On the comparisons of regional differences in the growth of red snappers from the Gulf of Mexico

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Abstract

In recent years, many studies have been carried out to evaluate the variability in the growth of red snappers between regions and habitats in the Gulf of Mexico. However, most of these studies did not take into consideration the cluster sampling used to collect red snapper samples. The present analysis compares the regional differences in growth curves estimated from samples collected from two different sources during 1999-2001 (NMFS and Fischer et al. (2004)) and uses a simulated data set to demonstrate the effect of non-representative sampling on the precision of growth curves and lengths-at-age. A reweighting method is proposed here to improve the precision of growth curves and lengths at age when the clustering effect is strong or when otolith samples were not randomly collected. The effects of clustering sampling on the precision of length frequency distributions and mean lengths for red snappers collected from commercial fisheries were also analyzed. Results from this study showed that the regional differences in growth rates and lengths-at-age seen in Fischer et al. (2004) may be due to clustering effects or non-representative sampling. Also, these results show that, in order to draw any conclusions regarding regional differences in growth of a species, (1) the length frequency distributions of otolith samples need to be representative of the populations intended for study, and (2) the effective sample size should be used for any statistical tests regarding differences in length or age related parameters between different regions or habitats.

Introduction

Fischer et al. (2004) reported a regional difference in growth curves between red snappers collected from Texas and red snappers collected from Alabama and Louisiana. Other studies also found that growth rates of red snappers from different years (Nieland and Wilson, 2007), among different sexes (Wilson and Nieland, 2001), or from different habitats (Sarri, 2008; Syc, 2011) may be different. Differences in growth rates between different regions or types of habitat may have important implications for the management of red snapper stocks. However, these studies did not take into consideration that red snapper samples were collected through cluster sampling. The effective sample sizes of cluster samples can be much smaller than the actual sample sizes when the within cluster correlation is high (Chih 2010, 2011). As a result, a cluster sample may not be representative of a population intended for study even when the sample size appears to be adequate.

The present study evaluated the effects of sampling on the precision of growth curves and mean lengths-at-age. First, the length frequency distributions estimated from red snapper samples collected from all fisheries in Alabama, Louisiana and Texas during 1999-2001 were compared with those obtained by Fischer et al., (2004) to evaluate if red snapper samples used in that study were representative of fish landings in those states during the same period. Second, a simulated data set based on the lengths-at-age and age frequency distributions estimated from otolith samples collected by state and NMFS samplers from the Gulf of Mexico during 1999-2001 was generated. The effects of non-representative sampling on the precision of growth curves and lengths at age were determined by the use of resampled samples with length frequency distributions that were different from the original simulated data. Also, a re-weighting method was used to re-adjust the growth curves, lengths-at-age and age frequency distributions of non-representative samples. Third, the design effect of cluster sampling and the within trip correlation of red snapper samples collected from commercial fisheries were analyzed to illustrate the effect of cluster sampling on the precision of length frequency distributions and mean lengths.

Materials and Methods

Length samples for commercial fisheries were collected from the Gulf of Mexico by samplers of the Trip Interview Program (TIP) between 1999 and 2001. Length samples for recreational fisheries were obtained from (1) the Marine Recreational Fisheries Statistics Survey, (2) the head boat survey, (3) the Texas Parks and Wildlife Department database, and (4) the TIP database. All lengths used were fork lengths in millimeters. Otolith samples were obtained from the age database of the Panama City Laboratory, SEFSC. Otolith data were from both commercial and recreational fisheries.

An age data set was simulated to demonstrate the effect of non-representative sampling on the precision of growth curves and lengths-at-age. The simulated data set was based on the mean lengths-at-age, standard deviations of lengths-at-age and proportions-at-age of the combined age data from 1999 to 2001 obtained from the Panama City Laboratory database (Table 2). Various data sets were resampled with replacement from the simulated data set to study the effects of non-representative sampling on the precision of growth curves and lengths-at-age. These data sets were resampled in such way that they had similar length frequency distributions as those reported by Fischer et al. (2004). Reweighting procedures for growth curves, age frequency distributions and lengths-at-age can be found in previous papers (Chih 2009a,b). The re-weighting factor for each observation was calculated with the formula

$$RW_i = \frac{NLi \big/ TN}{OLi \big/ TO},$$

where RW_i is the reweighting factor for samples belonging to length interval i, NL_i is the number of samples belonging to length i in the original simulated data set, TN is the total number of samples in the original simulated data set, OL_i is the number of samples of length interval i in otolith samples, and TO is the total number of otolith samples.

Estimations of dispersion index, effective sample sizes, within trip correlations and design effects have also been discussed previously (Chih, 2010, 2011). The dispersion index (DI) for a length frequency distribution was defined as:

$$\mathrm{DI} = \sum_{i=1}^{n} (P_i \times (1 - P_i)),$$

where n is the number of length intervals, and P_i is the proportion-at-length for length interval i of the length frequency distribution. The effective sample sizes were estimated by bootstrapping: a fixed number of trips were randomly selected from all available trips first, and then all fish in these trips were combined to form one group sample. Effective sample sizes for these group samples were estimated by comparing the variance estimated from 200 bootstrap runs with the nominal variance (see Chih (2010)). The within trip correlation (ρ) was estimated with the equation:

$$\rho = \frac{s_b^2 - \frac{s_w^2}{m}}{s_b^2 + \frac{m-1}{m} s_w^2}$$

where s_w^2 is the within trip variance:

$$s_w^2 = \frac{1}{N-n} \sum_i^n \sum_j^m (X_{ij} - \bar{x}_{i.})^2$$

and s_b^2 is the between trip variance:

$$s_b^2 = \frac{1}{n-1} \sum_i^n (\bar{x}_{i.} - \bar{x}_{..})^2$$

where m is the average trip sample size, n is the number of trips, N is the total sample size, X_{ij} is the length of the jth sample in the ith trip, $\bar{x}_{i.}$ is the mean length of the ith trip, $\bar{x}_{..}$ is the mean length of all samples. The design effect (Deff) of cluster sampling on mean length was estimated with the equation:

$$\text{Deff} = 1 + (m-1)\rho$$

where m is the average trip sample size.

Results & Discussion

Length samples

The length frequency distributions reported here for red snapper length samples collected from commercial and recreational fisheries in Alabama, Louisiana and Texas during 1999-2001 are very different from those reported by Fischer et al. (2004) (Fig 1). These differences are not surprising since the red snapper samples used by Fischer et al. came only from recreational hand line fisheries. The length frequency distributions of red snapper samples from commercial and recreational fisheries as well as those from handline and longline fisheries are different (Fig 2). Also, the maximum trip sample size in the Fischer et al. study was 75, which means the cluster sampling effect may have been high (Chih, 2010; also see below). In addition, some larger tournament fishing samples were 'opportunistically' sampled in their Alabama and Louisiana samples (Fischer et al. 2004), which means that their samples may not be representative of the overall landings.

The length frequency distributions found in this study for all red snapper samples from recreational fisheries were also different from those reported by Fischer et al. (2004) (Fig 3). In either combined samples from all fisheries or recreational samples, there were no drastic differences in length frequency distributions between Texas and Louisiana or Alabama. Since the sample sizes for the NMFS data were much larger than those for the Fischer et al. study (Table 1), the drastic differences in length frequency distributions between different states seen in the Fischer et al. study may be due to the effects of cluster sampling or non-representative sampling.

Otolith samples

Length frequency distributions for otolith samples collected from Alabama, Louisiana and Texas were also different from those for length samples and for those observed by Fischer et al. (2004) (Fig 4). These differences may also be due to cluster sampling. Growth curves estimated for these three different states showed that the growth curve for Alabama is significantly different from those for Louisiana and Texas (Fig 5, Table 3, likelihood ratio test). The growth curves estimated from Alabama may have been biased because of the lack of enough otolith samples from larger fish. These results are different from those found in the Fischer et al. study, which showed that the growth curve for Texas was significantly different from the growth curves for the other two states. These inconsistences suggest that comparisons of growth curves from different regions may be invalid if the cluster sample sizes are not large enough to reflect the population intended for study or if the samples were not sampled randomly.

Simulation and resampling

The probability distributions for lengths-at-age for red snappers overlap considerably (Fig 6). The resampled data based on the length frequency distributions of three different states in the Fischer et al. study showed that the simulated data for Texas have many more smaller fish than the other two states (Fig 7). The mean lengths-at-age (Fig 8), the probability distribution of lengths-at-age of five-year-old fish (Fig 9), and the age frequency distribution (Fig 10) estimated from simulated Texas data were significantly different from those estimated for Alabama and Louisiana. The growth curve estimated from simulated Texas data was also very different from those estimated for Alabama and Louisiana (Fig 11), as found with the likelihood ratio test (Table 4). These results were consistent with the findings of Fischer et al. (2004). Thus, samples with different length frequency distributions may have different growth curves and lengths-at-age even when they are derived from the same stock. Thus, non-representative samples (including cluster samples with inadequate sample sizes), may not be used to estimate growth curves and lengths-at-age. Since the length frequency distributions for the three states reported by Fischer et al. were different from those estimated from length samples collected by NMFS and state samplers, it is likely that the observed differences in lengths-at-age or growth curves between different states in their study were due to cluster sampling or non-representative sampling.

Reweighting by the original length frequency distribution

The age frequency distributions (Fig 12), growth curves (Fig 13) and lengths-at-age (Fig 14) estimated from simulated Alabama and Louisiana data were significantly improved (Table 5) after they were reweighted by the length frequency distribution of the original simulated data. However, age frequency distributions, growth curves, and lengths-at-age estimated from simulated Texas data were improved less by the re-weighting process. This is because few data from larger fish were available in the simulated Texas data. These results showed that reweighting is an effective way to re-adjust age frequency distributions, growth curves and lengths-at-age as long as enough otolith samples from larger fish were available to reflect the age-length relationship for all ages.

Design effect and effective sample size

The clustering effect of red snapper length samples collected from commercial fisheries is shown in Fig 15 (From Chih, 2010). Smaller fish tend to school together and have a lower trip dispersion index. That is, the clustering effect is more prominent for smaller fish. The design effect of cluster sampling on the precision of length frequency distributions estimated from red snapper samples collected from commercial fisheries is shown in Fig 16. For example, for a trip sample size of 50, the effective sample size could be less than 20% of the actual sample size. The design effect of cluster sampling on the precision of mean lengths is more substantial (Table 6). For a cluster sample with a trip sample size of 50 and a within trip correlation of 0.2, the design effect is more than 10 (see Chih (2011)). That is, the effective sample size is less than 10% of the actual sample size. The design effects for cluster sampling are different for different parameters. Using the actual sample size instead of the effective sample size can yield misleading results when conducting statistical testing for cluster samples.

Conclusions

1. The regional differences in growth among different states reported by Fischer et al. (2004) may be due to a clustering effect or non-representative sampling. This is evident by the fact that (a) the length frequency distributions for the states reported in their study were greatly different from those estimated from NMFS's length samples and (b) simulation analyses showed that such deviations in the length frequency distributions of red snapper samples can cause significant differences in growth curves and lengths-at-age.

2. Reweighting of growth curves, lengths-at-age and age frequency distributions by the length frequency distribution of the original population can improve the precision of these parameters. However, the reweighting will only work if

sufficient numbers of otolith samples are taken from all length categories. For that reason, it may be better to use the age-length-key sampling method than random otolith sampling methods.

3. The clustering effect among red snapper fish samples is high due to fish schooling, gear selectivity, and environmental factors. The clustering effect is especially obvious for smaller red snappers. Consequently, any statistical testing regarding length or age related parameters should be based on effective sample sizes and not on actual sample sizes.

4. The effects of sampling must be considered before drawing any conclusions regarding regional differences in growth among fish: (1) The length frequency distributions of the samples collected from regions intended for study should be representative of the fish populations in those regions and should be consistent over reasonably long periods of time. (2) Fish samples collected from regions being compared should be subjected to the same sampling practices (e.g., similar size limits, fishing regulations, gears, etc.). (3) Effective sample sizes should be large enough to reflect the age and length relationships over all length categories.

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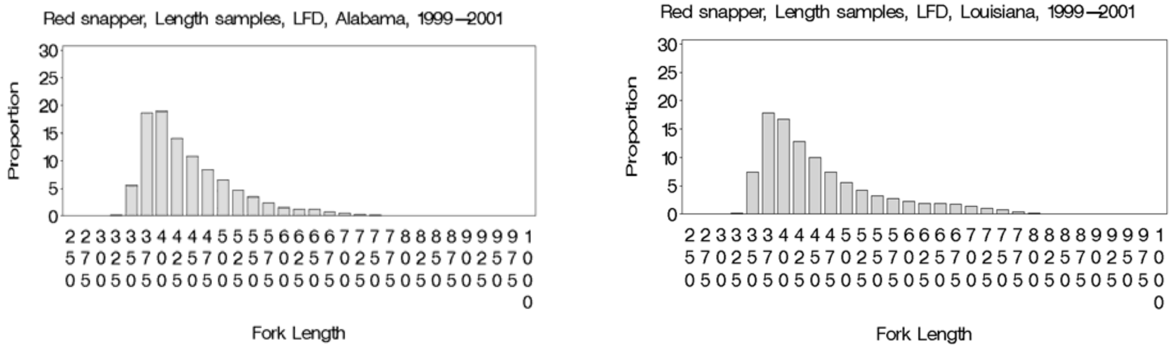
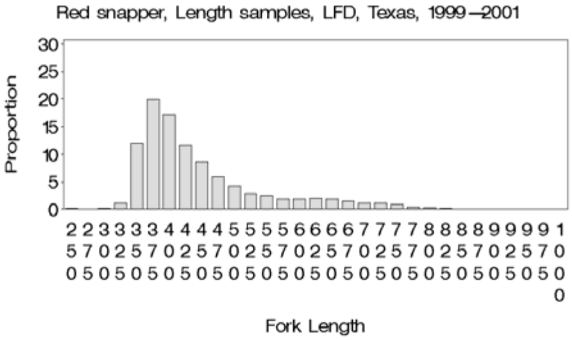
Fig 1. Length frequency distributions for red snapper length samples collected from all fisheries during 1999-2001 from (a) Alabama (n=15273), (b) Louisiana (n=16802) and (c) Texas (n=7703), and (d) the length frequency distribution determined by Fischer et al. (2004) for samples collected from Alabama (n= 2010), Louisiana (n= 1905) and Texas (n=1277).

(a) Alabama (b) Louisiana



(c) Texas



(d) Fischer et.al. (2004)

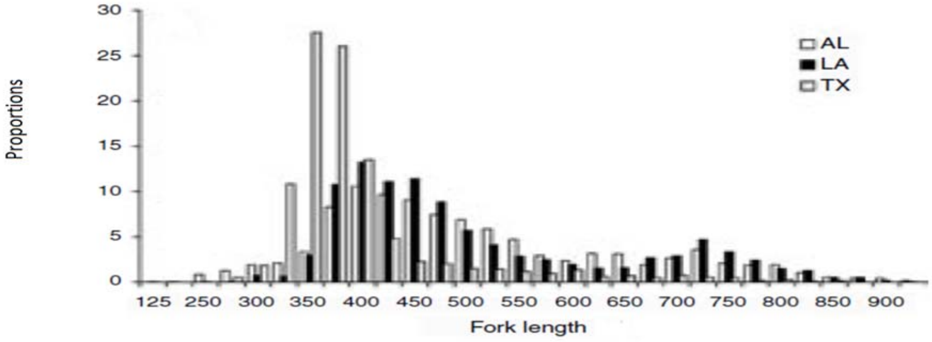
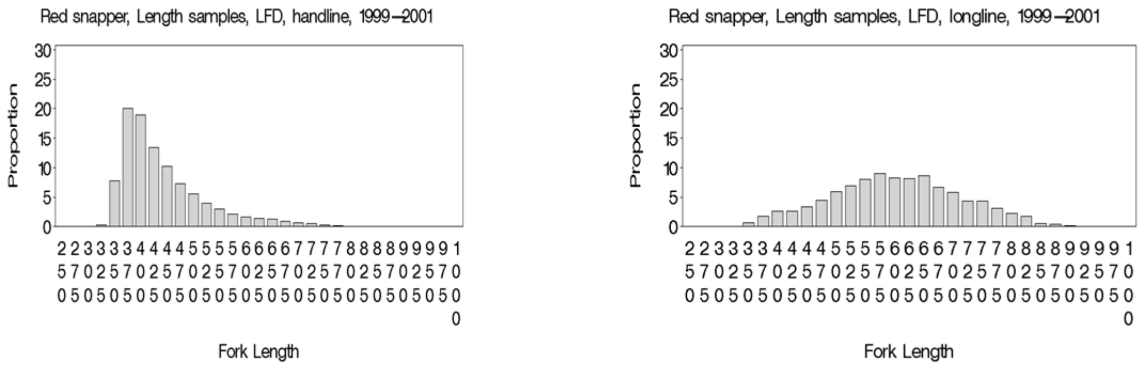


Fig 2. Length frequency distributions for red snapper length samples collected from different fisheries in the Gulf of Mexico from 1999 to 2001: (a) handline fishery (n=61255), (b) longline fishery (n=1754), (c) commercial fishery (n=31552), and (d) recreational fishery (n=38055).

(a) Handline

(b) Longline



(a) Commercial

(d) Recreational

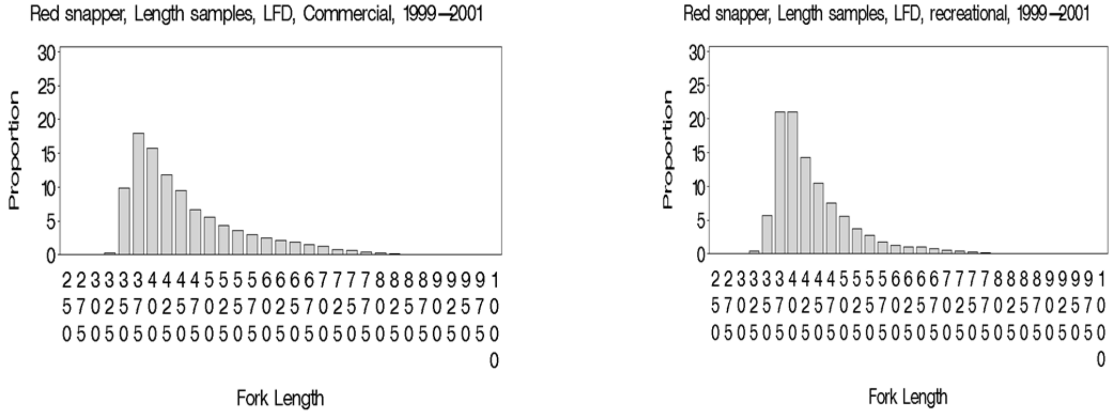
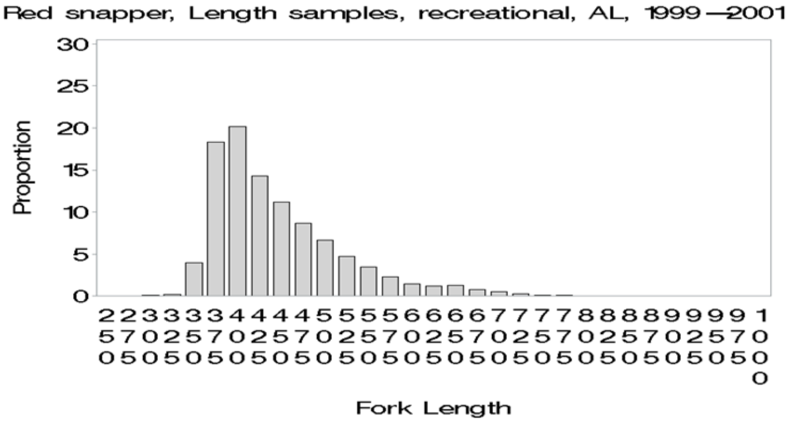
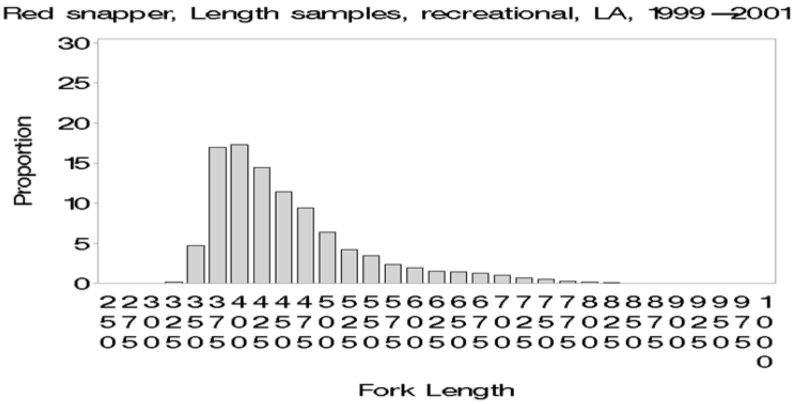


Fig 3. Length frequency distributions for red snapper samples collected from recreational fisheries in different states: (a) Alabama (n=13212), (b) Louisiana (n=6447), and (c) Texas (n=5725).

(a) Alabama



(b) Louisiana



(c) Texas

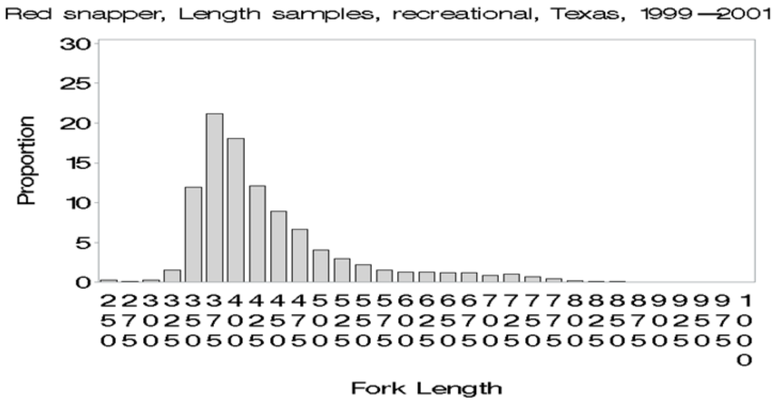
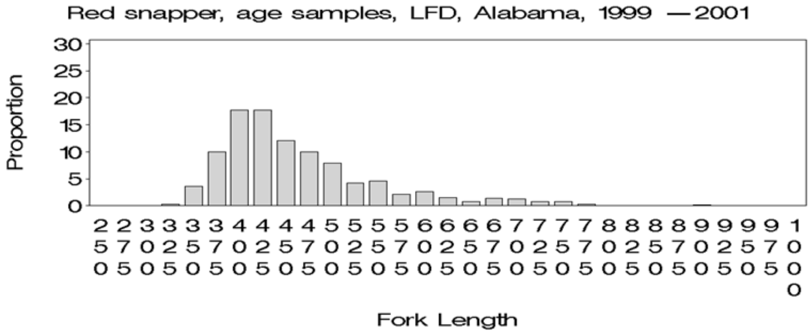
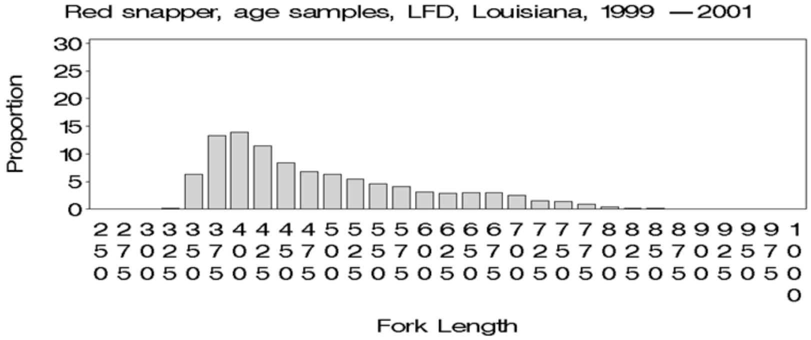


Figure 4. Length frequency distribution (LFD) for red snapper othlith samples processed by the Panama City Laboratory from 1999 to 2001. . Individual length frequency distribution: (a) Alabama (n=1147), (b) Louisiana (n=4299) , and (c) Texas (n=1252).

(a)Alabama



(b) Louisiana



(c) Texas

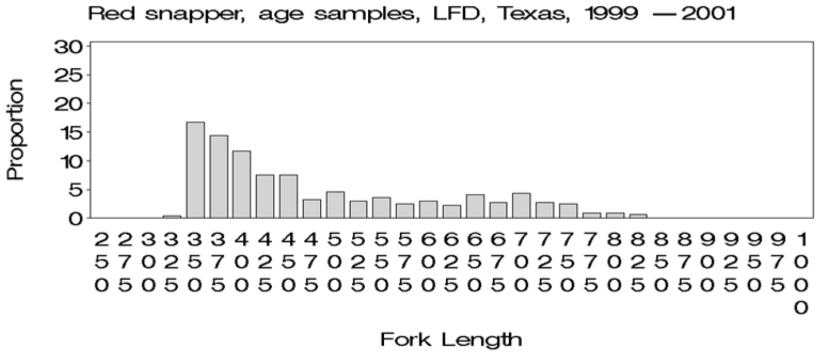
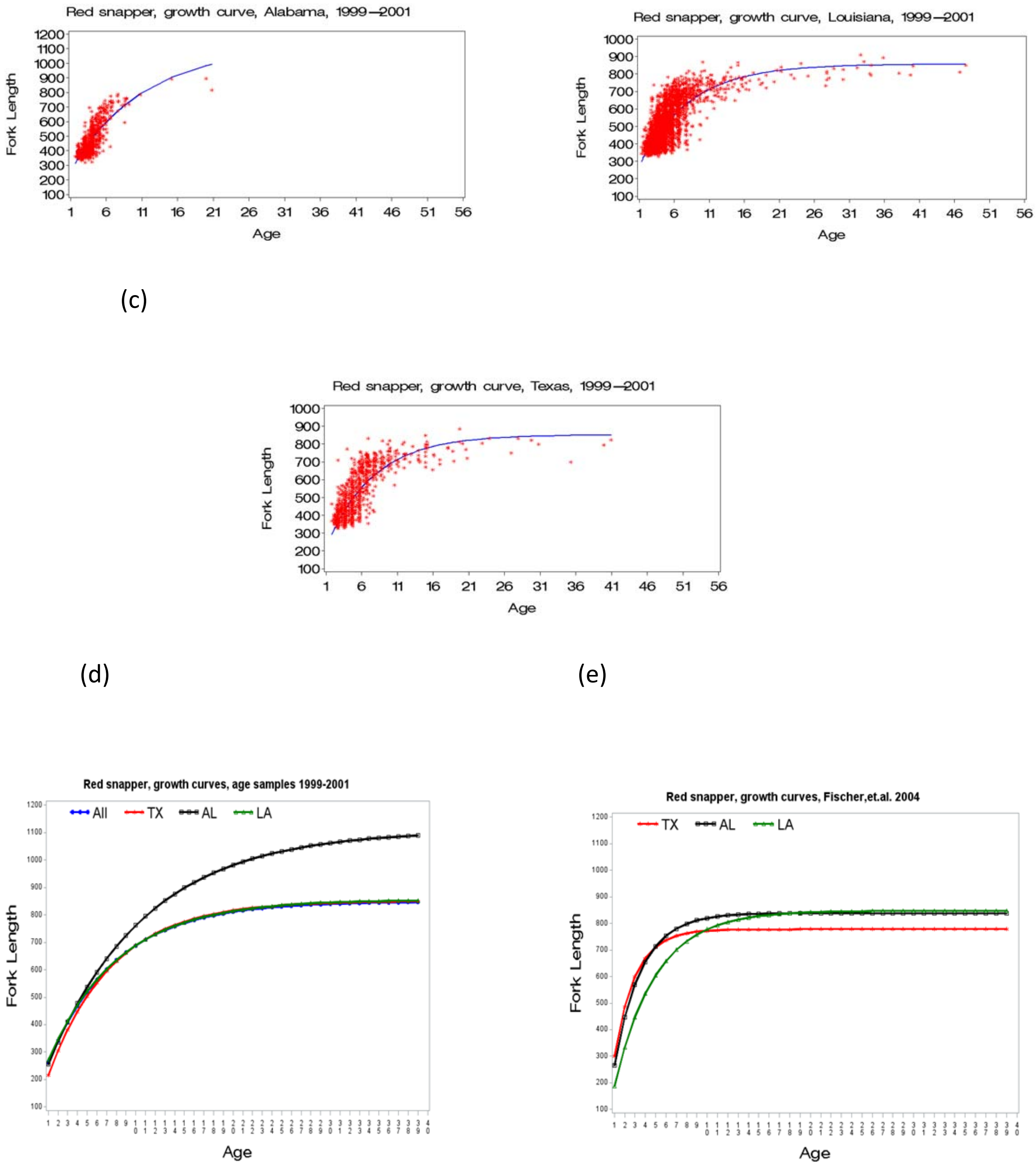


Figure 5. Comparisons of growth curves estimated from otolith samples collected from three different states and processed by the Panama City Laboratory from 1999 to 2001. Individual growth curves: (a) Alabama, (b)Louisiana, and (c) Texas. Comparisons: (d) all three states and (e) comparison of three growth curves obtained from Fischer et al. (2004).



(a)

(b)

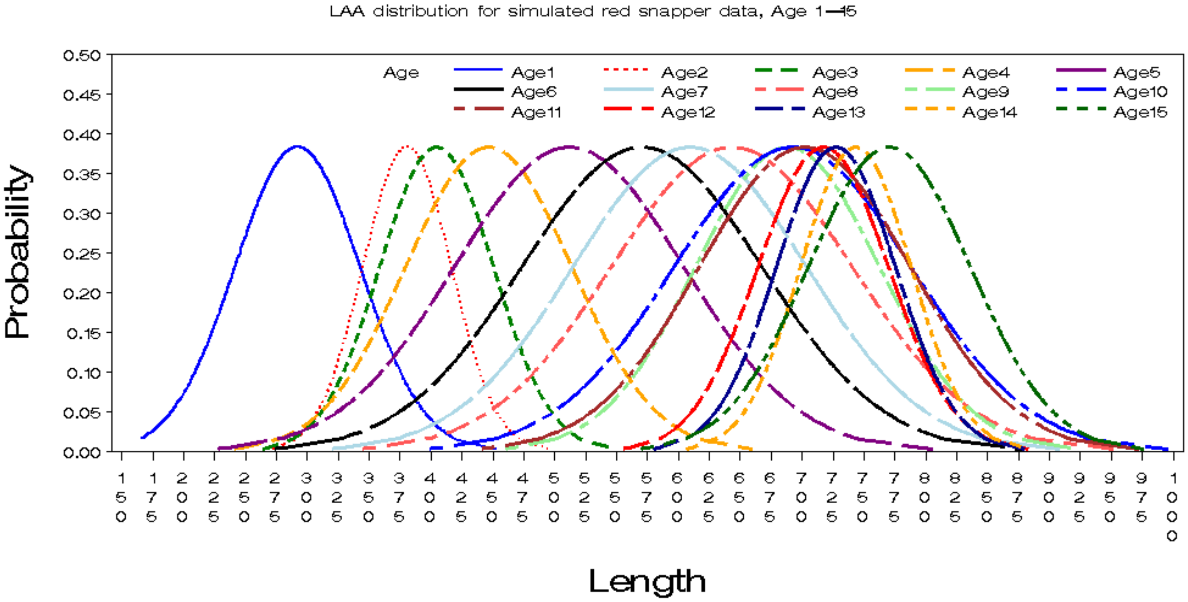
(c)

(d)

(e)

Figure 6. Simulated red snapper data based on the length at age matrix and age frequency distribution estimated from all red snapper otolith samples collected from Gulf of Mexico between 1999 and 2001 (also see Table 2): (a) probability distributions for lengths-at-age for ages 1 to 15 years, and (b) age frequency distribution for the simulated data.

(a)



(b)

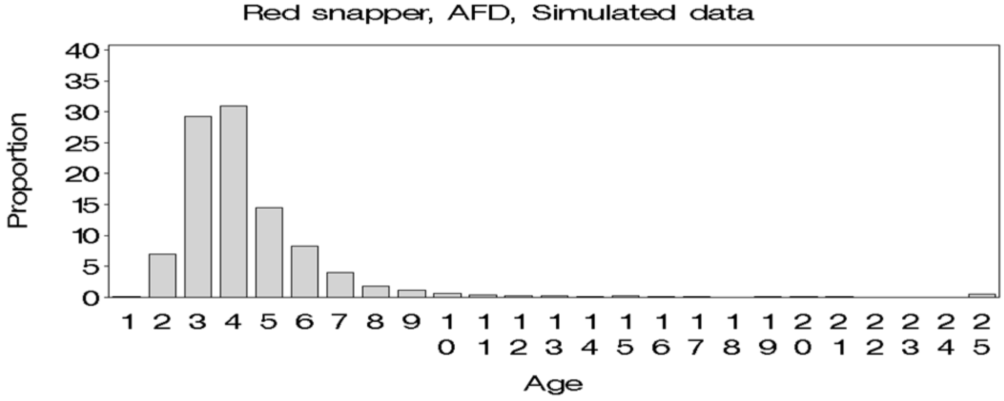


Figure 7. Length frequency distributions (LFD) (a) for the simulated data set, (b) for resampled data based on the Alabama LFD data from Fischer et al. (2004), (c) for resampled data based on the Louisiana LFD data from Fischer et al. (2004), and (d) for resampled data based on the Texas LFD of data from Fischer et al. (2004).

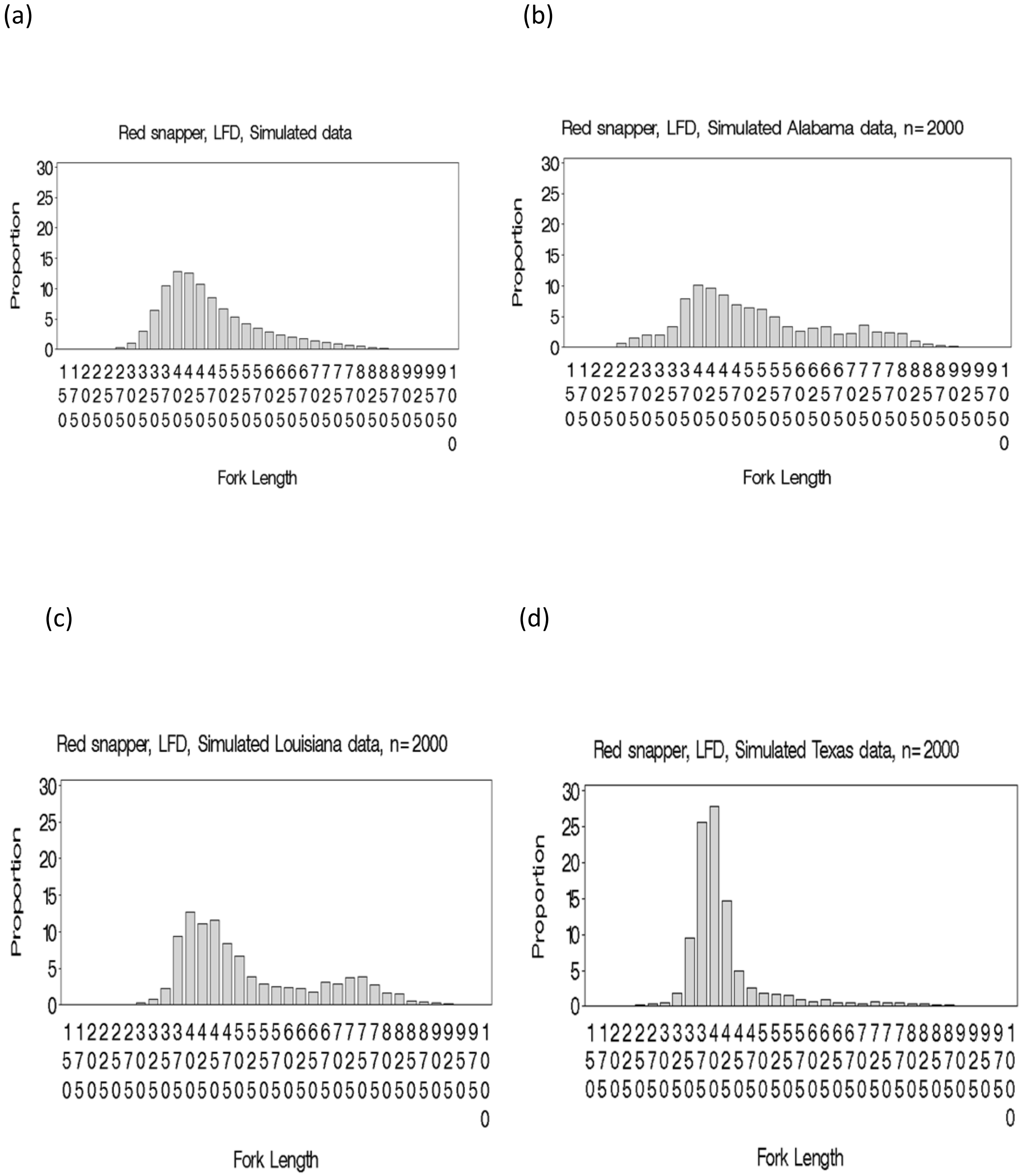


Figure 8. Length frequency distribution for simulated data at age 5 years: (a) simulated Alabama data, (b) simulated Louisiana data, (c) simulated Texas data, and (d) all simulated data.

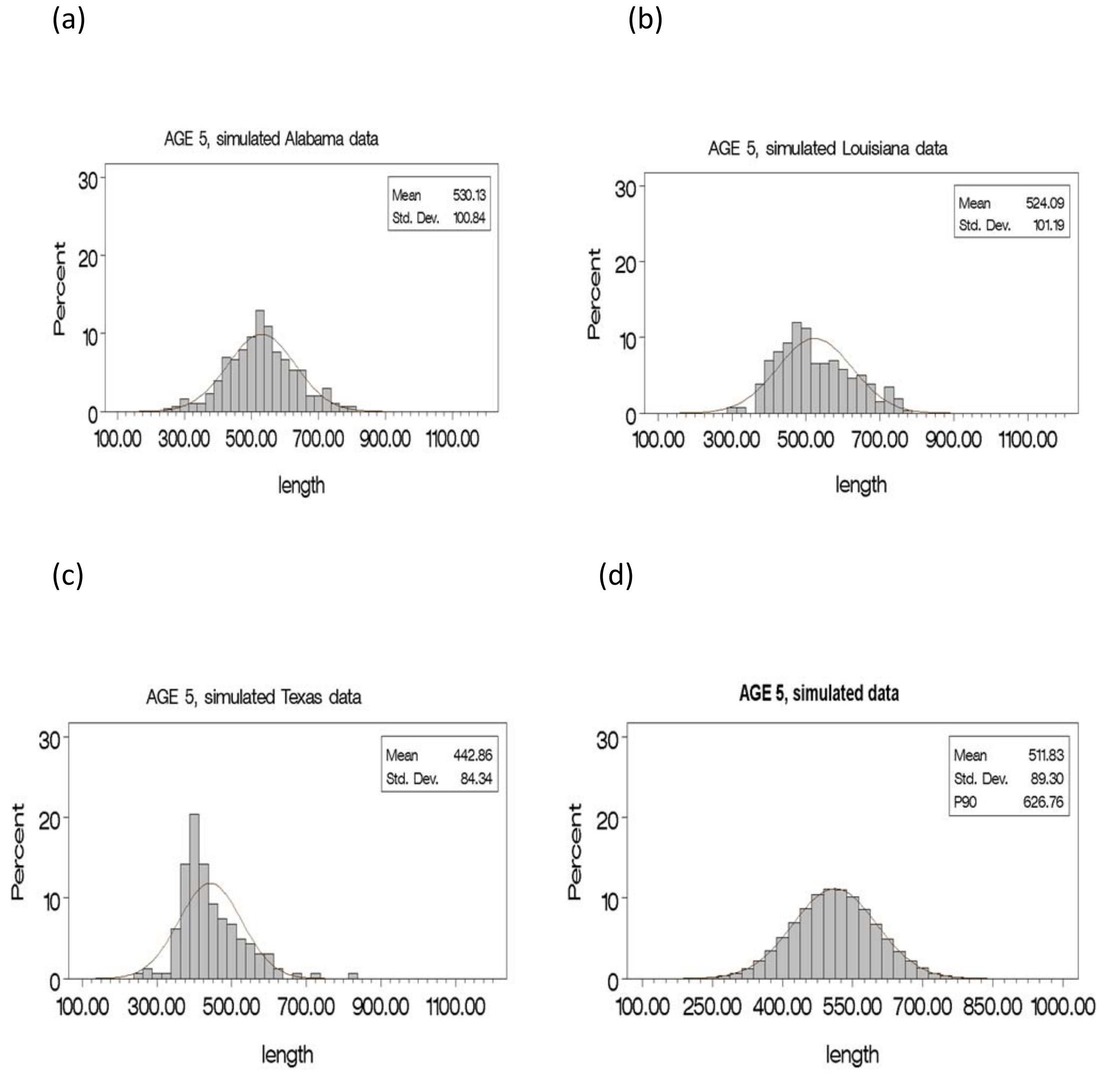


Figure 9. Mean length- at- age for ages 2 to 7 years estimated from resampled data (All-original simulated data, TX-Texas, AL-Alabama, LA- Louisiana, random- simple random sample with n=2000)

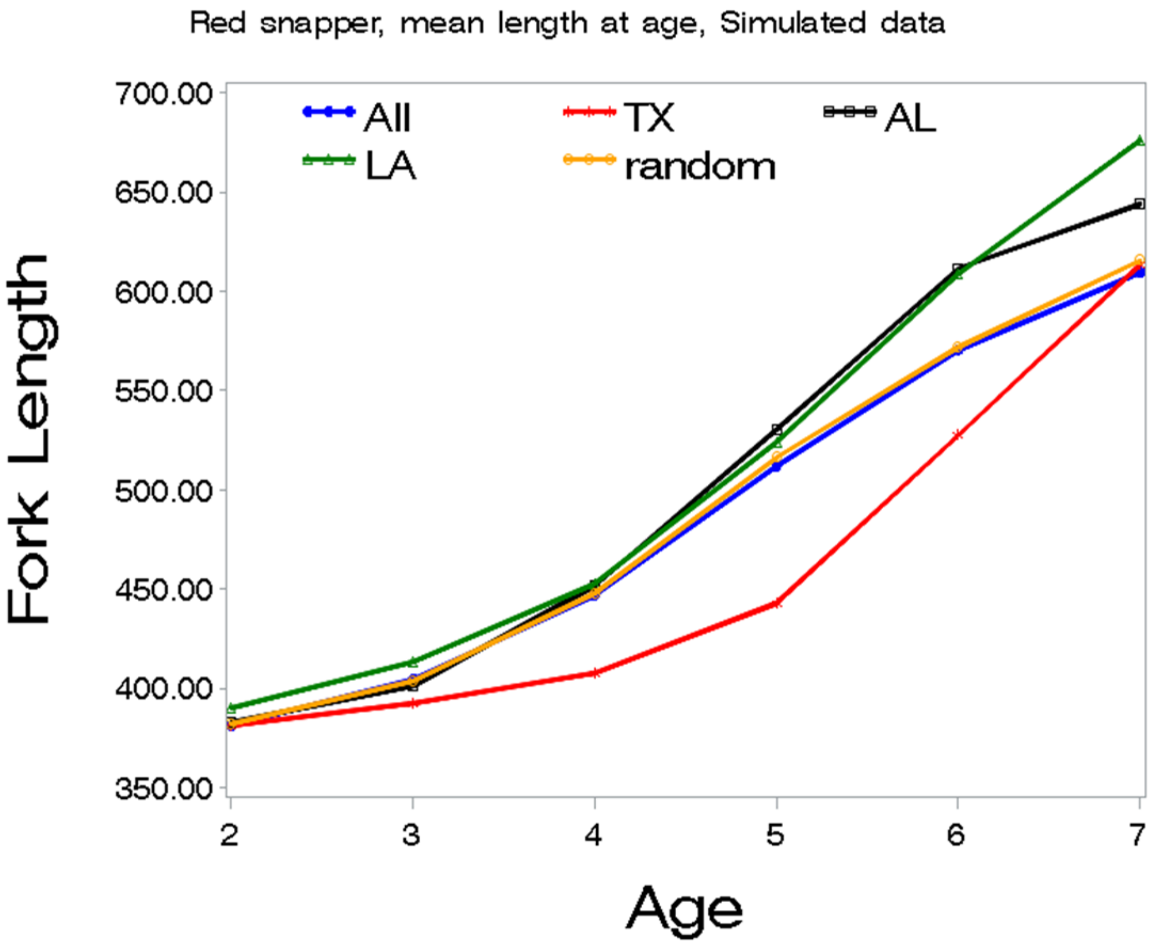


Figure 10. Estimated age frequency distributions from simulated data: (a) all simulated data, (b) simulated Alabama data, (c) simulated Louisiana data, and (d) simulated Texas data.

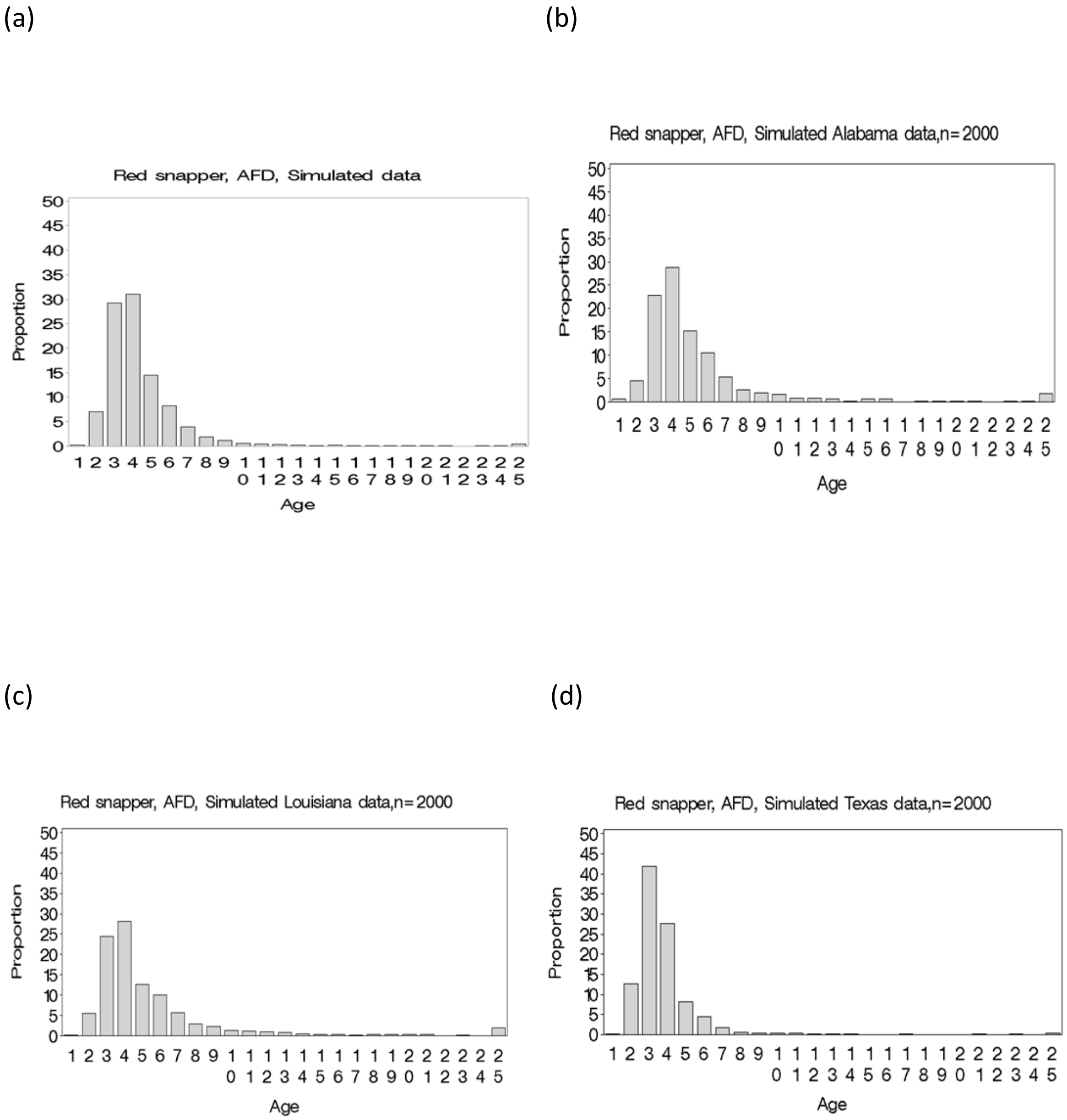


Figure 11. Estimated growth curves from simulated data: (a) all simulated data, (b) simulated Alabama data, (c) simulated Louisiana data, (d) simulated Texas data, and (e) comparison of growth curves.

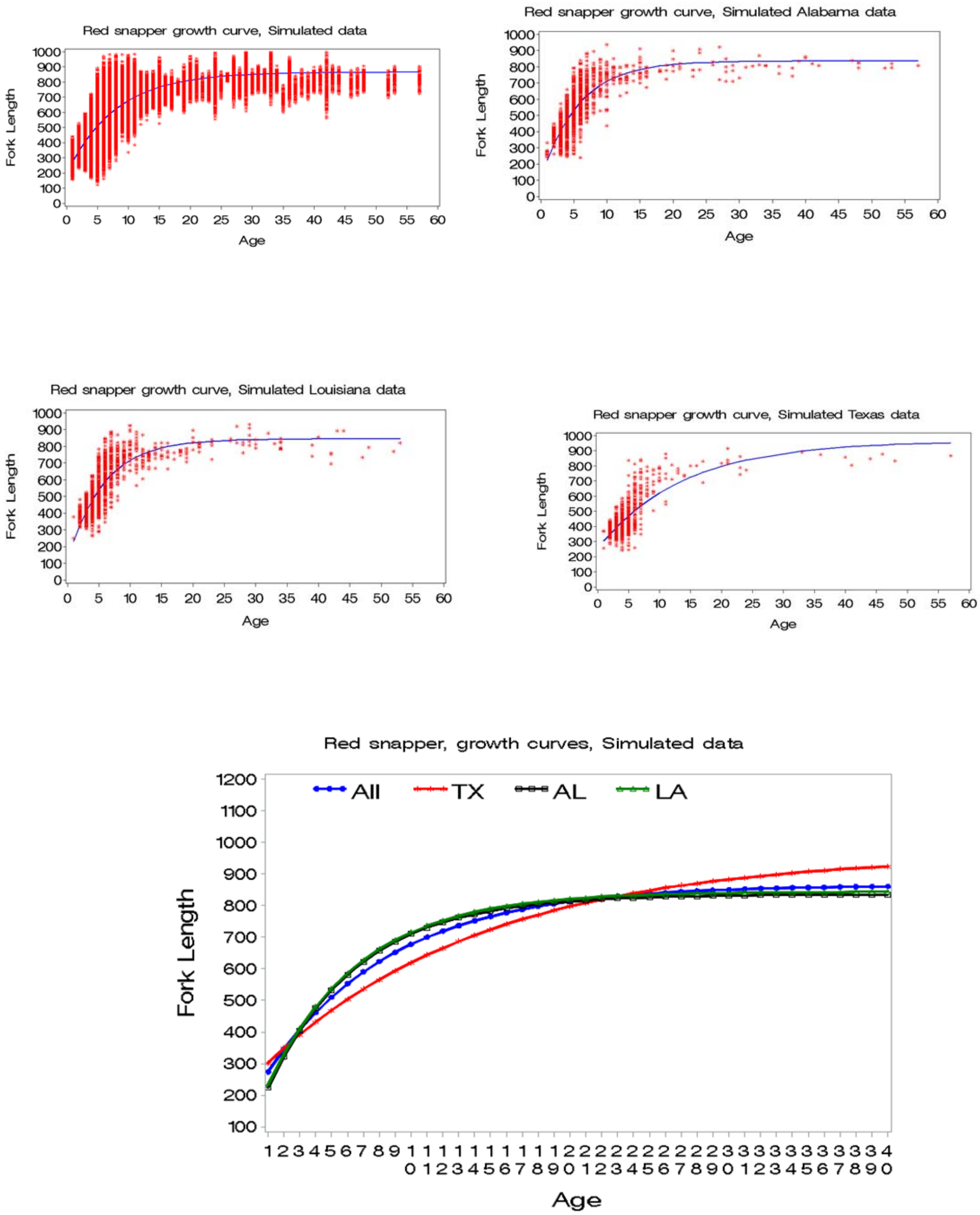


Figure 12. Age frequency distributions of (a) all simulated data, and reweighted age frequency distributions of (b) simulated Alabama data, (c) simulated Louisiana data, and (d) simulated Texas data.

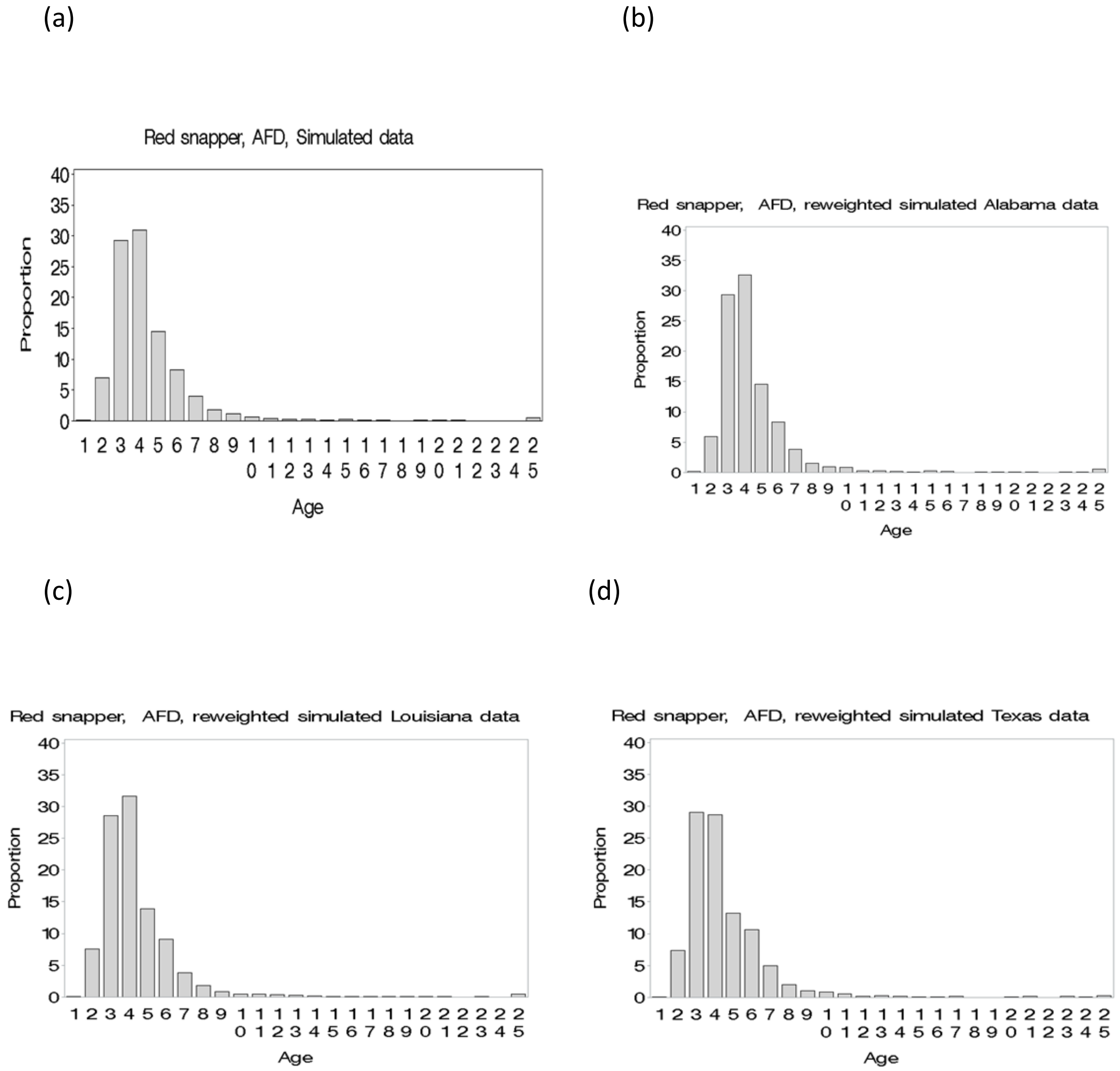
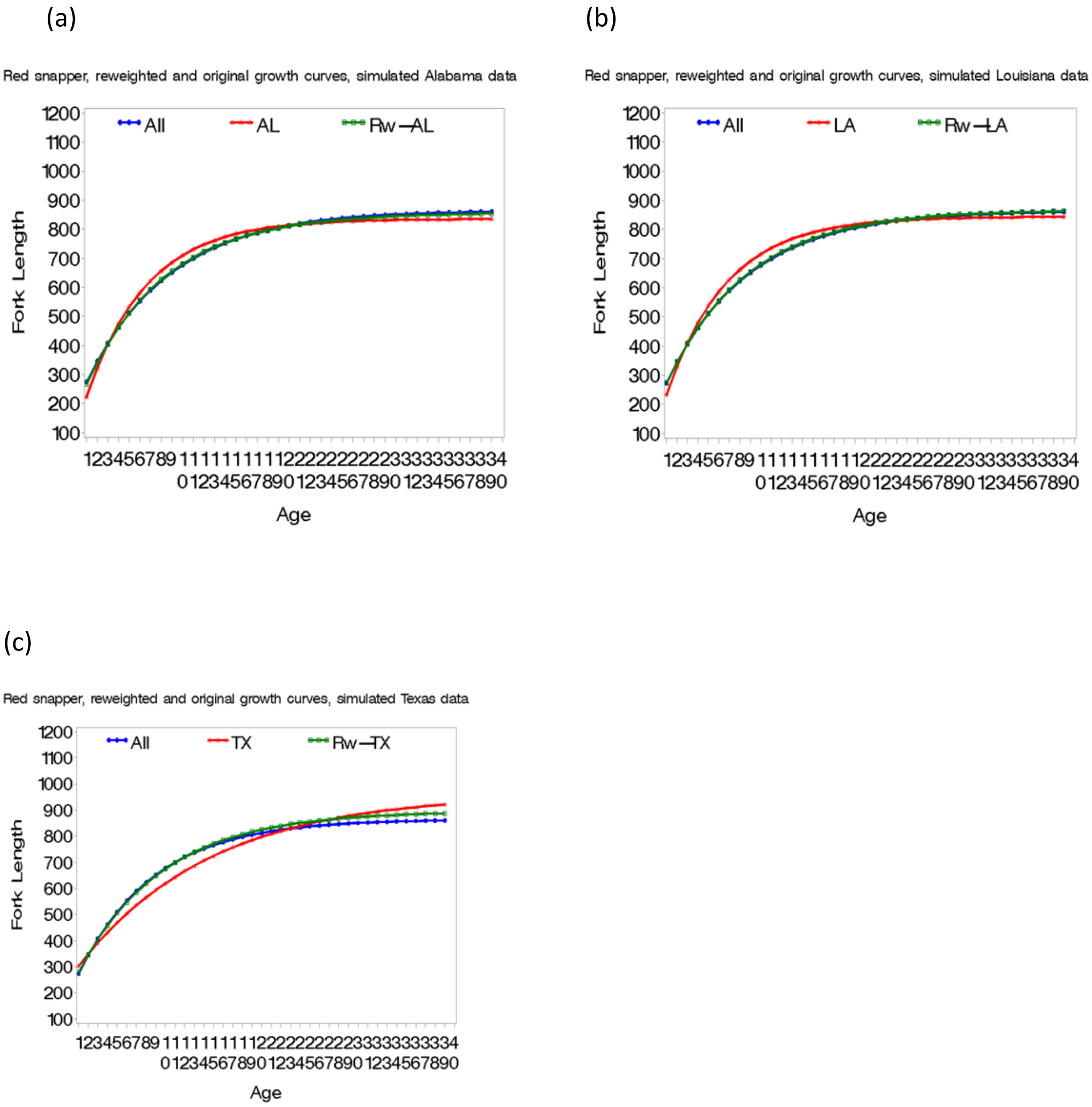


Figure 13. Comparisons of red snapper growth curves estimated from resampled state data with the original growth curve and with the reweighted growth curve: (a) Alabama (AL), (b) Louisiana (LA), and (c) Texas (TX).



(a)

Red snapper, reweighted and original growth curves, simulated Alabama data

(b)

Red snapper, reweighted and original growth curves, simulated Louisiana data

(c)

Red snapper, reweighted and original growth curves, simulated Texas data

Figure 14. Comparison of mean lengths-at-age for simulated red snapper data and reweighted data (AL-Alabama, LA-Louisiana, TX- Texas, All- original simulated data).

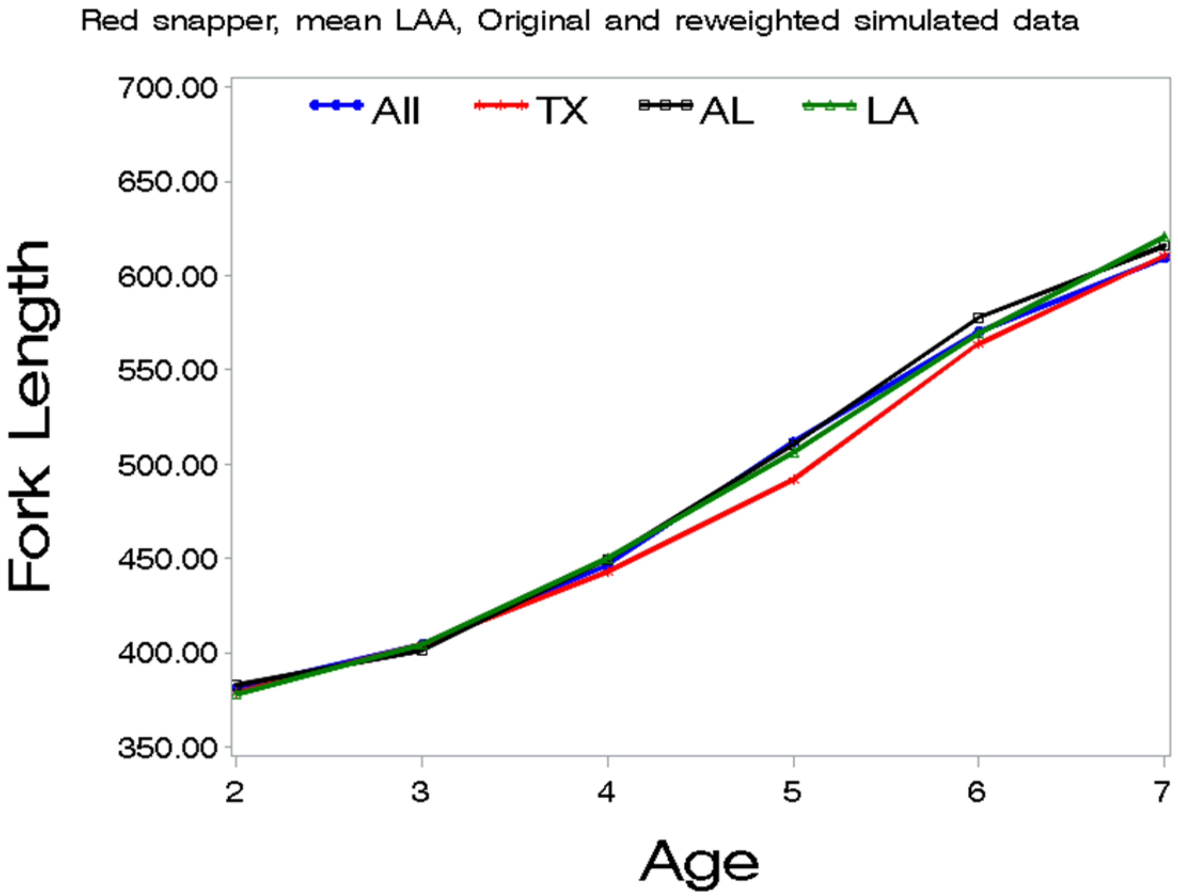


Figure 15. Scatter plots of the tripdispersion index (DI) and trip mean length (in cm) for red snapper samples collected from commercial fisheries from 1996-2008. Trip sample sizes were greater than 50 for all sampling trips (from Chih (2010)).

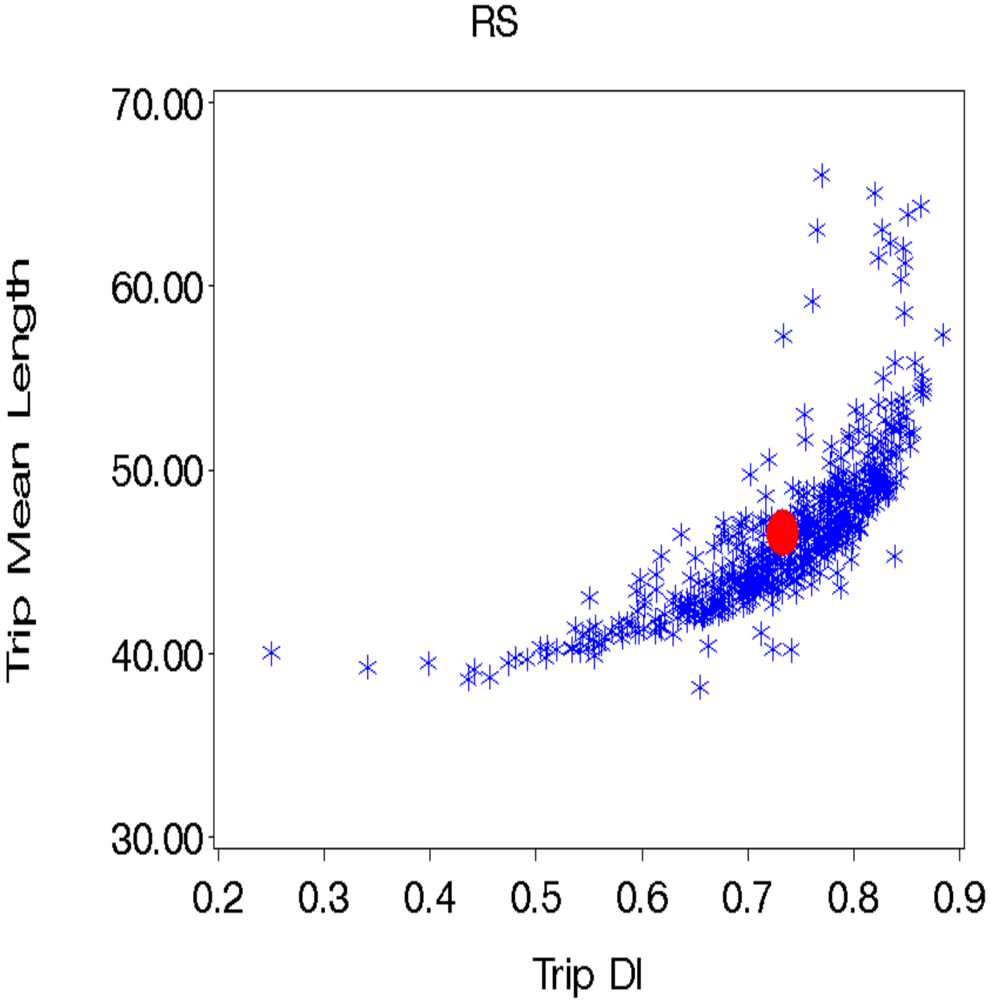


Figure 16. Effects of different sampling designs on effective sample sizes. Each data point represents the result from 200 bootstrap runs. TS: trip sample size. (from Chih (2010))

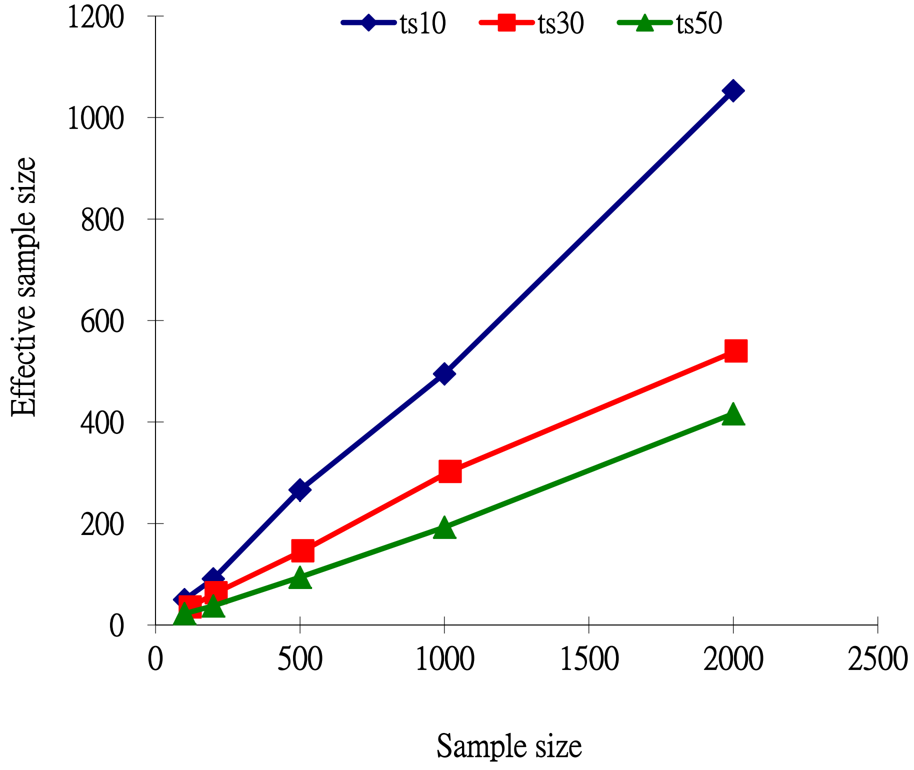


Table 1. Otolith and length sample sizes collected from different type of fisheries and states.

(a). Otolith samples

Year	Mode	Sample sizes
1999	Commercial	2949
1999	Charter boat	712
1999	Head boat	256
1999	Private boat	654
2000	Commercial	2535
2000	Charter boat	509
2000	Head boat	382
2000	Private boat	3
2000	Survey	203
2001	Commercial	2605
2001	Charter boat	383
2001	Head boat	291
2001	Private boat	2
2001	Survey	90

State	Sample sizes
Alabama	1147
Florida	3859
Louisiana	4299
Mississippi	1015
Texas	1252

(b) Length samples

State	Sample sizes
AL	15273
FL	26509
LA	16802
MS	3320
TX	7703

Source	Sample sizes
Head boat	11682
MRFSS	23480
TIP	31552
TPWD	2893

Table 2 – Mean lengths-at-age, standard deviations, original sample sizes, proportions and the simulated numbers of the simulated data set.

Age	Mean Length	Standard deviation	Original sample sizes	Proportions	Simulated numbers
1	292.44	48.56	18	0.002	1555
2	381.14	34.39	809	0.070	69904
3	404.50	44.15	3385	0.292	292491
4	446.63	64.50	3586	0.310	309859
5	511.73	89.03	1679	0.145	145079
6	570.58	93.20	960	0.083	82952
7	609.31	90.61	458	0.040	39575
8	643.19	93.51	215	0.019	18578
9	688.20	71.42	133	0.011	11492
10	692.34	91.94	72	0.006	6221
11	702.29	81.93	50	0.004	4320
12	717.09	50.57	34	0.003	2938
13	727.30	46.23	26	0.002	2247
14	743.34	42.87	17	0.001	1469
15	770.51	62.91	22	0.002	1901
16	744.28	35.28	12	0.001	1037
17	741.37	45.45	6	0.001	518
18	766.86	18.45	4	0.000	346
19	750.74	55.13	7	0.001	605
20	811.51	52.56	8	0.001	691
21	807.84	49.00	7	0.001	605
22	776.78	40.00	1	0.000	86
23	767.52	35.67	5	0.000	432
24	796.42	86.43	5	0.000	432
25	789.05	40.00	1	0.000	86

Age	Mean Length	Standard deviation	Original sample sizes	Proportions	Simulated numbers
26	833.89	11.33	2	0.000	173
27	821.33	67.21	3	0.000	259
28	787.95	35.74	6	0.001	518
29	855.15	88.38	5	0.000	432
30	799.68	28.56	4	0.000	346
31	826.07	37.12	2	0.000	173
32	813.13	32.72	2	0.000	173
33	850.43	72.16	3	0.000	259
34	815.18	30.89	3	0.000	259
35	699.35	40.00	1	0.000	86
36	819.90	64.27	3	0.000	259
37	761.67	40.00	1	0.000	86
38	805.11	40.00	1	0.000	86
39	783.39	40.00	1	0.000	86
40	811.72	29.44	3	0.000	259
41	823.99	40.00	1	0.000	86
42	795.66	89.47	2	0.000	173
43	829.66	40.00	1	0.000	86
44	820.22	40.00	1	0.000	86
46	796.61	40.00	1	0.000	86
47	810.84	40.00	1	0.000	86
48	816.12	30.01	3	0.000	259
52	795.66	40.00	1	0.000	86
53	823.99	40.00	1	0.000	86
57	823.05	40.00	1	0.000	86

Table 3. Comparisons of growth curves estimated from all otolith samples from the PC lab with those estimated from three different states. L_{max} =asymptotic length, k=growth coefficient, t_0 = age at zero length. (AL-Alabama, LA-Louisiana, TX- Texas, All- original simulated data)

(1) All vs AL

Model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
All samples	849.270	0.144	-1.554	.	.	.	.	.	.	.
AL samples	1109.139	0.100	-1.616	.	.	.	.	.	.	.
H_0: equal L_{max}	855.089	.	.	0.000	0.142	0.168	-1.588	-0.918	.	.
H_0: equal k	.	0.142	.	0.002	.	.	-1.589	-1.038	853.005	939.851
H_0: equal t_0	.	.	-1.558	0.799	0.144	0.103	.	.	849.534	1097.069
H_0: equal L_{max},k, t_0	851.890	0.144	-1.533	0.000	.	.	.	.	.	.

(2) All vs TX

Model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
All samples	849.270	0.144	-1.554	.	.	.	.	.	.	.
TX samples	851.993	0.151	-0.939	.	.	.	.	.	.	.
H_0: equal L_{max}	849.754	.	.	0.864	0.144	0.152	-1.557	-0.925	.	.
H_0: equal k	.	0.145	.	0.358	.	.	-1.534	-1.050	847.103	863.080
H_0: equal t_0	.	.	-1.477	0.000	0.147	0.129	.	.	844.183	884.307
H_0: equal L_{max},k, t_0	850.390	0.144	-1.518	0.000	.	.	.	.	.	.

(3) All vs LA

Model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
All samples	849.270	0.144	-1.554	.	.	.	.	.	.	.
LA samples	856.109	0.139	-1.755	.	.	.	.	.	.	.
H_0: equal L_{max}	851.125	.	.	0.597	0.143	0.141	-1.565	-1.722	.	.
H_0: equal k	.	0.143	.	0.408	.	.	-1.578	-1.684	851.854	848.969
H_0: equal t_0	.	.	-1.606	0.115	0.142	0.145	.	.	852.662	846.382
H_0: equal L_{max},k, t_0	850.952	0.143	-1.599	0.004	.	.	.	.	.	.

Table 3. (Continued)

(4) LA vs TX

Model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
LA samples	851.993	0.151	-0.939	.	.	.	.	.	.	.
TX samples	856.109	0.139	-1.755	.	.	.	.	.	.	.
H_0: equal L_{max}	854.614	.	.	0.832	0.150	0.140	-0.955	-1.745	.	.
H_0: equal k	.	0.143	.	0.194	.	.	-1.087	-1.676	866.832	848.154
H_0: equal t_0	.	.	-1.517	0.000	0.128	0.149	.	.	886.733	840.518
H_0: equal L_{max},k, t_0	855.575	0.141	-1.585	0.000	.	.	.	.	.	.

(5) TX vs AL

Model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
TX samples	856.109	0.139	-1.755	.	.	.	.	.	.	.
AL samples	1109.139	0.100	-1.616	.	.	.	.	.	.	.
H_0: equal L_{max}	870.712	.	.	0.000	0.133	0.161	-1.852	-0.967	.	.
H_0: equal k	.	0.135	.	0.008	.	.	-1.842	-1.124	864.838	962.837
H_0: equal t_0	.	.	-1.732	0.611	0.140	0.095	.	.	854.631	1134.015
H_0: equal L_{max},k, t_0	861.851	0.140	-1.676	0.000	.	.	.	.	.	.

(6) LA vs AL

Model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
LA samples	851.993	0.151	-0.939	.	.	.	.	.	.	.
AL samples	1109.139	0.100	-1.616	.	.	.	.	.	.	.
H_0: equal L_{max}	877.074	.	.	0.000	0.140	0.159	-1.093	-0.987	.	.
H_0: equal k	.	0.141	.	0.001	.	.	-1.127	-1.051	870.823	943.175
H_0: equal t_0	.	.	-1.163	0.010	0.142	0.123	.	.	865.483	1018.586
H_0: equal L_{max},k, t_0	861.752	0.148	-1.217	0.000	.	.	.	.	.	.

Table 4. Comparisons of growth curves estimated from a random sample (n=2000) taken from the simulated data set with growth curves estimated from resampled state data. L_{max} =asymptotic length, k=growth coefficient, t_0 = age at zero length. (AL-Alabama, LA-Louisiana, TX- Texas, RS- a simple random sample of the original simulated data)

(1) RS vs LA

Model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
RS samples	895.329	0.122	-1.967	.	.	.	.	.	.	.
LA samples	844.298	0.173	-0.867	.	.	.	.	.	.	.
H_0: equal L_{max}	851.317	.	.	0.028	0.138	0.169	-1.722	-0.911	.	.
H_0: equal k	.	0.159	.	0.000	.	.	-1.328	-1.107	814.749	861.125
H_0: equal t_0	.	.	-1.258	0.000	0.155	0.156	.	.	834.698	858.697
H_0: equal L_{max},k, t_0	856.225	0.152	-1.267	0.000	.	.	.	.	.	.

(2) RS vs TX

Model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
RS samples	895.329	0.122	-1.967	.	.	.	.	.	.	.
TX samples	963.938	0.073	-4.198	.	.	.	.	.	.	.
H_0: equal L_{max}	928.577	.	.	0.030	0.112	0.078	-2.147	-4.007	.	.
H_0: equal k	.	0.091	.	0.000	.	.	-2.747	-3.386	1004.467	885.139
H_0: equal t_0	.	.	-3.032	0.000	0.090	0.093	.	.	989.351	904.894
H_0: equal L_{max},k, t_0	935.777	0.098	-2.664	0.000	.	.	.	.	.	.

(3) RS vs AL

model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
RS samples	895.329	0.122	-1.967	.	.	.	.	.	.	.
AL samples	835.317	0.176	-0.767	.	.	.	.	.	.	.
H_0: equal L_{max}	844.493	.	.	0.012	0.141	0.171	-1.684	-0.822	.	.
H_0: equal k	.	0.161	.	0.000	.	.	-1.309	-1.020	812.363	854.121
H_0: equal t_0	.	.	-1.205	0.000	0.158	0.156	.	.	830.206	851.996
H_0: equal L_{max},k, t_0	848.767	0.154	-1.218	0.000	.	.	.	.	.	.

Table 4. (Continued)

(4) AL vs LA

model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
AL samples	835.317	0.176	-0.767	.	.	.	.	.	.	.
LA samples	844.298	0.173	-0.867	.	.	.	.	.	.	.
H_0: equal L_{max}	840.065	.	.	0.481	0.173	0.176	-0.796	-0.840	.	.
H_0: equal k	.	0.174	.	0.753	.	.	-0.789	-0.845	837.024	842.719
H_0: equal t_0	.	.	-0.818	0.533	0.173	0.175	.	.	837.329	842.417
H_0: equal L_{max},k, t_0	840.143	0.174	-0.821	0.058	.	.	.	.	.	.

(5) TX vs LA

model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
TX samples	963.938	0.073	-4.198	.	.	.	.	.	.	.
LA samples	844.298	0.173	-0.867	.	.	.	.	.	.	.
H_0: equal L_{max}	858.420	.	.	0.000	0.092	0.165	-3.648	-0.958	.	.
H_0: equal k	.	0.139	.	0.000	.	.	-2.194	-1.551	760.310	890.392
H_0: equal t_0	.	.	-2.012	0.000	0.121	0.131	.	.	844.543	884.022
H_0: equal L_{max},k, t_0	878.844	0.131	-1.645	0.000	.	.	.	.	.	.

(6) AL vs TX

model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
AL samples	835.317	0.176	-0.767	.	.	.	.	.	.	.
TX samples	963.938	0.073	-4.198	.	.	.	.	.	.	.
H_0: equal L_{max}	852.039	.	.	0.000	0.167	0.093	-0.869	-3.616	.	.
H_0: equal k	.	0.139	.	0.000	.	.	-1.469	-2.185	885.130	759.348
H_0: equal t_0	.	.	-1.982	0.000	0.130	0.123	.	.	878.438	842.594
H_0: equal L_{max},k, t_0	872.539	0.131	-1.647	0.000	.	.	.	.	.	.

Table 5. Comparisons of growth curves estimated from a random sample (n=2000) taken from the simulated data set with growth curves estimated from **reweighted** simulated data from different states. L_{max} =asymptotic length, k=growth coefficient, t_0 = age at zero length. (AL-Alabama, LA-Louisiana, TX- Texas, RS- a simple random sample of the original simulated data)

(1) RS vs LA

model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
RS samples	895.329	0.122	-1.967	.	.	.	.	.	.	.
LA samples	866.219	0.129	-1.932	.	.	.	.	.	.	.
H_0: equal L_{max}	878.213	.	.	0.295	0.128	0.125	-1.873	-1.999	.	.
H_0: equal k	.	0.126	.	0.519	.	.	-1.891	-1.993	885.429	872.928
H_0: equal t_0	.	.	-1.948	0.883	0.123	0.128	.	.	893.707	867.275
H_0: equal L_{max},k, t_0	878.245	0.126	-1.933	0.577	.	.	.	.	.	.

(2) RS vs TX

model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
RS samples	895.329	0.122	-1.967	.	.	.	.	.	.	.
TX samples	895.245	0.114	-2.286	.	.	.	.	.	.	.
H_0: equal L_{max}	895.284	.	.	0.998	0.122	0.114	-1.967	-2.286	.	.
H_0: equal k	.	0.118	.	0.392	.	.	-2.067	-2.198	908.587	885.154
H_0: equal t_0	.	.	-2.132	0.199	0.116	0.119	.	.	909.615	884.528
H_0: equal L_{max},k, t_0	895.128	0.118	-2.124	0.013	.	.	.	.	.	.

(3) RS vs AL

model	**lmax**	**k**	**t**	**p**	**k1**	**k2**	**t1**	**t2**	**lmax1**	**lmax2**
RS samples	895.329	0.122	-1.967	.	.	.	.	.	.	.
AL samples	895.245	0.114	-2.286	.	.	.	.	.	.	.
H_0: equal L_{max}	895.284	.	.	0.998	0.122	0.114	-1.967	-2.286	.	.
H_0: equal k	.	0.118	.	0.392	.	.	-2.067	-2.198	908.587	885.154
H_0: equal t_0	.	.	-2.132	0.199	0.116	0.119	.	.	909.615	884.528
H_0: equal L_{max},k, t_0	895.128	0.118	-2.124	0.013	.	.	.	.	.	.

Table 5. (Continued).

(4) LA vs AL

model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
LA samples	866.219	0.129	-1.932	.	.	.	.	.	.	.
AL samples	857.010	0.134	-1.788	.	.	.	.	.	.	.
H_0: equal L_{max}	861.515	.	.	0.701	0.131	0.132	-1.905	-1.814	.	.
H_0: equal k	.	0.131	.	0.606	.	.	-1.880	-1.840	860.589	862.478
H_0: equal t_0	.	.	-1.861	0.532	0.132	0.131	.	.	861.765	861.429
H_0: equal L_{max},k, t_0	861.621	0.131	-1.862	0.905	.	.	.	.	.	.

(5) LA vs TX

model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
LA samples	866.219	0.129	-1.932	.	.	.	.	.	.	.
TX samples	895.245	0.114	-2.286	.	.	.	.	.	.	.
H_0: equal L_{max}	879.560	.	.	0.257	0.124	0.119	-2.007	-2.196	.	.
H_0: equal k	.	0.122	.	0.101	.	.	-2.095	-2.108	883.977	874.897
H_0: equal t_0	.	.	-2.105	0.135	0.123	0.120	.	.	877.049	882.584
H_0: equal L_{max},k, t_0	879.432	0.121	-2.107	0.079	.	.	.	.	.	.

(6) AL vs TX

model	lmax	k	t	p	k1	k2	t1	t2	lmax1	lmax2
AL samples	857.010	0.134	-1.788	.	.	.	.	.	.	.
TX samples	895.245	0.114	-2.286	.	.	.	.	.	.	.
H_0: equal L_{max}	874.159	.	.	0.129	0.128	0.121	-1.886	-2.165	.	.
H_0: equal k	.	0.124	.	0.032	.	.	-2.003	-2.054	879.419	868.721
H_0: equal t_0	.	.	-2.037	0.036	0.125	0.122	.	.	871.750	877.799
H_0: equal L_{max},k, t_0	874.242	0.124	-2.036	0.060	.	.	.	.	.	.

Table 6 – The with trip correlations and design effects of red snapper samples collected from commercial fisheries from 1984 to 2008. All trip sample sizes are larger than 30.

YEAR	No. Trips	Avg. Trip size	Within trip correlation	Design effect
1984	59	78	0.261	21
1985	62	60	0.44	27
986	39	67	0.427	29
1987	10	70	0.182	14
1988	10	45	0.235	11
1989	21	53	0.428	23
1990	146	55	0.142	9
1991	192	48	0.134	7
1992	213	51	0.115	7
1993	171	55	0.133	8
1994	109	71	0.149	11
1995	86	81	0.17	15
1996	103	86	0.211	19
1997	136	76	0.158	13
1998	151	70	0.237	17
1999	117	51	0.242	13
2000	77	51	0.168	9
2001	94	45	0.138	7
2002	99	49	0.192	10
2003	123	45	0.204	10
2004	105	36	0.146	6
2005	165	34	0.158	6
2006	167	36	0.165	7
2007	179	35	0.353	13
2008	173	36	0.223	9