

Package ‘LifeTables’

July 2, 2014

Type Package

Title A package to implement HMD model life table system

Depends R (>= 2.10), mclust

Suggests gWidgets, gWidgetsRGtk2, RGtk2

Version 0.2

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Description Functions supplied in this package will implement discriminant analysis to select an appropriate life table family, select an appropriate alpha level based on a desired life expectancy at birth, produce a model mortality pattern based on family and level as well as plot the results.

License Unlimited

LazyLoad yes

LazyData yes

Repository CRAN

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NeedsCompilation no

R topics documented:

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LifeTables-package	<i>HMD Model Life Tables</i>
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Description

Provides functions for using a model life table system generated from the Human Mortality Database

Details

Package:	LifeTables
Type:	Package
Version:	1.0
Date:	2011-06-01
License:	
LazyLoad:	yes

`mortmod` is the mortality model that is the basis for the system. The user can supply the two input parameters - family and level - and a complete mortality rate schedule can be generated. If the user has some measure of child mortality (or a partial schedule) and optionally 45q15, the function `hmd.DA` can be used to find the appropriate family. Then `alpha.e0` can calculate an alpha value to generate a life table with a desired life expectancy. The function `mod.lt` combines the steps outlined above. It will find the family and level based on the child (and possibly adult) mortality indicator and a desired life expectancy and return a complete life table generated with the appropriate input parameter values.

There is a graphical user interface implemented in the package that allows for generating model life tables, exporting them and plotting various measures of the life table. It can be invoked using the function `modelLT.gui()`.

Author(s)

David J. Sharrow, GUI by Hana Sevcikova

Maintainer: David Sharrow <dsharrow@uw.edu>

References

S. Clark and D. Sharrow (2011) "Contemporary Model Life Tables for Developed Countries: An Application of Model-Based Clustering." Working Paper No. 107, Center for Statistics and the Social Sciences, University of Washington, www.csss.washington.edu/Papers/

C. Fraley and A. E. Raftery (2002) "Model-based clustering, discriminant analysis, and density estimation." *Journal of the American Statistical Association* **97**:611-631.

C. Fraley, A. E. Raftery, T. B. Murphy, L. Scrucca (2012) "mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation", Technical Report no. 597, Department of Statistics, University of Washington

Human Mortality Database University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany). Available at www.mortality.org or www.humanmortality.de (data downloaded on [November 2009]).

Examples

```
# first get the appropriate family #
hmd.DA(x=.09, sex="male", child.mort=4, adult.mort=.28)$classification

# then get the appropriate level (alpha) #
alpha.e0(pattern=1, e0.target=59, sex="male")

# put in the family and alpha to model to produce complete schedule #
mortmod(pattern=1, alpha=.034, sex="male")
```

alpha.e0	<i>Alpha to match life expectancy</i>
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Description

Finds the alpha value to reproduce a desired life expectancy given a life table family/pattern

Usage

```
alpha.e0(pattern, e0.target, sex="female")
```

Arguments

pattern	An integer (1-5) which indicates the desired life table family
e0.target	The desired life expectancy
sex	"male" or "female"

Details

An appropriate life table family (pattern) can be found using [hmd.DA](#) or [hmd.DA.mx](#)

Value

The alpha value to produce the life expectancy entered in `e0.target`

Author(s)

David Sharrow

See Also

[lt.mx](#), [mortmod](#), [hmd.DA](#)

Examples

```
alpha.e0(pattern=2, e0.target=65, sex="male")
```

hmd.DA

Discriminant analysis to determine life table family

Description

Returns the results of a discriminant analysis to find the appropriate life table family based on either a single indicator of child mortality (1m0, 5m0, 1q0, 5q0) or a child indicator and adult mortality indicator (45q15)

Usage

```
hmd.DA(x, child.mort=4, sex="female", adult.mort = NULL)
```

Arguments

<code>x</code>	A numeric value for the child mortality indicator to be classified
<code>sex</code>	"male" or "female" indicates the sex for the indicators
<code>child.mort</code>	An interger (1-4) to indicate which child mortality indicator is being supplied (1 - 1m0; 2 - 5m0; 3 - 1q0; 4 - 5q0)
<code>adult.mort</code>	The value for 45q15 (if no value is supplied, defaults to NULL and uses just the single child mortality measure to classify)

Details

The training models based on the known classification of the training data can be found in the workspace `MLTobs` in the "data" subdirectory of this package.

Value

train	The output from the function <code>MclustDA</code> , the parameters and other summary information for the model best fitting each class according to BIC.
out.dens	The output from the function <code>predict(MclustDA model name)</code> , A matrix in which the <code>[i,j]</code> th entry is the density for observation <code>i</code> in the model for class <code>j</code> .
classification	The classification for the test data

Author(s)

David Sharrow

References

S. Clark and D. Sharrow (2011) "Contemporary Model Life Tables for Developed Countries: An Application of Model-Based Clustering." Working Paper No. 107, Center for Statistics and the Social Sciences, University of Washington, www.csss.washington.edu/Papers/

C. Fraley and A. E. Raftery (2002) "Model-based clustering, discriminant analysis, and density estimation." *Journal of the American Statistical Association* **97**:611-631.

C. Fraley, A. E. Raftery, T. B. Murphy, L. Scrucca (2012) "mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation", Technical Report no. 597, Department of Statistics, University of Washington

Human Mortality Database University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany). Available at www.mortality.org or www.humanmortality.de (data downloaded on [November 2009]).

See Also

[MclustDA](#), [Mclust](#), [MLTobs](#)

Examples

```
# classifying with 1m0
examp.out <- hmd.DA(x=.05, sex="male", child.mort=1)
examp.out$classification

# classifying with 5q0 and 45q15
examp.out2 <- hmd.DA(x=.03, sex="male", child.mort=4, adult.mort=.18)
examp.out2$classification
```

hmd.DA.mx

Model Life Table Discriminant Analysis

Description

Training and testing steps to perform a discriminant analysis for a partial or complete human mortality rate schedules with the Human Mortality database as the training set.

Usage

```
hmd.DA.mx(data, sex="female")
```

Arguments

data	a partial or complete human mortality rate schedule to be classified. Must have contiguous age groups (with standard 5-year age intervals 0, 1-4, 5-9, 10-14...110+) and be in log scale. This can be a single schedule or many organized into a matrix with the columns representing the age groups.
sex	"male" or "female". The sex for the schedule to be classified.

Details

This function can only take contiguous age groups as arguments. Whatever age groups are used, the function uses that portion of the HMD schedules to generate the training models and then clasifies the test schedules.

Value

train	The output from the function <code>MclustDA</code> , the parameters and other summary information for the model best fitting each class according to BIC.
out.dens	The output from the function <code>predict(MclustDA model name)</code> , A matrix in which the [i,j]th entry is the density for observation i in the model for class j.
classification	The classification for the test data

Author(s)

David Sharrow

References

S. Clark and D. Sharrow (2011) "Contemporary Model Life Tables for Developed Countries: An Application of Model-Based Clustering." Working Paper No. 107, Center for Statistics and the Social Sciences, University of Washington, www.csss.washington.edu/Papers/

C. Fraley and A. E. Raftery (2002) "Model-based clustering, discriminant analysis, and density estimation." *Journal of the American Statistical Association* **97**:611-631.

C. Fraley, A. E. Raftery, T. B. Murphy, L. Scrucca (2012) "mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation", Technical Report no. 597, Department of Statistics, University of Washington

Human Mortality Database University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany). Available at www.mortality.org or www.humanmortality.de (data downloaded on [November 2009]).

See Also

[MclustDA](#), [Mclust](#), [MLTobs](#)

Examples

```
# some test data
data(MLTobs)
examp.data <- t(flt.mx[1:2,1:10])

# classify the test data
examp.out <- hmd.DA.mx(data=examp.data, sex="female")
examp.out$classification
```

lt.mx

Life tables from nmx

Description

Builds a life table by using the mortality rate schedule to calculate the subsequent columns of the table

Usage

```
lt.mx(nmx, sex="female", age=c(0,1,seq(5,110,5)), nax=NULL)
```

Arguments

nmx	A vector of age-specific mortality rates
age	The start age of each age interval (will also be the start age for each interval of the subsequent life table)
sex	"male" or "female". The sex determines the nax value for the childhood age intervals using the Coale and Demeney West values when nax=NULL
nax	A set of nax values for the life table. Must have the same length as nmx and if no values of provided, this argument defaults to half the length of the age interval except for the first two childhood age groups.

Value

<code>e0</code>	Life expectancy at birth
<code>lt</code>	A life table with age intervals matching those of the <code>nmx</code> schedule on which the table is built and with columns for age, <code>nax</code> , <code>nmx</code> , <code>nqx</code> , <code>npq</code> , <code>ndx</code> , <code>lx</code> , <code>nLx</code> , <code>Tx</code> , and <code>ex</code> .
<code>lt.5q0</code>	The probability of death between birth and age 5
<code>lt.45q15</code>	The probability of death between age 15 and 60

Author(s)

David Sharrow

Examples

```
# some data to build the table
data(MLTobs)
mx <- mlt.mx[,1]

# build the life table
lt.mx(nmx=mx, sex="male")
```

MLTobs

Background objects necessary for certain functions

Description

This data set contains 28 objects which are necessary for certain package functions and are described in detail below

Usage

```
data(MLTobs)
```

Format

28 objects:

- `averages.smooth` A 48x5 matrix whose columns contain the five underlying family patterns. Rows 1:24 are the male pattern and rows 25:48 are the female patterns. Used in [mortmod](#).
- `class5` A vector of length 844 which contains the classification for the 844 HMD mortality rate schedules. Used in [hmd.DA.mx](#).
- `f.csd.weight` A function to determine the weight for the family-specific deviation. Used in [mortmod](#).
- `fitted.ms.pca.scores` A 48x10 matrix whose columns contain the first 10 component score vectors a SVD of the HMD mortality rate schedules.

- `flt.mx` A 24x844 matrix whose columns contain the 844 female mortality rate schedules in the Human Mortality Database
- `flt.mx.info` A 844x28 matrix. The first four columns contain the Location ID, Location Name, Subgroup type and Period. The remaining columns contain the age-specific mortality rates contained in `flt.mx`.
- `hi.devs` A 6x48 matrix whose first five rows contain the family-age-specific high deviations for when alpha is positive. The 6th row contains the age-specific high deviations from the entire HMD dataset. Used in `mortmod`.
- `hmd.1m0.train.f` Training models for females when the input parameters include 1m0. Used in `hmd.DA`.
- `hmd.1m0.train.m` Training models for males when the input parameters include 1m0. Used in `hmd.DA`.
- `hmd.1m0a.train.f` Training models for females when the input parameters include 1m0 and 45q15. Used in `hmd.DA`.
- `hmd.1m0a.train.m` Training models for males when the input parameters include 1m0 and 45q15. Used in `hmd.DA`.
- `hmd.5m0.train.f` Training models for females when the input parameters include 5m0. Used in `hmd.DA`.
- `hmd.5m0.train.m` Training models for males when the input parameters include 5m0. Used in `hmd.DA`.
- `hmd.5m0a.train.f` Training models for females when the input parameters include 5m0 and 45q15. Used in `hmd.DA`.
- `hmd.5m0a.train.m` Training models for males when the input parameters include 5m0 and 45q15. Used in `hmd.DA`.
- `hmd.1q0.train.f` Training models for females when the input parameters include 1q0. Used in `hmd.DA`.
- `hmd.1q0.train.m` Training models for males when the input parameters include 1q0. Used in `hmd.DA`.
- `hmd.1q0a.train.f` Training models for females when the input parameters include 1q0 and 45q15. Used in `hmd.DA`.
- `hmd.1q0a.train.m` Training models for males when the input parameters include 1q0 and 45q15. Used in `hmd.DA`.
- `hmd.5q0.train.f` Training models for females when the input parameters include 5q0. Used in `hmd.DA`.
- `hmd.5q0.train.m` Training models for males when the input parameters include 5q0. Used in `hmd.DA`.
- `hmd.5q0a.train.f` Training models for females when the input parameters include 5q0 and 45q15. Used in `hmd.DA`.
- `hmd.5q0a.train.m` Training models for males when the input parameters include 5q0 and 45q15. Used in `hmd.DA`.
- `lo.devs` A 6x48 matrix whose first five rows contain the family-age-specific low deviations for when alpha is positive. The 6th row contains the age-specific low deviations from the entire HMD dataset. Used in `mortmod`.

- `mlt.mx` A 24x844 matrix whose columns contain the 844 male mortality rate schedules in the Human Mortality Database
- `mlt.mx.info` A 844x28 matrix. The first four columns contain the Location ID, Location Name, Subgroup type and Period. The remaining columns contain the age-specific mortality rates contained in `mlt.mx`.
- `opt.alpha.f` A 25x5 matrix whose columns contain the female family-specific alpha values to produce life tables with life expectancies at 25 levels from 30-90 in 2.5 year increments
- `opt.alpha.m` A 25x5 matrix whose columns contain the male family-specific alpha values to produce life tables with life expectancies at 25 levels from 30-90 in 2.5 year increments
- `Patterns.final.coeffs` A 5x5 matrix whose columns contain the set of median coefficients for each family which are used to calculate the underlying family patterns

References

S. Clark and D. Sharrow (2011) "Contemporary Model Life Tables for Developed Countries: An Application of Model-Based Clustering." Working Paper No. 107, Center for Statistics and the Social Sciences, University of Washington, www.csss.washington.edu/Papers/

C. Fraley and A. E. Raftery (2002) "Model-based clustering, discriminant analysis, and density estimation." *Journal of the American Statistical Association* **97**:611-631.

C. Fraley, A. E. Raftery, T. B. Murphy, L. Scrucca (2012) "mclust Version 4 for R: Normal Mixture Modeling for Model-Based Clustering, Classification, and Density Estimation", Technical Report no. 597, Department of Statistics, University of Washington

Human Mortality Database University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany). Available at www.mortality.org or www.humanmortality.de (data downloaded on [November 2009]).

`mod.lt`

Calculate a Model Life Table

Description

This function takes as arguments a value for child mortality, an indication of which child mortality indicator is supplied (defaults to 5q0), a possible value for 45q15, a possible target life expectancy to determine the level of mortality and the sex of the desired life table (defaults to "female"). The function selects the appropriate family (and level if a desired life expectancy is supplied or a value for alpha) and returns a life table. The resulting life table defaults to alpha=0.

Usage

```
mod.lt(child.value, child.mort=4, e0.target=NULL, adult.mort=NULL,
sex="female", alpha=0)
```

Arguments

child.value	A numeric value for one of four child mortality measures.
child.mort	An interger (1-4) to indicate which child mortality indicator is being supplied (1 - 1m0; 2 - 5m0; 3 - 1q0; 4 - 5q0). Defaults to 5q0.
e0.target	The desired life expentacy for the life table. If no life expectancy is supplied the resulting life table defaults to alpha=0.
sex	"male" or "female" indicates the sex for the desired life table. Defaults to "female".
adult.mort	Optional. If supplied, the function uses both the child mortality measure and 45q15 to select the family. Otherwise, just the child mortality indicator is used.
alpha	If e0.target is not supplied, alpha defaults to 0. This can be any number with negative values producing lower mortality and positive values producing higher mortality.

Value

lt.out	The life table output from the function <code>lt.mx</code> including e_0 , life expectancy at birth, $l_t \cdot 5q_0$, the probability of death between birth and age 5, $l_t \cdot 4q_{15}$, the probability of death between age 15 and 60, and l_t , the complete, resulting life table with columns for age, nax , nm_x , nq_x , np_x , ndx , lx , nL_x , T_x , and ex .
alpha	The alpha value which produced the table. This value is either user supplied or calculated from the user supplied <code>e0.target</code> .
sex	Sex of the life table.
family	An integer (1-5) to indicate the life table family/pattern.

Author(s)

David Sharrow, Hana Sevcikova

References

S. Clark and D. Sharrow (2011) "Contemporary Model Life Tables for Developed Countries: An Application of Model-Based Clustering." Working Paper No. 107, Center for Statistics and the Social Sciences, University of Washington, www.csss.washington.edu/Papers/

Human Mortality Database University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany). Available at www.mortality.org or www.humanmortality.de (data downloaded on [November 2009]).

See Also

[hmd.DA](#), [alpha.e0](#), [mortmod](#), [lt.mx](#)

Examples

```
mod.lt(child.value=.04, child.mort=4, sex="male", adult.mort=.18,
e0.target=60)
```

Description

The function launches a graphical user interface (GUI) from which various functionality of this package can be accessed.

Usage

```
modelLT.gui()
```

Details

In the main window of the GUI, select an indicator of child mortality and enter its value. Optionally, choose if an adult mortality should be added and if it is the case, enter its value. Then select a sex for the life table. Pressing the ‘Generate Life Table’ button creates a window containing the corresponding life table.

Now you can enter the desired life expectancy target (e_0). Press the Enter key to update the life table and the alpha value. Alternatively, you can update the alpha value directly. Again, press the Enter key to update the content of the window.

To export the life table into a csv file, press the ‘Export’ button. To plot any of the life table columns as a function of age, select the column in the drop-list at the bottom of the window, choose if the y-axis should be on a log scale and press ‘Plot’. From here, you can save the plot in various formats.

For the GUI to run the user will first need to install GTK+.

GTK+ can be downloaded here <http://www.gtk.org/download.html>.

If the user does not first install GTK and invokes the GUI from the R console, a dialogue box will appear to ask if you want to install GTK.

Author(s)

Hana Sevcikova, David Sharrow, Samuel Clark

Examples

```
## Not run:  
modelLT.gui()  
## End(Not run)
```

mortmod *Underlying model in the HMD life table system*

Description

This function generates a complete (up to age 110+) human mortality rate profile given a certain family and level of mortality

Usage

```
mortmod(pattern, sex="female", alpha=0)
```

Arguments

pattern	An integer from 1 to 5 indicating the family which determines the underlying pattern
sex	"male" or "female". Indicates the sex of the desired schedule
alpha	A scalar which determines the quantity to add or subtract from the underlying cluster pattern. Typical alpha values will not exceed an absolute value of 3. Defaults to 0.

Details

The pattern argument identifies the shape or pattern of mortality and then alpha determines the quantity to add or subtract (depending on the sign of alpha) to the underlying cluster pattern.

Value

model.patt	A vector of length 24 which contains a complete set of age-specific logged mortality rates for age intervals 0-1, 1-4, 5-9, 10-14, ..., 110+
------------	--

Author(s)

David Sharrow

References

S. Clark and D. Sharrow (2011) "Contemporary Model Life Tables for Developed Countries: An Application of Model-Based Clustering." Working Paper No. 107, Center for Statistics and the Social Sciences, University of Washington, www.csss.washington.edu/Papers/

Human Mortality Database University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany). Available at www.mortality.org or www.humanmortality.de (data downloaded on [November 2009]).

See Also

[hmd.DA](#), [alpha.e0](#)

Examples

```
mortmod(pattern=2, alpha=0.5, sex="female")
mortmod(pattern=5, alpha=-0.1, sex="male")
```

plotMLT

*Plotting function for life table quantities***Description**

Plots either a single column or scrolls through a plot for each column from a life table calculated from a user supplied mortality rate schedule

Usage

```
plotMLT(..., mx.out, sex, lt.col = "All", log = FALSE,
age = c(0, 1, seq(5, 110, 5)))
```

Arguments

...	Arguments to pass to par
mx.out	A mortality rate schedule with age groups 0-1, 1-4, 5-9, 10-14,..., up to any open interval.
sex	The sex for the calculated life table. "male" or "female"
lt.col	The desired life table quantity to plot. lt.col="All", the default, will scroll through a plot of each quantity when the user keys "return" after each plot. Otherwise a specific column can be selected by using the following intergers (1-nmx, 2-nqx, 3-npx, 4-ndx, 5-lx, 6-nLx, 7-Tx, 8-ex)
log	Logical. If TRUE and lt.col is not set to "All", the y-axis will be in log scale.
age	The start ages for each interval in the life table

Details

If lt.col=3 (npx) and log=TRUE, a warning message will appear noting that a y value ≤ 0 is omitted. This is the probability of surviving the final interval, which is by definition, 0.

Author(s)

David Sharrow

See Also

[lt.mx](#)

Examples

```
## Not run:  
mx.examp <- exp(mortmod(pattern=1, alpha=.05, sex="male"))  
plotMLT(mx.out=mx.examp, sex="male", lt.col="All")  
  
plotMLT(mx.out=mx.examp, sex="male", lt.col=3, log=TRUE)  
  
## End(Not run)
```

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