

# Package ‘MortalityLaws’

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**Type** Package

**Title** Parametric Mortality Models, Life Tables and HMD

**Version** 2.2.0

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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.

**License** MIT + file LICENSE

**LazyData** TRUE

**Depends** R (>= 3.0.0)

**Imports** 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>

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**VignetteBuilder** knitr

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ahmd	<i>MortalityLaws Test Data</i>
------	--------------------------------

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### 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. This dataset 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	<i>Check Data Availability in HMD</i>
--------------	---------------------------------------

---

**Description**

Returns information about the data available in the Human Mortality Database (HMD), including the range of years covered by the life tables for each country or region.

**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	<i>Check Available Mortality Laws</i>
---------------	---------------------------------------

---

**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 following 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

### References

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### See Also

[MortalityLaw](#)

### Examples

```
availableLaws()
```

---

availableLF

*Check Available Loss Functions*

---

### Description

Returns information about the loss functions implemented for use with the optimisation 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 <a href="#">MortalityLaw</a> .
legend	Table with details about the abbreviation used.

**Author(s)**

Marius D. Pascariu

**See Also**[MortalityLaw](#)**Examples**

availableLF()

---

`convertFx`*Convert Life Table Indicators*

---

**Description**

Easily convert between different life table indicators (e.g., from death rates  $m_x$  to death probabilities  $q_x$ , or from survivorship  $l_x$  to life expectancy  $e_x$ ). The function wraps [LifeTable](#) internally, so the conversion relies on the same constant-force-of-mortality (CFM) assumption and life-table methodology used throughout the package.

**Usage**`convertFx(x, data, from, to, ...)`**Arguments**

<code>x</code>	Numeric vector of ages at the beginning of each age interval. For a full life table, use single-year ages (e.g., $0:110$ ). For an abridged life table, use the lower bound of each interval (e.g., $c(0, 1, 5, 10, \dots, 110)$ ).
<code>data</code>	A numeric vector, matrix, or data frame containing the mortality indicator to be converted. Each row should correspond to an age, each column to a separate population or time period.
<code>from</code>	The type of indicator supplied in data. One of: "mx", "qx", "dx", or "lx".
<code>to</code>	The desired output indicator. One of: "mx", "qx", "dx", "lx", "Lx", "Tx", or "ex".
<code>...</code>	Further arguments passed to <a href="#">LifeTable</a> that may affect the results, such as <code>sex</code> , <code>lx0</code> , or <code>ax</code> .

## Details

This function provides a convenient interface for converting a single mortality indicator into another, without having to call [LifeTable](#) directly and extract the desired column.

The supported **input** types (from) are: mx, qx, dx, and lx.

The supported **output** types (to) are: mx, qx, dx, lx, Lx, Tx, and ex.

There are 28 possible from-to combinations (4 inputs  $\times$  7 outputs). All conversions pass through the full life-table computation; for example, converting mx to ex will internally compute qx, lx, dx, Lx, and Tx in sequence.

When data is a vector, the function returns a named vector. When data is a matrix or data frame with multiple columns, the function applies the conversion column-wise and returns a matrix with the same row and column names as the input.

## Value

A numeric vector or matrix containing the converted life table indicator. If the input was a named object, the output retains those names.

## Author(s)

Marius D. Pascariu

## See Also

[LifeTable](#) for the underlying life-table construction; [LawTable](#) for generating life tables from parametric mortality laws.

## Examples

```
# ---- Basic conversions ----

x <- 0:110
mx <- ahmd$mx

# Convert death rates to death probabilities
qx <- convertFx(x, data = mx, from = "mx", to = "qx")

# Convert death rates to death distribution
dx <- convertFx(x, data = mx, from = "mx", to = "dx")

# Convert death rates to survivorship
lx <- convertFx(x, data = mx, from = "mx", to = "lx")

# ---- All 28 possible conversions ----

from <- c("mx", "qx", "dx", "lx")
to <- c("mx", "qx", "dx", "lx", "Lx", "Tx", "ex")
K <- expand.grid(from = from, to = to)

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")
assign(N, convertFx(x = x, data = get(In), from = In, to = Out))
}

```

---

LawTable

*Compute Life Tables from Parameters of a Mortality Law*


---

### Description

Generate a complete life table directly from the fitted parameters of a parametric mortality model. This function evaluates the mortality law at the given ages and passes the resulting death rates ( $m_x$ ) or death probabilities ( $q_x$ ) to [LifeTable](#) for further computation of all standard life-table columns ( $l_x$ ,  $dx$ ,  $L_x$ ,  $T_x$ ,  $ex$ , etc.).

### Usage

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

### Arguments

<code>x</code>	Numeric vector of ages at the beginning of each age interval. For a full life table, use single-year ages (e.g., 0:110). For an abridged life table, use the lower bound of each interval (e.g., c(0, 1, 5, 10, ..., 110)).
<code>par</code>	The parameters of the mortality model. Can be: <ul style="list-style-type: none"> <li>• A numeric <b>vector</b> containing the coefficients (for a single life table).</li> <li>• A numeric <b>matrix</b> or <b>data.frame</b> where each row corresponds to a separate set of parameters (producing multiple life tables). Column names should match the parameter names of the chosen law.</li> </ul>
<code>law</code>	The name of the mortality law to be used (e.g., "gompertz", "makeham"). Run <a href="#">availableLaws</a> to see all options.
<code>sex</code>	Sex of the population. Options are NULL (default), "male", "female", or "total". When specified, the first two entries of the <code>ax</code> column are adjusted using Coale-Demeny coefficients, producing more accurate life-table values at the youngest ages. The adjustment differs slightly between males and females.
<code>lx0</code>	Radix, the starting population (or probability scale) at age 0. Default is 100,000. All subsequent life-table columns ( $l_x$ , $dx$ , $L_x$ , $T_x$ ) are scaled accordingly.
<code>ax</code>	Numeric vector representing the average number of person-years lived in the age interval by those who die in that interval. If NULL (the default), <code>ax</code> is estimated internally using a standard formula. You may supply a single value (applied to all intervals) or a vector of the same length as <code>x</code> . A common assumption is <code>ax = 0.5</code> , which places deaths at the midpoint of each interval.

## Details

This function is designed to work with models that have been fitted externally (e.g., via [MortalityLaw](#) or by hand). The `par` argument must contain the estimated coefficients of the mortality law, and `law` must be one of the valid codes listed by [availableLaws](#).

### Important caveat: age scaling during fitting

Several mortality laws (e.g., Gompertz, Makeham) internally *scale* the age vector during optimisation to ensure numerical stability. If the model was fitted using `MortalityLaw` over an age range  $[a, b]$ , the published coefficients correspond to the *scaled* ages, not the original ages. Consequently, `LawTable` will only produce valid life tables for ages  $\geq a$  (the lower bound of the fitting range). Attempting to use the same coefficients at younger ages will yield incorrect results (e.g., life expectancy at age 25 will equal that at age 45).

To determine which models apply age scaling, run:

```
A <- availableLaws()$table
A[, c("CODE", "SCALE_X")]
```

Models with `SCALE_X = TRUE` rescale the age vector internally. When using `LawTable` with such a model, make sure the `x` argument starts from the same lower age bound used during fitting.

For models that do *not* scale (e.g., Heligman-Pollard "HP"), this limitation does not apply, and `LawTable` can be used for any age range.

## Value

An object of class "LifeTable" containing the following components:

<code>lt</code>	A data.frame with the complete life table, including columns for age interval ( <code>x.int</code> ), exact age ( <code>x</code> ), death rate ( <code>mx</code> ), death probability ( <code>qx</code> ), person-years lived by decedents ( <code>ax</code> ), survivorship ( <code>lx</code> ), death distribution ( <code>dx</code> ), person-years lived ( <code>Lx</code> ), total person-years remaining ( <code>Tx</code> ), and life expectancy ( <code>ex</code> ).
<code>call</code>	The matched function call.
<code>process_date</code>	Timestamp of when the life table was computed.

## Author(s)

Marius D. Pascariu

## See Also

[LifeTable](#) for constructing life tables from raw mortality data; [MortalityLaw](#) for fitting parametric mortality models; [availableLaws](#) for the list of implemented laws and their scaling behaviour.

## Examples

```
# Example 1 --- Makeham --- multiple life tables from a matrix of parameters

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 = x1, par = C1, law = L1)

# ---- Important note on age scaling ----

# The Makeham model applies internal age scaling during fitting.
# If the coefficients above were estimated over ages 45-100, the life
# table produced by LawTable is valid only from age 45 onward.

# ---- Example 1B: correct usage ----
LawTable(x = 45:100, par = c(0.00717, 0.07789, 0.00363), law = L1)

# ---- Example 1C: incorrect usage ----
# The code below uses the same coefficients but starts at age 25.
# Because the model was fitted on scaled ages (starting at 45),
# the life table at age 25 will be meaningless (e.g., e25 equals e45).
## Not run:
LawTable(x = 25:100, par = c(0.00717, 0.07789, 0.00363), law = L1)

## End(Not run)

# ---- How to check which laws apply scaling ----
A <- availableLaws()$table
A[, c("CODE", "SCALE_X")]

# Example 2 --- Heligman-Pollard (no scaling) ---

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" does NOT scale the age vector, the output is valid for
# any starting age. Compare:
LawTable(x = 3:110, par = C2, law = L2)
# Note that e3 = 70.31 in both tables, confirming consistency.

```

## Description

Construct either a full (single-year age intervals) or an abridged (wider age intervals) life table from a variety of input data types. The function accepts:

- Death counts and mid-interval population estimates ( $D_x$ ,  $E_x$ )
- Age-specific death rates ( $m_x$ )
- Death probabilities ( $q_x$ )
- Survivorship curve ( $l_x$ )
- Distribution of deaths ( $dx$ )

Only one of these input options needs to be provided; the others are ignored if present. The input can be a numeric vector, `matrix`, or `data.frame`. When a `matrix` or `data.frame` with multiple columns is supplied, the function computes one life table per column.

## Usage

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

## Arguments

<code>x</code>	Numeric vector of ages at the beginning of each age interval. For a full life table, use single-year ages (e.g., <code>0:110</code> ). For an abridged life table, use the lower bound of each interval (e.g., <code>c(0, 1, 5, 10, ..., 110)</code> ).
<code>Dx</code>	Death counts. Each element represents the total number of deaths during the calendar year to persons aged $x$ to $x + n$ (where $n$ is the length of the age interval). Must be provided together with <code>Ex</code> .
<code>Ex</code>	Exposure-to-risk in the period. This is usually approximated by the mid-year population aged $x$ to $x + n$ . Must be provided together with <code>Dx</code> .
<code>mx</code>	Age-specific death rate in the age interval $[x, x+n)$ . Defined as $D_x / E_x$ .
<code>qx</code>	Probability of dying within the age interval $[x, x+n)$ .
<code>lx</code>	Probability of surviving to exact age $x$ (if $lx0 = 1$ ), or the number of survivors at exact age $x$ (if $lx0 > 1$ ). When <code>lx</code> is the sole input, the values are re-scaled to the chosen radix $lx0$ .
<code>dx</code>	Number of deaths in the life-table population occurring in the age interval $[x, x+n)$ . When <code>dx</code> is the sole input, the values are re-scaled to sum to $lx0$ .
<code>sex</code>	Sex of the population. Options are <code>NULL</code> (default), <code>"male"</code> , <code>"female"</code> , or <code>"total"</code> . When specified, the first two entries of the <code>ax</code> column are adjusted using Coale-Demeny coefficients, producing more accurate life-table values at the youngest ages. The adjustment differs slightly between males and females.

<code>lx0</code>	Radix, the starting population (or probability scale) at age 0. Default is 100,000. All subsequent life-table columns ( <code>lx</code> , <code>dx</code> , <code>Lx</code> , <code>Tx</code> ) are scaled accordingly.
<code>ax</code>	Numeric vector representing the average number of person-years lived in the age interval by those who die in that interval. If NULL (the default), <code>ax</code> is estimated internally using a standard formula. You may supply a single value (applied to all intervals) or a vector of the same length as <code>x</code> . A common assumption is <code>ax = 0.5</code> , which places deaths at the midpoint of each interval.

### Details

A life table (also called a mortality table or actuarial table) summarises the mortality experience of a population. For each age (or age interval) it reports:

- Death rates (`mx`) and death probabilities (`qx`)
- Survivorship (`lx`)
- Distribution of deaths (`dx`)
- Person-years lived (`Lx`) and total person-years remaining (`Tx`)
- Life expectancy (`ex`)

The life table is constructed sequentially: from the input data the function derives `mx`, then `qx`, then `lx`, `dx`, `Lx`, `Tx`, and finally `ex`. The constant-force-of-mortality (CFM) assumption is used to convert between `mx` and `qx`. If the `sex` argument is supplied, the first two values of the `ax` column are adjusted using the Coale-Demeny method, which accounts for the different infant mortality patterns between males and females.

### Value

An object of class "LifeTable" containing the following components:

<code>lt</code>	A <code>data.frame</code> with the complete life table, including columns for age interval ( <code>x.int</code> ), exact age ( <code>x</code> ), death rate ( <code>mx</code> ), death probability ( <code>qx</code> ), person-years lived by decedents ( <code>ax</code> ), survivorship ( <code>lx</code> ), death distribution ( <code>dx</code> ), person-years lived ( <code>Lx</code> ), total person-years remaining ( <code>Tx</code> ), and life expectancy ( <code>ex</code> ).
<code>call</code>	The matched function call.
<code>process_date</code>	Timestamp of when the life table was computed.

### Author(s)

Marius D. Pascariu

### See Also

[LawTable](#) for generating life tables from a fitted parametric mortality law; [convertFx](#) for converting between mortality measures.

**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 automatically.

# 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 using a custom 'ax' -----
# This example reuses the ages (x) and death rates (mx) from Example 3.
# Note that 'ax' must have the same length as 'x', otherwise an error
# 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, 2, 1, 1, 1)

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

```

## Description

Fit parametric mortality models given a set of input data. The data can be supplied as death counts and mid-interval population estimates ( $D_x$ ,  $E_x$ ), age-specific death rates ( $m_x$ ), or death probabilities ( $q_x$ ). Use the `law` argument to specify the model to be fitted. Over 30 parametric models are currently implemented; run [availableLaws](#) to see the full list. Models can be fitted using maximum likelihood or by optimising a loss function. See the [availableLF](#) function for the implemented options.

## 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

<code>x</code>	Numeric vector of ages at the beginning of each age interval. For a full life table, use single-year ages (e.g., 0:110). For an abridged life table, use the lower bound of each interval (e.g., c(0, 1, 5, 10, ..., 110)).
<code>Dx</code>	Death counts. Each element represents the total number of deaths during the calendar year to persons aged $x$ to $x + n$ (where $n$ is the length of the age interval). Must be provided together with <code>Ex</code> .
<code>Ex</code>	Exposure-to-risk in the period. This is usually approximated by the mid-year population aged $x$ to $x + n$ . Must be provided together with <code>Dx</code> .
<code>mx</code>	Age-specific death rate in the age interval $[x, x+n)$ . Defined as $D_x / E_x$ .
<code>qx</code>	Probability of dying within the age interval $[x, x+n)$ .
<code>law</code>	The name of the mortality law to be used (e.g., "gompertz", "makeham"). Run <a href="#">availableLaws</a> to see all options.
<code>opt.method</code>	The function to optimise. Available options: <ul style="list-style-type: none"> <li>• "poissonL": Poisson log-likelihood.</li> <li>• "binomialL": Binomial log-likelihood.</li> <li>• "LF1": Squared relative error <math>(1 - \mu/\nu)^2</math>.</li> <li>• "LF2": Squared log-ratio <math>\log(\mu/\nu)^2</math>.</li> <li>• "LF3": Chi-squared-type <math>((\nu - \mu)^2)/\nu</math>.</li> <li>• "LF4": Squared error <math>(\nu - \mu)^2</math>.</li> <li>• "LF5": Deviance-type <math>(\nu - \mu) * \log(\nu/\mu)</math>.</li> <li>• "LF6": Absolute error <math>\text{abs}(\nu - \mu)</math>.</li> </ul> See <a href="#">availableLF</a> for details.
<code>parS</code>	Optional starting parameter values for the optimisation. If NULL, sensible defaults are automatically chosen via <a href="#">bring_parameters</a> .

<code>fit.this.x</code>	A subset of <code>x</code> over which to fit the model. The default is the entire <code>x</code> vector. Use this to exclude, for example, advanced ages where data are sparse.
<code>custom.law</code>	A user-defined function for fitting a model not included in the package. The function must accept arguments <code>x</code> (age vector) and <code>par</code> (named parameter vector) and return a list containing at least an element named <code>hx</code> (the hazard or force of mortality). See the examples below.
<code>show</code>	Logical. If TRUE, a progress bar is displayed during fitting. Default: FALSE.
<code>...</code>	Additional arguments passed to or from other methods.

### Details

**Optimisation:** The PORT routines (via `nlminb`) are used for unconstrained and box-constrained optimisation. Parameters are estimated on the log scale to ensure positivity, and the routine is set to allow up to 5000 iterations. When the optimisation method is "poissonL" or "binomialL", the AIC, BIC and log-likelihood are computed from the likelihood. Otherwise these are set to NaN.

**Scaling of the age vector:** For models that cover only a portion of the lifespan (e.g., adult or old-age mortality), the age vector `x` is automatically re-scaled as  $x = x - \min(x) + 1$  before fitting. This transformation improves numerical stability and helps the optimisation algorithm converge, especially when the starting age is far from zero. Models that apply this scaling are flagged with `SCALE_X = TRUE` in the table returned by `availableLaws`. When using `predict.MortalityLaw` or `LawTable` with such models, the same scaling is applied internally, so predictions remain consistent with the fitted coefficients.

**Handling matrix input:** If `Dx`, `Ex`, `mx` or `qx` are provided as matrices (with one column per population or time period), the function iterates over the columns and fits a separate model to each, returning a collection of results.

### Value

An object of class "MortalityLaw", which is a list with the following components:

<code>input</code>	List of input arguments, stored for reproducibility.
<code>info</code>	Model information (name, formula, date of fitting).
<code>coefficients</code>	Estimated parameters of the mortality law. A named vector for a single fit, or a matrix for multiple fits.
<code>fitted.values</code>	Fitted hazard rates (or death probabilities) evaluated at the input ages <code>x</code> .
<code>residuals</code>	Deviance residuals, computed as observed minus fitted values.
<code>goodness.of.fit</code>	List or matrix of goodness-of-fit measures: AIC, BIC and log-likelihood (available only for likelihood-based methods).
<code>opt.diagnosis</code>	Object returned by the optimisation routine, useful for checking convergence.
<code>df</code>	Number of parameters and residual degrees of freedom.
<code>deviance</code>	Sum of squared log-residuals, used as a deviance measure.

### Author(s)

Marius D. Pascariu

**See Also**

[availableLaws](#) for a list of all implemented models; [availableLF](#) for loss function details; [LifeTable](#) for life table construction; [ReadHMD](#) for downloading data from the Human Mortality Database.

**Examples**

```
# Example 1: Fitting the Makeham model -----
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
#  $hx = b \cdot \exp(b \cdot (x - m))$  (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](https://doi.org/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)

**Maintainer:** Marius D. Pascariu <[mpascariu@outlook.com](mailto:mpascariu@outlook.com)> ([ORCID](#)) [copyright holder]

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 Method for MortalityLaw*

---

**Description**

Plot Method for MortalityLaw

**Usage**

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

**Arguments**

x                      An object of class "MortalityLaw".  
...                     Further arguments passed to graphical methods, such as parameters (see [par](#)).

**Value**

A plot is generated as a side effect.

**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	<p>What type of data are you looking for? The following options might be available for some or all the countries and regions:</p> <ul style="list-style-type: none"> <li>• "births" – birth records;</li> <li>• "Dx_lexis" – deaths by Lexis triangles;</li> <li>• "Ex_lexis" – exposure-to-risk by Lexis triangles;</li> <li>• "population" – population size;</li> <li>• "Dx" – death counts;</li> <li>• "Ex" – exposure-to-risk;</li> <li>• "mx" – central death-rates;</li> <li>• "LT_f" – period life tables for females;</li> <li>• "LT_m" – period life tables for males;</li> <li>• "LT_t" – period life tables both sexes combined;</li> <li>• "e0" – period life expectancy at birth;</li> <li>• "Exc" – cohort exposures;</li> <li>• "mxc" – cohort death-rates;</li> <li>• "LT_fc" – cohort life tables for females;</li> <li>• "LT_mc" – cohort life tables for males;</li> <li>• "LT_tc" – cohort life tables both sexes combined;</li> <li>• "e0c" – cohort life expectancy at birth;</li> </ul>
regions	<p>Specify the region specific data you want to download by adding the AHMD region code/s. Options:</p> <ul style="list-style-type: none"> <li>• "ACT" – Australian Capital Territory;</li> <li>• "NSW" – New South Wales;</li> <li>• "NT" – Northern Territory;</li> <li>• "QLD" – Queensland;</li> <li>• "SA" – South Australia;</li> <li>• "TAS" – Tasmania;</li> <li>• "VIC" – Victoria;</li> <li>• "WA" – Western Australia;</li> <li>• NULL – if NULL data for all the regions are downloaded.</li> </ul>
interval	<p>Datasets are given in various age and time formats based on which the records are aggregated. Interval options:</p> <ul style="list-style-type: none"> <li>• "1x1" – by age and year;</li> <li>• "1x5" – by age and 5-year time interval;</li> <li>• "1x10" – by age and 10-year time interval;</li> <li>• "5x1" – by 5-year age group and year;</li> <li>• "5x5" – by 5-year age group and 5-year time interval;</li> <li>• "5x10" – by 5-year age group and 10-year time interval.</li> </ul>
save	<p>Do you want to save a copy of the dataset on your local machine? Logical. Default: FALSE.</p>
show	<p>Choose whether to display a progress bar. Logical. Default: TRUE.</p>

## 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    | <p>What type of data are you looking for? The following options are available:</p> <ul style="list-style-type: none"> <li>• "births" – birth records;</li> <li>• "Dx_lexis" – deaths by Lexis triangles;</li> <li>• "population" – population size;</li> <li>• "Dx" – death counts;</li> <li>• "Ex" – exposure-to-risk;</li> <li>• "mx" – central death-rates;</li> <li>• "LT_f" – period life tables for females;</li> <li>• "LT_m" – period life tables for males;</li> <li>• "LT_t" – period life tables both sexes combined;</li> <li>• "e0" – period life expectancy at birth;</li> </ul> |
| regions | <p>Specify the region specific data you want to download by adding the CHMD region code/s. Options:</p> <ul style="list-style-type: none"> <li>• "CAN" – Canada - Sum of Canadian provinces and territories;</li> <li>• "NFL" – Newfoundland &amp; Labrador;</li> <li>• "PEI" – Prince Edward Island;</li> <li>• "NSC" – Nova Scotia;</li> <li>• "NBR" – New Brunswick;</li> <li>• "QUE" – Quebec;</li> <li>• "ONT" – Ontario;</li> <li>• "MAN" – Manitoba;</li> <li>• "SAS" – Saskatchewan;</li> <li>• "ALB" – Alberta;</li> <li>• "BCO" – British Columbia;</li> </ul>                       |

	<ul style="list-style-type: none"> <li>• "NWT" – Northwest Territories &amp; Nunavut;</li> <li>• "YUK" – Yukon;</li> <li>• NULL – if NULL data for all the regions are downloaded.</li> </ul>
interval	<p>Datasets are given in various age and time formats based on which the records are aggregated. Interval options:</p> <ul style="list-style-type: none"> <li>• "1x1" – by age and year;</li> <li>• "1x5" – by age and 5-year time interval;</li> <li>• "1x10" – by age and 10-year time interval;</li> <li>• "5x1" – by 5-year age group and year;</li> <li>• "5x5" – by 5-year age group and 5-year time interval;</li> <li>• "5x10" – by 5-year age group and 10-year time interval.</li> </ul>
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, Université de Montréal, under the supervision of Professor Robert Bourbeau, in collaboration with demographers at the Max Planck Institute for Demographic Research (Rostock, Germany) and the Department of Demography, University of California at Berkeley. Nadine Ouellette, researcher at the Institut national d'études démographiques in Paris and member of the Mortality and Longevity research team at the Université de Montréal, 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	<p>What type of data are you looking for? The following options might be available for some or all the countries and regions:</p> <ul style="list-style-type: none"> <li>• "births" – birth records;</li> <li>• "Dx_lexis" – deaths by Lexis triangles;</li> <li>• "Ex_lexis" – exposure-to-risk by Lexis triangles;</li> <li>• "population" – population size;</li> <li>• "Dx" – death counts;</li> <li>• "Ex" – exposure-to-risk;</li> <li>• "mx" – central death-rates;</li> <li>• "LT_f" – period life tables for females;</li> <li>• "LT_m" – period life tables for males;</li> <li>• "LT_t" – period life tables both sexes combined;</li> <li>• "e0" – period life expectancy at birth;</li> <li>• "Exc" – cohort exposures;</li> <li>• "mxc" – cohort death-rates;</li> <li>• "LT_fc" – cohort life tables for females;</li> <li>• "LT_mc" – cohort life tables for males;</li> <li>• "LT_tc" – cohort life tables both sexes combined;</li> <li>• "e0c" – cohort life expectancy at birth;</li> </ul>
countries	<p>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;</p>
interval	<p>Datasets are given in various age and time formats based on which the records are aggregated. Interval options:</p> <ul style="list-style-type: none"> <li>• "1x1" – by age and year;</li> <li>• "1x5" – by age and 5-year time interval;</li> <li>• "1x10" – by age and 10-year time interval;</li> <li>• "5x1" – by 5-year age group and year;</li> <li>• "5x5" – by 5-year age group and 5-year time interval;</li> <li>• "5x10" –by 5-year age group and 10-year time interval.</li> </ul>
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	<p>What type of data are you looking for? The following options might be available for some or all the countries and regions:</p> <ul style="list-style-type: none"> <li>• "births" – birth records;</li> <li>• "Dx_lexis" – deaths by Lexis triangles;</li> <li>• "Ex_lexis" – exposure-to-risk by Lexis triangles;</li> <li>• "population" – population size;</li> <li>• "Dx" – death counts;</li> <li>• "Ex" – exposure-to-risk;</li> <li>• "mx" – central death-rates;</li> <li>• "LT_f" – period life tables for females;</li> <li>• "LT_m" – period life tables for males;</li> <li>• "LT_t" – period life tables both sexes combined;</li> <li>• "e0" – period life expectancy at birth;</li> <li>• "Exc" – cohort exposures;</li> <li>• "mxc" – cohort death-rates;</li> <li>• "LT_fc" – cohort life tables for females;</li> <li>• "LT_mc" – cohort life tables for males;</li> <li>• "LT_tc" – cohort life tables both sexes combined;</li> <li>• "e0c" – cohort life expectancy at birth;</li> </ul>
regions	<p>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",</p>

"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 aggregated. Interval options: <ul style="list-style-type: none"> <li>• "1x1" – by age and year;</li> <li>• "1x5" – by age and 5-year time interval;</li> <li>• "1x10" – by age and 10-year time interval;</li> <li>• "5x1" – by 5-year age group and year;</li> <li>• "5x5" – by 5-year age group and 5-year time interval;</li> <li>• "5x10" –by 5-year age group and 10-year time interval.</li> </ul>
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)**

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**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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