

# Package ‘RkMetrics’

July 29, 2017

**Title** Hybrid Mortality Estimation

**Version** 1.3

**Date** 2017-07-25

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**Description** Hybrid Mortality Modelling (HMM) provides a framework in which mortality around “the accident hump” and at very old ages can be modelled under a single model. The graphics’ codes necessary for visualization of the models’ output are included here. Specifically, the graphics are based on the assumption that, the mortality rates can be expressed as a function of the area under the curve between the crude mortality rates plots and the tangential transform of the force of mortality.

**Depends** R (>= 3.4.0)

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2017-07-29 12:43:55 UTC

## R topics documented:

iplot . . . . .	2
lplot . . . . .	2
mmplot . . . . .	3
Mortality . . . . .	4
pccopula . . . . .	5
pgcopula . . . . .	5
vplot . . . . .	6
<b>Index</b>	<b>7</b>

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 iplot

*A Plotting Function*


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**Description**

Produces a plot of the area-under-the-curve for the mortality data, but lplot() inverted

**Usage**

```
iplot(n, x, add = F)
```

**Arguments**

n	the length of the vector Defaults to TRUE.
x	the vector argument.
add	whether to add lines. Default is FALSE

**Examples**

```
m1 <- Mortality$D.Male[which(Mortality$Year == 2008)]
m2 <- Mortality$E.Male[which(Mortality$Year == 2008)]
male.1 <- m1/m2
male.2 <- log(male.1[!is.na(male.1)])
iplot(1:length(male.2),male.2)

iplot(1:length(male.2),male.2,add=TRUE)
```

---

 lplot

*A Plotting Function*


---

**Description**

Produces a plot of the area-under-the-curve for the mortality data

**Usage**

```
lplot(n, x, add = F)
```

**Arguments**

n	the length of the vector Defaults to TRUE.
x	the vector argument.
add	whether to add lines. Default is FALSE

**Examples**

```

m1 <- Mortality$D.Male[which(Mortality$Year == 2008)]
m2 <- Mortality$E.Male[which(Mortality$Year == 2008)]
male.1 <- m1/m2
male.2 <- log(male.1[!is.na(male.1)])
lplot(1:length(male.2),male.2)

lplot(1:length(male.2),male.2,add=TRUE)

```

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mmpplot

*A Plotting Function*


---

**Description**

Produces a plot of the difference between the area-under-the-curve for the mortality data and the extended mortality boundaries

**Usage**

```
mmpplot(n, x, young, old)
```

**Arguments**

n	the length of the vector Defaults to TRUE.
x	the vector argument.
young	the age at which the accident hump begins. Must be entered
old	age at which, either mortality experience between males and females converge, or rapid acceleration of mortality. This is typically over 80 years.

**Examples**

```

#Examples
m1 <- Mortality$D.Male[which(Mortality$Year == 2008)]
m2 <- Mortality$E.Male[which(Mortality$Year == 2008)]
male.1 <- m1/m2
male.2 <- log(male.1[!is.na(male.1)])
lplot(1:length(male.2),male.2)

mmpplot(1:length(male.2),male.2,young=17,old=80)

```

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Mortality

*Switzerland Mortality Data*

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### **Description**

Exposed to Risk and number of deaths data.

### **Usage**

Mortality

### **Format**

A data frame with 6 columns corresponding to:

**Year** Corresponding year of data collected

**Age** Age of the individual

**E.Male** Male Exposed-to-Risk Population

**E.Female** Female Exposed-to-Risk Population

**D.Male** Number of male death counts, for the given year and age

**D.Female** Number of female death counts, for the given year and age

### **Details**

Mortality data for both Males and Females in Switzerland, from 1981 to 2014.

These data are freely available at the Human Mortality Database

### **Source**

<http://www.mortality.org/cgi-bin/hmd/country.php?cntr=CHE&level=1>

### **References**

Glei, D. and Andreeva, M. (2016). About mortality data for switzerland.

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pccopula

*A Plotting Function*

---

**Description**

Produces a plot of a copula, which can be used to assess the dependency between two sexes bounded by the actual and the expanded mortality estimates

**Usage**

```
pccopula(theta, pl = 1, z)
```

**Arguments**

theta	gives the order.
pl	gives the association.
z	the length of the z axis Defaults to 10.

**Examples**

```
#Examples  
  
pccopula(theta=3,pl=.5,z=10)
```

---

pgcopula

*A Plotting Function*

---

**Description**

Similar to pccopula(), but suitable when the dependence is stronger at the older ages

**Usage**

```
pgcopula(theta, pl = 1, z)
```

**Arguments**

theta	gives the order.
pl	gives the association, with a correction for the direction of dependence
z	the length of the z axis Defaults to 10.

**Examples**

```
#Examples  
pgcopula(theta=1.3,pl=2,z=10)
```

---

vplot

*A Plotting Function*

---

**Description**

Produces a similar plot as lplot(), only a transposition of ages is made

**Usage**

```
vplot(n, x, add = F)
```

**Arguments**

n	the length of the vector Defaults to TRUE.
x	the vector argument.
add	whether to add lines. Default is FALSE

**Examples**

```
m1 <- Mortality$D.Male[which(Mortality$Year == 2008)]  
m2 <- Mortality$E.Male[which(Mortality$Year == 2008)]  
male.1 <- m1/m2  
male.2 <- log(male.1[!is.na(male.1)])  
vplot(1:length(male.2),male.2)
```

# Index

- \*Topic **datasets**
  - Mortality, 4
- \*Topic **iplot**
  - iplot, 2
- \*Topic **lplot**
  - lplot, 2
- \*Topic **mmpplot**
  - mmpplot, 3
- \*Topic **pccopula()**
  - pccopula, 5
- \*Topic **pgcopula()**
  - pgcopula, 5
- \*Topic **vplot**
  - vplot, 6

iplot, 2

lplot, 2

mmpplot, 3  
Mortality, 4

pccopula, 5  
pgcopula, 5

vplot, 6