-cprob_lzero; //removes any probability mass below zero

//most other length bins
//population
for (ilen=2;ilen<nlenbins;ilen++)
{
    zscore_len=((lenbins(ilen)+0.5*lenbins_width)-meanlen_FL_oct15(iyear,iage)) / len_sd_nad(iyear,iage);
        cprob_lenvec(ilen)=cumd_norm(zscore_len);
    lenprob_oct15(iyear,iage,ilen)=cprob_lenvec(ilen)-cprob_lenvec(ilen-1);
}

//last length bin is a plus group
//population
zscore_len=((lenbins(nlenbins)-0.5*lenbins_width)-meanlen_FL_oct15(iyear,iage)) / len_sd_nad(iyear,iage);
    lenprob_oct15(iyear,iage,nlenbins)=1.0-cum_norm(zscore_len);
    lenprob_oct15(iyear,iage)=lenprob_oct15(iyear,iage)/(1.0-cprob_lzero); //renormalize to account for any prob
mass below size=0
}

//fleet and survey specific length probs
//lenprob_nad(iyear)=lenprob_oct15(iyear);
lenprob_nad=lenprob_oct15;
}

FUNCTION get_weight_at_age_landings ///whole weight in mt

for (iyear=styr; iyear<=endyr; iyear++)
{
    wholewgt_cR_mt(iyear)=tv_wgt_middle_mt(iyear);
}

FUNCTION get_spr_F0

```

```

//at mdyr, apply half this yr's mortality, half next yr's
N_spr_F0(1)=1.0*mfexp(-1.0*M(1)*spawn_time_frac); //at peak spawning time
N_bpr_F0(1)=1.0; //at start of year
for (iage=2; iage<=nages; iage++)
{ N_spr_F0(iage)=N_spr_F0(iage-1)*mfexp(-1.0*(M(iage-1)*(1.0-spawn_time_frac) + M(iage)*spawn_time_frac));
  N_bpr_F0(iage)=N_bpr_F0(iage-1)*mfexp(-1.0*(M(iage-1)));
}
N_spr_F0(nages)=N_spr_F0(nages)/(1.0-mfexp(-1.0*M(nages))); //plus group (sum of geometric series)
N_bpr_F0(nages)=N_bpr_F0(nages)/(1.0-mfexp(-1.0*M(nages)));

spr_F0=sum(elem_prod(N_spr_F0,reprod));
bpr_F0=sum(elem_prod(N_bpr_F0,wgt_spawn_mt));

```

FUNCTION get\_selectivity

```

sel_cRn_block1=logistic_double(agebins, selpar_A50_cRn, selpar_slope_cRn,
selpar_A502_cRn,selpar_slope2_cRn);

sel_cRn_block2=logistic_double(agebins, selpar_A50_cRn2, selpar_slope_cRn2,
selpar_A502_cRn2,selpar_slope2_cRn2);

sel_cRn_block3=logistic_double(agebins, selpar_A50_cRn3, selpar_slope_cRn3,
selpar_A502_cRn3,selpar_slope2_cRn3);

sel_cRn_block4=logistic_double(agebins, selpar_A50_cRn4, selpar_slope_cRn4,
selpar_A502_cRn4,selpar_slope2_cRn4);

sel_cRs_block1=logistic_double(agebins, selpar_A50_cRs, selpar_slope_cRs, selpar_A502_cRs,selpar_slope2_cRs);

sel_cRs_block2=logistic_double(agebins, selpar_A50_cRs2, selpar_slope_cRs2,
selpar_A502_cRs2,selpar_slope2_cRs2);

sel_cRs_block3=logistic_double(agebins, selpar_A50_cRs3, selpar_slope_cRs3,
selpar_A502_cRs3,selpar_slope2_cRs3);

sel_cRs_block4=logistic_double(agebins, selpar_A50_cRs4, selpar_slope_cRs4,
selpar_A502_cRs4,selpar_slope2_cRs4);

sel_cBn_block1=logistic_double(agebins, selpar_A50_cBn, selpar_slope_cBn,
selpar_A502_cBn,selpar_slope2_cBn);

sel_cBn_block2=logistic_double(agebins, selpar_A50_cBn2, selpar_slope_cBn2,
selpar_A502_cBn2,selpar_slope2_cBn2);

```

```
sel_cBs_block1=logistic_double(agebins, selpar_A50_cBs, selpar_slope_cBs, selpar_A502_cBs,selpar_slope2_cBs);  
//sel_cBs_block2=logistic_double(agebins, selpar_A50_cBs2, selpar_slope_cBs2,  
selpar_A502_cBs2,selpar_slope2_cBs2);
```

```
sel_nad_block1=logistic(agebins, selpar_A50_nad, selpar_slope_nad);  
//sel_nad_block1=logistic_double(agebins, selpar_A50_nad, selpar_slope_nad,  
selpar_A502_nad,selpar_slope2_nad);
```

```
sel_mad_block1=logistic_double(agebins, selpar_A50_mad, selpar_slope_mad,  
selpar_A502_mad,selpar_slope2_mad);
```

```
//sel_sad_block1=logistic_double(agebins, selpar_A50_sad, selpar_slope_sad,  
selpar_A502_sad,selpar_slope2_sad);
```

```
//selpar_age0_cRn=1.0/(1.0+mfexp(-sel_age0_cRn_logit)); //block 1
```

```
//selpar_age1_cRn=1.0/(1.0+mfexp(-sel_age1_cRn_logit));
```

```
//selpar_age2_cRn=1.0/(1.0+mfexp(-sel_age2_cRn_logit));
```

```
//selpar_age2_cRn=1.0;
```

```
//selpar_age3_cRn=1.0/(1.0+mfexp(-sel_age3_cRn_logit));
```

```
//selpar_age4_cRn=1.0/(1.0+mfexp(-sel_age4_cRn_logit));
```

```
//selpar_age5_cRn=1.0/(1.0+mfexp(-sel_age5_cRn_logit));
```

```
//selpar_age6_cRn=1.0/(1.0+mfexp(-sel_age6_cRn_logit));
```

```
//sel_age_cRn_vec(1)=selpar_age0_cRn;
```

```
//sel_age_cRn_vec(2)=selpar_age1_cRn;
```

```
//sel_age_cRn_vec(3)=selpar_age2_cRn;
```

```
//sel_age_cRn_vec(4)=selpar_age3_cRn;
```

```
//sel_age_cRn_vec(5)=selpar_age4_cRn;
```

```
//sel_age_cRn_vec(6)=selpar_age5_cRn;
```

```
//sel_age_cRn_vec(7)=selpar_age6_cRn;
```

```
//sel_cRn_block1=sel_age_cRn_vec;
```

```
//selpar_age0_cRn2=1.0/(1.0+mfexp(-sel_age0_cRn2_logit)); //block 2
```

```
//selpar_age1_cRn2=1.0/(1.0+mfexp(-sel_age1_cRn2_logit));
```

```
//selpar_age2_cRn2=1.0/(1.0+mfexp(-sel_age2_cRn2_logit));
```

```
//selpar_age3_cRn2=1.0;
```

```
//selpar_age3_cRn2=1.0/(1.0+mfexp(-sel_age3_cRn2_logit));
```

```
//selpar_age4_cRn2=1.0/(1.0+mfexp(-sel_age4_cRn2_logit));
```

```
//selpar_age5_cRn2=1.0/(1.0+mfexp(-sel_age5_cRn2_logit));
```

```
//selpar_age6_cRn2=1.0/(1.0+mfexp(-sel_age6_cRn2_logit));  
//sel_age_cRn2_vec(1)=selpar_age0_cRn2;  
//sel_age_cRn2_vec(2)=selpar_age1_cRn2;  
//sel_age_cRn2_vec(3)=selpar_age2_cRn2;  
//sel_age_cRn2_vec(4)=selpar_age3_cRn2;  
//sel_age_cRn2_vec(5)=selpar_age4_cRn2;  
//sel_age_cRn2_vec(6)=selpar_age5_cRn2;  
//sel_age_cRn2_vec(7)=selpar_age6_cRn2;  
//sel_cRn_block2=sel_age_cRn2_vec;
```

```
//selpar_age0_cRn3=1.0/(1.0+mfexp(-sel_age0_cRn3_logit)); //block 3  
//selpar_age1_cRn3=1.0/(1.0+mfexp(-sel_age1_cRn3_logit));  
//selpar_age2_cRn3=1.0/(1.0+mfexp(-sel_age2_cRn3_logit));  
//selpar_age3_cRn3=1.0;  
//selpar_age3_cRn3=1.0/(1.0+mfexp(-sel_age3_cRn3_logit));  
//selpar_age4_cRn3=1.0/(1.0+mfexp(-sel_age4_cRn3_logit));  
//selpar_age5_cRn3=1.0/(1.0+mfexp(-sel_age5_cRn3_logit));  
//selpar_age6_cRn3=1.0/(1.0+mfexp(-sel_age6_cRn3_logit));  
//sel_age_cRn3_vec(1)=selpar_age0_cRn3;  
//sel_age_cRn3_vec(2)=selpar_age1_cRn3;  
//sel_age_cRn3_vec(3)=selpar_age2_cRn3;  
//sel_age_cRn3_vec(4)=selpar_age3_cRn3;  
//sel_age_cRn3_vec(5)=selpar_age4_cRn3;  
//sel_age_cRn3_vec(6)=selpar_age5_cRn3;  
//sel_age_cRn3_vec(7)=selpar_age6_cRn3;  
//sel_cRn_block3=sel_age_cRn3_vec;
```

```
//selpar_age0_cRn4=1.0/(1.0+mfexp(-sel_age0_cRn4_logit)); //block 4  
//selpar_age1_cRn4=1.0/(1.0+mfexp(-sel_age1_cRn4_logit));  
//selpar_age2_cRn4=1.0/(1.0+mfexp(-sel_age2_cRn4_logit));  
//selpar_age3_cRn4=1.0;  
//selpar_age3_cRn4=1.0/(1.0+mfexp(-sel_age3_cRn4_logit));  
//selpar_age4_cRn4=1.0/(1.0+mfexp(-sel_age4_cRn4_logit));  
//selpar_age5_cRn4=1.0/(1.0+mfexp(-sel_age5_cRn4_logit));  
//selpar_age6_cRn4=1.0/(1.0+mfexp(-sel_age6_cRn4_logit));
```

```
//sel_age_cRn4_vec(1)=selpar_age0_cRn4;  
//sel_age_cRn4_vec(2)=selpar_age1_cRn4;  
//sel_age_cRn4_vec(3)=selpar_age2_cRn4;  
//sel_age_cRn4_vec(4)=selpar_age3_cRn4;  
//sel_age_cRn4_vec(5)=selpar_age4_cRn4;  
//sel_age_cRn4_vec(6)=selpar_age5_cRn4;  
//sel_age_cRn4_vec(7)=selpar_age6_cRn4;  
//sel_cRn_block4=sel_age_cRn4_vec;
```

```
//selpar_age0_cRs=1.0/(1.0+mfexp(-sel_age0_cRs_logit)); //block 1  
//selpar_age1_cRs=1.0/(1.0+mfexp(-sel_age1_cRs_logit));  
//selpar_age2_cRs=1.0/(1.0+mfexp(-sel_age2_cRs_logit));  
//selpar_age2_cRs=1.0;  
//selpar_age3_cRs=1.0/(1.0+mfexp(-sel_age3_cRs_logit));  
//selpar_age4_cRs=1.0/(1.0+mfexp(-sel_age4_cRs_logit));  
//selpar_age5_cRs=1.0/(1.0+mfexp(-sel_age5_cRs_logit));  
//selpar_age6_cRs=1.0/(1.0+mfexp(-sel_age6_cRs_logit));  
//sel_age_cRs_vec(1)=selpar_age0_cRs;  
//sel_age_cRs_vec(2)=selpar_age1_cRs;  
//sel_age_cRs_vec(3)=selpar_age2_cRs;  
//sel_age_cRs_vec(4)=selpar_age3_cRs;  
//sel_age_cRs_vec(5)=selpar_age4_cRs;  
//sel_age_cRs_vec(6)=selpar_age5_cRs;  
//sel_age_cRs_vec(7)=selpar_age6_cRs;  
//sel_cRs_block1=sel_age_cRs_vec;
```

```
//selpar_age0_cRs2=1.0/(1.0+mfexp(-sel_age0_cRs2_logit)); //block 2  
//selpar_age1_cRs2=1.0/(1.0+mfexp(-sel_age1_cRs2_logit));  
//selpar_age2_cRs2=1.0/(1.0+mfexp(-sel_age2_cRs2_logit));  
//selpar_age2_cRs2=1.0;  
//selpar_age3_cRs2=1.0/(1.0+mfexp(-sel_age3_cRs2_logit));  
//selpar_age4_cRs2=1.0/(1.0+mfexp(-sel_age4_cRs2_logit));  
//selpar_age5_cRs2=1.0/(1.0+mfexp(-sel_age5_cRs2_logit));  
//selpar_age6_cRs2=1.0/(1.0+mfexp(-sel_age6_cRs2_logit));  
//sel_age_cRs2_vec(1)=selpar_age0_cRs2;
```

```
//sel_age_cRs2_vec(2)=selpar_age1_cRs2;  
//sel_age_cRs2_vec(3)=selpar_age2_cRs2;  
//sel_age_cRs2_vec(4)=selpar_age3_cRs2;  
//sel_age_cRs2_vec(5)=selpar_age4_cRs2;  
//sel_age_cRs2_vec(6)=selpar_age5_cRs2;  
//sel_age_cRs2_vec(7)=selpar_age6_cRs2;  
//sel_cRs_block2=sel_age_cRs2_vec;
```

```
//selpar_age0_cRs3=1.0/(1.0+mfexp(-sel_age0_cRs3_logit)); //block 3  
//selpar_age1_cRs3=1.0/(1.0+mfexp(-sel_age1_cRs3_logit));  
//selpar_age2_cRs3=1.0/(1.0+mfexp(-sel_age2_cRs3_logit));  
//selpar_age2_cRs3=1.0;  
//selpar_age3_cRs3=1.0/(1.0+mfexp(-sel_age3_cRs3_logit));  
//selpar_age4_cRs3=1.0/(1.0+mfexp(-sel_age4_cRs3_logit));  
//selpar_age5_cRs3=1.0/(1.0+mfexp(-sel_age5_cRs3_logit));  
//selpar_age6_cRs3=1.0/(1.0+mfexp(-sel_age6_cRs3_logit));  
//sel_age_cRs3_vec(1)=selpar_age0_cRs3;  
//sel_age_cRs3_vec(2)=selpar_age1_cRs3;  
//sel_age_cRs3_vec(3)=selpar_age2_cRs3;  
//sel_age_cRs3_vec(4)=selpar_age3_cRs3;  
//sel_age_cRs3_vec(5)=selpar_age4_cRs3;  
//sel_age_cRs3_vec(6)=selpar_age5_cRs3;  
//sel_age_cRs3_vec(7)=selpar_age6_cRs3;  
//sel_cRs_block3=sel_age_cRs3_vec;
```

```
//selpar_age0_cRs4=1.0/(1.0+mfexp(-sel_age0_cRs4_logit)); //block 4  
//selpar_age1_cRs4=1.0/(1.0+mfexp(-sel_age1_cRs4_logit));  
//selpar_age2_cRs4=1.0/(1.0+mfexp(-sel_age2_cRs4_logit));  
//selpar_age2_cRs4=1.0;  
//selpar_age3_cRs4=1.0/(1.0+mfexp(-sel_age3_cRs4_logit));  
//selpar_age4_cRs4=1.0/(1.0+mfexp(-sel_age4_cRs4_logit));  
//selpar_age5_cRs4=1.0/(1.0+mfexp(-sel_age5_cRs4_logit));  
//selpar_age6_cRs4=1.0/(1.0+mfexp(-sel_age6_cRs4_logit));  
//sel_age_cRs4_vec(1)=selpar_age0_cRs4;  
//sel_age_cRs4_vec(2)=selpar_age1_cRs4;
```

```
//sel_age_cRs4_vec(3)=selpar_age2_cRs4;  
//sel_age_cRs4_vec(4)=selpar_age3_cRs4;  
//sel_age_cRs4_vec(5)=selpar_age4_cRs4;  
//sel_age_cRs4_vec(6)=selpar_age5_cRs4;  
//sel_age_cRs4_vec(7)=selpar_age6_cRs4;  
//sel_cRs_block4=sel_age_cRs4_vec;
```

```
//selpar_age0_cBn=1.0/(1.0+mfexp(-sel_age0_cBn_logit)); //block 1  
//selpar_age1_cBn=1.0/(1.0+mfexp(-sel_age1_cBn_logit));  
//selpar_age2_cBn=1.0/(1.0+mfexp(-sel_age2_cBn_logit));  
//selpar_age3_cBn=1.0;  
//selpar_age3_cBn=1.0/(1.0+mfexp(-sel_age3_cBn_logit));  
//selpar_age4_cBn=1.0/(1.0+mfexp(-sel_age4_cBn_logit));  
//selpar_age5_cBn=1.0/(1.0+mfexp(-sel_age5_cBn_logit));  
//selpar_age6_cBn=1.0/(1.0+mfexp(-sel_age6_cBn_logit));  
//sel_age_cBn_vec(1)=selpar_age0_cBn;  
//sel_age_cBn_vec(2)=selpar_age1_cBn;  
//sel_age_cBn_vec(3)=selpar_age2_cBn;  
//sel_age_cBn_vec(4)=selpar_age3_cBn;  
//sel_age_cBn_vec(5)=selpar_age4_cBn;  
//sel_age_cBn_vec(6)=selpar_age5_cBn;  
//sel_age_cBn_vec(7)=selpar_age6_cBn;  
//sel_cBn_block1=sel_age_cBn_vec;
```

```
//selpar_age0_cBn2=1.0/(1.0+mfexp(-sel_age0_cBn2_logit)); //block 2  
//selpar_age1_cBn2=1.0/(1.0+mfexp(-sel_age1_cBn2_logit));  
//selpar_age2_cBn2=1.0/(1.0+mfexp(-sel_age2_cBn2_logit));  
//selpar_age3_cBn2=1.0;  
//selpar_age3_cBn2=1.0/(1.0+mfexp(-sel_age3_cBn2_logit));  
//selpar_age4_cBn2=1.0/(1.0+mfexp(-sel_age4_cBn2_logit));  
//selpar_age5_cBn2=1.0/(1.0+mfexp(-sel_age5_cBn2_logit));  
//selpar_age6_cBn2=1.0/(1.0+mfexp(-sel_age6_cBn2_logit));  
//sel_age_cBn2_vec(1)=selpar_age0_cBn2;  
//sel_age_cBn2_vec(2)=selpar_age1_cBn2;  
//sel_age_cBn2_vec(3)=selpar_age2_cBn2;
```

```
//sel_age_cBn2_vec(4)=selpar_age3_cBn2;  
//sel_age_cBn2_vec(5)=selpar_age4_cBn2;  
//sel_age_cBn2_vec(6)=selpar_age5_cBn2;  
//sel_age_cBn2_vec(7)=selpar_age6_cBn2;  
//sel_cBn_block2=sel_age_cBn2_vec;
```

```
//selpar_age0_cBs=1.0/(1.0+mfexp(-sel_age0_cBs_logit)); //block 1  
//selpar_age1_cBs=1.0/(1.0+mfexp(-sel_age1_cBs_logit));  
//selpar_age2_cBs=1.0/(1.0+mfexp(-sel_age2_cBs_logit));  
//selpar_age2_cBs=1.0;  
//selpar_age3_cBs=1.0/(1.0+mfexp(-sel_age3_cBs_logit));  
//selpar_age4_cBs=1.0/(1.0+mfexp(-sel_age4_cBs_logit));  
//selpar_age5_cBs=1.0/(1.0+mfexp(-sel_age5_cBs_logit));  
//selpar_age6_cBs=1.0/(1.0+mfexp(-sel_age6_cBs_logit));  
//sel_age_cBs_vec(1)=selpar_age0_cBs;  
//sel_age_cBs_vec(2)=selpar_age1_cBs;  
//sel_age_cBs_vec(3)=selpar_age2_cBs;  
//sel_age_cBs_vec(4)=selpar_age3_cBs;  
//sel_age_cBs_vec(5)=selpar_age4_cBs;  
//sel_age_cBs_vec(6)=selpar_age5_cBs;  
//sel_age_cBs_vec(7)=selpar_age6_cBs;  
//sel_cBs_block1=sel_age_cBs_vec;
```

```
//selpar_age0_cBs2=1.0/(1.0+mfexp(-sel_age0_cBs2_logit)); //block 2  
//selpar_age1_cBs2=1.0/(1.0+mfexp(-sel_age1_cBs2_logit));  
//selpar_age2_cBs2=1.0/(1.0+mfexp(-sel_age2_cBs2_logit));  
//selpar_age2_cBs2=1.0;  
//selpar_age3_cBs2=1.0/(1.0+mfexp(-sel_age3_cBs2_logit));  
//selpar_age4_cBs2=1.0/(1.0+mfexp(-sel_age4_cBs2_logit));  
//selpar_age5_cBs2=1.0/(1.0+mfexp(-sel_age5_cBs2_logit));  
//selpar_age6_cBs2=1.0/(1.0+mfexp(-sel_age6_cBs2_logit));  
//sel_age_cBs2_vec(1)=selpar_age0_cBs2;  
//sel_age_cBs2_vec(2)=selpar_age1_cBs2;  
//sel_age_cBs2_vec(3)=selpar_age2_cBs2;  
//sel_age_cBs2_vec(4)=selpar_age3_cBs2;
```



```
//sel_age_cBs2_vec(5)=selpar_age4_cBs2;  
//sel_age_cBs2_vec(6)=selpar_age5_cBs2;  
//sel_age_cBs2_vec(7)=selpar_age6_cBs2;  
//sel_cBs_block2=sel_age_cBs2_vec;
```

```
//selpar_age0_nad=1.0/(1.0+mfexp(-sel_age0_nad_logit));  
//selpar_age1_nad=1.0/(1.0+mfexp(-sel_age1_nad_logit));  
//selpar_age2_nad=1.0/(1.0+mfexp(-sel_age2_nad_logit));  
//selpar_age2_nad=1.0;  
//selpar_age3_nad=1.0/(1.0+mfexp(-sel_age3_nad_logit));  
//selpar_age4_nad=1.0/(1.0+mfexp(-sel_age4_nad_logit));  
//selpar_age5_nad=1.0/(1.0+mfexp(-sel_age5_nad_logit));  
//selpar_age6_nad=1.0/(1.0+mfexp(-sel_age6_nad_logit));  
//sel_age_nad_vec(1)=selpar_age0_nad;  
//sel_age_nad_vec(2)=selpar_age1_nad;  
//sel_age_nad_vec(3)=selpar_age2_nad;  
//sel_age_nad_vec(4)=selpar_age3_nad;  
//sel_age_nad_vec(5)=selpar_age4_nad;  
//sel_age_nad_vec(6)=selpar_age5_nad;  
//sel_age_nad_vec(7)=selpar_age6_nad;  
//sel_nad_block1=sel_age_nad_vec;
```

```
//selpar_age0_mad=1.0/(1.0+mfexp(-sel_age0_mad_logit));  
//selpar_age1_mad=1.0/(1.0+mfexp(-sel_age1_mad_logit));  
//selpar_age2_mad=1.0/(1.0+mfexp(-sel_age2_mad_logit));  
//selpar_age2_mad=1.0;  
//selpar_age3_mad=1.0/(1.0+mfexp(-sel_age3_mad_logit));  
//selpar_age4_mad=1.0/(1.0+mfexp(-sel_age4_mad_logit));  
//selpar_age5_mad=1.0/(1.0+mfexp(-sel_age5_mad_logit));  
//selpar_age6_mad=1.0/(1.0+mfexp(-sel_age6_mad_logit));  
//sel_age_mad_vec(1)=selpar_age0_mad;  
//sel_age_mad_vec(2)=selpar_age1_mad;  
//sel_age_mad_vec(3)=selpar_age2_mad;  
//sel_age_mad_vec(4)=selpar_age3_mad;  
//sel_age_mad_vec(5)=selpar_age4_mad;
```

```
//sel_age_mad_vec(6)=selpar_age5_mad;
//sel_age_mad_vec(7)=selpar_age6_mad;
//sel_mad_block1=sel_age_mad_vec;

//selpar_age0_sad=1.0/(1.0+mfexp(-sel_age0_sad_logit));
//selpar_age1_sad=1.0/(1.0+mfexp(-sel_age1_sad_logit));
//selpar_age2_sad=1.0/(1.0+mfexp(-sel_age2_sad_logit));
//selpar_age2_sad=1.0;
//selpar_age3_sad=1.0/(1.0+mfexp(-sel_age3_sad_logit));
//selpar_age4_sad=1.0/(1.0+mfexp(-sel_age4_sad_logit));
//selpar_age5_sad=1.0/(1.0+mfexp(-sel_age5_sad_logit));
//selpar_age6_sad=1.0/(1.0+mfexp(-sel_age6_sad_logit));
//sel_age_sad_vec(1)=selpar_age0_sad;
//sel_age_sad_vec(2)=selpar_age1_sad;
//sel_age_sad_vec(3)=selpar_age2_sad;
//sel_age_sad_vec(4)=selpar_age3_sad;
//sel_age_sad_vec(5)=selpar_age4_sad;
//sel_age_sad_vec(6)=selpar_age5_sad;
//sel_age_sad_vec(7)=selpar_age6_sad;
//sel_sad_block1=sel_age_sad_vec;
```

```
//BLOCK 1 for selex - 1955 to 1969
```

```
for (iyear=styr; iyear<=endyr_selex_phase1; iyear++)
```

```
{
  sel_cRn(iyear)=sel_cRn_block1;
  sel_cRs(iyear)=sel_cRs_block1;
  sel_cBn(iyear)=sel_cBn_block1;
  sel_cBs(iyear)=sel_cBs_block1;
}
```

```
//BLOCK 2 for selex - 1970 to 1971
```

```
for (iyear=(endyr_selex_phase1+1); iyear<=endyr_selex_phase2; iyear++)
```

```
{
  //sel_cRn(iyear)=sel_cRn_block1;
  sel_cRn(iyear)=sel_cRn_block2;
```

```
sel_cRs(iyear)=sel_cRs_block1;
sel_cBn(iyear)=sel_cBn_block1;
sel_cBs(iyear)=sel_cBs_block1;
}
```

```
//BLOCK 3 for selex - 1972 to 1984
```

```
for (iyear=(endyr_selex_phase2+1); iyear<=endyr_selex_phase3; iyear++)
```

```
{
//sel_cRn(iyear)=sel_cRn_block1;
sel_cRn(iyear)=sel_cRn_block2;
//sel_cRs(iyear)=sel_cRs_block1;
sel_cRs(iyear)=sel_cRs_block2;
sel_cBn(iyear)=sel_cBn_block1;
sel_cBs(iyear)=sel_cBs_block1;
}
```

```
//BLOCK 4 for selex - 1985 to 1989
```

```
for (iyear=(endyr_selex_phase3+1); iyear<=endyr_selex_phase4; iyear++)
```

```
{
//sel_cRn(iyear)=sel_cRn_block1;
sel_cRn(iyear)=sel_cRn_block2;
//sel_cRs(iyear)=sel_cRs_block1;
sel_cRs(iyear)=sel_cRs_block2;
sel_cBn(iyear)=sel_cBn_block1;
sel_cBs(iyear)=sel_cBs_block1;
```

```
sel_mad(iyear)=sel_mad_block1;
}
```

```
//BLOCK 5 for selex - 1990 to 1993
```

```
for (iyear=(endyr_selex_phase4+1); iyear<=endyr_selex_phase5; iyear++)
```

```
{
//sel_cRn(iyear)=sel_cRn_block1;
sel_cRn(iyear)=sel_cRn_block2;
//sel_cRs(iyear)=sel_cRs_block1;
```

```
sel_cRs(iyear)=sel_cRs_block2;  
sel_cBn(iyear)=sel_cBn_block1;  
sel_cBs(iyear)=sel_cBs_block1;
```

```
sel_nad(iyear)=sel_nad_block1;  
sel_mad(iyear)=sel_mad_block1;  
//sel_sad(iyear)=sel_sad_block1;  
}
```

```
//BLOCK 6 for selex - 1994 to 2004
```

```
for (iyear=(endyr_selex_phase5+1); iyear<=endyr_selex_phase6; iyear++)
```

```
{  
  //sel_cRn(iyear)=sel_cRn_block1;  
  sel_cRn(iyear)=sel_cRn_block3;  
  //sel_cRs(iyear)=sel_cRs_block1;  
  sel_cRs(iyear)=sel_cRs_block2;  
  sel_cBn(iyear)=sel_cBn_block1;  
  sel_cBs(iyear)=sel_cBs_block1;
```

```
  sel_nad(iyear)=sel_nad_block1;  
  sel_mad(iyear)=sel_mad_block1;  
  //sel_sad(iyear)=sel_sad_block1;  
}
```

```
//BLOCK 7 for selex - 2005 to 2012
```

```
for (iyear=(endyr_selex_phase6+1); iyear<=endyr_selex_phase7; iyear++)
```

```
{  
  //sel_cRn(iyear)=sel_cRn_block1;  
  sel_cRn(iyear)=sel_cRn_block3;  
  //sel_cRs(iyear)=sel_cRs_block1;  
  sel_cRs(iyear)=sel_cRs_block3;  
  sel_cBn(iyear)=sel_cBn_block1;  
  sel_cBs(iyear)=sel_cBs_block1;
```

```
  sel_nad(iyear)=sel_nad_block1;
```

```
sel_mad(iyear)=sel_mad_block1;
//sel_sad(iyear)=sel_sad_block1;
}
```

```
//BLOCK 8 for selex - 2012 to 2017
```

```
for (iyear=(endyr_selex_phase7+1); iyear<=endyr; iyear++)
```

```
{
//sel_cRn(iyear)=sel_cRn_block1;
//sel_cRn(iyear)=sel_cRn_block3;
sel_cRn(iyear)=sel_cRn_block4;
//sel_cRs(iyear)=sel_cRs_block1;
//sel_cRs(iyear)=sel_cRs_block3;
sel_cRs(iyear)=sel_cRs_block4;
//sel_cBn(iyear)=sel_cBn_block1;
sel_cBn(iyear)=sel_cBn_block2;
sel_cBs(iyear)=sel_cBs_block1;
//sel_cBs(iyear)=sel_cBs_block2;
```

```
sel_nad(iyear)=sel_nad_block1;
sel_mad(iyear)=sel_mad_block1;
//sel_sad(iyear)=sel_sad_block1;
}
```

```
FUNCTION get_mortality
```

```
Fsum.initialize();
```

```
Fapex.initialize();
```

```
F.initialize();
```

```
//initialization F is avg from first 3 yrs of observed landings
```

```
log_F_dev_init_cRn=sum(log_F_dev_cRn(styr_cRn_L,(styr_cRn_L+2)))/3.0;
```

```
log_F_dev_init_cRs=sum(log_F_dev_cRs(styr_cRs_L,(styr_cRs_L+2)))/3.0;
```

```
log_F_dev_init_cBn=sum(log_F_dev_cBn(styr_cBn_L,(styr_cBn_L+2)))/3.0;
```

```
log_F_dev_init_cBs=sum(log_F_dev_cBs(styr_cBs_L,(styr_cBs_L+2)))/3.0;
```

```
for (iyear=styr; iyear<=endyr; iyear++)
```

```

{
if(iyear>=styr_cRn_L & iyear<=endyr_cRn_L)//spans full time series
{F_cRn_out(iyear)=mfexp(log_avg_F_cRn+log_F_dev_cRn(iyear));}
F_cRn(iyear)=sel_cRn(iyear)*F_cRn_out(iyear);
Fsum(iyear)+=F_cRn_out(iyear);

if(iyear>=styr_cRs_L & iyear<=endyr_cRs_L)//spans full time series
{F_cRs_out(iyear)=mfexp(log_avg_F_cRs+log_F_dev_cRs(iyear));}
F_cRs(iyear)=sel_cRs(iyear)*F_cRs_out(iyear);
Fsum(iyear)+=F_cRs_out(iyear);

if(iyear>=styr_cBn_L & iyear<=endyr_cBn_L)//spans full time series
{F_cBn_out(iyear)=mfexp(log_avg_F_cBn+log_F_dev_cBn(iyear));}
F_cBn(iyear)=sel_cBn(iyear)*F_cBn_out(iyear);
Fsum(iyear)+=F_cBn_out(iyear);

if(iyear>=styr_cBs_L & iyear<=endyr_cBs_L)//spans full time series
{F_cBs_out(iyear)=mfexp(log_avg_F_cBs+log_F_dev_cBs(iyear));}
F_cBs(iyear)=sel_cBs(iyear)*F_cBs_out(iyear);
Fsum(iyear)+=F_cBs_out(iyear);

//Total F at age
F(iyear)=F_cRn(iyear); //first in additive series (NO +=)
F(iyear)+=F_cRs(iyear);
F(iyear)+=F_cBn(iyear);
F(iyear)+=F_cBs(iyear);

Fapex(iyear)=max(F(iyear));
Z(iyear)=tv_M(iyear)+F(iyear);

} //end iyear

FUNCTION get_bias_corr
var_rec_dev=norm2(log_rec_dev(styr_rec_dev,endyr_rec_dev)-
sum(log_rec_dev(styr_rec_dev,endyr_rec_dev))/nyrs_rec)

```

```

        /(nyrs_rec-1.0);
//if (set_BiasCor <= 0.0) {BiasCor=mfexp(var_rec_dev/2.0);} //bias correction based on empirical residuals
rec_sigma_sq=square(rec_sigma);
if (set_BiasCor <= 0.0) {BiasCor=mfexp(rec_sigma_sq/2.0);} //bias correction based on Rsigma
else {BiasCor=set_BiasCor;}

FUNCTION get_numbers_at_age
//Initialization
R0=mfexp(log_R0);
S0=spr_F0*R0;
R_virgin=SR_eq_func(R0, steep, spr_F0, spr_F0, BiasCor, SR_switch);

B0=bpr_F0*R_virgin*1000000; //virgin biomass
B0_q_DD=R_virgin*sum(elem_prod(N_bpr_F0(set_q_DD_stage,nages),wgt_spawn_mt(set_q_DD_stage,nages)));

F_initial=sel_cRn(styr)*mfexp(log_avg_F_cRn+log_F_dev_init_cRn)
            +sel_cRs(styr)*mfexp(log_avg_F_cRs+log_F_dev_init_cRs)
            +sel_cBn(styr)*mfexp(log_avg_F_cBn+log_F_dev_init_cBn)
            +sel_cBs(styr)*mfexp(log_avg_F_cBs+log_F_dev_init_cBs);

Z_initial=tv_M(styr)+F_initial;

//Initial equilibrium age structure
N_spr_initial(1)=1.0*mfexp(-1.0*Z_initial(1)*spawn_time_frac); //at peak spawning time;
for (iage=2; iage<=nages; iage++)
{
    N_spr_initial(iage)=N_spr_initial(iage-1)*
        mfexp(-1.0*(Z_initial(iage-1)*(1.0-spawn_time_frac) + Z_initial(iage)*spawn_time_frac));
}
N_spr_initial(nages)=N_spr_initial(nages)/(1.0-mfexp(-1.0*Z_initial(nages))); //plus group
spr_initial=sum(elem_prod(N_spr_initial,reprod));
//if (styr==styr_rec_dev) {R1=SR_eq_func(R0, steep, spr_F0, spr_initial, 1.0, SR_switch);} //without bias correction
(deviation added later)
//else {R1=SR_eq_func(R0, steep, spr_F0, spr_initial, BiasCor, SR_switch);} //with bias correction
R1=SR_eq_func(R0, steep, spr_F0, spr_initial, BiasCor, SR_switch);
if(R1<0.0) {R1=10.0;} //Avoid unrealistically low popn sizes during search algorithm

```

```

//Compute equilibrium age structure for first year
N_initial_eq(1)=R1;
for (iage=2; iage<=nages; iage++)
{
  N_initial_eq(iage)=N_initial_eq(iage-1)*
    mfexp(-1.0*(Z_initial(iage-1)));
}
//plus group calculation
N_initial_eq(nages)=N_initial_eq(nages)/(1.0-mfexp(-1.0*Z_initial(nages))); //plus group

//Add deviations to initial equilibrium N
N(styr)(2,nages)=elem_prod(N_initial_eq(2,nages),mfexp(log_Nage_dev));

if (styr==styr_rec_dev) {N(styr,1)=N_initial_eq(1)*mfexp(log_rec_dev(styr_rec_dev));}
else {N(styr,1)=N_initial_eq(1);}
//N(styr,1)=N_initial_eq(1)*mfexp(log_rec_dev(styr_rec_dev));
//cout << "N initialization " << N(styr) << endl;

N_mdyr(styr)(1,nages)=elem_prod(N(styr)(1,nages),(mfexp(-1.*(Z_initial(1,nages))*0.5))); //mid year
N_spawn(styr)(1,nages)=elem_prod(N(styr)(1,nages),(mfexp(-1.*(Z_initial(1,nages))*spawn_time_frac))); //peak
spawning time
N_nad(styr)(1,nages)=elem_prod(N(styr)(1,nages),(mfexp(-1.*(Z_initial(1,nages))*0.63))); //October 15
N_mad(styr)(1,nages)=elem_prod(N(styr)(1,nages),(mfexp(-1.*(Z_initial(1,nages))*0.13))); //April 15
N_sad(styr)(1,nages)=elem_prod(N(styr)(1,nages),(mfexp(-1.*(Z_initial(1,nages))*0.13))); //April 15

SSB(styr)=sum(elem_prod(N_spawn(styr),reprod_tv(styr)));
//B_q_DD(styr)=sum(elem_prod(N(styr)(set_q_DD_stage,nages),wgt_spawn_mt(set_q_DD_stage,nages)));

//Rest of years
for (iyear=styr; iyear<endyr; iyear++)
{
  if(iyear<(styr_rec_dev-1) | iyear>(endyr_rec_dev-1)) //recruitment follows S-R curve (with bias correction)
  exactly
  {
    //N(iyear+1,1)=BiasCor*SR_func(R0, steep, spr_F0, SSB(iyear),SR_switch);
  }
}

```



```

N(iyear+1)(2,nages)=++elem_prod(N(iyear)(1,nages-1),(mfexp(-1.*Z(iyear)(1,nages-1))));
N(iyear+1,nages)+=N(iyear,nages)*mfexp(-1.*Z(iyear,nages)); //plus group
//N_mdyr(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.5))); //mid
year
N_spawn(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-
1.*(Z(iyear+1)(1,nages))*spawn_time_frac))); //peak spawning time
SSB(iyear+1)=sum(elem_prod(N_spawn(iyear+1),reprod_tv(iyear+1)));
//B_q_DD(iyear+1)=sum(elem_prod(N(iyear+1)(set_q_DD_stage,nages),wgt_spawn_mt(set_q_DD_stage,
nages)));

N(iyear+1,1)=BiasCor*SR_func(R0, steep, spr_F0, SSB(iyear+1),SR_switch);

N_mdyr(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.5))); //mid year
N_nad(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.63))); //October
15
N_mad(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.13))); //April 15
N_sad(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.13))); //April 15

}
else //recruitment follows S-R curve with lognormal deviation
{
//N(iyear+1,1)=SR_func(R0, steep, spr_F0, SSB(iyear),SR_switch)*mfexp(log_rec_dev(iyear+1));
N(iyear+1)(2,nages)=++elem_prod(N(iyear)(1,nages-1),(mfexp(-1.*Z(iyear)(1,nages-1))));
N(iyear+1,nages)+=N(iyear,nages)*mfexp(-1.*Z(iyear,nages)); //plus group
//N_mdyr(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.5))); //mid
year
N_spawn(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-
1.*(Z(iyear+1)(1,nages))*spawn_time_frac))); //peak spawning time
SSB(iyear+1)=sum(elem_prod(N_spawn(iyear+1),reprod_tv(iyear+1)));

N(iyear+1,1)=SR_func(R0, steep, spr_F0, SSB(iyear+1),SR_switch)*mfexp(log_rec_dev(iyear+1));

//cout << "R0 " << R0 << endl;
//cout << "steep " << steep << endl;
//cout << "SSB " << SSB(iyear+1) << endl;
//cout << "SR_switch " << SR_switch << endl;
//cout << "rec dev " << mfexp(log_rec_dev(iyear+1)) << endl;

```

```

//cout << "iyear " << iyear << endl;
//cout << "N " << N(iyear+1) << endl;

N_mdyr(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.5))); //mid year
N_nad(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.63))); //October
15
N_mad(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.13))); //April 15
N_sad(iyear+1)(1,nages)=elem_prod(N(iyear+1)(1,nages),(mfexp(-1.*(Z(iyear+1)(1,nages))*0.13))); //April 15

}
}

//last year (projection) has no recruitment variability
N(endyr+1)(2,nages)=++elem_prod(N(endyr)(1,nages-1),(mfexp(-1.*Z(endyr)(1,nages-1))));
N(endyr+1,nages)+=N(endyr,nages)*mfexp(-1.*Z(endyr,nages)); //plus group
SSB(endyr+1)=sum(elem_prod(N(endyr+1),reprod));
N(endyr+1,1)=BiasCor*SR_func(R0, steep, spr_F0, SSB(endyr+1),SR_switch);

//Time series of interest
rec=column(N,1);
SdS0=SSB/S0;

FUNCTION get_landings_numbers //Baranov catch eqn
for (iyear=styr; iyear<=endyr; iyear++)
{
for (iage=1; iage<=nages; iage++)
{
L_cRn_num(iyear,iage)=N(iyear,iage)*F_cRn(iyear,iage)*
(1.-mfexp(-1.*Z(iyear,iage)))/Z(iyear,iage);
L_cRs_num(iyear,iage)=N(iyear,iage)*F_cRs(iyear,iage)*
(1.-mfexp(-1.*Z(iyear,iage)))/Z(iyear,iage);
L_cBn_num(iyear,iage)=N(iyear,iage)*F_cBn(iyear,iage)*
(1.-mfexp(-1.*Z(iyear,iage)))/Z(iyear,iage);
L_cBs_num(iyear,iage)=N(iyear,iage)*F_cBs(iyear,iage)*
(1.-mfexp(-1.*Z(iyear,iage)))/Z(iyear,iage);
}
}
}

```

```
}  
}
```

FUNCTION get\_landings\_wgt

```
for (iyear=styr; iyear<=endyr; iyear++)
```

```
{
```

```
  L_cRn_mt(iyear)=elem_prod(L_cRn_num(iyear),wholewgt_cR_mt(iyear))*1000000; //in 1000 mt whole weight
```

```
  L_cRs_mt(iyear)=elem_prod(L_cRs_num(iyear),wholewgt_cR_mt(iyear))*1000000; //in 1000 mt whole weight
```

```
  L_cBn_mt(iyear)=elem_prod(L_cBn_num(iyear),wholewgt_cR_mt(iyear))*1000000; //in 1000 mt whole weight
```

```
  L_cBs_mt(iyear)=elem_prod(L_cBs_num(iyear),wholewgt_cR_mt(iyear))*1000000; //in 1000 mt whole weight
```

```
  pred_cRn_L_mt(iyear)=sum(L_cRn_mt(iyear));
```

```
  pred_cRs_L_mt(iyear)=sum(L_cRs_mt(iyear));
```

```
  pred_cBn_L_mt(iyear)=sum(L_cBn_mt(iyear));
```

```
  pred_cBs_L_mt(iyear)=sum(L_cBs_mt(iyear));
```

```
}
```

FUNCTION get\_catchability\_fcns

```
//Get rate increase if estimated, otherwise fixed above
```

```
if (set_q_rate_phase>0.0)
```

```
{
```

```
  for (iyear=styr_nad_cpue; iyear<=endyr_nad_cpue; iyear++)
```

```
    { if (iyear>styr_nad_cpue & iyear <=2003)
```

```
      { //q_rate_fcn_nad(iyear)=(1.0+q_rate)*q_rate_fcn_nad(iyear-1); //compound
```

```
        q_rate_fcn_nad(iyear)=(1.0+(iyear-styr_nad_cpue)*q_rate)*q_rate_fcn_nad(styr_nad_cpue); //linear
```

```
      }
```

```
    } if (iyear>2003) {q_rate_fcn_nad(iyear)=q_rate_fcn_nad(iyear-1);}
```

```
}
```

```
for (iyear=styr_mad_cpue; iyear<=endyr_mad_cpue; iyear++)
```

```
{ if (iyear>styr_mad_cpue & iyear <=2003)
```

```
  { //q_rate_fcn_mad(iyear)=(1.0+q_rate)*q_rate_fcn_mad(iyear-1); //compound
```

```

    q_rate_fcn_mad(iyear)=(1.0+(iyear-styr_mad_cpue)*q_rate)*q_rate_fcn_mad(styr_mad_cpue); //linear
}
if (iyear>2003) {q_rate_fcn_mad(iyear)=q_rate_fcn_mad(iyear-1);}
}

for (iyear=styr_sad_cpue; iyear<=endyr_sad_cpue; iyear++)
{ if (iyear>styr_sad_cpue & iyear <=2003)
  //{q_rate_fcn_sad(iyear)=(1.0+q_rate)*q_rate_fcn_sad(iyear-1); //compound
  q_rate_fcn_sad(iyear)=(1.0+(iyear-styr_sad_cpue)*q_rate)*q_rate_fcn_sad(styr_sad_cpue); //linear
  }
  if (iyear>2003) {q_rate_fcn_sad(iyear)=q_rate_fcn_sad(iyear-1);}
}

for (iyear=styr_jai_cpue; iyear<=endyr_jai_cpue; iyear++)
{ if (iyear>styr_jai_cpue & iyear <=2003)
  //{q_rate_fcn_jai(iyear)=(1.0+q_rate)*q_rate_fcn_jai(iyear-1); //compound
  q_rate_fcn_jai(iyear)=(1.0+(iyear-styr_jai_cpue)*q_rate)*q_rate_fcn_jai(styr_jai_cpue); //linear
  }
  if (iyear>2003) {q_rate_fcn_jai(iyear)=q_rate_fcn_jai(iyear-1);}
}

//for (iyear=styr_mar_cpue; iyear<=endyr_mar_cpue; iyear++)
//{ if (iyear>styr_mar_cpue & iyear <=2003)
//  //{q_rate_fcn_mar(iyear)=(1.0+q_rate)*q_rate_fcn_mar(iyear-1); //compound
//  q_rate_fcn_mar(iyear)=(1.0+(iyear-styr_mar_cpue)*q_rate)*q_rate_fcn_mar(styr_mar_cpue); //linear
//  }
//  if (iyear>2003) {q_rate_fcn_mar(iyear)=q_rate_fcn_mar(iyear-1);}
//}

//for (iyear=styr_eco_cpue; iyear<=endyr_eco_cpue; iyear++)
//{ if (iyear>styr_eco_cpue & iyear <=2003)
//  //{q_rate_fcn_eco(iyear)=(1.0+q_rate)*q_rate_fcn_eco(iyear-1); //compound
//  q_rate_fcn_eco(iyear)=(1.0+(iyear-styr_eco_cpue)*q_rate)*q_rate_fcn_eco(styr_eco_cpue); //linear
//  }
//  if (iyear>2003) {q_rate_fcn_eco(iyear)=q_rate_fcn_eco(iyear-1);}

```

```

    //}
} //end q_rate conditional

//Get density dependence scalar (=1.0 if density independent model is used)
if (q_DD_beta>0.0)
{
  B_q_DD+=dzero;
  for (iyear=styr;iyear<=endyr;iyear++)
    {q_DD_fcn(iyear)=pow(B0_q_DD,q_DD_beta)*pow(B_q_DD(iyear),-q_DD_beta);}
    //{q_DD_fcn(iyear)=1.0+4.0/(1.0+mfexp(0.75*(B_q_DD(iyear)-0.1*B0_q_DD))); }
}

FUNCTION get_indices
//---Predicted CPUEs-----

//Northern Adult index
q_nad(styr_nad_cpue)=mfexp(log_q_nad);
for (iyear=styr_nad_cpue; iyear<=endyr_nad_cpue; iyear++)
{
  q_nad(iyear)=q_nad(styr_nad_cpue);
  N_nad_cpue(iyear)=elem_prod(N_nad(iyear),sel_nad(iyear)); //matched with October 15
  pred_nad_cpue(iyear)=q_nad(iyear)*sum(N_nad_cpue(iyear));
  //pred_nad_cpue(iyear)=q_nad(iyear)*q_rate_fcn_nad(iyear)*q_DD_fcn(iyear)*sum(N_nad_cpue(iyear));
  //if (iyear<endyr_nad_cpue){q_nad(iyear+1)=q_nad(iyear)*mfexp(q_RW_log_dev_nad(iyear));}
}

//Middle Adult index
q_mad(styr_mad_cpue)=mfexp(log_q_mad);
for (iyear=styr_mad_cpue; iyear<=endyr_mad_cpue; iyear++)
{
  q_mad(iyear)=q_mad(styr_mad_cpue);
  N_mad_cpue(iyear)=elem_prod(N_mad(iyear),sel_mad(iyear)); //matched with April 15
  pred_mad_cpue(iyear)=q_mad(iyear)*sum(N_mad_cpue(iyear));
  //pred_mad_cpue(iyear)=q_mad(iyear)*q_rate_fcn_mad(iyear)*q_DD_fcn(iyear)*sum(N_mad_cpue(iyear));
}

```

```

    //if (iyear<endyr_mad_cpue){q_mad(iyear+1)=q_mad(iyear)*mfexp(q_RW_log_dev_mad(iyear));}
}

//Southern Adult index
q_sad(styr_sad_cpue)=mfexp(log_q_sad);
for (iyear=styr_sad_cpue; iyear<=endyr_sad_cpue; iyear++)
{
    q_sad(iyear)=q_sad(styr_sad_cpue);
    N_sad_cpue(iyear)=N_sad(iyear,2); //matched with April 15
    pred_sad_cpue(iyear)=q_sad(iyear)*N_sad_cpue(iyear);
    //pred_sad_cpue(iyear)=q_sad(iyear)*q_rate_fcn_sad(iyear)*q_DD_fcn(iyear)*sum(N_sad_cpue(iyear));
    //if (iyear<endyr_sad_cpue){q_sad(iyear+1)=q_sad(iyear)*mfexp(q_RW_log_dev_sad(iyear));}
}

//Juvenile abundance index
q_jai(styr_jai_cpue)=mfexp(log_q_jai);
q2_jai(styr_jai_cpue)=mfexp(log_q2_jai);
for (iyear=styr_jai_cpue; iyear<=endyr_jai_cpue; iyear++)
{
    q_jai(iyear)=q_jai(styr_jai_cpue);
    N_jai_cpue(iyear)=N(iyear,1)*mfexp(-1.*(Z(iyear)(1)*0.25));//matching seine index with June 1
    pred_jai_cpue(iyear)=q_jai(iyear)*N_jai_cpue(iyear);
    if(iyear>yr_q_change)
    {
        q2_jai(iyear)=q2_jai(styr_jai_cpue);
        pred_jai_cpue(iyear)=q2_jai(iyear)*N_jai_cpue(iyear);
    }
    //pred_jai_cpue(iyear)=q_jai(iyear)*q_rate_fcn_jai(iyear)*q_DD_fcn(iyear)*N_jai_cpue(iyear);
    //if (iyear<endyr_jai_cpue){q_jai(iyear+1)=q_jai(iyear)*mfexp(q_RW_log_dev_jai(iyear));}
}

//MARMAP and ECOMON
q_mar(1)=mfexp(log_q_mar);
//cout << "q_mar" << q_mar << endl;
q_eco(9)=mfexp(log_q_eco);

```

```

//cout << "q_eco" << q_eco << endl;
for (iyear=1; iyear<=8; iyear++)
{
  q_mar(iyear)=q_mar(1);
  //cout << "q_mar" << q_mar << endl;
  SSB_mareco_cpue(iyear)=SSB(1980+iyear); //matched with SSB
  //cout << "SSB_mareco_cpue" << SSB_mareco_cpue << endl;
  pred_mareco_cpue(iyear)=q_mar(iyear)*SSB_mareco_cpue(iyear);
  //cout << "pred_mareco_cpue" << pred_mareco_cpue << endl;
}
for (iyear=9; iyear<=nyr_mareco_cpue; iyear++)
{
  q_eco(iyear)=q_eco(9);
  //cout << "q_eco" << q_eco << endl;
  SSB_mareco_cpue(iyear)=SSB(1991+iyear);
  //cout << "SSB_mareco_cpue2" << SSB_mareco_cpue << endl;
  pred_mareco_cpue(iyear)=q_eco(iyear)*SSB_mareco_cpue(iyear);
  //cout << "pred_mareco_cpue2" << pred_mareco_cpue << endl;
}
FUNCTION get_length_comps

//Northern adult index
for (iyear=1;iyear<=nyr_nad_lenc;iyear++)
{
  pred_nad_lenc(iyear)=(N_nad_cpue(yrs_nad_lenc(iyear))
    *lenprob_nad(yrs_nad_lenc(iyear)))
    /sum(N_nad_cpue(yrs_nad_lenc(iyear)));
}

//Middle adult index
for (iyear=1;iyear<=nyr_mad_lenc;iyear++)
{
  pred_mad_lenc(iyear)=(N_mad_cpue(yrs_mad_lenc(iyear))
    *lenprob_mad(yrs_mad_lenc(iyear)))
    /sum(N_mad_cpue(yrs_mad_lenc(iyear)));
}

```

```
}
```

```
//Southern adult index
```

```
//for (iyear=1;iyear<=nyr_sad_lenc;iyear++)
```

```
//{
```

```
// pred_sad_lenc(iyear)=(N_sad_cpue(yrs_sad_lenc(iyear))
```

```
//      *lenprob_sad(yrs_sad_lenc(iyear)))
```

```
//      /sum(N_sad_cpue(yrs_sad_lenc(iyear)));
```

```
//}
```

```
FUNCTION get_age_comps
```

```
//Commerical reduction - north
```

```
for (iyear=1;iyear<=nyr_cRn_agec;iyear++)
```

```
{
```

```
  ErrorFree_cRn_agec(iyear)=L_cRn_num(yrs_cRn_agec(iyear))/sum(L_cRn_num(yrs_cRn_agec(iyear)));
```

```
  pred_cRn_agec_allages(iyear)=age_error*(ErrorFree_cRn_agec(iyear)/sum(ErrorFree_cRn_agec(iyear)));
```

```
  for (iage=1; iage<=nages_agec; iage++) {pred_cRn_agec(iyear,iage)=pred_cRn_agec_allages(iyear,iage);}
```

```
  //for (iage=(nages_agec+1); iage<=nages; iage++)
```

```
{pred_cRn_agec(iyear,nages_agec)+=pred_cRn_agec_allages(iyear,iage);} //plus group
```

```
}
```

```
//Commerical reduction - south
```

```
for (iyear=1;iyear<=nyr_cRs_agec;iyear++)
```

```
{
```

```
  ErrorFree_cRs_agec(iyear)=L_cRs_num(yrs_cRs_agec(iyear))/sum(L_cRs_num(yrs_cRs_agec(iyear)));
```

```
  pred_cRs_agec_allages(iyear)=age_error*(ErrorFree_cRs_agec(iyear)/sum(ErrorFree_cRs_agec(iyear)));
```

```
  for (iage=1; iage<=nages_agec; iage++) {pred_cRs_agec(iyear,iage)=pred_cRs_agec_allages(iyear,iage);}
```

```
  //for (iage=(nages_agec+1); iage<=nages; iage++)
```

```
{pred_cRs_agec(iyear,nages_agec)+=pred_cRs_agec_allages(iyear,iage);} //plus group
```

```
}
```

```
//Commerical bait - north
```

```
for (iyear=1;iyear<=nyr_cBn_agec;iyear++)
```

```
{
```



```

ErrorFree_cBn_agec(iyear)=L_cBn_num(yrs_cBn_agec(iyear))/sum(L_cBn_num(yrs_cBn_agec(iyear)));
pred_cBn_agec_allages(iyear)=age_error*(ErrorFree_cBn_agec(iyear)/sum(ErrorFree_cBn_agec(iyear)));
for (iage=1; iage<=nages_agec; iage++) {pred_cBn_agec(iyear,iage)=pred_cBn_agec_allages(iyear,iage);}
//for (iage=(nages_agec+1); iage<=nages; iage++)
{pred_cBn_agec(iyear,nages_agec)+=pred_cBn_agec_allages(iyear,iage);} //plus group
}

```

```

//Commerical bait - south
for (iyear=1;iyear<=nyr_cBs_agec;iyear++)
{
ErrorFree_cBs_agec(iyear)=L_cBs_num(yrs_cBs_agec(iyear))/sum(L_cBs_num(yrs_cBs_agec(iyear)));
pred_cBs_agec_allages(iyear)=age_error*(ErrorFree_cBs_agec(iyear)/sum(ErrorFree_cBs_agec(iyear)));
for (iage=1; iage<=nages_agec; iage++) {pred_cBs_agec(iyear,iage)=pred_cBs_agec_allages(iyear,iage);}
//for (iage=(nages_agec+1); iage<=nages; iage++)
{pred_cBs_agec(iyear,nages_agec)+=pred_cBs_agec_allages(iyear,iage);} //plus group
}

```

////-----  
-----

FUNCTION get\_weighted\_current

F\_temp\_sum=0.0;

F\_temp\_sum+=mfexp((selpar\_n\_yrs\_wgted\*log\_avg\_F\_cRn+  
sum(log\_F\_dev\_cRn((endyr-selpar\_n\_yrs\_wgted+1),endyr)))/selpar\_n\_yrs\_wgted);

F\_temp\_sum+=mfexp((selpar\_n\_yrs\_wgted\*log\_avg\_F\_cRs+  
sum(log\_F\_dev\_cRs((endyr-selpar\_n\_yrs\_wgted+1),endyr)))/selpar\_n\_yrs\_wgted);

F\_temp\_sum+=mfexp((selpar\_n\_yrs\_wgted\*log\_avg\_F\_cBn+  
sum(log\_F\_dev\_cBn((endyr-selpar\_n\_yrs\_wgted+1),endyr)))/selpar\_n\_yrs\_wgted);

F\_temp\_sum+=mfexp((selpar\_n\_yrs\_wgted\*log\_avg\_F\_cBs+  
sum(log\_F\_dev\_cBs((endyr-selpar\_n\_yrs\_wgted+1),endyr)))/selpar\_n\_yrs\_wgted);

F\_cRn\_prop=mfexp((selpar\_n\_yrs\_wgted\*log\_avg\_F\_cRn+  
sum(log\_F\_dev\_cRn((endyr-selpar\_n\_yrs\_wgted+1),endyr)))/selpar\_n\_yrs\_wgted)/F\_temp\_sum;

F\_cRs\_prop=mfexp((selpar\_n\_yrs\_wgted\*log\_avg\_F\_cRs+  
sum(log\_F\_dev\_cRs((endyr-selpar\_n\_yrs\_wgted+1),endyr)))/selpar\_n\_yrs\_wgted)/F\_temp\_sum;

```

F_cBn_prop=mfexp((selpar_n_yrs_wgted*log_avg_F_cBn+
  sum(log_F_dev_cBn((endyr-selpar_n_yrs_wgted+1),endyr)))/selpar_n_yrs_wgted)/F_temp_sum;
F_cBs_prop=mfexp((selpar_n_yrs_wgted*log_avg_F_cBs+
  sum(log_F_dev_cBs((endyr-selpar_n_yrs_wgted+1),endyr)))/selpar_n_yrs_wgted)/F_temp_sum;

log_F_dev_end_cRn=sum(log_F_dev_cRn((endyr-selpar_n_yrs_wgted+1),endyr))/selpar_n_yrs_wgted;
log_F_dev_end_cRs=sum(log_F_dev_cRs((endyr-selpar_n_yrs_wgted+1),endyr))/selpar_n_yrs_wgted;
log_F_dev_end_cBn=sum(log_F_dev_cBn((endyr-selpar_n_yrs_wgted+1),endyr))/selpar_n_yrs_wgted;
log_F_dev_end_cBs=sum(log_F_dev_cBs((endyr-selpar_n_yrs_wgted+1),endyr))/selpar_n_yrs_wgted;

F_end_L=sel_cRn(endyr)*mfexp(log_avg_F_cRn+log_F_dev_end_cRn)+
  sel_cRs(endyr)*mfexp(log_avg_F_cRs+log_F_dev_end_cRs)+
  sel_cBn(endyr)*mfexp(log_avg_F_cBn+log_F_dev_end_cBn)+
  sel_cBs(endyr)*mfexp(log_avg_F_cBs+log_F_dev_end_cBs);

F_end=F_end_L;
F_end_apex=max(F_end);

sel_wgted_tot=F_end/F_end_apex;
sel_wgted_L=elem_prod(sel_wgted_tot, elem_div(F_end_L,F_end));

wgt_wgted_L_denom=F_cRn_prop+F_cRs_prop+F_cBn_prop+F_cBs_prop;
wgt_wgted_L_mt=F_cRn_prop/wgt_wgted_L_denom*wholewgt_cR_mt(endyr)*1000+ //to scale to 1000s mt
  F_cRs_prop/wgt_wgted_L_denom*wholewgt_cR_mt(endyr)*1000+ //to scale to 1000s mt
  F_cBn_prop/wgt_wgted_L_denom*wholewgt_cR_mt(endyr)*1000+ //to scale to 1000s mt
  F_cBs_prop/wgt_wgted_L_denom*wholewgt_cR_mt(endyr)*1000; //to scale to 1000s mt

```

```

FUNCTION get_msy

```

```

  //compute values as functions of F
  for(ff=1; ff<=n_iter_msy; ff++)
  {
    //uses fishery-weighted F's
    Z_age_msy=0.0;

```

```

F_L_age_msy=0.0;

F_L_age_msy=F_msy(ff)*sel_wgted_L;
Z_age_msy=M+F_L_age_msy;

N_age_msy(1)=1.0;
for (iage=2; iage<=nages; iage++)
  {N_age_msy(iage)=N_age_msy(iage-1)*mfexp(-1.*Z_age_msy(iage-1));}
N_age_msy(nages)=N_age_msy(nages)/(1.0-mfexp(-1.*Z_age_msy(nages)));
N_age_msy_spawn(1,(nages-1))=elem_prod(N_age_msy(1,(nages-1)),
    mfexp((-1.*Z_age_msy(1,(nages-1)))*spawn_time_frac));
N_age_msy_spawn(nages)=(N_age_msy_spawn(nages-1)*(mfexp(-1.*Z_age_msy(nages-1)*(1.0-
spawn_time_frac) +
    Z_age_msy(nages)*spawn_time_frac)))/(1.0-mfexp(-1.*Z_age_msy(nages)));

spr_msy(ff)=sum(elem_prod(N_age_msy_spawn,reprod));

R_eq(ff)=SR_eq_func(R0, steep, spr_msy(1), spr_msy(ff), BiasCor, SR_switch);

if (R_eq(ff)<dzero) {R_eq(ff)=dzero;}
N_age_msy*=R_eq(ff);
N_age_msy_spawn*=R_eq(ff);

for (iage=1; iage<=nages; iage++)
{
  L_age_msy(iage)=N_age_msy(iage)*(F_L_age_msy(iage)/Z_age_msy(iage))*
    (1.-mfexp(-1.*Z_age_msy(iage)));
}

SSB_eq(ff)=sum(elem_prod(N_age_msy_spawn,reprod));
B_eq(ff)=sum(elem_prod(N_age_msy,wgt_spawn_mt))*1000000; //to scale to 1000s mt and catch in 1000s
L_eq_mt(ff)=sum(elem_prod(L_age_msy,wgt_wgted_L_mt))*1000; //to scale to catch in 1000s,
wgt_wgted_L_mt is already scaled to 1000s mt
//L_eq_knum(ff)=sum(L_age_msy)/1000.0;
}

```

```
msy_mt_out=max(L_eq_mt); //msy in whole weight
```

```
for(ff=1; ff<=n_iter_msy; ff++)
```

```
{
```

```
if(L_eq_mt(ff) == msy_mt_out)
```

```
{
```

```
SSB_msy_out=SSB_eq(ff);
```

```
B_msy_out=B_eq(ff);
```

```
R_msy_out=R_eq(ff);
```

```
//msy_knum_out=L_eq_knum(ff);
```

```
F_msy_out=F_msy(ff);
```

```
spr_msy_out=spr_msy(ff);
```

```
}
```

```
}
```

```
//-----  
-----
```

```
FUNCTION get_per_recruit_stuff
```

```
//static per-recruit stuff
```

```
for(iyear=styr; iyear<=endyr; iyear++)
```

```
{
```

```
N_age_spr(1)=1.0;
```

```
for(iage=2; iage<=nages; iage++)
```

```
{N_age_spr(iage)=N_age_spr(iage-1)*mfexp(-1.*Z(iyear,iage-1));}
```

```
N_age_spr(nages)=N_age_spr(nages)/(1.0-mfexp(-1.*Z(iyear,nages)));
```

```
N_age_spr_spawn(1,(nages-1))=elem_prod(N_age_spr(1,(nages-1)),  
mfexp(-1.*Z(iyear)(1,(nages-1))*spawn_time_frac));
```

```
N_age_spr_spawn(nages)=(N_age_spr_spawn(nages-1)*  
(mfexp(-1.*Z(iyear)(nages-1)*(1.0-spawn_time_frac) + Z(iyear)(nages)*spawn_time_frac )))  
/(1.0-mfexp(-1.*Z(iyear)(nages)));
```

```
spr_static(iyear)=sum(elem_prod(N_age_spr_spawn,reprod))/spr_F0;
```

```
}
```

```
//compute SSB/R and YPR as functions of F
```

```

for(ff=1; ff<=n_iter_spr; ff++)
{
//uses fishery-weighted F's, same as in MSY calculations
Z_age_spr=0.0;
F_L_age_spr=0.0;

F_L_age_spr=F_spr(ff)*sel_wgted_L;
Z_age_spr=M+F_L_age_spr;

N_age_spr(1)=1.0;
for (iage=2; iage<=nages; iage++)
{N_age_spr(iage)=N_age_spr(iage-1)*mfexp(-1.*Z_age_spr(iage-1));}
N_age_spr(nages)=N_age_spr(nages)/(1-mfexp(-1.*Z_age_spr(nages)));
N_age_spr_spawn(1,(nages-1))=elem_prod(N_age_spr(1,(nages-1)),
mfexp((-1.*Z_age_spr(1,(nages-1)))*spawn_time_frac));
N_age_spr_spawn(nages)=(N_age_spr_spawn(nages-1)*
(mfexp(-1.*(Z_age_spr(nages-1)*(1.0-spawn_time_frac) + Z_age_spr(nages)*spawn_time_frac)))
/(1.0-mfexp(-1.*Z_age_spr(nages))));
spr_spr(ff)=sum(elem_prod(N_age_spr_spawn,reprod));
L_spr(ff)=0.0;
for (iage=1; iage<=nages; iage++)
{
L_age_spr(iage)=N_age_spr(iage)*(F_L_age_spr(iage)/Z_age_spr(iage))*
(1.-mfexp(-1.*Z_age_spr(iage)));
L_spr(ff)+=L_age_spr(iage)*wgt_wgted_L_mt(iage)*1000.0; //already scaled to 1000s mt, but need to scale to
1000s fish
}
}
spr_ratio=spr_spr/spr_F0;
F35_dum=min(fabs(spr_ratio-0.35));
F30_dum=min(fabs(spr_ratio-0.3));
F40_dum=min(fabs(spr_ratio-0.4));
for(ff=1; ff<=n_iter_spr; ff++)
{
if (fabs(spr_ratio(ff)-0.35)==F35_dum) {F35_out=F_spr(ff);}
if (fabs(spr_ratio(ff)-0.3)==F30_dum) {F30_out=F_spr(ff);}
}

```

```

        if (fabs(spr_ratio(ff)-0.4)==F40_dum) {F40_out=F_spr(ff);}
    }
    rec=column(N,1);
    rec_mean=sum(rec(styr_rec_spr, endyr_rec_spr))/nyrs_rec_spr;
    R_F30_out=rec_mean;
    F_L_age_spr=F30_out*sel_wgted_L;
    Z_age_spr=M+F_L_age_spr;

    N_age_spr(1)=R_F30_out;
    for (iage=2; iage<=nages; iage++)
        {N_age_spr(iage)=N_age_spr(iage-1)*mfexp(-1.*Z_age_spr(iage-1));}
    N_age_spr(nages)=N_age_spr(nages)/(1-mfexp(-1.*Z_age_spr(nages)));
    N_age_spr_spawn(1,(nages-1))=elem_prod(N_age_spr(1,(nages-1)),
        mfexp((-1.*Z_age_spr(1,(nages-1)))*spawn_time_frac));
    N_age_spr_spawn(nages)=(N_age_spr_spawn(nages-1)*
        (mfexp(-1.*(Z_age_spr(nages-1)*(1.0-spawn_time_frac) + Z_age_spr(nages)*spawn_time_frac) )))
        /(1.0-mfexp(-1.*Z_age_spr(nages)));

    for (iage=1; iage<=nages; iage++)
    {
        L_age_F30(iage)=N_age_spr(iage)*(F_L_age_spr(iage)/Z_age_spr(iage))*
            (1.-mfexp(-1.*Z_age_spr(iage)));
    }
    SSB_F30_out=sum(elem_prod(N_age_spr_spawn,reprod));
    B_F30_out=sum(elem_prod(N_age_spr,wgt_spawn))*1000000;
    L_F30_mt_out=sum(elem_prod(L_age_F30,wgt_wgted_L_mt))*1000; //in whole weight
    L_F30_knum_out=sum(L_age_F30)/1000.0;

//-----
//-----

FUNCTION get_miscellaneous_stuff

//switch here if var_rec_dev <=dzero
if(var_rec_dev>0.0)
    {sigma_rec_dev=sqrt(var_rec_dev);} //sample SD of predicted residuals (may not equal rec_sigma)

```

```

else{sigma_rec_dev=0.0;}

//len_cv=elem_div(len_sd,meanlen_FL);
for (iyear=styr; iyear<=endyr; iyear++)
{
len_cv_apr15=mean(elem_div(len_sd_mad(iyear),meanlen_FL_apr15(iyear)));
//len_cv_jun1=mean(elem_div(len_sd_sad(iyear),meanlen_FL_jun1(iyear)));
len_cv_oct15=mean(elem_div(len_sd_nad(iyear),meanlen_FL_oct15(iyear)));
}
//len_cv=(len_cv_apr15+len_cv_jun1+len_cv_oct15)/3;
len_cv_mad=len_cv_apr15;
//len_cv_sad=len_cv_jun1;
len_cv_nad=len_cv_oct15;

//compute total landings-at-age in 1000 fish and 1000s mt whole weight
L_total_num.initialize();
L_total_mt.initialize();
//L_total_knum_yr.initialize();
L_total_mt_yr.initialize();

for(iyear=styr; iyear<=endyr; iyear++)
{
L_total_mt_yr(iyear)=pred_cRn_L_mt(iyear)+pred_cRs_L_mt(iyear)+
pred_cBn_L_mt(iyear)+pred_cBs_L_mt(iyear);
//L_total_knum_yr(iyear)=pred_cR_L_knum(iyear);

B(iyear)=elem_prod(N(iyear),tv_wgt_spawn_mt(iyear))*1000000; //scale to 1000s mt and 1000s fish landed
B_mdyr(iyear)=elem_prod(N_mdyr(iyear),tv_wgt_middle_mt(iyear))*1000000;
totN(iyear)=sum(N(iyear)); //in 1000s of fish
totB(iyear)=sum(B(iyear)); //in 1000s of mt
SSBatage(iyear)=elem_prod(N(iyear),reprod_tv(iyear));
}

L_total_num=L_cRn_num+L_cRs_num+L_cBn_num+L_cBs_num; //landings at age in 1000s fish
L_total_mt=L_cRn_mt+L_cRs_mt+L_cBn_mt+L_cBs_mt; //landings at age in 1000s mt whole weight

```

```

//Time series of interest
B(endyr+1)=elem_prod(N(endyr+1),wgt_spawn_mt)*1000000; //scale to 1000s mt and 1000s fish
//B_mdyr(endyr+1)=elem_prod(N_mdyr(endyr+1),wgt_fish_mt)*1000000; //scale to 1000s mt and 1000s fish
totN(endyr+1)=sum(N(endyr+1)); //in 1000s of fish
totB(endyr+1)=sum(B(endyr+1)); //in 1000s of mt
SdS0=SSB/S0;

Fend_mean_temp=1.0;
for (iyear=1; iyear<=selpar_n_yrs_wgted; iyear++) {Fend_mean_temp*=Fapex(endyr-iyear+1);}
Fend_mean=pow(Fend_mean_temp,(1.0/selpar_n_yrs_wgted));
if(F_msy_out>0)
{
  FdF_msy=Fapex/F_msy_out;
  FdF_msy_end=FdF_msy(endyr);
  FdF_msy_end_mean=Fend_mean/F_msy_out;
}
if(SSB_msy_out>0)
{
  SdSSB_msy=SSB/SSB_msy_out;
  SdSSB_msy_end=SdSSB_msy(endyr);
}

  if(F30_out>0)
{
  FdF30=Fapex/F30_out;
  FdF30_end_mean=Fend_mean/F30_out;
}

if(SSB_F30_out>0)
{
  SdSSB_F30=SSB/SSB_F30_out;
  SdSSB_F30_end=SdSSB_F30(endyr);
}
//fill in log recruitment deviations for yrs they are nonzero

```



```

for(iyear=styr_rec_dev; iyear<=endyr_rec_dev; iyear++)
  {log_rec_dev_output(iyear)=log_rec_dev(iyear);}
//fill in log Nage deviations for ages they are nonzero (ages2+)
for(iage=2; iage<=nages; iage++)
  {log_Nage_dev_output(iage)=log_Nage_dev(iage);}

```

```

//-----
-----

```

```

FUNCTION get_projection

```

```

switch(Fproj_switch){
  case 1: //F=Fcurrent
    F_reg_proj=Fend_mean;
    break;
  case 2: //F=Fmsy
    F_reg_proj=F_msy_out;
    break;
  case 3: //F=F30
    F_reg_proj=F30_out;
    break;
  case 4: //F=F40
    F_reg_proj=F40_out;
    break;
  default: // no such switch available
    cout << "Error in input: Projection switch Fproj_switch must be set to 1, 2, 3, or 4." << endl;
    cout << "Presently it is set to " << Fproj_switch << "." << endl;
    exit(0);
}

```

```

N_proj(styr_proj)=N(endyr+1); //initial conditions computed previously

```

```

for (iyear=styr_proj; iyear<=endyr_proj; iyear++) //recruitment follows S-R curve (with bias correction) exactly
{
  if (iyear<styr_regs) {F_proj(iyear)=Fend_mean;}
  else {F_proj(iyear)=Fproj_mult*F_reg_proj;}
}

```

```

FL_age_proj=sel_wgted_L*F_proj(iyear);

Z_proj(iyear)=M+FL_age_proj;
N_spawn_proj(iyear)(1,nages)=elem_prod(N_proj(iyear)(1,nages),(mfexp(-
1.*(Z_proj(iyear)(1,nages))*spawn_time_frac)); //peak spawning time
SSB_proj(iyear)= sum(elem_prod(N_spawn_proj(iyear),reprod));
B_proj(iyear)=sum(elem_prod(N_proj(iyear),wgt_spawn_mt))*1000000; //uses spawning weight

for (iage=1; iage<=nages; iage++)
{
L_age_proj(iyear,iage)=N_proj(iyear,iage)*FL_age_proj(iage)*(1.-mfexp(-
1.*Z_proj(iyear,iage)))/Z_proj(iyear,iage);
}
L_knum_proj(iyear)=sum(L_age_proj(iyear))/1000.0;
L_mt_proj(iyear)=sum(elem_prod(L_age_proj(iyear),wgt_wgted_L_mt)); //in 1000 mt

if (iyear<endyr_proj) {
N_proj(iyear+1,1)=BiasCor*SR_func(R0, steep, spr_F0, SSB_proj(iyear),SR_switch);
N_proj(iyear+1)(2,nages)=++elem_prod(N_proj(iyear)(1,nages-1),(mfexp(-
1.*Z_proj(iyear)(1,nages-1))));
N_proj(iyear+1,nages)+=N_proj(iyear,nages)*mfexp(-1.*Z_proj(iyear,nages)); //plus
group
}
}
R_proj=column(N_proj,1);
//-----
-----

FUNCTION evaluate_objective_function
//fval=square(xdum-9.0);

fval=0.0;
fval_data=0.0;

//---likelihoods-----

```

//---Indices-----

f\_nad\_cpue=0.0;

f\_nad\_cpue=lk\_lognormal(pred\_nad\_cpue, obs\_nad\_cpue, nad\_cpue\_cv, w\_l\_nad);

fval+=f\_nad\_cpue;

fval\_data+=f\_nad\_cpue;

f\_mad\_cpue=0.0;

f\_mad\_cpue=lk\_lognormal(pred\_mad\_cpue, obs\_mad\_cpue, mad\_cpue\_cv, w\_l\_mad);

fval+=f\_mad\_cpue;

fval\_data+=f\_mad\_cpue;

f\_sad\_cpue=0.0;

f\_sad\_cpue=lk\_lognormal(pred\_sad\_cpue, obs\_sad\_cpue, sad\_cpue\_cv, w\_l\_sad);

fval+=f\_sad\_cpue;

fval\_data+=f\_sad\_cpue;

f\_jai\_cpue=0.0;

f\_jai\_cpue=lk\_lognormal(pred\_jai\_cpue, obs\_jai\_cpue, jai\_cpue\_cv, w\_l\_jai);

fval+=f\_jai\_cpue;

fval\_data+=f\_jai\_cpue;

f\_mareco\_cpue=0.0;

f\_mareco\_cpue=lk\_lognormal(pred\_mareco\_cpue, obs\_mareco\_cpue, mareco\_cpue\_cv, w\_l\_mareco);

fval+=f\_mareco\_cpue;

fval\_data+=f\_mareco\_cpue;

//---Landings-----

//f\_cRn\_L in 1000 mt whole wgt

f\_cRn\_L=lk\_lognormal(pred\_cRn\_L\_mt(styr\_cRn\_L, endyr\_cRn\_L), obs\_cRn\_L(styr\_cRn\_L, endyr\_cRn\_L),  
cRn\_L\_cv(styr\_cRn\_L, endyr\_cRn\_L), w\_L);

fval+=f\_cRn\_L;

fval\_data+=f\_cRn\_L;

```

//f_cRs_L in 1000 mt whole wgt
f_cRs_L=lk_lognormal(pred_cRs_L_mt(styr_cRs_L,endyr_cRs_L), obs_cRs_L(styr_cRs_L,endyr_cRs_L),
                    cRs_L_cv(styr_cRs_L,endyr_cRs_L), w_L);
fval+=f_cRs_L;
fval_data+=f_cRs_L;

//f_cBn_L in 1000 mt whole wgt
f_cBn_L=lk_lognormal(pred_cBn_L_mt(styr_cBn_L,endyr_cBn_L), obs_cBn_L(styr_cBn_L,endyr_cBn_L),
                    cBn_L_cv(styr_cBn_L,endyr_cBn_L), w_L);
fval+=f_cBn_L;
fval_data+=f_cBn_L;

//f_cBs_L in 1000 mt whole wgt
f_cBs_L=lk_lognormal(pred_cBs_L_mt(styr_cBs_L,endyr_cBs_L), obs_cBs_L(styr_cBs_L,endyr_cBs_L),
                    cBs_L_cv(styr_cBs_L,endyr_cBs_L), w_L);
fval+=f_cBs_L;
fval_data+=f_cBs_L;

//---Length comps-----

//f_nad_lenc
//f_nad_lenc=lk_robust_multinomial(nsamp_nad_lenc, pred_nad_lenc, obs_nad_lenc, nyr_nad_lenc,
double(nlenbins), minSS_nad_lenc, w_lc_nad);
//f_nad_lenc=lk_logistic_normal(nsamp_nad_lenc, pred_nad_lenc, obs_nad_lenc, nyr_nad_lenc,
double(nlenbins), minSS_nad_lenc);
f_nad_lenc=lk_dirichlet_multinomial(nsamp_nad_lenc, pred_nad_lenc, obs_nad_lenc, nyr_nad_lenc,
double(nlenbins), minSS_nad_lenc, log_dm_nad_lc);
fval+=f_nad_lenc;
fval_data+=f_nad_lenc;

//f_mad_lenc
//f_mad_lenc=lk_robust_multinomial(nsamp_mad_lenc, pred_mad_lenc, obs_mad_lenc, nyr_mad_lenc,
double(nlenbins), minSS_mad_lenc, w_lc_mad);
//f_mad_lenc=lk_logistic_normal(nsamp_mad_lenc, pred_mad_lenc, obs_mad_lenc, nyr_mad_lenc,
double(nlenbins), minSS_mad_lenc);

```

```

f_mad_lenc=lk_dirichlet_multinomial(nsamp_mad_lenc, pred_mad_lenc, obs_mad_lenc, nyr_mad_lenc,
double(nlenbins), minSS_mad_lenc, log_dm_mad_lc);

fval+=f_mad_lenc;
fval_data+=f_mad_lenc;

//f_sad_lenc
//f_sad_lenc=lk_robust_multinomial(nsamp_sad_lenc, pred_sad_lenc, obs_sad_lenc, nyr_sad_lenc,
double(nlenbins), minSS_sad_lenc, w_lc_sad);
//f_sad_lenc=lk_logistic_normal(nsamp_sad_lenc, pred_sad_lenc, obs_sad_lenc, nyr_sad_lenc, double(nlenbins),
minSS_sad_lenc);
//f_sad_lenc=lk_dirichlet_multinomial(nsamp_sad_lenc, pred_sad_lenc, obs_sad_lenc, nyr_sad_lenc,
double(nlenbins), minSS_sad_lenc, log_dm_sad_lc);
//fval+=f_sad_lenc;
//fval_data+=f_sad_lenc;

//---Age comps-----

//f_cRn_agec
//f_cRn_agec=lk_robust_multinomial(nsamp_cRn_agec, pred_cRn_agec, obs_cRn_agec, nyr_cRn_agec,
double(nages_agec), minSS_cRn_agec, w_ac_cRn);
//f_cRn_agec=lk_logistic_normal(nsamp_cRn_agec, pred_cRn_agec, obs_cRn_agec, nyr_cRn_agec,
double(nages_agec), minSS_cRn_agec);
f_cRn_agec=lk_dirichlet_multinomial(nsamp_cRn_agec, pred_cRn_agec, obs_cRn_agec, nyr_cRn_agec,
double(nages_agec), minSS_cRn_agec, log_dm_cRn_ac);
fval+=f_cRn_agec;
fval_data+=f_cRn_agec;

//f_cRs_agec
//f_cRs_agec=lk_robust_multinomial(nsamp_cRs_agec, pred_cRs_agec, obs_cRs_agec, nyr_cRs_agec,
double(nages_agec), minSS_cRs_agec, w_ac_cRs);
//f_cRs_agec=lk_logistic_normal(nsamp_cRs_agec, pred_cRs_agec, obs_cRs_agec, nyr_cRs_agec,
double(nages_agec), minSS_cRs_agec);
f_cRs_agec=lk_dirichlet_multinomial(nsamp_cRs_agec, pred_cRs_agec, obs_cRs_agec, nyr_cRs_agec,
double(nages_agec), minSS_cRs_agec, log_dm_cRs_ac);
fval+=f_cRs_agec;
fval_data+=f_cRs_agec;

//f_cBn_agec

```

```

//f_cBn_aged=lk_robust_multinomial(nsamp_cBn_aged, pred_cBn_aged, obs_cBn_aged, nyr_cBn_aged,
double(nages_aged), minSS_cBn_aged, w_ac_cBn);

//f_cBn_aged=lk_logistic_normal(nsamp_cBn_aged, pred_cBn_aged, obs_cBn_aged, nyr_cBn_aged,
double(nages_aged), minSS_cBn_aged);

f_cBn_aged=lk_dirichlet_multinomial(nsamp_cBn_aged, pred_cBn_aged, obs_cBn_aged, nyr_cBn_aged,
double(nages_aged), minSS_cBn_aged, log_dm_cBn_ac);

fval+=f_cBn_aged;
fval_data+=f_cBn_aged;

//f_cBs_aged

//f_cBs_aged=lk_robust_multinomial(nsamp_cBs_aged, pred_cBs_aged, obs_cBs_aged, nyr_cBs_aged,
double(nages_aged), minSS_cBs_aged, w_ac_cBs);

//f_cBs_aged=lk_logistic_normal(nsamp_cBs_aged, pred_cBs_aged, obs_cBs_aged, nyr_cBs_aged,
double(nages_aged), minSS_cBs_aged);

f_cBs_aged=lk_dirichlet_multinomial(nsamp_cBs_aged, pred_cBs_aged, obs_cBs_aged, nyr_cBs_aged,
double(nages_aged), minSS_cBs_aged, log_dm_cBs_ac);

fval+=f_cBs_aged;
fval_data+=f_cBs_aged;

//-----Constraints and penalties-----

//Light penalty applied to log_Nage_dev for deviation from zero. If not estimated, this penalty equals zero.
f_Nage_init=norm2(log_Nage_dev);
fval+=w_Nage_init*f_Nage_init;

f_rec_dev=0.0;
//rec_sigma_sq=square(rec_sigma);
rec_logL_add=nyrs_rec*log(rec_sigma);
f_rec_dev=(square(log_rec_dev(styr_rec_dev) + rec_sigma_sq/2.0)/(2.0*rec_sigma_sq));
for(iyear=(styr_rec_dev+1); iyear<=endyr_rec_dev; iyear++)
{f_rec_dev+=(square(log_rec_dev(iyear)-R_autocorr*log_rec_dev(iyear-1) + rec_sigma_sq/2.0)/
(2.0*rec_sigma_sq));}
f_rec_dev+=rec_logL_add;
fval+=w_rec*f_rec_dev;

f_rec_dev_early=0.0; //possible extra constraint on early rec deviations
if (w_rec_early>0.0)

```

```

{ if (styr_rec_dev<endyr_rec_phase1)
  {
    for(iyear=styr_rec_dev; iyear<=endyr_rec_phase1; iyear++)
      //{{f_rec_dev_early+=(square(log_rec_dev(iyear)-R_autocorr*log_rec_dev(iyear-1) + rec_sigma_sq/2.0)/
      //      (2.0*rec_sigma_sq)) + rec_logL_add;}}
      {f_rec_dev_early+=square(log_rec_dev(iyear));}}
  }
fval+=w_rec_early*f_rec_dev_early;
}

f_rec_dev_end=0.0; //possible extra constraint on ending rec deviations
if (w_rec_end>0.0)
{ if (endyr_rec_phase2<endyr_rec_dev)
  {
    for(iyear=(endyr_rec_phase2+1); iyear<=endyr_rec_dev; iyear++)
      //{{f_rec_dev_end+=(square(log_rec_dev(iyear)-R_autocorr*log_rec_dev(iyear-1) + rec_sigma_sq/2.0)/
      //      (2.0*rec_sigma_sq)) + rec_logL_add;}}
      {f_rec_dev_end+=square(log_rec_dev(iyear));}}
  }
  fval+=w_rec_end*f_rec_dev_end;
}

//Ftune penalty: does not apply in last phase
f_Ftune=0.0;
if (w_Ftune>0.0)
{if (set_Ftune>0.0 && !last_phase()) {f_Ftune=square(Fapex(set_Ftune_yr)-set_Ftune);}}
fval+=w_Ftune*f_Ftune;
}

//Penalty if apical F exceeds 3.0
f_fullF_constraint=0.0;
if (w_fullF>0.0)
{for (iyear=styr; iyear<=endyr; iyear++)
  {if(Fapex(iyear)>3.0) {f_fullF_constraint+=(mfexp(Fapex(iyear)-3.0)-1.0);}}}}
fval+=w_fullF*f_fullF_constraint;

```

```
}
```

```
//Random walk components of fishery dependent indices - we don't have any fishery dependent indices
```

```
//f_cH_RWq_cpue=0.0;
```

```
//for (iyear=styr_cH_cpue; iyear<endyr_cH_cpue; iyear++)
```

```
// {f_cH_RWq_cpue+=square(q_RW_log_dev_cH(iyear))/(2.0*set_RWq_var);}
```

```
//fval+=f_cH_RWq_cpue;
```

```
//---Priors-----
```

```
//neg_log_prior arguments: estimate, prior mean, prior var/-CV, pdf type
```

```
//Variance input as a negative value is considered to be CV in arithmetic space (CV=-1 implies loose prior)
```

```
//pdf type 1=none, 2=lognormal, 3=normal, 4=beta
```

```
f_priors=0.0;
```

```
f_priors+=neg_log_prior(len_cv_nad_val,set_len_cv_nad(5),set_len_cv_nad(6),set_len_cv_nad(7));
```

```
f_priors+=neg_log_prior(len_cv_mad_val,set_len_cv_mad(5),set_len_cv_mad(6),set_len_cv_mad(7));
```

```
//f_priors+=neg_log_prior(len_cv_sad_val,set_len_cv_sad(5),set_len_cv_sad(6),set_len_cv_sad(7));
```

```
f_priors+=neg_log_prior(steep,set_steep(5),set_steep(6),set_steep(7));
```

```
f_priors+=neg_log_prior(log_R0,set_log_R0(5),set_log_R0(6),set_log_R0(7));
```

```
f_priors+=neg_log_prior(R_autocorr,set_R_autocorr(5),set_R_autocorr(6),set_R_autocorr(7));
```

```
f_priors+=neg_log_prior(rec_sigma,set_rec_sigma(5),set_rec_sigma(6),set_rec_sigma(7));
```

```
f_priors+=neg_log_prior(selpar_A50_cRn,set_selpar_A50_cRn(5), set_selpar_A50_cRn(6),  
set_selpar_A50_cRn(7));
```

```
f_priors+=neg_log_prior(selpar_slope_cRn,set_selpar_slope_cRn(5), set_selpar_slope_cRn(6),  
set_selpar_slope_cRn(7));
```

```
f_priors+=neg_log_prior(selpar_A502_cRn,set_selpar_A502_cRn(5), set_selpar_A502_cRn(6),  
set_selpar_A502_cRn(7));
```

```
f_priors+=neg_log_prior(selpar_slope2_cRn,set_selpar_slope2_cRn(5), set_selpar_slope2_cRn(6),  
set_selpar_slope2_cRn(7));
```

```
f_priors+=neg_log_prior(selpar_A50_cRn2,set_selpar_A50_cRn2(5), set_selpar_A50_cRn2(6),  
set_selpar_A50_cRn2(7));
```

```
f_priors+=neg_log_prior(selpar_slope_cRn2,set_selpar_slope_cRn2(5), set_selpar_slope_cRn2(6),  
set_selpar_slope_cRn2(7));
```

```
f_priors+=neg_log_prior(selpar_A502_cRn2,set_selpar_A502_cRn2(5), set_selpar_A502_cRn2(6),  
set_selpar_A502_cRn2(7));
```



```
f_priors+=neg_log_prior(selpar_slope2_cRn2,set_selpar_slope2_cRn2(5), set_selpar_slope2_cRn2(6),  
set_selpar_slope2_cRn2(7));
```

```
f_priors+=neg_log_prior(selpar_A50_cRn3,set_selpar_A50_cRn3(5), set_selpar_A50_cRn3(6),  
set_selpar_A50_cRn3(7));
```

```
f_priors+=neg_log_prior(selpar_slope_cRn3,set_selpar_slope_cRn3(5), set_selpar_slope_cRn3(6),  
set_selpar_slope_cRn3(7));
```

```
f_priors+=neg_log_prior(selpar_A502_cRn3,set_selpar_A502_cRn3(5), set_selpar_A502_cRn3(6),  
set_selpar_A502_cRn3(7));
```

```
f_priors+=neg_log_prior(selpar_slope2_cRn3,set_selpar_slope2_cRn3(5), set_selpar_slope2_cRn3(6),  
set_selpar_slope2_cRn3(7));
```

```
f_priors+=neg_log_prior(selpar_A50_cRn4,set_selpar_A50_cRn4(5), set_selpar_A50_cRn4(6),  
set_selpar_A50_cRn4(7));
```

```
f_priors+=neg_log_prior(selpar_slope_cRn4,set_selpar_slope_cRn4(5), set_selpar_slope_cRn4(6),  
set_selpar_slope_cRn4(7));
```

```
f_priors+=neg_log_prior(selpar_A502_cRn4,set_selpar_A502_cRn4(5), set_selpar_A502_cRn4(6),  
set_selpar_A502_cRn4(7));
```

```
f_priors+=neg_log_prior(selpar_slope2_cRn4,set_selpar_slope2_cRn4(5), set_selpar_slope2_cRn4(6),  
set_selpar_slope2_cRn4(7));
```

```
f_priors+=neg_log_prior(selpar_A50_cRs,set_selpar_A50_cRs(5), set_selpar_A50_cRs(6), set_selpar_A50_cRs(7));
```

```
f_priors+=neg_log_prior(selpar_slope_cRs,set_selpar_slope_cRs(5), set_selpar_slope_cRs(6),  
set_selpar_slope_cRs(7));
```

```
f_priors+=neg_log_prior(selpar_A502_cRs,set_selpar_A502_cRs(5), set_selpar_A502_cRs(6),  
set_selpar_A502_cRs(7));
```

```
f_priors+=neg_log_prior(selpar_slope2_cRs,set_selpar_slope2_cRs(5), set_selpar_slope2_cRs(6),  
set_selpar_slope2_cRs(7));
```

```
f_priors+=neg_log_prior(selpar_A50_cRs2,set_selpar_A50_cRs2(5), set_selpar_A50_cRs2(6),  
set_selpar_A50_cRs2(7));
```

```
f_priors+=neg_log_prior(selpar_slope_cRs2,set_selpar_slope_cRs2(5), set_selpar_slope_cRs2(6),  
set_selpar_slope_cRs2(7));
```

```
f_priors+=neg_log_prior(selpar_A502_cRs2,set_selpar_A502_cRs2(5), set_selpar_A502_cRs2(6),  
set_selpar_A502_cRs2(7));
```

```
f_priors+=neg_log_prior(selpar_slope2_cRs2,set_selpar_slope2_cRs2(5), set_selpar_slope2_cRs2(6),  
set_selpar_slope2_cRs2(7));
```

```
f_priors+=neg_log_prior(selpar_A50_cRs3,set_selpar_A50_cRs3(5), set_selpar_A50_cRs3(6),  
set_selpar_A50_cRs3(7));
```

f\_priors+=neg\_log\_prior(selpar\_slope\_cRs3,set\_selpar\_slope\_cRs3(5), set\_selpar\_slope\_cRs3(6),  
set\_selpar\_slope\_cRs3(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_cRs3,set\_selpar\_A502\_cRs3(5), set\_selpar\_A502\_cRs3(6),  
set\_selpar\_A502\_cRs3(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_cRs3,set\_selpar\_slope2\_cRs3(5), set\_selpar\_slope2\_cRs3(6),  
set\_selpar\_slope2\_cRs3(7));

f\_priors+=neg\_log\_prior(selpar\_A50\_cRs4,set\_selpar\_A50\_cRs4(5), set\_selpar\_A50\_cRs4(6),  
set\_selpar\_A50\_cRs4(7));

f\_priors+=neg\_log\_prior(selpar\_slope\_cRs4,set\_selpar\_slope\_cRs4(5), set\_selpar\_slope\_cRs4(6),  
set\_selpar\_slope\_cRs4(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_cRs4,set\_selpar\_A502\_cRs4(5), set\_selpar\_A502\_cRs4(6),  
set\_selpar\_A502\_cRs4(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_cRs4,set\_selpar\_slope2\_cRs4(5), set\_selpar\_slope2\_cRs4(6),  
set\_selpar\_slope2\_cRs4(7));

f\_priors+=neg\_log\_prior(selpar\_A50\_cBn,set\_selpar\_A50\_cBn(5), set\_selpar\_A50\_cBn(6),  
set\_selpar\_A50\_cBn(7));

f\_priors+=neg\_log\_prior(selpar\_slope\_cBn,set\_selpar\_slope\_cBn(5), set\_selpar\_slope\_cBn(6),  
set\_selpar\_slope\_cBn(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_cBn,set\_selpar\_A502\_cBn(5), set\_selpar\_A502\_cBn(6),  
set\_selpar\_A502\_cBn(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_cBn,set\_selpar\_slope2\_cBn(5), set\_selpar\_slope2\_cBn(6),  
set\_selpar\_slope2\_cBn(7));

f\_priors+=neg\_log\_prior(selpar\_A50\_cBn2,set\_selpar\_A50\_cBn2(5), set\_selpar\_A50\_cBn2(6),  
set\_selpar\_A50\_cBn2(7));

f\_priors+=neg\_log\_prior(selpar\_slope\_cBn2,set\_selpar\_slope\_cBn2(5), set\_selpar\_slope\_cBn2(6),  
set\_selpar\_slope\_cBn2(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_cBn2,set\_selpar\_A502\_cBn2(5), set\_selpar\_A502\_cBn2(6),  
set\_selpar\_A502\_cBn2(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_cBn2,set\_selpar\_slope2\_cBn2(5), set\_selpar\_slope2\_cBn2(6),  
set\_selpar\_slope2\_cBn2(7));

f\_priors+=neg\_log\_prior(selpar\_A50\_cBs,set\_selpar\_A50\_cBs(5), set\_selpar\_A50\_cBs(6), set\_selpar\_A50\_cBs(7));

f\_priors+=neg\_log\_prior(selpar\_slope\_cBs,set\_selpar\_slope\_cBs(5), set\_selpar\_slope\_cBs(6),  
set\_selpar\_slope\_cBs(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_cBs,set\_selpar\_A502\_cBs(5), set\_selpar\_A502\_cBs(6),  
set\_selpar\_A502\_cBs(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_cBs,set\_selpar\_slope2\_cBs(5), set\_selpar\_slope2\_cBs(6),  
set\_selpar\_slope2\_cBs(7));

f\_priors+=neg\_log\_prior(selpar\_A50\_cBs2,set\_selpar\_A50\_cBs2(5), set\_selpar\_A50\_cBs2(6),  
set\_selpar\_A50\_cBs2(7));

f\_priors+=neg\_log\_prior(selpar\_slope\_cBs2,set\_selpar\_slope\_cBs2(5), set\_selpar\_slope\_cBs2(6),  
set\_selpar\_slope\_cBs2(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_cBs2,set\_selpar\_A502\_cBs2(5), set\_selpar\_A502\_cBs2(6),  
set\_selpar\_A502\_cBs2(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_cBs2,set\_selpar\_slope2\_cBs2(5), set\_selpar\_slope2\_cBs2(6),  
set\_selpar\_slope2\_cBs2(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRn\_logit,set\_sel\_age0\_cRn(5),set\_sel\_age0\_cRn(6), set\_sel\_age0\_cRn(7));

f\_priors+=neg\_log\_prior(sel\_age1\_cRn\_logit,set\_sel\_age1\_cRn(5),set\_sel\_age1\_cRn(6), set\_sel\_age1\_cRn(7));

f\_priors+=neg\_log\_prior(sel\_age2\_cRn\_logit,set\_sel\_age2\_cRn(5),set\_sel\_age2\_cRn(6), set\_sel\_age2\_cRn(7));

f\_priors+=neg\_log\_prior(sel\_age3\_cRn\_logit,set\_sel\_age3\_cRn(5),set\_sel\_age3\_cRn(6), set\_sel\_age3\_cRn(7));

f\_priors+=neg\_log\_prior(sel\_age4\_cRn\_logit,set\_sel\_age4\_cRn(5),set\_sel\_age4\_cRn(6), set\_sel\_age4\_cRn(7));

f\_priors+=neg\_log\_prior(sel\_age5\_cRn\_logit,set\_sel\_age5\_cRn(5),set\_sel\_age5\_cRn(6), set\_sel\_age5\_cRn(7));

f\_priors+=neg\_log\_prior(sel\_age6\_cRn\_logit,set\_sel\_age6\_cRn(5),set\_sel\_age6\_cRn(6), set\_sel\_age6\_cRn(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRn2\_logit,set\_sel\_age0\_cRn2(5),set\_sel\_age0\_cRn2(6),  
set\_sel\_age0\_cRn2(7));

f\_priors+=neg\_log\_prior(sel\_age1\_cRn2\_logit,set\_sel\_age1\_cRn2(5),set\_sel\_age1\_cRn2(6),  
set\_sel\_age1\_cRn2(7));

f\_priors+=neg\_log\_prior(sel\_age2\_cRn2\_logit,set\_sel\_age2\_cRn2(5),set\_sel\_age2\_cRn2(6),  
set\_sel\_age2\_cRn2(7));

f\_priors+=neg\_log\_prior(sel\_age3\_cRn2\_logit,set\_sel\_age3\_cRn2(5),set\_sel\_age3\_cRn2(6),  
set\_sel\_age3\_cRn2(7));

f\_priors+=neg\_log\_prior(sel\_age4\_cRn2\_logit,set\_sel\_age4\_cRn2(5),set\_sel\_age4\_cRn2(6),  
set\_sel\_age4\_cRn2(7));

f\_priors+=neg\_log\_prior(sel\_age5\_cRn2\_logit,set\_sel\_age5\_cRn2(5),set\_sel\_age5\_cRn2(6),  
set\_sel\_age5\_cRn2(7));

f\_priors+=neg\_log\_prior(sel\_age6\_cRn2\_logit,set\_sel\_age6\_cRn2(5),set\_sel\_age6\_cRn2(6),  
set\_sel\_age6\_cRn2(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRn3\_logit,set\_sel\_age0\_cRn3(5),set\_sel\_age0\_cRn3(6),  
set\_sel\_age0\_cRn3(7));

f\_priors+=neg\_log\_prior(sel\_age1\_cRn3\_logit,set\_sel\_age1\_cRn3(5),set\_sel\_age1\_cRn3(6),  
set\_sel\_age1\_cRn3(7));

f\_priors+=neg\_log\_prior(sel\_age2\_cRn3\_logit,set\_sel\_age2\_cRn3(5),set\_sel\_age2\_cRn3(6),  
set\_sel\_age2\_cRn3(7));

f\_priors+=neg\_log\_prior(sel\_age3\_cRn3\_logit,set\_sel\_age3\_cRn3(5),set\_sel\_age3\_cRn3(6),  
set\_sel\_age3\_cRn3(7));

f\_priors+=neg\_log\_prior(sel\_age4\_cRn3\_logit,set\_sel\_age4\_cRn3(5),set\_sel\_age4\_cRn3(6),  
set\_sel\_age4\_cRn3(7));

f\_priors+=neg\_log\_prior(sel\_age5\_cRn3\_logit,set\_sel\_age5\_cRn3(5),set\_sel\_age5\_cRn3(6),  
set\_sel\_age5\_cRn3(7));

f\_priors+=neg\_log\_prior(sel\_age6\_cRn3\_logit,set\_sel\_age6\_cRn3(5),set\_sel\_age6\_cRn3(6),  
set\_sel\_age6\_cRn3(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRn4\_logit,set\_sel\_age0\_cRn4(5),set\_sel\_age0\_cRn4(6),  
set\_sel\_age0\_cRn4(7));

f\_priors+=neg\_log\_prior(sel\_age1\_cRn4\_logit,set\_sel\_age1\_cRn4(5),set\_sel\_age1\_cRn4(6),  
set\_sel\_age1\_cRn4(7));

f\_priors+=neg\_log\_prior(sel\_age2\_cRn4\_logit,set\_sel\_age2\_cRn4(5),set\_sel\_age2\_cRn4(6),  
set\_sel\_age2\_cRn4(7));

f\_priors+=neg\_log\_prior(sel\_age3\_cRn4\_logit,set\_sel\_age3\_cRn4(5),set\_sel\_age3\_cRn4(6),  
set\_sel\_age3\_cRn4(7));

f\_priors+=neg\_log\_prior(sel\_age4\_cRn4\_logit,set\_sel\_age4\_cRn4(5),set\_sel\_age4\_cRn4(6),  
set\_sel\_age4\_cRn4(7));

f\_priors+=neg\_log\_prior(sel\_age5\_cRn4\_logit,set\_sel\_age5\_cRn4(5),set\_sel\_age5\_cRn4(6),  
set\_sel\_age5\_cRn4(7));

f\_priors+=neg\_log\_prior(sel\_age6\_cRn4\_logit,set\_sel\_age6\_cRn4(5),set\_sel\_age6\_cRn4(6),  
set\_sel\_age6\_cRn4(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRs\_logit,set\_sel\_age0\_cRs(5),set\_sel\_age0\_cRs(6), set\_sel\_age0\_cRs(7));

f\_priors+=neg\_log\_prior(sel\_age1\_cRs\_logit,set\_sel\_age1\_cRs(5),set\_sel\_age1\_cRs(6), set\_sel\_age1\_cRs(7));

f\_priors+=neg\_log\_prior(sel\_age2\_cRs\_logit,set\_sel\_age2\_cRs(5),set\_sel\_age2\_cRs(6), set\_sel\_age2\_cRs(7));

f\_priors+=neg\_log\_prior(sel\_age3\_cRs\_logit,set\_sel\_age3\_cRs(5),set\_sel\_age3\_cRs(6), set\_sel\_age3\_cRs(7));

f\_priors+=neg\_log\_prior(sel\_age4\_cRs\_logit,set\_sel\_age4\_cRs(5),set\_sel\_age4\_cRs(6), set\_sel\_age4\_cRs(7));

f\_priors+=neg\_log\_prior(sel\_age5\_cRs\_logit,set\_sel\_age5\_cRs(5),set\_sel\_age5\_cRs(6), set\_sel\_age5\_cRs(7));

f\_priors+=neg\_log\_prior(sel\_age6\_cRs\_logit,set\_sel\_age6\_cRs(5),set\_sel\_age6\_cRs(6), set\_sel\_age6\_cRs(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRs2\_logit,set\_sel\_age0\_cRs2(5),set\_sel\_age0\_cRs2(6), set\_sel\_age0\_cRs2(7));

f\_priors+=neg\_log\_prior(sel\_age1\_cRs2\_logit,set\_sel\_age1\_cRs2(5),set\_sel\_age1\_cRs2(6), set\_sel\_age1\_cRs2(7));

f\_priors+=neg\_log\_prior(sel\_age2\_cRs2\_logit,set\_sel\_age2\_cRs2(5),set\_sel\_age2\_cRs2(6), set\_sel\_age2\_cRs2(7));

f\_priors+=neg\_log\_prior(sel\_age3\_cRs2\_logit,set\_sel\_age3\_cRs2(5),set\_sel\_age3\_cRs2(6), set\_sel\_age3\_cRs2(7));

f\_priors+=neg\_log\_prior(sel\_age4\_cRs2\_logit,set\_sel\_age4\_cRs2(5),set\_sel\_age4\_cRs2(6), set\_sel\_age4\_cRs2(7));

f\_priors+=neg\_log\_prior(sel\_age5\_cRs2\_logit,set\_sel\_age5\_cRs2(5),set\_sel\_age5\_cRs2(6), set\_sel\_age5\_cRs2(7));

f\_priors+=neg\_log\_prior(sel\_age6\_cRs2\_logit,set\_sel\_age6\_cRs2(5),set\_sel\_age6\_cRs2(6), set\_sel\_age6\_cRs2(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRs3\_logit,set\_sel\_age0\_cRs3(5),set\_sel\_age0\_cRs3(6), set\_sel\_age0\_cRs3(7));  
f\_priors+=neg\_log\_prior(sel\_age1\_cRs3\_logit,set\_sel\_age1\_cRs3(5),set\_sel\_age1\_cRs3(6), set\_sel\_age1\_cRs3(7));  
f\_priors+=neg\_log\_prior(sel\_age2\_cRs3\_logit,set\_sel\_age2\_cRs3(5),set\_sel\_age2\_cRs3(6), set\_sel\_age2\_cRs3(7));  
f\_priors+=neg\_log\_prior(sel\_age3\_cRs3\_logit,set\_sel\_age3\_cRs3(5),set\_sel\_age3\_cRs3(6), set\_sel\_age3\_cRs3(7));  
f\_priors+=neg\_log\_prior(sel\_age4\_cRs3\_logit,set\_sel\_age4\_cRs3(5),set\_sel\_age4\_cRs3(6), set\_sel\_age4\_cRs3(7));  
f\_priors+=neg\_log\_prior(sel\_age5\_cRs3\_logit,set\_sel\_age5\_cRs3(5),set\_sel\_age5\_cRs3(6), set\_sel\_age5\_cRs3(7));  
f\_priors+=neg\_log\_prior(sel\_age6\_cRs3\_logit,set\_sel\_age6\_cRs3(5),set\_sel\_age6\_cRs3(6), set\_sel\_age6\_cRs3(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cRs4\_logit,set\_sel\_age0\_cRs4(5),set\_sel\_age0\_cRs4(6), set\_sel\_age0\_cRs4(7));  
f\_priors+=neg\_log\_prior(sel\_age1\_cRs4\_logit,set\_sel\_age1\_cRs4(5),set\_sel\_age1\_cRs4(6), set\_sel\_age1\_cRs4(7));  
f\_priors+=neg\_log\_prior(sel\_age2\_cRs4\_logit,set\_sel\_age2\_cRs4(5),set\_sel\_age2\_cRs4(6), set\_sel\_age2\_cRs4(7));  
f\_priors+=neg\_log\_prior(sel\_age3\_cRs4\_logit,set\_sel\_age3\_cRs4(5),set\_sel\_age3\_cRs4(6), set\_sel\_age3\_cRs4(7));  
f\_priors+=neg\_log\_prior(sel\_age4\_cRs4\_logit,set\_sel\_age4\_cRs4(5),set\_sel\_age4\_cRs4(6), set\_sel\_age4\_cRs4(7));  
f\_priors+=neg\_log\_prior(sel\_age5\_cRs4\_logit,set\_sel\_age5\_cRs4(5),set\_sel\_age5\_cRs4(6), set\_sel\_age5\_cRs4(7));  
f\_priors+=neg\_log\_prior(sel\_age6\_cRs4\_logit,set\_sel\_age6\_cRs4(5),set\_sel\_age6\_cRs4(6), set\_sel\_age6\_cRs4(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cBn\_logit,set\_sel\_age0\_cBn(5),set\_sel\_age0\_cBn(6), set\_sel\_age0\_cBn(7));  
f\_priors+=neg\_log\_prior(sel\_age1\_cBn\_logit,set\_sel\_age1\_cBn(5),set\_sel\_age1\_cBn(6), set\_sel\_age1\_cBn(7));  
f\_priors+=neg\_log\_prior(sel\_age2\_cBn\_logit,set\_sel\_age2\_cBn(5),set\_sel\_age2\_cBn(6), set\_sel\_age2\_cBn(7));  
f\_priors+=neg\_log\_prior(sel\_age3\_cBn\_logit,set\_sel\_age3\_cBn(5),set\_sel\_age3\_cBn(6), set\_sel\_age3\_cBn(7));  
f\_priors+=neg\_log\_prior(sel\_age4\_cBn\_logit,set\_sel\_age4\_cBn(5),set\_sel\_age4\_cBn(6), set\_sel\_age4\_cBn(7));  
f\_priors+=neg\_log\_prior(sel\_age5\_cBn\_logit,set\_sel\_age5\_cBn(5),set\_sel\_age5\_cBn(6), set\_sel\_age5\_cBn(7));  
f\_priors+=neg\_log\_prior(sel\_age6\_cBn\_logit,set\_sel\_age6\_cBn(5),set\_sel\_age6\_cBn(6), set\_sel\_age6\_cBn(7));

f\_priors+=neg\_log\_prior(sel\_age0\_cBn2\_logit,set\_sel\_age0\_cBn2(5),set\_sel\_age0\_cBn2(6),  
set\_sel\_age0\_cBn2(7));

f\_priors+=neg\_log\_prior(sel\_age1\_cBn2\_logit,set\_sel\_age1\_cBn2(5),set\_sel\_age1\_cBn2(6),  
set\_sel\_age1\_cBn2(7));

f\_priors+=neg\_log\_prior(sel\_age2\_cBn2\_logit,set\_sel\_age2\_cBn2(5),set\_sel\_age2\_cBn2(6),  
set\_sel\_age2\_cBn2(7));

f\_priors+=neg\_log\_prior(sel\_age3\_cBn2\_logit,set\_sel\_age3\_cBn2(5),set\_sel\_age3\_cBn2(6),  
set\_sel\_age3\_cBn2(7));

f\_priors+=neg\_log\_prior(sel\_age4\_cBn2\_logit,set\_sel\_age4\_cBn2(5),set\_sel\_age4\_cBn2(6),  
set\_sel\_age4\_cBn2(7));

f\_priors+=neg\_log\_prior(sel\_age5\_cBn2\_logit,set\_sel\_age5\_cBn2(5),set\_sel\_age5\_cBn2(6),  
set\_sel\_age5\_cBn2(7));

```
f_priors+=neg_log_prior(sel_age6_cBn2_logit,set_sel_age6_cBn2(5),set_sel_age6_cBn2(6),  
set_sel_age6_cBn2(7));
```

```
f_priors+=neg_log_prior(sel_age0_cBs_logit,set_sel_age0_cBs(5),set_sel_age0_cBs(6), set_sel_age0_cBs(7));  
f_priors+=neg_log_prior(sel_age1_cBs_logit,set_sel_age1_cBs(5),set_sel_age1_cBs(6), set_sel_age1_cBs(7));  
f_priors+=neg_log_prior(sel_age2_cBs_logit,set_sel_age2_cBs(5),set_sel_age2_cBs(6), set_sel_age2_cBs(7));  
f_priors+=neg_log_prior(sel_age3_cBs_logit,set_sel_age3_cBs(5),set_sel_age3_cBs(6), set_sel_age3_cBs(7));  
f_priors+=neg_log_prior(sel_age4_cBs_logit,set_sel_age4_cBs(5),set_sel_age4_cBs(6), set_sel_age4_cBs(7));  
f_priors+=neg_log_prior(sel_age5_cBs_logit,set_sel_age5_cBs(5),set_sel_age5_cBs(6), set_sel_age5_cBs(7));  
f_priors+=neg_log_prior(sel_age6_cBs_logit,set_sel_age6_cBs(5),set_sel_age6_cBs(6), set_sel_age6_cBs(7));
```

```
f_priors+=neg_log_prior(sel_age0_cBs2_logit,set_sel_age0_cBs2(5),set_sel_age0_cBs2(6), set_sel_age0_cBs2(7));  
f_priors+=neg_log_prior(sel_age1_cBs2_logit,set_sel_age1_cBs2(5),set_sel_age1_cBs2(6), set_sel_age1_cBs2(7));  
f_priors+=neg_log_prior(sel_age2_cBs2_logit,set_sel_age2_cBs2(5),set_sel_age2_cBs2(6), set_sel_age2_cBs2(7));  
f_priors+=neg_log_prior(sel_age3_cBs2_logit,set_sel_age3_cBs2(5),set_sel_age3_cBs2(6), set_sel_age3_cBs2(7));  
f_priors+=neg_log_prior(sel_age4_cBs2_logit,set_sel_age4_cBs2(5),set_sel_age4_cBs2(6), set_sel_age4_cBs2(7));  
f_priors+=neg_log_prior(sel_age5_cBs2_logit,set_sel_age5_cBs2(5),set_sel_age5_cBs2(6), set_sel_age5_cBs2(7));  
f_priors+=neg_log_prior(sel_age6_cBs2_logit,set_sel_age6_cBs2(5),set_sel_age6_cBs2(6), set_sel_age6_cBs2(7));
```

```
f_priors+=neg_log_prior(selpar_A50_nad,set_selpar_A50_nad(5), set_selpar_A50_nad(6),  
set_selpar_A50_nad(7));
```

```
f_priors+=neg_log_prior(selpar_slope_nad,set_selpar_slope_nad(5), set_selpar_slope_nad(6),  
set_selpar_slope_nad(7));
```

```
f_priors+=neg_log_prior(selpar_A502_nad,set_selpar_A502_nad(5), set_selpar_A502_nad(6),  
set_selpar_A502_nad(7));
```

```
f_priors+=neg_log_prior(selpar_slope2_nad,set_selpar_slope2_nad(5), set_selpar_slope2_nad(6),  
set_selpar_slope2_nad(7));
```

```
f_priors+=neg_log_prior(sel_age0_nad_logit,set_sel_age0_nad(5),set_sel_age0_nad(6), set_sel_age0_nad(7));  
f_priors+=neg_log_prior(sel_age1_nad_logit,set_sel_age1_nad(5),set_sel_age1_nad(6), set_sel_age1_nad(7));  
f_priors+=neg_log_prior(sel_age2_nad_logit,set_sel_age2_nad(5),set_sel_age2_nad(6), set_sel_age2_nad(7));  
f_priors+=neg_log_prior(sel_age3_nad_logit,set_sel_age3_nad(5),set_sel_age3_nad(6), set_sel_age3_nad(7));  
f_priors+=neg_log_prior(sel_age4_nad_logit,set_sel_age4_nad(5),set_sel_age4_nad(6), set_sel_age4_nad(7));  
f_priors+=neg_log_prior(sel_age5_nad_logit,set_sel_age5_nad(5),set_sel_age5_nad(6), set_sel_age5_nad(7));  
f_priors+=neg_log_prior(sel_age6_nad_logit,set_sel_age6_nad(5),set_sel_age6_nad(6), set_sel_age6_nad(7));
```

f\_priors+=neg\_log\_prior(selpar\_A50\_mad,set\_selpar\_A50\_mad(5), set\_selpar\_A50\_mad(6),  
set\_selpar\_A50\_mad(7));

f\_priors+=neg\_log\_prior(selpar\_slope\_mad,set\_selpar\_slope\_mad(5), set\_selpar\_slope\_mad(6),  
set\_selpar\_slope\_mad(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_mad,set\_selpar\_A502\_mad(5), set\_selpar\_A502\_mad(6),  
set\_selpar\_A502\_mad(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_mad,set\_selpar\_slope2\_mad(5), set\_selpar\_slope2\_mad(6),  
set\_selpar\_slope2\_mad(7));

f\_priors+=neg\_log\_prior(sel\_age0\_mad\_logit,set\_sel\_age0\_mad(5),set\_sel\_age0\_mad(6), set\_sel\_age0\_mad(7));

f\_priors+=neg\_log\_prior(sel\_age1\_mad\_logit,set\_sel\_age1\_mad(5),set\_sel\_age1\_mad(6), set\_sel\_age1\_mad(7));

f\_priors+=neg\_log\_prior(sel\_age2\_mad\_logit,set\_sel\_age2\_mad(5),set\_sel\_age2\_mad(6), set\_sel\_age2\_mad(7));

f\_priors+=neg\_log\_prior(sel\_age3\_mad\_logit,set\_sel\_age3\_mad(5),set\_sel\_age3\_mad(6), set\_sel\_age3\_mad(7));

f\_priors+=neg\_log\_prior(sel\_age4\_mad\_logit,set\_sel\_age4\_mad(5),set\_sel\_age4\_mad(6), set\_sel\_age4\_mad(7));

f\_priors+=neg\_log\_prior(sel\_age5\_mad\_logit,set\_sel\_age5\_mad(5),set\_sel\_age5\_mad(6), set\_sel\_age5\_mad(7));

f\_priors+=neg\_log\_prior(sel\_age6\_mad\_logit,set\_sel\_age6\_mad(5),set\_sel\_age6\_mad(6), set\_sel\_age6\_mad(7));

f\_priors+=neg\_log\_prior(selpar\_A50\_sad,set\_selpar\_A50\_sad(5), set\_selpar\_A50\_sad(6), set\_selpar\_A50\_sad(7));

f\_priors+=neg\_log\_prior(selpar\_slope\_sad,set\_selpar\_slope\_sad(5), set\_selpar\_slope\_sad(6),  
set\_selpar\_slope\_sad(7));

f\_priors+=neg\_log\_prior(selpar\_A502\_sad,set\_selpar\_A502\_sad(5), set\_selpar\_A502\_sad(6),  
set\_selpar\_A502\_sad(7));

f\_priors+=neg\_log\_prior(selpar\_slope2\_sad,set\_selpar\_slope2\_sad(5), set\_selpar\_slope2\_sad(6),  
set\_selpar\_slope2\_sad(7));

f\_priors+=neg\_log\_prior(sel\_age0\_sad\_logit,set\_sel\_age0\_sad(5),set\_sel\_age0\_sad(6), set\_sel\_age0\_sad(7));

f\_priors+=neg\_log\_prior(sel\_age1\_sad\_logit,set\_sel\_age1\_sad(5),set\_sel\_age1\_sad(6), set\_sel\_age1\_sad(7));

f\_priors+=neg\_log\_prior(sel\_age2\_sad\_logit,set\_sel\_age2\_sad(5),set\_sel\_age2\_sad(6), set\_sel\_age2\_sad(7));

f\_priors+=neg\_log\_prior(sel\_age3\_sad\_logit,set\_sel\_age3\_sad(5),set\_sel\_age3\_sad(6), set\_sel\_age3\_sad(7));

f\_priors+=neg\_log\_prior(sel\_age4\_sad\_logit,set\_sel\_age4\_sad(5),set\_sel\_age4\_sad(6), set\_sel\_age4\_sad(7));

f\_priors+=neg\_log\_prior(sel\_age5\_sad\_logit,set\_sel\_age5\_sad(5),set\_sel\_age5\_sad(6), set\_sel\_age5\_sad(7));

f\_priors+=neg\_log\_prior(sel\_age6\_sad\_logit,set\_sel\_age6\_sad(5),set\_sel\_age6\_sad(6), set\_sel\_age6\_sad(7));

f\_priors+=neg\_log\_prior(log\_q\_nad,set\_log\_q\_nad(5),set\_log\_q\_nad(6),set\_log\_q\_nad(7));

f\_priors+=neg\_log\_prior(log\_q\_mad,set\_log\_q\_mad(5),set\_log\_q\_mad(6),set\_log\_q\_mad(7));

f\_priors+=neg\_log\_prior(log\_q\_sad,set\_log\_q\_sad(5),set\_log\_q\_sad(6),set\_log\_q\_sad(7));

f\_priors+=neg\_log\_prior(log\_q\_jai,set\_log\_q\_jai(5),set\_log\_q\_jai(6),set\_log\_q\_jai(7));

f\_priors+=neg\_log\_prior(log\_q2\_jai,set\_log\_q2\_jai(5),set\_log\_q2\_jai(6),set\_log\_q2\_jai(7));

```

f_priors+=neg_log_prior(log_q_mar,set_log_q_mar(5),set_log_q_mar(6),set_log_q_mar(7));
f_priors+=neg_log_prior(log_q_eco,set_log_q_eco(5),set_log_q_eco(6),set_log_q_eco(7));

f_priors+=neg_log_prior(log_dm_nad_lc,set_log_dm_nad_lc(5),set_log_dm_nad_lc(6),set_log_dm_nad_lc(7));
f_priors+=neg_log_prior(log_dm_mad_lc,set_log_dm_mad_lc(5),set_log_dm_mad_lc(6),set_log_dm_mad_lc(7));
//f_priors+=neg_log_prior(log_dm_sad_lc,set_log_dm_sad_lc(5),set_log_dm_sad_lc(6),set_log_dm_sad_lc(7));

f_priors+=neg_log_prior(log_dm_cRn_ac,set_log_dm_cRn_ac(5),set_log_dm_cRn_ac(6),set_log_dm_cRn_ac(7));
f_priors+=neg_log_prior(log_dm_cRs_ac,set_log_dm_cRs_ac(5),set_log_dm_cRs_ac(6),set_log_dm_cRs_ac(7));
f_priors+=neg_log_prior(log_dm_cBn_ac,set_log_dm_cBn_ac(5),set_log_dm_cBn_ac(6),set_log_dm_cBn_ac(7));
f_priors+=neg_log_prior(log_dm_cBs_ac,set_log_dm_cBs_ac(5),set_log_dm_cBs_ac(6),set_log_dm_cBs_ac(7));

fval+=f_priors;

```

```
//-----
```

```
//Logistic function: 2 parameters
```

```
FUNCTION dvar_vector logistic(const dvar_vector& ages, const dvariable& A50, const dvariable& slope)
```

```
//ages=vector of ages, A50=age at 50% selectivity, slope=rate of increase
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvar_vector Sel_Tmp(ages.indexmin(),ages.indexmax());
```

```
Sel_Tmp=1./(1.+mfexp(-1.*slope*(ages-A50))); //logistic;
```

```
RETURN_ARRAYS_DECREMENT();
```

```
return Sel_Tmp;
```

```
//-----
```

```
//Logistic-exponential: 4 parameters (but 1 is fixed)
```

```
FUNCTION dvar_vector logistic_exponential(const dvar_vector& ages, const dvariable& A50, const dvariable& slope, const dvariable& sigma, const dvariable& joint)
```

```
//ages=vector of ages, A50=age at 50% sel (ascending limb), slope=rate of increase, sigma=controls rate of descent (descending)
```

```
//joint=age to join curves
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvar_vector Sel_Tmp(ages.indexmin(),ages.indexmax());
```

```
Sel_Tmp=1.0;
```

```
for (iage=1; iage<=nages; iage++)
```

```
{
```



```

if (ages(iage)<joint) {Sel_Tmp(iage)=1./(1.+mfexp(-1.*slope*(ages(iage)-A50)));}
if (ages(iage)>joint){Sel_Tmp(iage)=mfexp(-1.*square((ages(iage)-joint)/sigma));}
}
Sel_Tmp=Sel_Tmp/max(Sel_Tmp);
RETURN_ARRAYS_DECREMENT();
return Sel_Tmp;

```

```
//-----
```

```
//Logistic function: 4 parameters
```

```
FUNCTION dvar_vector logistic_double(const dvar_vector& ages, const dvariable& A501, const dvariable& slope1,
const dvariable& A502, const dvariable& slope2)
```

```
//ages=vector of ages, A50=age at 50% selectivity, slope=rate of increase, A502=age at 50% decrease additive to
A501, slope2=slope of decrease
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvar_vector Sel_Tmp(ages.indexmin(),ages.indexmax());
```

```
Sel_Tmp=elem_prod( (1./(1.+mfexp(-1.*slope1*(ages-A501)))),(1.-(1./(1.+mfexp(-1.*slope2*(ages-
(A501+A502)))))) );
```

```
Sel_Tmp=Sel_Tmp/max(Sel_Tmp);
```

```
RETURN_ARRAYS_DECREMENT();
```

```
return Sel_Tmp;
```

```
//-----
```

```
//Jointed logistic function: 6 parameters (increasing and decreasing logistcs joined at peak selectivity)
```

```
FUNCTION dvar_vector logistic_joint(const dvar_vector& ages, const dvariable& A501, const dvariable& slope1,
const dvariable& A502, const dvariable& slope2, const dvariable& satval, const dvariable& joint)
```

```
//ages=vector of ages, A501=age at 50% sel (ascending limb), slope1=rate of increase,A502=age at 50% sel
(descending), slope1=rate of increase (ascending),
```

```
//satval=saturation value of descending limb, joint=location in age vector to join curves (may equal age or age + 1
if age-0 is included)
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvar_vector Sel_Tmp(ages.indexmin(),ages.indexmax());
```

```
Sel_Tmp=1.0;
```

```
for (iage=1; iage<=nages; iage++)
```

```
{
```

```
if (double(iage)<joint) {Sel_Tmp(iage)=1./(1.+mfexp(-1.*slope1*(ages(iage)-A501)));}
```

```
if (double(iage)>joint){Sel_Tmp(iage)=1.0-(1.0-satval)/(1.+mfexp(-1.*slope2*(ages(iage)-A502)));}
```

```
}
```

```
Sel_Tmp=Sel_Tmp/max(Sel_Tmp);  
RETURN_ARRAYS_DECREMENT();  
return Sel_Tmp;
```

```
//-----
```

```
//Double Gaussian function: 6 parameters (as in SS3)
```

```
FUNCTION dvar_vector gaussian_double(const dvar_vector& ages, const dvariable& peak, const dvariable& top,  
const dvariable& ascwid, const dvariable& deswid, const dvariable& init, const dvariable& final)
```

```
//ages=vector of ages, peak=ascending inflection location (as logistic), top=width of plateau, ascwid=ascent width  
(as log(width))
```

```
//deswid=descent width (as log(width))
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvar_vector Sel_Tmp(ages.indexmin(),ages.indexmax());  
dvar_vector sel_step1(ages.indexmin(),ages.indexmax());  
dvar_vector sel_step2(ages.indexmin(),ages.indexmax());  
dvar_vector sel_step3(ages.indexmin(),ages.indexmax());  
dvar_vector sel_step4(ages.indexmin(),ages.indexmax());  
dvar_vector sel_step5(ages.indexmin(),ages.indexmax());  
dvar_vector sel_step6(ages.indexmin(),ages.indexmax());  
dvar_vector pars_tmp(1,6); dvar_vector sel_tmp_iq(1,2);
```

```
pars_tmp(1)=peak;
```

```
pars_tmp(2)=peak+1.0+(0.99*ages(nages)-peak-1.0)/(1.0+mfexp(-top));
```

```
pars_tmp(3)=mfexp(ascwid);
```

```
pars_tmp(4)=mfexp(deswid);
```

```
pars_tmp(5)=1.0/(1.0+mfexp(-init));
```

```
pars_tmp(6)=1.0/(1.0+mfexp(-final));
```

```
sel_tmp_iq(1)=mfexp(-(square(ages(1)-pars_tmp(1))/pars_tmp(3)));
```

```
sel_tmp_iq(2)=mfexp(-(square(ages(nages)-pars_tmp(2))/pars_tmp(4)));
```

```
sel_step1=mfexp(-(square(ages-pars_tmp(1))/pars_tmp(3)));
```

```
sel_step2=pars_tmp(5)+(1.0-pars_tmp(5))*(sel_step1-sel_tmp_iq(1))/(1.0-sel_tmp_iq(1));
```

```
sel_step3=mfexp(-(square(ages-pars_tmp(2))/pars_tmp(4)));
```

```
sel_step4=1.0+(pars_tmp(6)-1.0)*(sel_step3-1.0)/(sel_tmp_iq(2)-1.0);
```

```
sel_step5=1.0/(1.0+mfexp(-(20.0* elem_div((ages-pars_tmp(1)), (1.0+sfabs(ages-pars_tmp(1)))))));
```

```
sel_step6=1.0/(1.0+mfexp(-(20.0*elem_div((ages-pars_tmp(2)),(1.0+sfabs(ages-pars_tmp(2)))))));
```

```
Sel_Tmp=elem_prod(sel_step2,(1.0-sel_step5))+  
    elem_prod(sel_step5,((1.0-sel_step6)+ elem_prod(sel_step4,sel_step6)) );
```

```
Sel_Tmp=Sel_Tmp/max(Sel_Tmp);  
RETURN_ARRAYS_DECREMENT();  
return Sel_Tmp;
```

```
//-----
```

```
//Spawner-recruit function (Beverton-Holt or Ricker)
```

```
FUNCTION dvariable SR_func(const dvariable& R0, const dvariable& h, const dvariable& spr_F0, const dvariable&  
SSB, int func)
```

```
//R0=virgin recruitment, h=steepness, spr_F0=spawners per recruit @ F=0, SSB=spawning biomass
```

```
//func=1 for Beverton-Holt, 2 for Ricker
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvariable Recruits_Tmp;
```

```
switch(func) {
```

```
case 1: //Beverton-Holt
```

```
    Recruits_Tmp=((0.8*R0*h*SSB)/(0.2*R0*spr_F0*(1.0-h)+(h-0.2)*SSB));
```

```
break;
```

```
case 2: //Ricker
```

```
    Recruits_Tmp=((SSB/spr_F0)*mfexp(h*(1-SSB/(R0*spr_F0))));
```

```
break;
```

```
}
```

```
RETURN_ARRAYS_DECREMENT();
```

```
return Recruits_Tmp;
```

```
//-----
```

```
//Spawner-recruit equilibrium function (Beverton-Holt or Ricker)
```

```
FUNCTION dvariable SR_eq_func(const dvariable& R0, const dvariable& h, const dvariable& spr_F0, const  
dvariable& spr_F, const dvariable& BC, int func)
```

```
//R0=virgin recruitment, h=steepness, spr_F0=spawners per recruit @ F=0, spr_F=spawners per recruit @ F,  
BC=bias correction
```

```
//func=1 for Beverton-Holt, 2 for Ricker
```

```
RETURN_ARRAYS_INCREMENT();
```

```

dvariable Recruits_Tmp;
switch(func) {
  case 1: //Beverton-Holt
    Recruits_Tmp=(R0/((5.0*h-1.0)*spr_F))*(BC*4.0*h*spr_F-spr_F0*(1.0-h));
  break;
  case 2: //Ricker
    Recruits_Tmp=R0/(spr_F/spr_F0)*(1.0+log(BC*spr_F/spr_F0)/h);
  break;
}
RETURN_ARRAYS_DECREMENT();
return Recruits_Tmp;

//-----
//compute multinomial effective sample size for a single yr
FUNCTION dvariable multinom_eff_N(const dvar_vector& pred_comp, const dvar_vector& obs_comp)
//pred_comp=vector of predicted comps, obscomp=vector of observed comps
dvariable EffN_Tmp; dvariable numer; dvariable denom;
RETURN_ARRAYS_INCREMENT();
numer=sum( elem_prod(pred_comp,(1.0-pred_comp)) );
denom=sum( square(obs_comp-pred_comp) );
if (denom>0.0) {EffN_Tmp=numer/denom;}
else {EffN_Tmp=-missing;}
RETURN_ARRAYS_DECREMENT();
return EffN_Tmp;

//-----
//Likelihood contribution: lognormal
FUNCTION dvariable lk_lognormal(const dvar_vector& pred, const dvar_vector& obs, const dvar_vector& cv, const
dvariable& wgt_dat)
//pred=vector of predicted vals, obs=vector of observed vals, cv=vector of CVs in arithmetic space,
wgt_dat=constant scaling of CVs
//small_number is small value to avoid log(0) during search
RETURN_ARRAYS_INCREMENT();
dvariable LkvalTmp;
dvariable small_number=0.0001;
dvar_vector var(cv.indexmin(),cv.indexmax()); //variance in log space

```

```

var=log(1.0+square(cv/wgt_dat)); // convert cv in arithmetic space to variance in log space
LkvalTmp=sum(0.5*elem_div(square(log(elem_div((pred+small_number),(obs+small_number))))),var) );
RETURN_ARRAYS_DECREMENT();
return LkvalTmp;

```

```
//-----
```

```
//Likelihood contribution: multinomial
```

```
FUNCTION dvariable lk_multinomial(const dvar_vector& nsamp, const dvar_matrix& pred_comp, const
dvar_matrix& obs_comp, const double& ncomp, const double& minSS, const dvariable& wgt_dat)
```

```
//nsamp=vector of N's, pred_comp=matrix of predicted comps, obs_comp=matrix of observed comps, ncomp =
number of yrs in matrix, minSS=min N threshold, wgt_dat=scaling of N's
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvariable LkvalTmp;
```

```
dvariable small_number=0.0001;
```

```
LkvalTmp=0.0;
```

```
for (int ii=1; ii<=ncomp; ii++)
```

```
{if (nsamp(ii)>=minSS)
```

```
  {LkvalTmp-=wgt_dat*nsamp(ii)*sum(elem_prod((obs_comp(ii)+small_number),
    log(elem_div((pred_comp(ii)+small_number), (obs_comp(ii)+small_number)))));
```

```
  }
```

```
}
```

```
RETURN_ARRAYS_DECREMENT();
```

```
return LkvalTmp;
```

```
//-----
```

```
//Likelihood contribution: robust multinomial
```

```
FUNCTION dvariable lk_robust_multinomial(const dvar_vector& nsamp, const dvar_matrix& pred_comp, const
dvar_matrix& obs_comp, const double& ncomp, const dvariable& mbin, const double& minSS, const dvariable&
wgt_dat)
```

```
//nsamp=vector of N's, pred_comp=matrix of predicted comps, obs_comp=matrix of observed comps, ncomp =
number of yrs in matrix, mbin=number of bins, minSS=min N threshold, wgt_dat=scaling of N's
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvariable LkvalTmp;
```

```
dvariable small_number=0.0001;
```

```
LkvalTmp=0.0;
```

```
dvar_matrix Eprime=elem_prod((1.0-obs_comp), obs_comp)+0.1/mbin; //E' of Francis 2011, p.1131
```

```
dvar_vector nsamp_wgt=nsamp*wgt_dat;
```

```

//cout<<nsamp_wgt<<endl;
for (int ii=1; ii<=ncomp; ii++)
{if (nsamp(ii)>=minSS)
    {LkvalTmp+= sum(0.5*log(Eprime(ii))-log(small_number+mfexp(elem_div((-square(obs_comp(ii)-pred_comp(ii))
, (Eprime(ii)*2.0/nsamp_wgt(ii) ))) ));
    }
}
RETURN_ARRAYS_DECREMENT();
return LkvalTmp;

```

```
//-----
```

```
//Likelihood contribution: Dirichlet-multinomial
```

```
FUNCTION dvariable lk_dirichlet_multinomial(const dvar_vector& nsamp, const dvar_matrix& pred_comp, const
dvar_matrix& obs_comp, const double& ncomp, const dvariable& mbin, const double& minSS, const dvariable&
log_dir_par)
```

```
//nsamp=vector of N's, pred_comp=matrix of predicted comps, obs_comp=matrix of observed comps, ncomp =
number of yrs in matrix, mbin=number of bins, minSS=min N threshold, wgt_dat=scaling of N's
```

```
RETURN_ARRAYS_INCREMENT();
```

```
dvariable LkvalTmp;
```

```
LkvalTmp=0.0;
```

```
dvar_vector nsamp_adjust=nsamp*mfexp(log_dir_par);
```

```
//dvar_vector nsamp_adjust=mfexp(log_dir_par);
```

```
for (int ii=1; ii<=ncomp; ii++)
```

```
{
```

```
    if (nsamp(ii)>=minSS)
```

```
    {
```

```
        LkvalTmp-=gammln(nsamp_adjust(ii))-gammln(nsamp(ii)+nsamp_adjust(ii));
```

```
        LkvalTmp-=sum(gammln(nsamp(ii)*obs_comp(ii)+nsamp_adjust(ii)*pred_comp(ii)));
```

```
        LkvalTmp+=sum(gammln(nsamp_adjust(ii)*pred_comp(ii)));
```

```
    }
```

```
}
```

```
RETURN_ARRAYS_DECREMENT();
```

```
return LkvalTmp;
```

```
//-----
```

```
//Likelihood contribution: logistic normal (aka multivariate logistic in iSCAM; logistic normal in Francis'
terminology)
```

```

FUNCTION dvariable lk_logistic_normal(const dvar_vector& nsamp, const dvar_matrix& pred_comp, const
dvar_matrix& obs_comp, const double& ncomp, const dvariable& mbin, const double& minSS)

//nsamp=vector of N's, pred_comp=matrix of predicted comps, obs_comp=matrix of observed comps, ncomp =
number of yrs in matrix, mbin=number of bins, minSS=min N threshold

RETURN_ARRAYS_INCREMENT();

dvariable LkvalTmp;

dvariable small_number=0.0001;

LkvalTmp=0.0;

dvar_matrix nu=pred_comp+0.0;

dvar_matrix pred_plus=pred_comp+small_number;

dvar_matrix obs_plus=obs_comp+small_number;

dvariable nu_mean;

dvariable nu_sum_sq;

dvariable tau_hat_sq;

dvariable year_count; //keeps track of years included in likelihood (i.e., that meet the sample size requirement)

LkvalTmp=0.0;

nu_sum_sq=0.0;

year_count=0.0;

for (int ii=1; ii<=ncomp; ii++)
{if (nsamp(ii)>=minSS)
{
    year_count+=1.0;
    nu_mean=sum( log(obs_plus(ii))-log(pred_plus(ii)) )/mbin; //year-specific mean log residual
    for (int jj=1; jj<=mbin;jj++)
    {
        nu(ii,jj) = log(obs_plus(ii,jj)) - log(pred_plus(ii,jj)) - nu_mean;
        nu_sum_sq += square(nu(ii,jj));
    }
}
}

if (year_count>0.0)
{
    tau_hat_sq = nu_sum_sq/((mbin-1.0)*year_count);
    LkvalTmp = (mbin-1.0)*year_count*log(tau_hat_sq);
}

```

```

}
RETURN_ARRAYS_DECREMENT();
return LkvalTmp;

//-----
//-----
//Likelihood contribution: priors
FUNCTION dvariable neg_log_prior(dvariable pred, const double& prior, dvariable var, int pdf)
//prior=prior point estimate, var=variance (if negative, treated as CV in arithmetic space), pred=predicted value,
pdf=prior type (1=none, 2=lognormal, 3=normal, 4=beta)
dvariable LkvalTmp;
dvariable alpha, beta, ab_iq;
dvariable big_number=1e10;
LkvalTmp=0.0;
// compute generic pdf's
switch(pdf) {
case 1: //option to turn off prior
LkvalTmp=0.0;
break;
case 2: // lognormal
if(prior<=0.0) cout << "YIKES: Don't use a lognormal distn for a negative prior" << endl;
else if(pred<=0) LkvalTmp=big_number=1e10;
else {
if(var<0.0) var=log(1.0+var*var); // convert cv to variance on log scale
LkvalTmp= 0.5*( square(log(pred/prior))/var + log(var) );
}
break;
case 3: // normal
if(var<0.0 && prior!=0.0) var=square(var*prior); // convert cv to variance on observation scale
else if(var<0.0 && prior==0.0) var=-var; // cv not really appropriate if prior value equals zero
LkvalTmp= 0.5*( square(pred-prior)/var + log(var) );
break;
case 4: // beta
if(var<0.0) var=square(var*prior); // convert cv to variance on observation scale
if(prior<=0.0 || prior>=1.0) cout << "YIKES: Don't use a beta distn for a prior outside (0,1)" << endl;
ab_iq=prior*(1.0-prior)/var - 1.0; alpha=prior*ab_iq; beta=(1.0-prior)*ab_iq;
}
}

```



```

        if(pred>=0 && pred<=1) LkvalTmp= (1.0-alpha)*log(pred)+(1.0-beta)*log(1.0-pred)-
        gammln(alpha+beta)+gammln(alpha)+gammln(beta);
        else LkvalTmp=big_number;
        break;
    default: // no such prior pdf currently available
        cout << "The prior must be either 1(lognormal), 2(normal), or 3(beta)." << endl;
        cout << "Presently it is " << pdf << endl;
        exit(0);
    }
    return LkvalTmp;

//-----
//SDNR: age comp likelihood (assumes fits are done with the robust multinomial function)
FUNCTION dvariable sdnr_multinomial(const double& ncomp, const dvar_vector& ages, const dvar_vector&
nsamp,
                                const dvar_matrix& pred_comp, const dvar_matrix& obs_comp, const dvariable& wgt_dat)
//ncomp=number of years of data, ages=vector of ages, nsamp=vector of N's,
//pred_comp=matrix of predicted comps, obs_comp=matrix of observed comps, wgt_dat=likelihood weight for
data source
RETURN_ARRAYS_INCREMENT();
dvariable SdnrTmp;
dvar_vector o(1,ncomp);
dvar_vector p(1,ncomp);
dvar_vector ose(1,ncomp);
dvar_vector res(1,ncomp);
SdnrTmp=0.0;
for (int ii=1; ii<=ncomp; ii++)
{
    o(ii)=sum(elem_prod(ages,obs_comp(ii)));
    p(ii)=sum(elem_prod(ages,pred_comp(ii)));
    ose(ii)=sqrt((sum(elem_prod(square(ages),pred_comp(ii)))-square(p(ii)))/(nsamp(ii)*wgt_dat));
}
res=elem_div((o-p),ose);
SdnrTmp=sqrt(sum(square(res-(sum(res)/ncomp)))/(ncomp-1.0));
RETURN_ARRAYS_DECREMENT();
return SdnrTmp;

```

```
//-----
//SDNR: lognormal likelihood
FUNCTION dvariable sdnr_lognormal(const dvar_vector& pred, const dvar_vector& obs, const dvar_vector& cv,
const dvariable& wgt_dat)
//nyr=number of years of data, pred=vector of predicted data, obs=vector of observed data, cv=vector of cv's,
wgt_dat=likelihood weight for data source
RETURN_ARRAYS_INCREMENT();
dvariable SdnrTmp;
dvariable small_number=0.00001;
dvariable n;
dvar_vector res(cv.indexmin(),cv.indexmax());
SdnrTmp=0.0;
res=elem_div(log(elem_div(obs+small_number,pred+small_number)),sqrt(log(1+square(cv/wgt_dat))));
n=cv.indexmax()-cv.indexmin()+1;
SdnrTmp=sqrt(sum(square(res-(sum(res)/n))/(n-1.0)));
RETURN_ARRAYS_DECREMENT();
return SdnrTmp;
```

```
//-----
REPORT_SECTION
```

```
if (last_phase())
{
cout<<"start report"<<endl;
//cout<<"xdum = "<<xdum<<endl;
get_weighted_current();
//cout<<"got weighted"<<endl;
get_msy();
//cout<<"got msy"<<endl;
get_per_recruit_stuff();
//cout<<"got per recruit"<<endl;
get_miscellaneous_stuff();
//cout<<"got misc stuff"<<endl;
get_projection();
//cout<<"got projection"<<endl;
```

```

grad_max=objective_function_value::pobjfun->gmax;
time(&finish);
    elapsed_time=difftime(finish,start);
    hour=long(elapsed_time)/3600;
    minute=long(elapsed_time)%3600/60;
    second=(long(elapsed_time)%3600)%60;
    cout<<endl<<endl<<"*****"<<endl;
    cout<<"--Start time: "<<ctime(&start)<<endl;
    cout<<"--Finish time: "<<ctime(&finish)<<endl;
    cout<<"--Runtime: ";
    cout<<hour<<" hours, "<<minute<<" minutes, "<<second<<" seconds"<<endl;
    cout << "--TotalLikelihood: " << fval << endl;
    cout<<"--Final gradient: "<<objective_function_value::pobjfun->gmax << endl;
    cout<<"*****"<<endl;

cout <<endl;
cout << "><--><--><--><--><--><--><--><--><--><--><--><--><-->" <<endl;
//cout << "BC Fmsy=" << F_msy_out<< " BC SSBmsy=" << SSB_msy_out <<endl;
cout <<"F status="<<FdF_msy_end<<endl;
cout <<"Pop status="<<SdSSB_msy_end<<endl;
cout << "h="<<steep<<" R0="<<R0<<endl;
//cout << "xdum " << xdum << endl;
cout << "><--><--><--><--><--><--><--><--><--><--><-->" <<endl;

report << "TotalLikelihood " << fval << endl;
report << "N" << endl;
report << N<<endl;
report << "F" << endl;
report << F <<endl;

    sdnr_lc_nad=sdnr_multinomial(nyr_nad_lenc, lenbins, nsamp_nad_lenc, pred_nad_lenc, obs_nad_lenc,
w_lc_nad);
    sdnr_lc_mad=sdnr_multinomial(nyr_mad_lenc, lenbins, nsamp_mad_lenc, pred_mad_lenc, obs_mad_lenc,
w_lc_mad);

```

```
//sdnr_lc_sad=sdnr_multinomial(nyr_sad_lenc, lenbins, nsamp_sad_lenc, pred_sad_lenc, obs_sad_lenc, w_lc_sad);
```

```
sdnr_ac_cRn=sdnr_multinomial(nyr_cRn_agec, agebins_agec, nsamp_cRn_agec, pred_cRn_agec, obs_cRn_agec, w_ac_cRn);
```

```
sdnr_ac_cRs=sdnr_multinomial(nyr_cRs_agec, agebins_agec, nsamp_cRs_agec, pred_cRs_agec, obs_cRs_agec, w_ac_cRs);
```

```
sdnr_ac_cBn=sdnr_multinomial(nyr_cBn_agec, agebins_agec, nsamp_cBn_agec, pred_cBn_agec, obs_cBn_agec, w_ac_cBn);
```

```
sdnr_ac_cBs=sdnr_multinomial(nyr_cBs_agec, agebins_agec, nsamp_cBs_agec, pred_cBs_agec, obs_cBs_agec, w_ac_cBs);
```

```
sdnr_l_nad=sdnr_lognormal(pred_nad_cpue, obs_nad_cpue, nad_cpue_cv, w_l_nad);
```

```
sdnr_l_mad=sdnr_lognormal(pred_mad_cpue, obs_mad_cpue, mad_cpue_cv, w_l_mad);
```

```
sdnr_l_sad=sdnr_lognormal(pred_sad_cpue, obs_sad_cpue, sad_cpue_cv, w_l_sad);
```

```
sdnr_l_jai=sdnr_lognormal(pred_jai_cpue, obs_jai_cpue, jai_cpue_cv, w_l_jai);
```

```
sdnr_l_mareco=sdnr_lognormal(pred_mareco_cpue, obs_mareco_cpue, mareco_cpue_cv, w_l_mareco);
```

```
//#####  
#####
```

```
//## Passing parameters to vector for bounds check plotting
```

```
//#####  
#####
```

```
Linf_out(8)=Linf; Linf_out(1,7)=set_Linf;
```

```
K_out(8)=K; K_out(1,7)=set_K;
```

```
t0_out(8)=t0; t0_out(1,7)=set_t0;
```

```
len_cv_nad_val_out(8)=len_cv_nad_val; len_cv_nad_val_out(1,7)=set_len_cv_nad;
```

```
len_cv_mad_val_out(8)=len_cv_mad_val; len_cv_mad_val_out(1,7)=set_len_cv_mad;
```

```
//len_cv_sad_val_out(8)=len_cv_sad_val; len_cv_sad_val_out(1,7)=set_len_cv_sad;
```

```
log_R0_out(8)=log_R0; log_R0_out(1,7)=set_log_R0;
```

```
steep_out(8)=steep; steep_out(1,7)=set_steep;
```

```
rec_sigma_out(8)=rec_sigma; rec_sigma_out(1,7)=set_rec_sigma;
```

```
R_autocorr_out(8)=R_autocorr; R_autocorr_out(1,7)=set_R_autocorr;
```

log\_dm\_nad\_lc\_out(8)=log\_dm\_nad\_lc; log\_dm\_nad\_lc\_out(1,7)=set\_log\_dm\_nad\_lc;  
log\_dm\_mad\_lc\_out(8)=log\_dm\_mad\_lc; log\_dm\_mad\_lc\_out(1,7)=set\_log\_dm\_mad\_lc;  
//log\_dm\_sad\_lc\_out(8)=log\_dm\_sad\_lc; log\_dm\_sad\_lc\_out(1,7)=set\_log\_dm\_sad\_lc;

log\_dm\_cRn\_ac\_out(8)=log\_dm\_cRn\_ac; log\_dm\_cRn\_ac\_out(1,7)=set\_log\_dm\_cRn\_ac;  
log\_dm\_cRs\_ac\_out(8)=log\_dm\_cRs\_ac; log\_dm\_cRs\_ac\_out(1,7)=set\_log\_dm\_cRs\_ac;  
log\_dm\_cBn\_ac\_out(8)=log\_dm\_cBn\_ac; log\_dm\_cBn\_ac\_out(1,7)=set\_log\_dm\_cBn\_ac;  
log\_dm\_cBs\_ac\_out(8)=log\_dm\_cBs\_ac; log\_dm\_cBs\_ac\_out(1,7)=set\_log\_dm\_cBs\_ac;

selpar\_A50\_cRn\_out(8)=selpar\_A50\_cRn; selpar\_A50\_cRn\_out(1,7)=set\_selpar\_A50\_cRn;  
selpar\_slope\_cRn\_out(8)=selpar\_slope\_cRn; selpar\_slope\_cRn\_out(1,7)=set\_selpar\_slope\_cRn;  
selpar\_A502\_cRn\_out(8)=selpar\_A502\_cRn; selpar\_A502\_cRn\_out(1,7)=set\_selpar\_A502\_cRn;  
selpar\_slope2\_cRn\_out(8)=selpar\_slope2\_cRn; selpar\_slope2\_cRn\_out(1,7)=set\_selpar\_slope2\_cRn;

selpar\_A50\_cRn2\_out(8)=selpar\_A50\_cRn2; selpar\_A50\_cRn2\_out(1,7)=set\_selpar\_A50\_cRn2;  
selpar\_slope\_cRn2\_out(8)=selpar\_slope\_cRn2; selpar\_slope\_cRn2\_out(1,7)=set\_selpar\_slope\_cRn2;  
selpar\_A502\_cRn2\_out(8)=selpar\_A502\_cRn2; selpar\_A502\_cRn2\_out(1,7)=set\_selpar\_A502\_cRn2;  
selpar\_slope2\_cRn2\_out(8)=selpar\_slope2\_cRn2; selpar\_slope2\_cRn2\_out(1,7)=set\_selpar\_slope2\_cRn2;

selpar\_A50\_cRn3\_out(8)=selpar\_A50\_cRn3; selpar\_A50\_cRn3\_out(1,7)=set\_selpar\_A50\_cRn3;  
selpar\_slope\_cRn3\_out(8)=selpar\_slope\_cRn3; selpar\_slope\_cRn3\_out(1,7)=set\_selpar\_slope\_cRn3;  
selpar\_A502\_cRn3\_out(8)=selpar\_A502\_cRn3; selpar\_A502\_cRn3\_out(1,7)=set\_selpar\_A502\_cRn3;  
selpar\_slope2\_cRn3\_out(8)=selpar\_slope2\_cRn3; selpar\_slope2\_cRn3\_out(1,7)=set\_selpar\_slope2\_cRn3;

selpar\_A50\_cRn4\_out(8)=selpar\_A50\_cRn4; selpar\_A50\_cRn4\_out(1,7)=set\_selpar\_A50\_cRn4;  
selpar\_slope\_cRn4\_out(8)=selpar\_slope\_cRn4; selpar\_slope\_cRn4\_out(1,7)=set\_selpar\_slope\_cRn4;  
selpar\_A502\_cRn4\_out(8)=selpar\_A502\_cRn4; selpar\_A502\_cRn4\_out(1,7)=set\_selpar\_A502\_cRn4;  
selpar\_slope2\_cRn4\_out(8)=selpar\_slope2\_cRn4; selpar\_slope2\_cRn4\_out(1,7)=set\_selpar\_slope2\_cRn4;

selpar\_A50\_cRs\_out(8)=selpar\_A50\_cRs; selpar\_A50\_cRs\_out(1,7)=set\_selpar\_A50\_cRs;  
selpar\_slope\_cRs\_out(8)=selpar\_slope\_cRs; selpar\_slope\_cRs\_out(1,7)=set\_selpar\_slope\_cRs;  
selpar\_A502\_cRs\_out(8)=selpar\_A502\_cRs; selpar\_A502\_cRs\_out(1,7)=set\_selpar\_A502\_cRs;  
selpar\_slope2\_cRs\_out(8)=selpar\_slope2\_cRs; selpar\_slope2\_cRs\_out(1,7)=set\_selpar\_slope2\_cRs;

selpar\_A50\_cRs2\_out(8)=selpar\_A50\_cRs2; selpar\_A50\_cRs2\_out(1,7)=set\_selpar\_A50\_cRs2;

selpar\_slope\_cRs2\_out(8)=selpar\_slope\_cRs2; selpar\_slope\_cRs2\_out(1,7)=set\_selpar\_slope\_cRs2;  
selpar\_A502\_cRs2\_out(8)=selpar\_A502\_cRs2; selpar\_A502\_cRs2\_out(1,7)=set\_selpar\_A502\_cRs2;  
selpar\_slope2\_cRs2\_out(8)=selpar\_slope2\_cRs2; selpar\_slope2\_cRs2\_out(1,7)=set\_selpar\_slope2\_cRs2;

selpar\_A50\_cRs3\_out(8)=selpar\_A50\_cRs3; selpar\_A50\_cRs3\_out(1,7)=set\_selpar\_A50\_cRs3;  
selpar\_slope\_cRs3\_out(8)=selpar\_slope\_cRs3; selpar\_slope\_cRs3\_out(1,7)=set\_selpar\_slope\_cRs3;  
selpar\_A502\_cRs3\_out(8)=selpar\_A502\_cRs3; selpar\_A502\_cRs3\_out(1,7)=set\_selpar\_A502\_cRs3;  
selpar\_slope2\_cRs3\_out(8)=selpar\_slope2\_cRs3; selpar\_slope2\_cRs3\_out(1,7)=set\_selpar\_slope2\_cRs3;

selpar\_A50\_cRs4\_out(8)=selpar\_A50\_cRs4; selpar\_A50\_cRs4\_out(1,7)=set\_selpar\_A50\_cRs4;  
selpar\_slope\_cRs4\_out(8)=selpar\_slope\_cRs4; selpar\_slope\_cRs4\_out(1,7)=set\_selpar\_slope\_cRs4;  
selpar\_A502\_cRs4\_out(8)=selpar\_A502\_cRs4; selpar\_A502\_cRs4\_out(1,7)=set\_selpar\_A502\_cRs4;  
selpar\_slope2\_cRs4\_out(8)=selpar\_slope2\_cRs4; selpar\_slope2\_cRs4\_out(1,7)=set\_selpar\_slope2\_cRs4;

selpar\_A50\_cBn\_out(8)=selpar\_A50\_cBn; selpar\_A50\_cBn\_out(1,7)=set\_selpar\_A50\_cBn;  
selpar\_slope\_cBn\_out(8)=selpar\_slope\_cBn; selpar\_slope\_cBn\_out(1,7)=set\_selpar\_slope\_cBn;  
selpar\_A502\_cBn\_out(8)=selpar\_A502\_cBn; selpar\_A502\_cBn\_out(1,7)=set\_selpar\_A502\_cBn;  
selpar\_slope2\_cBn\_out(8)=selpar\_slope2\_cBn; selpar\_slope2\_cBn\_out(1,7)=set\_selpar\_slope2\_cBn;

selpar\_A50\_cBn2\_out(8)=selpar\_A50\_cBn2; selpar\_A50\_cBn2\_out(1,7)=set\_selpar\_A50\_cBn2;  
selpar\_slope\_cBn2\_out(8)=selpar\_slope\_cBn2; selpar\_slope\_cBn2\_out(1,7)=set\_selpar\_slope\_cBn2;  
selpar\_A502\_cBn2\_out(8)=selpar\_A502\_cBn2; selpar\_A502\_cBn2\_out(1,7)=set\_selpar\_A502\_cBn2;  
selpar\_slope2\_cBn2\_out(8)=selpar\_slope2\_cBn2; selpar\_slope2\_cBn2\_out(1,7)=set\_selpar\_slope2\_cBn2;

selpar\_A50\_cBs\_out(8)=selpar\_A50\_cBs; selpar\_A50\_cBs\_out(1,7)=set\_selpar\_A50\_cBs;  
selpar\_slope\_cBs\_out(8)=selpar\_slope\_cBs; selpar\_slope\_cBs\_out(1,7)=set\_selpar\_slope\_cBs;  
selpar\_A502\_cBs\_out(8)=selpar\_A502\_cBs; selpar\_A502\_cBs\_out(1,7)=set\_selpar\_A502\_cBs;  
selpar\_slope2\_cBs\_out(8)=selpar\_slope2\_cBs; selpar\_slope2\_cBs\_out(1,7)=set\_selpar\_slope2\_cBs;

selpar\_A50\_cBs2\_out(8)=selpar\_A50\_cBs2; selpar\_A50\_cBs2\_out(1,7)=set\_selpar\_A50\_cBs2;  
selpar\_slope\_cBs2\_out(8)=selpar\_slope\_cBs2; selpar\_slope\_cBs2\_out(1,7)=set\_selpar\_slope\_cBs2;  
selpar\_A502\_cBs2\_out(8)=selpar\_A502\_cBs2; selpar\_A502\_cBs2\_out(1,7)=set\_selpar\_A502\_cBs2;  
selpar\_slope2\_cBs2\_out(8)=selpar\_slope2\_cBs2; selpar\_slope2\_cBs2\_out(1,7)=set\_selpar\_slope2\_cBs2;

selpar\_age0\_cRn\_out(8)=sel\_age0\_cRn\_logit; selpar\_age0\_cRn\_out(1,7)=set\_sel\_age0\_cRn;

selpar\_age1\_cRn\_out(8)=sel\_age1\_cRn\_logit; selpar\_age1\_cRn\_out(1,7)=set\_sel\_age1\_cRn;  
selpar\_age2\_cRn\_out(8)=sel\_age2\_cRn\_logit; selpar\_age2\_cRn\_out(1,7)=set\_sel\_age2\_cRn;  
selpar\_age3\_cRn\_out(8)=sel\_age3\_cRn\_logit; selpar\_age3\_cRn\_out(1,7)=set\_sel\_age3\_cRn;  
selpar\_age4\_cRn\_out(8)=sel\_age4\_cRn\_logit; selpar\_age4\_cRn\_out(1,7)=set\_sel\_age4\_cRn;  
selpar\_age5\_cRn\_out(8)=sel\_age5\_cRn\_logit; selpar\_age5\_cRn\_out(1,7)=set\_sel\_age5\_cRn;  
selpar\_age6\_cRn\_out(8)=sel\_age6\_cRn\_logit; selpar\_age6\_cRn\_out(1,7)=set\_sel\_age6\_cRn;

selpar\_age0\_cRn2\_out(8)=sel\_age0\_cRn2\_logit; selpar\_age0\_cRn2\_out(1,7)=set\_sel\_age0\_cRn2;  
selpar\_age1\_cRn2\_out(8)=sel\_age1\_cRn2\_logit; selpar\_age1\_cRn2\_out(1,7)=set\_sel\_age1\_cRn2;  
selpar\_age2\_cRn2\_out(8)=sel\_age2\_cRn2\_logit; selpar\_age2\_cRn2\_out(1,7)=set\_sel\_age2\_cRn2;  
selpar\_age3\_cRn2\_out(8)=sel\_age3\_cRn2\_logit; selpar\_age3\_cRn2\_out(1,7)=set\_sel\_age3\_cRn2;  
selpar\_age4\_cRn2\_out(8)=sel\_age4\_cRn2\_logit; selpar\_age4\_cRn2\_out(1,7)=set\_sel\_age4\_cRn2;  
selpar\_age5\_cRn2\_out(8)=sel\_age5\_cRn2\_logit; selpar\_age5\_cRn2\_out(1,7)=set\_sel\_age5\_cRn2;  
selpar\_age6\_cRn2\_out(8)=sel\_age6\_cRn2\_logit; selpar\_age6\_cRn2\_out(1,7)=set\_sel\_age6\_cRn2;

selpar\_age0\_cRn3\_out(8)=sel\_age0\_cRn3\_logit; selpar\_age0\_cRn3\_out(1,7)=set\_sel\_age0\_cRn3;  
selpar\_age1\_cRn3\_out(8)=sel\_age1\_cRn3\_logit; selpar\_age1\_cRn3\_out(1,7)=set\_sel\_age1\_cRn3;  
selpar\_age2\_cRn3\_out(8)=sel\_age2\_cRn3\_logit; selpar\_age2\_cRn3\_out(1,7)=set\_sel\_age2\_cRn3;  
selpar\_age3\_cRn3\_out(8)=sel\_age3\_cRn3\_logit; selpar\_age3\_cRn3\_out(1,7)=set\_sel\_age3\_cRn3;  
selpar\_age4\_cRn3\_out(8)=sel\_age4\_cRn3\_logit; selpar\_age4\_cRn3\_out(1,7)=set\_sel\_age4\_cRn3;  
selpar\_age5\_cRn3\_out(8)=sel\_age5\_cRn3\_logit; selpar\_age5\_cRn3\_out(1,7)=set\_sel\_age5\_cRn3;  
selpar\_age6\_cRn3\_out(8)=sel\_age6\_cRn3\_logit; selpar\_age6\_cRn3\_out(1,7)=set\_sel\_age6\_cRn3;

selpar\_age0\_cRn4\_out(8)=sel\_age0\_cRn4\_logit; selpar\_age0\_cRn4\_out(1,7)=set\_sel\_age0\_cRn4;  
selpar\_age1\_cRn4\_out(8)=sel\_age1\_cRn4\_logit; selpar\_age1\_cRn4\_out(1,7)=set\_sel\_age1\_cRn4;  
selpar\_age2\_cRn4\_out(8)=sel\_age2\_cRn4\_logit; selpar\_age2\_cRn4\_out(1,7)=set\_sel\_age2\_cRn4;  
selpar\_age3\_cRn4\_out(8)=sel\_age3\_cRn4\_logit; selpar\_age3\_cRn4\_out(1,7)=set\_sel\_age3\_cRn4;  
selpar\_age4\_cRn4\_out(8)=sel\_age4\_cRn4\_logit; selpar\_age4\_cRn4\_out(1,7)=set\_sel\_age4\_cRn4;  
selpar\_age5\_cRn4\_out(8)=sel\_age5\_cRn4\_logit; selpar\_age5\_cRn4\_out(1,7)=set\_sel\_age5\_cRn4;  
selpar\_age6\_cRn4\_out(8)=sel\_age6\_cRn4\_logit; selpar\_age6\_cRn4\_out(1,7)=set\_sel\_age6\_cRn4;

selpar\_age0\_cRs\_out(8)=sel\_age0\_cRs\_logit; selpar\_age0\_cRs\_out(1,7)=set\_sel\_age0\_cRs;  
selpar\_age1\_cRs\_out(8)=sel\_age1\_cRs\_logit; selpar\_age1\_cRs\_out(1,7)=set\_sel\_age1\_cRs;  
selpar\_age2\_cRs\_out(8)=sel\_age2\_cRs\_logit; selpar\_age2\_cRs\_out(1,7)=set\_sel\_age2\_cRs;  
selpar\_age3\_cRs\_out(8)=sel\_age3\_cRs\_logit; selpar\_age3\_cRs\_out(1,7)=set\_sel\_age3\_cRs;

selpar\_age4\_cRs\_out(8)=sel\_age4\_cRs\_logit; selpar\_age4\_cRs\_out(1,7)=set\_sel\_age4\_cRs;  
selpar\_age5\_cRs\_out(8)=sel\_age5\_cRs\_logit; selpar\_age5\_cRs\_out(1,7)=set\_sel\_age5\_cRs;  
selpar\_age6\_cRs\_out(8)=sel\_age6\_cRs\_logit; selpar\_age6\_cRs\_out(1,7)=set\_sel\_age6\_cRs;

selpar\_age0\_cRs2\_out(8)=sel\_age0\_cRs2\_logit; selpar\_age0\_cRs2\_out(1,7)=set\_sel\_age0\_cRs2;  
selpar\_age1\_cRs2\_out(8)=sel\_age1\_cRs2\_logit; selpar\_age1\_cRs2\_out(1,7)=set\_sel\_age1\_cRs2;  
selpar\_age2\_cRs2\_out(8)=sel\_age2\_cRs2\_logit; selpar\_age2\_cRs2\_out(1,7)=set\_sel\_age2\_cRs2;  
selpar\_age3\_cRs2\_out(8)=sel\_age3\_cRs2\_logit; selpar\_age3\_cRs2\_out(1,7)=set\_sel\_age3\_cRs2;  
selpar\_age4\_cRs2\_out(8)=sel\_age4\_cRs2\_logit; selpar\_age4\_cRs2\_out(1,7)=set\_sel\_age4\_cRs2;  
selpar\_age5\_cRs2\_out(8)=sel\_age5\_cRs2\_logit; selpar\_age5\_cRs2\_out(1,7)=set\_sel\_age5\_cRs2;  
selpar\_age6\_cRs2\_out(8)=sel\_age6\_cRs2\_logit; selpar\_age6\_cRs2\_out(1,7)=set\_sel\_age6\_cRs2;

selpar\_age0\_cRs3\_out(8)=sel\_age0\_cRs3\_logit; selpar\_age0\_cRs3\_out(1,7)=set\_sel\_age0\_cRs3;  
selpar\_age1\_cRs3\_out(8)=sel\_age1\_cRs3\_logit; selpar\_age1\_cRs3\_out(1,7)=set\_sel\_age1\_cRs3;  
selpar\_age2\_cRs3\_out(8)=sel\_age2\_cRs3\_logit; selpar\_age2\_cRs3\_out(1,7)=set\_sel\_age2\_cRs3;  
selpar\_age3\_cRs3\_out(8)=sel\_age3\_cRs3\_logit; selpar\_age3\_cRs3\_out(1,7)=set\_sel\_age3\_cRs3;  
selpar\_age4\_cRs3\_out(8)=sel\_age4\_cRs3\_logit; selpar\_age4\_cRs3\_out(1,7)=set\_sel\_age4\_cRs3;  
selpar\_age5\_cRs3\_out(8)=sel\_age5\_cRs3\_logit; selpar\_age5\_cRs3\_out(1,7)=set\_sel\_age5\_cRs3;  
selpar\_age6\_cRs3\_out(8)=sel\_age6\_cRs3\_logit; selpar\_age6\_cRs3\_out(1,7)=set\_sel\_age6\_cRs3;

selpar\_age0\_cRs4\_out(8)=sel\_age0\_cRs4\_logit; selpar\_age0\_cRs4\_out(1,7)=set\_sel\_age0\_cRs4;  
selpar\_age1\_cRs4\_out(8)=sel\_age1\_cRs4\_logit; selpar\_age1\_cRs4\_out(1,7)=set\_sel\_age1\_cRs4;  
selpar\_age2\_cRs4\_out(8)=sel\_age2\_cRs4\_logit; selpar\_age2\_cRs4\_out(1,7)=set\_sel\_age2\_cRs4;  
selpar\_age3\_cRs4\_out(8)=sel\_age3\_cRs4\_logit; selpar\_age3\_cRs4\_out(1,7)=set\_sel\_age3\_cRs4;  
selpar\_age4\_cRs4\_out(8)=sel\_age4\_cRs4\_logit; selpar\_age4\_cRs4\_out(1,7)=set\_sel\_age4\_cRs4;  
selpar\_age5\_cRs4\_out(8)=sel\_age5\_cRs4\_logit; selpar\_age5\_cRs4\_out(1,7)=set\_sel\_age5\_cRs4;  
selpar\_age6\_cRs4\_out(8)=sel\_age6\_cRs4\_logit; selpar\_age6\_cRs4\_out(1,7)=set\_sel\_age6\_cRs4;

selpar\_age0\_cBn\_out(8)=sel\_age0\_cBn\_logit; selpar\_age0\_cBn\_out(1,7)=set\_sel\_age0\_cBn;  
selpar\_age1\_cBn\_out(8)=sel\_age1\_cBn\_logit; selpar\_age1\_cBn\_out(1,7)=set\_sel\_age1\_cBn;  
selpar\_age2\_cBn\_out(8)=sel\_age2\_cBn\_logit; selpar\_age2\_cBn\_out(1,7)=set\_sel\_age2\_cBn;  
selpar\_age3\_cBn\_out(8)=sel\_age3\_cBn\_logit; selpar\_age3\_cBn\_out(1,7)=set\_sel\_age3\_cBn;  
selpar\_age4\_cBn\_out(8)=sel\_age4\_cBn\_logit; selpar\_age4\_cBn\_out(1,7)=set\_sel\_age4\_cBn;  
selpar\_age5\_cBn\_out(8)=sel\_age5\_cBn\_logit; selpar\_age5\_cBn\_out(1,7)=set\_sel\_age5\_cBn;  
selpar\_age6\_cBn\_out(8)=sel\_age6\_cBn\_logit; selpar\_age6\_cBn\_out(1,7)=set\_sel\_age6\_cBn;



selpar\_age0\_cBn2\_out(8)=sel\_age0\_cBn2\_logit; selpar\_age0\_cBn2\_out(1,7)=set\_sel\_age0\_cBn2;  
selpar\_age1\_cBn2\_out(8)=sel\_age1\_cBn2\_logit; selpar\_age1\_cBn2\_out(1,7)=set\_sel\_age1\_cBn2;  
selpar\_age2\_cBn2\_out(8)=sel\_age2\_cBn2\_logit; selpar\_age2\_cBn2\_out(1,7)=set\_sel\_age2\_cBn2;  
selpar\_age3\_cBn2\_out(8)=sel\_age3\_cBn2\_logit; selpar\_age3\_cBn2\_out(1,7)=set\_sel\_age3\_cBn2;  
selpar\_age4\_cBn2\_out(8)=sel\_age4\_cBn2\_logit; selpar\_age4\_cBn2\_out(1,7)=set\_sel\_age4\_cBn2;  
selpar\_age5\_cBn2\_out(8)=sel\_age5\_cBn2\_logit; selpar\_age5\_cBn2\_out(1,7)=set\_sel\_age5\_cBn2;  
selpar\_age6\_cBn2\_out(8)=sel\_age6\_cBn2\_logit; selpar\_age6\_cBn2\_out(1,7)=set\_sel\_age6\_cBn2;

selpar\_age0\_cBs\_out(8)=sel\_age0\_cBs\_logit; selpar\_age0\_cBs\_out(1,7)=set\_sel\_age0\_cBs;  
selpar\_age1\_cBs\_out(8)=sel\_age1\_cBs\_logit; selpar\_age1\_cBs\_out(1,7)=set\_sel\_age1\_cBs;  
selpar\_age2\_cBs\_out(8)=sel\_age2\_cBs\_logit; selpar\_age2\_cBs\_out(1,7)=set\_sel\_age2\_cBs;  
selpar\_age3\_cBs\_out(8)=sel\_age3\_cBs\_logit; selpar\_age3\_cBs\_out(1,7)=set\_sel\_age3\_cBs;  
selpar\_age4\_cBs\_out(8)=sel\_age4\_cBs\_logit; selpar\_age4\_cBs\_out(1,7)=set\_sel\_age4\_cBs;  
selpar\_age5\_cBs\_out(8)=sel\_age5\_cBs\_logit; selpar\_age5\_cBs\_out(1,7)=set\_sel\_age5\_cBs;  
selpar\_age6\_cBs\_out(8)=sel\_age6\_cBs\_logit; selpar\_age6\_cBs\_out(1,7)=set\_sel\_age6\_cBs;

selpar\_age0\_cBs2\_out(8)=sel\_age0\_cBs2\_logit; selpar\_age0\_cBs2\_out(1,7)=set\_sel\_age0\_cBs2;  
selpar\_age1\_cBs2\_out(8)=sel\_age1\_cBs2\_logit; selpar\_age1\_cBs2\_out(1,7)=set\_sel\_age1\_cBs2;  
selpar\_age2\_cBs2\_out(8)=sel\_age2\_cBs2\_logit; selpar\_age2\_cBs2\_out(1,7)=set\_sel\_age2\_cBs2;  
selpar\_age3\_cBs2\_out(8)=sel\_age3\_cBs2\_logit; selpar\_age3\_cBs2\_out(1,7)=set\_sel\_age3\_cBs2;  
selpar\_age4\_cBs2\_out(8)=sel\_age4\_cBs2\_logit; selpar\_age4\_cBs2\_out(1,7)=set\_sel\_age4\_cBs2;  
selpar\_age5\_cBs2\_out(8)=sel\_age5\_cBs2\_logit; selpar\_age5\_cBs2\_out(1,7)=set\_sel\_age5\_cBs2;  
selpar\_age6\_cBs2\_out(8)=sel\_age6\_cBs2\_logit; selpar\_age6\_cBs2\_out(1,7)=set\_sel\_age6\_cBs2;

selpar\_A50\_nad\_out(8)=selpar\_A50\_nad; selpar\_A50\_nad\_out(1,7)=set\_selpar\_A50\_nad;  
selpar\_slope\_nad\_out(8)=selpar\_slope\_nad; selpar\_slope\_nad\_out(1,7)=set\_selpar\_slope\_nad;  
selpar\_A502\_nad\_out(8)=selpar\_A502\_nad; selpar\_A502\_nad\_out(1,7)=set\_selpar\_A502\_nad;  
selpar\_slope2\_nad\_out(8)=selpar\_slope2\_nad; selpar\_slope2\_nad\_out(1,7)=set\_selpar\_slope2\_nad;

selpar\_age0\_nad\_out(8)=sel\_age0\_nad\_logit; selpar\_age0\_nad\_out(1,7)=set\_sel\_age0\_nad;  
selpar\_age1\_nad\_out(8)=sel\_age1\_nad\_logit; selpar\_age1\_nad\_out(1,7)=set\_sel\_age1\_nad;  
selpar\_age2\_nad\_out(8)=sel\_age2\_nad\_logit; selpar\_age2\_nad\_out(1,7)=set\_sel\_age2\_nad;  
selpar\_age3\_nad\_out(8)=sel\_age3\_nad\_logit; selpar\_age3\_nad\_out(1,7)=set\_sel\_age3\_nad;  
selpar\_age4\_nad\_out(8)=sel\_age4\_nad\_logit; selpar\_age4\_nad\_out(1,7)=set\_sel\_age4\_nad;

selpar\_age5\_nad\_out(8)=sel\_age5\_nad\_logit; selpar\_age5\_nad\_out(1,7)=set\_sel\_age5\_nad;  
selpar\_age6\_nad\_out(8)=sel\_age6\_nad\_logit; selpar\_age6\_nad\_out(1,7)=set\_sel\_age6\_nad;

selpar\_A50\_mad\_out(8)=selpar\_A50\_mad; selpar\_A50\_mad\_out(1,7)=set\_selpar\_A50\_mad;  
selpar\_slope\_mad\_out(8)=selpar\_slope\_mad; selpar\_slope\_mad\_out(1,7)=set\_selpar\_slope\_mad;  
selpar\_A502\_mad\_out(8)=selpar\_A502\_mad; selpar\_A502\_mad\_out(1,7)=set\_selpar\_A502\_mad;  
selpar\_slope2\_mad\_out(8)=selpar\_slope2\_mad; selpar\_slope2\_mad\_out(1,7)=set\_selpar\_slope2\_mad;

selpar\_age0\_mad\_out(8)=sel\_age0\_mad\_logit; selpar\_age0\_mad\_out(1,7)=set\_sel\_age0\_mad;  
selpar\_age1\_mad\_out(8)=sel\_age1\_mad\_logit; selpar\_age1\_mad\_out(1,7)=set\_sel\_age1\_mad;  
selpar\_age2\_mad\_out(8)=sel\_age2\_mad\_logit; selpar\_age2\_mad\_out(1,7)=set\_sel\_age2\_mad;  
selpar\_age3\_mad\_out(8)=sel\_age3\_mad\_logit; selpar\_age3\_mad\_out(1,7)=set\_sel\_age3\_mad;  
selpar\_age4\_mad\_out(8)=sel\_age4\_mad\_logit; selpar\_age4\_mad\_out(1,7)=set\_sel\_age4\_mad;  
selpar\_age5\_mad\_out(8)=sel\_age5\_mad\_logit; selpar\_age5\_mad\_out(1,7)=set\_sel\_age5\_mad;  
selpar\_age6\_mad\_out(8)=sel\_age6\_mad\_logit; selpar\_age6\_mad\_out(1,7)=set\_sel\_age6\_mad;

selpar\_A50\_sad\_out(8)=selpar\_A50\_sad; selpar\_A50\_sad\_out(1,7)=set\_selpar\_A50\_sad;  
selpar\_slope\_sad\_out(8)=selpar\_slope\_sad; selpar\_slope\_sad\_out(1,7)=set\_selpar\_slope\_sad;  
selpar\_A502\_sad\_out(8)=selpar\_A502\_sad; selpar\_A502\_sad\_out(1,7)=set\_selpar\_A502\_sad;  
selpar\_slope2\_sad\_out(8)=selpar\_slope2\_sad; selpar\_slope2\_sad\_out(1,7)=set\_selpar\_slope2\_sad;

selpar\_age0\_sad\_out(8)=sel\_age0\_sad\_logit; selpar\_age0\_sad\_out(1,7)=set\_sel\_age0\_sad;  
selpar\_age1\_sad\_out(8)=sel\_age1\_sad\_logit; selpar\_age1\_sad\_out(1,7)=set\_sel\_age1\_sad;  
selpar\_age2\_sad\_out(8)=sel\_age2\_sad\_logit; selpar\_age2\_sad\_out(1,7)=set\_sel\_age2\_sad;  
selpar\_age3\_sad\_out(8)=sel\_age3\_sad\_logit; selpar\_age3\_sad\_out(1,7)=set\_sel\_age3\_sad;  
selpar\_age4\_sad\_out(8)=sel\_age4\_sad\_logit; selpar\_age4\_sad\_out(1,7)=set\_sel\_age4\_sad;  
selpar\_age5\_sad\_out(8)=sel\_age5\_sad\_logit; selpar\_age5\_sad\_out(1,7)=set\_sel\_age5\_sad;  
selpar\_age6\_sad\_out(8)=sel\_age6\_sad\_logit; selpar\_age6\_sad\_out(1,7)=set\_sel\_age6\_sad;

log\_q\_nad\_out(8)=log\_q\_nad; log\_q\_nad\_out(1,7)=set\_log\_q\_nad;  
log\_q\_mad\_out(8)=log\_q\_mad; log\_q\_mad\_out(1,7)=set\_log\_q\_mad;  
log\_q\_sad\_out(8)=log\_q\_sad; log\_q\_sad\_out(1,7)=set\_log\_q\_sad;  
log\_q\_jai\_out(8)=log\_q\_jai; log\_q\_jai\_out(1,7)=set\_log\_q\_jai;  
log\_q2\_jai\_out(8)=log\_q2\_jai; log\_q2\_jai\_out(1,7)=set\_log\_q2\_jai;  
log\_q\_mar\_out(8)=log\_q\_mar; log\_q\_mar\_out(1,7)=set\_log\_q\_mar;

```
log_q_eco_out(8)=log_q_eco; log_q_eco_out(1,7)=set_log_q_eco;
```

```
log_avg_F_cRn_out(8)=log_avg_F_cRn; log_avg_F_cRn_out(1,7)=set_log_avg_F_cRn;
```

```
log_avg_F_cRs_out(8)=log_avg_F_cRs; log_avg_F_cRs_out(1,7)=set_log_avg_F_cRs;
```

```
log_avg_F_cBn_out(8)=log_avg_F_cBn; log_avg_F_cBn_out(1,7)=set_log_avg_F_cBn;
```

```
log_avg_F_cBs_out(8)=log_avg_F_cBs; log_avg_F_cBs_out(1,7)=set_log_avg_F_cBs;
```

```
log_rec_dev_out(styr_rec_dev, endyr_rec_dev)=log_rec_dev;
```

```
log_F_dev_cRn_out(styr_cRn_L, endyr_cRn_L)=log_F_dev_cRn;
```

```
log_F_dev_cRs_out(styr_cRs_L, endyr_cRs_L)=log_F_dev_cRs;
```

```
log_F_dev_cBn_out(styr_cBn_L, endyr_cBn_L)=log_F_dev_cBn;
```

```
log_F_dev_cBs_out(styr_cBs_L, endyr_cBs_L)=log_F_dev_cBs;
```

```
#include "am_make_Robject19.cxx" // write the R-compatible report
```

```
} //endl last phase loop
```