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

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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)
}
################
```

```r
## 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)
```