MortalityLaws User Manual

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Contents

1 Package structure

MortalityLaws in an **R** package which exploits the available optimization methods to provide tools for fitting and analyzing a wide range of complex mortality models. The package can be used to construct full and abridge life tables given various input indices and to download data from Human Mortality Database as well. The main functions in the package are: `MortalityLaw`, `LifeTable` and `ReadHMD`. The package provides also support functions like `availableLaws`, `availableLF` and `availableHMD` that return information about the mortality laws implemented in the package and loss functions used in optimization process and HMD data availability. Generic functions like `predict`, `plot`, `summary`, `fitted.values` are created for MortalityLaws objects. Small data set for testing purposes `ahmd` is saved in the package.
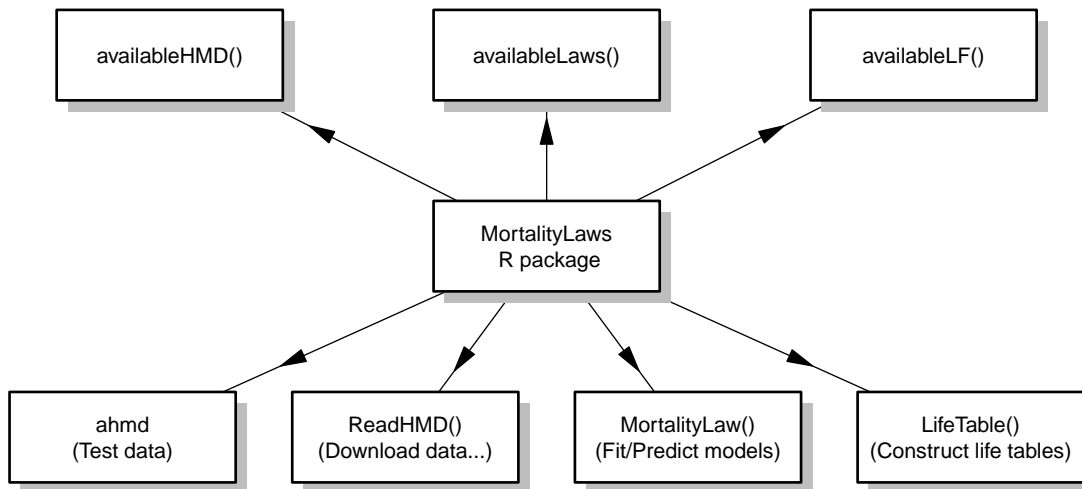

Figure 1: MortalityLaws R Package Structure

2 Downloading HMD Data

Download data form Human Mortality Database (2016) using the `ReadHMD` function:

```
library(MortalityLaws)
```

```
# Download HMD data - death counts
HMD_Dx <- ReadHMD(what = "Dx",
                  countries = "SWE",          # HMD country code for Sweden
                  interval  = "1x1",          # specify data format
                  username  = "user@email.com", # here add your HMD username
                  password  = "password",     # here add your password account
                  save = FALSE)               # save data outside R
```

Here we download all the registered death counts `Dx` in Sweden from 1751 until 2014. In the same way one can download the following records: birth records `births`, exposure-to-risk `Ex`, deaths by Lexis triangles `lexis`, population size `population`, death-rates `mx`, life tables for females

LT_f, life tables for males `LT_m`, life tables both sexes combined `LT_t`, life expectancy at birth `e0`, cohort death-rates `mxc` and cohort exposures `Exc` for over 39 countries and regions in different formats.

3   Model fitting and diagnosis

Once we have data from HMD or other sources we can start analyzing it. For example, let's fit a (Heligman and Pollard 1980) model under a Poisson setting which is already implemented as one of the standard models in the package. We have to use the `MortalityLaw` function in this regard.

```r
year     <- 1950
ages     <- 0:100
deaths   <- ahmd$Dx[paste(ages), paste(year)]
exposure <- ahmd$Ex[paste(ages), paste(year)]

fit <- MortalityLaw(x   = ages,
                    Dx  = deaths,    # vector with death counts
                    Ex  = exposure,  # vector containing exposures
                    law = "HP",
                    opt.method = "LF2")
```

```r
# inspect the output object
ls(fit)
## [1] "coefficients"    "fitted.values"   "goodness.of.fit" "info"
## [5] "input"           "opt.diagnosis"   "residuals"
```

A summary can be obtained using the `summary` function:

```r
summary(fit)
## Heligman-Pollard:
## q[x]/p[x] = A^[(x + B)^C] + D exp[-E log(x/F)^2] + G H^x
##
## Call: MortalityLaw(x = ages, Dx = deaths, Ex = exposure, law = "HP",
##     opt.method = "LF2")
##
## Deviance Residuals:
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## -0.03121 -0.00021  0.00000  0.00089  0.00026  0.04616
##
## Fitted values: mx
## Coefficients:
##        A        B        C        D        E       F_        G        H
##  0.00223  0.01461  0.12292  0.00091  2.75651 29.00797  0.00002  1.11411
```

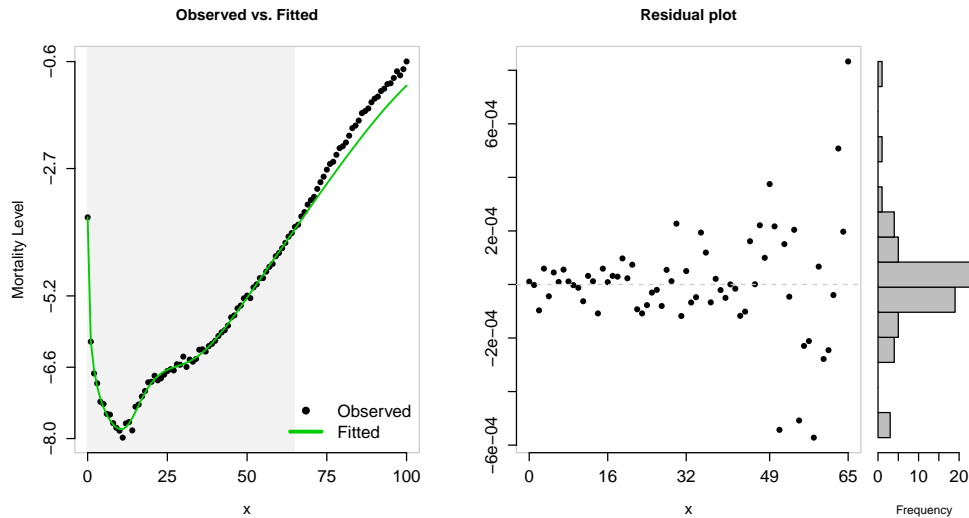The standard plot helps us to investigate visually the goodness of fit.

```
plot(fit)
```
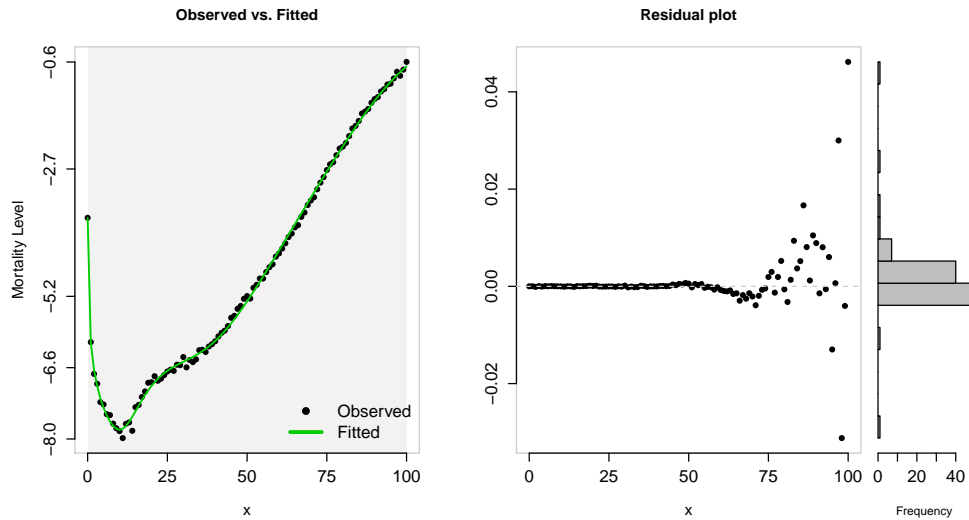

A model can be fitted using a subset of the data only by specifying in `fit.this.x` age range to be covered:

```
fit.subset <- MortalityLaw(x   = ages,
                           Dx  = deaths,
                           Ex  = exposure,
                           law = "HP",
                           opt.method = "LF2",
                           fit.this.x = 0:65)
plot(fit.subset)
```


The gray area on the plot showing the fitted value indicates the age range used in fitting the model.

4 Mortality laws in the package

In **R** one can check the availability of the implemented models using `availableLaws`:

```
availableLaws()
```

See table 1.

5 Loss function in the package

A parametric model is fitted by optimizing a loss function e.g. a likelihood function or a function that minimizes errors. In `MortalityLaws` 8 such functions are implemented and can be used to better capture different portions of a mortality curve. Check `availableLF` for more details.

```
availableLF()
##
## Loss functions available in the package:
##
##   LOSS FUNCTION                                CODE
##   L = -[Dx * log(mu) - mu*Ex]                  poissonL
##   L = -[Dx * log(1 - exp(-mu)) - (Ex - Dx)*mu]  binomialL
##   L =  [1 - mu/ov]^2                           LF1
##   L =  log[mu/ov]^2                            LF2
##   L =  [(ov - mu)^2]/ov                        LF3
##   L =  [ov - mu]^2                             LF4
##   L =  [ov - mu] * log[ov/mu]                  LF5
##   L =  abs(ov - mu)                            LF6
##
## LEGEND:
## Dx: Death counts
## Ex: Population exposed to risk
## mu: Estimated value
## ov: Observed value
```

6 Custom mortality laws

Now let's fit a mortality law that is not defined in the package, say a reparametrize version of Gompertz in terms of modal age at death (Missov et al. 2015),

$$\mu_x = \beta e^{\beta(x-M)}. \tag{1}$$

We have to define a function containing the desired hazard function and then using the `custom.law` argument it can be used in the `MortalityLaw` function.

```r
# Here we define a function for our new model and provide start parameters
my_gompertz <- function(x, par = c(b = 0.13, M = 45)){
  hx  <- with(as.list(par), b*exp(b*(x - M)) )
  # return everything inside this function
  return(as.list(environment()))
}
```

```r
# Select data
year     <- 1950
ages     <- 45:85
deaths   <- ahmd$Dx[paste(ages), paste(year)]
exposure <- ahmd$Ex[paste(ages), paste(year)]
```

```r
# Use 'custom.law' argument to instruct the MortalityLaw function how to behave
my_model <- MortalityLaw(x = ages,
                         Dx = deaths,
                         Ex = exposure,
                         custom.law = my_gompertz)
```

```r
summary(my_model)
## CUSTOM MORTALITY LAW
##
## Call: MortalityLaw(x = ages, Dx = deaths, Ex = exposure, custom.law = my_gompertz)
##
## Deviance Residuals:
##     Min.  1st Qu.   Median      Mean  3rd Qu.      Max.
## -0.00290 -0.00079 -0.00008  0.00030  0.00068  0.00758
##
## Fitted values: mx
## Coefficients:
##        b        M
##  0.10204 79.82816
##
## Goodness of fit:
## logLik    AIC     BIC
##  13.62 -23.24 -19.81
```

```r
plot(my_model)
```

Observed vs. Fitted — **Residual plot**
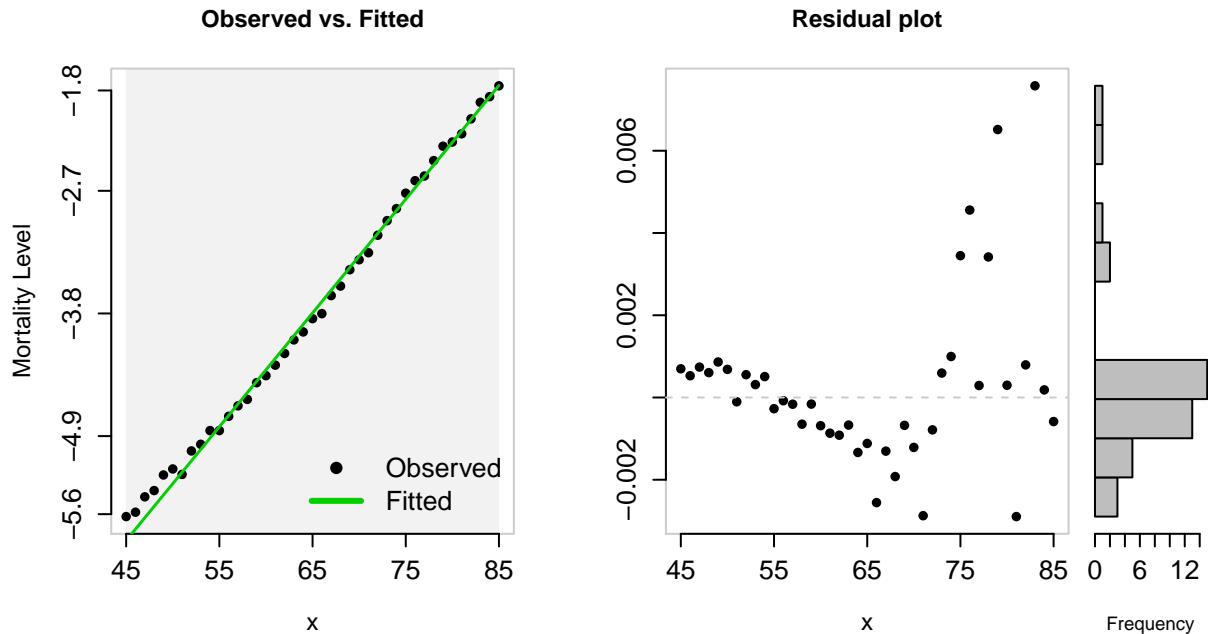
7 Full life tables

Using `LifeTable` function one can build full or abridge 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 are specified, the other can be ignored.

```r
# Life table for year of 1900
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
##
## Full Life Table
##
## Number of life tables: 1
## Dimension: 111 x 10
## Age intervals: [0,1) [1,2) [2,3) ...   ... [108,109) [109,110) [110,+)
##
```

```
##       x.int    x      mx      qx   ax    lx     dx    Lx       Tx      ex
##       [0,1)    0 0.1513 0.1404 0.49 1e+05 14042 92802 4808384 51.62
##       [1,2)    1 0.0479 0.0468  0.5 85958  4023 83931 4715582 56.16
##       [2,3)    2 0.0191 0.0189  0.5 81935  1552 81157 4631651 57.07
##       [3,4)    3  0.013 0.0129  0.5 80383  1041 79861 4550494 56.98
##       [4,5)    4 0.0094 0.0093  0.5 79342   740 78971 4470633 56.61
##       [5,6)    5 0.0067 0.0067  0.5 78602   523 78340 4391661 56.06
##        <NA> ...    ...    ...  ...   ...   ...   ...     ...    ...
##   [108,109) 108      0      1 0.15     0     0     0       0      0
##   [109,110) 109      0      1 0.15     0     0     0       0      0
##     [110,+) 110      0      1 0.15     0     0     0       0      0
```

```
ls(LT1)
## [1] "call"         "lt"          "process_date"
```

8 Abridge life tables

```
# Example
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)

lt <- LifeTable(x, mx = mx, sex = "female")
```

```
lt
##
## Abridge Life Table
##
## Number of life tables: 1
## Dimension: 24 x 10
## Age intervals: [0,1) [1,5) [5,10) ...   ... [100,105) [105,110) [110,+)
##
##       x.int    x      mx      qx   ax    lx    dx     Lx       Tx      ex
##       [0,1)    0   0.053 0.0516  0.2 1e+05  5162  95878 6485467 65.54
##       [1,5)    1   0.005 0.0198 1.44 94838  1878 374547 6389590 67.86
##      [5,10)    5   0.001  0.005  2.5 92960   464 463640 6015042 64.87
##    [10,15)    10  0.0012  0.006  2.5 92496   553 461098 5551402  60.2
##    [15,20)    15  0.0018  0.009  2.5 91943   824 457653 5090304 55.61
##    [20,25)    20   0.002   0.01  2.5 91119   907 453326 4632651  51.1
##        <NA> ...     ...    ...  ...   ...   ...    ...     ...    ...
##  [100,105) 100    0.39 0.8577 1.73   407   349    896    1014   3.55
##  [105,110) 105   0.478 0.9084 1.59    58    53    110     119   2.88
##    [110,+) 110   0.551      1 1.59     5     5      8       8   1.59
```

Refrences

Heligman, Larry, and John H Pollard. 1980. "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* 107 (01). Cambridge Univ Press: 49–80.

Missov, Trifon I, Adam Lenart, Laszlo Nemeth, Vladimir Canudas-Romo, and James W Vaupel. 2015. "The Gompertz Force of Mortality in Terms of the Modal Age at Death." *Demographic Research* 32: 1031–48.

University of California Berkeley, USA, and Max Planck Institute for Demographic Research, Germany. 2016. "Human Mortality Database." http://www.mortality.org/.

Table 1: Parametric functions build in the MortalityLaws package

Mortality laws	Predictor	Code
Gompertz	$\mu(x) = Ae^{Bx}$	gompertz
Gompertz	$\mu(x) = \frac{1}{\sigma}exp\left\{\frac{x-M}{\sigma}\right\}$	gompertz0
Inverse-Gompertz	$\mu(x) = \frac{1}{\sigma}exp\left\{\frac{x-M}{\sigma}\right\}/\left(exp\left\{e^{\frac{-(x-M)}{\sigma}}\right\} - 1\right)$	invgompertz
Makeham	$\mu(x) = Ae^{Bx} + C$	makeham
Makeham	$\mu(x) = \frac{1}{\sigma}exp\left\{\frac{x-M}{\sigma}\right\} + C$	makeham0
Opperman	$\mu(x) = \frac{A}{\sqrt{x}} + B + C\sqrt[3]{x}$	opperman
Thiele	$\mu(x) = A_1e^{-B_1x} + A_2e^{-\frac{1}{2}B_2(x-C)^2} + A_3e^{B_3x}$	thiele
Wittstein & Bumstead	$q(x) = \frac{1}{B}A^{-(Bx)^N} + A^{-(M-x)^N}$	wittstein
Perks	$\mu(x) = (A + BC^x)/(BC^{-x} + 1 + DC^x)$	perks
Weibull	$\mu(x) = \frac{1}{\sigma}\left(\frac{x}{M}\right)^{\frac{M}{\sigma}-1}$	weibull
Inverse-Weibull	$\mu(x) = \frac{1}{\sigma}\left(\frac{x}{M}\right)^{-\frac{M}{\sigma}-1}/\left(exp\left\{\left(\frac{x}{M}\right)^{-\frac{M}{\sigma}}\right\} - 1\right)$	invweibull
Van der Maen	$\mu(x) = A + Bx + Cx^2 + I/(N-x)$	vandermaen
Van der Maen	$\mu(x) = A + Bx + I/(N-x)$	vandermaen2
Quadratic	$\mu(x) = A + Bx + Cx^2$	quadratic
Beard	$\mu(x) = Ae^{Bx}/(1 + KAe^{Bx})$	beard
Makeham-Beard	$\mu(x) = Ae^{Bx}/(1 + KAe^{Bx}) + C$	makehambeard
Siler	$\mu(x) = A_1e^{-B_1x} + A_2 + A_3e^{B_3x}$	siler
Heligman - Pollard	$q(x)/p(x) = A^{(x+B)^C} + De^{-E(\ln x\ -\ln F\ )^2} + GH^x$	HP
Heligman - Pollard	$q(x) = A^{(x+B)^C} + De^{-E(\ln x\ -\ln F\ )^2} + \frac{GH^x}{1+GH^x}$	HP2
Heligman - Pollard	$q(x) = A^{(x+B)^C} + De^{-E(\ln x\ -\ln F\ )^2} + \frac{GH^x}{1+KGH^x}$	HP3
Heligman - Pollard	$q(x) = A^{(x+B)^C} + De^{-E(\ln x\ -\ln F\ )^2} + \frac{GH^{x^K}}{1+GH^{x^K}}$	HP3
Rogers-Planck	$q(x) = A_0 + A_1e^{-Ax} + A_2e^{\left\{B(x-U)-e^{-C(x-U)}\right\}} + A_3e^{Dx}$	rogersplanck
Martinelle	$\mu(x) = (Ae^{Bx} + C)/(1 + De^{Bx}) + Ke^{Bx}$	martinelle
Carriere	$S(x) = \psi_1 S_1(x) +\ \psi_2 S_2(x) +\ \psi_3 S_3(x)$	carriere1
Carriere	$S(x) = \psi_1 S_1(x) +\ \psi_4 S_4(x) +\ \psi_3 S_3(x)$	carriere2
Kostaki	$q(x)/p(x) = A^{(x+B)^C} + De^{-E_i(\ln x\ -\ln F\ )^2} + GH^x$	kostaki
Kannisto	$\mu(x) = Ae^{Bx}/(1 + Ae^{Bx}) + C$	kannisto