Package 'strandCet'

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Type Package

Title Estimation of biological parameters from stranded cetaceans

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Description Analysis of biological data from stranded marine mammals: mortality-at-age, survivorship, creation of life tables, leslie matrices, etc.

Depends R (>= 3.2.5)

Imports numDeriv, corpcor, MASS, mvtnorm, boot, minpack.lm, stats

License GPL (>=2)

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

R topics documented:

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calc.ro   *Caclulate net reproduction number from a demographic projection matrix.*

Description

Calculate the net reproduction number (R_0) from an age or stage-classified demographic projection matrix.

Usage

```
calc.ro(A, N.out = FALSE)
```

Arguments

A	A demographic projection matrix
N.out	Return the fundamental matrix (N) of the Markov chain.

Details

Calculates the net reproduction number (R_0) from an age or stage-classified demographic projection matrix by first decomposing the k x k projection matrix A into two component matrices, T and F. T collects the transitions between life-cycle stages while F collects the fertility transitions. For an age-classified Leslie matrix, T will contain only the sub-diagonal of A and F will contain only the first row of A. The fundamental matrix is given by $N = (I-T)^{-1}$, where I is a k x k identity matrix. R_0 is the leading eigenvalue of the matrix FN.

Value

If the (default) option N.out=FALSE is used, the net reproduction number is returned as a single value. If N.out = TRUE, the returned value is a list of two items:

ro	Net reproduction number.
N	Fundamental matrix.

References

Caswell, H. (2001). Matrix population models: construction, analysis, and interpretation, Second edition. Sinauer, Sunderland, Massachusetts, USA.

See Also

Leslie.matrix

---

coale	*Coale method.*

Description

Used to graduate the individuals-years lived by those dying in the interval by the method of Coale et al. (1983).

Usage

```
coale(b1, b4, nMx)
```

Arguments

b1	Two-element vector of regression coefficients for graduating 1 to 0 age-classes provided in Coale et al. (1983).
b4	Two-element vector of regression coefficients for graduating 4 to 1 age-classes provided in Coale et al. (1983).
nMx	Period central death rates = nDx/nKx.

Note

Utility function called by life.Leslie.

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cohort	*Cohort method*

Description

Dummy function called in life.Leslie

Usage

```
cohort(width12)
```

Arguments

width12	Width of the first two age classes.

Value

A two element vector representing the first two values of the nax column of the life table.

Note

Utility function called by life.Leslie.

See Also

life.Leslie

---

dens.prior   *Density of priors.*

Description

This function calculates the density of the prior distribution for the 9 parameters of the adapted Heligman-Pollard model. The density is calculated using a uniform distribution.

Usage

```
dens.prior(x, pri.lo = c(0, 0, 0, 0, 0, 0, 15, 0, 0), pri.hi = c(0.15, 1, 1,
  0.5, 0.25, 15, 55, 0.1, 1.25))
```

Arguments

x	A 1 * 9 vector or n * 9 matrix containing values for the eight Heligman-Pollard Parameters.
pri.lo	A vector giving the lower bounds of the uniform priors.
pri.hi	A vector giving the upper bounds of the uniform priors.

Value

A scalar describing the density of the prior distribution.

References

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

---

eigen.analysis   *Analysis of Eigen values*

Description

Calculates the asymptotic growth rate and related quantities from a demographic projection matrix.

Usage

```
eigen.analysis(A)
```

Arguments

A   Demographic projection matrix.

Details

Calculates the asymptotic growth rate (lambda) of a population described by demographic projection matrix A. The asymptotic growth rate of the population is given by the dominant eigenvalue of the projection matrix. By the Perron-Frobenius Theorem, this eigenvalue is guaranteed to be real, positive and strictly greater than all the other eigenvalues if the matrix A is non-negative, irreducible, and primitive (for details see Caswell (2001)).

Also calculates the damping ratio (rho), eigenvalue sensitivities, eigenvalue elasticities, the stable age distribution (for the communicating parts of the life cycle), and scaled reproductive values.

The damping ratio is the ratio of the dominant eigenvalue and the absolute value of the second eigenvalue. rho is a measure of the rate of convergence to the stable age-distribution. A population characterized by damping ratio rho will converge asymptotically to the stable age distribution exponentially with rate at least as fast as log(rho). Clearly, a population already at or very near the stable age distribution will converge faster, but rho provides an upper bound.

The eigenvalue sensitivities are the partial derivatives of lambda with respect to a perturbation in matrix element a_{ij}. The sensitivities measure the selection gradient on the life-cycle (Lande 1982). The eigenvalue elasticities are scaled to be proportional sensitivities of lambda to a perturbation in a_{ij}. Elasticities have a number of desirable properties including, their sum across all life-cycle transitions is unity and the sum of the elasticities of all incoming arcs to a life-cycle stage must equal the sum of all outgoing arcs (van Groenendael et al 1994).

The stable age distribution is normalized to represent the proportion in each of the communicating age classes. If the population is characterized by post-reproductive survival (and hence age classes that do not communicate with the rest of the life cycle graph), then other methods should be used to calculate to stable distribution. For example, from classic stable population theory, we know that the stable age distribution of the population c(x) is given by the relationship:

c(x) = b l(x) exp(-r*x)

where b is the gross birth rate, l(x) is survivorship to age x and r is the rate of increase of the population (=log(lambda)). See Coale (1972) or Preston et al. (2001) for details.

The age-specific reproductive values are normalized so that the reproductive value of the first age class is unity. Problems associated with post-reproductive survival are irrelevant for reproductive value since the reproductive value of post-reproductive individuals is, by definition, zero.

Value

A list with six components:

lambda1   the asymptotic growth rate (dominant eigenvalue) of A

rho   damping ratio of A

sensitivities   eigenvalue sensitivities of A

elasticities   eigenvalue elasticities of A

stable.age   stable age distribution of A

repro.value   reproductive values of A

References

Caswell, H. (2001). Matrix population models: Construction, analysis, and interpretation. 2nd ed. Sunderland, MA: Sinauer.

Coale, A.J. (1972). The growth and structure of human populations: A mathematical investigation. Princeton: Princeton University Press.

Lande, R. A. (1982). A quantitative genetic theory of life history evolution. Ecology 63:607-615.

van Groenendael, J., H. De Kroon, S. Kalisz, and S. Tuljapurkar. (1994). Loop analysis: Evaluating life history pathways in population projection matrices. Ecology 75 (8):2410-2415.

See Also

Leslie.matrix

---

entropy.wts	*Entropy of the rescaled weights relative to uniformity.*

Description

Performance measure for the IMIS algorithm that calculates the entropy of the importance weights relative to uniformity.

Usage

```
entropy.wts(w)
```

Arguments

w   A vector of importance weights corresponding to each row of the mixture of the prior and multivariate gaussian draws.

Value

Vector of entropy values relative to uniformity for a vector of weights.

Note

For use in the function final.resamp.

References

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Poole, D. and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

final.resamp

Est.life.tab   *Estimated life table.*

Description

Performs a regular life table from estimated and smoothed mortality rates at age.

Usage

```
Est.life.tab(Est.qx, age = age, n = 1000)
```

Arguments

Est.qx	Estimated mortality vector with same length as age.
age	The age at the beginning of the age classes of the life table.
n	The amount of individuals of the first age class in the theoretical population.

Details

Constructs a cohort life table from estimated and smoothed mortality rates calculated with mortality functions as Si.mod or HP.mod

Value

A dataframe with seven columns:

age	Age at the beginning of the interval.
qx	Probability of death between ages x and x + n.
nx	Number of survivors at age x in a theoretical cohort starting with n individuals.
dx	Number of deaths at age x in a theoretical cohort starting with n individuals.
lx	Probability of survival to exact age x.
ex	Life expectancy at age x.
Zx	Instant death rate at age x

References

Preston, S.H., Heuveline, P. and Guillot, F. (2001). Demography: Measuring and modeling population processes. Oxford: Blackwell.

See Also

Si.mod HP.mod

---

expt.upts   *Expected number of unique inputs after the final IMIS re-sample.*

Description

Performance measure for the IMIS algorithm that calculates the expected number of unique points after re-sampling.

Usage

```
expt.upts(w, m)
```

Arguments

w   A vector of importance weights corresponding to each row of the mixture of the prior and multivariate gaussian distributions.

m   The final re-sample size.

Value

A scalar describing the number of unique points from the final re-sample.

Note

For use in the function final.resamp.

References

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

final.resamp

final.resamp	*Final re-sampling step in Bayesian Melding using IMIS.*

Description

Performs the final re-sampling step in the Bayesian Melding with IMIS procedure for the nine adapted Heligman-Pollard parameters.

Usage

```
final.resamp(K, B1, H.new, H.k, log.like, d.keep, prior, h.mu, h.sig, nrisk,
    ndeath, age, B = 400, theta.dim = 9)
```

Arguments

K	The number of iterations of the importance sampling stage.
B1	Sample size at the importance sampling stage multiplied by the number of local optimums.
H.new	A matrix with dimensions ((B * d.keep) * 9) containing the B*d.keep inputs drawn from the multivariate gaussians.
H.k	A matrix containing the prior plus new inputs from the multivariate gaussians.
log.like	A vector of log-likelihoods corresponding to each row of H.k.
d.keep	The number of local optimums found in the optimizer step.
prior	A matrix containing the prior.
h.mu	A (d.keep * 9) matrix containing the results of the optimizer step.
h.sig	An array containing the covariance matrix for each row of h.mu.
nrisk	A vector containing the number of persons at risk in each age group.
ndeath	A vector containing the number of deaths in each age group.
age	A vector containing the ages at which each age interval begins.
B	Sample size at the importance sampling stage.
theta.dim	The number of columns of the prior matrix.

Value

H.new	A (B * theta.dim) matrix containing the posterior distribution for each parameter.
vwts	A vector containing the variance of the rescaled weights at each IMIS iteration
ewts	A vector containing the entropy of the rescaled weights at each IMIS iteration.
mwts	A vector containing the maximum of the rescaled weights at each IMIS iteration.
nup	A vector containing the expected number of unique points at each IMIS iteration.
frac.up	A vector containing the proportion of unique points in the final resample at each IMIS iteration.
wts.k	A vector containing the importance weights for the final iteration.
mwt.case	The maximum weight value and associated case.

Note

The function HP.mod performs this along with all other steps in a single function.

References

Heligman, L. and Pollard, J.H. (1980) The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

Poole, D. and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

mod ll.binom dens.prior var.rwts entropy.wts expt.upts

---

gen.time *Generation time*

Description

Calculates the generation time for an age or stage-classified demographic projection matrix.

Usage

```
gen.time(A, peryear = 5)
```

Arguments

A	Demographic projection matrix.
peryear	Width of the age classes.

Details

Calculates the generation time (T) for an age or stage-classified demographic projection matrix using the identity:

Ro = exp(r*T)

where Ro is the net reproduction number and r is the intrinsic rate of increase = log(lambda).

Generation time is the amount of time that it takes a typical female to produce Ro offspring or, equivalently, the amount of time it takes a population growing with instantaneous rate r to increase by a factor of Ro.

Value

The generation time implied by the demographic projection matrix.

Note

Calls function `calc.ro`, which calculates R_0 from the fundamental matrix of the Markov transition matrix (Caswell 2001).

References

Keyfitz, N., and Caswell. H. (2005). Applied mathematical demography. 3rd ed. New York: Springer.

Caswell, H. (2001). Matrix population models: Construction, analysis, and interpretation. 2nd ed. Sunderland, MA: Sinauer.

Preston, S.H., Heuveline, P. and Guillot, F. (2001). Demography: Measuring and modeling population processes. Oxford: Blackwell.

See Also

`calc.ro` `eigen.analysis`

HP.CI   *Helligman-Pollard confidence intervals with 9 parameters*

Description

Predicts Helligman-Pollard model with the estimated parameters both "natural" mortality, "total" mortality and mortality due to an external risk with confidence intervals.

Usage

```
HP.CI(HPout, age, CI = 95, M = "total")
```

Arguments

HPout	A model object created with HP.mod with the Heligman-Pollard estimated params
age	A vector of the ages at which the probabilities of death will be calculated.
CI	Defines the width of the credible interval (Defaults to 95 percent). A summary table is printed with the median estimate and lower and upper confidence bounds. Setting CI = 95 prints a table with the first column representing the 2.5th percentile for each parameter distribution, the second column represents the median value for each parameter distribution and the third column represents the 97.5th percentile for each parameter distribution.
M	The type of probabilities to be calculated. Can be both "natural" mortality, "total" mortality and mortality due to an external risk.

Details

The type of mortality to be calculated must be defined. By default the total probability of death is calculated but only natural mortality or due to an external risk can be calculad if previously defined.

Value

Return a dataframe with number of rows equal to the number of age classes and four columns:

age	Vetor with age classes.
Med	Median prediction of probabilities of death at age.
Mlo	Lower limit of prediction of probabilities of death at age with CI = (100 - CI)/2.
Mhi	Higher limit of prediction of probabilities of death at age with CI = 1- (100 - CI)/2.

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

See Also

hp.nqx mod mod.nat mod.risk

HP.mod	*Heligman-Pollard parameter estimator using Bayesian Melding with Incremental Mixture Importance Sampling.*

Description

Runs all the necessary functions to estimate the nine adapted Heligman-Pollard parameters in one step via Bayesian Melding with IMIS and optimization. In this order and with the proper arguments imputed the functions run are loop.optim, samp.postopt, like.resamp, final.resamp.

Usage

```
HP.mod(prior, lifeTab, K = 10, d = 10, B = 500, CI = 95, rm = 0)
```

Arguments

prior	A matrix with dimensions (9000 * theta.dim) containing the prior distribution for each Heligman-Pollard parameter.
lifeTab	A life table object from life.tab with a column containing the total number of individuals at risk of death in each age group. A column containing the total number of deaths in each age group. Length should equal the length of age. and a column of the ages at which the probabilities of death will be calculated.
K	The number of IMIS iterations.
d	The number of optimizer iterations.
B	The sample size at each importance sampling iteration.
CI	Defines the width of the confidence interval. A summary table is printed with the median estimate and lower and upper confidence bounds. Setting CI=95 prints a table with the first column representing the 2.5th percentile for each parameter distribution, the second column represents the median value for each parameter distribution and the third column represents the 97.5th percentile for each parameter distribution.
rm	The number of age classes that want to be removed from optimization

Details

All age classes are used for adjustment, in case of whish to remove any of the first age classes due to bias in the sample, indicate it with the parameter "rm" and these will be removed starting from the first age class

Value

A list with:

out	A summary table of the results with the median parameter values in the middle column, the lower bound results in the left column, and upper bound result in the right column.
H.final	A (B * theta.dim) matrix containing the posterior distribution for each parameter.
h.mu	The sets of parameters found in the optimizer step.
h.sig	The covariance matrix for each set of parameters in h.mu.
log.like	A vector of likelihoods for the prior plus resamples.
log.like.0	A vector of the likelihoods for the prior.
wts.0	A vector of importance weights for each set of parameters in the prior.
d.keep	The number of optimizer runs where the likelihood exceeded the maximum likelihood of the prior.
vwts	A vector containing the variance of the rescaled weights at each IMIS iteration.
ewts	A vector containing the entropy of the rescaled weights at each IMIS iteration.
mwts	A vector containing the maximum of the rescaled weights at each IMIS iteration.
mwt.case	The maximum weight and associated case.
nup	A vector containing the expected number of unique points at each IMIS iteration.
frac.up	A vector containing the proportion of unique points in the final resample at each IMIS iteration.
wts.k	A vector containing the importance weights for the final IMIS iteration.

Note

Because there are multiple sampling steps sometimes with upper and lower bound restricitions, this function can take several minutes to run depending on the sample size, K.

References

Heligman, L. and Pollard, J.H. (1980) The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

Poole, D. and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

loop.optim samp.postopt like.resamp final.resamp

---

hp.nqx   *Heligman-Pollard parameter conversion to age-specifc probabilites of*
                                death.

Description

Converts a set of Heligman-Pollard mortality model parameters into age-specific probabilities of
death.

Usage

```
hp.nqx(HPout, age, M = "total")
```

Arguments

HPout   A model object created with HP.mod with the Heligman-Pollard estimated params.

age   A vector containing the ages at which the probability of death will be calculated.

M   The type of probabilities to be calculated. Can be both "natural" mortality, "to-
            tal" mortality and mortality due to an external risk.

Value

Set of age specific probabilities of death equal to the length of age.

Note

Utility function called by HP.CI.

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of
Actuaries 107:49–80.

See Also

HP.CI

HP.pred   *Prediction of Heligman-Pollard model.*

Description

Predicts Heligman-Pollard model from Heligman-Pollard's parameters.

Usage

```
HP.pred(life, HPout, M = "med", age = seq(0, 29, 0.1), rm = 0)
```

Arguments

life	A life table created with life.tab or a dataframe with a vector of ages in the first column.
HPout	A model object created with HP.mod with the Heligman-Pollard estimated params.
M	Defines the statistic to predict. Median by default (med), Low CI (low) or High CI (high)
age	A vector containing the ages at which each age interval begins. See Details
rm	The number of age classes that want to be removed from optimization.

Details

Mx is returned only if number of ages required for prediction is equal to the number of ages in the life table.

Value

A dataframe with seven columns:

age	Age at the beginning of the interval.
Mx	Number of observed deaths at age x.
qx.tot	Total probability of death between ages x and x + n.
qx.nat	Natural probability of death between ages x and x + n.
qx.young	Young probability of death between ages x and x + n.
qx.risk	Probability of death due to an externl risk between ages x and x + n.
qx.adult	Adult or senescent probability of death between ages x and x + n.

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

HP.mod

HP.pri.start	*Estimation of starting values for priors of the Heligman-Pollard model.*

Description

Estimates starting values for the priors of the modified 9-parameter Heligman-Pollard model from mortality rates by age and proportion of individuals death from non natural causes.

Usage

```
HP.pri.start(Si.qx, Prop.risk, Life.qx, age, rg = 0.25,
  control = nls.lm.control(maxiter = 100))
```

Arguments

Si.qx	A vector of the same length as "age" containing the total mortality rates by age (qx).
Prop.risk	A vector of the same length as "age" containing the proportion of death animals identified as death by external effects (other different than natural mortality).
Life.qx	Mortality vector qx form life table created with life.tab.
age	A vector containing the ages at which each age interval begins.
rg	The variation of the range at which the mean prior values will be multiplied to calculate low and high limits.
control	Allow the user to set some characteristics Levenberg-Marquardt nonlinear least squares algorithm implemented in nls.lm. see nls.lm.control

Value

A dataframe with low, high and mean starting values for priors, to be used for fitting a adapted 9-parametres Heligman-Pollard model

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

Moré, J.J. (1978). The Levenberg-Marquardt algorithm: implementation and theory, in: Lecture Notes in Mathematics 630: Numerical Analysis, G.A. Watson (Ed.), Springer-Verlag: Berlin, pp. 105-116.

See Also

HP.priors HP.mod nlsLM life.tab

HP.priors	*Heligman-Pollard Parameter prior formation.*

Description

Draws from a uniform distribution with bounds "pri.lo" and "pri.hi" to create the prior distribution of the Heligman-Pollard parameters necessary for the Bayesian Melding procedure.

Usage

```
HP.priors(pri.lo = c(0, 0, 0, 0.001, 0, 0, 15, 0, 0), pri.hi = c(0.15, 1, 1,
  0.5, 0.25, 15, 55, 0.1, 1.25), theta.dim = 9)
```

Arguments

`pri.lo`	Lower bound of the uniform from which the prior is drawn.
`pri.hi`	Upper bound of the uniform from which the prior is drawn.
`theta.dim`	The number of parameters to be estimated.

Value

A ((1000 * theta.dim) x theta.dim) matrix containing the 1000 * theta.dim sets of the Heligman-Pollard parameters drawn from a uniform distribution.

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

Poole, D. and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

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keyfitz	*Keyfitz and Flieger method.*

Description

Utility used by `life.Leslie` to graduate the person-years lived by those dying in the interval by the method of Keyfitz and Flieger (1990).

Usage

```
keyfitz(b0, nMx)
```

Arguments

`b0`	Two-element vector of regression coefficients provided in Keyfitz and Flieger (1990).
`nMx`	Period central death rates = nDx/nKx.

Value

The first two values (age classes 0-1 and 1-5) of the nax column of a period life table.

Note

Utility function called by `life.Leslie`

References

Keyfitz, N. and Flieger, W. (1990). World population growth and aging: Demographic trends in the late twentieth century. Chicago: University of Chicago Press.

See Also

life.Leslie.

Leslie.matrix   *Leslie matrix*

Description

Generates a Leslie matrix for demographic projection from vectors of age-specific cumulative survival and fertility.

Usage

```
Leslie.matrix(lx, mx, L = TRUE, peryear = 5, one.sex = TRUE, SRB = 1,
  infant.class = TRUE)
```

Arguments

lx	A vector of either age-specific cumulative survival or person-years lived in the interval
mx	Age-specific fertility rates.
L	Logical. If 'TRUE', lx is taken to be individuals-years lived in the interval nLx, while if 'FALSE', lx is taken to be cumulative survival to exact age x + n.
peryear	Multiplier for fertility.
one.sex	Logical. If 'TRUE', fertility rates will be divided by 1/(1+SRB).
SRB	Sex ratio at birth.
infant.class	Logical. 'TRUE' if lx contains a value for the infant age-class.

Details

Constructs a k x k age-classified demographic projection matrix with age-specific survival probabilities along the sub-diagonal and age-specific fertilities along the first row of the matrix.

lx and mx are assumed to be of the same length. The resulting matrix is truncated to insure that there are no post-reproductive classes. This is important for ensuring irreducibility of the resulting matrix.

If mx is longer than lx, mx is trucated to be the same length as lx. If lx is longer than mx, a warning is issed and lx is truncated to be the same length as mx.

Fertility is assumed to be birth-flow (Caswell 2001). That is, breeding is assumed to be continuous and the individual elements of the first row of the Leslie matrix are averaged over successive age-classes. Fertility rates are typically given in annualized form. If this is the case and the age-classes are wider than one year, then peryear can be used to appropriately scale up the annual values.

The default behavior is to use person-years lived in the interval as the survival measure. If infant.class=TRUE, lx is taken to have a value for the infant age class (i.e., a shorter class width than

the other elements of lx. What is done when there is an infant class depends on what the values in lx represent. If L=TRUE, then the first two values of lx are combined to form the total person-years for the first ageclass in the Leslie matrix. Human demographic data from abridged life tables typically come with age classes x = 0, 1, 5, 10, ... Thus, combining the person-years for the first two age classes gives an initial age class of the correct width. If infant.class=TRUE and L=FALSE, the second element of lx is deleted. Creating a Leslie matrix from other forms of non-standard early age-classes can be accomplished by pre-processing lx and using the option infant.class=FALSE.

The human sex ratio at birth (male births/female births) is remarkably close to SRB=1.05 across a wide range of populations and this is the default value for SRB.

The resulting matrix has class "leslie.matrix". This class is not used extensively but will be in future evelopment.

Value

A k x k age-classified demographic projection matrix with class "leslie.matrix".

References

Keyfitz, N. (1977). Introduction to the mathematics of populations. 2nd ed. Menlo Park: Addison-Wesley.

Preston, S.H., Heuveline, P. and Guillot, F. (2001). Demography: Measuring and modeling population processes. Oxford: Blackwell.

Caswell, H. (2001). Matrix population models: Construction, analysis, and interpretation. 2nd ed. Sunderland, MA: Sinauer.

Leslie.pred   *Project Leslie matrix*

Description

Projects an population vector tmax intervals by pre-multiplication with a Leslie matrix.

Usage

```
Leslie.pred(A, no, tmax = 100, pop.sum = FALSE)
```

Arguments

A	A k * k projection matrix.
no	A k * 1 population vector.
tmax	Number of time steps to project the vector.
pop.sum	Logical: If 'TRUE', the age-classes of the projected population are summed, yielding a single total population vector

Details

Takes an initial population vector, no, and pre-multiplies by the demographic projection matrix, A, tmax times. This projection will be tmax*n years into the future, where n is the width of the age-classes in the Leslie matrix, A.

Value

If pop.sum=FALSE (the default), the value will be a k x tmax+1 matrix. The first column of the matrix is no and each subsequent column represents the population structure at time step 1, 2, ..., tmax. If pop.sum=TRUE, the value will be a vector of length tmax+1, where each element of the vector is the total population at time t=0, 1, ..., tmax.

References

Caswell, H. (2001). Matrix population models: Construction, analysis, and interpretation. 2nd ed. Sunderland, MA: Sinauer.

van Groenendael, J., De Kroon, H., Kalisz, S. and Tuljapurkar. S. (1994). Loop analysis: Evaluating life history pathways in population projection matrices. Ecology 75 (8):2410-2415.

See Also

Leslie.matrix eigen.analysis

---

life.Leslie   *Life table for Leslie matrix projections.*

Description

Constructs either a period or cohort life table from enumerated deaths and mid-interval population estimates.

Usage

```
life.Leslie(x, nDx, nKx, b0 = c(0.07, 1.7), b1 = c(0.053, 2.8),
  b4 = c(1.522, 1.518), type = "kf", nxx = 0, iwidth = 5,
  width12 = c(1, 4))
```

Arguments

x	Age at the beginning of the age classes of the life table.
nDx	Number of deaths.
nKx	Population size.
b0	Coefficients used in Keyfitz-Flieger graduation.
b1	First set of coefficients used in Coale-Demeny graduation.
b4	Second set of coefficients used in Coale-Demeny graduation.
type	Type of life table calculation: "kf", "cd", or "cohort". Default is "kf".
nxx	individuals-years lived by those dying in the last (possibly open) age-class. If nxx=0, the person-years lived by those dying in the interval is the inverse of the central death rate (corresponding to exponentially distributed failure times).
iwidth	Width of the age intervals.
width12	Width of the first two age classes.

Details

Constructs a period or cohort life tables from enumerated deaths and mid-interval population sizes (period) or enumerated deaths and person-years at risk (cohort). x, nDx, and nKx must all the be same length.

There are currently three options for life table construction. The first two are for the construction of period life tables. They differ only in the way that person-years lived by those dying in the first two intervals are handled. For type="kf", the default, the first two values of nax estimated using Keyfitz and Fleiger's (1990) regression method. For type="cd", Coale and Demeny's method (1983) is used. The Coale-Demeny method uses different coefficients depending on the level of early mortality. As a result, this method may work better for high-mortality populations.

The third type of life table is a cohort life table, for which the conversion from mortality rates to probabilities of death is unnecessary, so the nax column of the life table is of limited interest.

Value

A dataframe with nine columns:

x	Age at the beginning of the interval.
nax	Individuals-years lived by those dying in the interval x to x + n.
nMx	Period central death rate.
nqx	Probability of death between ages x and x + n.
lx	Probability of survival to exact age x.
ndx	Proportion of deaths occurring between ages x and x + n.
nLx	Individuals-years lived in the interval x to x + n.
Tx	Individuals-years of life left in the cohort at age x.
ex	Life expectancy at age x.

Note

Calls functions keyfitz, coale or cohort

References

Keyfitz, N. (1977). Introduction to the mathematics of populations. 2nd ed. Menlo Park: Addison-Wesley.

Coale, A., Demeny, P. and Vaughn, B. (1983). Regional model life tables and stable populations. 2nd ed. New York: Academic Press.

Keyfitz, N. and Flieger, W. (1990). World population growth and aging: Demographic trends in the late twentieth century. Chicago: University of Chicago Press.

Preston, S.H. Heuveline, P. and Guillot, F. (2001). Demography: Measuring and modeling population processes. Oxford: Blackwell.

See Also

keyfitz coale cohort Leslie.matrix

---

life.tab *Life table*

Description

Performs a regular life table from a dataframe with ages and number of death individuals.

Usage

```
life.tab(x, n = 1000)
```

Arguments

x	A dataframe withtwo columns: Ages and number of deaths.
n	Inicial number of individuals in the theoretical population.

Details

Constructs a cohort life table from a dataframe with age classes and enumerated deaths.

Value

A dataframe with nine columns:

age	Age at the beginning of the interval.
Mx	Number of observed deaths at age x.
Sx	Number of survivors at age x in the observed cohort of sum(length(M)) individuals.
nx	Number of survivors at age x in a theoretical cohort starting with n individuals.
dx	Number of deaths at age x in a theoretical cohort starting with n individuals.
qx	Probability of death between ages x and x + n.
lx	Probability of survival to exact age x.
ex	Life expectancy at age x.
Zx	Instant death rate at age x

References

Preston, S.H., Heuveline, P. and Guillot, F. (2001). Demography: Measuring and modeling population processes. Oxford: Blackwell.

---

like.resamp   *Local Optimums and Covariance from the optimizer step.*

Description

Defines some necessary arguments for the function final.resamp. Removes NAs from the opt.mu.d and opt.cov.d matrixes.

Usage

```
like.resamp(K, log.like.0, opt.cov.d, opt.mu.d, d.keep, d = 10,
  theta.dim = 9)
```

Arguments

K	Number of iterations at the importance sampling stage.
log.like.0	A vector containing the likelihoods for each row of the prior.
opt.cov.d	Covariance matrixes for the local optimums.
opt.mu.d	A d x 8 matrix containing the local optimums (sets of parameters from the optimizer step).
d.keep	Number of local optimums found in the optimizer step.
d	A scalar defining the number of optimizer interations.
theta.dim	Number of columns in the prior matrix.

Value

h.mu	A d.keep * 8 matrix containing the local optimum result.
h.sig	An array with (theta.dim * theta.dim * (K + d.keep)) dimensions containing the covariance matrix for each local optimum.
log.like	A vector of likelihoods for each row of H.k.

Note

Typically for use immediately before running final.resamp or within the function HP.mod

References

Poole, D. and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

final.resamp HP.mod

`ll.binom`   *Binomial likelihood.*

Description

Calculates a log likelihood from a binomial distribution.

Usage

```
ll.binom(x, n, p)
```

Arguments

x	Same as x from [dbinom](#) - successes.
n	Same as size from [dbinom](#) - trials.
p	Same as prob from [dbinom](#) - observed probability.

References

R Development Core Team. (2009). R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing Vienna, Austria.

See Also

[dbinom](#)

`loop.optim`   *Optimizer step for estimating the Heligman-Pollard Parameters using the Bayesian Melding with IMIS-opt procedure.*

Description

Performs the optimizer step in the IMIS procedure for the eight Heligman-Pollard parameters.

Usage

```
loop.optim(prior, nrisk, ndeath, age, d = 10, theta.dim = 9)
```

Arguments

prior	A matrix containing the prior.
nrisk	A vector containing the number of persons at risk in each age group.
ndeath	A vector containing the number of deaths in each age group.
age	A vector containing the ages at which each age interval begins.
d	Number of optimizer iterations.
theta.dim	Number of columns of the prior (This should be 9 if estimating all parameters. Functionality for estimation a limited number of parameters does not exist yet).

Value

opt.mu.d	A matrix containing the local optimums resulting from the optimizer step. Each local optimum contains a set of 9 parameter values.
opt.cov.d	An array containing the covariance matrix for each of the local optimums.
d.keep	The number of local optimums found whose likelihood is greater than the maximum likelihood from the prior.
theta.new	The set of parameters from the prior with the greatest weight as calculated with prior.likewts.
log.like.0	A vector containing a likelihood for each row of the prior.
wts.0	A vector containing an importance weight for each row of the prior.

Warning

If the likelihood for the initial local maximum does not exceed the highlest likelihood from the prior, a warning will be issued.

Note

Occasionally, this step fails to produce an initial local maximum that exceeds the highest likelihood of the prior and a warning is issued. Usually drawing a new prior or selecting a different algorithm solves this problem.

References

Poole, D. and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

mod ll.binom prior.likewts HP.mod

---

mod	*Heligman-Pollard parameter coversion to age-specific probabilites of death.*

Description

Calculates the age-specific probabilities of death using the Heligman-Pollard model.

Usage

```
mod(theta, x)
```

Arguments

theta	A vector containing values for the 9 parameters of the adapted Heligman-Pollard model.
x	A vector containing the ages at which to calculate the probabilities of death.

Value

A vector of probabilities of death at ages defined by x.

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

---

mod.nat	*Heligman-Pollard parameter coversion to natural age-specific proba-bilites of death.*

Description

Calculates the age-specific probabilities of death using the Heligman-Pollard model.

Usage

```
mod.nat(theta, x)
```

Arguments

theta	A vector containing values for the 9 parameters of the adapted Heligman-Pollard model.
x	A vector containing the ages at which to calculate the probabilities of death.

Value

A vector of probabilities of natural death at ages.

Note

Utility function called by HP.CI.

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

See Also

HP.CI

---

mod.risk | *Heligman-Pollard parameter coversion to age-specific probabilites of death due to an external risk.*

Description

Calculates the age-specific probabilities of death due to an external risk using the Heligman-Pollard model.

Usage

```
mod.risk(theta, x)
```

Arguments

theta | A vector containing values for the 9 parameters of the adapted Heligman-Pollard model.

x | A vector containing the ages at which to calculate the probabilities of death.

Value

A vector of probabilities of death at ages due to an external risk.

Note

Utility function called by HP.CI.

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

See Also

HP.CI

---

prior.likewts | *Prior likelihoods and weights.*

Description

Calculates the log-likelihood and importance weight for each set (i.e. each row) of Heligman-Pollard parameters in the prior.

Usage

```
prior.likewts(prior, nrisk, ndeath, age, theta.dim = 9)
```

Arguments

prior	A ((theta.dim * 1000) * theta.dim) matrix containing the prior distribution.
nrisk	A vector containing the number of persons at risk in each age group.
ndeath	A vector containing the number of deaths in each age group.
age	A vector containing the ages at which each age interval begins.
theta.dim	Number of columns of the prior matrix.

Value

wts.0	A vector containing an importance weight for each set of parameters from the prior.
log.like.0	A vector containing a log likelihood for each set of parameters from the prior.

Note

Used in the loop.optim function

References

Heligman, L. and Pollard, J.H. (1980). The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

Poole, D and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Gen- eralized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

mod ll.binom loop.optim HP.mod

---

samp.postopt	*Multivariate Gaussian Sampling for Heligman-Pollard model estimated via Bayesian Melding.*

Description

Samples the eight Heligman-Pollard parameters from the mvnorm distribution for each run of optimizer step where the likelihood for that run exceeds the maximum likelihood from the prior.

Usage

```
samp.postopt(opt.cov.d, opt.mu.d, d.keep, prior, B = 400, B0 = 8000,
  d = 10)
```

Arguments

`opt.cov.d`	An array containing a covariance matrix for each run of optimizer where the likelihood for that run exceeds the maximum likelihood from the prior.
`opt.mu.d`	A matrix containing the results of the optimizer step.
`d.keep`	Number of runs of optimizer where the likelihood for that run exceeds the maximum likelihood from the prior.
`prior`	A matrix containing the prior distribution (see HP.priors).
`B`	Sample size at the importance sampling stage.
`B0`	Sample size of the prior. This is equal to (theta.dim * 1000).
`d`	Number of optimizer iterations.

Value

`H.k`	The prior plus new samples.
`H.new`	The new samples from the multivariate normal.
`B1`	The number of new samples - should be equal to B * d.keep.

Note

For use within the function HP.mod.

References

Heligman, L. and Pollard, J.H. (1980) The Age Pattern of Mortality. Journal of the Institute of Actuaries 107:49–80.

Poole, D and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A and Bao, L. (2009). "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

Si.mod	*Siler model.*

Description

Fit a 5-parameters Competing-Risk Siler model for Animal Mortality.

Usage

```
Si.mod(data, par = c(-0.15, 1.1, 0.15, 0.005, 0.15), rm = 0,
  method = "Nelder-Mead", control = list(fnscale = -1, maxit = 10000))
```

Arguments

data	Data frame with age clases and frequency of occurrence (see Details).
par	Initial values for the Siler parameters to be optimized over.
rm	The number of age classes that want to be removed from optimization (see Details).
method	The method to be used: "Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN" or "Brent" (see optim).
control	A list of control parameters (see optim).

Details

The data used must be a data frame whose first column is a vector of the estimated ages of the animals found dead and the second the frequency of occurrence of those ages.

All age classes are used for adjustment, in case of whish to remove any of the first age classes due to bias in the sample, indicate it with the parameter "rm" and these will be removed starting from the first age class.

References

Siler, W. (1979). A Competing-Risk Model for Animal Mortality. Ecology 60, 750–757.

Siler, W. (1983). Parameters of mortality in human populations with widely varying life spans. Stat. Med. 2, 373–380.

Nocedal, J. and Wright, S. J. (1999). Numerical Optimization. Springer.

See Also

optim

Si.pred	*Predict Siler model*

Description

Predict Siler model from Siler's parameters

Usage

```
Si.pred(data, Sout, rm = 0)
```

Arguments

data	frame with age clases and frequency of occurrence (see Details).
Sout	A model object created with Si.mod with the 5 Siler's parameters.
rm	The number of age classes that want to be removed from optimization (see Details).

Details

The data used must be the data frame from which the Siler's patameters were estimated, whose first column is a vector of the estimated ages of the animals found dead and the second the frequency of occurrence of those ages.

In case that any age class had been removed for the estimation of the parameters that are going to be used for predicting the model, indicate it with the parameter "rm" and these age classes will be removed starting from the first age class.

References

Siler, W. (1979). A Competing-Risk Model for Animal Mortality. Ecology 60, 750–757.

Siler, W. (1983). Parameters of mortality in human populations with widely varying life spans. Stat. Med. 2, 373–380.

See Also

Si.mod

---

var.rwts	*Variance of the rescaled weights when estimating the Heligman-Pollard parameters using Bayesian Melding with IMIS.*

Description

Calculates the variance of the rescaled weights.

Usage

```
var.rwts(w)
```

Arguments

w   A vector of importance weights corresponding to each row of the mixture of the prior and multivariate gaussian draws.

Value

A scalar representing the variance of the rescaled weights.

Note

Used in the final.resamp function.

References

Poole, D. and Raftery, A. (2000). Inference for Deterministic Simulation Models: The Bayesian Melding Approach. Journal of the American Statistical Association 95:1244–1255.

Raftery, A. and Bao, L. (2009). Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling. Technical Report 560, Department of Statistics, University of Washington.

Sharrow, D.J., Clark, S.J., Collinson, M.A., Kahn, K. and Tollman, S.M. (2013). The Age Pattern of Increases in Mortality Affected by HIV: Bayesian Fit of the Heligman-Pollard Model to Data from the Agincourt HDSS Field Site in Rural Northeast South Africa. Demogr. Res. 29, 1039–1096.

See Also

final.resamp HP.mod

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