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Title Functions for Medical Statistics Book with some Demographic Data

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Depends R (>= 2.2.0)

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.

License GPL (>= 2)

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Contents

CaretakerRatio   *Caretaker Ratio*

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

Preston SH, Heuveline P, Guillot M (2001) Demography: Measuring and Modeling Population Processes. Blackwell Publishing, Oxford.

Newell C (1988) Methods and Models in Demography. The Guilford Press, New York.

Rowland DT (2003) Demographic methods and concepts. Oxford Univ. Press, Oxford.

Examples

```
# 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)
```

CM	*Coale and McNeil's model nupitiality and its fitting*

Description

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

Usage

```
 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 nupitiality. 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 nupitiality 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

Coale AJ, McNeil DR (1972) The distribution by age of the frequency of first marriage in a female cohort. Journal of the American Statistical Association, 67(340): 743-749.doi:10.1080/01621459.1972.10481287

Newell C (1988) Methods and Models in Demography. The Guilford Press, New York.

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=000001034991&cycode=0
 Ages <- 15:60
 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,
 0.479789489, 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, 0.909329207, 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\n for 2010 Japanese females")
fitted <- CM(res[1], res[2], res[3])
lines(Ages, fitted$G[6:51], col="red")
NoteForm <- "C=%3.1f, a0=%3.1f, k=%3.1f\n mu=%3.1f, sd=%3.1f"
text(40, 0.2, sprintf(NoteForm, res[1], res[2], res[3], fitted$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

Bland JM, Altman DG (1997) Statistics notes: Cronbach's alpha. BMJ, 314: 572.

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

Coale AJ, Trussell TJ (1978) Technical Note: Finding the Two Parameters That Specify a Model Schedule of Marital Fertility. Population Index, 44(2): 203-213.

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)
fitDenny(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

Denny C (1997) A model of the probability of survival from birth. Mathematical and Computer Modelling, 26: 69-78. doi:10.1016/S08957177(97)001702

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.

Author(s)

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

Examples

```
geary.test(rnorm(100))
geary.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*exp(B*t)+C.
B	The parameter B of the Gompertz-Makeham model u(t)=A*exp(B*t)+C.
C	The parameter C of the Gompertz-Makeham model u(t)=A*exp(B*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

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

---

gstem   *Draw 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/>

Examples

```
x <- rnorm(100, 10, 1)
stem(x)
stem(x, 2)
layout(t(1:2))
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

Tamura K. (2008) How do we die?: death date from vital statistics of the Japanese population. *The Waseda study of politics and public law*, 87: 27-57.

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*b/c*(c/x)^1.5*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*b/c*(c/x)^1.5*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*b/c*(c/x)^1.5*exp(-b^2*(c/x+x/c-2)) for age x from 15 to 54.
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

Chandola T, Coleman DA, Horns RW (1999) Recent European fertility patterns: fitting curves to 'distorted' distributions. Population Studies, 53(3): 317-329. doi:10.1080/00324720308089

See Also

Jfert

Examples

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

IndexOfDissimilarity   *Index of dissimilarity (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

Preston SH, Heuveline P, Guillot M (2001) Demography: Measuring and Modeling Population Processes. Blackwell Publishing, Oxford.

Newell C (1988) Methods and Models in Demography. The Guilford Press, New York.

Rowland DT (2003) Demographic methods and concepts. Oxford Univ. Press, Oxford.

Examples

```
# Dissimilarities of Japanese population structure were increasing
# from 1960-1980 (0.132) to 1980-2000 (0.156).
IndexOfDissimilarity(Jpopl$M1980+Jpopl$F1980, Jpopl$M2000+Jpopl$F2000)
IndexOfDissimilarity(Jpopl$M1980+Jpopl$F1980, Jpopl$M1960+Jpopl$F1960)
```

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/

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
IRCI(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/

References

https://www.statsdirect.com/help/rates/poisson_rate_ci.htm

Examples

```
IRCIPois(8, 85000)
```

| IRDMH | *Calculate pooled incidence rate difference and its confidence intervals with Mantel-Haenszel's method* |

Description

Calculate pooled incidence rate difference and its confidence intervals with Mantel-Haenszel's method.

Usage

```
IRDMH(XTAB, conf.level=0.9)
```

Arguments

XTAB   A matrix with 4 columns. The first column is the incidence in the exposed cohort. The second column is the incidence in the unexposed cohort. The third column is the observed person-time of exposed cohort. The forth column is the observed person-time of unexposed cohort. Rows should be composed of different strata or studies.

conf.level   Probability for confidence intervals. Default is 0.9.

Value

estimate   Calculated point estimate of pooled incidence rate difference with Manterl-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/

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
# Table 10-5 of Rothman's textbook (Chapter 10).
IRDMH(matrix(c(196, 111, 62119, 15763, 167, 157, 6085, 2780), 2, byrow=TRUE), conf.level=0.9)
```

IRRMH   *Calculate pooled incidence rate ratio and its confidence intervals with Mantel-Haenszel's method*

Description

Calculate pooled incidence rate ratio and its confidence intervals with Mantel-Haenszel's method.

Usage

```
IRRMH(XTAB, conf.level=0.9)
```

Arguments

XTAB	A matrix with 4 columns. The first column is the incidence in the exposed cohort. The second column is the incidence in the unexposed cohort. The third column is the observed person-time of exposed cohort. The forth column is the observed person-time of unexposed cohort. Rows should be composed of different strata or studies.
conf.level	Probability for confidence intervals. Default is 0.9.

Value

estimate	Calculated point estimate of pooled incidence rate ratio with Manterl-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/

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
# Table 10-5 of Rothman's textbook (Chapter 10).
IRRMH(matrix(c(196, 111, 62119, 15763, 167, 157, 6085, 2780), 2, byrow=TRUE), conf.level=0.9)
```

| 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
[, 8]	H27M	numeric	Number of males' death by age classes in 2015
[, 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
[,14]	H27F	numeric	Number of females' death by age classes in 2015
[,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
[,20]	H27MP	numeric	Number of males' population by age classes in 2015
[,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
[,25]	H17FP	numeric	Number of females' population by age classes in 2005
[,26]	H22FP	numeric	Number of females' population by age classes in 2010
[,26]	H27FP	numeric	Number of females' population by age classes in 2015

Details

Japanese mortality data by sex and age-class (by five) given as national official vital statitistics 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.
- `S60MP-H27MP`: Age class specific number of males' population in 1985-2015.
- `S60FP-H27FP`: Age class specific number of females' population in 1985-2015.

Source

https://www.stat.go.jp/english/data/nenkan/66nenkan/index.html

References

Ministry of Health, Labor and Welfare of Japan: Vital Statistics.

Jfert	*Age-specific fertility rates and age-specific marital fertility rates in Japan.*

Description

Age-specific fertility and marital fertility rates for aged 15-54 Japanese wowmen in Japan, from 1950 to 2020, every five years.

Usage

```
Jfert
```

Format

A data frame with 40 observations on 31 variables.

[, 1]	Age	integer	Ages of women
[, 2]	ASFR1950	numeric	Age-specific fertility rates of Japanese women in 1950.
[, 3]	ASFR1955	numeric	Age-specific fertility rates of Japanese women in 1955.
[, 4]	ASFR1960	numeric	Age-specific fertility rates of Japanese women in 1960.
[, 5]	ASFR1965	numeric	Age-specific fertility rates of Japanese women in 1965.
[, 6]	ASFR1970	numeric	Age-specific fertility rates of Japanese women in 1970.
[, 7]	ASFR1975	numeric	Age-specific fertility rates of Japanese women in 1975.

```
[, 8]    ASFR1980    numeric    Age-specific fertility rates of Japanese women in 1980.
[, 9]    ASFR1985    numeric    Age-specific fertility rates of Japanese women in 1985.
[,10]    ASFR1990    numeric    Age-specific fertility rates of Japanese women in 1990.
[,11]    ASFR1995    numeric    Age-specific fertility rates of Japanese women in 1995.
[,12]    ASFR2000    numeric    Age-specific fertility rates of Japanese women in 2000.
[,13]    ASFR2005    numeric    Age-specific fertility rates of Japanese women in 2005.
[,14]    ASFR2010    numeric    Age-specific fertility rates of Japanese women in 2010.
[,15]    ASFR2015    numeric    Age-specific fertility rates of Japanese women in 2015.
[,16]    ASFR2020    numeric    Age-specific fertility rates of Japanese women in 2020.
[,17]    ASMFR1950   numeric    Age-specific marital fertility rates of Japanese married women in 1950.
[,18]    ASMFR1955   numeric    Age-specific marital fertility rates of Japanese married women in 1955.
[,19]    ASMFR1960   numeric    Age-specific marital fertility rates of Japanese married women in 1960.
[,20]    ASMFR1965   numeric    Age-specific marital fertility rates of Japanese married women in 1965.
[,21]    ASMFR1970   numeric    Age-specific marital fertility rates of Japanese married women in 1970.
[,22]    ASMFR1975   numeric    Age-specific marital fertility rates of Japanese married women in 1975.
[,23]    ASMFR1980   numeric    Age-specific marital fertility rates of Japanese married women in 1980.
[,24]    ASMFR1985   numeric    Age-specific marital fertility rates of Japanese married women in 1985.
[,25]    ASMFR1990   numeric    Age-specific marital fertility rates of Japanese married women in 1990.
[,26]    ASMFR1995   numeric    Age-specific marital fertility rates of Japanese married women in 1995.
[,27]    ASMFR2000   numeric    Age-specific marital fertility rates of Japanese married women in 2000.
[,28]    ASMFR2005   numeric    Age-specific marital fertility rates of Japanese married women in 2005.
[,29]    ASMFR2010   numeric    Age-specific marital fertility rates of Japanese married women in 2010.
[,30]    ASMFR2015   numeric    Age-specific marital fertility rates of Japanese married women in 2015.
[,31]    ASMFR2020   numeric    Age-specific marital fertility rates of Japanese married women in 2020.
```

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.

- ASFR1950-ASFR2020: Age-specific fertility rates for all women aged 15-54 for 1950-2020, every 5 years.

- ASMFR1950-ASMFR2020: Age-specific marital fertility rates for married women aged 15-54 for 1950-2020, every 5 years.

Source

https://warp.da.ndl.go.jp/info:ndljp/pid/1334623/www.stat.go.jp/english/data/chouki/02.htm https://warp.da.ndl.go.jp/info:ndljp/pid/1334623/www.stat.go.jp/data/chouki/zuhyou/02-29-b.xls https://www.ipss.go.jp/syoushika/tohkei/Popular/P_Detail2022.asp?fname=T04-09.htm https://www.e-stat.go.jp/stat-search/file-download?statInfId=000032118572&fileKind=1 https://www.e-stat.go.jp/stat-search/file-download?statInfId=000032142474&fileKind=0

References

Ministry of Health, Labor and Welfare of Japan: Vital Statistics. / Ministry of Internal Affairs and Communications, Statistics Bureau: Population Census.

Jlife   *Completed lifetables in Japan.*

Description

The qx column of the completed lifetables in Japan, from "1891-1898" to "2020", mostly every 5 years.

Usage

```
Jlife
```

Format

A data frame with 117 observations (NAs are filled for the ages with no survivors) on 45 variables.

[, 1]	Age	integer	Ages of women
[, 2]	qx1895M	numeric	qx of completed lifetable functions of Japanese men in 1891-1898.
[, 3]	qx1895F	numeric	qx of completed lifetable functions of Japanese women in 1891-1898.
[, 4]	qx1901M	numeric	qx of completed lifetable functions of Japanese men in 1899-1903.
[, 5]	qx1901F	numeric	qx of completed lifetable functions of Japanese women in 1899-1903.
[, 6]	qx1911M	numeric	qx of completed lifetable functions of Japanese men in 1909-1913.
[, 7]	qx1911F	numeric	qx of completed lifetable functions of Japanese women in 1909-1913.
[, 8]	qx1923M	numeric	qx of completed lifetable functions of Japanese men in 1921-1925.
[, 9]	qx1923F	numeric	qx of completed lifetable functions of Japanese women in 1921-1925.
[,10]	qx1928M	numeric	qx of completed lifetable functions of Japanese men in 1926-1930.
[,11]	qx1928F	numeric	qx of completed lifetable functions of Japanese women in 1926-1930.
[,12]	qx1935M	numeric	qx of completed lifetable functions of Japanese men in 1935-1936.
[,13]	qx1935F	numeric	qx of completed lifetable functions of Japanese women in 1935-1936.
[,14]	qx1947M	numeric	qx of completed lifetable functions of Japanese men in 1947.
[,15]	qx1947F	numeric	qx of completed lifetable functions of Japanese women in 1947.
[,16]	qx1951M	numeric	qx of completed lifetable functions of Japanese men in 1950-1952.
[,17]	qx1951F	numeric	qx of completed lifetable functions of Japanese women in 1950-1952.
[,18]	qx1955M	numeric	qx of completed lifetable functions of Japanese men in 1955.
[,19]	qx1955F	numeric	qx of completed lifetable functions of Japanese women in 1955.
[,20]	qx1960M	numeric	qx of completed lifetable functions of Japanese men in 1960.
[,21]	qx1960F	numeric	qx of completed lifetable functions of Japanese women in 1960.
[,22]	qx1965M	numeric	qx of completed lifetable functions of Japanese men in 1965.
[,23]	qx1965F	numeric	qx of completed lifetable functions of Japanese women in 1965.
[,24]	qx1970M	numeric	qx of completed lifetable functions of Japanese men in 1970.
[,25]	qx1970F	numeric	qx of completed lifetable functions of Japanese women in 1970.
[,26]	qx1975M	numeric	qx of completed lifetable functions of Japanese men in 1975.

```
[,27]   qx1975F   numeric   qx of completed lifetable functions of Japanese women in 1975.
[,28]   qx1980M   numeric   qx of completed lifetable functions of Japanese men in 1980.
[,29]   qx1980F   numeric   qx of completed lifetable functions of Japanese women in 1980.
[,30]   qx1985M   numeric   qx of completed lifetable functions of Japanese men in 1985.
[,31]   qx1985F   numeric   qx of completed lifetable functions of Japanese women in 1985.
[,32]   qx1990M   numeric   qx of completed lifetable functions of Japanese men in 1990.
[,33]   qx1990F   numeric   qx of completed lifetable functions of Japanese women in 1990.
[,34]   qx1995M   numeric   qx of completed lifetable functions of Japanese men in 1995.
[,35]   qx1995F   numeric   qx of completed lifetable functions of Japanese women in 1995.
[,36]   qx2000M   numeric   qx of completed lifetable functions of Japanese men in 2000.
[,37]   qx2000F   numeric   qx of completed lifetable functions of Japanese women in 2000.
[,38]   qx2005M   numeric   qx of completed lifetable functions of Japanese men in 2005.
[,39]   qx2005F   numeric   qx of completed lifetable functions of Japanese women in 2005.
[,40]   qx2010M   numeric   qx of completed lifetable functions of Japanese men in 2010.
[,41]   qx2010F   numeric   qx of completed lifetable functions of Japanese women in 2010.
[,42]   qx2015M   numeric   qx of completed lifetable functions of Japanese men in 2015.
[,43]   qx2015F   numeric   qx of completed lifetable functions of Japanese women in 2015.
[,44]   qx2020M   numeric   qx of completed lifetable functions of Japanese men in 2020.
[,45]   qx2020F   numeric   qx of completed lifetable functions of Japanese women in 2020.
```

Details

qx columns were cited from the completed life tables in Japan for the 1st to 23rd one (7th one was not made, so that it is missing).

- `Age`: Ages from 0 to 116.

- `qx1895M-qx2020M`: qx of 1st to 23rd completed lifetables for Japanese men.

- `qx1895F-qx2020F`: qx of 1st to 23rd completed lifetables for Japanese women.

Source

https://warp.da.ndl.go.jp/info:ndljp/pid/1334623/www.stat.go.jp/english/data/chouki/02.htm https://warp.da.ndl.go.jp/collections/content/info:ndljp/pid/11423429/www.stat.go.jp/data/chouki/zuhyou/02-35.xls https://www.mhlw.go.jp/toukei/saikin/hw/life/20th/index.html https://www.mhlw.go.jp/toukei/saikin/hw/life/21th/index.html https://www.mhlw.go.jp/toukei/saikin/hw/life/22th/index.html https://www.mhlw.go.jp/toukei/saikin/hw/life/23th/index.html

References

Ministry of Health, Labor and Welfare of Japan: Completed lifetables. / Ministry of Internal Affairs and Communications, Statistics Bureau: Historical Statistics of Japan.

	Jpop		*Japanese population data*

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.

[, 1]	Age	Factor w/86 levels	Ages (years old, combined for 85+)
[, 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
[,10]	M1908	numeric	Age specific population of males in 1908
[,11]	F1908	numeric	Age specific population of females in 1908
[,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
[,16]	M1920	numeric	Age specific population of males in 1920
[,17]	F1920	numeric	Age specific population of females in 1920
[,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
[,23]	F1935	numeric	Age specific population of females in 1935
[,24]	M1940	numeric	Age specific population of males in 1940
[,25]	F1940	numeric	Age specific population of females in 1940
[,26]	M1947	numeric	Age specific population of males in 1947
[,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

[,33]	F1960	numeric	Age specific population of females in 1960
[,34]	M1965	numeric	Age specific population of males in 1965
[,35]	F1965	numeric	Age specific population of females in 1965
[,36]	M1970	numeric	Age specific population of males in 1970
[,37]	F1970	numeric	Age specific population of females in 1970
[,38]	M1975	numeric	Age specific population of males in 1975
[,39]	F1975	numeric	Age specific population of females in 1975
[,40]	M1980	numeric	Age specific population of males in 1980
[,41]	F1980	numeric	Age specific population of females in 1980
[,42]	M1985	numeric	Age specific population of males in 1985
[,43]	F1985	numeric	Age specific population of females in 1985
[,44]	M1990	numeric	Age specific population of males in 1990
[,45]	F1990	numeric	Age specific population of females in 1990
[,46]	M1995	numeric	Age specific population of males in 1995
[,47]	F1995	numeric	Age specific population of females in 1995
[,48]	M2000	numeric	Age specific population of males in 2000
[,49]	F2000	numeric	Age specific population of females in 2000
[,50]	M2005	numeric	Age specific population of males in 2005
[,51]	F2005	numeric	Age specific population of females in 2005
[,52]	M2010	numeric	Age specific population of males in 2010
[,53]	F2010	numeric	Age specific population of females in 2010
[,54]	M2015	numeric	Age specific population of males in 2015
[,55]	F2015	numeric	Age specific population of females in 2015
[,56]	M2015J	numeric	Age specific population of Japanese males in 2015
[,57]	F2015J	numeric	Age specific population of Japanese females in 2015
[,58]	M2020	numeric	Age specific population of males in 2020
[,59]	F2020	numeric	Age specific population of females in 2020
[,60]	M2020J	numeric	Age specific population of Japanese males in 2020
[,61]	F2020J	numeric	Age specific population of Japanese females in 2020

Details

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

- Age: Ages, combined for 85+.
- M1888-M2020: Age specific number of males' population in 1988-2020.
- F1888-F2020: Age specific number of females' population in 1988-2020.
- M2015J-M2020J: Age specific number of the Japanese population of males in 2015-2020.
- F2015J-F2020J: Age specific number of the Japanese population of females in 2015-2020.

Source

https://www.stat.go.jp/english/data/kokusei/index.html https://warp.da.ndl.go.jp/info:ndljp/pid/1334623/www.stat.go.jp/english/data/chouki/02.htm https://www.e-stat.go.jp/stat-search/files/data?fileid=000007809775&rcount=3 https://www.e-stat.go.jp/stat-search/file-download?statInfId=000032142404&fileKind=0

References

Statistics Bureau, Ministry of Internal Affairs and Communications: Population Census, 1888-2020.

Jpopl	*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
[,10]	M1908	numeric	Age specific population of males in 1908
[,11]	F1908	numeric	Age specific population of females in 1908
[,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
[,16]	M1920	numeric	Age specific population of males in 1920
[,17]	F1920	numeric	Age specific population of females in 1920
[,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
[,23]	F1935	numeric	Age specific population of females in 1935
[,24]	M1940	numeric	Age specific population of males in 1940
[,25]	F1940	numeric	Age specific population of females in 1940
[,26]	M1947	numeric	Age specific population of males in 1947
[,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
[,33]	F1960	numeric	Age specific population of females in 1960
[,34]	M1965	numeric	Age specific population of males in 1965
[,35]	F1965	numeric	Age specific population of females in 1965
[,36]	M1970	numeric	Age specific population of males in 1970
[,37]	F1970	numeric	Age specific population of females in 1970
[,38]	M1975	numeric	Age specific population of males in 1975
[,39]	F1975	numeric	Age specific population of females in 1975
[,40]	M1980	numeric	Age specific population of males in 1980
[,41]	F1980	numeric	Age specific population of females in 1980
[,42]	M1985	numeric	Age specific population of males in 1985
[,43]	F1985	numeric	Age specific population of females in 1985
[,44]	M1990	numeric	Age specific population of males in 1990
[,45]	F1990	numeric	Age specific population of females in 1990
[,46]	M1995	numeric	Age specific population of males in 1995
[,47]	F1995	numeric	Age specific population of females in 1995
[,48]	M2000	numeric	Age specific population of males in 2000
[,49]	F2000	numeric	Age specific population of females in 2000
[,50]	M2000J	numeric	Age specific population of Japanese males in 2000
[,51]	F2000J	numeric	Age specific population of Japanese females in 2000
[,52]	M2005	numeric	Age specific population of males in 2005
[,53]	F2005	numeric	Age specific population of females in 2005
[,54]	M2005J	numeric	Age specific population of Japanese males in 2005
[,55]	F2005J	numeric	Age specific population of Japanese females in 2005
[,56]	M2010	numeric	Age specific population of males in 2010
[,57]	F2010	numeric	Age specific population of females in 2010
[,58]	M2010J	numeric	Age specific population of Japanese males in 2010
[,59]	F2010J	numeric	Age specific population of Japanese females in 2010
[,60]	M2015	numeric	Age specific population of males in 2015
[,61]	F2015	numeric	Age specific population of females in 2015
[,62]	M2015J	numeric	Age specific population of Japanese males in 2015
[,63]	F2015J	numeric	Age specific population of Japanese females in 2015
[,64]	M2020	numeric	Age specific population of males in 2020
[,65]	F2020	numeric	Age specific population of females in 2020
[,66]	M2020J	numeric	Age specific population of Japanese males in 2020
[,67]	F2020J	numeric	Age specific population of Japanese females in 2020

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.

Source

https://www.stat.go.jp/english/data/kokusei/index.html https://warp.da.ndl.go.jp/info:ndljp/pid/1334623/www.stat.go.jp/english/data/chouki/02.htm https://www.e-stat.go.jp/stat-search/files/data?fileid=000007809775&rcount=3 https://www.e-stat.go.jp/stat-search/file-download?statInfId=000032142404&fileKind=0

References

Statistics Bureau, Ministry of Internal Affairs and Communications: Population Census, 1888-2020.

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 121 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 statitistics every year from 1899 to 2022, except for 1944-1946.

- YEAR: Calender year.
- 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.
- 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)] per 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)* 100,000.

Source

https://www.mhlw.go.jp/toukei/list/dl/81-1a2.pdf https://www.mhlw.go.jp/toukei/saikin/
hw/jinkou/geppo/nengai10/toukei02.html https://www.ipss.go.jp/p-info/e/psj2012/PSJ2012-05.
xls https://www.mhlw.go.jp/english/database/db-hw/vs01.html https://www.e-stat.go.
jp/stat-search/files/data?sinfid=000022220050&ext=csv https://www.mhlw.go.jp/toukei/
saikin/hw/jinkou/kakutei12/ https://www.e-stat.go.jp/stat-search/files/data?sinfid=
000022220091&ext=csv https://www.mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei13/ https:
//www.mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei14/ https://www.mhlw.go.jp/toukei/
saikin/hw/jinkou/kakutei15/ https://www.mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei16/
https://www.mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei17/ https://www.mhlw.go.jp/
toukei/saikin/hw/jinkou/kakutei18/ https://www.mhlw.go.jp/toukei/saikin/hw/jinkou/
kakutei19/ https://www.mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei20/ https://www.
mhlw.go.jp/toukei/saikin/hw/jinkou/kakutei21/ https://www.mhlw.go.jp/toukei/saikin/
hw/jinkou/kakutei22/ https://www.ipss.go.jp/syoushika/tohkei/Popular/P_Detail2021.
asp?fname=T05-28.htm https://www.e-stat.go.jp/stat-search/file-download?statInfId=
000040098325&fileKind=1

References

Ministry of Health, Labor and Welfare of Japan: Vital Statistics.

National Institute for Population and Social Security Research: Table 5-28 of Population Statistics of Japan 2019.

Jvital2013byPref	*Cross sectional data of several vital statistics in Japan 2013 for each prefecture*

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
[,10]   ACRPB        numeric       Artificial contraception rates
[,11]   PNMPB        numeric       Perinatal mortalities per birth
[,12]   SBRA22W      numeric       Stillbirth rate after gestational age of 22 weeks per birth
[,13]   ENMR         numeric       Early neonatal mortality rate per live birth
[,14]   MR           numeric       Marriage rates
[,15]   DR           numeric       Divorce rates
[,16]   TFR          numeric       Total fertility rates
[,17]   CSM.ALL      numeric       Cause-specific mortality for all causes
[,18]   CSM.CANCER   numeric       Cause-specific mortality for cancer
[,19]   CSM.HD       numeric       Cause-specific mortality for heart disease except for hypertention
[,20]   CSM.PNEUM    numeric       Cause-specific mortality for pneumonia
[,21]   CSM.CEVD     numeric       Cause-specific mortality for cerebrovascular disease
[,22]   CSM.SEN      numeric       Cause-specific mortality for senescence
[,23]   CSM.ACC      numeric       Cause-specific mortality for accidents
[,24]   CSM.SUI      numeric       Cause-specific mortality for suicide
[,25]   CSM.KF       numeric       Cause-specific mortality for kidney failure
[,26]   CSM.COPD     numeric       Cause-specific mortality for chronic obstructive pulmonary disease
[,27]   CSM.AA       numeric       Cause-specific mortality for aneuysm of aorta
[,28]   CSM.LIVD     numeric       Cause-specific mortality for liver disease
[,29]   CSM.DIAB     numeric       Cause-specific mortality for diabetes
[,30]   CSM.SEP      numeric       Cause-specific mortality for sepsis
[,31]   CSM.MNP      numeric       Cause-specific mortality for miscellaneous neoplasms
[,32]   CSM.DEM      numeric       Cause-specific mortality for dementia
[,33]   CSM.TB       numeric       Cause-specific mortality for tuberculosis
[,34]   CSM.TA       numeric       Cause-specific mortality for traffic accidents
```

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 aneuysm 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

Ministry of Health, Labor and Welfare of Japan: Vital Statistics 2013.

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)

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References

Landis JR, Koch GG (1977) The measurement of observer agreement for categorical data. Biometrics, 33: 159-174.

See Also

Kappa

Examples

```
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

```
lifetable(mx, ns=NULL, class=5, mode=1)
lifetable2(mx, ax=0.5, n=1)
lifetable3(lx, ax=0.5, n=1)
clifetable(qx)
lxtodx(lx)
dxtolx(dx)
qxtodx(qx)
dxtoqx(dx)
qxtomx(qx, ax=0.5, n=1, mmax=NULL)
mxtoqx(mx, ax=0.5, n=1)
qxtolx(qx)
lxtoqx(lx)
uxtoqx(ux)
hlifetable(mx, ax=0.5, n=5, pix=0, Nx=NULL, conf.level=0.95)
getax(lx, Tx, n=5)
```

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

Preston SH, Heuveline P, Guillot M (2001) Demography: Measuring and Modeling Population Processes. Blackwell Publishing, Oxford.

Newell C (1988) Methods and Models in Demography. The Guilford Press, New York.

Sullivan DF (1971) A single index of mortality and morbidity. HSMHA Health Reports, 86: 347-354.

See Also

Jlife

Examples

```
lifetable(c(0.0087, 0.00015, 0.00019, 0.00098, 0.0013, 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, 0.002485, 0.004210, 0.007219, 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, 0.8070, 0.7876, 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, 20)), ax=c(0.3, rep(0.5, 24))) # Newell, Table 13.1
clifetable(Jlife$qx2000F)
```

---

mhchart	*Draw maternity history charts.*

Description

To compare the maternity histories among several human populations, this kind of graph is useful, inspired by Wood JW (1994) "Dynamics of Human Reproduction", Aldine de Gruyter, New York.

Usage

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

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

Nagelkerke N (1991) A note on a general definition of the coefficient of determination. Biometrika, 78: 691-692.

Faraway JJ (2006) Extending the linear models with R: Generalized linear, mixed effects and non-parametric regression models. Chapman and Hall.

<https://minato.sip21c.org/grad/infop-text2012.pdf>

Examples

```
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

```
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 disesase 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 disesase but not exposed. Otherwise, ignored.

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.
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.
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 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

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
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

```
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 Manterl-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/

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
# 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,
```

```
    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 occurences

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

```
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

```
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/

References

Kuroda T (1976) Japan's Changing Population Structure (in Japanese). Kokon-Shoin, Tokyo.

Kuroda T (1971) A study on population composition: Special reference to Japan. (in Japanese, with abstract in English) Journal of Population Problems (Jinko-Mondai-Kenkyu), No. 119: 1-12. https://www.ipss.go.jp/syoushika/bunken/data/pdf/j119.pdf

Examples

```
# 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}
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, 90, 107, 122, 142, 146, 125, 121, 131,
  157, 127, 101, 76, 84),
 Gumma = 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, 500, 494),
 Kanagawa = c(351, 374, 385, 423, 518, 490, 529, 592, 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, 230, 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),
```

```
    Mie = c(67, 75, 80, 87, 82, 81, 92, 102, 125, 135, 118, 111, 109, 135,
     122, 103, 80, 88),
    Shiga = c(61, 67, 69, 74, 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, 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, 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))
# }
```

```
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)

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Examples

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

Prefe0	*Changes of life expectancy at birth for each prefecture in Japan since 1965*

Description

The data gives the estimates of life expectancy at birth (e0) for each prefecture in Japan since 1965.

Usage

```
Prefe0
```

Format

A data frame with 47 observations on 26 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]	E0M.1965	numeric	Life expectancy at birth of each prefecture for males in 1965
[, 4]	E0M.1970	numeric	Life expectancy at birth of each prefecture for males in 1970
[, 5]	E0M.1975	numeric	Life expectancy at birth of each prefecture for males in 1975
[, 6]	E0M.1980	numeric	Life expectancy at birth of each prefecture for males in 1980
[, 7]	E0M.1985	numeric	Life expectancy at birth of each prefecture for males in 1985
[, 8]	E0M.1990	numeric	Life expectancy at birth of each prefecture for males in 1990
[, 9]	E0M.1995	numeric	Life expectancy at birth of each prefecture for males in 1995
[,10]	E0M.2000	numeric	Life expectancy at birth of each prefecture for males in 2000
[,11]	E0M.2005	numeric	Life expectancy at birth of each prefecture for males in 2005
[,12]	E0M.2010	numeric	Life expectancy at birth of each prefecture for males in 2010
[,13]	E0M.2015	numeric	Life expectancy at birth of each prefecture for males in 2015
[,14]	E0M.2020	numeric	Life expectancy at birth of each prefecture for males in 2020
[,15]	E0F.1965	numeric	Life expectancy at birth of each prefecture for females in 1965
[,16]	E0F.1970	numeric	Life expectancy at birth of each prefecture for females in 1970
[,17]	E0F.1975	numeric	Life expectancy at birth of each prefecture for females in 1975
[,18]	E0F.1980	numeric	Life expectancy at birth of each prefecture for females in 1980
[,19]	E0F.1985	numeric	Life expectancy at birth of each prefecture for females in 1985
[,20]	E0F.1990	numeric	Life expectancy at birth of each prefecture for females in 1990
[,21]	E0F.1995	numeric	Life expectancy at birth of each prefecture for females in 1995
[,22]	E0F.2000	numeric	Life expectancy at birth of each prefecture for females in 2000
[,23]	E0F.2005	numeric	Life expectancy at birth of each prefecture for females in 2005
[,24]	E0F.2010	numeric	Life expectancy at birth of each prefecture for females in 2010
[,25]	E0F.2015	numeric	Life expectancy at birth of each prefecture for females in 2015
[,26]	E0F.2020	numeric	Life expectancy at birth of each prefecture for females in 2020

Details

Life expectancy at birth for each prefecture in Japan since 1965.

- PNAME: The name (in roma-ji) for prefectures.

- JCODE: Prefecture number defined by Geographical Information Authority of Japan. From 1 to 47.

- E0[M|F].*: Life expectancy at birth (e0) of each prefecture for males ([M]) or for females ([F]) in year (*).

Source

https://www.mhlw.go.jp/toukei/saikin/hw/life/tdfk20/dl/tdfk20-08.xls

References

Ministry of Health, Labor and Welfare of Japan: Vital Statistics with Life Expectancy 2020. https://minato.sip21c.org/demography/how-to-make-pref-charts.html (in Japanese), WHO https://www.who.int/data/gho/data/themes/mortality-and-global-health-estimates

Examples

```
require(fmsb)
x <- Prefe0
males <- t(x[, 3:14])
colnames(males) <- x$PNAME
females <- t(x[, 15:26])
colnames(females) <- x$PNAME
COL <- ifelse(x$PNAME=="Nagano", "blue", ifelse(x$PNAME=="Okinawa", "red", "lightgrey"))
LWD <- ifelse(x$PNAME=="Nagano", 2, ifelse(x$PNAME=="Okinawa", 2, 1))
LTY <- ifelse(x$PNAME=="Nagano", 1, ifelse(x$PNAME=="Okinawa", 1, 3))
years <- 1965+0:11*5
layout(t(1:2))
matplot(years, males, type="l", col=COL, lwd=LWD, lty=LTY,
 main="Changes of e0 for males in each prefecture of Japan
 (Blue: Nagano, Red: Okinawa, Grey: Other)")
matplot(years, females, type="l", col=COL, lwd=LWD, lty=LTY,
 main="Changes of e0 for females in each prefecture of Japan
 (Blue: Nagano, Red: Okinawa, Grey: Other)")
```

PrefYLL2010   *Years of Life Lost by several causes in Japan 2010 for each prefecture*

Description

The data gives years of life lost by several causes in Japan 2010 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, 2010).

Usage

```
PrefYLL2010
```

Format

A data frame with 47 observations on 28 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]	CancerM	numeric	Years of Life Lost (YLL) of males by cancer
[, 4]	CardioM	numeric	Years of Life Lost (YLL) of males by heart diseases except for hypertention
[, 5]	CerebroM	numeric	Years of Life Lost (YLL) of males by cerebrovascular disease
[, 6]	Top3M	numeric	Years of Life Lost (YLL) of males by cancer, heart disease or cerebrovascular dis
[, 7]	PneumoniaM	numeric	Years of Life Lost (YLL) of males by pneumonia
[, 8]	AccidentM	numeric	Years of Life Lost (YLL) of males by accident
[, 9]	TrafficM	numeric	Years of Life Lost (YLL) of males by traffic accidents
[,10]	SuicideM	numeric	Years of Life Lost (YLL) of males by suicide
[,11]	KidneyM	numeric	Years of Life Lost (YLL) of males by kidney failure
[,12]	LiverM	numeric	Years of Life Lost (YLL) of males by liver disease
[,13]	DiabetesM	numeric	Years of Life Lost (YLL) of males by diabetes
[,14]	HypertensM	numeric	Years of Life Lost (YLL) of males by hypertension
[,15]	Covid19M	numeric	Years of Life Lost (YLL) of males by tuberculosis
[,16]	CancerF	numeric	Years of Life Lost (YLL) of females by cancer
[,17]	CardioF	numeric	Years of Life Lost (YLL) of females by heart diseases except for hypertention
[,18]	CerebroF	numeric	Years of Life Lost (YLL) of females by cerebrovascular disease
[,19]	Top3F	numeric	Years of Life Lost (YLL) of females by cancer, heart disease or cerebrovascular c
[,20]	PneumoniaF	numeric	Years of Life Lost (YLL) of females by pneumonia
[,21]	AccidentF	numeric	Years of Life Lost (YLL) of females by accident
[,22]	TrafficF	numeric	Years of Life Lost (YLL) of females by traffic accidents
[,23]	SuicideF	numeric	Years of Life Lost (YLL) of females by suicide
[,24]	KidneyF	numeric	Years of Life Lost (YLL) of females by kidney failure
[,25]	LiverF	numeric	Years of Life Lost (YLL) of females by liver disease
[,26]	DiabetesF	numeric	Years of Life Lost (YLL) of females by diabetes
[,27]	HypertensF	numeric	Years of Life Lost (YLL) of females by hypertension
[,28]	Covid19F	numeric	Years of Life Lost (YLL) of females by tuberculosis

Details

Years of Life Lost by several causes in Japan 2010 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.
- Cancer[M|F]: YLL by cancer for males ([M]) or for females ([F]).
- Cardio[M|F]: YLL by heart disease for males ([M]) or for females ([F]).
- Cerebro[M|F]: YLL by cerebrovascular disease for males ([M]) or for females ([F]).
- Top3[M|F]: YLL by above 3 major diseases for males ([M]) or for females ([F]).
- Peumonia[M|F]: YLL by pneumonia for males ([M]) or for females ([F]).
- Accident[M|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 diabates 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/tdfk10/dl/zuhyou.xls

References

Ministry of Health, Labor and Welfare of Japan: Vital Statistics with Life Expectancy 2010. https://minato.sip21c.org/demography/how-to-make-pref-charts.html (in Japanese), WHO https://www.who.int/data/gho/data/themes/mortality-and-global-health-estimates

Examples

```
require(fmsb)
x <- PrefYLL2010
COL <- ifelse(x$PNAME=="Nagano", "blue", ifelse(x$PNAME=="Okinawa", "red",
             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","Top3","Pneumonia",
 "Accident","(Traffic\n Accident)","Suicide","Kidney\n Failure","Liver\n Disease",
 "Diabetes","Hypertension","Tuberculosis")
males <- x[,3:15]
females <- x[,16:28]
layout(t(1:2))
radarchart(males, maxmin=FALSE, pcol=COL, axistype=2, pty=32, plty=LTY, plwd=LWD, vlabels=VX,
 title="YLLs in males (2010)\n (Blue: Nagano, Green: Shiga,\n Red: Okinawa, Gray: Others)")
radarchart(females, maxmin=FALSE, pcol=COL, axistype=2, pty=32, plty=LTY, plwd=LWD, vlabels=VX,
 title="YLL in females (2010)\n (Blue: Nagano, Green: Shiga,\n Red: Okinawa, Gray: Others)")
```

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.

[, 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]	CancerM	numeric	Years of Life Lost (YLL) of males by cancer
[, 4]	CardioM	numeric	Years of Life Lost (YLL) of males by heart diseases except for hypertention
[, 5]	CerebroM	numeric	Years of Life Lost (YLL) of males by cerebrovascular disease
[, 6]	PneumoniaM	numeric	Years of Life Lost (YLL) of males by pneumonia
[, 7]	AccidentM	numeric	Years of Life Lost (YLL) of males by accident
[, 8]	TrafficM	numeric	Years of Life Lost (YLL) of males by traffic accidents
[, 9]	SuicideM	numeric	Years of Life Lost (YLL) of males by suicide
[,10]	KidneyM	numeric	Years of Life Lost (YLL) of males by kidney failure
[,11]	LiverM	numeric	Years of Life Lost (YLL) of males by liver disease
[,12]	DiabetesM	numeric	Years of Life Lost (YLL) of males by diabetes
[,13]	HypertensM	numeric	Years of Life Lost (YLL) of males by hypertension
[,14]	TBM	numeric	Years of Life Lost (YLL) of males by tuberculosis
[,15]	CancerF	numeric	Years of Life Lost (YLL) of females by cancer
[,16]	CardioF	numeric	Years of Life Lost (YLL) of females by heart diseases except for hypertention
[,17]	CerebroF	numeric	Years of Life Lost (YLL) of females by cerebrovascular disease
[,18]	PneumoniaF	numeric	Years of Life Lost (YLL) of females by pneumonia
[,19]	AccidentF	numeric	Years of Life Lost (YLL) of females by accident
[,20]	TrafficF	numeric	Years of Life Lost (YLL) of females by traffic accidents
[,21]	SuicideF	numeric	Years of Life Lost (YLL) of females by suicide
[,22]	KidneyF	numeric	Years of Life Lost (YLL) of females by kidney failure
[,23]	LiverF	numeric	Years of Life Lost (YLL) of females by liver disease
[,24]	DiabetesF	numeric	Years of Life Lost (YLL) of females by diabetes
[,25]	HypertensF	numeric	Years of Life Lost (YLL) of females by hypertension
[,26]	TBF	numeric	Years of Life Lost (YLL) of females by tuberculosis

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.
- Cancer[M|F]: YLL by cancer for males ([M]) or for females ([F]).
- Cardio[M|F]: YLL by heart disease for males ([M]) or for females ([F]).
- Cerebro[M|F]: YLL by cerebrovascular disease for males ([M]) or for females ([F]).
- Peumonia[M|F]: YLL by pneumonia for males ([M]) or for females ([F]).
- Accident[M|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 diabates 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

Ministry of Health, Labor and Welfare of Japan: Vital Statistics with Life Expectancy 2015. https://minato.sip21c.org/demography/how-to-make-pref-charts.html (in Japanese), WHO https://www.who.int/data/gho/data/themes/mortality-and-global-health-estimates

Examples

```
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)")
```

PrefYLL2020   *Years of Life Lost by several causes in Japan 2020 for each prefecture*

Description

The data gives years of life lost by several causes in Japan 2020 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, 2020). Until 2015, deaths caused by tuberculosis were analyzed, but in 2020, deaths caused by COVID-19 are calculated instead.

Usage

```
PrefYLL2020
```

Format

A data frame with 47 observations on 28 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]	CancerM	numeric	Years of Life Lost (YLL) of males by cancer
[, 4]	CardioM	numeric	Years of Life Lost (YLL) of males by heart diseases except for hypertention
[, 5]	CerebroM	numeric	Years of Life Lost (YLL) of males by cerebrovascular disease
[, 6]	Top3M	numeric	Years of Life Lost (YLL) of males by cancer, heart disease or cerebrovascular dis
[, 7]	PneumoniaM	numeric	Years of Life Lost (YLL) of males by pneumonia
[, 8]	AccidentM	numeric	Years of Life Lost (YLL) of males by accident
[, 9]	TrafficM	numeric	Years of Life Lost (YLL) of males by traffic accidents
[,10]	SuicideM	numeric	Years of Life Lost (YLL) of males by suicide
[,11]	KidneyM	numeric	Years of Life Lost (YLL) of males by kidney failure
[,12]	LiverM	numeric	Years of Life Lost (YLL) of males by liver disease
[,13]	DiabetesM	numeric	Years of Life Lost (YLL) of males by diabetes
[,14]	HypertensM	numeric	Years of Life Lost (YLL) of males by hypertension
[,15]	Covid19M	numeric	Years of Life Lost (YLL) of males by tuberculosis
[,16]	CancerF	numeric	Years of Life Lost (YLL) of females by cancer
[,17]	CardioF	numeric	Years of Life Lost (YLL) of females by heart diseases except for hypertention
[,18]	CerebroF	numeric	Years of Life Lost (YLL) of females by cerebrovascular disease
[,19]	Top3F	numeric	Years of Life Lost (YLL) of females by cancer, heart disease or cerebrovascular c
[,20]	PneumoniaF	numeric	Years of Life Lost (YLL) of females by pneumonia
[,21]	AccidentF	numeric	Years of Life Lost (YLL) of females by accident
[,22]	TrafficF	numeric	Years of Life Lost (YLL) of females by traffic accidents
[,23]	SuicideF	numeric	Years of Life Lost (YLL) of females by suicide
[,24]	KidneyF	numeric	Years of Life Lost (YLL) of females by kidney failure
[,25]	LiverF	numeric	Years of Life Lost (YLL) of females by liver disease
[,26]	DiabetesF	numeric	Years of Life Lost (YLL) of females by diabetes
[,27]	HypertensF	numeric	Years of Life Lost (YLL) of females by hypertension
[,28]	Covid19F	numeric	Years of Life Lost (YLL) of females by tuberculosis

Details

Years of Life Lost by several causes in Japan 2020 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.
- Cancer[M|F]: YLL by cancer for males ([M]) or for females ([F]).
- Cardio[M|F]: YLL by heart disease for males ([M]) or for females ([F]).
- Cerebro[M|F]: YLL by cerebrovascular disease for males ([M]) or for females ([F]).
- Top3[M|F]: YLL by above 3 major diseases for males ([M]) or for females ([F]).
- Peumonia[M|F]: YLL by pneumonia for males ([M]) or for females ([F]).
- Accident[M|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 diabates for males ([M]) or for females ([F]).
- Hypertension[M|F]: YLL by hypertension for males ([M]) or for females ([F]).
- Covid19[M|F]: YLL by COVID-19 for males ([M]) or for females ([F]).

Source

https://www.mhlw.go.jp/toukei/saikin/hw/life/tdfk20/dl/tdfk20-08.xls

References

Ministry of Health, Labor and Welfare of Japan: Vital Statistics with Life Expectancy 2020. https://minato.sip21c.org/demography/how-to-make-pref-charts.html (in Japanese), WHO https://www.who.int/data/gho/data/themes/mortality-and-global-health-estimates

Examples

```
require(fmsb)
x <- PrefYLL2020
COL <- ifelse(x$PNAME=="Nagano", "blue", ifelse(x$PNAME=="Okinawa", "red",
              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","Top 3 causes","Pneumonia",
 "Accident","(Traffic\n Accident)","Suicide","Kidney\n Failure","Liver\n Disease",
 "Diabetes","Hypertension","Tuberculosis")
males <- x[,3:15]
females <- x[,16:28]
layout(t(1:2))
radarchart(males, maxmin=FALSE, pcol=COL, axistype=2, pty=32, plty=LTY, plwd=LWD, vlabels=VX,
```

```
 title="YLLs in males (2020)\n (Blue: Nagano, Green: Shiga,\n Red: Okinawa, Gray: Others)")
radarchart(females, maxmin=FALSE, pcol=COL, axistype=2, pty=32, plty=LTY, plwd=LWD, vlabels=VX,
 title="YLL in females (2020)\n (Blue: Nagano, Green: Shiga,\n Red: Okinawa, Gray: Others)")
```

pvalueplot	*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 logarythmic 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

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
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))
```

---

pvpORMH   *Drawing p-value function plot by stratified or pooled cross tables*

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

```
pvpORMH(XTAB, xrange, add, ...)
```

Arguments

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.

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

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

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. The radatchart() uses the polygons as radar grid, radarchartcirc() uses circles as radar grid.

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, ...)

 radarchartcirc(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 vari-
                ables, 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 usd.
cglty	Line type for radar grids: Default 3, dotted line. For radatchartcirc(), default 1, solid line.
cglwd	Line width for radar grids: Default 1, which means thinnest line.
cglcol	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)
VARNAMES <- c("Total\nQOL", "Physical\naspects", "Phychological\naspects",
 "Social\naspects", "Environmental\naspects")
op <- par(mar=c(1, 2, 2, 1), mfrow=c(2, 3))
radarchart(dat, axistype=1, seg=5, plty=1, vlabels=VARNAMES,
 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 with hatching, axis=2)")
radarchart(dat, axistype=2, pcol=topo.colors(3), plty=1,
 pfcol=adjustcolor(topo.colors(3), 0.3),
 title="(topo.colors, fill with transparency, axis=2)")
radarchart(dat, axistype=3, pty=32, plty=1, axislabcol="grey", na.itp=FALSE,
 title="(no points, axis=3, na.itp=FALSE)")
radarchartcirc(dat, axistype=3, pty=32, plty=1, axislabcol="grey", na.itp=FALSE,
 title="(no points, axis=3, na.itp=FALSE, circular radar grid)")
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   *Calculate incidence rate difference and its confidence intervals*

Description

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

Usage

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

Arguments

a	The number of disease occurence among exposed cohort.
b	The number of disease occurence among non-exposed cohort.
PT1	The observed person-time of the exposed cohort.
PT0	The observed person-time of the unexposed cohort.
CRC	Logical. If TRUE, calculate confidence intervals for each incidence rate. Default is FALSE.
conf.level	Probability for confidence intervals. Default is 0.95.

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/

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

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

---

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

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

Arguments

a	The number of disease occurence among exposed cohort.
b	The number of disease occurence 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

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
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

```
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/>

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

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)
```

RDMH	*Calculate pooled risk difference and its confidence intervals with Mantel-Haenszel's method*

Description

Calculate pooled risk difference and its confidence intervals with Mantel-Haenszel's method.

Usage

```
RDMH(XTAB, conf.level=0.9)
```

Arguments

XTAB	A matrix with 4 columns. The first column is the number of disease occurrence in exposed cohort. The second column is the number of disease occurrence in unexposed cohort. The third column is the total number of exposed cohort. The forth column is the total number of unexposed cohort. Rows should be composed of different strata or studies.
conf.level	Probability for confidence intervals. Default is 0.9.

Value

estimate	Calculated point estimate of pooled risk difference with Manterl-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/

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
# Table 10-3 of Rothman's textbook (Chapter 10).
RDMH(matrix(c(8, 5, 106, 120, 22, 16, 98, 85), 2, 4, byrow=TRUE), conf.level=0.9)
```

---

riskdifference	*Calculate risk difference and its confidence intervals*

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 occurence among exposed cohort.
b	The number of disease occurence 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

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
res <- riskdifference(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 occurence among exposed cohort.
Y	The number of disease occurence 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/>

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
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

```
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.
distance	The numeric vector of distance between actual performance set and the worst performance.
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)
```

RRMH	*Calculate pooled risk ratio and its confidence intervals with Mantel-Haenszel's method*

Description

Calculate pooled risk ratio and its confidence intervals with Mantel-Haenszel's method.

Usage

```
RRMH(XTAB, conf.level=0.9)
```

Arguments

XTAB   A matrix with 4 columns. The first column is the number of disease occurrence
              in exposed cohort. The second column is the number of disease occurrence
              in unexposed cohort. The third column is the total number of exposed cohort.
              The forth column is the total number of unexposed cohort. Rows should be
              composed of different strata or studies.

conf.level   Probability for confidence intervals. Default is 0.9.

Value

estimate   Calculated point estimate of pooled risk ratio with Manterl-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/

References

Rothman KJ (2012) Epidemiology: An Introduction. 2nd Ed., Oxford University Press, Oxford.

Examples

```
# Table 10-3 of Rothman's textbook (Chapter 10).
RRMH(matrix(c(8, 5, 106, 120, 22, 16, 98, 85), 2, 4, byrow=TRUE), conf.level=0.9)
```

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

<https://www.mhlw.go.jp/toukei/list/dl/81-1b1.pdf>, page 55.

References

Tamura K. (2008) How do we die?: death date from vital statistics of the Japanese population. *The Waseda study of politics and public law*, 87: 27-57.

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

```
 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

```
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/

Examples

```
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

https://support.sas.com/documentation/cdl/en/procstat/63104/HTML/default/viewer.htm#corr_toc.htm

Examples

```
data(airquality)
spearman.ci.sas(airquality$Ozone, airquality$Wind)
```

---

truemedian	*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

```
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/>

References

Grimm LG (1993) Statistical Applications for the Behavioral Sciences. John Wiley and Sons.

Examples

```
median(c(3, 3, 4, 4, 4))
truemedian(c(3, 3, 4, 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

WI   The Whipple's Index.

JUDGE   Based on Whipple's Index, accuracy of age-reporting is judged.

Author(s)

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References

Preston SH, Heuveline P, Guillot M (2001) Demography: Measuring and Modeling Population Processes. Blackwell Publishing, Oxford.

Newell C (1988) Methods and Models in Demography. The Guilford Press, New York.

Rowland DT (2003) Demographic methods and concepts. Oxford Univ. Press, Oxford.

Ministry of Home Affairs, India (2011) 2011 Census C-13. https://censusindia.gov.in/nada/index.php/catalog/22542/download/25673/PC01_C13_00.xls

Examples

```
 WhipplesIndex(Jpop$M2000)
# India <- read.delim("https://minato.sip21c.org/ldaR/India2011census.txt")
# CRAN requires the example code can work without internet connection
# since 2024, and thus I modified the code to include the data here.
 India <- data.frame(
  Males = c(10633298, 11381468, 11952853, 12331431, 12333024, 13725480,
  13394700, 12903364, 14061937, 12214985, 16089436, 12962604, 14637892,
  12563775, 13165128, 13739746, 13027935, 11349449, 15020851, 10844415,
  14892165, 10532278, 12392976, 9674189, 10093085, 14311524, 10315030,
  8552032, 10719926, 7445696, 15628996, 7157502, 8801105, 6108879,
  6964192, 15036666, 8067568, 5784879, 8090401, 5939867, 15173411,
```

```
 6172297, 6856826, 4468914, 4873938, 12685175, 5735540, 4043122,
 5568554, 4105723, 11379329, 4323584, 4068700, 2808043, 3263610,
 7769352, 3666804, 2339391, 3072508, 2607957, 8677046, 3095448,
 2892015, 1977207, 2060033, 6275854, 2278670, 1353711, 1640034,
 1396057, 5393714, 1584873, 1176727, 708381, 787804, 2278704, 832251,
 438394, 506957, 434297, 1725200, 491522, 306378, 192946, 210994,
 580527, 215850, 112348, 112374, 99007, 360237, 118606, 75430, 46220,
 51972, 124950, 57894, 35238, 48393, 28284, 289325),
Females = c(9677936, 10373729, 11103415, 11642610, 11377014, 12328750,
12259545, 11923276, 12906436, 11209653, 14462671, 11778342, 13239415,
11716908, 12093041, 12159708, 11564358, 9868018, 12937296, 10014673,
13990570, 9446694, 11135249, 9479866, 9787150, 13456554, 9761967,
8157318, 11407090, 7286828, 14770033, 6665743, 8812439, 6655662,
7030400, 13385965, 7760149, 5907352, 9381357, 5786480, 13355581,
5395597, 6523816, 4865438, 4752294, 11187786, 5257138, 3908175,
6081038, 3746076, 10083093, 3562382, 3666464, 2782747, 3131302,
7838194, 3405033, 2259635, 3646426, 2540755, 9133643, 2931365,
2853128, 2016898, 2026924, 6746498, 2233276, 1251371, 1908339,
1371173, 5592566, 1499310, 1074202, 658155, 733110, 2493642, 834882,
396654, 561458, 455264, 2059738, 536294, 297415, 187239, 212503,
684271, 232048, 109063, 123266, 114413, 472835, 139691, 78131,
48410, 55002, 147584, 62374, 36175, 56118, 36287, 316453),
Age = 0:100)
WhipplesIndex(India$Males)
# To check age-heaping graphically,
# you can install and load pyramid package from cran
# and pyramid(India, Cstep=5) may be useful.
```

Index