

## Using Bayesian Models to Reconstruct Small Mammal Populations

E.R. Unnsteinsdottir, P. Hersteinsson, J.P. Jonasson, B.J. McAdam

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### Supplementary Information

This supplementary information gives full details of the growth and birth model. Some details are replicated from the main paper, so that this may be read as a stand-alone document.

### Methods

#### Bayesian Model

The implementation of the Bayesian model simultaneously estimates growth parameters and possible birth dates for each mouse. For each observation,  $i$ , of any mouse the input to the model is a mouse ID ( $m_i$ ), weight on day of observation ( $w_i$ ), and day of the year ( $d_i$ ). For every mouse ID,  $m$ , we also know the mouse sex,  $s_m \in \{\text{female, male}\}$ .

#### Unknowns

The model estimates several unknown variables. The Gompertz growth model is a hierarchical model with parameters for population sex and individual, specifically there is a population average growth asymptote,  $K_\mu$ , and rate,  $\alpha_\mu$ ; sex specific asymptotes and rate,  $K_{\text{male}}, K_{\text{female}}, \alpha_{\text{male}}, \alpha_{\text{female}}$ ; and for each mouse,  $m$ , individual asymptote and rate,  $K_m, \alpha_m$ . The random variation in the growth model is characterised by precision parameters,  $\tau_{K_{\text{sex}}}, \tau_{\alpha_{\text{sex}}}, \tau_K, \tau_\alpha, \tau$ . Each mouse has an unknown birthday  $b_m$ .

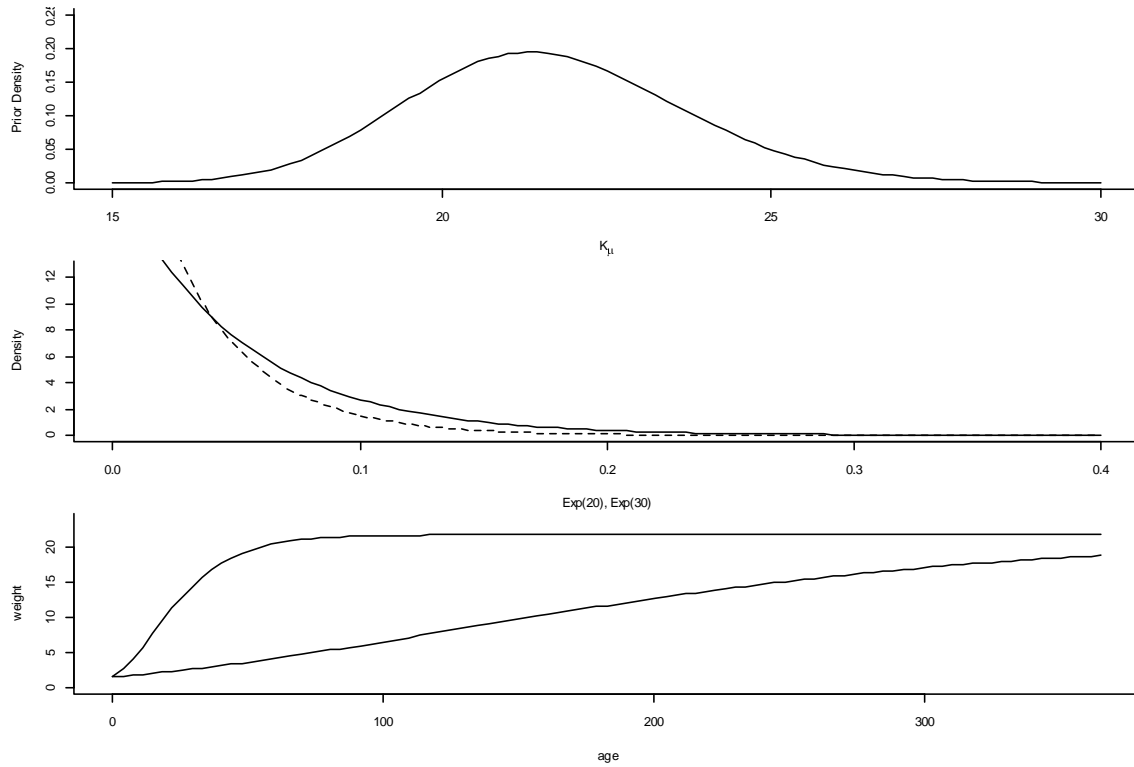
#### Priors

Prior distribution of population mean growth asymptote is based on measured size of individuals observed after day 330 (assumed to be near or fully grown), mean of logs  $\overline{\log(w)} = 3.06$  (equating to weight 21.3g), and standard deviation  $\sigma_{\log(w)} = 0.099$ . According to the Gompertz growth model, all weights should have a log normal distribution

$$K_\mu \sim \text{ln N}(\overline{\log(w)}, 1/\sigma_{\log(w)}^2)$$

(‘ln N’ denotes the lognormal distribution parameterised by log of mean and precision. All probability distributions are parameterised here as in the OpenBugs implementations, the probability density function of this distribution is shown in Figure S1a)

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**Figure S1:** Prior probability density distribution of parameters and example growth curves: (a) prior density of population mean growth asymptote; (b) density of Exp(20) (solid line) and Exp(30) (dashed line) used for unknown standard deviations; (c) example Gompertz growth curves with asymptotic size as population mean and rate  $\alpha = -0.008$  (upper line, fast growth) and  $\alpha = -0.064$  (lower line, slow growth).

Prior distribution of population mean growth rate is assumed to be uniform with limits chosen such that a mouse reaches 90% of asymptotic size after between 50 and 400 days.

$$\alpha_{\mu} = U(-0.064, -0.008)$$

The variation in growth between the sexes is characterised by the unknown precision parameters  $\tau_{K,sex}$  and  $\tau_{\alpha,sex}$ . These are given priors based on an exponential distribution of the corresponding standard deviation (distribution Exp(20) is exponential with has an expected value of 0.05, see Figure S1b, solid line)

$$\sigma_{K,sex}, \sigma_{\alpha,sex} \sim \text{Exp}(20)$$

$$\tau_{K,sex} = 1 / \sigma_{K,sex}^2$$

$$\tau_{\alpha,sex} = 1 / \sigma_{\alpha,sex}^2$$

$$K_{\text{male}}, K_{\text{female}} \sim \ln N(\log(K_{\mu}), \tau_{K,sex})$$

$$\alpha_{\text{male}}, \alpha_{\text{female}} \sim N(\alpha_{\mu}, \tau_{\alpha,sex})$$

In principal, this can be extended for any number of population components with differing growth parameters.

Individual mice vary from their sex mean growth parameters in the same manner

$$\sigma_K, \sigma_\alpha \sim \text{Exp}(20)$$

$$\tau_K = 1 / \sigma_K^2$$

$$\tau_\alpha = 1 / \sigma_\alpha^2$$

$$K_m \sim \ln N(\log(K_{s_m}), \tau_K) \text{ for all } m$$

$$\alpha_m \sim \ln N(\log(\alpha_{s_m}), \tau_\alpha) \text{ for all } m$$

And finally, growth is stochastic so there is an unknown variation between the individual growth curve and individual observations of weight, controlled by unknown precision  $\tau$ . As variation around the growth curve for an individual is likely to be smaller than variation between individuals, we use a narrower prior (dotted line on Figure S1b).

$$\sigma \sim \text{Exp}(30)$$

$$\tau = 1 / \sigma^2$$

The possible birthdays of each mouse are assumed to be uniformly distributed from the start of the breeding season (20<sup>th</sup> April=day 110, known from dissection of trapped mice, used as minbirthday<sub>m</sub> for all mice  $m$ ) and the day before the first observation of that mouse (maxbirthday<sub>m</sub>). An alternative approach used by Zhang et al (2009) is to use a Gamma distribution for age at first capture in order to exclude the possibility of trapping at very young age, and of individuals being exceptionally old. We do not consider that we have sufficient information to set a prior for such a Gamma distribution, and the short breeding season is likely to be the dominant effect.

$$b_m \sim U(\text{minbirthday}_m, \text{maxbirthday}_m)$$

## Model Equations

The expected size of a mouse on a day of observation depends upon its age and the individual growth parameters for that mouse, following the Gompertz growth model and with a fixed birth size  $w_0 = 1.5\text{g}$ , for all observations  $i$ :

$$E(w_i) = K_{m_i} \times \exp(\log(w_0 / K_{m_i}) \times \exp(\alpha_{m_i} \times (d_i - b_{m_i})))$$

The residual variation between  $E(w_i)$  and  $w_i$  has a lognormal distribution with precision  $\tau$

$$w_i \sim \ln N(\log(E(w_i)), \tau)$$

Example growth curves for high and low growth rates are shown in Figure S1c,d

## OpenBugs Implementation

The model is described using the OpenBugs model below

```
MouseModel {
```

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```
# The unknowns are:

# - population growth asymptote and rate: Kmu, alphaMu
# - sex specific growth asymptote and rate: Ksex[s], alphaSex[s]
# - level of sex variation: tauKSex, tauAlphaSex
# - individual growth asymptote and rate: K[m], alpha[m]
# - level of individual variation: tauK, tauAlpha
# - level of observation variation: tau
# - mice's birthdays, birth[m]


# known values (observations given as input) are:
# - mouse observed on each observation: mouse[i]
# - weight at each observation: weight[i]
# - day of each observation: day[i]
# - sex of each mouse: sex[m]
# - range of possible birthdays for each mouse:
#   minBirthday[m], maxBirthday[m]
# - number of observations: observations
# - number of mice: mice


# PRIORS


# K distributed log-normally according to 'adult' data
# This is the precision of the log of K in the data
log.KPrecision <- 1/(adultLogWeightSD * adultLogWeightSD)
Kmu ~ dlnorm(adultMeanLogWeight, log.KPrecision)
log.Kmu <- log(Kmu)


# alpha is the growth rate,
# to reach 90% of asymptote in 50 days alpha=-0.064
# to reach 90% of asymptote in 400 days, alpha=-0.008
# > 20 * exp(log(1.5/20) * exp(-0.064 * 50))
# [1] 17.99596
```

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```
# > 20 * exp(log(1.5/20) * exp(-0.008 * 400))

# [1] 17.99596

alphaMu ~ dunif(-0.064, -0.008)

# SEX SPECIFIC K AND ALPHA.

sigmaKSex ~ dexp(20) # expected value 0.05
                        # corresponds roughly to 1g variation of 20g mean

tauKSex <- 1/(sigmaKSex*sigmaKSex)

sigmaAlphaSex ~ dexp(20) # expected value 0.05
                        # scale corresponds to scale of alphaMu

tauAlphaSex <- 1/(sigmaAlphaSex*sigmaAlphaSex)

for(s in 1:2){

  Ksex[s] ~ dlnorm(log.Kmu, tauKSex)

  log.Ksex[s] <- log(Ksex[s])

  alphaSex[s] ~ dnorm(alphaMu, tauAlphaSex)

}

# tau is the unknown precision of the growth curve

# this is 1/variance of residuals

# our prior for tau is that large values should be more likely

# (i.e. smaller variance)

sigmaK ~ dexp(20) # expected value 0.05

tauK <- 1/(sigmaK*sigmaK)

sigmaAlpha ~ dexp(20) # expected value 0.05

tauAlpha <- 1/(sigmaAlpha*sigmaAlpha)

sigma ~ dexp(30) # expected value 0.05
                # could try smaller variation between samples
                # than between mice (e.g. 30)

tau <- 1/(sigma*sigma)

# individual growth

for(m in 1:mice){

  # individual K and alpha sampled from distributions for sex of mouse

  K[m] ~ dlnorm(log.Ksex[sex[m]], tauK)
```

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```
alpha[m] ~ dnorm(alphaSex[sex[m]], tauAlpha)I(-0.100, -0.020)

# individual growth rate
}

# birthday distributed normally through the breeding season
# but not after first observation of the mouse!
for(m in 1:mice){
  birthday[m] ~ dunif(minBirthday[m], maxBirthday[m])
}

# GROWTH MODEL
for(i in 1:observations){

  # age
  age[i] <- (day[i] - birthday[mouse[i]])

  # expected weight (given birthday, alpha and K)
  expectedWeight[i] <- K[mouse[i]] *
    exp( log(birthWeight/K[mouse[i]]) *
      exp(alpha[mouse[i]] * age[i]) )
  log.expectedWeight[i] <- log(expectedWeight[i])

  # residuals (not needed but useful for debugging)
  #residual[i] <- expectedWeight[i] - weight[i]

  # error in expected weight
  weight[i] ~ dlnorm(log.expectedWeight[i], tau)

} # end for(i in observations)

} # end MouseModel
```

### Model Fitting

Model fitting was performed by an R script that assembled the data set before using the BRugs library to fit the model in OpenBugs and extract the chains of estimates. An initial 10000 iterations

were used to burn-in the chain, then 50000 iterations thinned by every 10 observations yielded 5000 sets of estimates of each parameter.

A copy of the OpenBugs data file can be obtained from [NEED TO PUT THE DATA ONLINE](#)

## Results

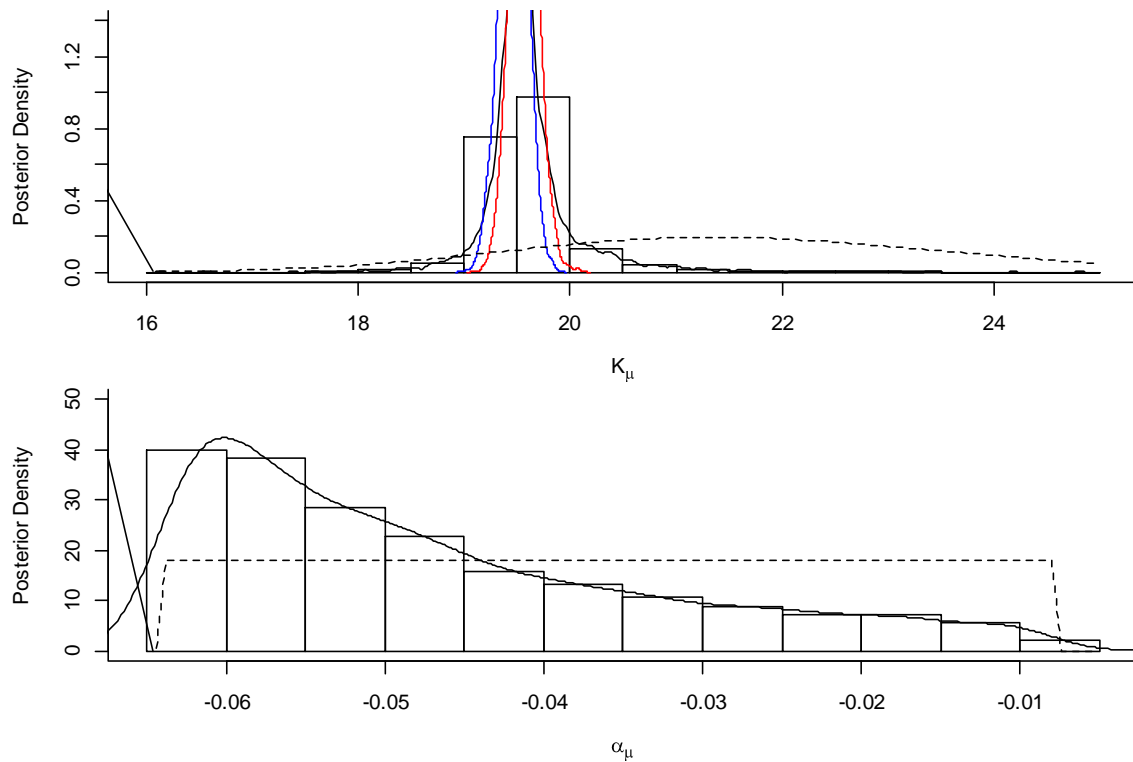
### Posterior Parameters

Table S1 shows median and 95% Bayesian confidence intervals for model parameters.

Variable	2.5%	50%	97.5%
$K_\mu$	18.9	19.5	20.8
$\tau_K$	71.2	85.3	105
$\alpha_\mu$	-0.063	-0.051	-0.012
$\tau_\alpha$	11500	789000	24100000
$K_{\mu,\text{female}}$	19.3	19.6	19.8
$K_{\mu,\text{male}}$	19.2	19.5	19.7
$\alpha_{\text{female}}$	-0.097	-0.091	-0.086
$\alpha_{\text{male}}$	-0.093	-0.088	-0.080
$\tau$	124	155	192

**Table S1:** median and 95% Bayesian confidence intervals for model parameters

Figure S2 shows posterior probability densities of parameters, and example growth curves.



**Figure S2:** Posterior probability density distributions for (a)  $K_\mu$ , and (b) rate  $\alpha_\mu$ .

Histogram of posterior distribution, smoothed kernel density plot as solid black

line, prior distribution as dashed line, and male and female specific parameter  $K_{\text{male}}$ ,  $K_{\text{female}}$  posterior distributions as blue and red respectively.

Figure 1 in the paper shows posterior distributions of growth curves and possible birth dates for example mice with different numbers of observations.

### **Estimated Birth Dates and Population Growth**

Figure 2 in the paper shows the overall distribution of birth dates of the observed mice, and cohort population size based on these birth dates and different values of estimated daily mortality.