Supplement for: Temperature-induced within-species variation in growth and reproduction revealed by an energy-based model

**Hui-Yu Wang, Hideyasu Shimadzu, Hsiu-Chin Lin, Ulf Dieckmann, Mikko Heino, Yongjun Tian\*, and Peng Sun\***

This supplement file provides some lines of essential R code used for the paper.

**Required packages**

library(bbmle)

library(faraway)

### Data preparation

data0 = read.table("Cutlassfish\_combined\_data\_2021.txt",header=TRUE,na.strings="NA")

data0$soma = data0$total\_w-data0$gonad\_w

data0$soma[which(is.na(data0$soma))] = data0$total\_w[which(is.na(data0$soma))]

#soma wt = total wt for immature fish

data0$soma1 = data0$soma/53.25 #normalize soma weight by average somatic weight at age 2

### Estimation of age-at-50 % maturity

##mean A50 for all stocks

mod1 = glm(I(maturity=="M")~round(age),family=binomial,data=data0)

A50\_all = (log(1)-mod1$coef[1]) /mod1$coef[2]

### Parameter estimation

## the model form of somatic growth, w\_t

w = function(a, alp, t, w0){

(w0^(1-alp) + a\*(1-alp)\*t)^{1/(1-alp)}

}

ssr0 = function(a, alp){

t = round(age)

s = soma1

w0 = mean(s[t==0], na.rm=T)

ry = log(s) - log(w(a, alp, t+0.5, w0))

sum(ry^2, na.rm=T)

}

################

## fitting a soma model for each location

################

results = list()

loc = levels(data0$site)

for(i in 1:length(loc)){

results[[i]] = mle2(ssr0, start=list(a=1,alp=0.5), data=subset(data0, site==loc[i]), lower = c(a=0.0001,alp=0.0001), upper=c(a=20,alp=0.999), method="L-BFGS-B")

}

## the estimated parameters: a and alpha

names(results) = loc

sapply(results, coef)

asite = c(0.939,0.928,0.743,0.965,0.884)

alpsite = c(0.89,0.84,0.882,0.859,0.957)

## the model form of gonadic growth, g\_t

g = function(gam,b, t){

a = asite[i]

alp = alpsite[i]

if(t>=1){

wt = w(a, alp, t, w0)

wt1 = w(a, alp, t-1, w0)

(b/(a\*(1-alp + gam)))\*(wt^(1-alp+gam)-wt1^(1-alp+gam))}

else 0

}

ssr1 = function(gam,b){

t = round(age)

z = gonad\_w /53.25 #standardize gt

rg = log(z) - log(g(gam,b,t+0.5))

sum(rg^2,na.rm=T)

}

################

## fitting a gonadic model for each location

################

results\_b = list()

for(i in 1:length(loc)){

locdata = subset(data0, site==loc[i])

s = locdata$soma1

w0 = mean(s[round(locdata$age)==0], na.rm=T)

results\_b[[i]] = mle2(ssr1, start=list(gam=1.2,b=0.01), data=subset(locdata,maturity=="M"),lower = c(gam=0.0001,b=0.0001), upper=c(gam=20,b=20), method="L-BFGS-B")

}

## the estimated parameters: b and gamma

names(results\_b) = loc

sapply(results\_b, coef)