Package ‘demogR’

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demogR-package

Description

demogR is a collection of functions to construct and analyze age-structured population models. For a list of functions, type: help(package="demogR").

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References


calc.ro  
Calculate 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 $k \times k$ 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 $k \times k$ 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

...
Author(s)

James Holland Jones

References


See Also

see leslie.matrix

Examples

## Create a Leslie matrix
Px <- c(0.77, 0.95, 0.98, 0.97)
Fx <- c(0, 0.1, 1.2, 1)
L <- matrix(Px, ncol = 4, byrow = TRUE)
L[1,] <- Fx
## Calculate R_0
calc.ro(L)
## look at the fundamental matrix
calc.ro(L, N.out=TRUE)

## Coale-Demeny Model Life Tables

Description

Coale-Demeny regional model life tables

Usage

cdmltw(sex = "F")
cdmlte(sex = "F")
cdmlts(sex = "F")
cdmltn(sex = "F")

Arguments

sex female or male life tables. Defaults to 'F' (female).

Details

Provides region-specific model life tables for 25 different levels of mortality, indexed by life expectancy at age 10 (with 1 being the lowest and 25 being the highest life expectancy at age 10).
The regions are West (cdmltw), East (cdmlte), South (cdmlts), and North (cdmltn).
**Value**

A list containing two 21 element vectors, one 25 element vector and eight 25 x 21 matrices: 25 mortality levels by 21 age classes. The eight matrices contain the standard columns of a life table for each mortality level:

- **age**: the 21 age classes
- **width**: widths of the 21 age classes
- **e10**: the 25 mortality levels as life expectancy at age 10
- **lx**: survival probabilities to exact age x
- **nqx**: probabilities of death between ages x and x+n
- **nax**: person-years lived by those dying between ages x and x+n
- **ndx**: proportion of all deaths occurring between ages x and x+n
- **nlx**: person-years lived in the interval x to x+n
- **nmx**: central death rate in the interval x to x+n
- **Tx**: person-years of life remaining to the cohort at age x
- **ex**: life expectancy at age x

**Author(s)**

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Corrected by Jim Oeppen, Southern Denmark University, Odense, Denmark

**References**


**See Also**

- `life.table`

**Examples**

```r
## Generate West model life table family for females
Wf <- cdmltw()

## Plot survivorship for the 25 levels
plot(Wf$age,Wf$lx[1,], type="l", xlab="Age", ylab="Survivorship")
for(i in 2:25) lines(Wf$age, Wf$lx[i,])
```
Description

Utility used by life.table to graduate the person-years lived by those dying in the interval by the method of Coale and Demeny.

Usage

coale(b1, b4, nMx)

Arguments

- **b1**: two element vector of regression coefficients for graduating 1a0 provided in Coale et al. (1983)
- **b4**: two element vector of regression coefficients for graduating 4a1 provided in Coale et al. (1983)
- **nMx**: period central death rates: \( nDx/nKx \)

Details

Utility function called by life.table.

Value

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

References


See Also

life.table

Examples

data(goodman)
vlt <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx, type="cd"))
cohort

cohort

description
dummy function called in life.table.

usage
cohort(width12)

arguments
width12 width of the first two age classes

details
this is essentially a place-holder function used when passing the option type="cohort" to life.table.

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

see also
life.table

examples
data(thar)
    thar.lt <- with(thar, life.table(x=age, nDx=deaths, nKx=count,
                               type="cohort", iwidth=1, width12=c(1,1)))
    thar.lt

eigen.analysis

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:

\[ c(x) = b\ l(x)\ \exp(-r\cdot x) \]

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


See Also

leslie.matrix, secdcr

Examples

data(goodman)
ven <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx))
ven.mx <- with(goodman, ven.bx/ven.nKx)
A <- leslie.matrix(lx=ven$nLx,mx=ven.mx)

usa <- with(goodman, life.table(x=age, nKx=usa.nKx, nDx=usa.nDx))
usa.mx <- with(goodman, usa.bx/usa.nKx)
B <- leslie.matrix(lx=usa$nLx,mx=usa.mx)

eav <- eigen-analysis(A)
eau <- eigen-analysis(B)

## compare rates of increase
eav$lambda1
eau$lambda1

## compare stable age distributions for Venezuela and the USA
op <- par(no.readonly = TRUE)
age <- seq(0,50,by=5)
par(mfrow=c(1,2))
barplot(eav$stable.age, names.arg=age,
       horiz=TRUE,
       col="grey",
       ylab="Age")
barplot(eau$stable.age, names.arg=age[-11],
       horiz=TRUE,
       col="blue",
       ylab="Age",
       xlim=c(0,0.2))

par(op)

## Compare reproductive values for Venezuela and the USA
plot(age, eau$repro.value, type="l", xlab="Age", ylab="Reproductive Value")
lines(age[-11], eau$repro.value, lty=2)
legend("topright", c("Venezuela (1965)", "USA (1967)"), lty=c(1,2))

Description
Calculates the partial derivatives of the eigenvalue elasticities of a demographic projection matrix.

Usage
elassens(A, k, l)

Arguments
- A: a demographic projection matrix
- k: row index of the transition that the partial is calculated with respect to
- l: column index of the transition that the partial is calculated with respect to

Details

Value
A matrix of class "leslie.matrix".

References

See Also
secder, leslie.matrix, eigen.analysis

Examples
data(goodman)
mlt <- with(goodman, life.table(x=age, nDx=mad.nDx, nKx=mad.nKx))
mx <- goodman$mad.bx/goodman$mad.nKx

## make the Leslie matrix
mad <- leslie.matrix(1x=mlt$lx, mx=mx)

## now calculate the sensitivities of the elasticities with respect
**fullsecder**

```r
##to infant survival
es21 <- elassens(mad,2,1)
```

**Description**

Calculates the second derivatives of the dominant eigenvalue of a square matrix, \( A \), with respect to all non-zero elements of \( A \).

**Usage**

```r
fullsecder(A)
```

**Arguments**

- `A` a demographic projection matrix

**Details**

Produces a matrix the columns of which are re-shaped matrices of second derivatives of the dominant eigenvalue of the projection matrix \( A \) with respect to each non-zero element in \( A \).


**Value**

A square matrix. If \( A \) is a Leslie matrix of rank \( k \), then the maximum rank of the resulting matrix is \( 2k-1 \) (since there are at most \( k \) non-zero fertilities and \( k-1 \) survival probabilities in a \( k \times k \) Leslie matrix).

**References**


**See Also**

`secder`, `lassens`, `eigen.analysis`, `stoch.sens`
Examples

```r
## eigenvalue second derivatives of the US projection matrix from 1967
data(goodman)
ult <- with(goodman, life.table(x=age, nKx=usa.nKx, nDx=usa.nDx))
mx <- goodman$usa.bx/goodman$usa.nKx
usa <- leslie.matrix(lx=ult$nLx,mx=mx)

fs <- fullsecder(usa)

## plot the survival cross-second derivatives of lambda with respect
## to infant survival
plot(seq(0,40,by=5), fs["21",10:18], type="l",
xlab="Age (j)",
ylab=expression(paste(partialdiff^2, lambda, "/",
   partialdiff, P[1], partialdiff, P[j])))
abline(h=0,lty=3)
```

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

\[ R_0 = \exp(r \cdot T) \]

where \( R_0 \) 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 \( R_0 \) offspring or, equivalently, the amount of time it takes a population growing with instantaneous rate \( r \) to increase by a factor of \( R_0 \).

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


See Also

calc.ro, eigen.analysis

Examples

```r
## compare generation times from two populations with very different
## R_0 values
data(goodman)
ven <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx))
ven.mx <- with(goodman, ven.bx/ven.nKx)
A <- leslie.matrix(lx=ven$nLx, mx=ven.mx)

usa <- with(goodman, life.table(x=age, nKx=usa.nKx, nDx=usa.nDx))
usa.mx <- with(goodman, usa.bx/usa.nKx)
B <- leslie.matrix(lx=usa$nLx, mx=usa.mx)

gen.time(A)
gen.time(B)
```

Description


Usage

data(goodman)
Format

A data frame with 19 observations on the following 10 variables.

- **age** age classes
- **ven.nKx** mid-year population structure for Venezuela
- **ven.nDx** enumerated deaths for Venezuela
- **ven.bx** enumerated births for Venezuela
- **mad.nKx** mid-year population structure for Madagascar
- **mad.nDx** enumerated deaths for Madagascar
- **mad.bx** enumerated births for Madagascar
- **usa.nKx** mid-year population structure for the United States
- **usa.nDx** enumerated deaths for the United States
- **usa.bx** enumerated births for the United States

Details

Vital event data tabulated by Keyfitz and Flieger (1990) and used by Goodman et al. (1974) to illustrate their kinship frequency calculations. The three female populations represent tremendous diversity in age-specific demographic schedules. Venezuela (1965) is characterized by low mortality and high fertility; Madagascar (1966) is characterized by very high mortality and fertility, while the United States (1967) is characterized by low mortality and low fertility.

Source

Keyfitz and Flieger (1990), Goodman et al. (1974)

References


Examples

data(goodman)
## Plot age-specific mortality rates for the three populations
with(goodman, plot(age, usa.nDx/usa.nKx, type="l", log="y", xlab="Age", ylab="nMx"))
with(goodman, lines(age, mad.nDx/mad.nKx, lty=2))
with(goodman, lines(age, ven.nDx/ven.nKx, lty=3))
legend("bottomright", c("USA","Madagascar","Venezuela"), lty=c(1,2,3))
Description

Utility used by `life.table` 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). Default value: `b0=c(0.07, 1.7)`.
- `nMx`: period central death rates: `=nDx/nKx`.

Details

Utility function called by `life.table`.

Value

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

References


See Also

`life.table`

Examples

```r
data(goodman)
## default type="kf"
vlt <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx))```
Description

Calculates the logarithm of the stochastic growth rate using Tuljapurkar's second order approximation for independent and identically distributed environments.

Usage

\texttt{lams(aseq, n = 5)}

Arguments

\begin{itemize}
\item \texttt{aseq} sequence of matrices with each matrix given as a re-shaped column of \texttt{aseq}
\item \texttt{n} width of the projection interval/age-class
\end{itemize}

Details

Uses Tuljapurkar's second order approximation for independent and identically distributed (i.i.d.) environments.

Value

The long-run growth rate for the population with projection matrices given by \texttt{aseq}.

References


See Also

\texttt{stoch.sens,eigen.analysis}

Examples

\begin{verbatim}
## simulate two matrices: good year/bad year
## beta distributed survival, gamma fertility
px1 <- rbeta(5,9,1)
px2 <- rbeta(5,7,3)
mx1 <- c(0,rgamma(5,10,10))
mx2 <- c(0,rgamma(5,7,10))
## good year matrix
A1 <- odiag(px1,-1)
\end{verbatim}
leslie.matrix

A1[1,] <- mx

## bad year matrix
A2 <- diag(px2,-1)
A2[1,] <- mx
aseq <- cbind(matrix(A1,nr=36,nc=1), matrix(A2,nr=36,nc=1))
lams(aseq)

---

**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 = 1.05, 
  infant.class = TRUE)
```

**Arguments**

- `lx` : 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 person-years lived in the interval \( nLx \), while if 'FALSE', `lx` is taken to be cumulative survival to exact age \( x+n \). Defaults to 'TRUE'.
- `peryear` : Multiplier for fertility. Defaults to `peryear`=5.
- `one.sex` : logical; If 'TRUE', fertility rates will be divided by \((1+SRB)\).
- `SRB` : sex ratio at birth. Defaults to \( SRB=1.05 \).
- `infant.class` : logical; 'TRUE' if `lx` contains a value for the infant age-class.

**Details**

Constructs a \( k \times k \) 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 truncated to be the same length as \( lx \). If \( lx \) is longer than \( mx \), a warning is issued 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 \( \text{peryear} \) 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 \( \text{infant.class}=\text{TRUE} \), \( lx \) 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 \( L=\text{TRUE} \), then the first two values of \( lx \) are combined to form the total person-years for the first age-class in the Leslie matrix. Human demographic data from abridged life tables typically come with age classes \( x = 0, 1, 5, 10, \ldots \) ... Thus, combining the person-years for the first two age classes gives an initial age class of the correct width. If \( \text{infant.class}=\text{FALSE} \) and \( L=\text{FALSE} \), 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 \( \text{infant.class}=\text{FALSE} \).

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

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

Value

A \( k \times k \) age-classified demographic projection matrix with class "leslie.matrix".

References


See Also

odiag, leslie.row

Examples

```r
## Construct lx and mx values
data(goodman)
mlt <- with(goodman, life.table(x=age, nDx=mad.nDx, nKx=mad.nKx))
mx <- goodman$mad.bx/goodman$mad.nKx

## Now make the Leslie matrix
mad <- leslie.matrix(lx=mlt$nLx, mx=mx)
```
## Description

A utility for calculating the first row of a Leslie matrix from vectors of interval survival probabilities and age-specific fertility rates.

## Usage

```r
leslie.row1(mx, px, L = NULL, SRB = 1.05, peryear = 5, one.sex = TRUE)
```

## Arguments

- **mx**: vector of age-specific fertilities (length=k)
- **px**: vector of interval survival probabilities (length=k-1)
- **L**: person-years lived in the first interval; default L=NULL in which case each element is multiplied by peryear*sqrt(px[1]), otherwise each element is multiplied by L.
- **SRB**: sex ratio at birth; default SRB=1.05.
- **peryear**: width of the age-class/projection interval
- **one.sex**: should each element be reduced by a factor 1/(1+SRB)? default one.sex=TRUE.

## Details

Calculates the first-row entries for a Leslie matrix. This utility is particularly useful for constructing simulated Leslie matrices.

## Value

A vector of length k, where k is the rank of the projection matrix A.

## See Also

- **leslie.matrix**
Examples

```r
## simulate survival values from a beta(9,1) distribution
px <- rbeta(10, 9, 1)

## simulate fertility values from a gamma(2,10) distribution with age
## at first reproduction = 10
mx <- c(0, 0, 0, rgamma(2, 10))
A <- odiag(px, -1)
Fx <- leslie.row1(mx, px)
A[1,] <- Fx
```

Description

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

Usage

```r
life.table(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`: 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`: person-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).
width of the age intervals. Default iwidth=5.
width12  width of the first two age classes. Default width12=c(1,4).

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 be the 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:
\[
x \quad \text{age at the beginning of the interval}
\]
\[
nax \quad \text{person-years lived by those dying in the interval x to x+n}
\]
\[
nMx \quad \text{period central death rate}
\]
\[
nqx \quad \text{probability of death between ages x and x+n}
\]
\[
lx \quad \text{probability of survival to exact age x}
\]
\[
ndx \quad \text{proportion of deaths occurring between ages x and x+n}
\]
\[
nLx \quad \text{person-years lived in the interval x to x+n}
\]
\[
Tx \quad \text{person-years of life left in the cohort at age x}
\]
\[
ex \quad \text{life expectancy at age x}
\]

References

See Also
cdmltw
Examples

data(goodman)
## default type="kf"
vlt <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx))
## compare nax values for cd vs kf life tables
vlt$1 <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx, type="cd"))
vlt$1[nax[1:2]]
vlt$1[nax[1:2]]
## now construct a cohort life table for Himalayan thar,
## (Hemitargus jemlahicus)
data(thar)
thar$Lt <- with(thar, life.table(x=age, nDx=deaths, nKx=count,
                           type="cohort", iwidth=1, width12=c(1,1)))

loop.elas

Description

Calculate and plot loop elasticities for a demographic projection matrix.

Usage

loop.elas(A,
          draw.plot = TRUE,
          peryear = 5,
          xlab = "Loop Elasticity",
          ylab = "Age",
          xlim = c(0, (maxe + 0.02)),
          ...)

Arguments

A    demographic projection matrix
draw.plot    should a plot be drawn? default: draw.plot=TRUE
peryear    width of the age-class/projection interval
xlab    x-axis label; default ylab="Age"
ylab    y-axis label; default ylab="Loop Elasticity"
xlim    plotting limits for x-axis
...    arguments to be passed to/from other methods

Details

Value

A vector of length k (the rank of the projection matrix A) giving the loop elasticities for each of the loops in the life-cycle graph.

References


See Also

eigen.analysis, leslie.matrix

Examples

data(goodman)
ven <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx))
ven.mx <- with(goodman, ven.bx/ven.nKx)
A <- leslie.matrix(lx=ven$nLx, mx=ven.mx)

usa <- with(goodman, life.table(x=age, nKx=usa.nKx, nDx=usa.nDx))
usa.mx <- with(goodman, usa.bx/usa.nKx)
B <- leslie.matrix(lx=usa$nLx, mx=usa.mx)
eav <- eigen.analysis(A)
eau <- eigen.analysis(B)

## Compare the loop elasticities of Venezuela (1965) and the USA (1967)
le.usa <- loop.elas(A)
le.usa <- loop.elas(B)

Description

Utility that takes a matrix n x m and stacks its columns to form a column vector of length mn.

Usage

m2v(A)

Arguments

A an m x n matrix
Value

For an m x n input matrix, returns a m*n x 1 matrix (i.e., a column vector).

Note

Meant to capture the MATLAB functionality of the colon operator, A(:,).

See Also

odiag

Examples

A <- matrix(rnorm(9), nr=3, nc=3)
m2v(A)

odiag

Description

Utility function that creates a square matrix with a vector on the off-diagonal or extracts the specified off-diagonal vector.

Usage

odiag(A, at = 0)

Arguments

A either a vector or a matrix
at which diagonal?

Details

If the first argument is a vector of length k, the result will be a square matrix of rank k+at with the provided vector along the 'at' diagonal. Positive values for 'at' place the vector above the diagonal, negative values below the diagonal, and at=0 (the default) places the vector on the diagonal.

Value

A vector if argument A is a matrix and a matrix if A is a vector.

Note

odiag is meant to capture some of the functionality of the MATLAB function diag().
See Also
diag

Examples

```r
## Construct a matrix from a vector
## random survival probabilities with mean 0.9 and variance 0.0082

y <- rbeta(4,9,1)
A <- odiag(y,-1)

## add fertilities
F <- c(0,rep(1,4))
A[1,] <- F

## Extract a vector from a matrix
A <- matrix(rnorm(25), nr=5, nc=5)
odiag(A,2)
```

Description

Plots Leslie matrices and other objects of class "leslie.matrix".

Usage

```r
## S3 method for class 'leslie.matrix'
plot(x, y=NULL,
     ..., main="", sub="",
     ann=TRUE,
     xlim=NULL, ylim=NULL,
     axes=TRUE,
     col=c("black","grey"),
     lwd=2,
     xlab="Age", ylab="Sensitivity",
     peryear=5 )
```

Arguments

- **x**: demographic projection matrix
- **y**: y axis values; NULL
- **...**: arguments to be passed to/from other methods
- **main**: an overall title for the plot
sub  a subtitle for the plot
ann  logical; if TRUE, annotate plot
xlim plotting limits for x-axis; if xlim=NULL, range of x values used
ylim plotting limits for y-axis; if ylim=NULL, range of y values used
axes logical; if TRUE, draw axes and box
col vector (length 2) of line colors for the plot; default col("black","grey")
lwd thickness of the plotted lines; default lwd=2
peryear width of the age-class/projection interval; default peryear=5
xlab x-axis label; default xlab="Age"
ylab y-axis label; default ylab="Sensitivity"

Details
Plots the subdiagonal and the first row of an object of class leslie.matrix on common axes. Probably most useful for plotting either eigenvalue sensitivities or elasticities of a projection matrix.

Value
NULL

See Also
eigenNanalysis, loopNelas

Examples
data(goodman)
ven <- with(goodman, life.table(x=age, nKx=ven.nKx, nDx=ven.nDx))
ven.mx <- with(goodman, ven.bx/ven.nKx)
A <- leslie.matrix(lx=ven$nlx, mx=ven.mx)
ea.ven <- eigenNanalysis(A)

usa <- with(goodman, life.table(x=age, nKx=usa.nKx, nDx=usa.nDx))
usa.mx <- with(goodman, usa.bx/usa.nKx)
B <- leslie.matrix(lx=usa$nlx, mx=usa.mx)
ea.usa <- eigenNanalysis(B)

## Compare sensitivities for Venezuela and the USA
plot(ea.ven$sens, main="Venezuela")
plot(ea.usa$sens, main="USA")
Description

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

Usage

```r
project.leslie(A, no, tmax, pop.sum = FALSE)
```

Arguments

- `A`: a k x k projection matrix
- `no`: a k x 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.

See Also

- `leslie.matrix`, `eigen.analysis`

Examples

```r
data(goodman)
ult <- with(goodman, life.table(x=age, nKx=usa.nKx, nDx=usa.nDx))
mx <- goodman$usa.bx/goodman$usa.nKx
usa <- leslie.matrix(1x=ult$nLx,mx=mx)

## initial population is the age structure in 1967
## this includes the number of 0-1 year-olds and the number of 1-4 year-olds, which need to be combined into a single 5-year wide
```
## element

```r
no <- goodman$usa.nKx[3:11]
no <- c(sum(goodman$usa.nKx[1:2]), no)/1e6
N <- project.leslie(usa, no, tmax=20)
plot(seq(1967, 2067, by=5), apply(N, 2, sum),
     type="l",
     xlab="Years",
     ylab="Projected Population (millions)"
     title="Projected Total Population Size (Ages 0-45) of the United States"

# Note that this is a lousy projection since it assumes constant demographic rates and a closed population and only accounts for ages 0-45
```

### Description

Calculates the second derivatives of the dominant eigenvalue of the demographic projection matrix for all non-zero transitions with respect to one specified transition.

### Usage

```r
secder(A, k, l)
```

### Arguments

- `A`: demographic projection matrix
- `k`: row index for the specified transition
- `l`: column index for the specified transition

### Details


### Value

A square matrix of the same rank as `A` where each element \( s_{ij} \) is the second derivative of the dominant eigenvalue of `A`, \( \partial^2 \lambda / \partial a_{ij} \partial a_{kl} \).

### Note

The eigenvalue second derivatives are essential for calculating both perturbation analyses of the eigenvalue elasticities and stochastic sensitivities. `secder` is used in functions to calculate both these quantities.
References


See Also

fullsecder, elassens, eigen.analysis, stoch.sens

Examples

```r
## eigenvalue second derivatives of the US projection matrix from 1967
## with respect to infant survival
data(goodman)
ult <- with(goodman, life.table(x=age, nKx=usa.nKx, nDx=usa.nDx))
mx <- goodman$usa.bx/goodman$usa.nKx
usa <- leslie.matrix(lx=ult$nLx,mx=mx)

sd21 <- secder(usa,2,1)
```

Description

Calculates the sensitivity of the stochastic growth rate to perturbations in the mean demographic projection matrix.

Usage

```r
stoch.sens(env, amat, k)
```

Arguments

- `env` environmental sequence
- `amat` matrices describing the population dynamics in the different environmental states, organized as columns of a matrix
- `k` rank of the projection matrices

Details

See Caswell (2001, section 14.4) for details.
Value

A list with two elements:

- sensitivities: sensitivities of the stochastic growth rate
- elasticities: elasticities of the stochastic growth rate

Note

This is essentially a translation of Caswell’s (2001, section 14.4.1.1) MATLAB code.

References


See Also

lams, eigen.analysis

Examples

```r
## Simulate an i.i.d. sequence of 3 environmental states

env <- floor(runif(100,0,3))+1
px1 <- rbeta(4,9.5,0.5)
px2 <- rbeta(4,7.5,2.5)
px3 <- rbeta(4,5.5)
mx <- c(0,rgamma(4,5,10))

A1 <- odiag(px1,-1)
A2 <- odiag(px2,-1)
A3 <- odiag(px3,-1)
A1[,1] <- leslie.row1(mx,px1)
A2[,1] <- leslie.row1(mx,px2)
A3[,1] <- leslie.row1(mx,px3)
amat <- cbind(matrix(A1,nr=25), matrix(A2,nr=25), matrix(A3,nr=25))
stoch.sens(env,amat,k=5)
```
Description

Caughley’s (1966) survival data on Himalayan thar (*Hemitragus jemlahicus*).

Usage

data(thar)

Format

A data frame with 13 observations on the following 3 variables.

- age: age class
- count: the number of individuals at the start of the age class
- deaths: observed deaths in the age class

Details

Caughley (1966) smoothed the counts within age classes and this data set used those reported smoothed counts.

Source


Examples

data(thar)
thar.lt <- with(thar,
  life.table(x=age,
    n Dx=deaths,
    n Kx=count,
    type="cohort",
    iwidth=1,
    width12=c(1,1)))

thar.lt
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