Supplement S1. Worked example for the analysis of growth variation in biological hard parts.

Morrongiello, J.R.[1,2], & Thresher, R.E.[1] A statistical framework to explore ontogenetic growth variation among individuals and populations: a marine fish example. Ecological Monographs

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Here we present worked examples for the analyses presented in the article. Executable R code is provided in Supplement S2 and datasets in Supplement S3 and S4. We refer the reader to Table 2 in the article for parameter descriptions and Table 3 for formal model descriptions and the paper text for model interpretation. The online supplementary material presented by Weisberg et al. (2010) provides additional R code and functions for performing mixed effect analyses on growth increment data. In especial, they provide code for a function called ‘`growthFrame`’ that translates ‘wide format’ measurements into the ‘long’ format required by the ‘lmer’ function in R. This function also automates the addition of Age and Year values to each increment measurement, which are essential for the following analyses.

Packages used:

```
> library(lme4)
> library(AICcmodavg)
> library(effects)
> library(lattice)
> library(plyr)
```

The data underpinning analyses presented in the manuscript are derived from the Southern and Eastern Scalefish and Shark Fishery and as such their reproduction is limited by commercial confidentiality. Therefore, we provide an example data set in Supplement S3 (‘S3 within zone example data.csv’) based on 200 randomly selected individuals from across the seven fishery zones to illustrate our below analyses. To read the data into R from a defined working directory (see `?setwd`) and explore its structure:

```
> Data<-read.csv('within zone example data.csv')
> head(Data)
    FishID sex AAC Cohort Age Year Increment     Temp
1 fish1014   F   6   2004   2 2005     0.283 14.66527
2 fish1014   F   6   2004   3 2006     0.282 14.48516
3 fish1014   F   6   2004   4 2007     0.234 14.79234
4 fish1014   F   6   2004   5 2008     0.192 14.52392
5 fish1014   F   6   2004   6 2009     0.195 14.52599
6 fish1066   F   5   2005   2 2006     0.300 15.67758
> str(Data)
'data.frame':   739 obs. of  8 variables:
 $ FishID   : Factor w/ 200 levels "fish1014","fish1066",..: 1 1 1 1 1 2 2
2 2 3 ...
```

```
 $ sex      : Factor w/ 2 levels "F","M": 1 1 1 1 1 1 2 2 2 2 ...
 $ AAC      : int  6 6 6 6 6 5 5 5 5 5 ...
 $ Cohort   : int  2004 2004 2004 2004 2004 2005 2005 2005 2005 1994 ...
 $ Age      : int  2 3 4 5 6 2 3 4 5 2 ...
 $ Year     : int  2005 2006 2007 2008 2009 2006 2007 2008 2009 1995 ...
 $ Increment: num  0.283 0.282 0.234 0.192 0.195 ...
 $ Temp     : num  14.7 14.5 14.8 14.5 14.5 ...
```

‘`Head`’ returns the first six lines of `Data` and ‘`str`’ its structure. We see that there are 739 observations and eight variables in this data set. The first column contains a categorical variable called FishID which has 200 levels. These correspond to the 200 fish in the sample. Each fish has an associated sex (‘M; and ‘F’), AAC (age-at-capture) and Cohort (year spawned) that are repeated across all increment measurements (Increment, in mm) for that individual. Each increment also has an associated age (Age) and year (Year) of formation as well as an estimate of annual average bottom temperature (Temp).

The individual growth trajectories can be visualised using the ‘`xyplot`’ from the ‘*lattice*’ package.

```
> xyplot(Increment ~ Age, group=FishID, Data, type=c('l','p'))
```

Here, we plot each fish’s increment measurements as a function of age. The ‘group’ argument ensures that data from each fish are associated and the ‘type’ argument plots both lines (‘l’) and points (‘p’).

Centring continuous variables prior to analysis aids in model convergence (especially with complex structures) and the interpretation of random slopes, interactions and polynomial terms. Therefore, I specify a function called ‘`c.`’ that centres existing variables within a model:

```
> c. <- function (x) scale(x, scale = FALSE)
```

Alternatively, this can be achieved by creating a scaled variable in the data.frame using the ‘`scale`’ function in the ‘*base*’ package.

It is also advisable to create new factor variables for random effects. ‘`lmer`’ in the ‘*lme4*’ package automatically treats random intercepts as factors (e.g. if your fish identifiers are numbers), but it helps with plotting to do it beforehand. FishID is already a factor, so here we convert Year and Cohort into new factorial variables:

```
> Data$fYear <- factor(Data$Year)
> Data$fCohort <- factor(Data$Cohort)
```

Within zone models- random effect structures

We first fit a series of models of increasing random effect complexity to the data. At this stage, all models included the full intrinsic fixed effect parameteriation of *Age* * *Sex* + *Age-at-capture* (AAC) (Zuur et al. 2009). *Age* and *age-at-capture* were log-transformed to satisfy model assumptions. These models are fit with REML (default for lmer, could also be specified with call ‘`REML=TRUE`’ within model). See ‘within zone models’ section in R code file (Supplment S2).

M1a: random intercept for FishID

```
> M1a<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (1|FishID),Data)
```

M1b: random slope and intercept for FishID and Age

```
> M1b<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID),Data)
```

Models were compared using AICc. This was achieved using the ‘aictab’ function from the ‘AICcmodavg’ package. ‘aictab’ requires a candidate list of models, a list of model names and asks whether you would like the results sorted in terms of ΔAICc.

```
##specify model list

> models<-list(M1a,M1b)

##specify model names

> Modnames <- c('M1a ', 'M1b ')

##return AICc model selection table:

> aictab(cand.set = models, modnames = Modnames, sort = TRUE)
```

```
Model selection based on AICc :

     K  AICc Delta_AICc AICcWt Cum.Wt Res.LL
M1b  9 29.19       0.00      1      1  -5.47
M1a  7 43.82      14.63      0      1 -14.83
```

AICc indicates that M1b is the better model.

M2a: random slope and intercept for FishID and Age, and random intercept for Year

```
> M2a<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|fYear), Data)
```

M2b: random slope and intercept for FishID and Age, and random intercept for Cohort

```
> M2b<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|fCohort), Data)
```

Intra-class correlations

Calculate the intra-class correlation coefficient (temporal growth synchrony, ICC) for either Year or Cohort temporal segregation using the variance estimates from the random intercept models M2a or M2b:

$$ICC_{\gamma|\delta} = \frac{\sigma^2_{\gamma|\delta}}{\sigma^2_{\gamma|\delta} + \sum_{l=1}^{u} \sigma_l^2 + \sigma_e^2} \qquad \text{eq. 1}$$

where $\sigma^2_{\gamma|\delta}$ is the *Year* or *Cohort* random intercept variance, u is the number of random effects in the model, σ_l^2 is the variance component for the *l*th random effect and σ_e^2 is the residual variance.

```
##extract variance components from the model using the ‘VarCorr’ function.
##Number in square brackets specifies particular variance components
required; the full list can be accessed using ‘str(VarCorr(model))’.

##Year random intercept variance

> vYear<-VarCorr(M2a)$fYear[1]

##FishID random intercept variance

> vFishID<-VarCorr(M2a)$FishID[1]

##FishID age slope variance

> vAge<-VarCorr(M2a)$FishID[4]

##age and FishID covariance (can also be estimated by
##corr*(sqrt(vFishID*VAge))

> covar<-VarCorr(M2a)$FishID[2]

##residual variance

> vErr<- (attr(VarCorr(M2a),'sc'))^2

##Calculate ICC for fYear:

> vYear / (vYear + vFishID + vAge + covar + vErr)

##For Cohort ICC, swap the model to M2b and replace ‘fYear’ with ‘fCohort’.
```

Among-individual annual growth correlation in this data set is 9.36%.

Within-cohort annual growth correlation in this data set is 12.68%.

M3a: random slope and intercept for FishID, Year and Age

```
> M3a<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID)+(c.(log(Age))|fYear), Data)
```

M3b: random slope and intercept for FishID, Cohort and Age

```
> M3b<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data)
```

M4a: random slope and intercept for FishID and Age, and random intercepts for Year and Cohort

```
> M4a<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|fYear) + (1|fCohort), Data)
```

M4b: random slope and intercept for FishID, Year and Age, and random intercept for Cohort

```
> M4b<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fYear) + (1|fCohort), Data)
```

M4c: random slope and intercept for FishID, Cohort and Age, and random intercept for Year

```
> M4c<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|fYear) + (c.(log(Age))|fCohort), Data)
```

M4d: random slope and intercept for FishID, Year, Cohort and Age

```
> M4d<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fYear) +
      (c.(log(Age))|fCohort), Data)
```

Models M2a – M4d can be compared using:

```
> models<-list(M2a,M2b,M3a,M3b,M4a,M4b,M4c,M4d)
> Modnames <- c('M2a', 'M2b', 'M3a', 'M3b', 'M4a', 'M4b', 'M4c', 'M4d')
> aictab(cand.set = models, modnames = Modnames, sort = TRUE)
```

```
Model selection based on AICc :

     K  AICc Delta_AICc AICcWt Cum.Wt Res.LL
M3b 12 -3.58       0.00   0.53   0.53  14.00
M4d 15 -1.84       1.74   0.22   0.76  16.25
M4c 13 -1.62       1.96   0.20   0.96  14.06
M4a 11  2.89       6.47   0.02   0.98   9.74
M2b 10  3.75       7.33   0.01   0.99   8.28
M4b 13  5.80       9.38   0.00   1.00  10.35
M2a 10 10.69      14.27   0.00   1.00   4.81
M3a 12 12.15      15.73   0.00   1.00   6.14
```

The best random effect structure is M3b: random age slope for FishID and Cohort.

R^2 for mixed models

Conditional and marginal R2 (R_(LMM(m))^2 and R_(LMM(c))^2) (Nakagawa and Schielzeth 2013) can be calculated using the ‘rsqaured.glmm’ function created by Jon Lefcheck (extract reproduced with permission). For a detailed description of what this function does and further code to derive these R2 values from ‘lmer’ and ‘lme’ models, see Jon’s blog page: (http://jslefche.wordpress.com/2013/03/13/r2-for-linear-mixed-effects-models/).

```
###function to calculate r squares
#Function rsquared.lme requires models to be input as a list (can include
#fixed-effects only models,but not a good idea to mix models of class "mer"
#with models of class "lme")
> rsquared.glmm=function(modlist) {
  do.call(rbind,lapply(modlist,function(i) {
    if(inherits(i,"merMod") | class(i)=="merLmerTest") {
      VarF=var(as.vector(fixef(i) %*% t(i@pp$X)))
      VarRand=colSums(do.call(rbind,lapply(VarCorr(i),function(j) j[1])))
      VarResid=attr(VarCorr(i),"sc")^2
      Rm=VarF/(VarF+VarRand+VarResid)
      Rc=(VarF+VarRand)/(VarF+VarRand+VarResid)
      Rsquared.mat=data.frame(Class=class(i),Marginal=Rm,Conditional=Rc,
      AIC=AIC(update(i,REML=F))) }
     else { print("Function requires models of class lm, lme, mer, or
merMod")
} } ) ) }
```

Conditional and marginal R2 values can be returned using the list specified above (order as per specified in ‘models’):

```
> rsquared.glmm(models)
    Class  Marginal Conditional       AIC
1 lmerMod 0.7007897   0.7927402 -16.45144
2 lmerMod 0.6611263   0.7757749 -22.89028
3 lmerMod 0.7012019   0.7926963 -14.77326
4 lmerMod 0.6715236   0.7841021 -29.70404
5 lmerMod 0.6764365   0.7824398 -23.91833
6 lmerMod 0.6612290   0.7794110 -25.36365
7 lmerMod 0.6733920   0.7849511 -27.84531
8 lmerMod 0.6750526   0.7866787 -25.62351
```

Random effect plots

Plots of the fYear and fCohort random effects (similar to figure 3 in manuscript) can be generated by extracting BLUPs for each of these terms from models just including either fYear or fCohort. Here, we chose M2a as the best ‘just year’ model and M3b as the best ‘just Cohort’ model (based on AICc from model selection table above). Random intercepts can still be interpreted even in the presence of random slopes (Weisberg et al. 2010). These BLUPs and their standard errors are extracted using the following code:

```
##for fYear

> (year.M2a<-ranef(M2a)$fYear[,1])###extracts the Year random effects
(BLUPs)
> (year.se.M2a<-sqrt (attr(ranef(M2a,postVar=TRUE)
      [["fYear"]],"postVar")[1,1,]))#####gets BLUP SE for each year

##create a new data frame with BLUPs, upper and lower SEs by Year
> M2ayear<-data.frame(y=year.M2a)##add BLUPs
> M2ayear$upper<-(M2ayear$y+year.se.M2a)##upper bound
> M2ayear$lower<-(M2ayear$y-year.se.M2a)##lower bound
> M2anew <- data.frame(year = (as.numeric(levels(Data$fYear))))##add years
> M2adata<-cbind(M2anew,M2ayear)##bring it all together

##for fCohort

> (Cohort.M3b<-ranef(M3b)$fCohort[,1])#extracts Cohort random effects
#(BLUPs)
> (Cohort.se.M3b <-sqrt (attr(ranef(M3b,postVar=TRUE)
      [["fCohort"]],"postVar")[1,1,]))#####gets BLUP SE for each year

##create a new data frame with BLUPs, upper and lower SEs by Cohort
> M3bCohort<-data.frame(y=Cohort.M3b)
> M3bCohort $SE<-( Cohort.se.M3b)##specify SEs
> M3bCohort $upper<-(M3bCohort$y+Cohort.se.M3b)
> M3bCohort $lower<-(M3bCohort$y-Cohort.se.M3b)
> M3bnew <- data.frame(Cohort = (as.numeric(levels(Data$fCohort))))
> M3bdata<-cbind(M3bnew,M3bCohort)
```

To plot a two panel figure of Year and Cohort random effects (± 1 SE):

```
##set up panels
```

```
> par(mfrow=c(2,1))
##plot year
> plot(range(M2anew$year), range(M2ayear), type = "n", ann =
      FALSE,axes=F,xlim=c(1970,2010))
> axis((1),las=1,tcl=-.2,cex.axis=1,xaxp=c(1970,2010,4),mgp=c(3,.4,0))
> axis((2),las=1,tcl=-.2,cex.axis=1,mgp=c(3,.4,0))
> box(bty='l')

> CI.U <- M2ayear[, "upper"]
> CI.L <- M2ayear[, "lower"]

# Create a 'loop' around the x values. Add values to 'close' the loop
> X.Vec <- c(M2anew$year, tail(M2anew$year, 1), rev(M2anew$year),
      M2anew$year[1])
# Same for y values
> Y.Vec <- c(CI.L, tail(CI.U, 1), rev(CI.U), CI.L[1])
# Use polygon() to create the enclosed shading area
# We are 'tracing' around the perimeter as created above
> polygon(X.Vec, Y.Vec, col = "grey", border = NA)
# Use matlines() to plot the fitted line and CI's
# Add after the polygon above so the lines are visible
> matlines(M2anew$year,M2ayear, lty = c(1, 2, 2), type = "l", col =
      c("black", "", ""),lwd=1.5)
> points(M2adata$year,M2adata$y,pch=16,cex=.8)
> lines(c(1950,2010),c(0,0),lwd=1,lty=2)
> mtext('predicted growth (mm)',side=2,cex=1,line=2.5)
> mtext('Year',side=1,cex=1,line=2.5)
> mtext('Year random effect',side=3,cex=2,line=2)
##plot cohort
##specify a function called xy.error.bars that has 4 components (xbar,
##ybar, x and y)
> xy.error.bars<-function (xbar,ybar,x,y){
      plot(x, y, pch=16,cex=1,axes=FALSE,ylab='',xlab='',ylim=c(-.25,.25),
      xlim=c(1970,2010))
      arrows(x, y-yb, x, y+yb, code=3, angle=90, length=0,lwd=1)
      axis((1),las=1,tcl=-.2,mgp=c(3,.4,0))
      axis((2),las=2,tcl=-.2,mgp=c(3,.4,0))
      box(bty='l')
}
> x<-M3bdata$Cohort##specify the x data
> y<- M3bdata$y##specify the y data
> xb<-c('')##specify x error bars- not used here so left blank
> yb<- M3bdata$SE##specify the data to be used for the y error bars (this
##is called by the ‘arrows’ above
> xy.error.bars(xb,yb,x,y)
> lines(c(1960,2010),c(0,0),lwd=1,lty=2)
> mtext('Cohort',side=1,line=2.5,cex=1)
> mtext('predicted growth (mm)',side=2,cex=1,line=2.5)
> mtext('Cohort random effect',side=3,cex=2,line=2)
```

Within zone models- intrinsic effect structures

Once an optimum random effect structure is selected (in this case M3b), we investigate fixed intrinsic sources of growth variation. Six models are fit with maximum likelihood ML (REML=F).

```
> M3b1<- lmer (log(Increment) ~ c.(log(Age)) + (c.(log(Age))|FishID) +
      (c.(log(Age))|fCohort), Data, REML=F)
> M3b2<- lmer (log(Increment) ~ c.(log(Age)) + sex + (c.(log(Age))|FishID)
      + (c.(log(Age))|fCohort), Data, REML=F)
> M3b3<- lmer (log(Increment) ~ c.(log(Age)) + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=F)
> M3b4<- lmer (log(Increment) ~ c.(log(Age)) * sex + (c.(log(Age))|FishID)
      + (c.(log(Age))|fCohort), Data, REML=F)
> M3b5<- lmer (log(Increment) ~ c.(log(Age)) + sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=F)
> M3b6<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=F)
> models<-list(M3b1,M3b2,M3b3,M3b4,M3b5,M3b6)
> Modnames <- c('M3b1','M3b2','M3b3','M3b4','M3b5','M3b6')
> aictab(cand.set = models, modnames = Modnames, sort = TRUE)
Model selection based on AICc :
     K   AICc Delta_AICc AICcWt Cum.Wt    LL
M3b1  9 -32.87       0.00   0.37   0.37 25.56
M3b3 10 -31.75       1.12   0.21   0.58 26.03
M3b2 10 -31.20       1.67   0.16   0.74 25.75
M3b4 11 -30.51       2.37   0.11   0.85 26.43
M3b5 11 -29.97       2.90   0.09   0.94 26.17
M3b6 12 -29.27       3.60   0.06   1.00 26.85
```

The best intrinsic effect structure is M3b1: growth is related to just age just Age. This model is refitted with REML to get unbiased parameter estimates (Zuur et al. 2009).

```
> M3b1reml<- lmer (log(Increment) ~ c.(log(Age)) + (c.(log(Age))|FishID) +
      (c.(log(Age))|fCohort), Data, REML=T)
```

The Age fixed effect can now be plotted. We use the ‘`Effect`’ function from the ‘*effects*’ package to generate model predictions across a range of ages (specified by the ‘xlevels’ argument). See the ‘Effect’ help page for more options. These predictions (with SEs and 95% CIs) are extracted to a data frame, the log-transformed growth predictions converted back to their original scale and then plotted using a xy error plot. We choose this graphical approach as whilst Age is continuous, values only take whole numbers.

To produce a plot with 95% confidence intervals:

```
> ageplot<- as.data.frame (Effect (c('Age'), M3b1reml, xlevels = list
      (Age=seq(2,15,by=1))))##extract model predictions to data frame
      ##called ageplot
> ageplot$transfit<-exp(ageplot$fit) ##back transform fitted values to
      ##original scale
> ageplot$transupper<-exp(ageplot$upper) ##transform upper CI
> ageplot$transCI<-ageplot$transupper-ageplot$transfit ##calculate value to
      ##be plotted as y error bar by subtracting upper CI from fit
> xy.error.bars<-function (xbar,ybar,x,y){
> plot(x, y, pch=16, cex=1, ljoin=2, axes=FALSE, ylab='', xlab='',
      xlim=c(2,15), ylim=c(0,.5))
> arrows(x, y-yb, x, y+yb, code=3, angle=90, length=0,lwd=1)
```

```
> axis((1),las=1, tcl=-.2, mgp=c(3,.4,0), xaxp=c(2,18,4), cex.axis=1)
> axis((2),las=2, tcl=-.2, mgp=c(3,.4,0), yaxp=c(0,.6,3), cex.axis=1)
> box(bty='l')}
> x<-ageplot$Age
> y<-ageplot$transfit
> xb<-c('')
> yb<-ageplot$transCI
> xy.error.bars(xb,yb,x,y)
> lines(x,y,lty=2)
> mtext('age',side=1,line=1.5,cex=1)
> mtext('predicted growth (mm)',side=2,line=2.5,cex=1)
```

Within zone models- extrinisc effect structures

We can now use this optimal intrinsic effects model to investigate how extrinsic factors (e.g. temperature) affect growth. We extend M3b1 to include a temperature term:

```
 > M3b7<- lmer (log(Increment) ~ c.(log(Age)) + c.(Temp) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=F)
> models<-list(M3b1,M3b7)
> Modnames <- c('M3b1','M3b7')
> aictab(cand.set = models, modnames = Modnames, sort = TRUE)
```

```
Model selection based on AICc :

      K   AICc Delta_AICc AICcWt Cum.Wt    LL
M3b7 10 -36.43       0.00   0.86   0.86 28.37
M3b1  9 -32.87       3.56   0.14   1.00 25.56
```

There is evidence for a negative temperature effect in this example data set. We refit M3b7 with REML to get parameter estimates and temperature effect plot (using the ‘`Effect`’ function).

```
> M3b7reml<- lmer (log(Increment) ~ c.(log(Age)) + c.(Temp) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=T)
> tempplot<- as.data.frame (Effect (c('Temp'), M3b7reml,xlevels= 10))
> tempplot$transfit<-exp(tempplot$fit)
> tempplot$transupper<-exp(tempplot$upper)
> tempplot$translower<-exp(tempplot$lower)
##plot temperature effect with 95% CIs (on original scale)
> summary(tempplot)
> plot(transfit ~ Temp, tempplot, type='l',ylim=c(0.135,0.185)) ##ylim
      ensures that the plot region is big enough to display CIs
> lines(transupper ~ Temp, tempplot, lty=2)
> lines(translower ~ Temp, tempplot, lty=2)
```

We can also investigate whether there is a linear (or curve-linear) temporal trend in the growth data by including a Year terms as a fixed effect:

```
> M3b8<- lmer (log(Increment) ~ c.(log(Age)) + c.(Year) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=F)
```

```
> M3b9<- lmer (log(Increment) ~ c.(log(Age)) + c.(Year) + I(c.(Year)^2) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=F)
> models<-list(M3b1,M3b8, M3b9)
> Modnames <- c('M3b1','M3b8', 'M3b9')
> aictab(cand.set = models, modnames = Modnames, sort = TRUE)
Model selection based on AICc :

      K   AICc Delta_AICc AICcWt Cum.Wt    LL
M3b9 11 -50.86       0.00   0.63   0.63 36.61
M3b8 10 -49.78       1.08   0.37   1.00 35.04
M3b1  9 -32.87      17.98   0.00   1.00 25.56
```

Model selection indicates a curve-linear temporal growth trend; growth rates are increasing through time. As for Temperature, we refit the Year model with REML and plot.

```
> M3b9reml<- lmer (log(Increment) ~ c.(log(Age)) + c.(Year) + I(c.(Year)^2)
      + (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=T)
> yearplot<- as.data.frame (Effect (c('Year'), M3b9reml,xlevels= 10))
> yearplot$transfit<-exp(yearplot$fit)
> yearplot$transupper<-exp(yearplot$upper)
> yearplot$translower<-exp(yearplot$lower)
##plot Year effect with 95% CIs (on original scale)
> summary(yearplot)
> plot(transfit ~ Year, yearplot, type='l',ylim=c(0.1,0.29)) ##ylim ensures
      ##that the plot region is big enough to display CIs
> lines(transupper ~ Year, yearplot, lty=2)
> lines(translower ~ Year, yearplot, lty=2)
```

Within versus among individual variation

We can partition Temperature into two components using within subject centring (van de Pol and Wright 2009) and the ‘`ave`’ (from ‘*stats*’ package), ‘`ddply`’ (from ‘*plyr*’ package) and ‘`transform`’ (from ‘*base*’ package) functions. We create new variables for the mean temperature experienced by an individual across its lifetime (amongIDV) and the deviation of each observation from the individual-specific mean (withinIDV).

```
> Data$amongIDV<-ave(Data$Temp,Data$FishID)
> Data<-ddply(Data, .(FishID), transform, withinIDV = scale(Temp,scale=F))
```

These new variables can now be fit to the growth data. The first step is to see whether there is evidence of individual-specific differences in temperature reaction norms (fitting random withinIDV slope for each FishID).

M8: within and among individual temperature- just fixed effects

```
> M8<- lmer (log(Increment) ~ c.(log(Age)) + c.(amongIDV) + c.(withinIDV)+
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=T)
```

M9: within and among individual temperature- with random within slope

```
> M9<- lmer (log(Increment) ~ c.(log(Age)) + c.(amongIDV) + c.(withinIDV)+
      (c.(log(Age))|FishID) + (c.(withinIDV) |FishID) +
      (c.(log(Age))|fCohort), Data, REML=T)
##the random age and withinIDV slopes are uncorrelated
> models<-list(M8,M9)
> Modnames <- c('M8','M9')
```

```
> aictab(cand.set = models, modnames = Modnames, sort = TRUE)
Model selection based on AICc :

    K   AICc Delta_AICc AICcWt Cum.Wt Res.LL
M8 11 -13.73       0.00   0.96   0.96  18.05
M9 14  -7.51       6.22   0.04   1.00  18.04
```

There is no evidence of individual-specific reaction norms. An inspection of the model output for M8 suggests that the majority of the negative population-level temperature effect (from M3b7reml) is due to among-individual differences in lifetime temperature. We can test whether the amongIDV and withinIDV effects differ from each other in magnitude or direction by fitting:

```
> M8a<- lmer (log(Increment) ~ c.(log(Age)) + c.(Temp) + c.(amongIDV) +
      (c.(log(Age))|FishID) + (c.(log(Age))|fCohort), Data, REML=T)
```

This suggests that there is in fact little difference between among and within individual growth responses (albeit both a weak in example data set). See van de Pol and Wright (2009) for further discussion on interpreting these model outputs.

Across zone models

As with the within-zone analyses, the data underpinning analyses presented in the manuscript are derived from the Southern and Eastern Scalefish and Shark Fishery and as such their reproduction is limited by commercial confidentiality. Therefore, we provide an example data set in Supplement S4 (‘S4 among zone example data.csv’) based on 1000 randomly selected individuals from across the seven fishery zones to illustrate our below analyses. We assigned these fish to 10 fishing zones (A to J).

```
> Data2<-read.csv('among zone example data.csv')
> head(Data2)
> str(Data2)
```

Convert Year and Cohort into factors:

```
> Data2$fYear <- factor(Data2$Year)
> Data2$fCohort <- factor(Data2$Cohort)
```

In Supplement S5 (‘S5 example temperature.csv’) we have generated temperature time series for each zone, with average temperatures ranging from 12 to 16.5 degrees.

```
> Temperature<-read.csv('example temperature.csv')
```

Having the temperature data in a separate file allows us to calculate temperature normals (averages) and temperature anomalies for each zone before we merge these to the increment data set. We use code similar to that for creating amongIDV and withinIDV above:

```
Temperature$normal<- ave(Temperature$Temp,Temperature$zone)
Temperature<- ddply(Temperature, .(zone), transform, anomaly =
scale(Temp,scale=F))
```

We merge the increment and temperature data frames

```
Data2<- merge(Data2, Temperature)
```

Now we can explore different random effect structures for the among-zone data. Below are sixteen models of varying random slope and random intercept complexity (ranging from model 5 to model 6 in table 2). The R mixed effects model wiki provides a detailed explanation of random effect formulation http://glmm.wikidot.com/faq.

```
> M5a<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) +
      (c.(log(Age))|zone) + (c.(log(Age))|zone:fCohort), Data2)
> M5b<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (c.(log(Age))|zone) +
      (c.(log(Age))|zone:fCohort), Data2)
> M5c<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) + (1|zone) +
      (c.(log(Age))|zone:fCohort), Data2)
> M5d<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (1|zone) +
      (c.(log(Age))|zone:fCohort), Data2)
> M5e<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) +
      (c.(log(Age))|zone) + (1|zone:fCohort),Data2)
> M5f<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (c.(log(Age))|zone) +
      (1|zone:fCohort), Data2)
> M5g<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) + (1|zone) +
      (1|zone:fCohort), Data2)
> M5h<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (1|zone) + (1|zone:fCohort),
      Data2)
> M5i<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) +
      (c.(log(Age))+c.(log(AAC))|zone) + (c.(log(Age))|zone:fCohort),
      Data2)
> M5j<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (c.(log(Age)) +
      c.(log(AAC))|zone) + (c.(log(Age))|zone:fCohort), Data2)
> M5k<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) +
      (c.(log(AAC))|zone) + (c.(log(Age))|zone:fCohort), Data2)
> M5l<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) + (c.(log(Age)) +
      c.(log(AAC))|zone) + (1|zone:fCohort), Data2)
> M5m<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (c.(log(AAC))|zone) +
      (c.(log(Age))|zone:fCohort), Data2)
> M5n<- lmer( log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (c.(log(Age)) +
      c.(log(AAC))|zone) + (1|zone:fCohort), Data2)
> M5o<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (c.(log(Age))|zone:fYear) +
      (c.(log(AAC))|zone) + (1|zone:fCohort), Data2)
> M5p<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (c.(log(AAC))|zone) +
      (1|zone:fCohort), Data2)
models<-list(M5a, M5b, M5c, M5d, M5e, M5f, M5g, M5h, M5i, M5j, M5k, M5l,
M5m, M5n, M5o, M5p)
Modnames <- paste("M5", letters[1:16], sep = "")##letters[1:16] equals a:p
aictab(cand.set = models, modnames = Modnames, sort = TRUE)
Model selection based on AICc :
```

```
      K   AICc Delta_AICc AICcWt Cum.Wt Res.LL
M5h 12 143.52       0.00   0.42   0.42 -59.72
M5d 14 145.02       1.51   0.20   0.61 -58.46
M5g 14 145.02       1.51   0.20   0.81 -58.46
M5f 14 147.54       4.03   0.06   0.86 -59.72
M5b 16 149.06       5.54   0.03   0.89 -58.46
M5e 16 149.06       5.54   0.03   0.92 -58.46
M5c 16 149.06       5.54   0.03   0.94 -58.46
M5o 16 149.06       5.54   0.03   0.97 -58.46
M5m 16 149.06       5.55   0.03   0.99 -58.46
M5k 18 154.03      10.52   0.00   1.00 -58.93
M5n 17 155.24      11.73   0.00   1.00 -60.54
M5j 19 155.49      11.98   0.00   1.00 -58.65
M5p 14 156.80      13.28   0.00   1.00 -64.34
M5a 18 159.63      16.12   0.00   1.00 -61.73
M5l 19 170.77      27.25   0.00   1.00 -66.29
M5i 21 173.60      30.08   0.00   1.00 -65.68
```

The best among-zone random effect structure is the simplest M5h: random intercepts for zone and FishID (the latter with a random Age slope) and Year and Cohort nested within zone.

You may receive a warning on some of these models regarding a convergence failure. This is likely due to the underlying data (randomised) not supporting the complexity of models being fit. The number of iterations can be increased by adding the below code to the model call, or alternatively simpler models can be fit:

```
control=lmerControl(optCtrl=list(maxfun=20000))
```

Model M5h can be extended to include different combinations of temperature normals and anomalies, including polynomials. The most complex is:

```
> M5h1<- lmer (log(Increment) ~ c.(log(Age)) * sex + c.(log(AAC)) +
      c.(normal) + I(c.(normal)^2) + c.(anomaly) + I(c.(anomaly)^2) +
      (c.(log(Age))|FishID) + (1|zone:fYear) + (1|zone) + (1|zone:fCohort),
      Data2)
```

References

van de Pol, M. V., and J. Wright. 2009. A simple method for distinguishing within- versus between-subject effects using mixed models. Animal Behaviour **77**:753-758.

Weisberg, S., G. Spangler, and L. S. Richmond. 2010. Mixed effects models for fish growth. Canadian Journal of Fisheries and Aquatic Sciences **67**:269-277.

Zuur, A. F., E. N. Ieno, N. J. Walker, A. A. Saveliev, and G. M. Smith. 2009. Mixed Effects Models and Extensions in Ecology with R. Springer, New York, USA.