

Bayesian Fertility Trajectory Analysis (BaFTA) tutorial.

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1 Brief introduction

This vignette provides an overview of the data needed and the use of the functions available in the R package BaFTA. The package allows to make inference on age-specific fertility for aggregated and individual level data. For details of the age-specific fertility models included in the package see [1].

2 Installing the package

Before installing BaFTA, You will need package **snowfall** for parallel computing, which you can install as

```
# Install snowfall:
install.packages("snowfall")
```

You can download the BaFTA package from the GitHub repository. Store the tar.gz file in your computer and install the package as

```
# Install package:
install.packages("My directory/BaFTA_1.0.0.tar.gz", type = "source",
                repos = FALSE)
```

Alternatively, you can install it directly from GitHub by typing the following code:

```
# Install devtools:
install.packages("devtools")

# Load devtools:
library(devtools)

# Install BaFTA from GitHub:
install_git("https://github.com/fercol/BaFTA", subdir = "pkg/")
```

To initialize BaFTA, simply type to the console:

```
# Load the library:
library(BaFTA)
```

which will also load **snowfall**.

3 Data formatting

3.1 Aggregated data

The data frame needed requires only the following four columns: **Age** with discrete ages; **nParents** with the number of available adults per age; **nOffspring** with the number of offspring produced in that age interval; **Fertility** with the age-specific fertility, calculated as $\text{Fertility} = \text{nOffspring} / \text{nParents}$. Here is an example of the first six rows of a simulated dataset:

	Age	nParents	nOffspring	Fertility
1	1	100	388	3.880000
2	2	100	727	7.270000
3	3	47	306	6.510638
4	4	17	101	5.941176
5	5	6	38	6.333333
6	6	2	2	1.000000

3.2 Individual data with discrete ages

When individual level data with discrete age intervals is available, then the data frame for analysis in BaFTA should include the following three columns: **indID** with character string of individual IDs of the parents; **Age** with the discrete ages of the parents at the time of birth; **nOffspring** with the number of offspring produced during that reproductive event by the given parent. Here is an example on simulated data:

	indID	Age	nOffspring
1	I0002	1	5
2	I0002	2	5
3	I0016	1	5
4	I0016	2	4
5	I0017	1	1
6	I0017	2	9

Uncertain number of offspring for discrete ages data In case there are occasions when parents were not observed constantly and only for fraction of the survey time, users can include an additional column for the proportion of time that parent was observed during the corresponding sampling occasion. The name of the additional column needs to be **obsProp** and should contain 1 for individuals that were fully observed, and values between 0 and 1 for individuals that were only partially observed. Here is an example:

	indID	Age	nOffspring	obsProp
1	I0002	1	5	1.00
2	I0002	2	0	0.25
3	I0016	1	4	0.25
4	I0016	2	4	1.00
5	I0017	1	1	0.75
6	I0017	2	9	1.00

As you can see, some rows depict individuals that the user assumes they were detected for only 75% or 25% of the time. The values assigned to those individuals need to represent the user's belief in what proportion of the reproductive season or effort they were able to follow.

3.3 Individual data with continuous ages and variable IBI

For individual data with continuous ages and variable IBIs, then the data needed consist of a data frame with individual rows per reproductive event, and with the following columns: **indID** with character string of individual IDs of the parents; **Age** with the discrete ages of the parents at the time of birth; **nOffspring** with the number of offspring produced during that reproductive event by the given parent, including failed events (i.e., **nOffspring** = 0); **IBI** with the time since last reproduction in years. Column **First** indicates whether the observation correspond to the first reproductive event of that parent. Here is an example on simulated data: Here is an example on simulated data:

	indID	Age	nOffspring	IBI	First
1	I0007	1.225655	5	0.2256546	0
2	I0007	1.505292	2	0.2796373	0
3	I0007	1.687194	6	0.1819023	0
4	I0007	2.113609	9	0.4264145	0
5	I0007	2.269594	6	0.1559857	0
6	I0007	2.450261	8	0.1806669	0

Unknown ages Often, parents are first detected as adults and their ages are uncertain or entirely unknown. In those cases, BaFTA allows users to specify lower and upper bounds for the ages when those individuals were detected. The package provides function **CalcMinMaxAge()** so users can automatically calculate the possible minimum and maximum ages for those individuals given the minimum age at sexual maturity, and the maximum possible reproductive age of the species. For instance, let's assume that for a given species, the minimum age at sexual maturity is 1 year, the maximum possible reproductive age is 10, and individuals 2, 4, and 5 are of unknown age. Then, the data object can be updated as:

```
object <- CalcMinMaxAge(object = object, minAge = 1, maxAge = 10,
  unkAgeID = c(2, 4, 5))
```

The resulting dataset includes two additional columns **MinAge** and **MaxAge** where individuals not included in the **unkAgeID** argument will have **MinAge** = **MaxAge** = **Age**, while those in the index will have a range of possible ages. Below is an example where the first three records have the same min and max ages to the recorded age by the user, while the last three records have different min, max, and proposed age. For the last three, BaFTA will estimate the ages as part of the inference process.

	indID	Age	nOffspring	IBI	First	MinAge	MaxAge
1	I0007	1.2256546	5	0.2256546	0	1.2256546	1.225655
2	I0007	1.5052919	2	0.2796373	0	1.5052919	1.505292
3	I0007	1.6871942	6	0.1819023	0	1.6871942	1.687194
27	I0160	0.4937211	2	0.0000000	1	0.2500000	10.816708

28	I0160	0.6770130	2	0.1832919	0	0.4332919	11.0000000
36	I0176	0.8331805	0	0.0000000	1	0.2500000	10.645818

4 Analysis

To run an analysis on aggregated data (**aggrRepr**), using the quadratic model, it is sufficient to use function **bafta()** as follows:

```
# Quadratic:
outAG0 <- bafta(object = aggrRepr, model = "quadratic",
               dataType = "aggregated", nsim = 4, ncpus = 4,
               niter = 11000, burnin = 1001, thinning = 20)
```

where argument **model** specifies the functional form for the age-specific fertility (i.e., expected number of offspring produced by individuals of a given age), and, as its name indicates, argument **dataType** specifies the type of data, with options “**aggregated**”, “**indivSimple**” for individual level data with discrete age information, and “**indivExtended**” for individual level data with continuous ages and variable IBIs.

To visualize the output of the model, functions **print()**

```
# Simple print:
outAG0

# Summary:
summary(outAG0)
```

which prints the following output to the console:

```
>
> Call:
> Model           : quadratic
> Data type       : aggregated
> Num. iterations : 31000
> Burnin          : 1001
> Thinning        : 20
> Number of sims. : 4
> Computing time  : 6.66 secs
>
> Coefficients:
>      Mean      SD    Lower  Upper Neff  Rhat
```

```

> b0      7.5324 0.49831 6.60490 8.5565 2747 1.001
> b1      0.1113 0.02199 0.06937 0.1554 2938 1.001
> b2      2.7717 0.22031 2.40271 3.2678 1876 1.000
> gamma 4.0636 1.46964 2.51441 8.1580 4738 1.000
>
> Convergence:
> All parameter chains converged.
>
> Model fit:
>
> DIC = 72.23
>
> Predictive loss:
> Good. Fit Penalty Deviance
>      13239      6260      19499

```

```

# Gamma distributional model:
outAG1 <- bafta(object = aggrRepr, model = "gamma",
               dataType = "aggregated", nsim = 4, ncpus = 4,
               niter = 11000, burnin = 1001, thinning = 20)

```

As shown in Fig. 1, to visually inspect the traces for proper convergence, simply type

```

# Plot traces:
plot(outAG1)

```

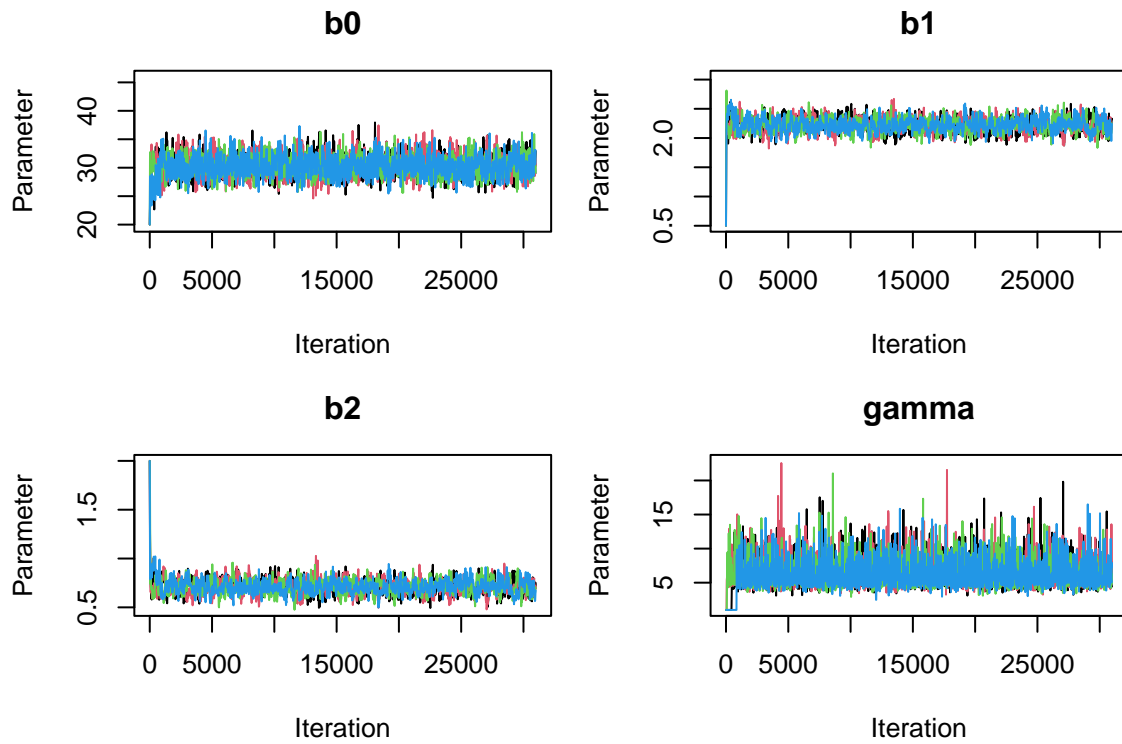


Figure 1: Plot of fertility parameter traces for BaFTA output.

Alternatively, it is possible to plot the posterior densities of the fertility parameters (Fig. 2) by typing

```
plot(outAG1, type = "density")
```

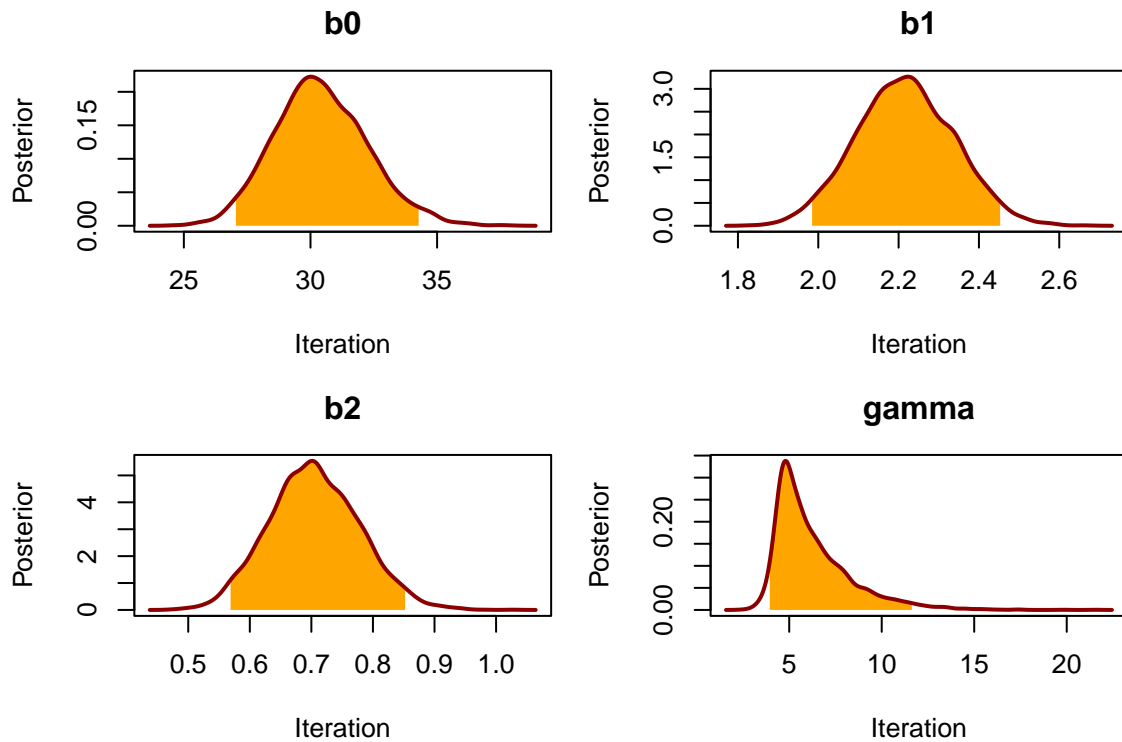


Figure 2: Plot of fertility parameter posterior densities for BaFTA output. The orange filled polygons depict the 95% credible intervals.

To plot the estimated fertility with its 95% credible intervals compared to the actual fertility just change the **type** argument as

```
plot(outAG1, type = "fertility")
```

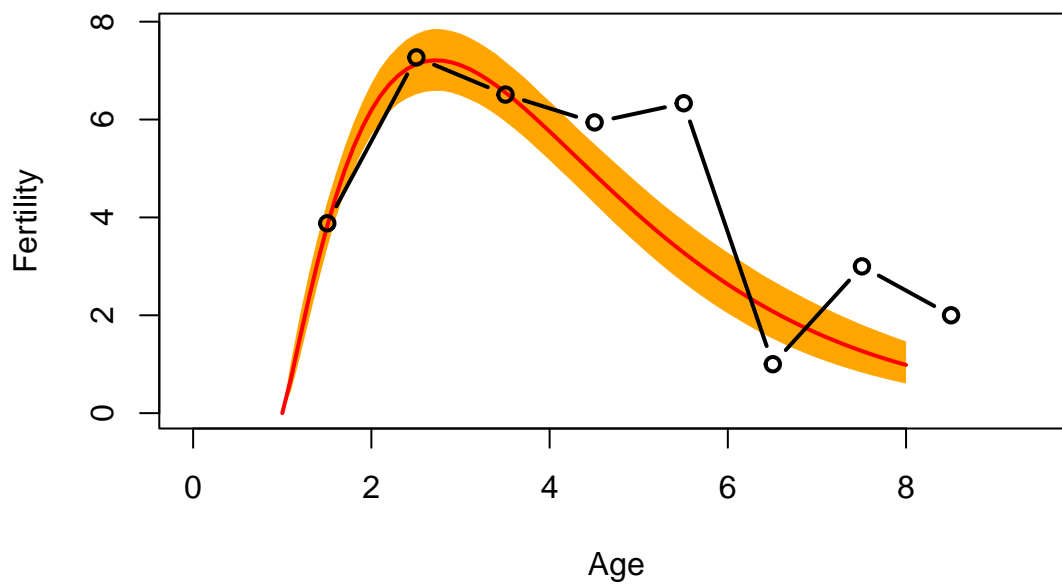



Figure 3: Plot of the estimated age-specific fertility with the 95% credible intervals (orange) against the actual fertility.

Finally, to plot the predicted number of offspring produced by parents of a given age against the actual number of offspring, modify the **type** argument as

```
plot(outAG1, type = "predictive")
```

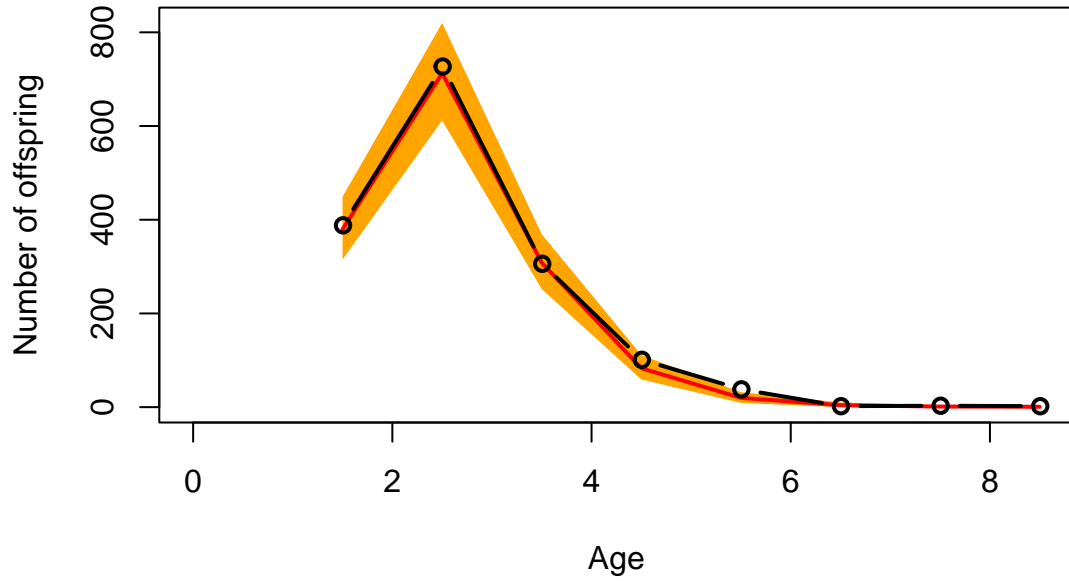


Figure 4: Plot of the predicted age-specific number of offspring with the 95% predictive intervals (orange) against the actual number of offspring.

5 Fertility models included in BaFTA

The following table shows the different models of age-specific fertility included in BaFTA. The parametrization is as in the package and therefore differs from that in Colchero [1] (i.e., $\theta^\top = [b_0, b_1, \dots, b_p]$). Note that the column **Model** shows the model name as it needs to be specified in argument **model** within function **bafta()**.

Model	Fertility function	References
quadratic	$g(x) = b_0 \exp \left[-b_1(x - b_2)^2 \right],$ where $b_0, b_1, b_2 \geq 0$.	[2, 3, 4]
ColcheroMuller	$g(x) = b_0 \exp \left[b_1x - b_2x^2 + b_3/(x + 1) \right],$ where $b_0, b_1, b_2 \geq 0$ and $b_3 \in \mathbb{R}$.	[4, 5]
PeristeraKostaki	$g(x) = b_0 \exp \left[- \left(\frac{x - b_3}{b(x)} \right)^2 \right],$ where $b_0 \geq 0$, $b_3 \in \mathbb{R}$, and $b(x) = b_1$ if $x \leq b_3$, $b(x) = b_2$ if $x > b_3$.	[6]
Hadwiger	$g(x) = b_0 \frac{b_1}{b_2} \left(\frac{b_2}{x} \right)^{3/2} \exp \left[-b_1^2 \left(\frac{b_2}{x} + \frac{x}{b_2} - 2 \right) \right],$ where $b_0, b_1, b_2 > 0$.	[7]
gamma	$g(x) = b_0 \left[\Gamma(b_1) b_2^{b_1} \right]^{-1} x^{b_1-1} e^{x/b_2},$ where $b_0, b_1, b_2 > 0$.	[8]
beta	$g(x) = b_0 \frac{(x - b_3)^{b_1-1} (b_4 - x)^{b_2-1}}{(b_4 - b_3)^{b_1+b_2-1} B(b_1, b_2)},$ where $b_0, b_1, b_2, b_3, b_4 > 0$, and B is the beta function.	[8]
skewNormal	$g(x) = b_0 2b_1^{-1} \phi \left(\frac{x - b_2}{b_1} \right) \Phi \left\{ b_3 \left(\frac{x - b_2}{b_1} \right) \right\},$ where $b_0, b_1, b_3 > 0$, $b_2 \in \mathbb{R}$, and ϕ and Φ are the standard normal PDF and CDF, respectively.	[9, 10]
gammaMixture	$g(x) = b_0(b_1) \left\{ \left[\Gamma(b_2) b_3^{b_2} \right]^{-1} x^{b_2-1} e^{x/b_3} \right\}$ $+ (1 - b_1) \left\{ \left[\Gamma(b_4) b_5^{b_4} \right]^{-1} x^{b_4-1} e^{x/b_5} \right\},$ where $b_0, \dots, b_5 > 0$.	[8]
HadwigerMixture	$g(x) = b_0 \left\{ b_1 \left(\frac{b_2}{b_3} \right) \left(\frac{b_3}{x} \right)^{3/2} \exp \left[-b_2^2 \left(\frac{b_3}{x} + \frac{x}{b_3} - 2 \right) \right] \right.$ $+ (1 - b_1) \left(\frac{b_4}{b_5} \right) \left(\frac{b_5}{x} \right)^{3/2}$ $\left. \times \exp \left[-b_4^2 \left(\frac{b_5}{x} + \frac{x}{b_5} - 2 \right) \right] \right\},$ where $b_0, \dots, b_5 > 0$.	[8]

Model	Fertility function	References
skewSymmetric	$g(x) = b_0 2b_1^{-1} \phi\left(\frac{x-b_2}{b_1}\right) \times \Phi\left\{b_3\left(\frac{x-b_2}{b_1}\right) + b_4\left(\frac{x-b_2}{b_1}\right)^3\right\},$ <p>where $b_0, b_1, b_3 > 0$, $b_2, b_4 \in \mathbb{R}$, and ϕ and Φ are the standard normal PDF and CDF, respectively.</p>	[9, 10]
skewLogistic	$g(x) = b_0 2b_1^{-1} \frac{e^{-(x-b_2)/b_1}}{(1 + e^{-(x-b_2)/b_1})^2} \times \frac{1}{(1 + e^{-b_3[(x-b_2)/b_1] - b_4[(x-b_2)/b_1]^3})},$ <p>where $b_0, b_1, b_3 > 0$, $b_2, b_4 \in \mathbb{R}$, and ϕ and Φ are the standard normal PDF and CDF, respectively.</p>	[11]

6 Inference details

6.1 Generals of the inference model

The model differs depending on the type of data. For data of type “**indivSimple**”, we can define the nonhomogeneous Poisson process $\{N(x), x \geq 0\}$ with intensity function $\lambda(x)$, where $N(x)$ are the cumulative number of offspring produce by a given individual up to age x . At a given discrete age interval $[x, x + 1)$ we can define the random variable for an average individuals as

$$Y_x = N(x + 1) - N(x) \sim \text{Pois}[\Lambda(x + 1) - \Lambda(x)], \quad (1)$$

where

$$\Lambda(x) = \int_0^x \lambda(t) dt. \quad (2)$$

For age intervals of one year, $\lambda(x)$ can be calculated at the midpoint of the interval $[x, x + 1)$ such that

$$\int_x^{x+1} \lambda(t) dt = \Lambda(x + 1) - \Lambda(x) = \lambda\left(x + \frac{1}{2}\right) + \varepsilon_x, \quad (3)$$

where, based on the error of the midpoint rule, $\varepsilon_x \leq \frac{K}{24}$ and $K \geq |\lambda''(t)|$ for all $t \in [x, x + 1]$. Given that g is a concave function of age we can therefore assume that the error ε_x is negligible.

The random variable Y_x in Eq. 1 represents the number of offspring produced within the age interval $[x, x + 1)$ by an average individual. However, given that individuals differ in their ability to reproduce, a hierarchical model is more appropriate [5, 4]. Here, we define the conditional random variable

$$\begin{aligned} Y_{i,x}|U_i &\sim \text{Pois}[\lambda(x, U_i)] \\ U_i &\sim \text{Ga}(\alpha, \alpha) \end{aligned} \quad (4)$$

where $\alpha > 0$, with observations $y_{i,x} \in \mathbb{N}_{\geq 0}$, U_1, \dots, U_{n_x} are i.i.d. random variables variable with $E(U_i) = 1$ for $i = 1, 2, \dots, n_x$ where n_x is the number of parents at age x , and $g : \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$ is a $k \geq 2$ times differentiable smooth concave function. The resulting random variable is marginally distributed as $Y_{i,x} \sim \text{NB}[\alpha, \alpha/(g(x) + \alpha)]$, with likelihood function

$$\mathcal{L}(\mathbf{y}|\boldsymbol{\theta}, \sigma^2) = \prod_{i=1}^n \prod_{x \in E_i} \frac{\Gamma(y_{i,x} + \alpha)}{\Gamma(\alpha) y_{i,x}!} \left(\frac{\alpha}{g(x) + \alpha} \right)^\alpha \left(\frac{g(x)}{g(x) + \alpha} \right)^{y_{i,x}}, \quad (5)$$

where E_i is the set of ages at which individual i was known to be present, $E[Y_{i,x}] = g(x)$ and $\text{Var}[Y_{i,x}] = g(x)[(g(x) + \alpha)/\alpha]$

For data type **aggregated**, the random variable of interest is then W_x . However, since $Y_{i,x}$ for $i \in I_x$ where I_x is an indexed set of individuals alive at age x are not identically distributed (i.e., $Y_{i,x}|U_i \sim \text{Pois}[\lambda(x, U_i)]$) for all $i \in I_x$, the distribution of W_x needs to be fully specified.

As shown in [1], the resulting random variable is $W_x \sim \text{NB}(n_x \alpha, \alpha/[g(x) + \alpha])$, with probability mass function

$$f_W(w_x) = \frac{\Gamma(w_x + n_x \alpha)}{\Gamma(n_x \alpha) w_x!} \left(\frac{g(x)}{g(x) + \alpha} \right)^{w_x} \left(\frac{\alpha}{g(x) + \alpha} \right)^{n_x \alpha}, \quad \text{for } x \in \mathbb{N}_{\geq 0} \quad (6)$$

where $E[W_x] = n_x g(x)$ and $\text{Var}[W_x] = n_x g(x)[g(x) + \alpha]/\alpha$.

If the data are **indivExtended** then $x > 0$ and we define two additional random variables, namely W_i with $w_i \geq 0$ for the time between the minimum age at maturity and the first birth, with exponential PDF, and $Z_{i,x} = \delta_{i,x} - \tau$ where $\delta_{i,x} \geq 0$ is the interbirth interval for individual i at age x and τ is the minimum gestation time (also including weaning if relevant). Here we need also a hierarchical model given by

$$\begin{aligned} Y_{i,x}|U_i, W \geq w_i \vee Z_x = z_{i,x} &\sim F_Y(y_{i,x}|u_i, w_i, z_{i,x}) \\ U_i &\sim N(0, \sigma_u^2) \\ W_i &\sim F_W(w_i) \\ Z_{i,x}|V_i &\sim F_Z(z_{i,x}, v_i) \\ V_i &\sim N(0, \sigma_v^2), \end{aligned} \tag{7}$$

and with likelihood

$$\mathcal{L}(\dots) = \begin{cases} \gamma e^{-\gamma w_i} f_Y(y_{i,x}|\theta, u_i) f_U(u_i) & \text{for } x = w_i \\ \eta e^{-e^{v_i} \eta z_{i,x}} f_Y(y_{i,x}|\theta, u_i) f_U(u_i) & \text{for } x > w_i \end{cases} \tag{8}$$

The posterior for the most parameterized model (i.e., **indivExtended**) is approximated as

$$\begin{aligned} p(\theta, \eta, \gamma, \sigma_u, \sigma_v | \mathbf{y}, \mathbf{w}, \mathbf{z}) &\propto p(\mathbf{y}, \mathbf{w}, \mathbf{z} | \theta, \eta, \gamma, \sigma_u, \sigma_v) \\ &\times p(\theta | \mu_\theta, \sigma_\theta) p(\eta | \mu_\eta, \sigma_\eta) p(\gamma | \mu_\gamma, \sigma_\gamma) \\ &\times p(\sigma_u | s_1, s_2) p(\sigma_v | r_1, r_2), \end{aligned} \tag{9}$$

where the first term on the right hand side of Eq. 9 is the likelihood function while the following terms are prior densities for the parameters. For the other two types of datasets, the posterior is simplified accordingly.

6.2 MCMC performance diagnostics

After the MCMC algorithms are finished, a range of diagnostics are calculated on the parameter chains. If multiple simulations are implemented and all of them run through, then potential scale reduction is calculated for each parameter to estimate convergence [12]. This diagnostic is calculated as $\hat{R} = \sqrt{\hat{v}^+/W}$, where W is a measure of the within-sequence variance and \hat{v}^+ is a weighted average of the between-sequence variance (B) and W . Convergence is attained when \hat{R} is close to 1. As a rule of thumb, we have assigned an arbitrary upper bound of $\hat{R} < 1.05$ above which it is assumed that parameters have not reached convergence.

6.3 Model fit

If all parameters have converged, BaFTA calculates deviance information criterion (DIC; [13]), which has been described as a measure of predictive power and a criterion for model fit. DIC approximates the expected predictive deviance, and is calculated as

$$\text{DIC} = 2\hat{D}_{avg}(\mathbf{y}) - D_{\hat{\theta}}(\mathbf{y})$$

where \mathbf{y} denotes the observed data, $\hat{D}_{avg}(\mathbf{y})$ is the mean discrepancy between the data and the model as a function of the parameters θ , averaged over the posterior distribution, while $D_{\hat{\theta}}(\mathbf{y})$ is the discrepancy at the posterior mode (here represented by the point estimate $\hat{\theta}$). It is important to outline that the use of DICs is still controversial

and therefore the results need to be taken with caution (see responses in [13]). In order to improve the measure provided, BaFTA's DIC is calculated as an approximation to the group-marginalized DIC presented by Millar [14].

In addition to the DIC, BaFTA calculates predictive loss as described by Gelfand *et al.* [15]. This measure requires producing a vector of predicted number of offspring $\hat{\mathbf{y}}|\mathbf{y}$, where \mathbf{y} are the observed number of offsprings. With these $\hat{\mathbf{y}}$ we can construct a prediction distribution, integrated across the posterior densities of the parameters as

$$p(\hat{\mathbf{y}}|\mathbf{y}) = \int \dots \int p(\hat{\mathbf{y}}|\boldsymbol{\theta})p(\boldsymbol{\theta}|\mathbf{y})d\theta_0 \dots d\theta_p. \quad (10)$$

The integrals in Eq. 10 are evaluated numerically by means of the converged parameter traces, and the expected predictions are approximated as

$$E[\hat{\mathbf{y}}|\mathbf{y}] = \frac{1}{M} \sum_{m=1}^M E[\hat{\mathbf{y}}|\hat{\boldsymbol{\theta}}_m], \quad (11)$$

where M is the total number of MCMC iterations, and $\hat{\boldsymbol{\theta}}_m$ is the vector of parameters estimated at step m . Mean and upper and lower 95% predictive intervals are included as part of the BaFTA output. With these, BaFTA calculate predictive loss, D , by first calculating a measure of goodness of fit

$$G = \sum_{i=1}^N (E[\hat{\mathbf{y}}|\mathbf{y}] - \mathbf{y})^2 \quad (12)$$

and a measure of model dispersion, or penalty term, given by the predictive variance

$$P = \sum Var[\hat{\mathbf{y}}|\mathbf{y}]. \quad (13)$$

Predictive loss is then calculated as $D = G + P$.

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