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Description Age-specific mortality rates are estimated and projected using the Kannisto, Lee-Carter and related methods as described in Sevcikova et al. (2016) <doi:10.1007/978-3-319-26603-9_15>.

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Description

Age-specific mortality rates are estimated and projected using the Kannisto, Lee-Carter and related methods as described in Sevcikova et al. (2016) doi:10.1007/9783319266039_15.

Details

The package implements methodology described in Sevcikova et al. (2016) that is related to estimating and predicting age-specific mortality rates. The main functions are:

- cokannisto: Extrapolates given mortality rates into higher ages using the Coherent Kannisto method. The original Kannisto method (with sex-independent extrapolation) is avalable in the function kannisto.

- lileecarter.estimate: Estimates the coherent Lee-Carter parameters for male and female mortality rates (Li and Lee 2005), i.e. sex-independent parameters a_x and k_t, and the coherent parameter b_x. In addition, it computes the ultimate b_x^u for rotation (Li et al. 2013). The underlying sex-independent estimation is implemented in the function leecarter.estimate.

- mortcast: Using estimated coherent Lee-Carter parameters and given future sex-specific life expectancies, it projects age-specific mortality rates, while (by default) rotating the b_x parameter as described in Li et al. (2013).

Functions contained in the package can be used to apply Algorithm 2 in Sevcikova et al. (2016) as shown in the Example below. It can be used for both, 5-year and 1-year age groups.

Other methods for forecasting mortality rates are available:

- pmd: pattern of mortality decline
- mlt: model life tables
- logquad: log-quadratic mortality model
- mortcast.blend: combining two different methods

A life table can be constructed using the life.table function.

Author(s)

Hana Sevcikova, Nan Li and Patrick Gerland

References

Li, N. and Lee, R. D. (2005). Coherent mortality forecasts for a group of populations: An extension of the Lee-Carter method. Demography, 42, 575-594.

Li, N., Lee, R. D. and Gerland, P. (2013). Extending the Lee-Carter method to model the rotation of age patterns of mortality decline for long-term projections. Demography, 50, 2037-2051.

Sevcikova H., Li N., Kantorova V., Gerland P., Raftery A.E. (2016). Age-Specific Mortality and Fertility Rates for Probabilistic Population Projections. In: Schoen R. (eds) Dynamic Demographic Analysis. The Springer Series on Demographic Methods and Population Analysis, vol 39. Springer, Cham. Earlier version.

Examples

```
# This example applies Algorithm 2 in Sevcikova et al. (2016)
# on data from WPP2017 for China
#
data(mxM, mxF, e0Fproj, e0Mproj, package = "wpp2017")
country <- "China"

# extract observed mortality rates for male and female
mxm <- subset(mxM, name == country)[,4:16]
mxf <- subset(mxF, name == country)[,4:16]
rownames(mxm) <- rownames(mxf) <- c(0,1, seq(5, 100, by=5))

# Step 1: extrapolate from 100+ to 130+ using Coherent Kannisto
mx130 <- cokannisto(mxm, mxf)

# Steps 2-5: estimate coherent Lee-Carter parameters
# (here ax is computed from the last observed period
# and smoothened over ages)
lc.est <- lileecarter.estimate(mx130$male, mx130$female,
            ax.index = ncol(mx130$male), ax.smooth = TRUE)

# Steps 6-9: project future mortality rates based on future
# life expectancies from WPP2017
e0f <- as.numeric(subset(e0Fproj, name == country)[-(1:2)])
e0m <- as.numeric(subset(e0Mproj, name == country)[-(1:2)])
names(e0f) <- names(e0m) <- colnames(e0Fproj)[-(1:2)]
pred <- mortcast(e0m, e0f, lc.est)

# plot projection for the first and last future time period
plot(pred$female$mx[,"2015-2020"], type="l", log="y",
    ylim=range(pred$female$mx, pred$male$mx), xaxt="n",
    ylab="mx", xlab="Age", main=country, col="red")
axis(1, at=1:nrow(pred$female$mx),
    labels=rownames(pred$female$mx))
lines(pred$male$mx[,"2015-2020"], col="blue")
lines(pred$female$mx[,"2095-2100"], col="red", lty=2)
```

```
lines(pred$male$mx[,"2095-2100"], col="blue", lty=2)
legend("topleft", legend=c("male 2015-2020", "female 2015-2020",
    "male 2095-2100", "female 2095-2100"), bty="n",
    col=rep(c("blue", "red"),2), lty=c(1,1,2,2))
```

---

cokannisto	*Coherent Kannisto Method*

Description

Extrapolate given mortality rates into higher ages using the Coherent Kannisto method as described
in Sevcikova et al. (2016).

Usage

```
cokannisto(
  mxM,
  mxF,
  est.ages = seq(80, 95, by = 5),
  proj.ages = seq(100, 130, by = 5)
)
```

Arguments

mxM	A vector or matrix of male mortality rates. If it is a matrix, rows correspond to age groups with rownames identifying the corresponding age as integers. By default five-years age groups are assigned to rows if rownames are not given.
mxF	A vector or matrix of female mortality rates. Its length or dimension should be the same mxM.
est.ages	A vector of integers identifying the ages to be used for estimation. It should be a subset of rownames of mxM. Change the defaults if 1-year age groups are used (see Example in kannisto).
proj.ages	A vector of integers identifying the age groups for which mortality rates are to be projected. Change the defaults if 1-year age groups are used (see Example in kannisto).

Details

The function first estimates the coherent Kannisto parameters by passing mortality rates for age
groups est.ages into the cokannisto.estimate function. The estimated parameters are then
passed to the projection function kannisto.predict to extrapolate into ages proj.ages. Lastly,
the input mortality objects are extended by results for the extrapolated ages. If proj.ages contains
age groups that are included in mxM and mxF, values for those age groups are overwritten.

Value

A list of two vectors or matrices (for male and female) containing the input motality objects extended by the extrapolated age groups.

References

Sevcikova H., Li N., Kantorova V., Gerland P., Raftery A.E. (2016). Age-Specific Mortality and Fertility Rates for Probabilistic Population Projections. In: Schoen R. (eds) Dynamic Demographic Analysis. The Springer Series on Demographic Methods and Population Analysis, vol 39. Springer, Cham

See Also

cokannisto.estimate, kannisto.predict

Examples

```
data(mxM, mxF, package = "wpp2017")
country <- "South Africa"
mxm <- subset(mxM, name == country)[,-(1:3)]
mxf <- subset(mxF, name == country)[,-(1:3)]
rownames(mxm) <- rownames(mxf) <- c(0,1, seq(5, 100, by=5))
mxnew <- cokannisto(mxm, mxf)
ages <- as.integer(rownames(mxnew$male))
plot(ages, mxnew$male[,"2095-2100"], type="l", log="y",
    xlab="age", ylab="mx", col="blue", main=country)
lines(ages, mxnew$female[,"2095-2100"], col="red")
lines(ages, mxnew$male[,"2010-2015"], lty=2, col="blue")
lines(ages, mxnew$female[,"2010-2015"], lty=2, col="red")
legend("bottomright", legend=c("male 2010-2015", "female 2010-2015",
    "male 2095-2100", "female 2095-2100"), bty="n",
    col=rep(c("blue", "red"),2), lty=c(2,2,1,1))
```

---

cokannisto.estimate *Coherent Kannisto Estimation*

Description

Estimate the coherent Kannisto parameters as described in Sevcikova et al. (2016).

Usage

```
cokannisto.estimate(mxM, mxF, ages, fitted = TRUE)
```

Arguments

`mxM`	A vector of male mortality rates.
`mxF`	A vector of female mortality rates.
`ages`	A vector of ages corresponding to `mxM` and `mxF`.
`fitted`	Logical. If `TRUE` the fitted values and residuals are returned.

Details

Given the Kannisto equation $logit(m_x) = \log(c) + dx$, the Coherent Kannisto method estimates the d parameter jointly for male and female data, in order to prevent mortality crossovers in higher ages.

Value

List of two lists, one for male and one for female. Each of the two lists contains the following components:

coefficients: named vector with the coherent Kannisto coefficients c and d. The d values are the same in both lists.

fitted.values: the fitted values (not included if `fitted` is `FALSE`)

residuals: input rates minus the fitted values (not included if `fitted` is `FALSE`)

References

Sevcikova H., Li N., Kantorova V., Gerland P., Raftery A.E. (2016). Age-Specific Mortality and Fertility Rates for Probabilistic Population Projections. In: Schoen R. (eds) Dynamic Demographic Analysis. The Springer Series on Demographic Methods and Population Analysis, vol 39. Springer, Cham

See Also

cokannisto, kannisto.predict, kannisto

Examples

```
data(mxM, mxF, package = "wpp2017")
country <- "Brazil"
mxm <- subset(mxM, name == country)[,"2010-2015"]
mxf <- subset(mxF, name == country)[,"2010-2015"]
cokannisto.estimate(mxm[18:21], mxf[18:21], ages = 18:21)
```

kannisto	*Kannisto Method*

Description

Extrapolate given mortality rates using the original Kannisto method.

Usage

```
kannisto(mx, est.ages = seq(80, 95, by = 5), proj.ages = seq(100, 130, by = 5))
```

Arguments

mx
: A vector or matrix of mortality rates. If it is a matrix, rows correspond to age groups with rownames identifying the corresponding age as integers. By default five-years age groups are assigned to rows if rownames are not given.

est.ages
: A vector of integers identifying the ages to be used for estimation. It should be a subset of rownames of mx. Change the defaults if 1-year age groups are used (see Example).

proj.ages
: A vector of integers identifying the age groups for which mortality rates are to be projected. Change the defaults if 1-year age groups are used (see Example).

Details

The function first estimates the original Kannisto parameters by passing mortality rates for age groups est.ages into the kannisto.estimate function. The estimated parameters are then passed to the projection function kannisto.predict to extrapolate into ages proj.ages. Lastly, the input mortality object is extended by results for the extrapolated ages. If proj.ages contains age groups that are included in mx, values for those age groups are overwritten.

Value

A vector or matrix containing the input mortality object mx extended by the extrapolated age groups.

References

Thatcher, A. R., Kannisto, V. and Vaupel, J. W. (1998). The Force of Mortality at Ages 80 to 120, volume 5 of Odense Monographs on Population Aging Series. Odense, Denmark: Odense University Press.

See Also

kannisto.estimate, kannisto.predict, cokannisto

Examples

```
data(mxM, package = "wpp2017")
mx <- subset(mxM, name == "Burkina Faso")[,-(1:3)]
rownames(mx) <- c(0,1, seq(5, 100, by=5))
mxnew <- kannisto(mx)
ages <- as.integer(rownames(mxnew))
plot(ages, mxnew[,"2095-2100"], type="l", log="y",
    xlab="age", ylab="mx", col="red")
lines(ages, mxnew[,"2010-2015"])

# Kannisto for 1-year age groups
# derive toy 1-year mx using model life tables at e0 of 70
mx1y <- mlt(70, sex = "male", nx = 1)
# Pretend we only observed mx for ages 0:100.
# Use 90-99 for estimation and extend mx from 100 to 140
mx1ynew <- kannisto(mx1y[1:100, , drop = FALSE], est.ages = 90:99, proj.ages = 100:140)
# Plot the new mx for old ages
plot(80:140, mx1ynew[81:141], type = "l", xlab="age", ylab="mx", col="red")
# Check how it compares to the original mx that was not used in the estimation
lines(100:130, mx1y[101:nrow(mx1y)])
```

---

kannisto.estimate   *Kannisto Estimation*

Description

Estimate the Kannisto parameters (Thatcher et al. 1998).

Usage

```
kannisto.estimate(mx, ages)
```

Arguments

mx	A vector of mortality rates.
ages	A vector of ages corresponding to mx. These can be indices of age groups or raw ages.

Details

Given the Kannisto equation $logit(m_x) = \log(c) + dx$, the function estimates the c and d parameters using values of ages as the covariate x.

Value

List with the following components:

coefficients: named vector with Kannisto coefficients c and d.

fitted.values: the fitted values

residuals: input rates minus the fitted values

References

Thatcher, A. R., Kannisto, V. and Vaupel, J. W. (1998). The Force of Mortality at Ages 80 to 120, volume 5 of Odense Monographs on Population Aging Series. Odense, Denmark: Odense University Press.

See Also

kannisto.predict, kannisto, cokannisto.estimate

Examples

```
data(mxM, package = "wpp2017")
mx <- subset(mxM, name == "Canada")[,"2010-2015"]
kannisto.estimate(mx[18:21], ages = 18:21)
```

---

  kannisto.predict   *Kannisto Prediction*

Description

Given estimated Kannisto parameters (coherent or original), it predicts mortality rates for given ages.

Usage

```
kannisto.predict(pars, ages)
```

Arguments

pars   A named vector with Kanisto coefficients c and d (e.g. result of kannisto.estimate or cokannisto.estimate).

ages   A vector of ages to make prediction for. These can be indices of age groups or raw ages, but on the same scale as used in the estimation.

Details

Given parameters c and d in pars, the function uses the Kannisto equation $logit(m_x) = \log(c) + dx$, to predict mortality rates for age groups x given by ages.

Value

Vector of predicted mortality rates.

References

Thatcher, A. R., Kannisto, V. and Vaupel, J. W. (1998). The Force of Mortality at Ages 80 to 120, volume 5 of Odense Monographs on Population Aging Series. Odense, Denmark: Odense University Press.

See Also

cokannisto, kannisto.estimate, cokannisto.estimate

Examples

```
data(mxM, mxF, package = "wpp2017")
mxm <- subset(mxM, name == "Germany")[,"2010-2015"]
ages <- c(0, 1, seq(5, 130, by=5))

# using original Kannisto parameters
pars <- kannisto.estimate(mxm[18:21], ages = ages[18:21])
mxm.pred <- kannisto.predict(pars$coefficients, ages = ages[22:28])
plot(ages, c(mxm[1:21], mxm.pred), type="l", log="y",
    xlab="age", ylab="mx")

# Coherent Kannisto
mxf <- subset(mxF, name == "Germany")[,"2010-2015"]
copars <- cokannisto.estimate(
   mxm[18:21], mxf[18:21], ages = ages[18:21])
cmxm.pred <- kannisto.predict(copars[["male"]]$coefficients, ages = ages[22:28])
cmxf.pred <- kannisto.predict(copars[["female"]]$coefficients, ages = ages[22:28])
plot(ages, c(mxm[1:21], cmxm.pred), type="l", log="y",
    xlab="age", ylab="mx", col="blue")
lines(ages, c(mxf[1:21], cmxf.pred), col="red")
```

---

leecarter.estimate   *Lee-Carter Estimation*

Description

Estimate Lee-Carter parameters (Lee and Carter 1992).

Usage

```
leecarter.estimate(
  mx,
  ax.index = NULL,
  ax.smooth = FALSE,
```

```
    ax.smooth.df = NULL,
    bx.postprocess = TRUE,
    nx = 5
)
```

Arguments

mx	A matrix of age-specific mortality rates where rows correspond to age groups and columns correspond to time periods. Rownames define the starting ages of the age groups.
ax.index	A vector of column indices of mx to be used to estimate the a_x parameter. By default all time periods are used.
ax.smooth	Logical allowing to smooth the a_x over ages.
ax.smooth.df	Degree of freedom for smoothing if ax.smooth is TRUE. Default is half the length of a_x.
bx.postprocess	Logical determining if numerical anomalies in b_x should be dealt with.
nx	Size of age groups. By default ages are determined by rownames of mx. This argument is only used if mx has no rownames. If nx is 5, the age groups are interpreted as 0, 1, 5, 10, ... For nx equals 1, the age groups are interpreted as 0, 1, 2, 3, ...

Details

The function estimates parameters of $\log(m_x(t)) = a_x + b_x k(t) + \epsilon_x(t)$ (Lee and Carter 1992). The argument ax.index determines which time periods to use to estimate the a_x parameter, while ax.smooth controls if the resulting a_x should be smoothened over ages (see Sevcikova et al. 2016 for details).

Value

List with elements ax, bx and kt corresponding to the estimated parameters.

References

Lee, R. D. and Carter, L. (1992). Modeling and forecasting the time series of US mortality. Journal of the American Statistical Association, 87, 659-671.

Sevcikova H., Li N., Kantorova V., Gerland P., Raftery A.E. (2016). Age-Specific Mortality and Fertility Rates for Probabilistic Population Projections. In: Schoen R. (eds) Dynamic Demographic Analysis. The Springer Series on Demographic Methods and Population Analysis, vol 39. Springer, Cham

See Also

mortcast, lileecarter.estimate

Examples

```
data(mxM, package = "wpp2017")
mx <- subset(mxM, name == "Netherlands")[,4:16]
rownames(mx) <- c(0,1, seq(5, 100, by=5))
lc.ax.avg <- leecarter.estimate(mx)
lc.ax.last <- leecarter.estimate(mx, ax.index=ncol(mx))
plot(lc.ax.avg$ax, type="l")
lines(lc.ax.last$ax, col="blue")
```

---

life.table   *Life Table Function*

Description

Function for obtaining life table quantities from mortality rates.

Usage

```
life.table(
  mx,
  sex = c("male", "female", "total"),
  abridged = TRUE,
  a0rule = c("ak", "cd"),
  radix = 1,
  open.age = 130
)
```

Arguments

mx	Vector of age-specific mortality rates nmx. If abridged is TRUE (default), the elements correspond to 1m0, 4m1, 5m5, 5m10, ... If abridged is FALSE, they correspond to 1m0, 1m1, 1m2, 1m3, ...
sex	Which sex the mortality rates correspond to.
abridged	Is it an abridged life table (TRUE, default) or not (FALSE). In the former case, the mx vector is interpreted as corresponding to age groups 0, 1-4, 5-9, 10-14, ... If FALSE, the mx vector is interpreted as corresponding to one-year age groups, i.e. 0, 1, 2, 3, ...
a0rule	Rule for approximation of a0. "ak" (default) uses the Andreev-Kingkade method (Andreev and Kingkade, 2015), "cd" uses the Coale-Demeany method.
radix	Base of the life table.
open.age	Open age group. If smaller than the last age group of mx, the life table is truncated. It does not have any effect if larger than the last age group.

Details

Computes a life table corresponding to given mortality rates for either 5- or 1-year age groups. The implementation follows Preston et al. (2001).

Value

Data frame with rows corresponding to age groups and the following columns:

age Starting year of the age group.

mx Age-specific mortality rates as passed into the mx argument.

qx Probability of dying between ages x and x+n.

lx Number of survivors at age x.

dx Number of deaths between ages x and x+n.

Lx Person-years lived between ages x and x+n.

sx Survival rate from age x to x+n. Note that in an abridged life table, sx always refers to 5-year intervals. Here, sx in the first row is the survival from births to the second age group, sx in the second row is the survival from age 0-4 to age 5-9, third row has the survival from 5-9 to 10-14 etc.

Tx Person-years lived after age x.

ex Life expectancy at age x.

ax Average person-years lived in the interval by those dying in the interval. For young ages, it follows Preston et al. (2001), Table 3.3 on page 48. If a0rule is "ak" (default) the Andreev-Kingkade method is used for a0. For compatibility with computations done at the UN, we set ax for ages 5 and 10 in the abridged version to 2.5. For an unabridged life table, ax is set to 0.5 for all but first and last age groups.

References

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

Andreev, E.M. and Kingkade, W.W. (2015). Average age at death in infancy and infant mortality level: Reconsidering the Coale-Demeny formulas at current levels of low mortality. Demographic Research, 33(13), p.363-390. DOI: 10.4054/DemRes.2015.33.13

Examples

```
data(mxF, e0Fproj, package = "wpp2017")
# get female mortality of Mexico for the current year
country <- "Mexico"
mxf <- subset(mxF, name == country)[,"2010-2015"]
life.table(mxf, sex = "female")
```

lileecarter.estimate   *Coherent Lee-Carter Estimation*

Description

Estimate coherent Lee-Carter parameters (Li and Lee 2005).

Usage

```
lileecarter.estimate(mxM, mxF, nx = 5, ...)
```

Arguments

mxM	A matrix of male age-specific mortality rates where rows correspond to age groups and columns correspond to time periods. For 5-year age groups, the first and second rows corresponds to 0-1 and 1-5 age groups, respectively. Rownames define the starting ages of the respective groups.
mxF	A matrix of female mortality rates of the same shape as mxM.
nx	Size of age groups. Should be either 5 or 1.
...	Additional arguments passed to leecarter.estimate.

Details

The coherent Lee-Carter parameters for male and female mortality rates share the same b_x which is the average of the age-specific b_x parameters.

The function in addition computes the ultimate b_x^u as defined in Li et al. (2013) based on the coherent b_x.

Value

List containing elements bx (coherent b_x parameter), ultimate.bx (ultimate b_x^u parameter), ages (age groups), nx (age group interval), and lists female and male, each with the Lee-Carter parameters.

References

Li, N. and Lee, R. D. (2005). Coherent mortality forecasts for a group of populations: An extension of the Lee-Carter method. Demography, 42, 575-594.

Li, N., Lee, R. D. and Gerland, P. (2013). Extending the Lee-Carter method to model the rotation of age patterns of mortality decline for long-term projections. Demography, 50, 2037-2051.

Examples

```
data(mxM, mxF, package = "wpp2017")
country <- "Germany"
mxm <- subset(mxM, name == country)[,4:16]
mxf <- subset(mxF, name == country)[,4:16]
rownames(mxm) <- rownames(mxf) <- c(0,1, seq(5, 100, by=5))
lc <- lileecarter.estimate(mxm, mxf)
plot(lc$bx, type="l")
lines(lc$ultimate.bx, lty=2)
```

---

logquad   *Log-Quadratic Mortality Model*

Description

Predict age-specific mortality rates using the Log-Quadratic Mortality Model (Wilmoth et al. 2012).

Usage

```
logquad(
  e0,
  sex = c("male", "female", "total"),
  my.coefs = NULL,
  q5ranges = c(1e-04, 0.9),
  k = 0,
  keep.lt = FALSE,
  ...
)

logquadj(e0m, e0f, ...)
```

Arguments

e0	Vector of target life expectancies.
sex	Which sex does the give e0 corresponds to.
my.coefs	Data frame with columns "sex", "age", "ax", "bx", "cx", "vx". The "sex" column should contain values "female", "male" and/or "total". The "age" column must be sorted so that it assures that rows correspond to ages in increasing order. Any NAs are internally converted to zeros. If not given, the dataset LQcoef is used.
q5ranges	A vector of size two, giving the min and max of 5q0 used in the bisection method.
k	Value of the k parameter.
keep.lt	Logical. If TRUE additional life table columns are kept in the resulting object.
...	Additional arguments passed to the underlying function.

| e0m | A time series of target male life expectancy. |
| e0f | A time series of target female life expectancy. |

Details

The LogQuad method in this implementation projects mortality rates using the equation

$$\log(m_x) = a_x + b_x h + c_x h^2 + v_x k$$

where a_x, b_x, c_x and v_x are age-specific coefficients, $h = \log(5q0)$ (i.e. reflects child mortality), and k should be chosen to match 45q15 (adult mortality) or set to 0 (default). The coefficients can be passed as inputs, or taken from the package default dataset LQcoef which are taken from https://u.demog.berkeley.edu/~jrw/LogQuad/.

For the given inputs and values of life expectancy e0, the function finds values of h that best match e0, using life tables and the bisection method. It returns the corresponding mortality schedule for each value of e0.

Function logquad is for one sex, while logquadj can be used for both sexes.

Value

Function logquad returns a list with the following elements: a matrix mx with the predicted mortality rates. If keep.lt is TRUE, it also contains matrices sr (survival rates), and life table quantities Lx and lx. Function logquadj returns a list of objects, one for each sex.

References

Wilmoth, J., Zureick, S., Canudas-Romo, V., Inoue, M., Sawyer, C. (2012). A Flexible Two-Dimensional Mortality Model for Use in Indirect Estimation. Population studies, 66(1), 1-28. doi:10.1080/00324728.2011.611411

See Also

LQcoef, mortcast.blend, mortcast, pmd, mlt

Examples

```
data(e0Mproj, package = "wpp2017")
country <- "Brazil"
# get target e0
e0m <- as.numeric(subset(e0Mproj, name == country)[-(1:2)])
# project into future
pred <- logquad(e0m, sex = "male")
# plot first projection in black and the remaining ones in heat colors
plot(pred$mx[,1], type = "l", log = "y", ylim = range(pred$mx),
    ylab = "male mx", xlab = "Age", main = country)
for(i in 2:ncol(pred$mx)) lines(pred$mx[,i],
    col = heat.colors(20)[i])
```

LQcoef   *Coefficients for the Log-Quadratic Mortality Model*

Description

Data object containing a table of coefficients to be used in the Log-Quadratic Model as implemented in the [logquad](#) function.

Usage

```
data(LQcoef)
```

Format

Data frame containing columns "sex", "age", "ax", "bx", "cx", "vx". Rows correspond to sex and age groups.

Source

<https://u.demog.berkeley.edu/~jrw/LogQuad/>

References

Wilmoth, J., Zureick, S., Canudas-Romo, V., Inoue, M., Sawyer, C. (2012). A Flexible Two-Dimensional Mortality Model for Use in Indirect Estimation. Population studies, 66(1), 1-28. doi:10.1080/00324728.2011.611411

See Also

[logquad](#)

Examples

```
data(LQcoef)
head(LQcoef)
```

---

mlt   *Model Life Tables Mortality Patterns*

Description

Predict age-specific mortality rates using Coale-Demeny and UN model life tables.

Usage

```
mlt(e0, sex = c("male", "female"), type = "CD_West", nx = 5, ...)

mltj(e0m, e0f, ..., nx = 5)
```

Arguments

e0	A time series of target life expectancy.
sex	Either "male" or "female".
type	Type of the model life table. Available options are "CD_East", "CD_North", "CD_South", "CD_West", "UN_Chilean", "UN_Far_Eastern", "UN_General", "UN_Latin_American", "UN_South_Asian".
nx	Size of age groups. Should be either 5 or 1.
...	Additional arguments passed to the underlying function.
e0m	A time series of target male life expectancy.
e0f	A time series of target female life expectancy.

Details

Given a level of life expectancy (e0), sex and a type of model life table, the function extracts the corresponding mortality pattern from `MLTlookup` (for abridged LT) or `MLT1Ylookup` (for 1-year LT), while interpolating between neighboring e0 groups. Function `mlt` is for one sex, while `mltj` can be used for both sexes.

Value

Function `mlt` returns a matrix with the predicted mortality rates. Columns correspond to the values in the e0 vector and rows correspond to age groups. Function `mltj` returns a list of such matrices, one for each sex.

References

https://www.un.org/development/desa/pd/data/extended-model-life-tables

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

See Also

mortcast, mortcast.blend, pmd, MLTlookup

Examples

```
data(e0Fproj, package = "wpp2017")
country <- "Uganda"
# get target e0
e0f <- subset(e0Fproj, name == country)[-(1:2)]
# project into future using life table Cole-Demeny North
mx <- mlt(e0f, sex = "female", type = "CD_North")
# plot first projection in black and the remaining ones in grey
plot(mx[,1], type = "l", log = "y", ylim = range(mx),
    ylab = "female mx", xlab = "Age",
    main = paste(country, "5-year age groups"))
for(i in 2:ncol(mx)) lines(mx[,i], col = "grey")

# MLT for 1-year age groups
mx1y <- mlt(e0f, sex = "female", type = "CD_North", nx = 1)
plot(mx1y[,1], type = "l", log = "y", ylim = range(mx1y),
    ylab = "female mx", xlab = "Age",
    main = paste(country, "1-year age groups"))
for(i in 2:ncol(mx1y)) lines(mx1y[,i], col = "grey")
```

MLTlookup   *Model Life Tables Lookup*

Description

Lookup tables containing values for various model life tables, including Coale-Demeny and UN life tables.

Usage

```
data(MLTlookup)
data(MLT1Ylookup)
```

Format

Data frame with the following columns:

type Type of the model life table. Available options are "CD_East", "CD_North", "CD_South", "CD_West", "UN_Chilean", "UN_Far_Eastern", "UN_General", "UN_Latin_American", "UN_South_Asian". For the CD types, see Coale et al. (1983). For the UN types, see the link in References below.

sex Code for distinguishing sexes. 1 is for male, 2 is for female.

age Starting age of an age group. In MLTlookup these are 0, 1, 5, 10, ... 130. The MLT1Ylookup table contains 1-year ages ranging from 0 to 130.

e0 Level of life expectancy, starting at 20 and going by steps of 2.5 up to 115.

mx Mortality rates.

lx, Lx, sx Other life table columns.

Source

An updated version of these datasets were provided by Sara Hertog, United Nations Population Division, in October 2021 (package version >= 2.6-0). For previous version of the tables, install MortCast 2.5-0: 'devtools::install_github("PPgp/MortCast@v2.5-0")'

References

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

https://www.un.org/development/desa/pd/data/extended-model-life-tables

See Also

mlt

Examples

```
data(MLTlookup)
str(MLTlookup)
# CD West life table for male at e0 of 80
subset(MLTlookup, type == "CD_West" & sex == 1 & e0 == 80)
```

---

mortcast   *Coherent Rotated Lee-Carter Prediction*

Description

Predict age-specific mortality rates using the coherent rotated Lee-Carter method.

Usage

```
mortcast(
  e0m,
  e0f,
  lc.pars,
  rotate = TRUE,
  keep.lt = FALSE,
  constrain.all.ages = FALSE,
  ...
)
```

Arguments

e0m	A time series of future male life expectancy.
e0f	A time series of future female life expectancy.
lc.pars	A list of coherent Lee-Carter parameters with elements bx, ultimate.bx, ages, nx, female and male as returned by [lileecarter.estimate](). The female and male objects are again lists that should contain a vector ax and optionally a matrix axt if the a_x parameter needs to be defined as time dependent. In such a case, rows are age groups and columns are time periods corresponding to the length of the e0f and e0m vectors.
rotate	If TRUE the rotation method of b_x is used as described in Li et al. (2013).
keep.lt	Logical. If TRUE additional life table columns are kept in the resulting object.
constrain.all.ages	
	By default the method constrains the male mortality to be above female mortality for old ages if the male life expectancy is below the female life expectancy. Setting this argument to TRUE causes this constraint to be applied to all ages.
...	Additional life table arguments.

Details

This function implements Steps 6-9 of Algorithm 2 in Sevcikova et al. (2016). It uses the abridged or unabridged life table function to find the level of mortality that coresponds to the given life expectancy. Thus, it can be used for both, mortality for 5- or 1-year age groups.

Value

List with elements female and male, each of which contains a matrix mx with the predicted mortality rates. If keep.lt is TRUE, it also contains matrices sr (survival rates), and life table quantities Lx and lx.

References

Li, N., Lee, R. D. and Gerland, P. (2013). Extending the Lee-Carter method to model the rotation of age patterns of mortality decline for long-term projections. Demography, 50, 2037-2051.

Sevcikova H., Li N., Kantorova V., Gerland P., Raftery A.E. (2016). Age-Specific Mortality and Fertility Rates for Probabilistic Population Projections. In: Schoen R. (eds) Dynamic Demographic Analysis. The Springer Series on Demographic Methods and Population Analysis, vol 39. Springer, Cham

See Also

[rotate.leecarter](), [leecarter.estimate](), [lileecarter.estimate](), [mortcast.blend]()

Examples

```
# estimate parameters from historical mortality data (5-year age groups)
data(mxM, mxF, e0Fproj, e0Mproj, package = "wpp2017")
country <- "Brazil"
```

```
mxm <- subset(mxM, name == country)[,4:16]
mxf <- subset(mxF, name == country)[,4:16]
rownames(mxm) <- rownames(mxf) <- c(0,1, seq(5, 100, by=5))
lc <- lileecarter.estimate(mxm, mxf)

# project into future for given levels of life expectancy
e0f <- as.numeric(subset(e0Fproj, name == country)[-(1:2)])
e0m <- as.numeric(subset(e0Mproj, name == country)[-(1:2)])
pred <- mortcast(e0m, e0f, lc)

# plot first projection in black and the remaining ones in grey
plot(lc$ages, pred$female$mx[,1], type="b", log="y", ylim=range(pred$female$mx),
    ylab="female mx", xlab="Age", main=paste(country, "(5-year age groups)"), cex=0.5)
for(i in 2:ncol(pred$female$mx)) lines(lc$ages, pred$female$mx[,i], col="grey")

# similarly for 1-year age groups
# derive toy 1-year mx using model life tables at given level of e0
mxm1y <- mlt(seq(65, 71, length = 4), sex = "male", nx = 1)
mxf1y <- mlt(seq(73, 78, length = 4), sex = "female", nx = 1)

# estimate parameters
lc1y <- lileecarter.estimate(mxm1y, mxf1y, nx = 1)

# project into the future
pred1y <- mortcast(e0m, e0f, lc1y)

# plot first projection in black and the remaining ones in grey
plot(lc1y$ages, pred1y$female$mx[,1], type="b", log="y", ylim=range(pred1y$female$mx),
    ylab="female mx", xlab="Age", main="1-year age groups", cex=0.5)
for(i in 2:ncol(pred1y$female$mx)) lines(lc1y$ages, pred1y$female$mx[,i], col="grey")
```

---

mortcast.blend   *Mortality Prediction by Method Blending*

Description

Predict age-specific mortality rates using a blend of two different methods (Coherent Lee-Carter, Coherent Pattern Mortality Decline, Log-Quadratic model, or Model Life Tables). Weights can be applied to fine-tune the blending mix.

Usage

```
mortcast.blend(
  e0m,
  e0f,
  meth1 = "lc",
  meth2 = "mlt",
  weights = c(1, 0.5),
```

```
    nx = 5,
    apply.kannisto = TRUE,
    min.age.groups = if (nx == 5) 28 else 131,
    match.e0 = TRUE,
    keep.lt = FALSE,
    meth1.args = NULL,
    meth2.args = NULL,
    kannisto.args = NULL,
    ...
)
```

Arguments

e0m	A time series of future male life expectancy.
e0f	A time series of future female life expectancy.
meth1	Character string giving the name of the first method to blend. It is one of "lc", "pmd", "mlt" or "logquad", corresponding to Coherent Lee-Carter (function [mortcast](#)), Pattern Mortality Decline (function [copmd](#)), Log-Quadratic model (function [logquadj](#)), and Model Life Tables (function [mltj](#)), respectively. The "logquad" method can only be used with 5-year age groups.
meth2	Character string giving the name of the second method to blend. One of the same choices as meth1.
weights	Numeric vector with values between 0 and 1 giving the weight of meth1. If it is a single value, the same weight is applied for all time periods. If it is a vector of size two, it is assumed these are weights for the first and the last time period. Remaining weights will be interpolated. Note that meth2 is weighted by 1 - weights.
nx	Size of age groups. Should be either 5 or 1.
apply.kannisto	Logical. If TRUE and if any of the methods results in less than min.age.groups age categories, the coherent Kannisto method ([cokannisto](#)) is applied to extend the age groups into old ages.
min.age.groups	Minimum number of age groups. Triggers the application of Kannisto, see above. For a 5-year age groups, the default is 28; for 1-year ages it is 131.
match.e0	Logical. If TRUE the blended mx is scaled so that it matches the input e0.
keep.lt	Logical. If TRUE additional life table columns are kept in the resulting object. Only used if match.e0 is TRUE.
meth1.args	List of arguments passed to the function that corresponds to meth1.
meth2.args	List of arguments passed to the function that corresponds to meth2.
kannisto.args	List of arguments passed to the [cokannisto](#) function if Kannisto is applied. If 1-year age groups are used various defaults in the Kannisto function need to be changed (see Example).
...	Additional life table arguments.

Details

The function allows to combine two different methods using given weights. The weights can change over time - by default they are interpolated from the starting weight to the end weight. As the blended mortality rates do not necessarily match the target life expectancy, scaling is applied to improve the match, controlled by the `match.e0` argument. The projection is done for both sexes, so that coherent methods can be applied.

Value

List with elements `female` and `male`, each of which contains a matrix `mx` with the predicted mortality rates. If the result has been scaled (`match.e0` is TRUE), the element `mx.rawblend` contains the mx before scaling. Also in such a case, if `keep.lt` is TRUE, it also contains matrices `sr` (survival rates), and life table quantities `Lx` and `lx`. In addition, the return object contains elements `meth1res` and `meth2res` which contain the results of the functions corresponding to the two methods. Elements `meth1` and `meth2` contain the names of the methods. A vector `weights` contains the final (possibly interpolated) weights.

See Also

mortcast, copmd, mltj, logquad, cokannisto

Examples

```
data(mxM, mxF, e0Fproj, e0Mproj, package = "wpp2017")
country <- "Brazil"
# estimate parameters from historical mortality data
mxm <- subset(mxM, name == country)[,4:16]
mxf <- subset(mxF, name == country)[,4:16]
rownames(mxm) <- rownames(mxf) <- c(0,1, seq(5, 100, by=5))
lcest <- lileecarter.estimate(mxm, mxf)
# project into future
e0f <- subset(e0Fproj, name == country)[-(1:2)]
e0m <- subset(e0Mproj, name == country)[-(1:2)]

# Blend LC and MLT
pred1 <- mortcast.blend(e0m, e0f, meth1 = "lc", meth2 = "mlt",
    meth1.args = list(lc.pars = lcest),
    meth2.args = list(type = "CD_North"),
    weights = c(1,0.25))

# Blend PMD and MLT
pred2 <- mortcast.blend(e0m, e0f, meth1 = "pmd", meth2 = "mlt",
    meth1.args = list(mxm0 = mxm[, "2010-2015"],
                      mxf0 = mxf[, "2010-2015"]))

# plot projection by time
plotmx <- function(pred, iage, main)
    with(pred, {
        # blended projections
        plot(female$mx[iage,], type="l",
            ylim=range(meth1res$female$mx[iage,],
```

```
                              meth2res$female$mx[iage,]),
              ylab="female mx", xlab="Time", main=main, col = "red")
         lines(meth1res$female$mx[iage,], lty = 2)
         lines(meth2res$female$mx[iage,], lty = 3)
         legend("topright", legend=c("blend", meth1, meth2),
                 lty = 1:3, col = c("red", "black", "black"), bty = "n")
    })
age.group <- 3 # 5-9 years old
par(mfrow=c(1,2))
plotmx(pred1, age.group, "LC-MLT (age 5-9)")
plotmx(pred2, age.group, "PMD-MLT (age 5-9)")

# Blend LC and MLT for 1-year age groups
##########################################
# First interpolate e0 to get 1-year life expectancies (for first five years)
e0m1y <- approx(as.double(e0m[,1:2]), n = 5)$y
e0f1y <- approx(as.double(e0f[,1:2]), n = 5)$y
# derive toy mx in order to get some LC parameters
mxm1y <- mlt(seq(70, 72, length = 4), sex = "male", nx = 1)
mxf1y <- mlt(seq(78, 79, length = 4), sex = "female", nx = 1)
lcest1y <- lileecarter.estimate(mxm1y, mxf1y, nx = 1)

# projections
pred3 <- mortcast.blend(e0m1y, e0f1y, meth1 = "lc", meth2 = "mlt",
    weights = c(1,0.25), min.age.groups = 131, nx = 1,
    meth1.args = list(lc.pars = lcest1y),
    kannisto.args = list(est.ages = 90:99, proj.ages = 100:130))

# plot results
par(mfrow=c(1,1))
plot(0:130, pred3$female$mx[,5], log = "y", type = "l", col = "red")
lines(0:130, pred3$male$mx[,5], col = "blue")
```

---

pmd	*Pattern of Mortality Decline Prediction*

Description

Predict age-specific mortality rates using the Pattern of mortality decline (PMD) method (Andreev et al. 2013).

Usage

```
pmd(
  e0,
  mx0,
  sex = c("male", "female"),
  nx = 5,
  interp.rho = FALSE,
```

```
  kranges = c(0, 25),
  keep.lt = FALSE,
  keep.rho = FALSE,
  ...
)

modpmd(
  e0,
  mx0,
  sex = c("male", "female"),
  nx = 5,
  interp.rho = FALSE,
  kranges = c(0, 25),
  ax.index = NULL,
  ax.smooth = FALSE,
  ax.smooth.df = NULL,
  keep.lt = FALSE,
  keep.rho = FALSE,
  ...
)

copmd(
  e0m,
  e0f,
  mxm0,
  mxf0,
  nx = 5,
  interp.rho = FALSE,
  keep.rho = FALSE,
  use.modpmd = FALSE,
  ...
)
```

Arguments

e0	A vector of target life expectancy, one element for each predicted time point.
mx0	A vector with starting age-specific mortality rates. In case of modpmd it can be a matrix where rows correspond to age groups and columns correspond to time periods. Row names define the starting ages of the age groups. As the ρ_x coefficients are only available up to age 100, the mx0 gets truncated if it contains values beyond 100. In such a case, a warning is issued.
sex	Either "male" or "female".
nx	Size of age groups. Should be either 5 or 1.
interp.rho	Logical controlling if the ρ coefficients should be interpolated (TRUE) or if the raw (binned) version should be used (FALSE), as stored in the dataset [PMDrho]().
kranges	A vector of size two, giving the min and max of the k parameter which is estimated to match the target e0 using the bisection method.

keep.lt	Logical. If TRUE additional life table columns are kept in the resulting object.
keep.rho	Logical. If TRUE the ρ coefficients are included in the resulting object.
...	Additional arguments passed to the underlying functions. For copmd, in addition to kranges and keep.lt, it can be sexratio.adjust which is a logical controlling if a sex-ratio adjustment should be applied to prevent crossovers between male and female mx. In such a case it uses coefficients from the PMDadjcoef dataset. However, if the argument adjust.with.mxf is set to TRUE (in addition to sexratio.adjust), the adjustment is done using the female mortality rates as the lower constraint for male mortality rates. If the argument adjust.sr.if.needed is set to TRUE, a sex-ratio adjustment is performed dynamically, using the sex ratio in the previous time point. In such a case, an adjustment in time t is applied only if there was a drop of sex ratio below one at time t-1. Other arguments passed here in copmd can be ax.index, ax.smooth and ax.smooth.df which control the estimation of the initial mx if use.modpmd is TRUE.
ax.index	A vector of column indices of mx to be used to estimate the $a_x = E[log(mx(t_0))]$ parameter. By default it is estimated as the average over all observed time periods, but this argument can restrict the time periods to use.
ax.smooth	Logical allowing to smooth the a_x over ages.
ax.smooth.df	Degree of freedom for smoothing if ax.smooth is TRUE. Default is half the length of a_x.
e0m	A time series of target male life expectancy.
e0f	A time series of target female life expectancy.
mxm0, mxf0	A vector with starting age-specific male/female mortality rates. If use.modpmd is TRUE, this can be a matrix of historical mx (age x time) from which the starting values are estimated.
use.modpmd	Logical determining if the modified version of PMD (modpmd) should be used. In such a case the starting values of mortality rates are estimated similarly to a_x in leecarter.estimate, possibly from more than one time periods. In addition, a smoothing can be applied.

Details

These functions implements the PMD method introduced in Andreev et al. (2013) and its modifications. It assumes that the future decline in age-specific mortality will follow a certain pattern with the increase in life expectancy at birth (e0):

$$log[mx(t)] = log[mx(t-1)] - k(t)\rho_x(t)$$

Here, $\rho_x(t)$ is the age-specific pattern of mortality decline between $t-1$ and t. Such patterns for each sex and various levels of e0 are stored in the dataset PMDrho. The pmd function can be instructed to interpolate between neighboring levels of e0 by setting the argument interp.rho to TRUE. The k parameter is estimated to match the e0 level using the bisection method.

Function pmd evaluates the method for a single sex, while copmd does it coherently for both sexes. In the latter case, the same ρ_x (namely the average over sex-specific ρ_x) is used for both, male and female.

Function modpmd implements a modified version of pmd where the initial $log[mx(t_0)]$ is replaced by an a_x estimated as in [leecarter.estimate](), i.e. using possibly multiple years of historical mx and optionally smoothed. Arguments ax.index, ax.smooth and ax.smooth.df determine the estimation years and parameters of the smoothing.

Value

Function pmd and modpmd return a list with the following elements: a matrix mx with the predicted mortality rates. If keep.lt is TRUE, it also contains matrices sr (survival rates), and life table quantities Lx and lx. If keep.rho is TRUE, it contains a matrix rho where columns correspond to the values in the e0 vector and rows correspond to age groups.

Function copmd returns a list with one element for each sex (male and female) where each of them is a list as described above. In addition if keep.rho is TRUE, element rho.sex gives the sex-dependent (i.e. not averaged) ρ_x coefficient.

References

Andreev, K., Gu, D., Gerland, P. (2013). Age Patterns of Mortality Improvement by Level of Life Expectancy at Birth with Applications to Mortality Projections. Paper presented at the Annual Meeting of the Population Association of America, New Orleans, LA. https://paa2013.populationassociation.org/papers/132554.

Gu, D., Pelletier, F., Sawyer, C. (2017). Projecting Age-sex-specific Mortality: A Comparison of the Modified Lee-Carter and Pattern of Mortality Decline Methods, UN Population Division, Technical Paper No. 6. New York: United Nations. https://population.un.org/wpp/Publications/Files/WPP2017_TechnicalPaperNo6.pdf

See Also

[mortcast](), [mortcast.blend](), [PMDrho]()

Examples

```
data(mxF, e0Fproj, package = "wpp2017")
country <- "Hungary"
# get initial mortality for the current year
mxf <- subset(mxF, name == country)[,"2010-2015"]
names(mxf) <- c(0,1, seq(5, 100, by=5))
# get target e0
e0f <- subset(e0Fproj, name == country)[-(1:2)]
# project into future
pred <- pmd(e0f, mxf, sex = "female")
# plot first projection in black and the remaining ones in grey
plot(pred$mx[,1], type = "l", log = "y", ylim = range(pred$mx),
    ylab = "female mx", xlab = "Age", main = country)
for(i in 2:ncol(pred$mx)) lines(pred$mx[,i], col = "grey")
```

PMDadjcoef   *Coefficients for Sex Ratio Adjustments in the PMD Method*

Description

Data object containing a table of coefficients to be used to adjust the sex ratio in the coherent Pattern Mortality Decline method as implemented in the copmd function. To invoke the adjustment, argument `sexratio.adjust` should be set to `TRUE`.

Usage

```
data(PMDadjcoef)
```

Format

Data frame containing columns "age", "intercept", "lmxf", "e0f", "e0f2", and "gap". Rows correspond to age groups. The values are estimates of the following regression

$$\log_{10} mx^M = \beta_0 + \beta_1 \log_{10} mx^F + \beta_2 e_0^F + \beta_3 (e_0^F)^2 + \beta_4 (e_0^F - e_0^M)$$

The order of the columns starting with intercept corresponds to the order of the coefficients in the above equation.

Source

The coefficients were estimated and provided by Danan Gu, UN Population Division.

References

Gu, D., Pelletier, F. and Sawyer, C. (2017). Projecting Age-sex-specific Mortality: A Comparison of the Modified Lee-Carter and Pattern of Mortality Decline Methods, UN Population Division, Technical Paper No. 6. New York: United Nations. https://population.un.org/wpp/Publications/Files/WPP2017_TechnicalPaperNo6.pdf

See Also

copmd

Examples

```
data(PMDadjcoef)
PMDadjcoef
```

PMDrho   *Pattern Mortality Decline Lookup Tables*

Description

Data object containing two tables with ρ coefficients for the Pattern Mortality Decline method as implemented in the [pmd](#) function.

Usage

```
data(PMDrho)
```

Format

Using `data(PMDrho)` loads two objects into memory: `RhoFemales` and `RhoMales`. They both are data frames with 22 rows corresponding to age groups, and 17 columns corresponding to different levels of life expectancy in 5-years intervals (from 50 to 135). The names of the columns reflect the middle of the respective interval.

References

Andreev, K. Gu, D., Gerland, P. (2013). Age Patterns of Mortality Improvement by Level of Life Expectancy at Birth with Applications to Mortality Projections. Paper presented at the Annual Meeting of the Population Association of America, New Orleans, LA. `https://paa2013.populationassociation.org/papers/132554`.

Gu, D., Pelletier, F. and Sawyer, C. (2017). Projecting Age-sex-specific Mortality: A Comparison of the Modified Lee-Carter and Pattern of Mortality Decline Methods, UN Population Division, Technical Paper No. 6. New York: United Nations. `https://population.un.org/wpp/Publications/Files/WPP2017_TechnicalPaperNo6.pdf`

See Also

[pmd](#)

Examples

```
data(PMDrho)
head(RhoFemales)
head(RhoMales)

# plot a few male patterns
e0lev <- colnames(RhoMales)[c(1, 5, 9, 13, 17)]
plot(RhoMales[, e0lev[1]], type="l", log="y", ylim=range(RhoMales[,e0lev]),
    ylab="male rho", xlab="Age")
for(i in 2:length(e0lev)) lines(RhoMales[,e0lev[i]], lty = i)
legend("bottomleft", legend = e0lev, lty = 1:length(e0lev), bty= "n")
```

`rotate.leecarter`   *Rotated Lee-Carter*

Description

Rotate the Lee-Carter parameter b_x over time to reach an ultimate b_x^u, as described in Li et al. (2013).

Usage

```
rotate.leecarter(bx, ultimate.bx, e0, e0l = 80, e0u = 102, p = 0.5)

ultimate.bx(bx)
```

Arguments

bx	A vector of the Lee-Carter b_x parameter (from e.g. `lileecarter.estimate` or `leecarter.estimate`).
ultimate.bx	A vector of the ultimate b_x^u parameter as defined in Li, Lee, Gerland (2013) (obtained using `lileecarter.estimate` or `ultimate.bx`).
e0	A time series of life expectancies.
e0l	Level of life expectancy at which the rotation starts.
e0u	Level of life expectancy at which the rotation finishes.
p	Exponent of the smooth function.

Value

Function `rotate.leecarter` returns a matrix of rotated $B_x(t)$ where rows correspond to age groups and columns correspond to time periods (given by the vector `e0`).

Function `ultimate.bx` returns a vector of the ultimate b_x^u.

References

Li, N., Lee, R. D. and Gerland, P. (2013). Extending the Lee-Carter method to model the rotation of age patterns of mortality decline for long-term projections. Demography, 50, 2037-2051.

Examples

```
data(mxF, mxM, e0Fproj, e0Mproj, package = "wpp2017")
country <- "Japan"
mxm <- subset(mxM, name == country)[,4:16]
mxf <- subset(mxF, name == country)[,4:16]
e0f <- as.numeric(subset(e0Fproj, name == country)[-(1:2)])
e0m <- as.numeric(subset(e0Mproj, name == country)[-(1:2)])
rownames(mxm) <- rownames(mxf) <- c(0,1, seq(5, 100, by=5))
lc <- lileecarter.estimate(mxm, mxf)
rotlc <- rotate.leecarter(lc$bx, lc$ultimate.bx, (e0f + e0m)/2)
```

```
plot(lc$bx, type="l")
lines(lc$ultimate.bx, col="red")
for(i in 1:ncol(rotlc)) lines(rotlc[,i], col="grey")
```

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