

Package ‘paramDemo’

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Type Package

Title Parametric and Non-Parametric Demographic Functions and Applications

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Description Calculate parametric mortality and Fertility models, following packages 'BaSTA' in Colchero, Jones and Rebke (2012) <[doi:10.1111/j.2041-210X.2012.00186.x](https://doi.org/10.1111/j.2041-210X.2012.00186.x)> and 'BaFTA' <<https://github.com/fercol/BaFTA>>, summary statistics (e.g. ageing rates, life expectancy, lifespan equality, etc.), life table and product limit estimators from census data.

License GPL

BugReports <https://github.com/fercol/paramDemo/issues>

NeedsCompilation no

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paramDemo-package	<i>Parametric and Non-Parametric Demographic Functions and Applications</i>
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Description

Functions for parametric and non-parametric calculations of survival, mortality and fertility

Details

Package: paramDemo
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This package contains functions for calculations of parametric mortality, survival and fertility models, as well as non-parametric methods for life tables and product limit estimators.

Author(s)

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CalcAgeingRateMort	<i>Calculating actuarial and reproduction aging rates.</i>
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Description

CalcAgeingRateMort and CalcAgeingRateFert are used to calculate actuarial and reproductive ageing rates from parametric models of mortality and fertility.

Usage

```
CalcAgeingRateMort(theta, x, model = "GO", shape = "simple",  
                    checkTheta = TRUE)  
  
CalcAgeingRateFert(beta, x, modelFert = "quadratic", ageMatur = 0,  
                    checkBeta = TRUE)
```

Arguments

theta	Numerical vector of age-specific mortality parameters (see details).
beta	Numerical vector of age-specific fertility parameters (see details.)
x	Numerical vector of ages at which to calculate mortality.
model	The underlying mortality model to be used. "EX" = exponential, "GO" = Gompertz, "WE" = Weibull and "LO" = logistic (see details).
shape	The overall shape of the model. Values are: simple = no extra parameters added; Makeham = a constant parameter is added to the mortality; and bathtub = a Gompertz declining mortality for early ages and a constant parameter are added to the mortality model (see details).
modelFert	Age-specific fertility model. Options are "quadratic" (default), "PeristeraKostaki", "ColcheroMuller", "Hadwiger", "gamma", "beta", "skewNormal", "gammaMixture", "HadwigerMixture", "skewSymmetric", "skewLogistic" (see details)
ageMatur	Numerical value for the age at sexual maturity.
checkTheta	Logical to verify that the theta parameters conform with the mortality model's specification (see details).
checkBeta	Logical to verify that the beta parameters conform with the fertility model's specification (see details).

Details

The function `CalcAgeingRateMort` uses parametric functions to calculate the actuarial (i.e., mortality) rate of ageing. The function follows the conventions from package `BaSTA` (Colchero and Clark 2012, Colchero *et al.* 2012, Colchero *et al.* 2021) to select the parametric model of mortality. The mortality function describes how the risk of mortality changes with age, and is defined as

$$\mu(x|\theta) = \lim_{\Delta x \rightarrow 0} \frac{\Pr[x < X < x + \Delta x | X > x]}{\Delta x},$$

where X is a random variable for ages at death, $x \geq 0$ are ages and θ is the vector of mortality parameters. (For further details on the mortality and survival models see [CalcMort](#)).

Given a vector of ages x_1, x_2, \dots, x_n specified by the user with argument `x`, the function calculates ageing rates at age x_i as

$$\frac{d}{dx} \ln[\mu(x)]|_{x=x_i},$$

for $i = 1, 2, \dots, n$.

Similarly, function `CalcAgeingRatesFert` calculate reproductive ageing rates from parametric models of age-specific fertility, $g(x)$. It uses a numerical approximation to

$$\frac{d}{dx} \ln[g(x)]|_{x=x_i},$$

for $i = 1, 2, \dots, n$.

Value

The functions output a matrix with the ages at which ageing rates were calculated, the estimated actuarial rate of ageing, and the level of survival at that age.

Author(s)

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See Also

[CalcSurv](#) to calculate age-specific survival, [CalcMort](#) to calculate age-specific mortality, [CalcFert](#) to calculate age-specific fertility.

[CalcAgeMaxFert](#) to calculate the age at maximum fertility from parametric models of age-specific fertility. [CalcRemainLifeExp](#) to calculate remaining life expectancy from parametric models of age-specific mortality.

Examples

```
# Calculate actuarial ageing rate from Gompertz model:
arm <- CalcAgeingRateMort(theta = c(b0 = -5, b1 = 0.1), x = 10)

# Calculate reproductive ageing rate from quadratic model:
arf <- CalcAgeingRateFert(beta = c(b0 = 2, b1 = 0.0025, b2 = 2), x = 10,
  modelFert = "quadratic")
```

CalcAgeMaxFert

Calculating Age at Maximum Fertility and Maximum Fertility.

Description

CalcAgeMaxFert is used to calculate the age at maximum fertility, and the maximum fertility level from parametric models of fertility.

Usage

```
CalcAgeMaxFert (beta, modelFert = "quadratic", ageMatur = 0,
  maxAge = 100)
```

Arguments

beta	Numerical vector of age-specific fertility parameters (see details).
modelFert	Age-specific fertility model. Options are “quadratic” (default), “PeristeraKostaki”, “ColcheroMuller”, “Hadwiger”, “gamma”, “beta”, “skewNormal”, “gammaMixture”, “HadwigerMixture”, “skewSymmetric”, “skewLogistic” (see details)
ageMatur	Numerical value for the age at sexual maturity.
maxAge	Numerical value for the maximum possible age of reproduction.

Details

For a given function g of age-specific fertility, `CalcAgeMaxFert` uses either an analytical solution to

$$\frac{dg}{dx} = 0$$

or a numerical approximation. For details of the parametric models available see [CalcFert](#).

Value

The function outputs a vector with the calculated or estimated age at maximum fertility, the maximum level of fertility, the error in the estimation and the number of iterations (for numerical approximations), and the age at maturity as specified by the user.

Author(s)

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See Also

[CalcSurv](#) to calculate age-specific survival, [CalcMort](#) to calculate age-specific mortality, [CalcFert](#) to calculate age-specific fertility.

[CalcAgeingRateMort](#) to calculate ageing rates from parametric models of age-specific mortality. [CalcRemainLifeExp](#) to calculate remaining life expectancy from parametric models of age-specific mortality.

Examples

```
# Calculate age at maximum fertility from quadratic model:
maxg <- CalcAgeMaxFert(beta = c(b0 = 0.5, b1 = 0.01, b2 = 10))

# Calculate age at maximum fertility from gamma model:
maxg <- CalcAgeMaxFert(beta = c(b0 = 13, b1 = 2, b2 = 0.15),
  modelFert = "gamma")
```

Description

`CalcDemo` is used to calculate age-specific demographic rates and summary statistics from parametric models of survival and fertility.

Usage

```
CalcDemo(theta = NULL, beta = NULL, x = NULL, dx = NULL,
          model = "GO", shape = "simple", modelFert = "quadratic",
          type = "both", minSx = 0.01, summarStats = TRUE,
          ageMatur = 0, maxAge = NULL, agesAR = NULL,
          SxValsAR = NULL)
```

Arguments

theta	Numerical vector of age-specific mortality parameters (see details).
beta	Numerical vector of age-specific fertility parameters (see details).
x	Numerical vector of ages. If NULL (default), ages are constructed from age 0 to the age when the survival function reaches 0.0001.
dx	Numerical value for age increments. If NULL, the default value is 0.01.
model	Mortality model, options are "EX" = exponential (i.e., constant mortality with age), "GO" = Gompertz (default), "WE" = Weibull, or "LO" = logistic.
shape	The overall shape of the mortality model. Values are: "simple" = no extra parameters added; "Makeham" = a constant parameter is added to the mortality; and "bathtub" = a Gompertz declining mortality for early ages and a constant parameter are added to the mortality model (see details).
modelFert	Age-specific fertility model. Options are "quadratic" (default), "PeristeraKostaki", "ColcheroMuller", "Hadwiger", "gamma", "beta", "skewNormal", "gammaMixture", "HadwigerMixture", "skewSymmetric", "skewLogistic" (see details)
type	Character string specifying the demographic rates to be calculated. Options are "both" (default), "survival", "fertility".
minSx	Numerical value specifying the lower bound of the survival function to find the maximum age. The default is 0.01.
summarStats	Logical specifying whether summary statistics such as life expectancy, lifespan equality and ageing rates at the specified ages should be calculated.
ageMatur	Numerical value specifying the age at sexual maturity, used as the lower bound for the age-specific fertility. Default is 0.
maxAge	Numerical values for the maximum age for survival and fertility demographic rates. If NULL (default), the maximum age is calculated when the survival function reaches minSx.
agesAR	Numerical vector of ages at which ageing rates should be calculated. If NULL (default) they are calculated at the ages when the survival function reaches 0.5, 0.2, and 0.05.
SxValsAR	Alternative to agesAR, numerical value for the levels of survival at which ageing rates should be calculated. If NULL (default) they are calculated at the ages when the survival function reaches 0.5, 0.2, and 0.05.

Details

1) Age-specific mortality and survival models:

The function `CalcDemo` uses parametric functions to calculate age-specific survival, defined as the probability of surviving to a given age. The function follows the conventions from package `BaSTA` (Colchero and Clark 2012, Colchero *et al.* 2012, Colchero *et al.* 2021). The mortality function describes how the risk of mortality changes with age, and is defined as

$$\mu(x|\theta) = \lim_{\Delta x \rightarrow 0} \frac{\Pr[x < X < x + \Delta x | X > x]}{\Delta x},$$

where X is a random variable for ages at death, $x \geq 0$ are ages and θ is the vector of mortality parameters. From the mortality function, the survival function is then given by

$$S(x|\theta) = \exp\left[-\int_0^x \mu(t|\theta) dt\right].$$

1.1) Argument “model”:

The `model` argument allows the user to choose between four basic mortality functions, namely

(a) `model = “EX”`: The exponential model (Cox and Oakes 1974), with constant mortality with age, specified as

$$\mu_b(x|\theta) = b,$$

where $b > 0$, with survival

$$S_b(x|\theta) = \exp[-bx].$$

(b) `model = “GO”`: The Gompertz mortality model (Gompertz 1925, Pletcher 1999), calculated as

$$\mu_b(x|\theta) = \exp(b_0 + b_1 x),$$

where $-\infty < b_0, b_1 < \infty$, with survival

$$S_b(x|\theta) = \exp\left[\frac{e^{b_0}}{b_1} (1 - e^{b_1 x})\right].$$

(c) `model = “WE”`: The Weibull mortality model (Pinder III *et al.* 1978) calculated as

$$\mu_b(x|\theta) = b_0 b_1^{b_0} x^{b_0-1},$$

where $b_0, b_1 > 0$, with survival

$$S_b(x|\theta) = \exp\left[-(b_1 x)^{b_0}\right].$$

(d) `model = “LO”`: The logistic mortality model (Pletcher 1999), calculated as

$$\mu_b(x|\theta) = \frac{\exp(b_0 + b_1 x)}{1 + b_2 \frac{e^{b_0}}{b_1} (e^{b_1 x} - 1)},$$

where $b_0, b_1, b_2 > 0$, with survival

$$S_b(x|\theta) = \left[1 + b_2 \frac{e^{b_0}}{b_1} (e^{b_1 x} - 1) \right]^{-1/b_2}.$$

1.2) Argument “shape”:

The shape argument allows the user to extend these models in order to explore more complex mortality shapes.

(a) shape = “simple”: (default) Leaves the model as defined above, with mortality given by

$$\mu(x|\theta) = \mu_b(x|\theta)$$

and survival

$$S(x|\theta) = S_b(x|\theta).$$

(b) shape = “Makeham”: A constant is added to the mortality, such that the mortality is given by

$$\mu(x|\theta) = c + \mu_b(x|\theta_1),$$

where $\theta = [c, \theta_1]$, and with survival

$$S(x|\theta) = e^{-cx} S_b(x|\theta_1)$$

The most common models with this shape is the Gompertz-Makeham model (Gompertz 1825, Makeham 1866).

(c) shape = “bathtub”: produces a concave shapes in mortality by adding a declining Gompertz term and a constant parameter to the basic mortality model, where the mortality function is

$$\mu(x|\theta) = \exp(a_0 - a_1 x) + c + \mu_b(x|\theta_1),$$

where $a_0 \in \mathbb{R}$, $a_1, c \geq 0$ and $\theta_1 \subset \theta$ are specified based on argument model, and with survival

$$S(x|\theta) = \exp \left[\frac{e^{a_0}}{a_1} (e^{a_1 x} - 1) - cx \right] S_b(x|\theta_1).$$

The most widely use “bathtub” shaped model is the **Siler mortality model** (Siler 1979), which provides considerably good fits to mammalian data. The arguments for the Siler model are:

```
CalcDemo(..., model = "GO", shape = "bathtub", ...)
```

2) Specifying theta parameters:

Argument theta requires a numerical vector of parameters. For instance, for a Gompertz model with simple shape and with parameter vector $\theta^\top = [b_0, b_1]$ where $b_0 = -5$ and $b_1 = 0.1$, the argument should be specified as

```
CalcDemo(theta = c(b0 = -5, b1 = 0.1), ...)
```

Note that in this example the parameter names are specified directly, this is required when checkTheta = FALSE. Although assigning the names to each parameter is not necessary when checkTheta = TRUE, it is advisable to ensure that the right values are assigned to the right parameter.

If argument `checkTheta` is set to `TRUE`, then the vector of `theta` parameters is verified for consistency with the requirements of the model and shape selected.

3) Age-specific fertility models:

The age-specific fertility models correspond to the expected number of offspring produced by adults of a given age. Therefore, for a random variable Y_x with realizations y_x for the number of offspring produced by adults of age x , we have that $E(Y_x) = g(x|\beta)$, where $g : \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$ is a non-negative smooth fertility function and β is a vector of parameters to be estimated. The functional forms of function g fall in two main categories, namely polynomial and distributional models.

3.a) Polynomial:

Of the models available in `paramDemo`, the “quadratic”, “PeristeraKostaki” (Peristera and Kostaki 2007), and “ColcheroMuller” (Colchero *et al.* 2021, Muller *et al.* 2020) fall within the polynomial category. Both, the “PeristeraKostaki” and “ColcheroMuller” are non-symmetric around the age at maximum fertility.

3.b) Distributional:

The distributional models are of the form

$$g(x|\beta) = Rf(x|\beta_1),$$

where $f : \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$ is a probability density function, $R > 0$ is a parameter for the total fertility rate, and $\beta_1 \subset \beta$ is a vector of parameters. The “Hadwiger” (Hadwiger 1940), “gamma” (Hoem *et al.* 1981), “beta” (Hoem *et al.* 1981), “skewNormal” (Mazzuco and Scarpa 2011, 2015), “gammaMixture” (Hoem *et al.* 1981), “HadwigerMixture” (Chandola *et al.* 1991), “skewSymmetric” (Mazzuco and Scarpa 2011, 2015), and “skewLogistic” (Asili *et al.* 2014) all fall in this category. Notably, the “gammaMixture”, “HadwigerMixture”, “skewSymmetric”, “skewLogistic” are appropriate when fertility might be bimodal (Hoem *et al.* 1981, Chandola *et al.* 1999, Mazzuco and Scarpa 2011, 2015, Asili *et al.* 2014).

4) Specifying beta parameters:

Argument `beta` requires a vector of parameters. For instance, for a quadratic model with parameter vector $\beta^T = [b_0, b_1, b_2]$ where $b_0 = 0.5$, $b_1 = 0.01$ and $b_2 = 10$, the argument should be specified as

```
CalcDemo(..., beta = c(b0 = 0.5, b1 = 0.01, b2 = 10), ...)
```

Note that in this example the parameter names are specified directly, this is required when `checkBeta = FALSE`. Although assigning the names to each parameter is not necessary when `checkBeta = TRUE`, it is advisable to ensure that the right values are assigned to the right parameter.

If argument `checkBeta` is set to `TRUE`, then the vector of `beta` parameters is verified for consistency with the requirements of the fertility model selected.

5) Summary statistics:

5.1) Ageing rates:

Given a vector of ages x_1, x_2, \dots, x_n specified by the user with argument `agesAR`, the function calculates ageing rates at age x_i as

$$\frac{d}{dx} \ln[\mu(x)]|_{x=x_i},$$

for $i = 1, 2, \dots, n$.

5.2) Ages at different levels of survival:

The function calculates the ages when the survival function reaches specific values (default at 0.2, 0.1, 0.05), commonly used as population measures of old age. Thus, for a given value $s = S(x)$, the function computes the inverse function

$$x = S^{-1}(s).$$

5.3) Remaining life expectancy:

The function calculates the life expectancy at birth as

$$e_0 = \int_0^{\infty} S(t) dt.$$

5.4) Measures of inequality and equality:

The function calculates different measures of inequality and equality in the distribution of ages at death that results from the parametric model:

- Lifespan inequality: (Demetrius 1974, Keyfitz and Caswell 2005) given by

$$H = - \frac{\int_0^{\infty} S(x) \ln[S(x)] dx}{e_0}$$

- Lifespan equality: (Colchero *et al.* 2016, Colchero *et al.* 2021) given by

$$\varepsilon = -\ln H.$$

- Gini coefficient: (Gini 1912, Shkolnikov *et al.* 2003) given by

$$G = 1 - \frac{1}{e_0} \int_0^{\infty} [l(x)]^2 dx$$

- Coefficient of variation: given by

$$CV = \frac{\sqrt{\sigma^2}}{e_0},$$

where σ^2 is the variance in ages at death.

Value

CalcDemo returns an object of class “paramDemo” with output consisting of two lists, one for survival and one for fertility. The survival list can be called as `object$surv` while the fertility list is in `object$fert`. Both include the following outputs:

functs	data.frame including the following columns for survival: age, mort for the mortality function, surv for the survival, pdf for the probability density function of ages at death, and cumhaz for the cumulative hazards. For fertility it includes columns for age and fert for the age-specific fertility.
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summStats	list with elements: calculated indicating whether summary statistics were calculated, ageingRates with the resulting actuarial ageing rates, and summStatsMort with ages at which the survival function reaches different levels (default 0.5, 0.2, 0.05) (e.g., AgeSx=0.5), with the life expectancy lifeExp, lifespIneq for the lifespan inequality (see Demetrius 1974), lifespEqual with the lifespan equality as in Colchero <i>et al.</i> (2021), Gini for the Gini coefficient, and CoeffVar for the coefficient of variation in the distribution of ages at death. For fertility, the list includes a logical calculated to indicate if summary statistics were calculated, and summStatsFert with the age at maximum fertility calculations (see CalcAgeMaxFert).
settings	list with the details of the parameters and the models used.
analyzed	logical indicating whether surv or fert were calculated.

Author(s)

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See Also

[CalcSurv](#) to calculate age-specific survival, [CalcMort](#) to calculate age-specific mortality, [CalcFert](#) to calculate age-specific fertility.

[CalcAgeingRateMort](#) to calculate ageing rates from parametric models of age-specific mortality. [CalcRemainLifeExp](#) to calculate remaining life expectancy from parametric models of age-specific mortality. [CalcAgeMaxFert](#) to calculate the age at maximum fertility from parametric models of age-specific fertility.

[CalcLifeHist](#) to calculate life history variables from parametric demographic models.

Examples

```
# Create paramDemo object from Gompertz mortality and
# quadratic fertility:
dem <- CalcDemo(theta = c(b0 = -5, b1 = 0.1),
                beta = c(b0 = 0.5, b1 = 0.01, b2 = 10),
                summarStats = TRUE, agesAR = c(5, 10))

# Plot demographic object:
plot(dem)
```

CalcDiscrDemo	<i>Calculating Demographic Rates on Discrete Age Intervals from Parametric Age-Specific Mortality</i>
---------------	---

Description

CalcDiscrDemo is used to calculate survival and fertility functions (i.e., lx , px , and qx) on discrete age intervals from an object of class “paramDemo” created with function CalcDemo.

Usage

```
CalcDiscrDemo(demo, dx = 1)
```

Arguments

demo	Object of class “paramDemo” created with function CalcDemo
dx	Numeric value for the age increments. Default is $dx = 1$

Details

CalcDiscrDemo takes the continuous survival functions from an object of class “paramDemo” and calculates the basic survival probabilities and, if available, fertility rates on discrete age intervals.

Let $x \geq 0$ and $\omega \in \mathbb{N}$ be the next integer of the age when the survival function $S(x)$ reaches the minimum. Given the age increments, Δx , specified with argument dx , the function creates a partition of $[0, \omega]$ such that $[x_i, x_i + \Delta x) \subset [0, \omega]$ for $i = 1, \dots, n$. At each age interval it calculates the discrete survival, lx , as

$$l_{x_i} = S(x_i).$$

The age- or stage-specific survival probability, px , is calculated as

$$p_{x_i} = \frac{S(x_i + \Delta x)}{S(x_i)},$$

while the age- or stage-specific mortality probability, qx , is $q_{x_i} = 1 - p_{x_i}$.

If fertility was also calculated with function CalcDemo, then the function includes the discrete age- or stage-specific fertility, bx , as

$$b_{x_i} = b\left(x_i + \frac{\Delta x}{2}\right) \Delta x,$$

where $b(x)$ is the continuous fertility function.

Value

CalcDiscrDemo returns an object of class “discrDemo” that consist of a matrix with the following columns:

age	Partition of the full age subset into discrete intervals
lx	Survival or cumulative survival

px	The age- or stage-specific survival probability
qx	The age- or stage-specific mortality probability
bx	If available, the age- or stage-specific fertility

Author(s)

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See Also

[CalcDemo](#) to create an object of class “paramDemo”.

Examples

```
# Create paramDemo object from Gompertz mortality and
# quadratic fertility:
dem <- CalcDemo(theta = c(b0 = -5, b1 = 0.1),
                beta = c(b0 = 0.5, b1 = 0.01, b2 = 10),
                summarStats = TRUE, agesAR = c(5, 10))

# Create discrete demographic object:
demDisc <- CalcDiscrDemo(dem, dx = 1)
```

CalcFert	<i>Calculating Parametric Age-Specific Fertility.</i>
----------	---

Description

CalcFert is used to calculate age-specific fertility from different parametric models.

Usage

```
CalcFert(beta, x, modelFert = "quadratic", checkBeta = TRUE)
```

Arguments

beta	Numerical vector of age-specific fertility parameters (see details).
x	Numerical vector of ages at which to calculate fertility.
modelFert	Age-specific fertility model. Options are “quadratic” (default), “PeristeraKostaki”, “ColcheroMuller”, “Hadwiger”, “gamma”, “beta”, “skewNormal”, “gammaMixture”, “HadwigerMixture”, “skewSymmetric”, “skewLogistic” (see details)
checkBeta	Logical to verify that the beta parameters conform with the model’s specification (see details).

Details

1) Age-specific fertility models:

The age-specific fertility models correspond to the expected number of offspring produced by adults of a given age. Therefore, for a random variable Y_x with realizations y_x for the number of offspring produced by adults of age x , we have that $E(Y_x) = g(x|\beta)$, where $g : \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$ is a non-negative smooth fertility function and β is a vector of parameters to be estimated. The functional forms of function g fall in two main categories, namely polynomial and distributional models.

2.a) Polynomial:

Of the models available in paramDemo, the “quadratic”, “PeristeraKostaki” (Peristera and Kostaki 2007), and “ColcheroMuller” (Colchero *et al.* 2021, Muller *et al.* 2020) fall within the polynomial category. Both, the “PeristeraKostaki” and “ColcheroMuller” are non-symmetric around the age at maximum fertility.

2.b) Distributional:

The distributional models are of the form

$$g(x|\beta) = Rf(x|\beta_1),$$

where $f : \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$ is a probability density function, $R > 0$ is a parameter for the total fertility rate, and $\beta_1 \in \beta$ is a vector of parameters. The “Hadwiger” (Hadwiger 1940), “gamma” (Hoem *et al.* 1981), “beta” (Hoem *et al.* 1981), “skewNormal” (Mazzuco and Scarpa 2011, 2015), “gammaMixture” (Hoem *et al.* 1981), “HadwigerMixture” (Chandola *et al.* 1991), “skewSymmetric” (Mazzuco and Scarpa 2011, 2015), and “skewLogistic” (Asili *et al.* 2014) all fall in this category. Notably, the “gammaMixture”, “HadwigerMixture”, “skewSymmetric”, “skewLogistic” are appropriate when fertility might be bimodal (Hoem *et al.* 1981, Chandola *et al.* 1999, Mazzuco and Scarpa 2011, 2015, Asili *et al.* 2014).

2) Specifying beta parameters:

Argument beta requires a vector of parameters. For instance, for a quadratic model with parameter vector $\beta^\top = [0.5, 0.01, 10]$, the argument should be specified as `theta = c(b0 = 0.5, b1 = 0.01, b2 = 10)`. Note that in this example the parameter names are specified directly, this is required when `checkBeta = FALSE`. Although assigning the names to each parameter is not necessary when `checkBeta = TRUE`, it is advisable to ensure that the right values are assigned to the right parameter.

If argument `checkBeta` is set to `TRUE`, then the vector of beta parameters is verified for consistency with the requirements of the model and shape selected.

Value

CalcFert returns a vector of class “numeric” with the fertility values at the specified ages.

Author(s)

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See Also

[CalcMort](#) to calculate age-specific mortality, [CalcSurv](#) to calculate age-specific survival

Examples

```
# Age specific fertility based on quadratic model (default):
fert <- CalcFert(beta = c(b0 = 0.5, b1 = 0.01, b2 = 10), x = 10)

# Age specific fertility based on gamma model:
fert <- CalcFert(beta = c(b0 = 13, b1 = 2, b2 = 0.15), x = 10,
                 modelFert = "gamma")
```

CalcLifeHist	<i>Calculating life history variables from parametric models of age-specific demographic rates.</i>
--------------	---

Description

CalcLifeHist uses parametric models of survival and fertility to calculate age-specific demographic rates, stable age structure, reproductive values, sensitivity and elasticities of the stable population growth rate to demographic rates, as well as different life history variables such as generation time or population entropy.

Usage

```
CalcLifeHist(theta = NULL, beta = NULL, dx = NULL,
             model = "GO", shape = "simple",
             modelFert = "quadratic", ageMatur = 0,
             maxAge = NULL, lambdaMethod = "matrix")
```

Arguments

theta	Numerical vector of age-specific mortality parameters (see details).
beta	Numerical vector of age-specific fertility parameters (see details).
dx	Numerical value for the age-interval increments, default is 1.
model	Mortality model, options are "EX" = exponential (i.e., constant mortality with age), "GO" = Gompertz (default), "WE" = Weibull, or "LO" = logistic.
shape	The overall shape of the mortality model. Values are: "simple" = no extra parameters added; "Makeham" = a constant parameter is added to the mortality; and "bathtub" = a Gompertz declining mortality for early ages and a constant parameter are added to the mortality model (see details).
modelFert	Age-specific fertility model. Options are "quadratic" (default), "PeristeraKostaki", "ColcheroMuller", "Hadwiger", "gamma", "beta", "skewNormal", "gammaMixture", "HadwigerMixture", "skewSymmetric", "skewLogistic" (see details)
ageMatur	Numerical value for the age at maturity.
maxAge	Numerical value for the maximum age. If NULL (default), it is calculated from the survival (see details).
lambdaMethod	Character string specifying the method to calculate the intrinsic population growth rate. Values are "matrix" for methods based on population projection matrices, or "Lotka" for numerical approximation of the root of the Lotka equation (see details)

Details

1) Age-specific mortality and survival models:

The function CalcDemo uses parametric functions to calculate age-specific survival, defined as the probability of surviving to a given age. The function follows the conventions from package BaSTA

(Colchero and Clark 2012, Colchero *et al.* 2012, Colchero *et al.* 2021). The mortality function describes how the risk of mortality changes with age, and is defined as

$$\mu(x|\theta) = \lim_{\Delta x \rightarrow 0} \frac{\Pr[x < X < x + \Delta x | X > x]}{\Delta x},$$

where X is a random variable for ages at death, $x \geq 0$ are ages and θ is the vector of mortality parameters. From the mortality function, the survival function is then given by

$$S(x|\theta) = \exp\left[-\int_0^x \mu(t|\theta)dt\right].$$

1.1)Argument “model”:

The model argument allows the user to choose between four basic mortality functions, namely

(a) model = “EX”: The exponential model (Cox and Oakes 1974), with constant mortality with age, specified as

$$\mu_b(x|\theta) = b,$$

where $b > 0$, with survival

$$S_b(x|\theta) = \exp[-bx].$$

(b) model = “G0”: The Gompertz mortality model (Gompertz 1925, Pletcher 1999), calculated as

$$\mu_b(x|\theta) = \exp(b_0 + b_1x),$$

where $-\infty < b_0, b_1 < \infty$, with survival

$$S_b(x|\theta) = \exp\left[\frac{e^{b_0}}{b_1} (1 - e^{b_1x})\right].$$

(c) model = “WE”: The Weibull mortality model (Pinder III *et al.* 1978) calculated as

$$\mu_b(x|\theta) = b_0 b_1^{b_0} x^{b_0-1},$$

where $b_0, b_1 > 0$, with survival

$$S_b(x|\theta) = \exp\left[-(b_1x)^{b_0}\right].$$

(d) model = “LO”: The logistic mortality model (Pletcher 1999), calculated as

$$\mu_b(x|\theta) = \frac{\exp(b_0 + b_1x)}{1 + b_2 \frac{e^{b_0}}{b_1} (e^{b_1x} - 1)},$$

where $b_0, b_1, b_2 > 0$, with survival

$$S_b(x|\theta) = \left[1 + b_2 \frac{e^{b_0}}{b_1} (e^{b_1x} - 1)\right]^{-1/b_2}.$$

1.2) Argument “shape”:

The shape argument allows the user to extend these models in order to explore more complex mortality shapes.

(a) shape = “simple”: (default) Leaves the model as defined above, with mortality given by

$$\mu(x|\boldsymbol{\theta}) = \mu_b(x|\boldsymbol{\theta})$$

and survival

$$S(x|\boldsymbol{\theta}) = S_b(x|\boldsymbol{\theta}).$$

(b) shape = “Makeham”: A constant is added to the mortality, such that the mortality is given by

$$\mu(x|\boldsymbol{\theta}) = c + \mu_b(x|\boldsymbol{\theta}_1),$$

where $\boldsymbol{\theta} = [c, \boldsymbol{\theta}_1]$, and with survival

$$S(x|\boldsymbol{\theta}) = e^{-cx} S_b(x|\boldsymbol{\theta}_1)$$

The most common models with this shape is the Gompertz-Makeham model (Gompertz 1825, Makeham 1866).

(c) shape = “bathtub”: produces a concave shapes in mortality by adding a declining Gompertz term and a constant parameter to the basic mortality model, where the mortality function is

$$\mu(x|\boldsymbol{\theta}) = \exp(a_0 - a_1 x) + c + \mu_b(x|\boldsymbol{\theta}_1),$$

where $a_0 \in \mathbb{R}$, $a_1, c \geq 0$ and $\boldsymbol{\theta}_1 \subset \boldsymbol{\theta}$ are specified based on argument model, and with survival

$$S(x|\boldsymbol{\theta}) = \exp \left[\frac{e^{a_0}}{a_1} (e^{a_1 x} - 1) - cx \right] S_b(x|\boldsymbol{\theta}_1).$$

The most widely use “bathtub” shaped model is the **Siler mortality model** (Siler 1979), which provides considerably good fits to mammalian data. The arguments for the Siler model are:

```
CalcLifeHist(..., model = "GO", shape = "bathtub", ...)
```

2) Specifying theta parameters:

Argument theta requires a numerical vector of parameters. For instance, for a Gompertz model with simple shape and with parameter vector $\boldsymbol{\theta}^\top = [b_0, b_1]$ where $b_0 = -5$ and $b_1 = 0.1$, the argument should be specified as

```
CalcDemo(theta = c(b0 = -5, b1 = 0.1), ...)
```

Note that in this example the parameter names are specified directly, this is required when checkTheta = FALSE. Although assigning the names to each parameter is not necessary when checkTheta = TRUE, it is advisable to ensure that the right values are assigned to the right parameter.

If argument checkTheta is set to TRUE, then the vector of theta parameters is verified for consistency with the requirements of the model and shape selected.

3) Age-specific fertility models:

The age-specific fertility models correspond to the expected number of offspring produced by adults of a given age. Therefore, for a random variable Y_x with realizations y_x for the number of offspring

produced by adults of age x , we have that $E(Y_x) = g(x|\beta)$, where $g : \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$ is a non-negative smooth fertility function and β is a vector of parameters to be estimated. The functional forms of function g fall in two main categories, namely polynomial and distributional models.

3.a) Polynomial:

Of the models available in paramDemo, the “quadratic”, “PeristeraKostaki” (Peristera and Kostaki 2007), and “ColcheroMuller” (Colchero *et al.* 2021, Muller *et al.* 2020) fall within the polynomial category. Both, the “PeristeraKostaki” and “ColcheroMuller” are non-symmetric around the age at maximum fertility.

3.b) Distributional:

The distributional models are of the form

$$g(x|\beta) = Rf(x|\beta_1),$$

where $f : \mathbb{R}_{\geq 0} \rightarrow \mathbb{R}_{\geq 0}$ is a probability density function, $R > 0$ is a parameter for the total fertility rate, and $\beta_1 \subset \beta$ is a vector of parameters. The “Hadwiger” (Hadwiger 1940), “gamma” (Hoem *et al.* 1981), “beta” (Hoem *et al.* 1981), “skewNormal” (Mazzuco and Scarpa 2011, 2015), “gammaMixture” (Hoem *et al.* 1981), “HadwigerMixture” (Chandola *et al.* 1991), “skewSymmetric” (Mazzuco and Scarpa 2011, 2015), and “skewLogistic” (Asili *et al.* 2014) all fall in this category. Notably, the “gammaMixture”, “HadwigerMixture”, “skewSymmetric”, “skewLogistic” are appropriate when fertility might be bimodal (Hoem *et al.* 1981, Chandola *et al.* 1999, Mazzuco and Scarpa 2011, 2015, Asili *et al.* 2014).

4) Specifying beta parameters:

Argument beta requires a vector of parameters. For instance, for a quadratic model with parameter vector $\beta^\top = [b_0, b_1, b_2]$ where $b_0 = 0.5$, $b_1 = 0.01$ and $b_2 = 10$, the argument should be specified as

```
CalcLifeHist(..., beta = c(b0 = 0.5, b1 = 0.01, b2 = 10), ...)
```

Note that in this example the parameter names are specified directly, this is required when checkBeta = FALSE. Although assigning the names to each parameter is not necessary when checkBeta = TRUE, it is advisable to ensure that the right values are assigned to the right parameter.

If argument checkBeta is set to TRUE, then the vector of beta parameters is verified for consistency with the requirements of the fertility model selected.

5) Methods to estimate lambda, r, stable age structure and reproductive values:

If argument lambdaMethod is set to “matrix”, the function calculates the asymptotic population growth rate λ as the dominant eigen-value of the resulting population projection matrix A (Caswell and Wegner 1978, Kroon *et al.* 1986, Caswell 2001). The intrinsic population growth rate is then $r = \log \lambda$, while the stable age-structure, $\omega^\top = [\omega_0, \omega_1, \dots, \omega_\tau]$, where τ is the maximum age of the population, is given by the corresponding right eigen vector, standardized by its norm. The reproductive value is the corresponding left eigen vector, $\nu^\top = [\nu_0, \nu_1, \dots, \nu_\tau]$, standardized such that $\nu_0 = 1$.

If argument lambdaMethod is set to “Lotka”, the function estimates the intrinsic population growth rate, r , by finding the real root of Lotka’ (1913) equation, given by

$$\int_0^\tau e^{-rx} S(x) m(x) dx = 1.$$

The stable population structure is then calculated as

$$\omega_x = \frac{e^{-rx} S(x)}{\sum_{k=0}^{\tau} e^{-rk} S(k)},$$

while the reproductive value is given by

$$\nu_x = \frac{\int_x^{\tau} e^{-r(k-x)} S(k) m(k) dk}{S(x)}.$$

The function then calculates the sensitivities of lambda to age-specific survival as

$$s_{p,x} = \frac{\nu_x \omega_{x+1}}{\langle \nu \omega \rangle}, \quad \text{for } x < \tau$$

where the denominator is the inner product, and the sensitivity of lambda to the reproductive value at x is given by

$$s_{m,x} = \frac{\nu_1 \omega_{x+1}}{\langle \nu \omega \rangle}, \quad \text{for } x < \tau$$

Elasticities are calculated as

$$e_{p,x} = \frac{p_x}{\lambda} s_{p,x} \text{ and } e_{m,x} = \frac{m_x}{\lambda} s_{m,x}.$$

6) Calculation of life history variables

The first life history variables are the intrinsic population growth rate r and the stable population growth rate $\lambda = e^r$, described in the previous section.

The function also provides a number of life history variables described by Tuljapurkar *et al.* (2009). For instance, it provides the generation time for the stable population as

$$T_s = \int_0^{\tau} x e^{-rx} S(x) m(x) dx,$$

as well as the cohort generation time, given by

$$T_c = \frac{\int_0^{\tau} x S(x) m(x) dx}{R_0},$$

where R_0 is the net reproductive rate, given by

$$R_0 = \int_0^{\tau} S(x) m(x) dx.$$

It provides the demographic dispersion given by

$$\sigma_d^2 = \frac{\int_0^{\tau} (x - T_c)^2 S(x) m(x) dx}{R_0}$$

which measures the dispersion of reproduction across ages.

Finally, it calculates the population entropy as proposed by Demetrius (1974), given by

$$H = - \frac{\int_0^{\tau} \rho(x) \log \rho(x) dx}{T_s}$$

where $\rho(x) = e^{-rx} S(x) m(x)$.

Value

The function produces an object of class “PDlifeHist”, which consists of a list with the following elements:

demoTab	A data frame with the resulting individual ages, the survival $S(x)$, the age-specific survival probability p_x , the age-specific mortality probability q_x , the age-specific fertility rate m_x , the stable age structure ω_x , the age specific reproductive value nu_x , and the sensitivities and elasticities.
lifeHist	A data frame with the life history variables described in details, including a description.
settings	A list with the information of the models and parameters as provided by the user.

Author(s)

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See Also

[CalcDemo](#) to calculate parametric demographic functions.

Examples

```
# Calculate life histories on the default models:
test <- CalcLifeHist(theta = c(b0 = -3, b1 = 0.1),
                    beta = c(b0 = 1, b1 = 0.01, b2 = 5),
                    ageMatur = 2)

# Print results:
test

# Plot results:
plot(test, type = "all")
```

CalcLifeTable

*Calculating a Life Table from Data.***Description**

CalcLifeTable uses non-parametric methods to calculate life tables and confidence intervals.

Usage

```
CalcLifeTable(ageLast, ageFirst = NULL, departType, dx = 1,
              calcCIs = FALSE, nboot = 1000, alpha = 0.05)
```

Arguments

ageLast	Numerical vector with the ages at last detection (i.e., death and censoring) (see details)
ageFirst	Numerical vector of ages at first detection (i.e., truncation). If NULL then all values are set to 0 (see details).
departType	Character string vector for the type of departure (i.e., last detection), with values “D” for death and “C” for censoring (see details).
dx	Age interval size, default set at 1 (see details)
calcCIs	Logical indicating whether confidence intervals should be calculated
nboot	Number of bootstrap iterations
alpha	Alpha level. Default is 0.05 for 95% CIs

Details**1) Data structure:**

CalcLifeTable allows to construct life tables for data that includes the following types of records:

- **Uncensored:** individuals with known ages at death;
- **right-censored:** individuals last seen alive;
- **left-truncated:** individuals born before the start of the study and are truncated at the age of entry.

The data required are the ages at last detection (i.e., *uncensored* or *right-censored*) passed through argument “ageLast”, the type of departure via argument “departType”, which takes two values, namely “D” for death, and “C” for censored (i.e., right-censored).

In addition, if there is *left-truncation*, it takes the ages at entry to the study by means of argument “ageFirst”. If all the individuals were born during the study, the value of “ageFirst” can be left as NULL, which will make them all equal to 0.

2) Computing life tables

To calculate life tables, the function uses conventional formal demographic methods as depicted by Preston *et al.* (2001). Argument “ageLast” provides a vector of ages at last detection, $x^\top =$

$[x_1, x_2, \dots, x_n]$, while argument “ageFirst” provides a vector of ages at first detection $\mathbf{y}^\top = [y_1, y_2, \dots, y_n]$. From argument “departType” the function produces an indicator vector for censoring $\mathbf{v} = \{v_i\}_{i \in \mathbb{N}_n}$ where $v_i = 1$ if individual i is censored and 0 otherwise.

The function creates a partition of the interval of ages between 0 and $\max(x)$, for age intervals $[x, x + \Delta x)$ where Δx is specified by argument “dx”. As default $\Delta x = 1$. At each age interval, the function calculates the following variables:

- N_x : which corresponds to number of individuals that entered the interval, but considering the proportion of time they were present within the interval as a function of left-truncation. It is given by

$$N_x = \sum_{i \in I_x} \lambda_{i,x},$$

where I_x is the subset of individuals recorded within the interval, and $\lambda_{i,x}$ is the proportion of time during the age interval each individual was present in the study. For individuals that entered the study before x then $\lambda_{i,x} = 1$, while for those that were truncated within the interval $\lambda_{i,x} = (x + \Delta x - y_i) / \Delta x$.

- D_x : the number of individuals dying in the interval.
- q_x : the age-specific mortality probability, calculated as $q_x = D_x / N_x$.
- p_x : the age-specific survival probability, given by $p_x = 1 - q_x$.
- l_x : the life table survival calculated as

$$l_x = \prod_{j=0}^{x-1} p_j$$

where $l_0 = 1$.

- a_x : Proportion of the interval lived by those that died in the interval, given by

$$a_x = \frac{\sum_{i \in J_x} \delta_{i,x}}{D_x}$$

where J_x is the subset of individuals that died within the interval, and $\delta_{i,x}$ is the proportion lived by those individuals from the start of the interval to their deaths, this is $\delta_{i,x} = (x_i - x) / \Delta x$.

- L_x : The number of individual years lived within the interval, given by

$$L_x = l_x(1 - a_x q_x)$$

- T_x : The total number of individual years lived after age x , given by $T_x = \sum_{j=x}^{\infty} L_j \Delta x$
- e_x : the remaining life expectancy at the beginning of each age interval, calculated as $e_x = T_x / l_x$.

3) Calculating confidence intervals If argument “calcCIs” is set to TRUE, the function uses a non-parametric bootstrap by sampling with replacement the data. Argument nboot specifies the number of bootstrap steps, with default nboot = 2000. From each re-sampled dataset, it uses function [CalcLifeTable](#) to construct the corresponding life table and stores the values of \$l_x\$, \$q_x\$, \$p_x\$, and \$e_x\$ from each iteration. From these, it calculates quantiles at the given alpha level.

Value

CalcLifeTable returns an object of class “paramDemoLT” with output consisting of a list with the life table and, if indicated by the user, with the confidence interval information. The life table in matrix format includes the following columns:

Ages	Ages with increments given by dx
Nx	Number of individuals entering the interval, does not need to be an integer since it considers truncation
Dx	Number of individuals that died within the age interval
lx	Survival (i.e., cumulative survival)
px	Age-specific survival probability
qx	Age-specific mortality probability
Lx	Number of individual years lived within the interval
Tx	Number of individual years lived after age x
ex	Remaining life expectancy at each age

If argument calcCIs = TRUE, the function also returns a list containing the following components:

lx	Matrix with Ages and mean and upper and lower CIs for the life table survival
qx	Matrix with Ages and mean and upper and lower CIs for the age-specific mortality probability
px	Matrix with Ages and mean and upper and lower CIs for the age-specific survival probability
ex	Matrix with Ages and mean and upper and lower CIs for the remaining life expectancy
Settings	Numerical vector including whether CIs were calculated, the number of bootstrap iterations, “nboot” and the alpha level “alpha”

Author(s)

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References

Preston, S.H., Heuveline, P. and Guillot, M. (2001) Demography: Measuring and Modeling Population Processes. Blackwell, Oxford.

See Also

[CalcProductLimitEst](#) to calculate product limit estimators.

Examples

```
# Simulate age at death data from Gompertz model:
ages <- SampleRandAge(n = 100, theta = c(b0 = -5, b1 = 0.1))

# Calculate life table:
lt <- CalcLifeTable(ageLast = ages, departType = rep("D", 100))

# Calculate life table with 95% CIs:
ltCIs <- CalcLifeTable(ageLast = ages, departType = rep("D", 100),
  calcCIs = TRUE, nboot = 100)
```

CalcMort

Calculating Parametric Age-Specific Mortality and survival.

Description

CalcMort and CalcSurv are used to calculate the age-specific mortality and survival functions from different parametric models.

Usage

```
CalcMort(theta, x, model = "GO", shape = "simple",
  checkTheta = TRUE)

CalcSurv(theta, x, model = "GO", shape = "simple",
  checkTheta = TRUE)
```

Arguments

theta	Numerical vector of age-specific mortality parameters (see details).
x	Numerical vector of ages at which to calculate mortality.
model	The underlying mortality model to be used. "EX" = exponential, "GO" = Gompertz, "WE" = Weibull and "LO" = logistic (see details).
shape	The overall shape of the model. Values are: simple = no extra parameters added; Makeham = a constant parameter is added to the mortality; and bathtub = a Gompertz declining mortality for early ages and a constant parameter are added to the mortality model (see details).
checkTheta	Logical to verify that the beta parameters conform with the model's specification (see details).

Details

1) Age-specific mortality and survival models:

The function `CalcMort` uses parametric functions to calculate age-specific survival, defined as the probability of surviving to a given age. The function follows the conventions from package `BaSTA` (Colchero and Clark 2012, Colchero *et al.* 2012, Colchero *et al.* 2021). The mortality function or hazard rate describes how the risk of mortality changes with age, and is defined as

$$\mu(x|\theta) = \lim_{\Delta x \rightarrow 0} \frac{\Pr[x < X < x + \Delta x | X > x]}{\Delta x},$$

where X is a random variable for ages at death, $x \geq 0$ are ages and θ is the vector of mortality parameters. From the mortality function, the survival function is then given by

$$S(x|\theta) = \Pr[X > x] = \exp\left[-\int_0^x \mu(t|\theta) dt\right],$$

with the cumulative distribution function $F(x|\theta) = 1 - S(x|\theta)$. The probability density function of ages at death is

$$f(x|\theta) = \mu(x|\theta)S(x|\theta),$$

for $x \geq 0$.

1.1) Argument “model”:

The `model` argument allows the user to choose between four basic mortality functions, namely

(a) `model = “EX”`: The exponential model (Cox and Oakes 1974), with constant mortality with age, specified as

$$\mu_b(x|\theta) = b,$$

where $b > 0$, with survival

$$S_b(x|\theta) = \exp[-bx].$$

(b) `model = “GO”`: The Gompertz mortality model (Gompertz 1925, Pletcher 1999), calculated as

$$\mu_b(x|\theta) = \exp(b_0 + b_1 x),$$

where $-\infty < b_0, b_1 < \infty$, with survival

$$S_b(x|\theta) = \exp\left[\frac{e^{b_0}}{b_1} (1 - e^{b_1 x})\right].$$

(c) `model = “WE”`: The Weibull mortality model (Pinder III *et al.* 1978) calculated as

$$\mu_b(x|\theta) = b_0 b_1^{b_0} x^{b_0-1},$$

where $b_0, b_1 > 0$, with survival

$$S_b(x|\theta) = \exp\left[-(b_1 x)^{b_0}\right].$$

(d) `model = “LO”`: The logistic mortality model (Pletcher 1999), calculated as

$$\mu_b(x|\boldsymbol{\theta}) = \frac{\exp(b_0 + b_1 x)}{1 + b_2 \frac{e^{b_0}}{b_1} (e^{b_1 x} - 1)},$$

where $b_0, b_1, b_2 > 0$, with survival

$$S_b(x|\boldsymbol{\theta}) = \left[1 + b_2 \frac{e^{b_0}}{b_1} (e^{b_1 x} - 1) \right]^{-1/b_2}.$$

1.2)Argument “shape”:

The shape argument allows the user to extend these models in order to explore more complex mortality shapes.

(a) shape = “simple”: (default) Leaves the model as defined above, with mortality given by

$$\mu(x|\boldsymbol{\theta}) = \mu_b(x|\boldsymbol{\theta})$$

and survival

$$S(x|\boldsymbol{\theta}) = S_b(x|\boldsymbol{\theta}).$$

(b) shape = “Makeham”: A constant is added to the mortality, such that the mortality is given by

$$\mu(x|\boldsymbol{\theta}) = c + \mu_b(x|\boldsymbol{\theta}_1),$$

where $\boldsymbol{\theta} = [c, \boldsymbol{\theta}_1]$, and with survival

$$S(x|\boldsymbol{\theta}) = e^{-cx} S_b(x|\boldsymbol{\theta}_1)$$

The most common models with this shape is the Gompertz-Makeham model (Gompertz 1825, Makeham 1866).

(c) shape = “bathtub”: produces a concave shapes in mortality by adding a declining Gompertz term and a constant parameter to the basic mortality model, where the mortality function is

$$\mu(x|\boldsymbol{\theta}) = \exp(a_0 - a_1 x) + c + \mu_b(x|\boldsymbol{\theta}_1),$$

where $a_0 \in \mathbb{R}$, $a_1, c \geq 0$ and $\boldsymbol{\theta}_1 \subset \boldsymbol{\theta}$ are specified based on argument model, and with survival

$$S(x|\boldsymbol{\theta}) = \exp \left[\frac{e^{a_0}}{a_1} (e^{a_1 x} - 1) - cx \right] S_b(x|\boldsymbol{\theta}_1).$$

The most widely use “bathtub” shaped model is the **Siler mortality model** (Siler 1979), which provides considerably good fits to mammalian data. The arguments for the Siler model are:

```
CalcMort(..., model = "GO", shape = "bathtub", ...)
```

2) Specifying theta parameters:

Argument theta requires a numerical vector of parameters. For instance, for a Gompertz model with simple shape and with parameter vector $\boldsymbol{\theta}^\top = [b_0, b_1]$ where $b_0 = -5$ and $b_1 = 0.1$, the argument should be specified as

```
CalcMort(theta = c(b0 = -5, b1 = 0.1), ...)
```

Note that in this example the parameter names are specified directly, this is required when checkTheta = FALSE. Although assigning the names to each parameter is not necessary when checkTheta = TRUE, it is advisable to ensure that the right values are assigned to the right parameter.

If argument checkTheta is set to TRUE, then the vector of theta parameters is verified for consistency with the requirements of the model and shape selected.

Value

CalcMort and CalcSurv return a vector of class “numeric” with the hazard rate or cumulative survival values at the specified ages, respectively.

Author(s)

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References

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See Also

[CalcSurv](#) to calculate age-specific survival, [CalcFert](#) to calculate age-specific fertility.

Examples

```
# Gompertz age specific mortality (default):
mort <- CalcMort(theta = c(b0 = -5, b1 = 0.1), x = 10)

# Siler age specific mortality:
mort <- CalcMort(theta = c(a0 = -1, a1 = 1, c = 0.0001,
                        b0 = -6, b1 = 0.15), x = 10,
                model = "GO", shape = "bathtub")

# Gompertz age specific survival (default):
surv <- CalcSurv(theta = c(b0 = -5, b1 = 0.1), x = 10)

# Siler age specific survival:
surv <- CalcSurv(theta = c(a0 = -1, a1 = 1, c = 0.0001,
                        b0 = -6, b1 = 0.15), x = 10,
                model = "GO", shape = "bathtub")
```

CalcProductLimitEst	<i>Calculating the product limit estimator from Data.</i>
---------------------	---

Description

CalcProductLimitEst uses non-parametric methods to calculate the product limit estimator and confidence intervals.

Usage

```
CalcProductLimitEst(ageLast, ageFirst = NULL, departType,
                    calcCIs = FALSE, nboot = 1000, alpha = 0.05)
```

Arguments

ageLast	Numerical vector with the ages at last detection (i.e., death and censoring) (see details)
ageFirst	Numerical vector of ages at first detection (i.e., truncation). If NULL then all values are set to 0 (see details).
departType	Character string vector for the type of departure (i.e., last detection), with values “D” for death and “C” for censoring (see details).
calcCIs	Logical indicating whether confidence intervals should be calculated
nboot	Number of bootstrap iterations
alpha	Alpha level. Default is 0.05 for 95% CIs

Details

1) Data structure:

The function allows to calculate product limit estimator (Wann *et al.* 1987) for data that includes the following types of records:

- **Uncensored:** individuals with known ages at death;
- **right-censored:** individuals last seen alive;
- **left-truncated:** individuals born before the start of the study and are truncated at the age of entry.

The data required are the ages at last detection (i.e., *uncensored* or *right-censored*) passed through argument “ageLast”, the type of departure via argument “departType”, which takes two values, namely “D” for death, and “C” for censored (i.e., right-censored).

In addition, if there is *left-truncation*, it takes the ages at entry to the study by means of argument “ageFirst”. If all the individuals were born during the study, the value of “ageFirst” can be left as NULL, which will make them all equal to 0.

Arguments

theta	Numerical vector of age-specific mortality parameters (see details).
x	Numerical vector of ages at which to calculate mortality.
dx	Numerical value for the width of age intervals used for integration. If NULL, default is $dx = 0.01$
xmax	Numerical value for the maximum age. If NULL, the value is obtain as the age when the surviva
atAllAges	Logical to indicate whether ageing rates should be provided between ages 0 and xmax
model	The underlying mortality model to be used. "EX" = exponential, "GO" = Gompertz, "WE" = Weibull and "LO" = logistic (see details).
shape	The overall shape of the model. Values are: simple = no extra parameters added; Makeham = a constant parameter is added to the mortality; and bathtub = a Gompertz declining mortality for early ages and a constant parameter are added to the mortality model (see details).
checkTheta	Logical to verify that the beta parameters conform with the model's specification (see details).

Details

The function `CalcAgeingRate` uses parametric functions to calculate the actuarial (i.e., survival) rate of ageing. The function follows the conventions from package `BaSTA` (Colchero and Clark 2012, Colchero *et al.* 2012, Colchero *et al.* 2021) to select the parametric model of mortality. The mortality function describes how the risk of mortality changes with age, and is defined as

$$\mu(x|\theta) = \lim_{\Delta x \rightarrow 0} \frac{\Pr[x < X < x + \Delta x | X > x]}{\Delta x},$$

where X is a random variable for ages at death, $x \geq 0$ are ages and θ is the vector of mortality parameters. From the mortality function, the survival function is then given by

$$S(x|\theta) = \exp\left[-\int_0^x \mu(t|\theta)dt\right].$$

(For further details on the mortality and survival models see [CalcMort](#)).

Given a vector of ages x_1, x_2, \dots, x_n specified by the user with argument `x`, the function calculates the remaining life expectancy at age x_i as

$$e_{x_i} = \frac{\int_{x_i}^{\infty} S(t)dt}{S(x_i)}$$

for $i = 1, 2, \dots, n$.

Value

The function outputs a matrix with the ages from which remaining life expectancies were calculated, and the values for the remaining life expectancy.

Author(s)

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See Also

[CalcSurv](#) to calculate age-specific survival, [CalcMort](#) to calculate age-specific mortality, [CalcFert](#) to calculate age-specific fertility.

[CalcAgeMaxFert](#) to calculate the age at maximum fertility from parametric models of age-specific fertility. [CalcAgeingRateMort](#) to calculate ageing rates from parametric models of age-specific mortality.

Examples

```
# Calculate ageing rate from Gompertz model:
rle <- CalcRemainLifeExp(theta = c(b0 = -5, b1 = 0.1), x = 10)

# Calculate ageing rate from Siler model:
rle <- CalcRemainLifeExp(theta = c(a0 = -1, a1 = 1, c = 0.0001,
                                b0 = -6, b1 = 0.15), x = 10,
                        model = "G0", shape = "bathtub")
```

plot.paramDemo

Functions to plot parametric demographic functions

Description

Draw a plot of demographic functions produced with function CalcDemo

Usage

```
## S3 method for class 'paramDemo'
plot(x, demofun = "all", ...)
```

Arguments

x	Object of class “paramDemo”
demofun	Character string for the demographic function to be plotted
...	Additional arguments passed to function plot

Value

No return value, called for plotting objects of class “paramDemo”

Author(s)

Fernando Colchero <fernando_colchero@eva.mpg.de>

See Also

[CalcDemo](#) to calculate parametric demographic functions.

Examples

```
# Create paramDemo object from Gompertz mortality and
# quadratic fertility:
dem <- CalcDemo(theta = c(b0 = -5, b1 = 0.1),
                beta = c(b0 = 0.5, b1 = 0.01, b2 = 10),
                summarStats = TRUE, agesAR = c(5, 10))

# Plot demographic object:
plot(dem)
```

plot.paramDemoLT

Functions to plot life tables and product limit estimators

Description

Draw a plot of demographic rates from a life table produced with function `CalcLifeTable` or of product limit estimator produced with function `CalcProductLimitEst`

Usage

```
## S3 method for class 'paramDemoLT'
plot(x, demorate = "lx", inclCIs = FALSE, ...)

## S3 method for class 'paramDemoPLE'
plot(x, inclCIs = FALSE, ...)
```

Arguments

<code>x</code>	Object of class <code>paramDemoLT</code> or <code>paramDemoPLE</code> produced with functions <code>CalcLifeTable</code> or <code>CalcProductLimitEst</code>
<code>demorate</code>	Demographic rate to be plotted, choices are “lx” for the survival, “px” for the age-specific survival probability, “qx” for the age-specific mortality probability, and “ex” for the remaining life expectancy
<code>inclCIs</code>	Logical indicating whether confidence intervals should be plotted in case they were calculated with function <code>CalcLifeTable</code> or <code>CalcProductLimitEst</code>
<code>...</code>	Additional arguments passed to function <code>plot</code>

Value

No return value, called for plotting objects of class “`paramDemoLT`”

Author(s)

Fernando Colchero <fernando_colchero@eva.mpg.de>

See Also

[CalcLifeTable](#) to calculate life tables. [CalcProductLimitEst](#) to calculate product limit estimators.

Examples

```
# Simulate age at death data from Gompertz model:
ages <- SampleRandAge(n = 100, theta = c(b0 = -5, b1 = 0.1))

# Calculate life table:
lt <- CalcLifeTable(ageLast = ages, departType = rep("D", 100))

# Plot life table:
plot(lt)
```

plot.PDlifeHist	<i>Summarizing and plotting life history variables from parametric demographic models.</i>
-----------------	--

Description

These functions are all generic methods for class PDlifeHist.

Usage

```
## S3 method for class 'PDlifeHist'
plot(x, type = "rates", ...)

## S3 method for class 'PDlifeHist'
summary(object, ...)

## S3 method for class 'PDlifeHist'
print(x, ...)
```

Arguments

x	Object of class “PDlifeHist” obtained from function CalcLifeHist
object	Object of class “PDlifeHist” obtained from function CalcLifeHist
type	Character string specifying the type of plot to be drawn, options are “rates”, “sensitivities”, “all”
...	Additional arguments passed to functions plot, print, and summary

Details

For objects of class “PDlifeHist”, function print displays on the console the data frame of life history variables produced by function [CalcLifeHist](#).

Function summary prints to the console, first the settings as specified by the user (i.e., theta and beta parameters, and the types of models used), and then, as function print, the table of life history variables.

Function plot with argument type = “rates” produces plots of the age-specific demographic rates (i.e., p_x and m_x) and the stable age structure and reproductive values (i.e., ω_x and ν_x). If argument type = “sensitivity”, then it produces plots of the sensitivities and elasticities of λ to p_x and m_x .

Value

No return value, called for plotting objects of class “PDlifeHist”

Author(s)

Fernando Colchero <fernando_colchero@eva.mpg.de>

See Also

[CalcLifeHist](#) to calculate life history variables from parametric demographic models.

Examples

```
# Calculate life histories on the default models:
test <- CalcLifeHist(theta = c(b0 = -3, b1 = 0.1),
                    beta = c(b0 = 1, b1 = 0.01, b2 = 5),
                    ageMatur = 2)

# Print results:
test

# Summary:
summary(test)

# Plot results:
plot(test, type = "all")
```

Description

SampleRandAge is used to randomly sample ages at death from a parametric mortality model

Usage

```
SampleRandAge(n, theta, dx = 0.001, model = "GO",
              shape = "simple", minSx = 1e-04)
```

Arguments

n	Number of individual ages at death to sample
theta	Numerical vector of age-specific mortality parameters (see details).
dx	Numeric value for the age increments (see details).
model	The underlying mortality model to be used. "EX" = exponential, "GO" = Gompertz, "WE" = Weibull and "LO" = logistic (see details).
shape	The overall shape of the model. Values are: simple = no extra parameters added; Makeham = a constant parameter is added to the mortality; and bathtub = a Gompertz declining mortality for early ages and a constant parameter are added to the mortality model (see details).
minSx	Minimum value for the survival function to set the maximum age (see details)

Details

SampleRandAge arguments "model" and "shape", to calculate the survival function, $S(x)$ for $x \geq 0$, at discrete age intervals $[x, x + \Delta x)$ where Δx is specified with argument "dx". It then calculates the CDF of ages at death, $F(x)$, and uses inverse sampling to sample n ages at death by random sampling from a uniform distribution bound as

$$u_i \sim \text{Unif}[F(x_m), F(x_M)],$$

where $x_m = \min(x)$ and $x_M = \max(x)$. It then finds the corresponding ages at death as

$$x_i = F^{-1}(u_i).$$

In most cases, this is achieved numerically and thus the lower the value for argument "dx" the higher the precision.

Value

SampleRandAge returns a vector of class "numeric" with randomly generated ages at death.

Author(s)

Fernando Colchero <fernando_colchero@eva.mpg.de>

Examples

```
# Simulate age at death data from Gompertz model:
ages <- SampleRandAge(n = 100, theta = c(b0 = -5, b1 = 0.1))

# Simulate age at death data from Siler model:
ages <- SampleRandAge(n = 100, theta = c(a0 = 0, a1 = 1, c = 0.001,
```

```
b0 = -5, b1 = 0.1), model = "GO",  
shape = "bathtub")
```

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