Package ‘fmsb’

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Author Minato Nakazawa <minatonakazawa@gmail.com>
Maintainer Minato Nakazawa <minatonakazawa@gmail.com>
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Suggests Epi, vcd
Description Several utility functions for the book entitled "Practices of Medical and Health Data Analysis using R" (Pearson Education Japan, 2007) with Japanese demographic data and some demographic analysis related functions.
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### Description

Caretaker ratio. Defined as the ratio of the aged population who may need care to caretaking females population.

### Usage

CaretakerRatio(PM, PF)
Arguments

**PM**  The integer vector to give age-specific population from age 0 to more than 80 for males.

**PF**  The integer vector to give age-specific population from age 0 to more than 80 for females.

Value

**CR**  Caretaker Ratio.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


Examples

```r
# Caretaker Ratio in Japan in 2015. The value 81.72 is much higher than
# 46 observed in UK in 1990.
CaretakerRatio(PM=Jpop$M2015, PF=Jpop$F2015)
```

Description

Implementing Coale and McNeil’s model (1972) for the age-specific probability of first marriage and fitting the model to actual data.

Usage

```r
CM(scale=0.8, a0=18, k=2)
fitCM(initialpar=c(0.8, 18, 2), data, ages=10:60, mode=1, Method="Nelder-Mead", ...)
```
Arguments

scale        The parameter C of the Coale-McNeil model, the scale parameter for total nuptiality. Almost same as 1-(probability of never marring for whole life)

a0          The parameter a0 of the Coale-McNeil model, the age of the beginning of first marriage. The beginning means about 1% of the population having ever married.

k           The parameter k of the Coale-McNeil model, how fast the population marry after a0.

initialpar  Initial value for the parameters to be estimated. If not given, c(0.8, 18, 2) is used.

data         Actual vector of the age-specific probability of first marriage when the mode is 1, otherwise the proportion ever married by each age.

ages        The age ranges for the data. It must be within the range from 10 to 60. Default is 10:60. It must have the same lengths as data.

mode        The mode of fitting, 1 means fitting for the probability of first marriage, otherwise fitting for the proportion ever married. Default is 1.

Method      The method to be used in optim() function. Default is "Nelder-Mead".

...         Other options to be passed to optim().

Value

CM() returns model schedule of nuptiality for ages from 10 to 60 as a list, composed of g (the numeric vector for the probability of first marriage happening for each age), G (the numeric vector for the proportion ever married by each age), mu (mean age of first marriage among total population), and sigma (standard deviation of the ages of first marriage). fitCM() returns the numeric vector of fitted parameters C, a0 and k, RMSE for those values, and the flag of convergence.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


See Also

CT

Examples

# The data of Japanese population census 2010 for the whole country
# The proportion of ever married females for ages from 15 to 60.
# https://www.e-stat.go.jp/SG1/estat/List.do?bid=00001034991&cycode=0
Ages <- 15:60
CronbachAlpha

 EverMarriedFemales <- c(0.003081039, 0.003203058, 0.006502558, 0.014261608, 0.028378604, 0.048903318, 0.07596101, 0.110311095, 0.153365573, 0.2090648, 0.273819118, 0.342672073, 0.41259517, 0.47979489, 0.536291775, 0.589919881, 0.631937609, 0.663719195, 0.691411757, 0.71775138, 0.740807817, 0.760155848, 0.775400475, 0.788445244, 0.799522713, 0.81108241, 0.821591503, 0.830695486, 0.840776283, 0.846773585, 0.85921777, 0.867991763, 0.876908992, 0.886388747, 0.894302114, 0.902385961, 0.908329207, 0.914662575, 0.920327092, 0.925013244, 0.929551158, 0.933150578, 0.935851652, 0.938421122, 0.940089719, 0.943223398)

 res <- fitCM(initialpar=c(0.8, 18, 2), data=EverMarriedFemales, ages=Ages, mode=2)
 print(res)
 plot(Ages, EverMarriedFemales, main="Proportion ever married by each age
 for 2010 Japanese females")
 fitted <- CM(res[1], res[2], res[3])
 lines(Ages, fitted$G[6:51], col="red")
 NoteForm <- "C=%3.1f, a0=%3.1f, k=%3.1f
 mu=%3.1f, sd=%3.1f"
 text(40, 0.2, sprintf(NoteForm, res[1], res[2], res[3], fitted$mu, fitted$sigma))
 # mean age of first marriage happening
 print(sum(Ages*fitted$g[Ages-9]/sum(fitted$g[Ages-9])))

---

CronbachAlpha

**Calculate Cronbach's alpha coefficient.**

**Description**

Calculate Cronbach's alpha coefficient from a matrix or data.frame with more than 2 columns.

**Usage**

CronbachAlpha(X)

**Arguments**

- **X**
  
A matrix or data.frame with more than 2 columns.

**Value**

Single numeric value of Cronbach's alpha.

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

**References**

Examples

QUEST <- data.frame(
  Q1=c(1, 5, 2, 3, 4, 2, 3, 4, 3, 2),
  Q2=c(2, 4, 1, 2, 4, 1, 2, 5, 2, 1),
  Q3=c(2, 5, 1, 3, 3, 2, 2, 4, 2, 2))
CronbachAlpha(QUEST)

CT
Coale and Trussell’s model marital fertility and its fitting

Description
Implementing Coale and Trussell’s model of age-specific marital fertility rates and fitting the model to actual ASMFR.

Usage

CT(M=1, m=0)
fitCT(initialpar=c(1.0, 1.0), data, Method="Nelder-Mead", ...)

Arguments

M
The parameter M of the CT model, the scale (peak height) parameter of fertility
m
The parameter m of the CT model, the strength of downward discordance from natural fertility with aging
initialpar
Initial value for the parameters to be estimated. If not given, c(1.0, 1.0) is used.
data
Actual vector of ASMFR (which must be given for from age 12 to age 49 for each age) to be used to obtain the best-fit parameters of the CT’s model.
Method
The method to be used in optim() function. Default is "Nelder-Mead".
...
Other options to be passed to optim().

Value

CT() returns model ASMFR for ages from 12 to 49. fitCT() returns the numeric vector of fitted parameters M and m, RMSE for those values, and the flag of convergence.

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References

Denny

See Also
Jfert

Examples
ASMFR <- c(0, 0, 0, Jfert$ASMFR2000[1:35])  # Jfert's ASMFR should be rearranged to 12:49
res <- fitCT(ASMFR)
FLAG <- res[4]
while (FLAG>0) {
  res <- fitCT(res[1:2], ASMFR)
  FLAG <- res[4]
}
print(res)

Denny

Denny's model mortality for lx and its fitting

Description
Implementing Denny's model mortality function of lx and fitting the model to actual lx of given lifetable.

Usage
Denny(a, b, c, t)
fittedDenny(initialpar=rep(0.1, 3), data, mode=3, Method="Nelder-Mead", ...)

Arguments
a
  The parameter a of the Denny model, l(t)=1/(1+a*(t/(105-t))^3+b*sqrt(exp(t/(105-t))-1)+c*(1-exp(-2*t))).
b
  The parameter b of the Denny model, l(t)=1/(1+a*(t/(105-t))^3+b*sqrt(exp(t/(105-t))-1)+c*(1-exp(-2*t))).
c
  The parameter c of the Denny model, l(t)=1/(1+a*(t/(105-t))^3+b*sqrt(exp(t/(105-t))-1)+c*(1-exp(-2*t))).
t
  Age (vector OK) in years. The t must be less than 105, otherwise the value by Denny() become 0.
initialpar
  Initial value for the parameters to be estimated. If not given, rep(0.1, 3) is used.
data
  Actual vector of qx in the lifetable to be used to obtain the best-fit parameters of the Denny's model. If the ages for qx are equal or elder than 105 years old, those will be ignored in fitting.
mode
  Which of lifetable functions should be used to calculate the RMSE: 1 qx, 2 dx, otherwise lx. Default is 3.
Method
  The method to be used in optim() function. Default is "Nelder-Mead".
  Other options to be passed to optim().
Value

Denny() returns model lx for the same length with t. fitDenny() returns the numeric vector of fitted parameters a, b, and c, RMSE for those values, and the flag of convergence.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


See Also

Jlife

Examples

res <- fitDenny(, qxtolx(Jlife$qx2005M))
FLAG <- res[5]
while (FLAG>0) {
  res <- fitDenny(res[1:3], qxtolx(Jlife$qx2005M))
  FLAG <- res[5]
}
print(res)

geary.test

Geary’s test for normality about kurtosis.

Description

Geary’s test for normality. Null hypothesis is that the data obeys to normal distribution.

Usage

geary.test(X)

Arguments

X A numeric vector.

Value

statistic Geary’s test statistic G
p.value The significant probability of the null-hypothesis testing.
GompertzMakeham

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

Examples

gerry.test(rnorm(100))
gerry.test(20:50)

GompertzMakeham

Gompertz-Makeham’s model mortality for \( u(x) \) and its fitting

Description
Implementing Gompertz-Makeham’s model mortality function of the force of mortality \( u(x) \) with conversion into \( qx \) and fitting the model to actual \( qx \) of given lifetable.

Usage

GompertzMakeham(A, B, C, t)
fitGM(initialpar=c(0.01, 0.0003, 0.07), data, mode=1, Method="Nelder-Mead", ...)

Arguments

A
The parameter A of the Gompertz-Makeham model \( u(t) = A \times \exp(B \times t) + C \).

B
The parameter B of the Gompertz-Makeham model \( u(t) = A \times \exp(B \times t) + C \).

C
The parameter C of the Gompertz-Makeham model \( u(t) = A \times \exp(B \times t) + C \).

t
Age (vector OK) in years

initialpar
Initial value for the parameters to be estimated. If not given, c(0.01, 0.0003, 0.07) is used.

data
Actual vector of \( qx \) in the lifetable to be used to obtain the best-fit parameters of the Gompertz-Makeham model.

mode
Which of lifetable functions should be used to calculate the RMSE, which is to be minimized in optim() function: 1 \( qx \), 2 \( dx \), otherwise \( lx \). Default is 1.

Method
The method to be used in optim() function. Default is "Nelder-Mead".

...
Other options to be passed to optim().

Value
GompertzMakeham() returns model \( qx \) for the same length with t, where \( u(x) \) is internally converted into \( qx \). fitGM() returns the numeric vector of fitted parameters of A, B and C, RMSE for those values, and the flag of convergence.

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/
See Also

Jlife

Examples

```r
res <- fitGM(Jlife$qx2005M)
FLAG <- res[5]
while (FLAG>0) {
  res <- fitGM(res[1:3], Jlife$qx2005M)
  FLAG <- res[5]
}
print(res)
```

gstem

`gstem` draws the stem and leaf plot in a graphic device.

Description

Capture the output of `stem()` function and plot them into graphic devices. However, the result of setting scale parameter as 2 may be controversial.

Usage

`gstem(X, scale)`

Arguments

- `X` A numeric vector.
- `scale` Parameter to control plot length of graph. Default is 1.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

Examples

```r
x <- rnorm(100, 10, 1)
stem(x)
gstem(x)
gstem(x, 2)
```
**H27MPJ**  
**Tentative model population of Japan in Heisei 27 (2015)**

### Description

The data gives the age-class specific model population of Japan in smoothed Heisei 27 (2015) to calculate directly adjusted mortality rate.

### Usage

H27MPJ

### Format

A named vector containing 21 observations, where names show age-classes.

### Source

https://www.mhlw.go.jp/content/12601000/000638712.pdf

### References


---

**Hadwiger**  
**Hadwiger's model fertility and its fitting**

### Description

Implementing Hadwiger's model of age-specific fertility rates and fitting the model to actual ASFR.

### Usage

Hadwiger(a=3.4, b=2.5, c=22.2)  
fitHad(initialpar=c(3.4, 2.5, 22.2), data, Method="Nelder-Mead", ...)

### Arguments

- **a**
  
The parameter a of the Hadwiger model, \( ASFR(x) = a \cdot b / c \cdot (c/x)^{1.5} \cdot \exp(-b^{2}(c/x+x/c-2)) \) for age x from 15 to 54.

- **b**
  
The parameter b of the Hadwiger model, \( ASFR(x) = a \cdot b / c \cdot (c/x)^{1.5} \cdot \exp(-b^{2}(c/x+x/c-2)) \) for age x from 15 to 54.

- **c**
  
The parameter c of the Hadwiger model, \( ASFR(x) = a \cdot b / c \cdot (c/x)^{1.5} \cdot \exp(-b^{2}(c/x+x/c-2)) \) for age x from 15 to 54.
IndexOfDissimilarity

initialpar
  Initial value for the parameters to be estimated. If not given, \(c(3.4, 2.5, 22.2)\) is used.

data
  Actual vector of ASFR (which must be given for from ages from 15 to 54 for each age) to be used to obtain the best-fit parameters of the Hadwiger’s model.

Method
  The method to be used in optim() function. Default is "Nelder-Mead".

... Other options to be passed to optim().

Value

Hadwiger() returns model ASFR for ages from 15 to 54. fitHad() returns the numeric vector of fitted parameters a, b and c, RMSE for those values, and the flag of convergence.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


See Also

Jfert

Examples

```r
res <- fitHad(Jfert$ASFR2000)
FLAG <- res[5]
while (FLAG>0) {
  res <- fitHad(res[1:3], Jfert$ASFR2000)
  FLAG <- res[5]
}
print(res)
```

IndexOfDissimilarity

**IndexOfDissimilarity (ID)**

Description

Index of dissimilarity between the 2 age-distributions.

Usage

```
IndexOfDissimilarity(X, Y)
```
Arguments

X A vector of age-specific standard populations (or percentage) for each age.
Y A vector of age-specific target populations (or percentage) for each age.

Value

ID Index of dissimilarity, which is a half of sum of absolute differences of percentages for each age, where NA is automatically treated as 0.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


Examples

# Dissimilarities of Japanese population structure were increasing
# from 1960-1980 (0.132) to 1980-2000 (0.156).

IRCI Calculate a incidence rate with confidence interval

Description

Calculate a incidence rate with confidence interval.

Usage

IRCI(a, PT, conf.level=0.9)

Arguments

a Number of cases
PT Person-years of observed population at risk
conf.level Probability for confidence intervals. Default is 0.9.
**Value**

| IR  | Point estimate of incidence rate. |
| IRL | Lower limit of confidence interval |
| IRU | Upper limit of confidence interval |

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

**References**


**Examples**

IRCIPois(8, 85000)

---

**IRCIPois**  
*Calculate incidence rate with its confidence intervals by exact method*

**Description**

Calculate incidence rate with its confidence intervals by exact method using Poisson distribution.

**Usage**

IRCIPois(a, PT, conf.level=0.9)

**Arguments**

- **a**: Number of cases
- **PT**: Person-years of observed population at risk
- **conf.level**: Probability for confidence intervals. Default is 0.9.

**Value**

| IR  | Point estimate of incidence rate. |
| IRL | Lower limit of confidence interval |
| IRU | Upper limit of confidence interval |

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

**References**

Examples

IRCIpois(8, 85000)

JASM  Japanese mortality data

Description

The data gives the sex and age-class (by five) specific numbers of death in Showa 60 (S60 = 1985), Heisei 2 (H02 = 1990), Heisei 7 (H07 = 1995), Heisei 12 (H12 = 2000), Heisei 17 (H17 = 2005), Heisei 22 (H22 = 2010) and Heisei 27 (H27 = 2015), and corresponding populations.

Usage

JASM

Format

A data frame with 18 observations on 30 variables.

| [, 1] AGECLASS | Factor w/18 levels | Age class (years old) |
| [ , 2] S60MODEL | numeric | Model population in 1985 |
| [ , 3] S60M | numeric | Number of males’ death by age classes in 1985 |
| [ , 4] H02M | numeric | Number of males’ death by age classes in 1990 |
| [ , 5] H07M | numeric | Number of males’ death by age classes in 1995 |
| [ , 6] H12M | numeric | Number of males’ death by age classes in 2000 |
| [ , 7] H17M | numeric | Number of males’ death by age classes in 2005 |
| [ , 8] H22M | numeric | Number of males’ death by age classes in 2010 |
| [ , 9] S60F | numeric | Number of females’ death by age classes in 1985 |
| [ ,10] H02F | numeric | Number of females’ death by age classes in 1990 |
| [ ,11] H07F | numeric | Number of females’ death by age classes in 1995 |
| [ ,12] H12F | numeric | Number of females’ death by age classes in 2000 |
| [ ,13] H17F | numeric | Number of females’ death by age classes in 2005 |
| [ ,14] H22F | numeric | Number of females’ death by age classes in 2010 |
| [ ,15] S60MP | numeric | Number of males’ population by age classes in 1985 |
| [ ,16] H02MP | numeric | Number of males’ population by age classes in 1990 |
| [ ,17] H07MP | numeric | Number of males’ population by age classes in 1995 |
| [ ,18] H12MP | numeric | Number of males’ population by age classes in 2000 |
| [ ,19] H17MP | numeric | Number of males’ population by age classes in 2005 |
| [ ,20] H22MP | numeric | Number of males’ population by age classes in 2010 |
| [ ,21] S60FP | numeric | Number of females’ population by age classes in 1985 |
| [ ,22] H02FP | numeric | Number of females’ population by age classes in 1990 |
| [ ,23] H07FP | numeric | Number of females’ population by age classes in 1995 |
| [ ,24] H12FP | numeric | Number of females’ population by age classes in 2000 |
Japanese mortality data by sex and age-class (by five) given as national official vital statistics from 1985 to 2015, every 5 years.

- AGECLASS: Labels for age classes. [0-4] to [85-].
- S60MODEL: Age class specific model population of Japan in 1985.
- S60M-H27M: Age class specific number of death of males in 1985-2015.
- S60F-H27F: Age class specific number of death of females in 1985-2015.
- S60FP-H27FP: Age class specific number of females’ population in 1985-2015.

Source


References


Description

Age-specific fertility and marital fertility rates for aged 15-54 Japanese women in Japan, from 1950 to 2015, every five years.

Usage

Jfert

Format

A data frame with 40 observations on 29 variables.

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Age-specific fertility rates and age-specific marital fertility rates in Japan.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Jfert</td>
</tr>
</tbody>
</table>

[1] Age | integer | Ages of women |
Details

The calculations were the numbers of live births divided by the numbers of women for ASFR (15-54), and the numbers of legitimate live births divided by the numbers of married women for ASMFR (15-54). Data sources are all official publication as vital statistics and national population census, so that the data are given with 5 years intervals.

- **Age**: Ages of women, from 15 to 54.

Source

https://www.ipss.go.jp/syoushika/tohkei/Popular/P_Detail2021.asp?fname=T04-09.htm
References


\[\text{Jlife} \quad \text{Completed lifetables in Japan.}\]

Description

The qx column of the completed lifetables in Japan, from "1891-1898" to "2015", mostly every 5 years.

Usage

\[\text{Jlife}\]

Format

A data frame with 117 observations (NAs are filled for the ages with no survivors) on 43 variables.

\[
\begin{array}{ccc}
[, 1] & \text{Age} & \text{integer} & \text{Ages of women} \\
[, 2] & qx1895M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1891-1898.} \\
[, 3] & qx1895F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1891-1898.} \\
[, 4] & qx1901M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1899-1903.} \\
[, 5] & qx1901F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1899-1903.} \\
[, 6] & qx1911M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1909-1913.} \\
[, 7] & qx1911F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1909-1913.} \\
[, 8] & qx1923M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1921-1925.} \\
[, 9] & qx1923F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1921-1925.} \\
[,10] & qx1928M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1926-1930.} \\
[,11] & qx1928F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1926-1930.} \\
[,12] & qx1935M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1935-1936.} \\
[,14] & qx1947M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1947.} \\
[,15] & qx1947F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1947.} \\
[,16] & qx1951M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1950-1952.} \\
[,17] & qx1951F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1950-1952.} \\
[,18] & qx1955M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1955.} \\
[,19] & qx1955F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1955.} \\
[,20] & qx1960M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1960.} \\
[,21] & qx1960F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1960.} \\
[,22] & qx1965M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1965.} \\
[,23] & qx1965F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1965.} \\
[,26] & qx1975M & \text{numeric} & \text{qx of completed lifetable functions of Japanese men in 1975.} \\
[,27] & qx1975F & \text{numeric} & \text{qx of completed lifetable functions of Japanese women in 1975.} \\
\end{array}
\]
- \( qx_{1990M} \) numeric qx of completed lifetable functions of Japanese men in 1990.
- \( qx_{1990F} \) numeric qx of completed lifetable functions of Japanese women in 1990.
- \( qx_{2010M} \) numeric qx of completed lifetable functions of Japanese men in 2010.
- \( qx_{2010F} \) numeric qx of completed lifetable functions of Japanese women in 2010.
- \( qx_{2015F} \) numeric qx of completed lifetable functions of Japanese women in 2015.

Details

- Age: Ages from 0 to 116.
- \( qx_{1895M}-qx_{2015M} \): qx of 1st to 22nd completed lifetables for Japanese men.
- \( qx_{1895F}-qx_{2015F} \): qx of 1st to 22nd completed lifetables for Japanese women.

Source


References


<table>
<thead>
<tr>
<th>Jpop</th>
<th>Japanese population data</th>
</tr>
</thead>
</table>

Description

The data gives the sex and age specific population for the all census results in Japan.
Usage

Jpop

Format

A data frame with 86 observations on 61 variables.

<table>
<thead>
<tr>
<th></th>
<th>Name</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>[,1]</td>
<td>Age</td>
<td>Factor w/86 levels</td>
<td>Ages (years old, combined for 85+)</td>
</tr>
<tr>
<td>[,2]</td>
<td>M1888</td>
<td>numeric</td>
<td>Age specific population of males in 1888</td>
</tr>
<tr>
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Details

Japanese population data by sex and age given as national official census record.

- Age: Ages, combined for 85+.

Source

https://www.e-stat.go.jp/stat-search/file-download?scriptId=000032142404&fileKind=0

References

Japanese population data (unshrunken version)

Description

The data gives the sex and age specific population for the all census results in Japan.

Usage

Jpopl

Format

A data frame with 111 observations on 67 variables.

[,1] Age Factor w/111 levels Ages (years old, combined for 110+)
[,2] M1888 numeric Age specific population of males in 1888
[,3] F1888 numeric Age specific population of females in 1888
[,4] M1893 numeric Age specific population of males in 1893
[,5] F1893 numeric Age specific population of females in 1893
[,6] M1898 numeric Age specific population of males in 1898
[,7] F1898 numeric Age specific population of females in 1898
[,8] M1903 numeric Age specific population of males in 1903
[,9] F1903 numeric Age specific population of females in 1903
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[,12] M1913 numeric Age specific population of males in 1913
[,13] F1913 numeric Age specific population of females in 1913
[,14] M1918 numeric Age specific population of males in 1918
[,15] F1918 numeric Age specific population of females in 1918
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[,18] M1925 numeric Age specific population of males in 1925
[,19] F1925 numeric Age specific population of females in 1925
[,20] M1930 numeric Age specific population of males in 1930
[,21] F1930 numeric Age specific population of females in 1930
[,22] M1935 numeric Age specific population of males in 1935
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[,27] F1947 numeric Age specific population of females in 1947
[,28] M1950 numeric Age specific population of males in 1950
[,29] F1950 numeric Age specific population of females in 1950
[,30] M1955 numeric Age specific population of males in 1955
[,31] F1955 numeric Age specific population of females in 1955
[,32] M1960 numeric Age specific population of males in 1960
### Details

Japanese population data by sex and age given as national official census record.

- **Age:** Ages, combined for 110+.
- **M1888-M2020:** Age specific number of males’ population in Japan for 1888-2020.
- **F1888-F2020:** Age specific number of females’ population in Japan for 1888-2020.
- **M2000J-M2020J:** Age specific number of Japanese males’ population in Japan for 2000-2020 by every 5 years.
- **F2000J-F2020J:** Age specific number of Japanese females’ population in Japan for 2000-2020 by every 5 years.
Jvital

Longitudinal data of several vital statistics in Japan

Description
The data gives longitudinal data of several vital statistics in Japan. Included indices are crude birth rates, crude death rates, infant mortality rates, and so on.

Usage
Jvital

Format
A data frame with 119 observations on 19 variables.

[, 1] YEAR numeric Year
[, 2] CBR numeric Crude birth rates of Japan
[, 3] CDR numeric Crude death rates of Japan
[, 4] IMR numeric Infant mortality rates of Japan
[, 5] NMR numeric Neonatal mortality rates of Japan
[, 6] NIR numeric Natural increase rates of Japan
[, 7] SBRPB numeric Stillbirth rates of Japan
[, 8] SARPB numeric Spontaneous abortion rates of Japan
[, 9] ACRPB numeric Artificial contraception rates of Japan
[,10] PNMPB numeric Perinatal mortalities per birth of Japan
[,11] MR numeric Marriage rates of Japan
[,12] DR numeric Divorce rates of Japan
[,13] TFR numeric Total fertility rates of Japan
[,14] ASMRM numeric Age-standardized mortality rates of males in Japan
[,15] ASMRM2 numeric Age-standardized mortality rates of males in Japan using new model population 2015
[,16] ASMRF numeric Age-standardized mortality rates of females in Japan
[,17] ASMRF2 numeric Age-standardized mortality rates of females in Japan using new model population 2015
[,18] PNMPLB numeric Perinatal mortalities per live births of Japan
[,19] MMR numeric Maternal mortality rates per 100000 births in Japan
Details

Longitudinal vital statistics in Japan provided as national official vital statistics every year from 1899 to 2020, except for 1944-1946.

- **YEAR**: Calendar year.
- **CBR**: Crude birth rate. Number of all live births / mid-year population 1000.
- **CDR**: Crude death rate. Number of death / mid-year population 1000.
- **IMR**: Infant mortality rate. Number of death at age 0 / 1000 live births.
- **NMR**: Neonatal mortality rate. Number of death within 4 weeks after birth / 1000 live births.
- **NIR**: Natural increase rate. CBR-CDR.
- **SBRPB**: Stillbirth rate per birth. Number of stillbirths / 1000 births.
- **SARPB**: Spontaneous abortion rate per birth. Number of spontaneous abortions / 1000 births.
- **ACRPB**: Artificial contraception (= induced abortion) rate per birth. Number of induced abortions / 1000 births.
- **PNMPB**: Perinatal mortality rate per birth. [(Number of stillbirths after gestational age 22 weeks) + (Number of early neonatal deaths within a week after birth)] per 1000 births. The denominator is the sum of the number of stillbirths after gestational age 22 weeks and the number of live births. This definition was established in 1995, but PNMPB also includes some values before 1995.
- **MR**: Marital rate. The number of marriages / mid-year population 1000.
- **DR**: Divorce rate. The number of divorces / mid-year population 1000.
- **TFR**: Total fertility rate. The sum of age-specific fertility rates, which is the number of births divided by the number of women’s population for each age.
- **ASMRM**: Age-standardized mortality rate of males, per mid-year population 1000, where the standard population is the model population in 1985 (S60MPJ).
- **ASMRM2**: Age-standardized mortality rate of males, per mid-year population 1000, where the standard population is the model population in 2015 (H27MPJ).
- **ASMRF**: Age-standardized mortality rate of females, per mid-year population 1000, where the standard population is the model population in 1985 (S60MPJ).
- **ASMRF2**: Age-standardized mortality rate of females, per mid-year population 1000, where the standard population is the model population in 2015 (H27MPJ).
- **PNMPLB**: Perinatal mortality per live birth. [(Number of stillbirths after gestational age 28 weeks) + (Number of early neonatal deaths within a week after birth)] / 1000 live births (Note: the denominator does not include stillbirths!). This definition stood until 1994, but PNMPLB also includes values after 1995, for comparison.
- **MMR**: Maternal mortality rate (actually ratio) per birth. (Number of maternal deaths during pregnancy or postpartum periods within 42 days [90 days until 1978] after the delivery due to reproduction-related causes) / (Number of total births = live births + stillbirths) x 100,000.
Source


References


---

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<th>Jvital2013byPref</th>
<th>Cross sectional data of several vital statistics in Japan 2013 for each prefecture</th>
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Description

The data gives cross sectional data of several vital statistics in Japan 2013 for each prefecture. Included indices are crude birth rates, crude death rates, infant mortality rates, and so on.

Usage

Jvital2013byPref

Format

A data frame with 47 observations on 34 variables.

```
[ , 1] PNAME  factor w/47 levels  The name (in roma-ji) for prefectures
[ , 2] JCODE  numeric  Prefecture number defined by Geographical Information Authority of Japan
[ , 3] CBR  numeric  Crude birth rates
[ , 4] CDR  numeric  Crude death rates
[ , 5] IMR  numeric  Infant mortality rates
[ , 6] NMR  numeric  Neonatal mortality rates
[ , 7] NIR  numeric  Natural increase rates
[ , 8] SBRPB  numeric  Stillbirth rates
[ , 9] SARPB  numeric  Spontaneous abortion rates
```
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<td>Cause-specific mortality for pneumonia</td>
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<td>Cause-specific mortality for cerebrovascular disease</td>
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<td>Cause-specific mortality for kidney failure</td>
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<td>Cause-specific mortality for chronic obstructive pulmonary disease</td>
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**Details**

Official vital statistics in Japan in 2013 for each prefecture.

- **PNAME**: The name (in roma-ji) for prefectures.
- **JCODE**: Prefecture number defined by Geographical Information Authority of Japan. From 1 to 47.
- **CBR**: Crude birth rate. Number of all live birth / mid-year population 1000.
- **CDR**: Crude death rate. Number of death / mid-year population 1000.
- **IMR**: Infant mortality rate. Number of death at age 0 / 1000 live births.
- **NMR**: Neonatal mortality rate. Number of death within 4 weeks after birth / 1000 live births.
- **NIR**: Natural increase rate. CBR-CDR.
- **SBRPB**: Stillbirth rate per birth. Number of stillbirths / 1000 births.
- **SARPB**: Spontaneous abortion rate per birth. Number of spontaneous abortions / 1000 births.
- **ACRPB**: Artificial contraception (= induced abortion) rate per birth. Number of induced abortions / 1000 births.
- **PNMPB**: Perinatal mortality per birth. [(Number of stillbirths after gestational age 22 weeks) + (Number of early neonatal deaths within a week after birth)] per 1000 births. The denominator is the sum of the number of stillbirths after gestational age 22 weeks and the number of live
births. This definition was established in 1995, but PNMPB also includes some values before 1995.

- **SBRA22W**: Stillbirth rate after gestational age of 22 weeks per 1000 births.
- **ENMR**: Early neonatal mortality rate per 1000 live births.
- **MR**: Marital rate. The number of marriages / mid-year population 1000.
- **DR**: Divorce rate. The number of divorces / mid-year population 1000.
- **TFR**: Total fertility rate. The sum of age-specific fertility rates, which is the number of births divided by the number of women’s population for each age.
- **CSM.ALL**: Cause-specific mortality for all causes. Similar to CDR, but the denominator is mid-year population 100000 instead of 1000.
- **CSM.CANCER**: Cause-specific mortality for cancer. The number of deaths caused by cancer / mid-year population 100000.
- **CSM.HD**: Cause-specific mortality for heart disease except for hypertention / mid-year population 100000.
- **CSM.PNEUM**: Cause-specific mortality for pneumonia / mid-year population 100000.
- **CSM.CEVD**: Cause-specific mortality for cerebrovascular disease / mid-year population 100000.
- **CSM.SEN**: Cause-specific mortality for senescence / mid-year population 100000.
- **CSM.ACC**: Cause-specific mortality for accidents / mid-year population 100000.
- **CSM.SUI**: Cause-specific mortality for suicide / mid-year population 100000.
- **CSM.KF**: Cause-specific mortality for kidney failure / mid-year population 100000.
- **CSM.COPD**: Cause-specific mortality for chronic obstructive pulmonary disease / mid-year population 100000.
- **CSM.AA**: Cause-specific mortality for aneusym of aorta / mid-year population 100000.
- **CSM.LIVD**: Cause-specific mortality for liver disease / mid-year population 100000.
- **CSM.DIAB**: Cause-specific mortality for diabetes / mid-year population 100000.
- **CSM.SEP**: Cause-specific mortality for sepsis / mid-year population 100000.
- **CSM.MNP**: Cause-specific mortality for miscellaneous neoplasms / mid-year population 100000.
- **CSM.DEM**: Cause-specific mortality for dementia / mid-year population 100000.
- **CSM.TB**: Cause-specific mortality for tuberculosis / mid-year population 100000.
- **CSM.TA**: Cause-specific mortality for traffic accidents / mid-year population 100000.

**Source**

https://www.mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei13/xls/hyo.xls
https://www.mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei13/xls/sankou.xls

**References**

Kappa.test

Calculate Cohen’s kappa statistics for agreement

Description

Calculate Cohen’s kappa statistics for agreement and its confidence intervals followed by testing null-hypothesis that the extent of agreement is same as random, kappa statistic equals zero.

Usage

Kappa.test(x, y=NULL, conf.level=0.95)

Arguments

x If y is not given, x must be the square matrix that the rows and columns show the ratings of different rater (or repeated measure) and the values indicate the numbers of data having that combination. If y is given, x must be the result of ratings by the first rater (or first time measurement).

y If given, y must be the result of ratings by the second rater (or second time measurement). As default, it is not given.

conf.level Probability for confidence intervals for kappa statistics. Default is 0.95.

Value

Result$statistic Z score to test null-hypothesis.

Result$estimate Calculated point estimate of Cohen’s kappa statistic.

Result$conf.int A numeric vector of length 2 to give upper/lower limit of confidence intervals.

Result$p.value The significant probability as the result of null-hypothesis testing.

Judgement The judgement for the estimated kappa about the extent of agreement, given by Landis JR, Koch GG (1977) Biometrics, 33: 159-174: If kappa is less than 0, "No agreement", if 0-0.2, "Slignt agreement", if 0.2-0.4, "Fair agreement", if 0.4-0.6, "Moderate agreement", if 0.6-0.8, "Substantial agreement", if 0.8-1.0, "Almost perfect agreement".

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References

See Also

Kappa

Examples

```r
res <- Kappa.test(matrix(c(20, 10, 5, 15), 2, 2))
str(res)
print(res)
Kappa.test(c(1, 1, 3, 1, 1, 2, 1, 2, 1, 1), c(2, 1, 3, 1, 3, 2, 1, 3, 3, 3))
```

---

lifetable

Lifetable functions with mutual conversions

Description

Lifetable related functions.

Usage

```r
lifetable(mx, ns=NULL, class=5, mode=1)
lifetable2(mx, ax=0.5, n=1)
lifetable3(lx, ax=0.5, n=1)
c lifetable(qx)
lxtodx(lx)
dxtolx(dx)
qxtodx(qx)
dxtoqx(dx)
qxtomx(qx, ax=0.5, n=1, mmax=NULL)
mxtqx(mx, ax=0.5, n=1)
qxtolx(qx)
lxtolx(lx)
uxtolx(ux)
```

Arguments

- **mx**: Lifetable function mx, meaning the age (class)-specific death rates.
- **ns**: If given as a vector with the same length as mx, the duration for each age (class). Default is NULL: same duration with class is automatically used.
- **n**: If given as a vector with the same length as mx or qx, the duration for each age (class). Default is 1, which means the length for all age-classes being 1 year.
- **class**: Age-class of lifetable() function. Default is 5.
mode

How to set ax and correction method in conversion from mx to qx. 1 and 11: all
ax is 0.5 except the open-ended class [where ax is reciprocal of mx], 2, 4, 12, 14:
ax is 0.1 for age 0, 0.4 for age 1-4, 0.5 for the other ages except the open-ended
class [where ax is reciprocal of mx], 3, 5, 13, 15: ax is 0.3 for age 0, 0.4 for age
1-4, 0.5 for the other ages except the open-ended class [where ax is reciprocal
of mx], 6 and 16: Males value given in Preston SH (2001), pp.48 Table 3.3,
7 and 17: Females value given in Preston SH (2001), pp.48 Table 3.3. If less
than 10, simply calculating qx as n*mx/(1+n*(1-ax)*mx) (Note: In the formula
of Preston SH (2001) pp.47, the function is given as n*mx/(1+(n-ax)*mx). The
difference is due to the formulation of ax. In this function, ax is given for single
age, same as Newell C (1988), pp.71) except for the open-ended class where
qx=1, otherwise calculating qx by Greville’s method. Default is 1.

ax

Lifetable function ax, fraction of last year lived. Default is 0.5 (scalar) for all
classes. It can be given as scalar or vector. Note: This argument can only be
specified in lifetable2() or lifetable3(), not in lifetable().

qx

Lifetable function qx, which means the probability of dying between age x and
x+1 (for lifetable(), x+class).

mmax

To calculate mx from qx, mx at the maximum open-ended age-class cannot be
calculated from qx. In such situation, mmax gives a value for it. Default is
NULL.

lx

Lifetable function lx, which means number of people left alive at age x from
100,000 newborns.

dx

Lifetable function dx, which means number of people dying between age x and
x+1 (for lifetable(), x+class) from 100,000 newborns. Differentials of lx.

ux

The force of mortality.

pix

age-(class-)specific proportions of unhealthy people.

Nx

Population of xth age-class, which is needed to calculate confidence intervals.

conf.level

The level of confidence intervals. Default is 0.95.

Tx

Lifetable function Tx, which means sum of person-years lived above age x.

Value

ages

Lifetable’s exact age x, which is the beginning of each interval.

n

Duration of each interval. If ns is not given, the value of the class is repeatedly
used.

mx

Lifetable function mx, meaning the age (class)-specific death rates.

qx

Lifetable function qx, which means the probability of dying between age x and
x+1 (for lifetable(), x+class).

ax

Lifetable function ax, which means the average number of person-years lived
in the interval by those dying in the interval. In lifetable(), it’s automatically
specified by mode.

lx

Lifetable function lx, which means number of people left alive at age x from
100,000 newborns.
dx Lifetable function dx, which means number of people dying between age x and x+1 (for lifetable(), x+class) from 100,000 newborns. Differentials of lx.
Lx Lifetable function Lx, which means person-years lived between age x and x+class.
Tx Lifetable function Tx, which means person-years lived above age x.
ex Lifetable function ex, which means expectation of life at age x.

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References

See Also
Jlife

Examples
lifetable(c(0.0087, 0.00015, 0.00019, 0.00098, 0.0011, 0.0014, 0.0019,
0.0029, 0.0048, 0.0071, 0.011, 0.019, 0.028, 0.041, 0.072, 0.11,
0.19), class=5, mode=11)
lifetable2(c(0.008314, 0.000408, 0.000181, 0.000187, 0.000282, 0.000307, 0.000364,
0.000566, 0.000884, 0.001445, 0.005495, 0.00719, 0.012054,
0.018259, 0.029920, 0.049689, 0.085545, 0.177987),
ax = c(0.1, 0.4, rep(0.5, 16), NA), n = c(1, 4, rep(5, 16), NA)
)
lifetable3(lx=c(1.0, 0.8499, 0.8786, 0.7762, 0.7691, 0.7502, 0.7362,
0.7130, 0.6826, 0.6525, 0.6223, 0.5898, 0.5535, 0.5106, 0.4585,
0.3965, 0.3210, 0.2380, 0.1516, 0.0768, 0.0276, 0.0059, 0.0006, 0),
n=c(rep(1, 5), rep(5, 16)), ax=c(0.3, rep(0.5, 24))) # Newell, Table 13.1
c lifetable(Jlife$qx2000F)

Description
Draw maternity history charts.

Usage
mhchart(LIST, XLIM=c(15,45), COL="black", FILL="white", BWD=1, ...)
NagelkerkeR2

Arguments

LIST
The list of groups with their maternity histories from first birth to the last birth. Usually the first childbirth age is estimated as median by Kaplan-Meier method, the second childbirth age was given by adding the median of first birth intervals to the first childbirth age by Kaplan-Meier method, and so on.

XLIM
The limit of x axis, which means the range of reproductive ages. Default is 15 and 45.

COL
The border color. Default is black.

FILL
The painting color. Default is white.

BWD
The line width of the boxes. Default is 1.

... Other parameters handed to barplot() to draw axes and background.

Value
No value is returned.

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

Examples

Developing <- c(18, 21, 24, 27, 30, 33.5, 37)
Hutterite <- c(23, 25, 27, 29, 31, 33, 35, 37, 39)
Gainj <- c(27, 31, 35, 39)
Japan <- c(29, 34)
x <- list(Developing=Developing, Hutterite=Hutterite, Gainj=Gainj, Japan=Japan)
mhchart(rev(x), COL="blue", FILL="pink", BWD=2, XLIM=c(15, 45), main="Maternity histories for selected populations", xlab="Maternal age (years)"

NagelkerkeR2

Calculate Nagelkerke’s R squared.

Description

To evaluate the goodness of fit of the logistic regression model, calculating Nagelkerke’s R squared from the result of glm(). The Nagelkerke’s R squared means the power of explanation of the model.

Usage

NagelkerkeR2(rr)
Arguments

`rr` The object with class "glm" and "lm", which would be generated by glm().

Value

`N` The number of observations in which the model were fitted.
`R2` Nagelkerke’s R squared.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


Examples

```r
res <- glm(cbind(ncases, ncontrols) ~ agegp + alcgp + tobgp, data=esoph, family=binomial())
summary(res)
NagelkerkeR2(res)
```

**oddsratio**

*Calculate odds ratio and its confidence intervals*

Description

Calculate odds ratio and its confidence intervals based on approximation, followed by null-hypothesis (odds ratio equals to 1) testing.

Usage

```r
oddsratio(a, b, c, d, conf.level=0.95, p.calc.by.independence=TRUE)
```

Arguments

`a` A scalar or a matrix. If matrix, it has to be 2 by 2, which contains the number of individuals who both suffer from exposure and disease as [1, 1], the number of individuals who suffer from disease but not exposed as [2, 1], the number of individuals who suffer from exposure but are healthy as [1, 2] and the number of individuals who neither suffered from exposure nor disease as [2, 2].

`b` If a is a scalar, this has to be given as the number of individuals who suffer from disease but not exposed. Otherwise, ignored.
oddsratio

\[ \text{c} \]
If \( a \) is a scalar, this has to be given as the number of individuals who suffer from exposure but are healthy. Otherwise, ignored.

\[ \text{d} \]
If \( a \) is a scalar, this has to be given as the number of individuals who neither suffered from exposure nor disease. Otherwise, ignored.

\[ \text{conf.level} \]
Probability for confidence intervals. Default is 0.95.

\[ \text{p.calc.by.independence} \]
Logical. If TRUE, calculating p-value by testing the null-hypothesis of independence between exposure and disease. Otherwise, calculating p-value by inverse-function of confidence intervals calculation (the result becomes the same as the vcd package). Default TRUE.

**Value**

- **estimate**
  Calculated point estimate of odds ratio.

- **conf.int**
  A numeric vector of length 2 to give upper/lower limit of confidence intervals.

- **p.value**
  The significant probability as the result of null-hypothesis testing.

**Note**

This function can also accept a matrix as argument, as suggested by Dr. Toshiaki Ara (<toshiaki.ara@gmail.com>). Thanks for a good suggestion.

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

**References**


**Examples**

```r
res <- oddsratio(5, 10, 85, 80)
str(res)
print(res)
oddsratio(12, 5, 6, 12)
oddsratio(12, 5, 6, 12, p.calc.by.independence=FALSE)
DH <- sample(c("Disease", "Health"), 100, replace=TRUE)
EN <- sample(c("Exposed", "Nonexposed"), 100, replace=TRUE)
x <- table(EN, DH)
oddsratio(x)
# same as oddsratio(x[1,1], x[2,1], x[1,2], x[2,2])
```
 ORMH  

*Calculate pooled odds ratio and its confidence intervals with Mantel-Haenszel’s method*

**Description**

Calculate pooled odds ratio and its confidence intervals with Mantel-Haenszel’s method.

**Usage**

```r
ORMH(TBL, conf.level=0.95)
```

**Arguments**

- **TBL**  
  A matrix with 4 columns. The first column is the number of exposed cases. The second column is the number of unexposed cases. The third column is the number of exposed controls. The forth column is the number of unexposed controls. Rows should be composed of different strata or studies.

- **conf.level**  
  Probability for confidence intervals. Default is 0.95.

**Value**

- **estimate**  
  Calculated point estimate of pooled odds ratio with Mantel-Haenszel’s method.

- **conf.int**  
  A numeric vector of length 2 to give upper/lower limit of confidence intervals.

- **conf.level**  
  Simply return the value of given conf.level.

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

**References**


**Examples**

```r
# Table 10-6 of Rothman's textbook (Chapter 10).
ORMH(matrix(c(3, 9, 104, 1059, 1, 3, 5, 86), 2, 4, byrow=TRUE), conf.level=0.9)

# Figure 8-4 of Rothman's textbook (Chapter 8)
# https://www.ncbi.nlm.nih.gov/pubmed/7630245
# https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(05)74403-2/fulltext
TenStudies <- matrix(
c(215, 229, 311-215, 306-229,  
38, 33, 59-38, 51-33,  
161, 174, 293-161, 293-174,  
76, 88, 164-76, 163-88,  
103, 105, 129-103, 133-105,  
65, 67, 120-65, 125-67),
```
pairwise.fisher.test

81, 75, 113-81, 110-75,
48, 63, 160-48, 159-63,
22, 21, 60-22, 62-21,
56, 51, 137-56, 140-51
), 10, 4, byrow=TRUE)

ORMH(TenStudies)

ElevenStudies <- rbind(TenStudies, c(468, 480, 229, 205))

ORMH(ElevenStudies)

---

pairwise.fisher.test  Exact version of pairwise.prop.test

Description
By conducting repeatedly Fisher's exact tests instead of chi-square tests, this function can test the null-hypothesis of no difference in any pair of proportions for more than 2 groups, with adjustment of type I error for multiple comparison.

Usage

pairwise.fisher.test(x, n, p.adjust.method, ...)

Arguments

x  A integer vector of event occurrences
n  A integer vector of trials
p.adjust.method  A name in p.adjust.methods to specify the method to adjust type I error for multiple comparisons. Default is "holm".
...  Miscellaneous arguments to be given for fisher.test().

Value
An object of adjusted p-values for all possible comparisons of pairs with class pairwise.htest.

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/. The code of this function was provided by Dr. Shigenobu AOKI (Gunma Univ.).

See Also
pairwise.prop.test, p.adjust.methods
Examples

```r
pairwise.fisher.test(c(2, 4, 5), c(10, 14, 17), p.adjust.method="bonferroni")
smoker <- c(2, 1, 7)
total <- c(11, 14, 10)
names(total) <- c("A", "B", "C")
pairwise.fisher.test(smoker, total)
```

---

**PEI**

*Population Expansion Index*

---

**Description**

Population Expansion Index (Bulge Index) for movement.

**Usage**

```r
PEI(X, CLS, MODE)
```

**Arguments**

- `X`  
  The vector to give age-specific population from age 0.
- `CLS`  
  The width of age-class in X. default is 1.
- `MODE`  
  If the MODE is 1, the ages of 20 to 39 years old are assumed as "easily movable ages" comparing with "relatively unmovable" 10 to 19 and 40 to 49, otherwise the ages of 15 to 34 years old are assumed as the former and 5 to 14 and 35 to 44 are assumed as the latter, as Dr. Toshio Kuroda suggested in his book. Then PEI (originally named as bulge index, but I prefer to use PEI instead) is calculated as the ratio of the population of "easily movable ages" to the population of "relatively unmovavle ages" times 100. If PEI is larger than 100, net migration may be positive and vise versa. Default 1.

**Value**

The value of PEI is returned.

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

**References**

# Prefectural population estimates in 2018 (unit=1000 persons)
# total of males and females, by 5 year age-class
# (Data source) Download Excel file and extracted
# ![url](https://www.e-stat.go.jp/stat-search/file-download?statInfId=000031807147&fileKind=0)

```r
PPT2018 <- data.frame(
  Hokkaido = c(175, 195, 207, 229, 235, 232, 266, 304, 367, 381, 344, 341, 354, 452, 368, 310, 252, 274),
  Aomori = c(41, 45, 51, 58, 48, 48, 59, 69, 82, 86, 83, 88, 94, 112, 89, 75, 67, 69),
  Iwate = c(41, 47, 52, 57, 47, 50, 59, 69, 81, 82, 78, 84, 91, 106, 82, 74, 67, 75),
  Miyagi = c(85, 93, 98, 109, 123, 119, 130, 144, 164, 163, 144, 146, 155, 182, 139, 116, 98, 108),
  Akita = c(28, 33, 37, 40, 30, 33, 42, 51, 61, 62, 59, 69, 78, 93, 72, 63, 61, 69),
  Yamagata = c(38, 42, 47, 51, 40, 43, 53, 61, 70, 69, 66, 73, 80, 95, 71, 62, 58, 73),
  Fukushima = c(67, 70, 79, 89, 73, 80, 94, 105, 122, 124, 117, 129, 139, 160, 119, 102, 89, 106),
  Ibaraki = c(106, 117, 127, 140, 132, 130, 152, 172, 204, 216, 185, 176, 190, 233, 196, 162, 116, 125),
  Tochigi = c(73, 80, 87, 92, 83, 98, 107, 122, 142, 146, 125, 121, 131, 157, 127, 101, 76, 84),
  Gunma = c(70, 79, 87, 97, 90, 88, 99, 113, 139, 148, 127, 117, 124, 153, 135, 110, 82, 94),
  Saitama = c(279, 299, 312, 343, 405, 381, 407, 458, 552, 608, 508, 428, 415, 524, 488, 411, 275, 235),
  Chiba = c(233, 251, 264, 289, 323, 310, 344, 387, 465, 513, 428, 367, 361, 460, 430, 358, 248, 225),
  Tokyo = c(539, 516, 495, 554, 867, 911, 961, 1013, 1109, 1167, 1005, 810, 687, 797, 750, 647, 508, 494),
  Kanagawa = c(351, 374, 385, 423, 518, 490, 529, 706, 788, 679, 551, 486, 599, 558, 479, 343, 326),
  Niigata = c(78, 88, 94, 103, 92, 94, 111, 127, 152, 154, 141, 141, 155, 190, 151, 129, 111, 135),
  Toyama = c(37, 40, 45, 50, 44, 44, 50, 58, 75, 79, 65, 62, 65, 84, 80, 63, 49, 60),
  Ishikawa = c(44, 48, 51, 57, 57, 53, 58, 65, 82, 86, 71, 68, 70, 86, 80, 63, 47, 58),
  Fukui = c(30, 33, 36, 39, 33, 34, 39, 43, 52, 54, 48, 49, 50, 62, 50, 43, 36, 44),
  Yamanashi = c(29, 32, 36, 41, 38, 35, 39, 44, 53, 60, 56, 53, 54, 64, 54, 47, 37, 46),
  Nagano = c(76, 85, 94, 101, 79, 83, 98, 114, 143, 150, 133, 127, 130, 159, 142, 122, 98, 129),
  Gifu = c(75, 86, 92, 101, 92, 86, 98, 112, 139, 148, 128, 122, 123, 155, 139, 116, 90, 96),
  Shizuoka = c(137, 155, 164, 175, 150, 162, 193, 214, 256, 276, 241, 225, 238, 284, 251, 212, 161, 173),
  Aichi = c(319, 339, 344, 374, 420, 414, 451, 484, 567, 610, 507, 434, 397, 492, 461, 387, 276, 259),
)
```

**Examples**
Mie = c(67, 75, 80, 87, 82, 81, 92, 102, 125, 135, 118, 111, 109, 135, 122, 103, 80, 88),
Shiga = c(61, 67, 74, 71, 79, 88, 105, 108, 89, 83, 81, 100, 85, 69, 52, 58),
Kyoto = c(94, 102, 107, 122, 159, 136, 137, 149, 183, 197, 167, 148, 142, 189, 180, 150, 112, 118),
Osaka = c(334, 352, 370, 418, 486, 461, 489, 529, 645, 727, 608, 507, 465, 614, 592, 519, 367, 329),
Hyogo = c(212, 230, 242, 267, 267, 247, 279, 317, 392, 430, 367, 334, 324, 410, 377, 313, 234, 244),
Nara = c(48, 54, 59, 67, 66, 58, 63, 71, 89, 100, 88, 81, 82, 107, 99, 85, 60, 63),
Wakayama = c(33, 37, 39, 45, 36, 37, 44, 48, 61, 67, 60, 60, 61, 77, 69, 59, 47, 54),
Tottori = c(22, 24, 25, 27, 22, 23, 28, 32, 37, 33, 35, 39, 46, 38, 30, 27, 36),
Shimane = c(26, 28, 29, 32, 25, 27, 32, 37, 43, 43, 38, 42, 46, 58, 48, 39, 37, 49),
Okayama = c(75, 81, 84, 93, 97, 90, 99, 107, 130, 136, 112, 108, 114, 142, 133, 106, 86, 104),
Hiroshima = c(113, 125, 126, 135, 136, 133, 150, 165, 201, 212, 175, 163, 167, 211, 194, 155, 119, 137),
Yamaguchi = c(49, 55, 58, 63, 57, 55, 64, 72, 89, 94, 80, 80, 90, 119, 104, 88, 71, 83),
Tokushima = c(26, 28, 29, 33, 29, 30, 36, 41, 48, 50, 45, 46, 52, 64, 53, 43, 37, 46),
Kagawa = c(37, 40, 42, 46, 40, 48, 54, 68, 69, 58, 57, 61, 79, 70, 54, 45, 56),
Ehime = c(49, 55, 58, 63, 52, 54, 65, 74, 91, 93, 83, 84, 90, 115, 98, 79, 66, 81),
Kochi = c(24, 26, 29, 32, 26, 26, 32, 37, 47, 48, 41, 44, 48, 61, 55, 44, 37, 49),
Fukuoka = c(218, 229, 226, 241, 275, 251, 285, 321, 363, 365, 311, 300, 315, 394, 320, 262, 205, 228),
Saga = c(34, 38, 39, 42, 35, 35, 42, 47, 53, 52, 48, 52, 57, 67, 51, 43, 37, 46),
Nagasaki = c(53, 57, 60, 63, 51, 54, 64, 72, 83, 87, 82, 89, 98, 117, 90, 77, 66, 79),
Kumamoto = c(74, 80, 81, 83, 75, 77, 91, 100, 112, 109, 104, 111, 122, 142, 111, 94, 85, 105),
Oita = c(44, 48, 49, 54, 47, 46, 56, 64, 75, 75, 66, 70, 78, 97, 81, 67, 57, 69),
Miyazaki = c(45, 50, 50, 51, 41, 42, 52, 61, 70, 67, 62, 69, 78, 92, 72, 60, 54, 64),
Kagoshima = c(68, 74, 74, 74, 62, 65, 80, 91, 100, 97, 96, 106, 123, 135, 101, 88, 80, 102),
Okinawa = c(82, 84, 81, 81, 72, 76, 88, 93, 104, 102, 89, 90, 93, 97, 60, 56, 48, 52)
)
# Calculate PEI for all prefectures
# for (i in 1:47) {
#  print(PEI(PPT2018[, i], CLS=5))
# }

# Calculate PEI for all prefectures
# for (i in 1:47) {
#  print(PEI(PPT2018[, i], CLS=5))
# }
percentile

print(apply(PPT2018, 2, PEI, CLS=5))

percentile

Convert numeric vector into its percentile

Description

Convert numeric vector into its percentile. For example, 1:5 will become c(0,25,50,75,100).

Usage

percentile(dat)

Arguments

dat A numeric vector, which will be converted into percentile value.

Value

A integer vector in [0,100]. Minimum value always becomes 0 and maximum always becomes 100.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

Examples

percentile(1:5)
X <- runif(1000, 10, 20)
percentile(X)

PrefYLL2015

Years of Life Lost by several causes in Japan 2015 for each prefecture

Description

The data gives years of life lost by several causes in Japan 2015 for each prefecture. There are several definitions of YLL. For example, WHO's Global Burden of Disease defines the YLL as the number of deaths multiplied by the standard life expectancy at the age at which death occurs, for a given cause, age and sex (WHO). However, Japanese Ministry of Health, Labor and Welfare gives the expected increase of the life expectancy at birth if the mortality due to each cause of death is removed from the age-specific mortality as the measure of YLL, and thus this dataset implements such data derived from the report of regional life tables in Japan (Ministry of Health, Labor and Welfare, 2015).
### Usage

PrefYLL2015

### Format

A data frame with 47 observations on 26 variables.

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>PNAME</td>
<td>factor w/47 levels</td>
</tr>
<tr>
<td></td>
<td>JCODE</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>CancerM</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>CardioM</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>CerebroM</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>PneumoniaM</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>AccidentM</td>
<td>numeric</td>
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<tr>
<td></td>
<td>TrafficM</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>SuicideM</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>KidneyM</td>
<td>numeric</td>
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<td></td>
<td>LiverM</td>
<td>numeric</td>
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<td></td>
<td>DiabetesM</td>
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<td>PneumoniaF</td>
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<td>TrafficF</td>
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<td>numeric</td>
</tr>
<tr>
<td></td>
<td>LiverF</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>DiabetesF</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>HypertensF</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>TBF</td>
<td>numeric</td>
</tr>
</tbody>
</table>

### Details

Years of Life Lost by several causes in Japan 2015 for each prefecture.

- **PNAME**: The name (in roma-ji) for prefectures.
- **JCODE**: Prefecture number defined by Geographical Information Authority of Japan. From 1 to 47.
- **CancerM/F**: YLL by cancer for males ([M]) or for females ([F]).
- **CardioM/F**: YLL by heart disease for males ([M]) or for females ([F]).
- **CerebroM/F**: YLL by cerebrovascular disease for males ([M]) or for females ([F]).
- **PneumoniaM/F**: YLL by pneumonia for males ([M]) or for females ([F]).
- **AccidentM/F**: YLL by accidents for males ([M]) or for females ([F]).
• Traffic[M|F]: YLL by traffic accidents (it’s also included in Accident[M|F] for males ([M]) or for females ([F]).
• Suicide[M|F]: YLL by suicide for males ([M]) or for females ([F]).
• Kidney[M|F]: YLL by kidney failure for males ([M]) or for females ([F]).
• Liver[M|F]: YLL by liver disease for males ([M]) or for females ([F]).
• Diabetes[M|F]: YLL by diabetes for males ([M]) or for females ([F]).
• Hypertension[M|F]: YLL by hypertension for males ([M]) or for females ([F]).
• TB[M|F]: YLL by tuberculosis for males ([M]) or for females ([F]).

Source
https://www.mhlw.go.jp/toukei/saikin/hw/life/tdfk15/dl/tdfk15-09.xls

References

Examples

```r
require(fmsb)
x <- PrefYLL2015
COL <- ifelse(x$PNAME=="Nagano", "blue", ifelse(x$PNAME=="Okinawa", "pink",
                   ifelse(x$PNAME=="Shiga", "green", "lightgrey")))
LWD <- ifelse(x$PNAME=="Nagano", 2, ifelse(x$PNAME=="Okinawa", 2, ifelse(x$PNAME=="Shiga", 2, 1)))
LTY <- ifelse(x$PNAME=="Nagano", 1, ifelse(x$PNAME=="Okinawa", 1, ifelse(x$PNAME=="Shiga", 1, 3)))
VX <- c("Cancer", "Heart\n Disease", "Cerebrovascular\n Disease", "Pneumonia", "Accident", "Traffic\n Accident", "Suicide", "Kidney\n Failure", "Liver\n Disease", "Diabetes", "Hypertension", "Tuberculosis")
males <- x[,3:14]
females <- x[,15:26]
layout(t(1:2))
radarchart(males, maxmin=FALSE, pcol=COL, axistype=2, pty=32, plty=LTY, plwd=LWD, vlabels=VX,
title="YLLs in males (2015)\n (Blue: Nagano, Green: Shiga, \n Pink: Okinawa, Gray: Others)")
radarchart(females, maxmin=FALSE, pcol=COL, axistype=2, pty=32, plty=LTY, plwd=LWD, vlabels=VX,
title="YLL in females (2015)\n (Blue: Nagano, Green: Shiga, \n Pink: Okinawa, Gray: Others)")
```

Drawing p-value function plot by a cross table
Description

Drawing the p-value function (a.k.a. nested confidence intervals) plot of risk ratio (RR) or odds ratio (OR) for a given 2 by 2 cross table, which is strongly recommended by Rothman KJ "Epidemiology: An introduction. 2nd Ed." Oxford Univ. Press.

Until fmsb-0.4.2, the formula to calculate p-values was not appropriate, so that the curve was not correct. Through discussion with Professor Rothman, I realized my mistake, then fixed it in fmsb-0.4.3. The feasible calculation is only possible in the manner of back-calculation from p-values to RR or OR, so that the calculation of p-values is restricted to the given range from 0.0005 to 1.

Usage

pvalueplot(XTAB, plot.OR, plot.log, xrange, add, ...)

Arguments

XTAB
A 2 by 2 matrix to draw p-value function (in another term, nested confidence intervals). The table should be given as the cross table for the exposure status being column and the health outcome status being row, opposite from usual manner for cross tabulation. To note, usually the numbers of incidence and the total observed numbers for exposed and nonexposed population as risk data, but in this function, the numbers of incidence and the remaining numbers without disease should be given as rows.

plot.OR
Logical. If you want to draw the p-value function for the odds ratio, it should be set at TRUE, otherwise the p-value function for the risk ratio is drawn. Default FALSE.

xrange
A numeric vector includes 2 elements for minimum and maximum of x axis. Default is c(0.01, 5).

plot.log
Logical. If TRUE, the horizontal axis becomes logarithmic scale. Default FALSE.

add
Logical. If TRUE, the line is overlayed on the existing pvalueplot, otherwise the graph is newly plotted. Default FALSE.

...
Other options handed down to plot() or lines(). pch, lty or col may be useful.

Value

The data.frame containing the set of p-values (ranging from 0.0005 to 1) and corresponding RR or OR is returned.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References

pvpORMH

Examples

\begin{verbatim}
  pvalueplot(matrix(c(321, 411, 686-321, 689-411), 2, 2), xrange=c(0.7, 0.9))
  pvalueplot(matrix(c(4, 386, 4, 1250), 2, 2), xrange=c(0.1, 20), plot.log=TRUE)
  pvalueplot(matrix(c(468, 480, 229, 205), 2, 2), plot.OR=TRUE, xrange=c(0.7, 1.0))
\end{verbatim}

\begin{verbatim}

Description

Drawing the p-value function (a.k.a. nested confidence intervals) plot of pooled odds ratios (pORs) for several 2 by 2 crosstables, which are stratified by a confounding variable or pooled for several studies, with Mantel-Haenszel's method.

Usage

\begin{verbatim}
pvpORMH(XTAB, xrange, add, ...)\end{verbatim}

Arguments

\begin{verbatim}
XTAB A matrix with 4 columns. The first column is the number of exposed cases. The second column is the number of unexposed cases. The third column is the number of exposed controls. The forth column is the number of unexposed controls. Rows should be composed of different strata or studies.
xrange A numeric vector includes 2 elements for minimum and maximum of x axis. Default is c(0.6, 1.2).
add Logical. If TRUE, the line is overlayed on the existing pvalueplot, otherwise the graph is newly plotted. Default FALSE.
... Other options handed down to plot() or lines(). pch, lty or col may be useful.
\end{verbatim}

Value

A data.frame containing the set of p-values (ranging from 0.0005 to 1) and corresponding pORs are returned.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References

Examples

TenStudies <- matrix(
  c(215, 229, 311-215, 306-229,
    38, 33, 59-38, 51-33,
    161, 174, 293-161, 293-174,
    76, 88, 164-76, 163-88,
    103, 105, 129-103, 133-105,
    65, 67, 120-65, 125-67,
    81, 75, 113-81, 110-75,
    48, 63, 160-48, 159-63,
    22, 21, 60-22, 62-21,
    56, 51, 137-56, 140-51
  ), 10, 4, byrow=TRUE)

ElevenStudies <- rbind(TenStudies, c(468, 480, 229, 205))

# Figure 8-4 in Chapter 8 of Rothman's textbook.
pvpORMH(TenStudies)
pvpORMH(ElevenStudies, add=TRUE, lty=2)
segments(1, 0, 1, 1, lwd=2)

---

radarchart

Drawing radar chart (a.k.a. spider plot)

Description

Drawing the radar chart with several lines from a data frame, which must be composed of more than 3 variables as axes and the rows indicate cases as series.

Usage

radarchart(df, axistype, seg, pty, pcol, plty, plwd, pdensity, pangle, pfcol, cglty, cglwd, cglcol, axislabcol, title, maxmin, na.itp, centerzero, vlabels, vlcex, caxislabels, calcex, paxislabels, palcex, ...)

Arguments

df          The data frame to be used to draw radarchart. If maxmin is TRUE, this must include maximum values as row 1 and minimum values as row 2 for each variables, and actual data should be given as row 3 and lower rows. The number of columns (variables) must be more than 2.

axistype    The type of axes, specified by any of 0:5. 0 means no axis label. 1 means center axis label only. 2 means around-the-chart label only. 3 means both center and around-the-chart (peripheral) labels. 4 is ** format of 1, 5 is *** format of 3. Default is 0.

seg          The number of segments for each axis (default 4).

pty          A vector to specify point symbol: Default 16 (closed circle), if you don’t plot data points, it should be 32. This is repeatedly used for data series.

pcol         A vector of color codes for plot data: Default 1:8, which are repeatedly used.
plty  A vector of line types for plot data: Default 1:6, which are repeatedly used.
plwd  A vector of line widths for plot data: Default 1, which is repeatedly used.
pdensity  A vector of filling density of polygons: Default NULL, which is repeatedly used.
pangle  A vector of the angles of lines used as filling polygons: Default 45, which is repeatedly used.
pfcol  A vector of color codes for filling polygons: Default NA, which is repeatedly used.
cglty  Line type for radar grids: Default 3, which means dotted line.
cglwd  Line width for radar grids: Default 1, which means thinnest line.
cgllcol  Line color for radar grids: Default "navy"
axislabcol  Color of axis label and numbers: Default "blue"
title  if any, title should be typed.
maxmin  Logical. If true, data frame includes possible maximum values as row 1 and possible minimum values as row 2. If false, the maximum and minimum values for each axis will be calculated as actual maximum and minimum of the data. Default TRUE.
na.itp  Logical. If true, items with NA values are interpolated from nearest neighbor items and connect them. If false, items with NA are treated as the origin (but not pointed, only connected with lines). Default FALSE.
centerzero  Logical. If true, this function draws charts with scaling originated from (0,0). If false, charts originated from (1/segments). Default FALSE.
vlabels  Character vector for the names for variables. If NULL, the names of the variables as colnames(df) are used. Default NULL.
vlcex  Font size magnification for vlabels. If NULL, the font size is fixed at text()’s default. Default NULL.
caxislabels  Character vector for center axis labels, overwriting values specified in axistype option. If NULL, the values specified by axistype option are used. Default is NULL.
calcex  Font size magnification for caxislabels. If NULL, the font size is fixed at text()’s default. Default NULL.
paxislabels  Character vector for around-the-chart (peripheral) labels, overwriting values specified in axistype option. If NULL, the values specified by axistype option are used. Default is NULL.
palcex  Font size magnification for paxislabels. If NULL, the font size is fixed at text()’s default. Default NULL.
...  Miscellaneous arguments to be given for plot.default().

Value
No value is returned.

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/
Examples

# Data must be given as the data frame, where the first cases show maximum.
maxmin <- data.frame(
  total=c(5, 1),
  phys=c(15, 3),
  psycho=c(3, 0),
  social=c(5, 1),
  env=c(5, 1))
# data for radarchart function version 1 series, minimum value must be omitted from above.
RNGkind("Mersenne-Twister")
set.seed(123)
dat <- data.frame(
  total=runif(3, 1, 5),
  phys=rnorm(3, 10, 2),
  psycho=c(0.5, NA, 3),
  social=runif(3, 1, 5),
  env=c(5, 2.5, 4))
dat <- rbind(maxmin,dat)

op <- par(mar=c(1, 2, 2, 1),mfrow=c(2, 2))
radarchart(dat, axistype=1, seg=5, plty=1, vlabels=c("Total\nQOL", "Physical\naspects", "Psychological\naspects", "Social\naspects", "Environmental\naspects"),
title="(axis=1, 5 segments, with specified vlabels)", vlcex=0.5)
radarchart(dat, axistype=2, pcol=topo.colors(3), plty=1, pdensity=c(5, 10, 30),
pangle=c(10, 45, 120), pfcol=topo.colors(3),
title="(topo.colors, fill, axis=2)"
)
radarchart(dat, axistype=3, pty=32, plty=1, axislabcol="grey", na.itp=FALSE,
title="(no points, axis=3, na.itp=FALSE)"
)
radarchart(dat, axistype=1, plwd=1:5, pcol=1, centerzero=TRUE,
seg=4, caxislabels=c("worst",",",",","best"),
title="(use lty and lwd but b/w, axis=1,\n centerzero=TRUE, with centerlabels)"
)
par(op)

ratedifference(a, b, PT1, PT0, CRC=FALSE, conf.level=0.95)

Arguments

a 
The number of disease occurrence among exposed cohort.
b 
The number of disease occurrence among non-exposed cohort.
**rateratio**

The observed person-time of the exposed cohort.

**PT1**

The observed person-time of the unexposed cohort.

**PT0**

Logical. If TRUE, calculate confidence intervals for each incidence rate. Default is FALSE.

**CRC**

Probability for confidence intervals. Default is 0.95.

**conf.level**

Calculate incidence rate ratio and its confidence intervals

**Value**

- **estimate**: Calculated point estimate of incidence rate difference.
- **conf.int**: A numeric vector of length 2 to give upper/lower limit of confidence intervals.
- **p.value**: The significant probability of the result of null-hypothesis testing.

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

**References**


**Examples**

```r
c <- ratedifference(136, 1709, 22050, 127650, CRC=TRUE)
str(c)
print(c)
```

---

**rateratio**  
_Calculate incidence rate ratio and its confidence intervals_

**Description**

Calculate incidence rate ratio (a kind of relative risk) and its confidence intervals based on approximation, followed by null hypothesis (incidence rate ratio equals to 1) testing.

**Usage**

```r
rateratio(a, b, PT1, PT0, conf.level=0.95)
```

**Arguments**

- **a**: The number of disease occurrence among exposed cohort.
- **b**: The number of disease occurrence among non-exposed cohort.
- **PT1**: The observed person-time of the exposed cohort.
- **PT0**: The observed person-time of the unexposed cohort.
- **conf.level**: Probability for confidence intervals. Default is 0.95.
Value

- `estimate`: Calculated point estimate of incidence rate ratio.
- `conf.int`: A numeric vector of length 2 to give upper/lower limit of confidence intervals.
- `p.value`: The significant probability of the result of null-hypothesis testing.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


Examples

```r
res <- rateratio(136, 1709, 22050, 127650)
str(res)
print(res)
```

---

RCI

*Calculate risk and its confidence interval*

Description

Calculate risk and its confidence interval by the simple asymptotic method.

Usage

```r
RCI(a, N, conf.level=0.9)
```

Arguments

- `a`: Number of cases
- `N`: Number of population at risk
- `conf.level`: Probability for confidence intervals. Default is 0.9.

Value

- `R`: Point estimate of risk.
- `RL`: Lower limit of confidence interval
- `RU`: Upper limit of confidence interval

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/
riskdifference

References

Examples
# By simple asymptotic method
RCI(20, 100)
# By Wilson Score (without continuity correction)
prop.test(20, 100, conf.level=0.9, correct=FALSE)
# By Exact method
binom.test(20, 100, conf.level=0.9)

Description
Calculate risk difference (a kind of attributable risk/excess risk) and its confidence intervals based on approximation, followed by null hypothesis (risk difference equals to 0) testing.

Usage
riskdifference(a, b, N1, N0, CRC=FALSE, conf.level=0.95)

Arguments
a The number of disease occurrence among exposed cohort.
b The number of disease occurrence among non-exposed cohort.
N1 The population at risk of the exposed cohort.
N0 The population at risk of the unexposed cohort.
CRC Logical. If TRUE, calculate confidence intervals for each risk. Default is FALSE.
conf.level Probability for confidence intervals. Default is 0.95.

Value
estimate Calculated point estimate of risk difference.
conf.int A numeric vector of length 2 to give upper/lower limit of confidence intervals.
p.value The significant probability of the result of null-hypothesis testing.

Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References
Examples

```r
res <- riskratio(321, 411, 686, 689, CRC=TRUE)
str(res)
print(res)
```

**riskratio**  
*Calculate risk ratio and its confidence intervals*

**Description**

Calculate risk ratio (a kind of relative risk) and its confidence intervals based on approximation, followed by null hypothesis (risk ratio equals to 1) testing.

**Usage**

```
riskratio(X, Y, m1, m2, conf.level=0.95, p.calc.by.independence=TRUE)
```

**Arguments**

- **X**: The number of disease occurrence among exposed cohort.
- **Y**: The number of disease occurrence among non-exposed cohort.
- **m1**: The number of individuals in exposed cohort group.
- **m2**: The number of individuals in non-exposed cohort group.
- **conf.level**: Probability for confidence intervals. Default is 0.95.
- **p.calc.by.independence**: Logical. If TRUE, calculating p-value by testing the null-hypothesis of independence between exposure and disease. Otherwise, calculating p-value by inverse-function of confidence intervals calculation (the result becomes the same as the vcd package). Default TRUE.

**Value**

- **estimate**: Calculated point estimate of risk ratio.
- **conf.int**: A numeric vector of length 2 to give upper/lower limit of confidence intervals.
- **p.value**: The significant probability of the result of null-hypothesis testing.

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

**References**

Examples

```r
res <- riskratio(5, 10, 90, 90)
str(res)
print(res)
riskratio(12, 5, 18, 17)
riskratio(12, 5, 18, 17, p.calc.by.independence=FALSE)
```

roc

**Calculate Receiver Operating Characteristic (ROC) curve**

Description

Calculate Receiver Operating Characteristic (ROC) curve’s each performance set of [sensitivity, 1-specificity], each distance of the performance from the worst performance [0, 1], and each piece of area under the curve, for each cutoff point, as list. Fittest cut off is suggested as the set of [sensitivity, 1-specificity] which gives the longest distance from [0, 1] (though it’s not common). If option maxdist=FALSE is given, the distances are calculated from the best performance [1, 0] and fittest cut off is the set of [sensitivity, 1-specificity] which gives minimum distance from best performance.

Usage

```r
roc(values, iscase, maxdist=TRUE)
```

Arguments

- `values`: A numeric vector of measured values.
- `iscase`: A logical (or 0/1) vector of diagnostics. Negative result must be given by `FALSE` or `0`.
- `maxdist`: A logical value to specify the method of distance calculation to seek the best cutoff. Default `TRUE`.

Value

- `cutoff`: The numeric vector of cutoff points, which are composed of the all unique values among the given measurements and the maximum cutoff is maximum measurement plus 1. Therefore, the minimum cutoff gives [1, 1] and the maximum cutoff gives [0, 0] as the performance set of [sensitivity, 1-specificity], respectively.
- `sens`: The numeric vector of sensitivities for all cutoff points.
- `falsepos`: The numeric vector of 1-specificities (false positiveness) for all cutoff points.
- `aucpiece`: The numeric vector of the pieces of areas under the curve.
- `maxdist`: Same as the given argument maxdist.
Author(s)
Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

See Also
ROC

Examples
```
scores <- c(15, 20, 19, 28, 26, 17, 13, 22, 23, 24)
diagno <- c(0, 0, 0, 1, 1, 1, 0, 1, 1, 1)
res <- roc(scores, diagno)
print(res)
plot(res)
```

S60MPJ Model population of Japan in Showa 60 (1985)

Description
The data gives the age-class (by five) specific model population of Japan in Showa 60 (1985) to calculate directly adjusted mortality rate.

Usage
S60MPJ

Format
A vector containing 18 observations.

Source

References
Siler Siler's model mortality for qx and its fitting

Description

Implementing Siler's model mortality function of qx and fitting the model to actual qx of given lifetable.

Usage

Siler(a1, b1, a2, a3, b3, t)
fitSiler(initialpar=c(0.01, 3, 1e-4, 1e-5, 0.1), data, mode=1, Method="Nelder-Mead", ...)

Arguments

a1 The parameter a1 of the Siler model, q(t)=a1*exp(-b1*t)+a2+a3*exp(b3*t).
b1 The parameter b1 of the Siler model, q(t)=a1*exp(-b1*t)+a2+a3*exp(b3*t).
a2 The parameter a2 of the Siler model, q(t)=a1*exp(-b1*t)+a2+a3*exp(b3*t).
a3 The parameter a3 of the Siler model, q(t)=a1*exp(-b1*t)+a2+a3*exp(b3*t).
b3 The parameter b3 of the Siler model, q(t)=a1*exp(-b1*t)+a2+a3*exp(b3*t).
t Age (vector OK) in years
initialpar Initial value for the parameters to be estimated. If not given, c(0.01, 0.0003, 0.07) is used.
data Actual vector of qx in the lifetable to be used to obtain the best-fit parameters of the Gompertz-Makeham model.
mode Which of lifetable functions should be used to calculate the RMSE: 1 qx, 2 dx, otherwise lx. Default is 1.
Method The method to be used in optim() function. Default is "Nelder-Mead".
... Other options to be passed to optim().

Value

Siler() returns model qx for the same length with t. fitSiler() returns the numeric vector of fitted parameters a1, b1, a2, a3 and b3, RMSE for those values, and the flag of convergence.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

See Also

Jlife
Examples

```r
res <- fitSiler(Jlife$qx2005M)
FLAG <- res[7]
while (FLAG>0) {
  res <- fitSiler(res[1:5], Jlife$qx2005M)
  FLAG <- res[7]
}
print(res)
```

---

**SIQR**

*Calculate semi-interquartile range*

Description

Calculate semi-interquartile range, using IQR or fivenum.

Usage

```r
SIQR(X, mode)
```

Arguments

- `X`: a numeric vector.
- `mode`: If 1, using fivenum, otherwise using IQR function. Default is 1.

Value

A numeric vector of length 1, giving the semi-interquartile range.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

Examples

```r
data <- rnorm(100, 10, 1)
SIQR(data)
SIQR(data, 2)
sd(data)
idata <- sample(50:80, 100, replace=TRUE)
SIQR(idata)
SIQR(idata, 2)
sd(idata)
```
spearman.ci.sas

Calculate Spearman’s rank correlation with its confidence intervals by SAS method

Description

Calculate Spearman’s rank correlation with its confidence intervals by the same method as SAS. Since fmsb-0.7.3, missing values are excluded pairwisely before calculation.

Usage

spearman.ci.sas(x, y, adj.bias=TRUE, conf.level=0.95)

Arguments

x A numeric vector.
y A numeric vector.
adj.bias Logical. If TRUE, adjustment for bias is taken. Default TRUE.
conf.level Probability for confidence intervals. Default is 0.95.

Value

rho Calculated point estimate of Spearman’s rank correlation coefficient.
rho.ll The lower limit of given confidence intervals.
rho.ul The upper limit of given confidence intervals.
adj.bias The option for bias adjustment taken.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


Examples

data(airquality)
spearman.ci.sas(airquality$Ozone, airquality$Wind)
Calculate true median for data with ties.

**Description**

Usually median for data with ties, tied values are treated as exactly same. For example, median of 3, 3, 4, 4, 4 will be 4. However, the measured values are usually rounded, so that we can assume evenly distributed true values for tied values. For example, the previous data can be treated as rounded values of 2.75, 3.25, 11/3, 4, 13/3. From this viewpoint, true median of 3, 3, 4, 4, 4 could be 11/3 (=3.66...). This function calculates this.

**Usage**

```r
truemedian(X, h)
```

**Arguments**

- **X**: A numeric vector. Usually integer.
- **h**: Width of measurement unit. Default is 1.

**Value**

A numeric vector of length 1, giving "true" median estimate.

**Author(s)**

Minato Nakazawa <minatonakazawa@gmail.com> [https://minato.sip21c.org/](https://minato.sip21c.org/)

**References**


**Examples**

```r
median(c(3, 3, 4, 4))
truedmedian(c(3, 3, 4, 4))
```
VIF

Calculate variance inflation factor (VIF) from the result of lm.

Description

To evaluate multicolinearity of multiple regression model, calculating the variance inflation factor (VIF) from the result of lm(). If VIF is more than 10, multicolinearity is strongly suggested.

Usage

VIF(X)

Arguments

X
  The object with class "lm", which would be generated by lm().

Value

A variance inflation factor is returned.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

Examples

# the target multiple regression model
res <- lm(Ozone ~ Wind+Temp+Solar.R, data=airquality)
summary(res)
# checking multicolinearity for independent variables.
VIF(lm(Wind ~ Temp+Solar.R, data=airquality))
VIF(lm(Temp ~ Wind+Solar.R, data=airquality))
VIF(lm(Solar.R ~ Wind+Temp, data=airquality))

WhipplesIndex

Whipple's Index

Description

Whipple's Index for age-heaping

Usage

WhipplesIndex(X)
Arguments

\( X \)  
The integer vector to give age-specific population from age 0 to more than 63 for each age.

Value

\( \text{WI} \)  
The Whipple's Index.

\( \text{JUDGE} \)  
Based on Whipple's Index, accuracy of age-reporting is judged.

Author(s)

Minato Nakazawa <minatonakazawa@gmail.com> https://minato.sip21c.org/

References


Examples

WhipplesIndex(Jpop$M2000)
India <- read.delim("https://minato.sip21c.org/ldaR/India2011census.txt")
WhipplesIndex(India$Males)
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