

Nonparametric growth model for Atlantic red drum, and changes to natural mortality (M) estimates.

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Abstract

There is evidence of misfit in the von Bertalanffy growth model for the northern region Atlantic red drum stock provided by the SEDAR 18 Data Workshop (DW). We used a nonparametric smooth monotone growth model which fit both the southern and northern region data very well. This growth model resulted in somewhat higher estimates of natural mortality (M) for younger ages based on the scaled Lorenzen method. The largest difference was for one-year old fish from the northern region, where the DW Lorenzen M estimate based on the von Bertalanffy model predicted length was 0.16 and the M estimate based on the nonparametric model was 0.20.

Introduction

Acronyms:

vonB - von Bertalanffy,
M - natural mortality,
DW - SEDAR 18 Data Workshop,
DWR - SEDAR 18 Data Workshop Report,
SR - southern region,
NR - northern region,

A standard von Bertalanffy (vonB) growth curve was used to model length-at-age growth data for Atlantic red drum (see Section 2.7 in SEDAR 18 Data Workshop Report, DWR). A weighted least squares approach was used for estimation, with the weighting designed to better fit older ages. Other models investigated (a 4 parameter model, and a double von Bertalanffy model) did not converge or resulted in some insignificant parameter estimates, and the standard vonB model was considered to be sufficient. One of the uses of the growth model was to estimate natural mortality (M) at age using the scaled Lorenzen method (see Section 2.4.1,2 SEDAR 18 DWR).

However, there is evidence of model misfit, particularly for the northern region Atlantic red drum stock (see Figure 2.17.1 in DWR). Model predicted lengths are at the “edge” of the data distribution for ages near 6 and 13. The data suggest more rapid growth than the vonB model for the first 5-7 years, and perhaps slower growth rates thereafter.

In this working paper we use nonparametric smooth monotone regression to better fit growth data for both the southern region (SR) and northern region (NR) Atlantic red drum stocks, and evaluate the impact of using this alternative growth model on estimates of M .

Methods

The individual growth measurements used in the SEDAR 18 DW were obtained for analysis. This is large data set, with 8 671 observations for the NR stock, and 26 041 observations for the SR stock. The data are shown in Figures 2.17.1 and 2.17.2 in the DWR.

The vonB model was estimates using unweighted least squares and the *nls()* function in the R statistical software package. Any length-at-age model should be monotone increasing and smooth as a function of age. For example, the standard vonB model has these properties. To better fit the red drum data we also used the *smooth.monotone()* function provided in the R package *fda* (functional data analysis). This is a spline based method that uses a type of monotone link function for smooth monotone regression. Its genesis was for fitting human growth data.

The growth data had a fairly simple structure so we selected a small number (8) of knots for the spline regression at points where the curvature seemed larger. We set the smoothing parameter (λ) equal to 10, although we tested several values and the growth estimates were largely insensitive to λ values. This is not unusual for monotone smoothing. Note that two missing values in the SR data had to be removed because *smooth.monotone()* of the version 2.1.0 of the *fda* R package does not accommodate missing values.

The code is provided in the Appendix.

The M estimation steps are:

1. Obtain mid-year length-at-age predictions, $Len(a)$, from the growth model, with ages backshifted by 1/6 to account for the September birthdate assumed for red drum.
2. Convert to weights, using stock-specific weight-length models, which are
 - a. NR: $wt(a) = 0.0000182*(Len(a)^{2.92})$,
 - b. SR : $wt(a) = 0.0000145*(Len(a)^{2.94})$.
3. Compute unscaled $M(a) = 3.69*(Wt(a)^{-0.305})$
4. Compute scaled M , $M_s(a) = -M(a)*\log(0.015)/\sum_a M(a)$

Results

The average lengths-at-age and model growth predictions are shown in Figures 1a and 1b for the NR and SR. Means lengths were computed within integer age classes (1a, and plotted versus mean partial age within the integer age classes. Confidence intervals were based on a normal approximation,

$$CI = \bar{l}_a \pm 2se(\bar{l}_a).$$

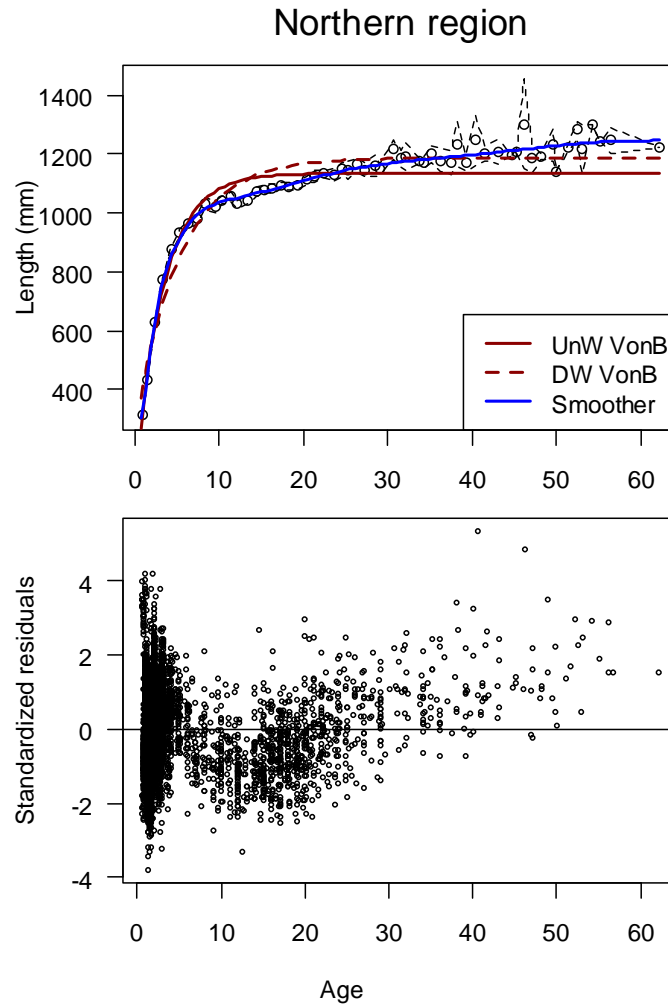


Figure 1a. Top panel: Growth data for the northern region Atlantic red drum stock. Mean lengths are shown as points. The black dashed lines denote approximate 95% confidence intervals. The solid lines denote model estimates using the unweighted von Bertalanffy growth curve (UnW vonB) and a nonparametric smooth monotone regression (Smoother). The brown dashed line shows the vonB predictions using the DW parameter estimates (DW vonB). Bottom panel: Residuals from the unweighted vonB model fitting.

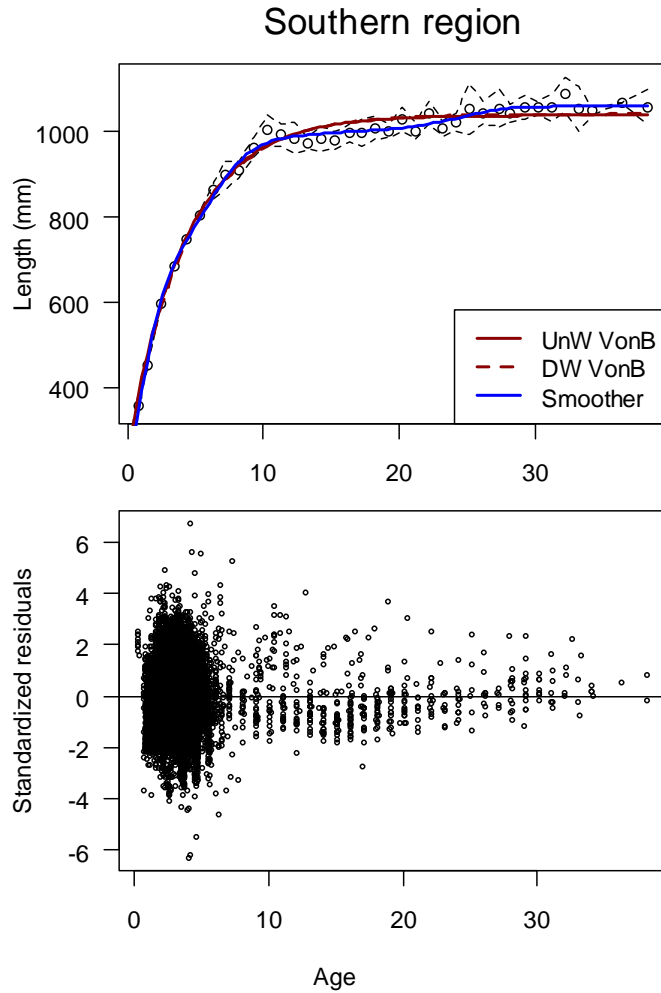


Figure 1b. Top panel: Growth data for the southern region Atlantic red drum stock. Mean lengths are shown as points. The black dashed lines denote approximate 95% confidence intervals. The solid lines denote model estimates using the unweighted von Bertalanffy growth curve (UnW vonB) and a nonparametric smooth monotone regression (Smoother). The brown dashed line shows the vonB predictions using the DW parameter estimates (DW vonB). Bottom panel: Residuals from the unweighted vonB model fitting.

Both the unweighted and DW vonB predictions do not fit the data for ranges of ages in the NR data. For the SR data the unweighted and DW vonB models gave very similar fits, and were good fits to the data. The nonparametric method fit the data closely for both stocks. The unweighted vonB parameter estimates are given in Table 1, along with the DW estimates for comparison purposes.

Table 1. Comparison on the unweighted (UnW) and DW vonB parameter estimates.

	UnW vonB		DW vonB	
	NR	SR	NR	SR
L_{inf}	1134	1039	1186.7	1041.5
K	0.2983	0.2356	0.1913	0.2285
t_0	-0.2461	-0.1120	-1.3027	-1.1377

Scaled estimates of M-at-age are shown in Figures 2a and 2b. They are very similar except at ages 1, and to a lesser extent age 2.

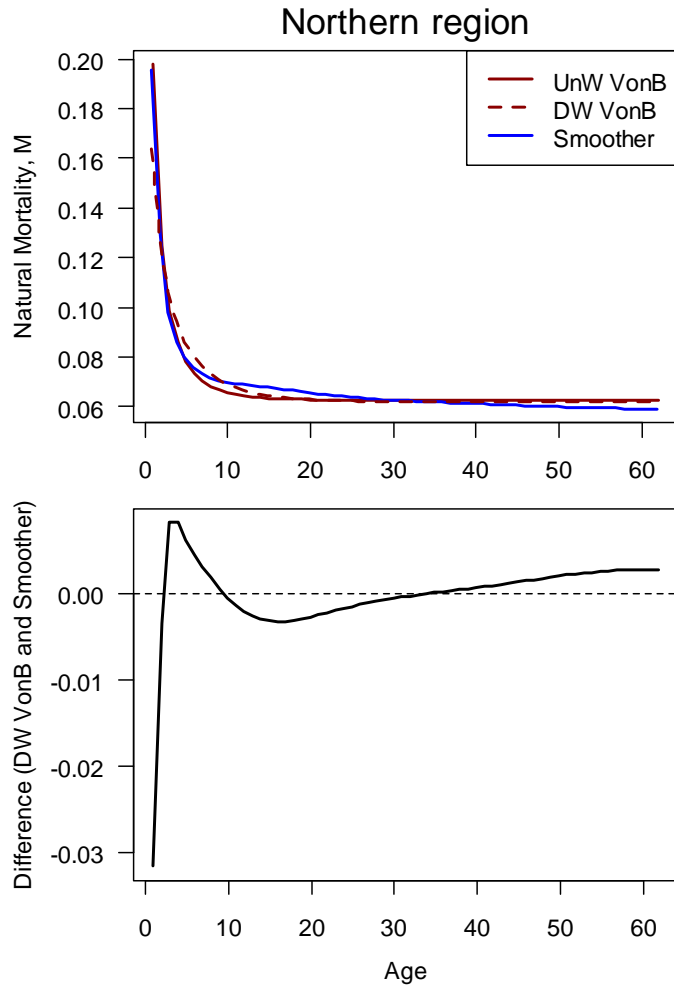


Figure 2a. Top panel: Comparison of scaled Lorenzen estimates of M-at-age for the northern region Atlantic red drum stock based on growth predicted by the von Bertalanffy model (unweighted - solid dark red line, DW – dashed line) and the smooth monotone regression model (blue line). Bottom panel: Differences in M-at-age estimates between the DW vonB and smoother methods.

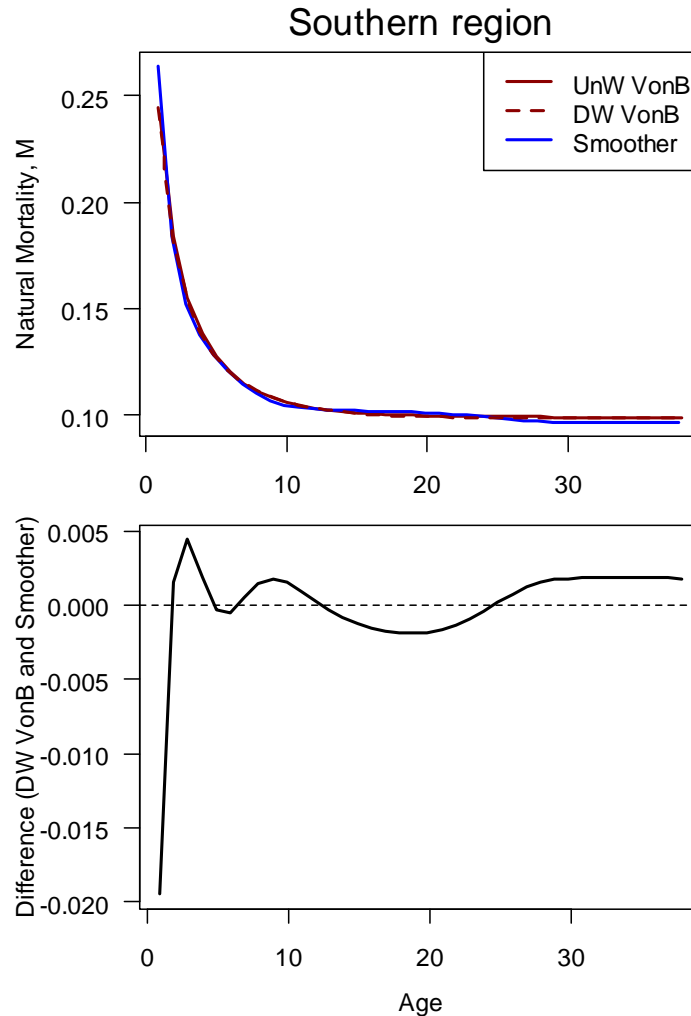


Figure 2b. Top panel: Comparison of scaled Lorenzen estimates of M-at-age for the southern region Atlantic red drum stock based on growth predicted by the von Bertalanffy model (unweighted - solid dark red line, DW – dashed line) and the smooth monotone regression model (blue line). Bottom panel: Differences in M-at-age estimates between the DW vonB and smoother methods.

Discussion

A nonparametric smooth monotone growth model fit the data very well, whereas for the northern region red drum stock the von Bertalanffy did not fit well. However, this smooth monotone growth model did not result in substantial differences in estimates of natural mortality (M) at age based on the scaled Lorenzen method. Largest differences were found at age one, where the DW Lorenzen M estimate based on the von Bertalanffy model predicted length was 0.16 and the M estimate based on the nonparametric model was 0.20

It is not surprising that the simple vonB growth model may not fit the data well for a stock like red drum. Juvenile red drum occur in inshore regions and grow extremely rapidly, especially during the warmer months. However, when the mature (A50=3 for females, and 1.5 for males), red drum move offshore and grow very little. The change in

growth with age is too abrupt for the standard von Bertalanffy curve to accommodate. An alternative approach is provided by Porch et al. (2002).

References

Porch, C. E., Wilson, C. A., and Nieland, D. L. 2002. A new growth model for red drum (*Sciaenops ocellatus*) that accommodates seasonal and ontogenic changes in growth rates. Fish. Bull. **100**: 149-152.

Appendix: R code

```
#read data from Excel Sheets;

#Northern Region ColA-B, Row2:8672
NR.data<-read.delim("clipboard",col.names=c('age','len'),header=F)
#Southern Region ColK-N, Row12:26042
SR.data<-read.delim("clipboard",col.names=c('age','len','n','cv'),header=F)

setwd("give a directory")
require("fda")

#Length-weight conversion parameters;
NR.LW <- c(0.0000182,2.92)
SR.LW <- c(0.0000145,2.94)

NR.DW.vonb <- c(1186.7,0.1913,-1.3027)
SR.DW.vonb <- c(1041.5,0.2285,-1.1377)

#VonB function;
VonB <- function(age,Linf,K,to){
  plen = Linf*(1 - exp(-K*(age - to)));
  return(plen)
}

fit <- function(age,len,Linf,K,to){
  plen <- VonB(age,Linf,K,to)
  resid <- ((len-plen)^2)
  return(resid/(length(plen)-3))}

#Length-Weight function;
LW <- function(parm,Len){
  pwt <- parm[1]*(Len^parm[2])
  return(pwt)
}

# Lorenzen M function;
LM <- function(wt){
  m.us <- 3.69*(wt^(-0.305))
  sc.m <- -log(0.015)/sum(m.us)
  m.s <- m.us*sc.m
  return(m.s)
}
```

```

for(i in c('NR','SR')){

  if(i=='NR'){
    data <- NR.data
    LW.parm <- NR.LW
    vonb.dw <- NR.DW.vonb
    ctext<-c('Northern region')}
  if(i=='SR'){
    data <- subset(SR.data,!is.na(SR.data$len))
    LW.parm <- SR.LW
    vonb.dw <- SR.DW.vonb
    ctext<-c('Southern region')}
  rng <- c(0,max(data$age)) # Range of observations
  age.knots <- c(0,2,4,6,8,10,30,rng[2])
  print(ctext)

  vonbfit <- nls( ~ fit(age,len,Linf,K,to),data = data,
                start = list(Linf = 1800, K = 0.1, to=0),
                trace = TRUE)

  sink(paste(i,"_output.txt",sep=""),type = "output")
  print(ctext)
  print(summary(vonbfit))
  sink()

  vonb.parm <- coef(vonbfit)

  # spline smoother parameters
  lambda <- 10 # smoothing parameter

## spline smoothing code
# First set up a basis for monotone smooth
# We use b-spline basis functions of order 6
# Knots are positioned at the ages in age.knots.
norder <- 6
nage <- length(age.knots)
nbasis <- nage + norder - 2
wbasis <- create.bspline.basis(rng, nbasis, norder, age.knots)

# starting values for coefficient
cvec0 <- matrix(0,nbasis,1)
Wfd0 <- fd(cvec0, wbasis)
# set up functional parameter object
Lfdobj <- 3 # penalize curvature of acceleration
growfdPar <- fdPar(Wfd0, Lfdobj, lambda)

# Smooth the data
result <- smooth.monotone(data$age,data$len, growfdPar)

# Extract the functional data object and regression
# coefficients
Wfd <- result$Wfdobj
beta <- result$beta
## end of spline smoothing code

# Evaluate the fitted height curve over a fine mesh

```



```

age <- seq(min(data$age),max(data$age),length=100)
plen.sm <- beta[1] + beta[2]*eval.monfd(age, Wfd)

# plotting code;

win.metafile(file=paste(i, "_growth.wmf", sep=" "),width=5,height=7)
par(mfrow=c(2,1),oma=c(2,1,2,1),mar=c(3,4,0,0))

plen.vonb <- VonB(age,Linf=vonb.parm[1],K=vonb.parm[2],to=vonb.parm[3])
plen.vonb1 <- VonB(age,Linf=vonb.dw[1],K=vonb.dw[2],to=vonb.dw[3]);# DW assessment fit;
mean.len <- tapply(data$len,floor(data$age),"mean")
ss.len <- tapply(data$len^2,floor(data$age),"mean")
n.len <- tapply(data$len,floor(data$age),"length")
se.len <- sqrt((ss.len - mean.len^2)/n.len)
len.l <- mean.len - 2*se.len
len.u <- mean.len + 2*se.len
mean.age <- tapply(data$age,floor(data$age),"mean")

yl <- c(min(len.l,na.rm=T),max(len.u,na.rm=T))
plot(mean.age,mean.len,ylim=yl,xlab='',ylab='Length (mm)',las=1)
lines(mean.age,len.l,lty=2)
lines(mean.age,len.u,lty=2)
lines(age,plen.vonb,lty=1,col='darkred',lwd=2)
lines(age,plen.vonb1,lty=2,col='darkred',lwd=2)
lines(age,plen.sm,lty=1,col='blue',lwd=2)
legend("bottomright",c("UnW VonB", "DW
VonB", "Smoother"),col=c('darkred', 'darkred', 'blue'),
lty=c(1,2,1),lwd=2)
mtext(side=3,ctext,line=1,cex=1.5)

resid <- data$len - VonB(data$age,Linf=vonb.parm[1],K=vonb.parm[2],to=vonb.parm[3])
std.resid <- resid/sqrt(mean(resid^2))
plot(data$age,std.resid,cex=0.5,ylab='Standardized residuals',xlab='Age',las=1)
abline(h=0,lty=1)
mtext(side=1,'Age',line=0,cex=1,outer=T)

dev.off()

#### Lorenzen Mortalities;

agefine1 <- seq(1,rng[2],by=1) -1/6 # backshifted by 1/6;
plen1.sm <- beta[1] + beta[2]*eval.monfd(agefine1, Wfd)
VonB.predict.len <- VonB(agefine1,Linf=vonb.parm[1],K=vonb.parm[2],to=vonb.parm[3]);
VonB.predict.len2 <- VonB(agefine1,Linf=vonb.dw[1],K=vonb.dw[2],to=vonb.dw[3]); # DW
assessment fit;
wt <- LW(LW.parm,VonB.predict.len) # Weight predicted from VonB length;
wt2 <- LW(LW.parm,VonB.predict.len2) # Weight predicted from VonB length;
wt1 <- LW(LW.parm,plen1.sm) # Weight predicted from smoother;

m.vonb <- LM(wt)
m.vonb2 <- LM(wt2)
m.sm <- LM(wt1)
age <- agefine1+1/6
# write smoother M to file;
write(file=paste(i, "_M.dat", sep=" "),t(cbind(age,m.sm)),ncolumns=2)

# plotting code;

```

```

win.metafile(file=paste(i, "_M.wmf", sep=" "),width=5,height=7)
par(mfrow=c(2,1),oma=c(1,1,2,1),mar=c(3,4,0,0))

y1 <- c(min(m.vonb,m.vonb2,m.sm),max(m.vonb,m.vonb2,m.sm))
plot(age,m.vonb,type='l',col='darkred',lwd=2,ylim=y1,xlab='',
ylab='',las=1)
lines(agefine1,m.sm,lty=1,col='blue',lwd=2)
lines(agefine1,m.vonb2,lty=2,col='darkred',lwd=2)
mtext(side=2,line=3.5,outer=F,'Natural Mortality, M')
legend("topright",c("UnW VonB","DW VonB","Smoother"),col=c('darkred','darkred','blue'),
lty=c(1,2,1),lwd=2)
mtext(side=3,ctext,line=0.5,cex=1.5)

plot(agefine1,m.vonb2-m.sm,type='l',lwd=2,xlab='',ylab='',las=1)
abline(h=0,lty=2)
mtext(side=2,line=3.5,outer=F,'Difference (DW VonB and Smoother)')
mtext(side=1,line=2.5,outer=F,'Age')
dev.off()
}

```