Supplemental Appendix B for ‘Museum specimens reveal life history variation in *Plethodon montanus*’ by Caruso and Rissler.

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**Table S1** Growth model parameters and descriptions

|  |  |
| --- | --- |
| Model parameters | Description |
| alpha | Alpha parameter for lost lag model |
| beta | Beta parameter for lost lag model |
| tau | Precision lost lag model |
| sigma.t | Standard deviation for lost lag model |
| a[1-5] | Site-specific asymptotic size |
| age0[1-5] | Site-specific age where size equals zero |
| k[1-5] | Site-specific growth rate |
| gamma | VB growth precision |
| sigma.g | Standard deviation for VB growth model |

**Table S2** Data and descriptions

|  |  |
| --- | --- |
| Name | Description |
| n.LL | Number of individuals for lost lag model |
| visible.lags | Number of visible LAGs for each individual |
| lags | Number of LAGs for individuals without bone resporption |
| pred.lags | Predicted number of LAGs |
| ALL | Number of individuals for VB growth model |
| site | Site identity |
| SITES | Number of sites |

### Growth model code

 model{
 ######## LOST LAG PRIORS ###################

 alpha.LL ~ dunif(0, 10)
 beta.LL ~ dunif(0, 10)

 tau <- pow(sigma2.t, -2)
 sigma.t ~ dunif(0, 5)

 ######## VB GROWTH PRIORS ###################

 for(s in 1:SITES){
 a[s] ~ dunif(50.0, 80.0)
 age.0[s] ~ dunif(-10, -0.01)
 logk[s] ~ dnorm(0, 0.01)
 }

 gamma <- pow(sigma.g, -2)
 sigma.g ~ dunif(0, 5)

 ######## PREDICTED VARIABLES ###############
 # Predict lost lags based on inner most LAGS

 for(i in 1:ALL){
 xx[i] <- inner.lag[i]/alpha.LL
 yy[i] <- 1/beta.LL
 zz[i] <- pow(xx[i], yy[i])
 lag.predict[i] <- exp(zz[i])-1
 trunc.lag.predict[i] <- trunc(lag.predict[i])
 # only integers - conservative round down
 pred.lags[i] <- visible.lags[i] + (trunc.lag.predict[i]\*lags.to.add[i])
 # only add to ones that lost lags
 } #i

 ######## LOST LAG MODEL ##################

 # Power relationship between lags and femur area (no lags lost)
 for(i in 1:n.LL){
 mu[i] <- alpha.LL \* pow(lags[i], beta.LL)
 area[i] ~ dnorm(mu[i], tau.area)
 } #i

 ############ VB GROWTH MODEL ###########

 for(p in 1:ALL){
 log(logk[p]) <- beta.k[site[p]]
 delta.age[p] <- (pred.lags[p] - age.0[site[p]])
 L.age[p] <- a[site[p]] \* (1-exp(-k[p] \* delta.age[p]))
 svl[p] ~ dnorm(L.age[p], tau.svl)
 } #p

 } #model

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