

Modelling sexed age-at-death profiles

We consider n age classes with bounds $\mathbf{t} = (0, t_1, \dots, t_n)$, resulting in lower and upper limits $\mathbf{l} = (l_1, \dots, l_n) = (0, t_1, \dots, t_{n-1})$, and $\mathbf{u} = (u_1, \dots, u_n) = (t_1, \dots, t_n)$.

The model is based on four assumptions. First, the male to female sex ratio is modelled by a sigmoidal decay function $r_\sigma = e^{-\frac{x^2}{2\sigma^2}}$, $\sigma > 0$, over continuous time x , implying that the sex ratio at birth ($x = 0$) is one, *i.e.* males and females are born in equal proportions, and that males outnumber females at no time. Second, we do not allow for the possibility that animals join the herd at a later age class, *i.e.* the number of births equals the number of deaths. Note that the last two assumptions imply that sex ratio change is driven solely by excess killing of males. Third, beyond the killing of males required to match a given sex ratio, males and females are killed in equal proportions. Lastly, no individual survives beyond the last age class, *i.e.* at time point u_n all individuals are dead.

In order to formalise the above assumptions, we introduce the following parameters besides the sigmoidal decay parameter σ . Let $\mathbf{f} = (f_1, \dots, f_n)$, $\mathbf{m} = (m_1, \dots, m_n)$, $\mathbf{a} = (a_1, \dots, a_{n-1})$, and $\mathbf{b} = (b_1, \dots, b_{n-1})$ be the proportion of females surviving per age class, the proportion of surviving males, the proportion of males killed due to sex ratio, and the remaining proportion of animals killed per sex, respectively. Note that proportion of animals killed per sex, b_i , is the same, single value for males and females, due to the third assumption. Under the four assumptions and with these definitions, the actual age-at-death profile is $\mathbf{p} = (a_1 + 2b_1, \dots, a_{n-1} + 2b_{n-1}, f_{n-1} + m_{n-1})$.

By definition we have the relations $f_{i-1} - b_i = f_i$ and $m_{i-1} - (a_i + b_i) = m_i$, $1 \leq i \leq n-1$, with $f_0 = m_0 = \frac{1}{2}$ and $f_n = m_n = 0$ following from the first and last assumption, respectively. Furthermore, the first assumption requires that males and females survive in proportions dictated by the sigmoidal decay function. We discretise $r_\sigma(x)$ using the definition of the mean of a function, *i.e.* $\bar{r}_\sigma(i) = \frac{1}{u_i - l_i} \int_{l_i}^{u_i} r_\sigma(x) dx = \frac{m_i}{f_i}$ for $0 \leq i \leq n-1$. Lastly, the second assumption constrains a_i and b_i to be positive, $a_i > 0$ and $b_i \geq 0$, where a_i is strictly greater than zero as the sigmoidal decay function is strictly decreasing, or equivalently $f_i > m_i$ for $1 \leq i \leq n-1$.

The above relations imply $\frac{m_{i-1} - (a_i + b_i)}{f_{i-1} - b_i} = \bar{r}_\sigma(i)$, for $1 \leq i \leq n-1$. Solving

the equation system (for example with [Wolfram Alpha®](#))

$$\begin{cases} \frac{m_{i-1}-(a_i+b_i)}{f_{i-1}-b_i} = \bar{r}_\sigma(i) \\ 0 < a_i \\ 0 \leq b_i \\ 0 < \bar{r}_\sigma(i) < \frac{m_{i-1}}{f_{i-1}} \leq 1 \end{cases} \quad (1)$$

for a_i and b_i yields the bounds and equation

$$0 < a_i \leq m_{i-1} - f_{i-1} \bar{r}_\sigma(i) \quad (2)$$

$$b_i = \frac{a_i + f_{i-1} \bar{r}_\sigma(i) - m_{i-1}}{\bar{r}_\sigma(i) - 1} \quad (3)$$

for successive age classes.

Simulating sexed age-at-death profiles

The last two relations suggest an easy heuristic for simulating age-at-death-profiles under the model, by iteratively sampling a_i uniformly in the interval given by inequality 2, for $1 \leq i \leq n-1$. However, the disadvantage is that for models with numerous age classes, killing becomes concentrated in the first age classes.

An alternative strategy is to sample an initial a in the bounds

$$0 < a < m_0 - f_0 \bar{r}_\sigma(n-1) = \frac{1 - \bar{r}_\sigma(n-1)}{2} \quad (4)$$

corresponding to the total proportion of males killed due to sex ratio before all animals are killed in the last age class, and recursively partition a until $n-1$ values for the desired $n-1$ age classes are reached. Partitioning a can be seen as sampling an α with $0 < \alpha < 1$, resulting in values αa and $(1-\alpha)a$ that by definition satisfy $\alpha a + (1-\alpha)a = a$. The bounds for valid α values can be obtained by solving the equation system (for example with [Wolfram Alpha®](#))

$$\begin{cases} \frac{m-(a+b)}{f-b} = r \\ \frac{m-(\alpha a + \beta b)}{f-\beta b} = r' \\ 0 < a \leq m - fr \\ b = \frac{a+fr-m}{r-1} \\ 0 < r < r' < 1 \\ 0 < \alpha < 1 \\ 0 < \beta < 1 \end{cases} \quad (5)$$

for α and β over the reals, yielding the bounds and equation

$$\max(0, \frac{br' - b - fr' + m}{br - b - fr + m}) < \alpha < \min(1, \frac{m - fr'}{br - b - fr + m}) \quad (6)$$

$$\beta = \frac{b\alpha(r - 1) + f(r' - \alpha r) + m(\alpha - 1)}{b(r' - 1)} \quad (7)$$

that partition an age class with m and f initial proportions of males respectively females, of which a are killed due to sex ratio and b are killed in both sexes to achieve a sex ratio of r , into two age classes with intermediate proportions $m - (\alpha a + \beta b)$ and $f - (\beta b)$ of males respectively females and sex ratio r' .

A feature of the above approach is that the the initial sample of a covering age classes 1 to $n - 1$ determines the proportion of animals surviving into the last age class, by definition $1 - (a + 2b)$. Replacing b by Equation 3 and $f_0 = m_0 = \frac{1}{2}$ yields $1 - (a + 2b) = a \frac{\bar{r}_\sigma(n-1)+1}{1-\bar{r}_\sigma(n-1)}$. Given a sample of actual proportions of animals surviving into the last class, its distribution can be matched when simulating data by sampling the initial a from a kernel density estimate over the actual proportions scaled with $\frac{1-\bar{r}_\sigma(n-1)}{\bar{r}_\sigma(n-1)+1}$ instead of sampling a uniformly from the interval specified by Equation 4.