Package 'MortalityLaws'

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Type Package

Title Parametric Mortality Models, Life Tables and HMD

Version 2.1.2

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Description Fit the most popular human mortality 'laws', and construct
full and abridge life tables given various input indices. A mortality
law is a parametric function that describes the dying-out process of
individuals in a population during a significant portion of their
life spans. For a comprehensive review of the most important mortality
laws see Tabeau (2001) <doi:10.1007/0-306-47562-6_1>.
Practical functions for downloading data from various human mortality
databases are provided as well.

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LazyData TRUE

Depends R (>= 3.0.0)

Imports minpack.lm (>= 1.2), RCurl (>= 1.95), pbapply (>= 1.3-4),
tidyr (>= 0.8.1), rvest (>= 1.0.3), httr (>= 1.4.5), methods

Suggests testthat, knitr, rmarkdown

URL https://github.com/mpascariu/MortalityLaws

BugReports https://github.com/mpascariu/MortalityLaws/issues

Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Contents

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ahmd   *MortalityLaws Test Data*

Description

Dataset containing altered death rates (mx), death counts (Dx) and exposures (Ex) for the female population living in England & Wales in four different years: 1850, 1900, 1950 and 2010. The data-set is provided for testing purposes only. Download the actual data free of charge from `https://www.mortality.org`. Once a username and a password are created on the website the function `ReadHMD` can be used for downloading.

Usage

```
ahmd
```

Format

An object of class `list` of length 3.

Source

Human Mortality Database

See Also

`ReadHMD`

Examples

```
head(ahmd$mx)
```

---

availableHMD   *Check Data Availability in HMD*

Description

The function returns information about available data in the Human Mortality Database, HMD (period life tables etc.), with the range of years covered by the life tables.

Usage

```
availableHMD(link = "https://www.mortality.org/Data/DataAvailability")
```

Arguments

link   URL to the HMD available data. Default: "https://www.mortality.org/Data/DataAvailability"

Value

A tibble.

Author(s)

Marius D. Pascariu

See Also

[ReadHMD](#)

Examples

```
availableHMD()
```

---

availableLaws   *Check Available Mortality Laws*

Description

The function returns information about the parametric models that can be called and fitted in the [MortalityLaw](#) function. For a comprehensive review of the most important mortality laws, Tabeau (2001) is a good starting point.

Usage

```
availableLaws(law = NULL)
```

Arguments

law   Optional. Default: `NULL`. One can extract details about a certain model by specifying its codename.

Value

The output is of the `"availableLaws"` class with the components:

table   Table with mortality models and codes to be used in MortalityLaw

legend   Table with details about the section of the mortality curve

Author(s)

Marius D. Pascariu

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See Also

MortalityLaw

Examples

```
availableLaws()
```

---

availableLF	*Check Available Loss Function*

Description

The function returns information about the implemented loss function used by the optimization procedure in the MortalityLaw function.

Usage

```
availableLF()
```

Value

A list of class `availableLF` with the components:

table   Table with loss functions and codes to be used in [MortalityLaw](#).

legend   Table with details about the abbreviation used.

Author(s)

Marius D. Pascariu

See Also

[MortalityLaw](#)

Examples

```
availableLF()
```

---

convertFx   *Convert Life Table Indicators*

Description

Easy conversion between the life table indicators. This function is based on the [LifeTable](#) function and methods behind it.

Usage

```
convertFx(x, data, from, to, ...)
```

Arguments

x   Vector of ages at the beginning of the age interval.

data   Vector or data.frame/matrix containing the mortality indicators.

from   Specify the life table indicator in the input `data`. Character. Options: `mx`, `qx`,
                 `dx`, `lx`.

to   What indicator would you like to obtain? Character. Options: `mx`, `qx`, `dx`, `lx`,
                 `Lx`, `Tx`, `ex`.

...   Further arguments to be passed to the [LifeTable](#) function with impact on the
                 results to be produced.

Value

A matrix or array containing life table indicators.

Author(s)

Marius D. Pascariu

See Also

LifeTable

Examples

```
# Data ---
x  <- 0:110
mx <- ahmd$mx

# mx to qx
qx <- convertFx(x, data = mx, from = "mx", to = "qx")
# mx to dx
dx <- convertFx(x, data = mx, from = "mx", to = "dx")
# mx to lx
lx <- convertFx(x, data = mx, from = "mx", to = "lx")


# There are 28 possible combinations -------------------------------
# Let generate all of them.
from <- c("mx", "qx", "dx", "lx")
to   <- c("mx", "qx", "dx", "lx", "Lx", "Tx", "ex")
K    <- expand.grid(from = from, to = to) # all possible cases/combinations

for (i in 1:nrow(K)) {
  In  <- as.character(K[i, "from"])
  Out <- as.character(K[i, "to"])
  N <- paste0(Out, "_from_", In)
  cat(i, " Create", N, "\n")
  # Create the 28 sets of results
  assign(N, convertFx(x = x, data = get(In), from = In, to = Out))
}
```

LawTable   *Compute Life Tables from Parameters of a Mortality Law*

Description

Compute Life Tables from Parameters of a Mortality Law

Usage

```
LawTable(x, par, law, sex = NULL, lx0 = 1e+05, ax = NULL)
```

Arguments

x	Vector of ages at the beginning of the age interval.
par	The parameters of the mortality model.
law	The name of the mortality law/model to be used. e.g. gompertz, makeham, ... To investigate all the possible options, see [availableLaws](#) function.
sex	Sex of the population considered here. Default: NULL. This argument affects the first two values in the life table ax column. If sex is specified the values are computed based on the Coale-Demeny method and are slightly different for males than for females. Options: NULL, male, female, total.
lx0	Radix. Default: 100 000.
ax	Numeric scalar. Subject-time alive in age-interval for those who die in the same interval. If NULL this will be estimated. A common assumption is ax = 0.5, i.e. the deaths occur in the middle of the interval. Default: NULL.

Details

The "life table" is also called "mortality table" or "actuarial table". This shows, for each age, what the probability is that a person of that age will die before his or her next birthday, the expectation of life across different age ranges or the survivorship of people from a certain population.

Value

The output is of the "LifeTable" class with the components:

lt	Computed life table;
call	Call in which all of the specified arguments are specified by their full names;
process_date	Time stamp.

Author(s)

Marius D. Pascariu

See Also

[LifeTable](#) [MortalityLaw](#)

Examples

```
# Example 1 --- Makeham --- 4 tables ----------
x1 = 45:100
L1 = "makeham"
C1 = matrix(c(0.00717, 0.07789, 0.00363,
              0.01018, 0.07229, 0.00001,
              0.00298, 0.09585, 0.00002,
              0.00067, 0.11572, 0.00078),
            nrow = 4, dimnames = list(1:4, c("A", "B", "C")))

LawTable(x = 45:100, par = C1, law = L1)
```

```
# WARNING!!!

# It is important to know how the coefficients have been estimated. If the
# fitting of the model was done over the [x, x+) age-range, the LawTable
# function can be used to create a life table only for age x onward.

# What can go wrong?

# ** Example 1B - is OK.
LawTable(x = 45:100, par = c(0.00717, 0.07789, 0.00363), law = L1)

# ** Example 1C - Not OK, because the life expectancy at age 25 is
# equal with life expectancy at age 45 in the previous example.
LawTable(x = 25:100, par = c(0.00717, 0.07789, 0.00363), law = L1)

# Why is this happening?

# If we have a model that covers only a part of the human mortality curve
# (e.g. adult mortality), in fitting the x vector is scaled down, meaning
# age (x) becomes (x - min(x) + 1). And, the coefficients are estimated on
# a scaled x in ordered to obtain meaningful estimates. Otherwise the
# optimization process might not converge.

# What can we do about it?

# a). Know which mortality laws are rescaling the x vector in the fitting
# process. If these models are fitted with the MortalityLaw() function, you
# can find out like so:
A <- availableLaws()$table
A[, c("CODE", "SCALE_X")]

# b). If you are using one of the models that are applying scaling,
# be aware over what age-range the coefficients have been estimated. If they
# have been estimated using, say, ages 50 to 80, you can use the
# LawTable() to build a life tables from age 50 onwards.


# Example 2 --- Heligman-Pollard -- 1 table ----
x2 = 0:110
L2 = "HP"
C2 = c(0.00223, 0.01461, 0.12292, 0.00091,
       2.75201, 29.01877, 0.00002, 1.11411)

LawTable(x = x2, par = C2, law = L2)

# Because "HP" is not scaling down the x vector, the output is not affected
# by the problem described above.

# Check
LawTable(x = 3:110, par = C2, law = L2)
# Note the e3 = 70.31 in both tables
```

LifeTable   *Compute Life Tables from Mortality Data*

Description

Construct either a full or abridged life table with various input choices like: death counts and mid-interval population estimates (Dx, Ex) or age-specific death rates (mx) or death probabilities (qx) or survivorship curve (lx) or a distribution of deaths (dx). If one of these options is specified, the other can be ignored. The input data can be an object of class: numerical vector, matrix or data.frame.

Usage

```
LifeTable(x, Dx = NULL, Ex = NULL,
             mx = NULL,
             qx = NULL,
             lx = NULL,
             dx = NULL,
             sex = NULL,
             lx0 = 1e5,
             ax  = NULL)
```

Arguments

x	Vector of ages at the beginning of the age interval.
Dx	Object containing death counts. An element of the Dx object represents the number of deaths during the year to persons aged x to x+n.
Ex	Exposure in the period. Ex can be approximated by the mid-year population aged x to x+n.
mx	Life table death rate in age interval [x, x+n).
qx	Probability of dying in age interval [x, x+n).
lx	Probability of survival up until exact age x (if l(0) = 1), or the number of survivors at exact age x, assuming l(0) > 1.
dx	Deaths by life-table population in the age interval [x, x+n).
sex	Sex of the population considered here. Default: NULL. This argument affects the first two values in the life table ax column. If sex is specified the values are computed based on the Coale-Demeny method and are slightly different for males than for females. Options: NULL, male, female, total.
lx0	Radix. Default: 100 000.
ax	Numeric scalar. Subject-time alive in age-interval for those who die in the same interval. If NULL this will be estimated. A common assumption is ax = 0.5, i.e. the deaths occur in the middle of the interval. Default: NULL.

Details

The "life table" is also called "mortality table" or "actuarial table". This shows, for each age, what the probability is that a person of that age will die before his or her next birthday, the expectation of life across different age ranges or the survivorship of people from a certain population.

Value

The output is of the "LifeTable" class with the components:

lt	Computed life table;
call	Call in which all of the specified arguments are specified by their full names;
process_date	Time stamp.

Author(s)

Marius D. Pascariu

See Also

LawTable convertFx

Examples

```
# Example 1 --- Full life tables with different inputs ---

y  <- 1900
x  <- as.numeric(rownames(ahmd$mx))
Dx <- ahmd$Dx[, paste(y)]
Ex <- ahmd$Ex[, paste(y)]

LT1 <- LifeTable(x, Dx = Dx, Ex = Ex)
LT2 <- LifeTable(x, mx = LT1$lt$mx)
LT3 <- LifeTable(x, qx = LT1$lt$qx)
LT4 <- LifeTable(x, lx = LT1$lt$lx)
LT5 <- LifeTable(x, dx = LT1$lt$dx)

LT1
LT5
ls(LT5)

# Example 2 --- Compute multiple life tables at once ---

LTs = LifeTable(x, mx = ahmd$mx)
LTs
# A warning is printed if the input contains missing values.
# Some of the missing values can be handled by the function.

# Example 3 --- Abridged life table ------------

x  <- c(0, 1, seq(5, 110, by = 5))
mx <- c(.053, .005, .001, .0012, .0018, .002, .003, .004,
```

```
          .004, .005, .006, .0093, .0129, .019, .031, .049,
          .084, .129, .180, .2354, .3085, .390, .478, .551)
LT6 <- LifeTable(x, mx = mx, sex = "female")
LT6

# Example 4 --- Abridged life table w using my own 'ax' -----------
# In this examples we are using the ages (x) and death rates (mx) from
# example 3. Note that 'ax' must have the same length as the 'x' vector
# otherwise an error message will be returned.

my_ax <- c(0.1, 1.5, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
            2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 1, 1)

LT7 <- LifeTable(x = x, mx = mx, ax = my_ax)
```

MortalityLaw   *Fit Mortality Laws*

Description

Fit parametric mortality models given a set of input data which can be represented by death counts
and mid-interval population estimates (Dx, Ex) or age-specific death rates (mx) or death proba-
bilities (qx). Using the argument law one can specify the model to be fitted. So far more than
27 parametric models have been implemented; check the availableLaws function to learn about
the available options. The models can be fitted under the maximum likelihood methodology or
by selecting a loss function to be optimised. See the implemented loss function by running the
availableLF function.

Usage

```
MortalityLaw(x, Dx = NULL, Ex = NULL, mx = NULL, qx = NULL,
                law = NULL,
                opt.method = "LF2",
                parS = NULL,
                fit.this.x = x,
                custom.law = NULL,
                show = FALSE, ...)
```

Arguments

x	Vector of ages at the beginning of the age interval.
Dx	Object containing death counts. An element of the Dx object represents the number of deaths during the year to persons aged x to x+n.
Ex	Exposure in the period. Ex can be approximated by the mid-year population aged x to x+n.
mx	Life table death rate in age interval [x, x+n).

qx	Probability of dying in age interval [x, x+n).
law	The name of the mortality law/model to be used. e.g. gompertz, makeham, ... To investigate all the possible options, see [availableLaws](#) function.
opt.method	How would you like to find the parameters? Specify the function to be optimize. Available options: the Poisson likelihood function poissonL; the Binomial likelihood function -binomialL; and 6 other loss functions. For more details, check the [availableLF](#) function.
parS	Starting parameters used in the optimization process (optional).
fit.this.x	Select the ages to be considered in model fitting. By default fit.this.x = x. One may want to exclude from the fitting procedure, say, the advanced ages where the data is sparse.
custom.law	Allows you to fit a model that is not defined in the package. Accepts as input a function.
show	Choose whether to display a progress bar during the fitting process. Logical. Default: FALSE.
...	Arguments to be passed to or from other methods.

Details

Depending on the complexity of the model, one of following optimization strategies is employed:

1. Nelder-Mead method: approximates a local optimum of a problem with n variables when the objective function varies smoothly and is unimodal. For details see [optim](#);
2. PORT routines: provides unconstrained optimization and optimization subject to box constraints for complicated functions. For details check [nlminb](#);
3. Levenberg-Marquardt algorithm: damped least-squares method. For details check [nls.lm](#).

Value

The output is of the "MortalityLaw" class with the components:

input	List with arguments provided in input. Saved for convenience.
info	Brief information about the model.
coefficients	Estimated coefficients.
fitted.values	Fitted values of the selected model.
residuals	Deviance residuals.
goodness.of.fit	
	List containing goodness of fit measures like AIC, BIC and log-Likelihood.
opt.diagnosis	Resultant optimization object useful for checking the convergence etc.

Author(s)

Marius D. Pascariu

See Also

[availableLaws](#) [availableLF](#) [LifeTable](#) [ReadHMD](#)

Examples

```
# Example 1: ------------------------
# Fit Makeham Model for Year of 1950.

x  <- 45:75
Dx <- ahmd$Dx[paste(x), "1950"]
Ex <- ahmd$Ex[paste(x), "1950"]

M1 <- MortalityLaw(x = x, Dx = Dx, Ex = Ex, law = 'makeham')

M1
ls(M1)
coef(M1)
summary(M1)
fitted(M1)
predict(M1, x = 45:95)
plot(M1)


# Example 2: ------------------------
# We can fit the same model using a different data format
# and a different optimization method.
x  <- 45:75
mx <- ahmd$mx[paste(x), ]
M2 <- MortalityLaw(x = x, mx = mx, law = 'makeham', opt.method = 'LF1')
M2
fitted(M2)
predict(M2, x = 55:90)

# Example 3: ------------------------
# Now let's fit a mortality law that is not defined
# in the package, say a reparameterized Gompertz in
# terms of modal age at death
# hx = b*exp(b*(x-m)) (here b and m are the parameters to be estimated)

# A function with 'x' and 'par' as input has to be defined, which returns
# at least an object called 'hx' (hazard rate).
my_gompertz <- function(x, par = c(b = 0.13, M = 45)){
  hx  <- with(as.list(par), b*exp(b*(x - M)) )
  return(as.list(environment()))
}

M3 <- MortalityLaw(x = x, Dx = Dx, Ex = Ex, custom.law = my_gompertz)
summary(M3)
# predict M3 for different ages
predict(M3, x = 85:130)


# Example 4: ------------------------
# Fit Heligman-Pollard model for a single
# year in the dataset between age 0 and 100 and build a life table.
```

```
x  <- 0:100
mx <- ahmd$mx[paste(x), "1950"] # select data
M4 <- MortalityLaw(x = x, mx = mx, law = 'HP', opt.method = 'LF2')
M4
plot(M4)

LifeTable(x = x, qx = fitted(M4))
```

MortalityLaws   *MortalityLaws: Parametric Mortality Models, Life Tables and HMD*

Description

Fit the most popular human mortality 'laws', and construct full and abridge life tables given various input indices. A mortality law is a parametric function that describes the dying-out process of individuals in a population during a significant portion of their life spans. For a comprehensive review of the most important mortality laws see Tabeau (2001) doi:10.1007/0306475626_1. Practical functions for downloading data from various human mortality databases are provided as well.

Details

To learn more about the package, start with the vignettes: browseVignettes(package = "MortalityLaws")

Author(s)

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Other contributors:

- Vladimir Canudas-Romo [contributor]

See Also

Useful links:

- https://github.com/mpascariu/MortalityLaws

- Report bugs at https://github.com/mpascariu/MortalityLaws/issues

---

plot.MortalityLaw   *Plot Function for MortalityLaw*

Description

Plot Function for MortalityLaw

Usage

```
## S3 method for class 'MortalityLaw'
plot(x, ...)
```

Arguments

x   An object of class MortalityLaw

...   Arguments to be passed to methods, such as graphical parameters (see [par](par)).

Value

generate a plot

Author(s)

Marius D. Pascariu

See Also

MortalityLaw

Examples

```
# See complete example in MortalityLaw help page
```

---

predict.MortalityLaw   *Predict function for MortalityLaw*

Description

Predict function for MortalityLaw

Usage

```
## S3 method for class 'MortalityLaw'
predict(object, x, ...)
```

Arguments

object	An object of class "MortalityLaw"
x	Vector of ages to be considered in prediction
...	Additional arguments affecting the predictions produced.

Value

A vector of predicted hazard rates

Author(s)

Marius D. Pascariu

See Also

MortalityLaw

Examples

```
# Extrapolate old-age mortality with the Kannisto model
# Fit ages 80-94 and extrapolate up to 120.

Mx <- ahmd$mx[paste(80:94), "1950"]
M1 <- MortalityLaw(x = 80:94, mx  = Mx, law = 'kannisto')
fitted(M1)
predict(M1, x = 80:120)

# See more examples in MortalityLaw function help page.
```

ReadAHMD *Download the Australian Human Mortality Database (AHMD)*

Description

Download detailed mortality and population data for different provinces and territories in Australia, in a single object from the Australian Human Mortality Database.

Usage

```
ReadAHMD(what, regions = NULL, interval = "1x1", save = FALSE, show = TRUE)
```

Arguments

what   What type of data are you looking for? The following options might be available
                      for some or all the countries and regions:

- "births" – birth records;
- "Dx_lexis" – deaths by Lexis triangles;
- "Ex_lexis" – exposure-to-risk by Lexis triangles;
- "population" – population size;
- "Dx" – death counts;
- "Ex" – exposure-to-risk;
- "mx" – central death-rates;
- "LT_f" – period life tables for females;
- "LT_m" – period life tables for males;
- "LT_t" – period life tables both sexes combined;
- "e0" – period life expectancy at birth;
- "Exc" – cohort exposures;
- "mxc" – cohort death-rates;
- "LT_fc" – cohort life tables for females;
- "LT_mc" – cohort life tables for males;
- "LT_tc" – cohort life tables both sexes combined;
- "e0c" – cohort life expectancy at birth;

regions   Specify the region specific data you want to download by adding the AHMD
                      region code/s. Options:

- "ACT" – Australian Capital Territory;
- "NSW" – New South Wales;
- "NT" – Northern Territory;
- "QLD" – Queensland;
- "SA" – South Australia;
- "TAS" – Tasmania;
- "VIC" – Victoria;
- "WA" – Western Australia;
- NULL – if NULL data for all the regions are downloaded.

interval   Datasets are given in various age and time formats based on which the records
                      are agregated. Interval options:

- "1x1" – by age and year;
- "1x5" – by age and 5-year time interval;
- "1x10" – by age and 10-year time interval;
- "5x1" – by 5-year age group and year;
- "5x5" – by 5-year age group and 5-year time interval;
- "5x10" –by 5-year age group and 10-year time interval.

save   Do you want to save a copy of the dataset on your local machine? Logical.
                      Default: FALSE.

show   Choose whether to display a progress bar. Logical. Default: TRUE.

Details

(Description taken from the AHMD website).

The Australian Human Mortality Database (AHMD) was created to provide detailed Australian mortality and population data to researchers, students, journalists, policy analysts, and others interested in the history of human longevity. The project is an achievement of the Mortality, Ageing & Health research team in the ANU School of Demography under the supervision of Associate Professor Vladimir Canudas-Romo, in collaboration with demographers at the Max Plank Institute for Demographic Research (Rostock, Germany) and the Department of Demography, University of California at Berkeley.

The AHMD is a "satellite" of the Human Mortality Database (HMD), an international database which currently holds detailed data for multiple countries or regions. Consequently, the AHMD's underlying methodology corresponds to the one used for the HMD.

The AHMD gathers all required data (deaths counts, births counts, population size, exposure-to-risk, death rates) to compute life tables for Australia, its states and its territories. One of the great advantages of the database is to include data that is validated and corrected, when required, and rendered comparable, if possible, for the period ranging from 1971 thru 2016. For comparison purposes, various life tables published by governmental organizations are also available for download in PDF format.

Value

A ReadAHMD object that contains:

input	List with the input values;
data	Data downloaded from AHMD;
download.date	Time stamp;
years	Numerical vector with the years covered in the data;
ages	Numerical vector with ages covered in the data.

Author(s)

Marius D. Pascariu

See Also

ReadHMD ReadCHMD

Examples

```
# Download demographic data for Australian Capital Territory and
# Tasmania regions in 5x1 format

# Death counts. We don't want to export data outside R.
AHMD_Dx <- ReadAHMD(what = "Dx",
                    regions = c('ACT', 'TAS'),
                    interval = "5x1",
                    save = FALSE)
AHMD_Dx
```

```
# Download life tables for female population in all the states and export data.
LTF <- ReadAHMD(what = "LT_f", interval  = "5x1", save = FALSE)
LTF
```

ReadCHMD   *Download the Canadian Human Mortality Database (CHMD)*

Description

Download detailed mortality and population data for different provinces and territories in Canada, in a single object from the Canadian Human Mortality Database.

Usage

```
ReadCHMD(what, regions = NULL, interval = "1x1", save = FALSE, show = TRUE)
```

Arguments

what
: What type of data are you looking for? The following options are available:
  - "births" – birth records;
  - "Dx_lexis" – deaths by Lexis triangles;
  - "population" – population size;
  - "Dx" – death counts;
  - "Ex" – exposure-to-risk;
  - "mx" – central death-rates;
  - "LT_f" – period life tables for females;
  - "LT_m" – period life tables for males;
  - "LT_t" – period life tables both sexes combined;
  - "e0" – period life expectancy at birth;

regions
: Specify the region specific data you want to download by adding the CHMD region code/s. Options:
  - "CAN" – Canada - Sum of Canadian provinces and territories;
  - "NFL" – Newfoundland & Labrador;
  - "PEI" – Prince Edward Island;
  - "NSC" – Nova Scotia;
  - "NBR" – New Brunswick;
  - "QUE" – Quebec;
  - "ONT" – Ontario;
  - "MAN" – Manitoba;
  - "SAS" – Saskatchewan;
  - "ALB" – Alberta;
  - "BCO" – British Columbia;

- ″NWT″ – Northwest Territories & Nunavut;
- ″YUK″ – Yukon;
- NULL – if NULL data for all the regions are downloaded.

interval Datasets are given in various age and time formats based on which the records are agregated. Interval options:

- ″1x1″ – by age and year;
- ″1x5″ – by age and 5-year time interval;
- ″1x10″ – by age and 10-year time interval;
- ″5x1″ – by 5-year age group and year;
- ″5x5″ – by 5-year age group and 5-year time interval;
- ″5x10″ –by 5-year age group and 10-year time interval.

save Do you want to save a copy of the dataset on your local machine? Logical. Default: FALSE.

show Choose whether to display a progress bar. Logical. Default: TRUE.

Details

(Description taken from the CHMD website).

The Canadian Human Mortality Database (CHMD) was created to provide detailed Canadian mortality and population data to researchers, students, journalists, policy analysts, and others interested in the history of human longevity. The project is an achievement of the Mortality and Longevity research team at the Department of Demography, Universite de Montreal, under the supervision of Professor Robert Bourbeau, in collaboration with demographers at the Max Plank Institute for Demographic Research (Rostock, Germany) and the Department of Demography, University of California at Berkeley. Nadine Ouellette, researcher at the Institut national d'etudes demographiques in Paris and member of the Mortality and Longevity research team at the Universite de Montreal, is in charge of computing all CHMD life tables and updating the CHMD web site.

The CHMD is a "satellite" of the Human Mortality Database (HMD), an international database which currently holds detailed data for multiple countries or regions. Consequently, the CHMD's underlying methodology corresponds to the one used for the HMD.

The CHMD gathers all required data (deaths counts, births counts, population size, exposure-to-risk, death rates) to compute life tables for Canada, its provinces and its territories. One of the great advantages of the database is to include data that is validated and corrected, when required, and rendered comparable, if possible, for the period ranging from 1921 thru 2011. For comparison purposes, various life tables published by governmental organizations are also available for download in PDF format.

Value

A ReadCHMD object that contains:

input List with the input values;

data Data downloaded from CHMD;

download.date Time stamp;

years Numerical vector with the years covered in the data;

ages Numerical vector with ages covered in the data.

Author(s)

Marius D. Pascariu

See Also

ReadHMD ReadAHMD

Examples

```
# Download demographic data for Quebec and Saskatchewan regions in 1x1 format

# Death counts. We don't want to export data outside R.
CHMD_Dx <- ReadCHMD(what = "Dx",
                    regions = c('QUE', 'SAS'),
                    interval  = "1x1",
                    save = FALSE)

# Download life tables for female population. To export data use save = TRUE.
LTF <- ReadCHMD(what = "LT_f",
                regions = c('QUE', 'SAS'),
                interval  = "1x1",
                save = FALSE)
```

ReadHMD   *Download The Human Mortality Database (HMD)*

Description

Download detailed mortality and population data for different countries and regions in a single object from the Human Mortality Database.

Usage

```
ReadHMD(
  what,
  countries = NULL,
  interval = "1x1",
  username,
  password,
  save = FALSE,
  show = TRUE
)
```

Arguments

what
: What type of data are you looking for? The following options might be available for some or all the countries and regions:

  - "births" – birth records;
  - "Dx_lexis" – deaths by Lexis triangles;
  - "Ex_lexis" – exposure-to-risk by Lexis triangles;
  - "population" – population size;
  - "Dx" – death counts;
  - "Ex" – exposure-to-risk;
  - "mx" – central death-rates;
  - "LT_f" – period life tables for females;
  - "LT_m" – period life tables for males;
  - "LT_t" – period life tables both sexes combined;
  - "e0" – period life expectancy at birth;
  - "Exc" – cohort exposures;
  - "mxc" – cohort death-rates;
  - "LT_fc" – cohort life tables for females;
  - "LT_mc" – cohort life tables for males;
  - "LT_tc" – cohort life tables both sexes combined;
  - "e0c" – cohort life expectancy at birth;

countries
: Specify the country data you want to download by adding the HMD country code/s. Options: "AUS" "AUT", "BEL", "BGR","BLR", "CAN", "CHL", "HRV","HKG", "CHE", "CZE", "DEUTNP","DEUTE", "DEUTW", "DNK", "ESP","EST", "FIN", "FRATNP","FRACNP","GRC", "HUN", "IRL", "ISL" "ISR", "ITA", "JPN", "KOR","LTU", "LUX", "LVA", "NLD","NOR", "NZL_NP", "NZL_MA" "NZL_NM","POL", "PRT" "RUS", "SVK","SVN", "SWE", "TWN", "UKR","GBR_NP","GBRTENW","GBRCENW","GBR_SCO","GBR_NI If NULL data for all the countries are downloaded at once;

interval
: Datasets are given in various age and time formats based on which the records are agregated. Interval options:

  - "1x1" – by age and year;
  - "1x5" – by age and 5-year time interval;
  - "1x10" – by age and 10-year time interval;
  - "5x1" – by 5-year age group and year;
  - "5x5" – by 5-year age group and 5-year time interval;
  - "5x10" –by 5-year age group and 10-year time interval.

username
: Your HMD username. If you don't have one you can sign up for free on the Human Mortality Database website.

password
: Your HMD password.

save
: Do you want to save a copy of the dataset on your local machine? Logical. Default: FALSE.

show
: Choose whether to display a progress bar. Logical. Default: TRUE.

Details

The Human Mortality Database (HMD) was created to provide detailed mortality and population data to researchers, students, journalists, policy analysts, and others interested in the history of human longevity. The project began as an outgrowth of earlier projects in the Department of Demography at the University of California, Berkeley, USA, and at the Max Planck Institute for Demographic Research in Rostock, Germany (see history). It is the work of two teams of researchers in the USA and Germany (see research teams), with the help of financial backers and scientific collaborators from around the world (see acknowledgements). The Center on the Economics and Development of Aging (CEDA) French Institute for Demographic Studies (INED) has also supported the further development of the database in recent years.

Value

A ReadHMD object that contains:

`input`	List with the input values (except the password).
`data`	Data downloaded from HMD.
`download.date`	Time stamp.
`years`	Numerical vector with the years covered in the data.
`ages`	Numerical vector with ages covered in the data.

Author(s)

Marius D. Pascariu

Examples

```
## Not run:


# Download demographic data for 3 countries in 1x1 format
age_int  <- 1  # age interval: 1,5
year_int <- 1  # year interval: 1,5,10
interval <- paste0(age_int, "x", year_int)  # --> 1x1
# And the 3 countries: Sweden Denmark and USA. We have to use the HMD codes
cntr  <- c('SWE', 'DNK', 'USA')

# Download death counts. We don't want to export data outside R.
HMD_Dx <- ReadHMD(what = "Dx",
                  countries = cntr,
                  interval  = interval,
                  username  = "user@email.com",
                  password  = "password",
                  save = FALSE)
HMD_Dx

# Download life tables for female population and export data.
LTF <- ReadHMD(what = "LT_f",
               countries = cntr,
               interval  = interval,
```

```
                  username = "user@email.com",
                  password = "password",
                  save = TRUE)
  LTF

  ## End(Not run)
```

ReadJMD   *Download the Japanese Mortality Database (JMD)*

Description

Download detailed mortality and population data of the 47 prefectures in Japan, in a single object. The source of data is the Japanese Mortality Database.

Usage

```
ReadJMD(what, regions = NULL, interval = "1x1", save = FALSE, show = TRUE)
```

Arguments

what   What type of data are you looking for? The following options might be available for some or all the countries and regions:

- "births" – birth records;
- "Dx_lexis" – deaths by Lexis triangles;
- "Ex_lexis" – exposure-to-risk by Lexis triangles;
- "population" – population size;
- "Dx" – death counts;
- "Ex" – exposure-to-risk;
- "mx" – central death-rates;
- "LT_f" – period life tables for females;
- "LT_m" – period life tables for males;
- "LT_t" – period life tables both sexes combined;
- "e0" – period life expectancy at birth;
- "Exc" – cohort exposures;
- "mxc" – cohort death-rates;
- "LT_fc" – cohort life tables for females;
- "LT_mc" – cohort life tables for males;
- "LT_tc" – cohort life tables both sexes combined;
- "e0c" – cohort life expectancy at birth;

regions   Specify the region specific data you want to download by adding the JMD region code/s. Options: "Japan", "Hokkaido", "Aomori","Iwate", "Miyagi","Akita", "Yamagata", "Fukushima", "Ibaraki", "Tochigi","Gunma", "Saitama", "Chiba", "Tokyo", "Kanagawa", "Niigata", "Toyama","Ishikawa", "Fukui", "Yamanashi",

"Nagano", "Gifu", "Shizuoka","Aichi","Mie", "Shiga", "Kyoto", "Osaka", "Hyogo", "Nara", "Wakayama", "Tottori","Shimane", "Okayama", "Hiroshima", "Yamaguchi", "Tokushima", "Kagawa","Ehime", "Kochi", "Fukuoka", "Saga", "Nagasaki", "Kumamoto", "Oita","Miyazaki", "Kagoshima", "Okinawa". If NULL data for all the regions are downloaded at once.

interval   Datasets are given in various age and time formats based on which the records are agregated. Interval options:

- "1x1" – by age and year;
- "1x5" – by age and 5-year time interval;
- "1x10" – by age and 10-year time interval;
- "5x1" – by 5-year age group and year;
- "5x5" – by 5-year age group and 5-year time interval;
- "5x10" –by 5-year age group and 10-year time interval.

save   Do you want to save a copy of the dataset on your local machine? Logical. Default: FALSE.

show   Choose whether to display a progress bar. Logical. Default: TRUE.

Details

(Description taken from the JMD website).

The Japanese Mortality Database is a comprehensively-reorganized mortality database that is optimized for mortality research and consistent with the Human Mortality Database. This database is provided as a part of the research project "Demographic research on the causes and the socio-economic consequence of longevity extension in Japan" (2011-2013), "Demographic research on longevity extension, population aging, and their effects on the social security and socio-economic structures in Japan" (2014-2016), and "Comprehensive research from a demographic viewpoint on the longevity revolution" (2017-2019) at the National Institute of Population and Social Security Research.

The Japanese Mortality Database is designed to provide the life tables to all the people who are interested in Japanese mortality including domestic and foreign mortality researchers for the purpose of mortality research. Especially because we have structured it to conform with the HMD, our database is suitable for international comparison, we put emphasis on the compatibility with the HMD more than our country's particular characteristics. Therefore, the life tables by JMD do not necessarily exhibit the same values as ones by the official life tables prepared and released by the Statistics and Information Department, Minister's Secretariat, Ministry of Health, Labor and Welfare according to the different base population or the methods for estimating the tables. When doing things other than mortality research, if life table that statistically displays our country's mortality situation is necessary, please use the official life table that has been prepared by the Statistics and Information Department, Minister's Secretariat, Ministry of Health, Labor and Welfare.

At the present time, we offer the data for All Japan and by prefecture. The project team is studying the methodology for estimating life tables along with data preparation. Therefore, the data may be updated when a new methodology is adopted. Please refer to "Methods" for further information.

Value

A ReadJMD object that contains:

input	List with the input values;
data	Data downloaded from JMD;
download.date	Time stamp;
years	Numerical vector with the years covered in the data;
ages	Numerical vector with ages covered in the data.

Author(s)

Marius D. Pascariu

See Also

ReadHMD ReadCHMD

Examples

```
# Download demographic data for Fukushima and Tokyo regions in 1x1 format

# Death counts. We don't want to export data outside R.
JMD_Dx <- ReadJMD(what = "Dx",
                  regions = c('Fukushima', 'Tokyo'),
                  interval  = "1x1",
                  save = FALSE)
JMD_Dx

# Download life tables for female population in all the states and export data.
LTF <- ReadJMD(what = "LT_f", interval  = "5x5", save = FALSE)
LTF
```

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