

Package ‘sasLM’

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Title 'SAS' Linear Model

Description This is a core implementation of 'SAS' procedures for linear models - GLM, REG, ANOVA, TTEST, FREQ, and UNIVARIATE. Some R packages provide type II and type III SS. However, the results of nested and complex designs are often different from those of 'SAS.' Different results does not necessarily mean incorrectness. However, many want the same results to SAS. This package aims to achieve that. Reference: Littell RC, Stroup WW, Freund RJ (2002, ISBN:0-471-22174-0).

Depends R (>= 3.5.0), mvtnorm

Imports methods

Suggests MASS

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sasLM-package

'SAS' Linear Model

Description

This is a core implementation of 'SAS' procedures for linear models - GLM, REG, and ANOVA. Some packages provide type II and type III SS. However, the results of nested and complex designs are often different from those of 'SAS'. A different result does not necessarily mean incorrectness. However, many want the same result with 'SAS'. This package aims to achieve that. Reference: Littell RC, Stroup WW, Freund RJ (2002, ISBN:0-471-22174-0).

Details

This will serve those who want SAS PROC GLM, REG, and ANOVA in R.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
## SAS PROC GLM Script for Typical Bioequivalence Data
# PROC GLM DATA=BEdata;
# CLASS SEQ SUBJ PRD TRT;
# MODEL LNCMAX = SEQ SUBJ(SEQ) PRD TRT;
# RANDOM SUBJ(SEQ)/TEST;
# LSMEANS TRT / DIFF=CONTROL("R") CL ALPHA=0.1;
# ODS OUTPUT LSMeansDiffCL=LSMD;

# DATA LSMD; SET LSMD;
# PE = EXP(DIFFERENCE);
# LL = EXP(LowerCL);
# UL = EXP(UpperCL);
# PROC PRINT DATA=LSMD; RUN;
##

## SAS PROC GLM equivalent
BEdata = af(BEdata, c("SEQ", "SUBJ", "PRD", "TRT")) # Columns as factor
formula1 = log(CMAX) ~ SEQ/SUBJ + PRD + TRT # Model
GLM(formula1, BEdata) # ANOVA tables of Type I, II, III SS
RanTest(formula1, BEdata, Random="SUBJ") # Hypothesis test with SUBJ as random
ci0 = CIest(formula1, BEdata, "TRT", c(-1, 1), 0.90) # 90% CI
exp(ci0[, c("Estimate", "Lower CL", "Upper CL")]) # 90% CI of GMR

## 'nlme' or SAS PROC MIXED is preferred for an unbalanced case
## SAS PROC MIXED equivalent
# require(nlme)
# Result = lme(log(CMAX) ~ SEQ + PRD + TRT, random=~1|SUBJ, data=BEdata)
# summary(Result)
# VarCorr(Result)
```

```
# ci = intervals(Result, 0.90) ; ci
# exp(ci$fixed["TRTT",])
##
```

af *Convert some columns of a data.frame to factors*

Description

Conveniently convert some columns of data.frame into factors.

Usage

```
af(DataFrame, Cols)
```

Arguments

DataFrame	a data.frame
Cols	column names or indices to be converted

Details

It performs conversion of some columns in a data.frame into factors conveniently.

Value

Returns a data.frame with converted columns.

Author(s)

Kyun-Seop Bae k@acr.kr

aov1 *ANOVA with Type I SS*

Description

ANOVA with Type I SS.

Usage

```
aov1(Formula, Data, BETA=FALSE, Resid=FALSE)
```

Arguments

Formula	a conventional formula for a linear model.
Data	a data.frame to be analyzed
BETA	if TRUE, coefficients (parameters) of REG will be returned. This is equivalent to SOLUTION option of SAS PROC GLM
Resid	if TRUE, fitted values (y hat) and residuals will be returned

Details

It performs the core function of SAS PROC GLM, and returns Type I SS. This accepts continuous independent variables also.

Value

The result table is comparable to that of SAS PROC ANOVA.

Df	degree of freedom
Sum Sq	sum of square for the set of contrasts
Mean Sq	mean square
F value	F value for the F distribution
Pr(>F)	probability of larger than F value

Next returns are optional.

Parameter	Parameter table with standard error, t value, p value. TRUE is 1, and FALSE is 0 in the Estimable column. This is returned only with BETA=TRUE option.
Fitted	Fitted value or y hat. This is returned only with Resid=TRUE option.
Residual	Weighted residuals. This is returned only with Resid=TRUE option.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
aov1(uptake ~ Plant + Type + Treatment + conc, C02)
aov1(uptake ~ Plant + Type + Treatment + conc, C02, BETA=TRUE)
aov1(uptake ~ Plant + Type + Treatment + conc, C02, Resid=TRUE)
aov1(uptake ~ Plant + Type + Treatment + conc, C02, BETA=TRUE, Resid=TRUE)
```

aov2
ANOVA with Type II SS

Description

ANOVA with Type II SS.

Usage

aov2(Formula, Data, BETA=FALSE, Resid=FALSE)

Arguments

Formula	a conventional formula for a linear model.
Data	a data.frame to be analyzed
BETA	if TRUE, coefficients (parameters) of REG will be returned. This is equivalent to SOLUTION option of SAS PROC GLM
Resid	if TRUE, fitted values (y hat) and residuals will be returned

Details

It performs the core function of SAS PROC GLM, and returns Type II SS. This accepts continuous independent variables also.

Value

The result table is comparable to that of SAS PROC ANOVA.

Df	degree of freedom
Sum Sq	sum of square for the set of contrasts
Mean Sq	mean square
F value	F value for the F distribution
Pr(>F)	probability of larger than F value

Next returns are optional.

Parameter	Parameter table with standard error, t value, p value. TRUE is 1, and FALSE is 0 in the Estimable column. This is returned only with BETA=TRUE option.
Fitted	Fitted value or y hat. This is returned only with Resid=TRUE option.
Residual	Weighted residuals. This is returned only with Resid=TRUE option.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```

aov2(uptake ~ Plant + Type + Treatment + conc, C02)
aov2(uptake ~ Plant + Type + Treatment + conc, C02, BETA=TRUE)
aov2(uptake ~ Plant + Type + Treatment + conc, C02, Resid=TRUE)
aov2(uptake ~ Plant + Type + Treatment + conc, C02, BETA=TRUE, Resid=TRUE)
aov2(uptake ~ Type, C02)
aov2(uptake ~ Type - 1, C02)

```

aov3

*ANOVA with Type III SS***Description**

ANOVA with Type III SS.

Usage

```
aov3(Formula, Data, BETA=FALSE, Resid=FALSE)
```

Arguments

Formula	a conventional formula for a linear model.
Data	a <code>data.frame</code> to be analyzed
BETA	if TRUE, coefficients (parameters) of REG will be returned. This is equivalent to SOLUTION option of SAS PROC GLM
Resid	if TRUE, fitted values (\hat{y}) and residuals will be returned

Details

It performs the core function of SAS PROC GLM, and returns Type III SS. This accepts continuous independent variables also.

Value

The result table is comparable to that of SAS PROC ANOVA.

Df	degree of freedom
Sum Sq	sum of square for the set of contrasts
Mean Sq	mean square
F value	F value for the F distribution
Pr(>F)	probability of larger than F value

Next returns are optional.

Parameter	Parameter table with standard error, t value, p value. TRUE is 1, and FALSE is 0 in the Estimable column. This is returned only with BETA=TRUE option.
Fitted	Fitted value or \hat{y} . This is returned only with Resid=TRUE option.
Residual	Weighted residuals. This is returned only with Resid=TRUE option.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
aov3(uptake ~ Plant + Type + Treatment + conc, C02)
aov3(uptake ~ Plant + Type + Treatment + conc, C02, BETA=TRUE)
aov3(uptake ~ Plant + Type + Treatment + conc, C02, Resid=TRUE)
aov3(uptake ~ Plant + Type + Treatment + conc, C02, BETA=TRUE, Resid=TRUE)
```

aspirinCHD

An example data for meta-analysis - aspirin in coronary heart disease

Description

The data is from 'Canner PL. An overview of six clinical trials of aspirin in coronary heart disease. Stat Med. 1987'

Usage

```
aspirinCHD
```

Format

A data frame with 6 rows.

y1 death event count of aspirin group

n1 total subject of aspirin group

y2 death event count of placebo group

n2 total subject of placebo group

Details

This data is for educational purpose.

References

Canner PL. An overview of six clinical trials of aspirin in coronary heart disease. Stat Med. 1987;6:255-263.

 BEdata

An Example Data of Bioequivalence Study

Description

Contains Cmax data from a real bioequivalence study.

Usage

BEdata

Format

A data frame with 91 observations on the following 6 variables.

ADM Admission or Hospitalization Group Code: 1, 2, or 3

SEQ Group or Sequence character code: 'RT' or 'TR'

PRD Period numeric value: 1 or 2

TRT Treatment or Drug code: 'R' or 'T'

SUBJ Subject ID

CMAX Cmax values

Details

This contains a real data of 2x2 bioequivalence study, which has three different hospitalization groups. See Bae KS, Kang SH. Bioequivalence data analysis for the case of separate hospitalization. *Transl Clin Pharmacol.* 2017;25(2):93-100. doi.org/10.12793/tcp.2017.25.2.93

 bk

Beautify the output of knitr::kable

Description

Trailing zeros after integer is somewhat annoying. This removes those in the vector of strings.

Usage

```
bk(ktab, rpltag=c("n", "N"), dig=10)
```

Arguments

ktab an output of knitr::kable

rpltag tag string of replacement rows. This is usually "n" which means the sample count.

dig maximum digits of decimals in the kable output

Details

This is convenient if used with `tsum0`, `tsum1`, `tsum2`, `tsum3`. This requires `knitr::kable`.

Value

A new processed vector of strings. The class is still `knitr_kable`.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[tsum0](#), [tsum1](#), [tsum2](#), [tsum3](#)

Examples

```
## OUTPUT example
# t0 = tsum0(CO2, "uptake", c("mean", "median", "sd", "length", "min", "max"))
# bk(kable(t0)) # requires knitr package
#
# |          |          x|
# |:-----|-----:|
# |mean   | 27.21310|
# |median | 28.30000|
# |sd     | 10.81441|
# |n      | 84      |
# |min    | 7.70000|
# |max    | 45.50000|

# t1 = tsum(uptake ~ Treatment, CO2,
#           e=c("mean", "median", "sd", "min", "max", "length"),
#           ou=c("chilled", "nonchilled"),
#           repl=list(c("median", "length"), c("med", "N")))
#
# bk(kable(t1, digits=3)) # requires knitr package
#
# |      | chilled| nonchilled| Combined|
# |:----|-----:|-----:|-----:|
# |mean | 23.783| 30.643| 27.213|
# |med  | 19.700| 31.300| 28.300|
# |sd   | 10.884| 9.705| 10.814|
# |min  | 7.700| 10.600| 7.700|
# |max  | 42.400| 45.500| 45.500|
# |N    | 42   | 42   | 84   |
```

 CIest *Confidence Interval Estimation*

Description

Get point estimate and its confidence interval with given contrast and alpha value using t distribution.

Usage

```
CIest(Formula, Data, Term, Contrast, conf.level=0.95)
```

Arguments

Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
Term	a factor name to be estimated
Contrast	a level vector. Level is alphabetically ordered by default.
conf.level	confidence level of confidence interval

Details

Get point estimate and its confidence interval with given contrast and alpha value using t distribution.

Value

Estimate	point estimate of the input linear contrast
Lower CL	lower confidence limit
Upper CL	upper confidence limit
Std. Error	standard error of the point estimate
t value	value for t distribution
Df	degree of freedom
Pr(> t)	probability of larger than absolute t value from t distribution with residual's degree of freedom

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
CIest(log(CMAX) ~ SEQ/SUBJ + PRD + TRT, BEdata, "TRT", c(-1, 1), 0.90) # 90% CI
```

`Coll`*Collinearity Diagnostics*

Description

Collinearity diagnostics with tolerance, VIF, eigenvalue, condition index, variance proportions

Usage

```
Coll(Formula, Data)
```

Arguments

Formula	formula of the model
Data	input data as a matrix or data.frame

Details

Sometimes collinearity diagnostics after multiple linear regression are necessary.

Value

Tol	tolerance of independent variables
VIF	variance inflation factor of independent variables
Eigenvalue	eigenvalue of $Z'Z$ (crossproduct) of standardized independent variables
Cond. Index	condition index
Proportions of variances	under the names of coefficients

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
Coll(mpg ~ disp + hp + drat + wt + qsec, mtcars)
```

CONTR *F Test with a Set of Contrasts*

Description

Do F test with a given set of contrasts.

Usage

```
CONTR(L, Formula, Data, mu=0)
```

Arguments

L	contrast matrix. Each row is a contrast.
Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
mu	a vector of mu for the hypothesis L. The length should be equal to the row count of L.

Details

It performs F test with a given set of contrasts (a matrix). It is similar to the CONTRAST clause of SAS PROC GLM. This can test the hypothesis that the linear combination (function)'s mean vector is mu.

Value

Returns sum of square and its F value and p-value.

Df	degree of freedom
Sum Sq	sum of square for the set of contrasts
Mean Sq	mean square
F value	F value for the F distribution
Pr(>F)	probability of larger than F value

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[cSS](#)

Examples

```
CONTR(t(c(0, -1, 1)), uptake ~ Type, C02) # sum of square
GLM(uptake ~ Type, C02) # compare with the above
```

`Cor.test`*Correlation test of multiple numeric columns*

Description

Testing correlation between numeric columns of data with Pearson method.

Usage

```
Cor.test(Data, conf.level=0.95)
```

Arguments

<code>Data</code>	a matrix or a data.frame
<code>conf.level</code>	confidence level

Details

It uses all numeric columns of input data. It uses "pairwise.complete.obs" rows.

Value

Row names show which columns are used for the test

Estimate	point estimate of correlation
Lower CL	upper confidence limit
Upper CL	lower confidence limit
t value	t value of the t distribution
Df	degree of freedom
$\Pr(> t)$	probability with the t distribution

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
Cor.test(mtcars)
```

corFisher *Correlation test by Fisher's Z transformation*

Description

Testing correlation between two numeric vectors by Fisher's Z transformation

Usage

```
corFisher(x, y, conf.level=0.95, rho=0)
```

Arguments

x	the first input numeric vector
y	the second input numeric vector
conf.level	confidence level
rho	population correlation rho under null hypothesis

Details

This accepts only two numeric vectors.

Value

N	sample size, length of input vectors
r	sample correlation
Fisher.z	Fisher's z
bias	bias to correct
rho.hat	point estimate of population rho
conf.level	confidence level for the confidence interval
lower	lower limit of confidence interval
upper	upper limit of confidence interval
rho0	population correlation rho under null hypothesis
p.value	p value under the null hypothesis

Author(s)

Kyun-Seop Bae k@acr.kr

References

Fisher RA. Statistical Methods for Research Workers. 14e. 1973

Examples

```
corFisher(mtcars$disp, mtcars$hp, rho=0.6)
```

cSS

*Sum of Square with a Given Contrast Set***Description**

Calculates sum of squares of a contrast from a `lfit` result.

Usage

```
cSS(K, rx, mu=0, eps=1e-8)
```

Arguments

K	contrast matrix. Each row is a contrast.
rx	a result of <code>lfit</code> function
mu	a vector of mu for the hypothesis K. The length should be equal to the row count of K.
eps	Less than this value is considered as zero.

Details

It calculates sum of squares with given a contrast matrix and a `lfit` result. It corresponds to SAS PROC GLM CONTRAST. This can test the hypothesis that the linear combination (function)'s mean vector is mu.

Value

Returns sum of square and its F value and p-value.

Df	degree of freedom
Sum Sq	sum of square for the set of contrasts
Mean Sq	mean square
F value	F value for the F distribution
Pr(>F)	probability of larger than F value

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[CONTR](#)

Examples

```
rx = REG(uptake ~ Type, CO2, summarize=FALSE)
cSS(t(c(0, -1, 1)), rx) # sum of square
GLM(uptake ~ Type, CO2) # compare with the above
```

CumAlpha

*Cumulative Alpha with various z's and ti***Description**

Cumulative alpha values with repeated hypothesis with changing bound z-value and time of test (ti).

Usage

```
CumAlpha(z, side=2, ti=NULL, c0=NULL, Seed=5)
```

Arguments

z	vector of upper z-value bounds for the repeated hypothesis test
side	1=one-side test, 2=two-side test
ti	vector of times (or information amount) of test. All values should be [0, 1] and sorted. If not specified, equal interval is assumed.
c0	correlation matrix. if not specified, Brownian motion assumed.
Seed	seed value for mtvtnorm::pmvnorm function

Details

It calculates cumulative alpha-values for the repeated hypothesis test with a vector of upper bound z-value. If the times of test is not specified, linear (proportional) increase of information amount and Brownian motion of z-value, i.e. the correlation is $\sqrt{t_i/t_j}$.

Value

The result is a matrix.

ti	time of test
cum.alpha	cumulative alpha valued

Author(s)

Kyun-Seop Bae k@acr.kr

References

Reboussin DM, DeMets DL, Kim K, Lan KKG. Computations for group sequential boundaries using the Lan-DeMets function method. *Controlled Clinical Trials*. 2000;21:190-207.

Examples

```
CumAlpha(z=rep(qnorm(1 - 0.05/2), 10)) # two-side Z-test with alpha=0.05 for ten times
```

CV *Coefficient of Variation in percentage*

Description

Coefficient of variation in percentage.

Usage

```
CV(y)
```

Arguments

y a numeric vector

Details

It removes NA.

Value

Coefficient of variation in percentage.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
CV(mtcars$mpg)
```

Diffogram *Plot Pairwise Differences*

Description

Plot pairwise differences by a common.

Usage

```
Diffogram(Formula, Data, Term, conf.level=0.95, adj="lsd", ...)
```

Arguments

Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
Term	a factor name to be estimated
conf.level	confidence level of confidence interval
adj	"lsd", "tukey", "scheffe", "bon", or "duncan" to adjust p-value and confidence limit
...	arguments to be passed to plot

Details

This usually shows the shortest interval. It corresponds to SAS PROC GLM PDIFF. For adjust method "dunnett", see PDIFF function.

Value

no return value, but a plot on the current device

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[LSM](#), [PDIFF](#)

Examples

```
Diffogram(uptake ~ Type*Treatment + as.factor(conc), CO2, "as.factor(conc)")
```

Drift

Drift defined by Lan and DeMets for Group Sequential Design

Description

Calculate the drift value with given upper bounds (z-valuse), times of test, and power.

Usage

```
Drift(bi, ti=NULL, Power=0.9)
```

Arguments

bi	upper bound z-values
ti	times of test. These should be in the range of [0, 1]. If omitted, even-interval is assumed.
Power	target power at the final test

Details

It calculates the drift value with given upper bound z-values, times of test, and power. If the times of test is not given, even-interval is assumed. `mvtnorm::pmvt` (with noncentrality) is better than `pmvnorm` in calculating power and sample size. But, Lan-DeMets used multi-variate normal rather than multi-variate noncentral t distribution. This function followed Lan-DeMets for the consistency with previous results.

Value

Drift value for the given condition

Author(s)

Kyun-Seop Bae `k@acr.kr`

References

Reboussin DM, DeMets DL, Kim K, Lan KKG. Computations for group sequential boundaries using the Lan-DeMets function method. *Controlled Clinical Trials*. 2000;21:190-207.

Examples

```
Drift(seqBound(ti=(1:5)/5)[, "up.bound"])
```

e1

Get a Contrast Matrix for Type I SS

Description

Makes a contrast matrix for type I SS using forward Doolittle method.

Usage

```
e1(XpX, eps=1e-8)
```

Arguments

<code>XpX</code>	crossproduct of a design or model matrix. This should have appropriate column names.
<code>eps</code>	Less than this value is considered as zero.

Details

It makes a contrast matrix for type I SS. If `zapsmall` is used, the result becomes more inaccurate.

Value

A contrast matrix for type I SS.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
x = ModelMatrix(uptake ~ Plant + Type + Treatment + conc, C02)
round(e1(crossprod(x$X)), 12)
```

e2

Get a Contrast Matrix for Type II SS

Description

Makes a contrast matrix for type II SS.

Usage

```
e2(x, eps=1e-8)
```

Arguments

x	an output of ModelMatrix
eps	Less than this value is considered as zero.

Details

It makes a contrast matrix for type II SS. If zapsmall is used, the result becomes more inaccurate.

Value

A contrast matrix for type II SS.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
round(e2(ModelMatrix(uptake ~ Plant + Type + Treatment + conc, C02)), 12)
round(e2(ModelMatrix(uptake ~ Type, C02)), 12)
round(e2(ModelMatrix(uptake ~ Type - 1, C02)), 12)
```

`e3`*Get a Contrast Matrix for Type III SS*

Description

Makes a contrast matrix for type III SS.

Usage

```
e3(x, eps=1e-8)
```

Arguments

`x` an output of `ModelMatrix`
`eps` Less than this value is considered as zero.

Details

It makes a contrast matrix for type III SS. If `zapsmall` is used, the result becomes more inaccurate.

Value

A contrast matrix for type III SS.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
round(e3(ModelMatrix(uptake ~ Plant + Type + Treatment + conc, C02)), 12)
```

`EMS`*Expected Mean Square Formula*

Description

Calculates a formula table for expected mean square of the given contrast. The default is for Type III SS.

Usage

```
EMS(Formula, Data, Type=3, eps=1e-8)
```

Arguments

Formula	a conventional formula for a linear model
Data	a <code>data.frame</code> to be analyzed
Type	type of sum of squares. The default is 3. Type 4 is not supported yet.
eps	Less than this value is considered as zero.

Details

This is necessary for further hypothesis tests of nesting factors.

Value

A coefficient matrix for Type III expected mean square

Author(s)

Kyun-Seop Bae `k@acr.kr`

Examples

```
f1 = log(CMAX) ~ SEQ/SUBJ + PRD + TRT
EMS(f1, BEdata)
EMS(f1, BEdata, Type=1)
EMS(f1, BEdata, Type=2)
```

 est

Estimate Linear Functions

Description

Estimates Linear Functions with a given GLM result.

Usage

```
est(L, X, rx, conf.level=0.95, adj="lsd", paired=FALSE)
```

Arguments

L	a matrix of linear contrast rows to be tested
X	a model (design) matrix from <code>ModelMatrix</code>
rx	a result of <code>lfit</code> function
conf.level	confidence level of confidence limit
adj	adjustment method for grouping. This supports "tukey", "bon", "scheffe", "duncan", and "dunnett". This only affects grouping, not the confidence interval.
paired	If this is TRUE, L matrix is for the pairwise comparison such as PDIFF function.

Details

It tests rows of linear function. Linear function means linear combination of estimated coefficients. It corresponds to SAS PROC GLM ESTIMATE. Same sample size per group is assumed for the Tukey adjustment.

Value

Estimate	point estimate of the input linear contrast
Lower CL	lower confidence limit by "lsd" method
Upper CL	upper confidence limit by "lsd" method
Std. Error	standard error of the point estimate
t value	value for t distribution for other than "scheffe" method
F value	value for F distribution for "scheffe" method only
Df	degree of freedom of residuals
Pr(> t)	probability of larger than absolute t value from t distribution with residual's degree of freedom, for other than "scheffe" method
Pr(>F)	probability of larger than F value from F distribution with residual's degree of freedom, for "scheffe" method only

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[ESTM](#), [PDIFF](#)

Examples

```
x = ModelMatrix(uptake ~ Type, C02)
rx = REG(uptake ~ Type, C02, summarize=FALSE)
est(t(c(0, -1, 1)), x$X, rx) # Quebec - Mississippi
t.test(uptake ~ Type, C02) # compare with the above
```

ESTM

Estimate Linear Function

Description

Estimates Linear Function with a formula and a dataset.

Usage

```
ESTM(L, Formula, Data, conf.level=0.95)
```

Arguments

L	a matrix of linear functions rows to be tested
Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
conf.level	confidence level of confidence limit

Details

It tests rows of linear functions. Linear function means linear combination of estimated coefficients. It is similar to SAS PROC GLM ESTIMATE. This is a convenient version of est function.

Value

Estimate	point estimate of the input linear contrast
Lower CL	lower confidence limit
Upper CL	upper confidence limit
Std. Error	standard error of the point estimate
t value	value for t distribution
Df	degree of freedom
Pr(> t)	probability of larger than absolute t value from t distribution with residual's degree of freedom

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[est](#)

Examples

```
ESTM(t(c(0, -1, 1)), uptake ~ Type, CO2) # Quevec - Mississippi
```

estmb

Estimability Check

Description

Check the estimability of row vectors of coefficients.

Usage

```
estmb(L, X, g2, eps=1e-8)
```

Arguments

L	row vectors of coefficients
X	a model (design) matrix from ModelMatrix
g2	g2 generalized inverse of crossprod(X)
eps	absolute value less than this is considered to be zero.

Details

It checks the estimability of L, row vectors of coefficients. This corresponds to SAS PROC GLM ESTIMATE. See <Kennedy Jr. WJ, Gentle JE. Statistical Computing. 1980> p361 or <Golub GH, Styan GP. Numerical Computations for Univariate Linear Models. 1971>.

Value

a vector of logical values indicating which row is estimable (as TRUE)

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[G2SWEEP](#)

ExitP

Exit Probability with cumulative Z-test in Group Sequential Design

Description

Exit probabilities with given drift, upper bounds, and times of test.

Usage

```
ExitP(Theta, bi, ti=NULL)
```

Arguments

Theta	drift value defined by Lan-DeMets. See the reference.
bi	upper bound z-values
ti	times of test. These should be in the range of [0, 1]. If omitted, even-interval is assumed.

Details

It calculates exit probabilities and cumulative exit probabilities with given drift, upper z-bounds and times of test. If the times of test is not given, even-interval is assumed. `mvtnorm::pmvt` (with noncentrality) is better than `pmvnorm` in calculating power and sample size. But, Lan-DeMets used multi-variate normal rather than multi-variate noncentral t distribution. This function followed Lan-DeMets for the consistency with previous results.

Value

The result is a matrix.

<code>ti</code>	time of test
<code>bi</code>	upper z-bound
<code>cum.alpha</code>	cumulative alpha-value

Author(s)

Kyun-Seop Bae `k@acr.kr`

References

Reboussin DM, DeMets DL, Kim K, Lan KKG. Computations for group sequential boundaries using the Lan-DeMets function method. *Controlled Clinical Trials*. 2000;21:190-207.

Examples

```
b0 = seqBound(ti=(1:5)/5)[, "up.bound"]
ExitP(Theta = Drift(b0), bi = b0)
```

`g2inv`

Generalized type 2 inverse matrix, g2 inverse

Description

Generalized inverse is usually not unique. Some programs use this algorithm to get a unique generalized inverse matrix. This uses SWEEP operator and works for non-square matrix also.

Usage

```
g2inv(A, eps=1e-08)
```

Arguments

<code>A</code>	a matrix to be inverted
<code>eps</code>	Less than this value is considered as zero.

Details

See 'SAS Technical Report R106, The Sweep Operator: Its importance in Statistical Computing' by J. H. Goodnight for the detail.

Value

g2 inverse

Author(s)

Kyun-Seop Bae k@acr.kr

References

Searle SR, Khuri AI. Matrix Algebra Useful for Statistics. 2e. John Wiley and Sons Inc. 2017.

See Also

[G2SWEEP](#)

Examples

```
A = matrix(c(1, 2, 4, 3, 3, -1, 2, -2, 5, -4, 0, -7), byrow=TRUE, ncol=4) ; A
g2inv(A)
```

G2SWEEP

Generalized inverse matrix of type 2 for linear regression

Description

Generalized inverse is usually not unique. Some programs use this algorithm to get a unique generalized inverse matrix.

Usage

```
G2SWEEP(A, Augmented=FALSE, eps=1e-08)
```

Arguments

A	a matrix to be inverted. If A is not a square matrix, G2SWEEP calls g2inv function.
Augmented	If this is TRUE and A is a model(design) matrix X, the last column should be X'y, the last row y'X, and the last cell y'y. See the reference and example for the detail. If the input matrix A is not a square matrix, Augmented option cannot be TRUE.
eps	Less than this value is considered as zero.

Details

Generalized inverse of g2-type is used by some softwares to do linear regression. See 'SAS Technical Report R106, The Sweep Operator: Its importance in Statistical Computing' by J. H. Goodnight for the detail.

Value

when Augmented=FALSE
ordinary g2 inverse

when Augmented=TRUE
g2 inverse and beta hats in the last column and the last row, and sum of square error (SSE) in the last cell

attribute "rank"
the rank of input matrix

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[lfit, ModelMatrix](#)

Examples

```
f1 = uptake ~ Type + Treatment # formula
x = ModelMatrix(f1, C02) # Model matrix and relevant information
y = model.frame(f1, C02)[, 1] # observation vector
nc = ncol(x$X) # number of columns of model matrix
XpY = crossprod(x$X, y)
aXpX = rbind(cbind(crossprod(x$X), XpY), cbind(t(XpY), crossprod(y)))
ag2 = G2SWEEP(aXpX, Augmented=TRUE)
b = ag2[1:nc, (nc + 1)] ; b # Beta hat
iXpX = ag2[1:nc, 1:nc] ; iXpX # g2 inverse of X'X
SSE = ag2[(nc + 1), (nc + 1)] ; SSE # Sum of Square Error
DFr = nrow(x$X) - attr(ag2, "rank") ; DFr # Degree of freedom for the residual

# Compare the below with the above
REG(f1, C02)
aov1(f1, C02)
```

geoCV

Geometric Coefficient of Variation in percentage

Description

Geometric coefficient of variation in percentage.

Usage

```
geoCV(y)
```

Arguments

y a numeric vector

Details

It removes NA. This is $\sqrt{\exp(\text{var}(\log(x))) - 1} * 100$.

Value

Geometric coefficient of variation in percentage.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[geoMean](#)

Examples

```
geoCV(mtcars$mpg)
```

geoMean

Geometric Mean without NA

Description

mean without NA values.

Usage

```
geoMean(y)
```

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

geometric mean value

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[geoCV](#)

Examples

```
geoMean(mtcars$mpg)
```

GLM

General Linear Model similar to SAS PROC GLM

Description

GLM is the main function of this package.

Usage

```
GLM(Formula, Data, BETA=FALSE, EMEAN=FALSE, Resid=FALSE, conf.level=0.95,  
Weights=1)
```

Arguments

Formula	a conventional formula for a linear model.
Data	a data.frame to be analyzed
BETA	if TRUE, coefficients (parameters) of REG will be returned. This is equivalent to SOLUTION option of SAS PROC GLM
EMEAN	if TRUE, least square means (or expected means) will be returned. This is equivalent to LSMEANS clause of SAS PROC GLM
Resid	if TRUE, fitted values (\hat{y}) and residuals will be returned
conf.level	confidence level for the confidence limit of the least square mean
Weights	weights for the weighted least square

Details

It performs the core function of SAS PROC GLM. Least square means for the interaction term of three variables is not supported yet.

Value

The result is comparable to that of SAS PROC GLM.

ANOVA	ANOVA table for the model
Fitness	Some measures of goodness of fit such as R-square and CV
Type I	Type I sum of square table
Type II	Type II sum of square table
Type III	Type III sum of square table
Parameter	Parameter table with standard error, t value, p value. TRUE is 1, and FALSE is 0 in the Estimable column. This is returned only with BETA=TRUE option.
Expected Mean	Least square (or expected) mean table with confidence limit. This is returned only with EMEAN=TRUE option.
Fitted	Fitted value or y hat. This is returned only with Resid=TRUE option.
Residual	Weighted residuals. This is returned only with Resid=TRUE option.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
GLM(uptake ~ Type*Treatment + conc, C02[-1,]) # Making data unbalanced
GLM(uptake ~ Type*Treatment + conc, C02[-1,], BETA=TRUE)
GLM(uptake ~ Type*Treatment + conc, C02[-1,], EMEAN=TRUE)
GLM(uptake ~ Type*Treatment + conc, C02[-1,], Resid=TRUE)
GLM(uptake ~ Type*Treatment + conc, C02[-1,], BETA=TRUE, EMEAN=TRUE)
GLM(uptake ~ Type*Treatment + conc, C02[-1,], BETA=TRUE, EMEAN=TRUE, Resid=TRUE)
```

is.cor

Is it a correlation matrix?

Description

Testing if the input matrix is a correlation matrix or not

Usage

```
is.cor(m, eps=1e-16)
```

Arguments

m	a presumed correlation matrix
eps	epsilon value. An absolute value less than this is considered as zero.

Details

A diagonal component should not be necessarily 1. But it should be close to 1.

Value

TRUE or FALSE

Author(s)

Kyun-Seop Bae k@acr.kr

Kurtosis

Kurtosis

Description

Kurtosis with a conventional formula.

Usage

```
Kurtosis(y)
```

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

Estimate of kurtosis

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[KurtosisSE](#)

KurtosisSE	<i>Standard Error of Kurtosis</i>
------------	-----------------------------------

Description

Standard error of the estimated kurtosis with a conventional formula.

Usage

```
KurtosisSE(y)
```

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

Standard error of the estimated kurtosis

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[Kurtosis](#)

LCL	<i>Lower Confidence Limit</i>
-----	-------------------------------

Description

The estimate of the lower bound of confidence limit using t-distribution

Usage

```
LCL(y, conf.level=0.95)
```

Arguments

y a vector of numerics
conf.level confidence level

Details

It removes NA in the input vector.

Value

The estimate of the lower bound of confidence limit using t-distribution

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[UCL](#)

lfit

Linear Fit

Description

Fits a least square linear model.

Usage

```
lfit(x, y, eps=1e-8)
```

Arguments

x	a result of ModelMatrix
y	a column vector of response, dependent variable
eps	Less than this value is considered as zero.

Details

Minimum version of least square fit of a linear model

Value

coefficients	beta coefficients
g2	g2 inverse
rank	rank of the model matrix
DFr	degree of freedom for the residual
SSE	sum of squares error
SST	sum of squares total
DFr2	degree of freedom of the residual for beta coefficient

Author(s)

Kyun-Seop Bae k@acr.kr

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

```
f1 = uptake ~ Type*Treatment + conc
x = ModelMatrix(f1, C02)
y = model.frame(f1, C02)[,1]
lfit(x, y)
```

lr

Linear Regression with g2 inverse

Description

Coefficients calculated with g2 inverse. Output is similar to `summary(lm())`.

Usage

```
lr(Formula, Data, eps=1e-8)
```

Arguments

Formula	a conventional formula for a linear model
Data	a <code>data.frame</code> to be analyzed
eps	Less than this value is considered as zero.

Details

It uses G2SWEEP to get g2 inverse. The result is similar to `summary(lm())` without options.

Value

The result is comparable to that of SAS PROC REG.

Estimate	point estimate of parameters, coefficients
Std. Error	standard error of the point estimate
t value	value for t distribution
Pr(> t)	probability of larger than absolute t value from t distribution with residual's degree of freedom

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
lr(uptake ~ Plant + Type + Treatment + conc, C02)
lr(uptake ~ Plant + Type + Treatment + conc - 1, C02)
lr(uptake ~ Type, C02)
lr(uptake ~ Type - 1, C02)
```

 lr0

Simple Linear Regressions with Each Independent Variable

Description

Usually, the first step to multiple linear regression is simple linear regressions with a single independent variable.

Usage

```
lr0(Formula, Data)
```

Arguments

Formula	a conventional formula for a linear model. Intercept will always be added.
Data	a data.frame to be analyzed

Details

It performs simple linear regression for each independent variable.

Value

Each row means one simple linear regression with that row name as the only independent variable.

Intercept	estimate of the intercept
SE(Intercept)	standard error of the intercept
Slope	estimate of the slope
SE(Slope)	standard error of the slope
Rsq	R-squared for the simple linear model
Pr(>F)	p-value of slope or the model

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
lrm0(uptake ~ Plant + Type + Treatment + conc, CO2)
lrm0(mpg ~ ., mtcars)
```

 LSM

Least Square Means

Description

Estimates least square means using g2 inverse.

Usage

```
LSM(Formula, Data, Term, conf.level=0.95, adj="lsd", hideNonEst=TRUE,
    PLOT=FALSE, descend=FALSE, ...)
```

Arguments

Formula	a conventional formula of model
Data	data.frame
Term	term name to be returned. If there is only one independent variable, this can be omitted.
conf.level	confidence level for the confidence limit
adj	adjustment method for grouping, "lsd"(default), "tukey", "bon", "duncan", "scheffe" are available. This does not affects SE, Lower CL, Upper CL of the output table.
hideNonEst	logical. hide non-estimables
PLOT	logical. whether to plot LSMs and their confidence intervals
descend	logical. This specifies the plotting order be ascending or descending.
...	arguments to be passed to plot

Details

It corresponds to SAS PROC GLM LSMEANS. The result of the second example below may be different from emmeans. This is because SAS or this function calculates mean of the transformed continuous variable. However, emmeans calculates the average before the transformation. Interaction of three variables is not supported yet. For adjust method "dunnett", see PDIFF function.

Value

Returns a table of expectations, t values and p-values.

Group	group character. This appears with one-way ANOVA or Term or adj argument is provided.
LSmean	point estimate of least square mean

LowerCL	lower confidence limit with the given confidence level by "lsd" method
UpperCL	upper confidence limit with the given confidence level by "lsd" method
SE	standard error of the point estimate
Df	degree of freedom of point estimate

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[PDIFF](#), [Diffogram](#)

Examples

```

LSM(uptake ~ Type, C02[-1,])
LSM(uptake ~ Type - 1, C02[-1,])
LSM(uptake ~ Type*Treatment + conc, C02[-1,])
LSM(uptake ~ Type*Treatment + conc - 1, C02[-1,])
LSM(log(uptake) ~ Type*Treatment + log(conc), C02[-1,])
LSM(log(uptake) ~ Type*Treatment + log(conc) - 1, C02[-1,])
LSM(log(uptake) ~ Type*Treatment + as.factor(conc), C02[-1,])
LSM(log(uptake) ~ Type*Treatment + as.factor(conc) - 1, C02[-1,])
LSM(log(CMAX) ~ SEQ/SUBJ + PRD + TRT, BEdata)
LSM(log(CMAX) ~ SEQ/SUBJ + PRD + TRT - 1, BEdata)

```

Max

Max without NA

Description

maximum without NA values.

Usage

```
Max(y)
```

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

maximum value

Author(s)

Kyun-Seop Bae k@acr.kr

Mean

Mean without NA

Description

mean without NA values.

Usage

Mean(y)

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

mean value

Author(s)

Kyun-Seop Bae k@acr.kr

Median

Median without NA

Description

median without NA values.

Usage

Median(y)

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

median value

Author(s)

Kyun-Seop Bae k@acr.kr

Min

Min without NA

Description

minimum without NA values.

Usage

Min(y)

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

minimum value

Author(s)

Kyun-Seop Bae k@acr.kr

 ModelMatrix

Model Matrix

Description

This model matrix is similar to `model.matrix`. But it does not omit unnecessary columns.

Usage

```
ModelMatrix(Formula, Data, KeepOrder=FALSE, XpX=FALSE)
```

Arguments

Formula	a conventional formula for a linear model
Data	a <code>data.frame</code> to be analyzed
KeepOrder	If <code>KeepOrder</code> is <code>TRUE</code> , terms in <code>Formula</code> will be kept. This is for Type I SS.
XpX	If <code>XpX</code> is <code>TRUE</code> , the cross-product of the design matrix (XpX , $X'X$) will be returned instead of the design matrix (X).

Details

It makes the `model(design)` matrix for GLM.

Value

Model matrix and attributes similar to the output of `model.matrix`.

X	design matrix, i.e. model matrix
XpX	cross-product of the design matrix, $X'X$
terms	detailed information about terms such as formula and labels
termsIndices	term indices
assign	assignment of columns for each term in order, different way of expressing term indices

Author(s)

Kyun-Seop Bae k@acr.kr

mtest	<i>Independent two groups t-test similar to PROC TTEST with summarized input</i>
-------	--

Description

This is comparable to SAS PROC TTEST except using summarized input (sufficient statistics).

Usage

```
mtest(m1, s1, n1, m0, s0, n0, conf.level=0.95)
```

Arguments

m1	mean of the first (test, active, experimental) group
s1	sample standard deviation of the first group
n1	sample size of the first group
m0	mean of the second (reference, control, placebo) group
s0	sample standard deviation of the second group
n0	sample size of the second group
conf.level	confidence level

Details

This uses summarized input. This also produces confidence intervals of means and variances by group.

Value

The output format is comparable to SAS PROC TTEST.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[TTEST](#), [tmtest](#), [ztest](#)

Examples

```
mtest(5.4, 10.5, 3529, 5.1, 8.9, 5190) # NEJM 388;15 p1386
```

N	<i>Number of observations</i>
---	-------------------------------

Description

Number of observations excluding NA values

Usage

N(y)

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

Count of the observation

Author(s)

Kyun-Seop Bae k@acr.kr

OBFBound	<i>O'Brien-Flemming bounds for cumulative Z-test in Group Sequential Design</i>
----------	---

Description

Sequential O'Brien-Flemming upper bounds for cumulative Z-test on accumaltive data. Z values are correlated. This is usually used for group sequential design.

Usage

OBFBound(K, alpha=0.05, side=2, ti=NULL, c0=NULL)

Arguments

K	count of tests including the final
alpha	goal alpha value for the last test at time 0.
side	1=one-side test, 2=two-side test
ti	times for test. These should be [0, 1]. If not specified, equal interval is assumed.
c0	correlation matrix. if not specified, Brownian motion assumed.

Details

It calculates O'Brien-Flemming upper z-bounds and cumulative alpha-values for the repeated test in group sequential design.

Value

The result is a matrix.

<code>t i</code>	time of test
<code>z</code>	O'Brien-Flemming upper z-bound
<code>cum.alpha</code>	cumulative alpha-value

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[seqBound](#), [PocockBound](#)

Examples

```
OBFBound(K=2)
OBFBound(K=3)
OBFBound(K=4)
OBFBound(K=5)
```

OR

Odds Ratio of two groups

Description

Odds Ratio between two groups

Usage

```
OR(y1, n1, y2, n2, conf.level=0.95)
```

Arguments

<code>y1</code>	positive event count of test (the first) group
<code>n1</code>	total count of the test (the first) group
<code>y2</code>	positive event count of control (the second) group
<code>n2</code>	total count of control (the second) group
<code>conf.level</code>	confidence level

Details

It calculates odds ratio of two groups. No continuity correction here. If you need percent scale, multiply the output by 100.

Value

The result is a data.frame.

odd1	proportion from the first group
odd2	proportion from the second group
OR	odds ratio, odd1/odd2
SElog	standard error of log(OR)
lower	lower confidence limit of OR
upper	upper confidence limit of OR

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[RD](#), [RR](#), [RDmn1](#), [RRmn1](#), [ORmn1](#), [RDmn](#), [RRmn](#), [ORmn](#)

Examples

```
OR(104, 11037, 189, 11034) # no continuity correction
```

ORcmh

Odds Ratio of two groups with strata by CMH method

Description

Odds ratio and its score confidence interval of two groups with stratification by Cochran-Mantel-Haenszel method

Usage

```
ORcmh(d0, conf.level=0.95)
```

Arguments

d0	A data.frame or matrix, of which each row means a strata. This should have four columns named y1, n1, y2, and n2; y1 and y2 for events of each group, n1 and n2 for sample size of each strata. The second group is usually the control group.
conf.level	confidence level

Details

It calculates odds ratio and its score confidence interval of two groups. This can be used for meta-analysis also.

Value

The following output will be returned for each stratum and common value. There is no standard error.

odd1	odd from the first group, $y1/(n1 - y1)$
odd2	odd from the second group, $y2/(n2 - y2)$
OR	odds ratio, odd1/odd2. The point estimate of common OR is calculated with MH weight.
lower	lower confidence limit of OR
upper	upper confidence limit of OR

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[RDmn1](#), [RRmn1](#), [ORMn1](#), [RDmn](#), [RRmn](#), [ORMn](#), [RDinv](#), [RRinv](#), [ORinv](#)

Examples

```
d1 = matrix(c(25, 339, 28, 335, 23, 370, 40, 364), nrow=2, byrow=TRUE)
colnames(d1) = c("y1", "n1", "y2", "n2")
ORcmh(d1)
```

ORinv

Odds Ratio of two groups with strata by inverse variance method

Description

Odds ratio and its score confidence interval of two groups with stratification by inverse variance method

Usage

```
ORinv(d0, conf.level=0.95)
```

Arguments

d0	A data.frame or matrix, of which each row means a stratum. This should have four columns named y1, n1, y2, and n2; y1 and y2 for events of each group, n1 and n2 for sample size of each strata. The second group is usually the control group.
conf.level	confidence level

Details

It calculates odds ratio and its confidence interval of two groups by inverse variance method. This supports stratification. This can be used for meta-analysis also.

Value

The following output will be returned for each stratum and common value. There is no standard error.

odd1	odd from the first group, $y1/(n1 - y1)$
odd2	odd from the second group, $y2/(n2 - y2)$
OR	odds ratio, odd1/odd2. The point estimate of common OR is calculated with MH weight.
lower	lower confidence limit of OR
upper	upper confidence limit of OR

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[RDmn1](#), [RRmn1](#), [ORmn1](#), [RDmn](#), [RRmn](#), [ORmn](#), [RDinv](#), [RRinv](#), [ORcmh](#)

Examples

```
d1 = matrix(c(25, 339, 28, 335, 23, 370, 40, 364), nrow=2, byrow=TRUE)
colnames(d1) = c("y1", "n1", "y2", "n2")
ORinv(d1)
```

ORmn

Odds Ratio and Score CI of two groups with strata by MN method

Description

Odds ratio and its score confidence interval of two groups with stratification by the Miettinen and Nurminen method

Usage

```
ORmn(d0, conf.level=0.95, eps=1e-8)
```

Arguments

<code>d0</code>	A data.frame or matrix, of which each row means a strata. This should have four columns named <code>y1</code> , <code>n1</code> , <code>y2</code> , and <code>n2</code> ; <code>y1</code> and <code>y2</code> for events of each group, <code>n1</code> and <code>n2</code> for sample size of each strata. The second group is usually the control group.
<code>conf.level</code>	confidence level
<code>eps</code>	absolute value less than <code>eps</code> is regarded as negligible

Details

It calculates odds ratio and its score confidence interval of the two groups. The confidence interval is asymmetric, and there is no standard error in the output. This supports stratification. This implementation uses `uniroot` function, which usually gives at least 5 significant digits. Whereas `PropCIs::orscoreci` function uses incremental or decremental search by the factor of 1.001 which gives only about 3 significant digits. This can be used for meta-analysis also.

Value

The following output will be returned for each stratum and common value. There is no standard error.

<code>odd1</code>	odd from the first group, $y1/(n1 - y1)$
<code>odd2</code>	odd from the second group, $y2/(n2 - y2)$
<code>OR</code>	odds ratio, <code>odd1/odd2</code> . The point estimate of common OR is calculated with MN weight.
<code>lower</code>	lower confidence limit of OR
<code>upper</code>	upper confidence limit of OR

Author(s)

Kyun-Seop Bae k@acr.kr

References

Miettinen O, Nurminen M. Comparative analysis of two rates. *Stat Med* 1985;4:213-26

See Also

[RDmn1](#), [RRmn1](#), [ORmn1](#), [RDmn](#), [RRmn](#), [RDinv](#), [RRinv](#), [ORinv](#), [ORcmh](#)

Examples

```
d1 = matrix(c(25, 339, 28, 335, 23, 370, 40, 364), nrow=2, byrow=TRUE)
colnames(d1) = c("y1", "n1", "y2", "n2")
ORmn(d1)
d2 = data.frame(y1=c(4, 2, 10), n1=c(20, 20, 20), y2=c(8, 11, 2), n2=c(20, 20, 20))
ORmn(d2)
```

ORmn1 *Odds Ratio and Score CI of two groups without strata by the MN method*

Description

Odds ratio and its score confidence interval of two groups without stratification

Usage

```
ORmn1(y1, n1, y2, n2, conf.level=0.95, eps=1e-8)
```

Arguments

y1	positive event count of test (the first) group
n1	total count of the test (the first) group
y2	positive event count of control (the second) group
n2	total count of control (the second) group
conf.level	confidence level
eps	absolute value less than eps is regarded as negligible

Details

It calculates odds ratio and its score confidence interval of the two groups. The confidence interval is asymmetric, and there is no standard error in the output. This does not support stratification. This implementation uses uniroot function, which usually gives at least 5 significant digits. Whereas PropCIs::orscoreci function uses incremental or decremental search by the factor of 1.001 which gives only less than 3 significant digits.

Value

There is no standard error.

odd1	odd from the first group, $y1/(n1 - y1)$
odd2	odd from the second group, $y2/(n2 - y2)$
OR	odds ratio, $odd1/odd2$
lower	lower confidence limit of OR
upper	upper confidence limit of OR

Author(s)

Kyun-Seop Bae k@acr.kr

References

Miettinen O, Nurminen M. Comparative analysis of two rates. Stat Med 1985;4:213-26

See Also

[RDmn1](#), [RRmn1](#), [RDmn](#), [RRmn](#), [ORmn](#)

Examples

```
ORmn1(104, 11037, 189, 11034)
```

pB

Plot Confidence and Prediction Bands for Simple Linear Regression

Description

It plots bands of the confidence interval and prediction interval for simple linear regression.

Usage

```
pB(Formula, Data, Resol=300, conf.level=0.95, lx, ly, ...)
```

Arguments

Formula	a formula
Data	a data.frame
Resol	resolution for the output
conf.level	confidence level
lx	x position of legend
ly	y position of legend
...	arguments to be passed to plot

Details

It plots. Discard return values. If lx or ly is missing, the legend position is calculated automatically.

Value

Ignore return values.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
pB(hp ~ disp, mtcars)
pB(mpg ~ disp, mtcars)
```

`Pcor.test`*Partial Correlation test of multiple columns*

Description

Testing partial correlation between many columns of data with Pearson method.

Usage

```
Pcor.test(Data, x, y)
```

Arguments

<code>Data</code>	a numeric matrix or data.frame
<code>x</code>	names of columns to be tested
<code>y</code>	names of control columns

Details

It performs multiple partial correlation test. It uses "complete.obs" rows of x and y columns.

Value

Row names show which columns are used for the test

<code>Estimate</code>	point estimate of correlation
<code>Df</code>	degree of freedom
<code>t value</code>	t value of the t distribution
<code>Pr(> t)</code>	probability with the t distribution

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
Pcor.test(mtcars, c("mpg", "hp", "qsec"), c("drat", "wt"))
```

pD *Diagnostic Plot for Regression*

Description

Four standard diagnostic plots for regression.

Usage

```
pD(rx, Title=NULL)
```

Arguments

rx a result of lm, which can give fitted, residuals, and rstandard.
Title title to be printed on the plot

Details

Most frequently used diagnostic plots are 'observed vs. fitted', 'standardized residual vs. fitted', 'distribution plot of standard residuals', and 'Q-Q plot of standardized residuals'.

Value

Four diagnostic plots in a page.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
pD(lm(uptake ~ Plant + Type + Treatment + conc, CO2), "Diagnostic Plot")
```

PDIF *Pairwise Difference*

Description

Estimates pairwise differences by a common method.

Usage

```
PDIF(Formula, Data, Term, conf.level=0.95, adj="lsd", ref, PLOT=FALSE,  
      reverse=FALSE, ...)
```

Arguments

Formula	a conventional formula for a linear model
Data	a <code>data.frame</code> to be analyzed
Term	a factor name to be estimated
conf.level	confidence level of confidence interval
adj	"lsd", "tukey", "scheffe", "bon", "duncan", or "dunnett" to adjust p-value and confidence limit
ref	reference or control level for Dunnett test
PLOT	whether to plot or not the diffogram
reverse	reverse A - B to B - A
...	arguments to be passed to plot

Details

It corresponds to PDIFF option of SAS PROC GLM.

Value

Returns a table of expectations, t values and p-values. Output columns may vary according to the adjustment option.

Estimate	point estimate of the input linear contrast
Lower CL	lower confidence limit
Upper CL	upper confidence limit
Std. Error	standard error of the point estimate
t value	value for t distribution
Df	degree of freedom
Pr(> t)	probability of larger than absolute t value from t distribution with residual's degree of freedom

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[LSM](#), [Diffogram](#)

Examples

```
PDIFF(uptake ~ Type*Treatment + as.factor(conc), C02, "as.factor(conc)")
PDIFF(uptake ~ Type*Treatment + as.factor(conc), C02, "as.factor(conc)", adj="tukey")
```

PocockBound	<i>Pocock (fixed) Bound for the cumulative Z-test with a final target alpha-value</i>
-------------	---

Description

Cumulative alpha values with cumulative hypothesis test with a fixed upper bound z-value in group sequential design.

Usage

```
PocockBound(K=2, alpha=0.05, side=2)
```

Arguments

K	total number of tests
alpha	alpha value at the final test
side	1=one-side test, 2=two-side test

Details

Pocock suggested a fixed upper bound z-value for the cumulative hypothesis test in group sequential designs.

Value

a fixed upper bound z-value for the K times repeated hypothesis test with a final alpha-value. Attributes are;

ti	time of test, Even-interval is assumed.
cum.alpha	cumulative alpha valued

Author(s)

Kyun-Seop Bae k@acr.kr

References

Reboussin DM, DeMets DL, Kim K, Lan KKG. Computations for group sequential boundaries using the Lan-DeMets function method. *Controlled Clinical Trials*. 2000;21:190-207.

See Also

[seqBound](#), [OBFBound](#)

Examples

```
PocockBound(K=2) # Z-value of upper bound for the two-stage design
PocockBound(K=3) # Z-value of upper bound for the two-stage design
PocockBound(K=4) # Z-value of upper bound for the two-stage design
PocockBound(K=5) # Z-value of upper bound for the two-stage design
```

pResD

Residual Diagnostic Plot for Regression

Description

Nine residual diagnostics plots.

Usage

```
pResD(rx, Title=NULL)
```

Arguments

rx	a result of lm, which can give fitted, residuals, and rstandard.
Title	title to be printed on the plot

Details

SAS-style residual diagnostic plots.

Value

Nine residual diagnostic plots in a page.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
pResD(lm(uptake ~ Plant + Type + Treatment + conc, CO2), "Residual Diagnostic Plot")
```

QuartileRange	<i>Inter-Quartile Range</i>
---------------	-----------------------------

Description

Interquartile range (Q3 - Q1) with a conventional formula.

Usage

```
QuartileRange(y, Type=2)
```

Arguments

y	a vector of numerics
Type	a type specifier to be passed to IQR function

Details

It removes NA in the input vector. Type 2 is SAS default, while Type 6 is SPSS default.

Value

The value of an interquartile range

Author(s)

Kyun-Seop Bae k@acr.kr

Range	<i>Range</i>
-------	--------------

Description

The range, maximum - minimum, as a scalar value.

Usage

```
Range(y)
```

Arguments

y	a vector of numerics
---	----------------------

Details

It removes NA in the input vector.

Value

A scalar value of a range

Author(s)

Kyun-Seop Bae k@acr.kr

RanTest

Test with Random Effects

Description

Hypothesis test of with specified type SS using random effects as error terms. This corresponds to SAS PROC GLM's RANDOM /TEST clause.

Usage

```
RanTest(Formula, Data, Random="", Type=3, eps=1e-8)
```

Arguments

Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
Random	a vector of random effects. All should be specified as primary terms, not as interaction terms. All interaction terms with random factor are regarded as random effects.
Type	Sum of square type to be used as contrast
eps	Less than this value is considered as zero.

Details

Type can be from 1 to 3. All interaction terms with random factor are regarded as random effects. Here the error term should not be MSE.

Value

Returns ANOVA and E(MS) tables with specified type SS.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
RanTest(log(CMAX) ~ SEQ/SUBJ + PRD + TRT, BEdata, Random="SUBJ")
fBE = log(CMAX) ~ ADM/SEQ/SUBJ + PRD + TRT
RanTest(fBE, BEdata, Random=c("ADM", "SUBJ"))
RanTest(fBE, BEdata, Random=c("ADM", "SUBJ"), Type=2)
RanTest(fBE, BEdata, Random=c("ADM", "SUBJ"), Type=1)
```

RD *Risk Difference between two groups*

Description

Risk (proportion) difference between two groups

Usage

```
RD(y1, n1, y2, n2, conf.level=0.95)
```

Arguments

y1	positive event count of test (the first) group
n1	total count of the test (the first) group
y2	positive event count of control (the second) group
n2	total count of control (the second) group
conf.level	confidence level

Details

It calculates risk difference between the two groups. No continuity correction here. If you need percent scale, multiply the output by 100.

Value

The result is a data.frame.

p1	proportion from the first group
p2	proportion from the second group
RD	risk difference, p1 - p2
SE	standard error of RD
lower	lower confidence limit of RD
upper	upper confidence limit of RD

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[RR](#), [OR](#), [RDmn1](#), [RRmn1](#), [ORMn1](#), [RDmn](#), [RRmn](#), [ORMn](#)

Examples

```
RD(104, 11037, 189, 11034) # no continuity correction
```

RDinv	<i>Risk Difference between two groups with strata by inverse variance method</i>
-------	--

Description

Risk difference and its score confidence interval between two groups with stratification by inverse variance method

Usage

```
RDinv(d0, conf.level=0.95)
```

Arguments

d0	A data.frame or matrix, of which each row means a stratum. This should have four columns named y1, n1, y2, and n2; y1 and y2 for events of each group, n1 and n2 for the sample size of each stratum. The second group is usually the control group.
conf.level	confidence level

Details

It calculates risk difference and its confidence interval between two groups by inverse variance method. If you need percent scale, multiply the output by 100. This supports stratification. This can be used for meta-analysis also.

Value

The following output will be returned for each stratum and common value. There is no standard error.

p1	proportion from the first group, $y1/n1$
p2	proportion from the second group, $y2/n2$
RD	risk difference, $p1 - p2$. The point estimate of common RD is calculated with MH weight.
lower	lower confidence limit of RD
upper	upper confidence limit of RD

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[RDMn1](#), [RRMn1](#), [ORMn1](#), [RDMn](#), [RRMn](#), [ORMn](#), [RRinv](#), [ORinv](#), [ORcmh](#)

Examples

```
d1 = matrix(c(25, 339, 28, 335, 23, 370, 40, 364), nrow=2, byrow=TRUE)
colnames(d1) = c("y1", "n1", "y2", "n2")
RDinv(d1)
```

RDmn	<i>Risk Difference and Score CI between two groups with strata by the MN method</i>
------	---

Description

Risk difference and its score confidence interval between two groups with stratification by the Miettinen and Nurminen method

Usage

```
RDmn(d0, conf.level=0.95, eps=1e-8)
```

Arguments

d0	A data.frame or matrix, of which each row means a stratum. This should have four columns named y1, n1, y2, and n2; y1 and y2 for events of each group, n1 and n2 for sample size of each stratum. The second group is usually the control group. Maximum allowable value for n1 and n2 is 1e8.
conf.level	confidence level
eps	absolute value less than eps is regarded as negligible

Details

It calculates risk difference and its score confidence interval between the two groups. The confidence interval is asymmetric, and there is no standard error in the output. If you need percent scale, multiply the output by 100. This supports stratification. This implementation uses uniroot function which usually gives at least 5 significant digits. This can be used for meta-analysis also.

Value

The following output will be returned for each stratum and common value. There is no standard error.

p1	proportion from the first group, $y1/n1$
p2	proportion from the second group, $y2/n2$
RD	risk difference, $p1 - p2$. The point estimate of common RD is calculated with MN weight.
lower	lower confidence limit of RD
upper	upper confidence limit of RD

Author(s)

Kyun-Seop Bae k@acr.kr

References

Miettinen O, Nurminen M. Comparative analysis of two rates. *Stat Med* 1985;4:213-26

See Also

[RDmn1](#), [RRmn1](#), [ORmn1](#), [RRmn](#), [ORmn](#), [RDinv](#), [RRinv](#), [ORinv](#), [ORcmh](#)

Examples

```
d1 = matrix(c(25, 339, 28, 335, 23, 370, 40, 364), nrow=2, byrow=TRUE)
colnames(d1) = c("y1", "n1", "y2", "n2")
RDmn(d1)
d2 = data.frame(y1=c(4, 2, 10), n1=c(20, 20, 20), y2=c(8, 11, 2), n2=c(20, 20, 20))
RDmn(d2)
```

RDmn1

Risk Difference and Score CI between two groups without strata by the MN method

Description

Risk difference and its score confidence interval between two groups without stratification

Usage

```
RDmn1(y1, n1, y2, n2, conf.level=0.95, eps=1e-8)
```

Arguments

y1	positive event count of test (the first) group
n1	total count of the test (the first) group. Maximum allowable value is 1e8.
y2	positive event count of control (the second) group
n2	total count of control (the second) group. Maximum allowable value is 1e8.
conf.level	confidence level
eps	absolute value less than eps is regarded as negligible

Details

It calculates risk difference and its score confidence interval between the two groups. The confidence interval is asymmetric, and there is no standard error in the output. If you need percent scale, multiply the output by 100. This does not support stratification. This implementation uses `uniroot` function which usually gives at least 5 significant digits.

Value

There is no standard error.

p1	proportion from the first group, y_1/n_1
p2	proportion from the second group, y_2/n_2
RD	risk difference, $p_1 - p_2$
lower	lower confidence limit of RD
upper	upper confidence limit of RD

Author(s)

Kyun-Seop Bae k@acr.kr

References

Miettinen O, Nurminen M. Comparative analysis of two rates. Stat Med 1985;4:213-26

See Also

[RRmn1](#), [ORmn1](#), [RDmn](#), [RRmn](#), [ORmn](#)

Examples

```
RDmn1(104, 11037, 189, 11034)
```

REG

Regression of Linear Least Square, similar to SAS PROC REG

Description

REG is similar to SAS PROC REG.

Usage

```
REG(Formula, Data, conf.level=0.95, HC=FALSE, Resid=FALSE, Weights=1,
    summarize=TRUE)
```

Arguments

Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
conf.level	confidence level for the confidence limit
HC	heteroscedasticity related output is required such as HC0, HC3, White's first and second moment specification test
Resid	if TRUE, fitted values (\hat{y}) and residuals will be returned
Weights	weights for each observation or residual square. This is usually the inverse of each variance.
summarize	If this is FALSE, REG returns just lfit result.

Details

It performs the core function of SAS PROC REG.

Value

The result is comparable to that of SAS PROC REG.

The first part is ANOVA table.

The second part is measures about fitness.

The third part is the estimates of coefficients.

Estimate	point estimate of parameters, coefficients
Estimable	estimability: 1=TRUE, 0=FALSE. This appears only when at least one inestimability occurs.
Std. Error	standard error of the point estimate
Lower CL	lower confidence limit with conf.level
Upper CL	lower confidence limit with conf.level
Df	degree of freedom
t value	value for t distribution
Pr(> t)	probability of larger than absolute t value from t distribution with residual's degree of freedom

The above result is repeated using HC0 and HC3, with following White's first and second moment specification test, if HC option is specified. The t values and their p values with HC1 and HC2 are between those of HC0 and H3.

Fitted	Fitted value or y hat. This is returned only with Resid=TRUE option.
--------	--

Residual	Weighted residuals. This is returned only with Resid=TRUE option.
----------	---

If summarize=FALSE, REG returns;

coefficients	beta coefficients
g2	g2 inverse
rank	rank of the model matrix
DFr	degree of freedom for the residual
SSE	sum of square error

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[lr](#)

Examples

```

REG(uptake ~ Plant + Type + Treatment + conc, C02)
REG(uptake ~ conc, C02, HC=TRUE)
REG(uptake ~ conc, C02, Resid=TRUE)
REG(uptake ~ conc, C02, HC=TRUE, Resid=TRUE)
REG(uptake ~ conc, C02, summarize=FALSE)

```

regD

*Regression of Conventional Way with Rich Diagnostics***Description**

regD provides rich diagnostics such as student residual, leverage(hat), Cook's D, studentized deleted residual, DFFITS, and DFBETAS.

Usage

```
regD(Formula, Data)
```

Arguments

Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed

Details

It performs the conventional regression analysis. This does not use g2 inverse, therefore it cannot handle a singular matrix. If the model(design) matrix is not full rank, use REG or fewer parameters.

Value

Coefficients	conventional coefficients summary with Wald statistics
Diagnostics	Diagnostics table for detecting outlier or influential/leverage points. This includes fitted (Predicted), residual (Residual), standard error of residual(se_resid), studentized residual(RStudent), hat(Leverage), Cook's D, studentized deleted residual(sdResid), DIFFITS, and COVRATIO.
DFBETAS	Column names are the names of coefficients. Each row shows how much each coefficient is affected by deleting the corresponding row of observation.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
regD(uptake ~ conc, C02)
```

RR *Relative Risk of the two groups*

Description

Relative Risk between the two groups

Usage

```
RR(y1, n1, y2, n2, conf.level=0.95)
```

Arguments

y1	positive event count of test (the first) group
n1	total count of the test (the first) group
y2	positive event count of control (the second) group
n2	total count of control (the second) group
conf.level	confidence level

Details

It calculates relative risk of the two groups. No continuity correction here. If you need percent scale, multiply the output by 100.

Value

The result is a data.frame.

p1	proportion from the first group
p2	proportion from the second group
RR	relative risk, p1/p2
SElog	standard error of log(RR)
lower	lower confidence limit of RR
upper	upper confidence limit of RR

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[RD](#), [OR](#), [RDmn1](#), [RRmn1](#), [ORMn1](#), [RDmn](#), [RRmn](#), [ORMn](#)

Examples

```
RR(104, 11037, 189, 11034) # no continuity correction
```

RRinv *Relative Risk of two groups with strata by inverse variance method*

Description

Relative risk and its score confidence interval of two groups with stratification by inverse variance method

Usage

```
RRinv(d0, conf.level=0.95)
```

Arguments

d0	A data.frame or matrix, of which each row means a stratum. This should have four columns named y1, n1, y2, and n2; y1 and y2 for events of each group, n1 and n2 for sample size of each stratum. The second group is usually the control group.
conf.level	confidence level

Details

It calculates relative risk and its confidence interval of two groups by inverse variance method. This supports stratification. This can be used for meta-analysis also.

Value

The following output will be returned for each stratum and common value. There is no standard error.

p1	proportion from the first group, $y1/n1$
p2	proportion from the second group, $y2/n2$
RR	relative risk, $p1/p2$. The point estimate of common RR is calculated with MH weight.
lower	lower confidence limit of RR
upper	upper confidence limit of RR

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[RDmn1](#), [RRmn1](#), [ORMn1](#), [RDmn](#), [RRmn](#), [ORMn](#), [RDinv](#), [ORinv](#), [ORcmh](#)

Examples

```
d1 = matrix(c(25, 339, 28, 335, 23, 370, 40, 364), nrow=2, byrow=TRUE)
colnames(d1) = c("y1", "n1", "y2", "n2")
RRinv(d1)
```

RRmn

*Relative Risk and Score CI of two groups with strata by the MN method***Description**

Relative risk and its score confidence interval of two groups with stratification by the Miettinen and Nurminen method

Usage

```
RRmn(d0, conf.level=0.95, eps=1e-8)
```

Arguments

d0	A data.frame or matrix, of which each row means a strata. This should have four columns named y1, n1, y2, and n2; y1 and y2 for events of each group, n1 and n2 for sample size of each stratum. The second group is usually the control group.
conf.level	confidence level
eps	absolute value less than eps is regarded as negligible

Details

It calculates relative risk and its score confidence interval of the two groups. The confidence interval is asymmetric, and there is no standard error in the output. This supports stratification. This implementation uses uniroot function, which usually gives at least 5 significant digits. Whereas PropCIs::riskscoreci function uses cubic equation approximation which gives only about 2 significant digits. This can be used for meta-analysis also.

Value

The following output will be returned for each strata and common value. There is no standard error.

p1	proportion from the first group, $y1/n1$
p2	proportion from the second group, $y2/n2$
RR	relative risk, $p1/p2$. Point estimate of common RR is calculated with MN weight.
lower	lower confidence limit of RR
upper	upper confidence limit of RR

Author(s)

Kyun-Seop Bae k@acr.kr

References

Miettinen O, Nurminen M. Comparative analysis of two rates. Stat Med 1985;4:213-26

See Also

[RDmn1](#), [RRmn1](#), [ORMn1](#), [RDmn](#), [ORMn](#), [RDinv](#), [RRinv](#), [ORinv](#), [ORcmh](#)

Examples

```
d1 = matrix(c(25, 339, 28, 335, 23, 370, 40, 364), nrow=2, byrow=TRUE)
colnames(d1) = c("y1", "n1", "y2", "n2")
RRmn(d1)
d2 = data.frame(y1=c(4, 2, 10), n1=c(20, 20, 20), y2=c(8, 11, 2), n2=c(20, 20, 20))
RRmn(d2)
```

RRmn1	<i>Relative Risk and Score CI of two groups without strata by by MN method</i>
-------	--

Description

Relative risk and its score confidence interval of the two groups without stratification

Usage

```
RRmn1(y1, n1, y2, n2, conf.level=0.95, eps=1e-8)
```

Arguments

y1	positive event count of test (the first) group
n1	total count of the test (the first) group
y2	positive event count of control (the second) group
n2	total count of control (the second) group
conf.level	confidence level
eps	absolute value less than eps is regarded as negligible

Details

It calculates the relative risk and its score confidence interval of the two groups. The confidence interval is asymmetric, and there is no standard error in the output. This does not support stratification. This implementation uses uniroot function, which usually gives at least 5 significant digits. Whereas PropCIs::riskscoreci function uses cubic equation approximation which gives only about 2 significant digits.

Value

There is no standard error.

p1	proportion from the first group, $y1/n1$
p2	proportion from the second group, $y2/n2$
RR	relative risk, $p1/p2$
lower	lower confidence limit of RR
upper	upper confidence limit of RR

Author(s)

Kyun-Seop Bae k@acr.kr

References

Miettinen O, Nurminen M. Comparative analysis of two rates. *Stat Med* 1985;4:213-26

See Also

[RDmn1](#), [ORmn1](#), [RDmn](#), [RRmn](#), [ORmn](#)

Examples

```
RRmn1(104, 11037, 189, 11034)
```

satt

Satterthwaite Approximation of Variance and Degree of Freedom

Description

Calculates pooled variance and degree of freedom using Satterthwaite equation.

Usage

```
satt(vars, dfs, ws=c(1, 1))
```

Arguments

vars	a vector of variances
dfs	a vector of degree of freedoms
ws	a vector of weights

Details

The input can be more than two variances.

Value

Variance	approximated variance
Df	degree of freedom

Author(s)

Kyun-Seop Bae k@acr.kr

ScoreCI

Score Confidence Interval for a Proportion or a Binomial Distribution

Description

Score confidence of a proportion in one group

Usage

```
ScoreCI(y, n, conf.level=0.95)
```

Arguments

y	positive event count of a group
n	total count of a group
conf.level	confidence level

Details

It calculates score confidence interval of a proportion in one group. The confidence interval is asymmetric and there is no standard error in the output. If you need percent scale, multiply the output by 100.

Value

The result is a data.frame. There is no standard error.

PE	point estimation for the proportion
Lower	lower confidence limit of Prop
Upper	upper confidence limit of Prop

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[binom.test](#), [prop.test](#)

Examples

```
ScoreCI(104, 11037)
```

SD	<i>Standard Deviation</i>
----	---------------------------

Description

Standard deviation of a sample.

Usage

```
SD(y)
```

Arguments

y a vector of numerics

Details

It removes NA in the input vector. The length of the vector should be larger than 1.

Value

Sample standard deviation

Author(s)

Kyun-Seop Bae k@acr.kr

SEM	<i>Standard Error of the Sample Mean</i>
-----	--

Description

The estimate of the standard error of the sample mean

Usage

```
SEM(y)
```

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

The estimate of the standard error of the sample mean

Author(s)

Kyun-Seop Bae k@acr.kr

 seqBound

Sequential bounds for cumulative Z-test in Group Sequential Design

Description

Sequential upper bounds for cumulative Z-test on accumaltive data. Z values are correlated. This is usually used for group sequential design.

Usage

```
seqBound(ti, alpha = 0.05, side = 2, t2 = NULL, asf = 1)
```

Arguments

ti	times for test. These should be [0, 1].
alpha	goal alpha value for the last test at time 0.
side	1=one-side test, 2=two-side test
t2	fractions of information amount. These should be [0, 1]. If not available, ti will be used instead.
asf	alpha spending function. 1=O'Brien-Flemming type (approximate not the exact), 2=Pocock type (approximate not the exact), 3=alpha*ti, 4=alpha*ti^1.5, 5=alpha*ti^2

Details

It calculates upper z-bounds and cumulative alpha-values for the repeated test in group sequential design. The correlation is assumed to be $\sqrt{t_i/t_j}$. Use [PocockBound](#) and [OBFBound](#) for more exact bounds.

Value

The result is a matrix.

ti	time of test
bi	upper z-bound
cum.alpha	cumulative alpha-value

Author(s)

Kyun-Seop Bae k@acr.kr

References

Reboussin DM, DeMets DL, Kim K, Lan KKG. Computations for group sequential boundaries using the Lan-DeMets function method. *Controlled Clinical Trials*. 2000;21:190-207.

See Also

[PocockBound](#), [OBFBound](#)

Examples

```
seqBound(ti=(1:5)/5)
seqBound(ti=(1:5)/5, asf=2)
```

seqCI

Confidence interval with the last Z-value for the group sequential design

Description

Confidence interval with given upper bounds, time of tests, the last Z-value, and confidence level.

Usage

```
seqCI(bi, ti, Zval, conf.level=0.95)
```

Arguments

bi	upper bound z-values
ti	times for test. These should be [0, 1].
Zval	the last z-value from the observed data. This is not necessarily the planned final Z-value.
conf.level	confidence level

Details

It calculates confidence interval with given upper bounds, time of tests, the last Z-value, and confidence level. It assumes two-side test. `mvtnorm`: `pmt` (with noncentrality) is better than `pvmnorm` in calculating power, sample size, and confidence interval. But, Lan-DeMets used multi-variate normal rather than multi-variate noncentral t distribution. This function followed Lan-DeMets for the consistency with previous results. For the theoretical background, see the reference.

Value

confidence interval of Z-value for the given confidence level.

Author(s)

Kyun-Seop Bae k@acr.kr

References

Reboussin DM, DeMets DL, Kim K, Lan KKG. Computations for group sequential boundaries using the Lan-DeMets function method. *Controlled Clinical Trials*. 2000;21:190-207.

Examples

```
seqCI(bi = c(2.53, 2.61, 2.57, 2.47, 2.43, 2.38),  
      ti = c(.2292, .3333, .4375, .5833, .7083, .8333), Zval=2.82)
```

Skewness

Skewness

Description

Skewness with a conventional formula.

Usage

```
Skewness(y)
```

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

Estimate of skewness

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[SkewnessSE](#)

SkewnessSE

Standard Error of Skewness

Description

Standard error of the skewness with a conventional formula.

Usage

SkewnessSE(y)

Arguments

y a vector of numerics

Details

It removes NA in the input vector.

Value

Standard error of the estimated skewness

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[Skewness](#)

SLICE

F Test with Slice

Description

Do F test with a given slice term.

Usage

SLICE(Formula, Data, Term, By)

Arguments

Formula	a conventional formula for a linear model
Data	a <code>data.frame</code> to be analyzed
Term	a factor name (not interaction) to calculate the sum of square and do F test with least square means
By	a factor name to be used for slice

Details

It performs F test with a given slice term. It is similar to the `SLICE` option SAS PROC GLM.

Value

Returns sum of square and its F value and p-value. Row names are the levels of the slice term.

Df	degree of freedom
Sum Sq	sum of square for the set of contrasts
Mean Sq	mean square
F value	F value for the F distribution
Pr(>F)	probability of larger than F value

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
SS(uptake ~ Type*Treatment, CO2, "Type", "Treatment")
SS(uptake ~ Type*Treatment, CO2, "Treatment", "Type")
```

SS	<i>Sum of Square</i>
----	----------------------

Description

Sum of squares with ANOVA.

Usage

```
SS(x, rx, L, eps=1e-8)
```

Arguments

x	a result of <code>ModelMatrix</code> containing design information
rx	a result of <code>lfit</code>
L	linear hypothesis, a full matrix matching the information in x
eps	Less than this value is considered as zero.

Details

It calculates sum of squares and completes the ANOVA table.

Value

ANOVA table a classical ANOVA table without the residual(Error) part.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[ModelMatrix](#), [lfit](#)

T3MS

Type III Expected Mean Square Formula

Description

Calculates a formula table for expected mean square of Type III SS.

Usage

```
T3MS(Formula, Data, L0, eps=1e-8)
```

Arguments

Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
L0	a matrix of row linear contrasts, if missed, e3 is used
eps	Less than this value is considered as zero.

Details

This is necessary for further hypothesis tests of nesting factors.

Value

A coefficient matrix for Type III expected mean square

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
T3MS(log(CMAX) ~ SEQ/SUBJ + PRD + TRT, BEdata)
```

T3test	<i>Test Type III SS using error term other than MSE</i>
--------	---

Description

Hypothesis test of Type III SS using an error term other than MSE. This corresponds to SAS PROC GLM's RANDOM /TEST clause.

Usage

```
T3test(Formula, Data, H="", E="", eps=1e-8)
```

Arguments

Formula	a conventional formula for a linear model
Data	a data.frame to be analyzed
H	Hypothesis term
E	Error term
eps	Less than this value is considered as zero.

Details

It tests a factor of type III SS using some other term as an error term. Here the error term should not be MSE.

Value

Returns one or more ANOVA table(s) of type III SS.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
T3test(log(CMAX) ~ SEQ/SUBJ + PRD + TRT, BEdata, E=c("SEQ:SUBJ"))  
T3test(log(CMAX) ~ SEQ/SUBJ + PRD + TRT, BEdata, H="SEQ", E=c("SEQ:SUBJ"))
```

tmtest *Independent two means test similar to t.test with summarized input*

Description

This produces essentially the same to t.test except using summarized input (sufficient statistics).

Usage

```
tmtest(m1, s1, n1, m0, s0, n0, conf.level=0.95, nullHypo=0, var.equal=FALSE)
```

Arguments

m1	mean of the first (test, active, experimental) group
s1	sample standard deviation of the first group
n1	sample size of the first group
m0	mean of the second (reference, control, placebo) group
s0	sample standard deviation of the second group
n0	sample size of the second group
conf.level	confidence level
nullHypo	value for the difference of means under null hypothesis
var.equal	assumption on the variance equality

Details

The default is Welch t-test with Satterthwaite approximation.

Value

The output format is very similar to t.test

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[mtest](#), [TTEST](#), [ztest](#)

Examples

```
tmtest(5.4, 10.5, 3529, 5.1, 8.9, 5190) # NEJM 388;15 p1386
tmtest(5.4, 10.5, 3529, 5.1, 8.9, 5190, var.equal=TRUE)
```

trimmedMean	<i>Trimmed Mean</i>
-------------	---------------------

Description

Trimmed mean wrapping mean function.

Usage

```
trimmedMean(y, Trim=0.05)
```

Arguments

y	a vector of numerics
Trim	trimming proportion. Default is 0.05

Details

It removes NA in the input vector.

Value

The value of trimmed mean

Author(s)

Kyun-Seop Bae k@acr.kr

tsum	<i>Table Summary</i>
------	----------------------

Description

Summarize a continuous dependent variable with or without independent variables.

Usage

```
tsum(Formula=NULL, Data=NULL, ColNames=NULL, MaxLevel=30, ...)
```

Arguments

Formula	a conventional formula
Data	a data.frame or a matrix
ColNames	If there is no Formula, this will be used.
MaxLevel	More than this will not be handled.
...	arguments to be passed to tsum0, tsum1, tsum2, or tsum3

Details

A convenient summarization function for a continuous variable. This is a wrapper function to tsum0, tsum1, tsum2, or tsum3.

Value

A data.frame of descriptive summarization values.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[tsum0](#), [tsum1](#), [tsum2](#), [tsum3](#)

Examples

```
tsum(lh)
t(tsum(CO2))
t(tsum(uptake ~ Treatment, CO2))
tsum(uptake ~ Type + Treatment, CO2)
print(tsum(uptake ~ conc + Type + Treatment, CO2), digits=3)
```

tsum0

Table Summary 0 independent(x) variable

Description

Summarize a continuous dependent(y) variable without any independent(x) variable.

Usage

```
tsum0(d, y, e=c("Mean", "SD", "N"), repl=list(c("length"), c("n")))
```

Arguments

d	a data.frame or matrix with colnames
y	y variable name, a continuous variable
e	a vector of summarize function names
repl	list of strings to replace after summarize. The length of list should be 2, and both should have the same length.

Details

A convenient summarization function for a continuous variable.

Value

A vector of summarized values

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[tsum](#), [tsum1](#), [tsum2](#), [tsum3](#)

Examples

```
tsum0(CO2, "uptake")
tsum0(CO2, "uptake", repl=list(c("mean", "length"), c("Mean", "n")))
```

tsum1

Table Summary 1 independent(x) variable

Description

Summarize a continuous dependent(y) variable with one independent(x) variable.

Usage

```
tsum1(d, y, u, e=c("Mean", "SD", "N"), ou="", repl=list(c("length"), ("n")))
```

Arguments

d	a data.frame or matrix with colnames
y	y variable name. a continuous variable
u	x variable name, upper side variable
e	a vector of summarize function names
ou	order of levels of upper side x variable
repl	list of strings to replace after summarize. The length of list should be 2, and both should have the same length.

Details

A convenient summarization function for a continuous variable with one x variable.

Value

A data.frame of summarized values. Row names are from e names. Column names are from the levels of x variable.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also[tsum](#), [tsum0](#), [tsum2](#), [tsum3](#)**Examples**

```
tsum1(CO2, "uptake", "Treatment")
tsum1(CO2, "uptake", "Treatment",
      e=c("mean", "median", "sd", "min", "max", "length"),
      ou=c("chilled", "nonchilled"),
      repl=list(c("median", "length"), c("med", "n")))
```

tsum2

Table Summary 2 independent(x) variables

Description

Summarize a continuous dependent(y) variable with two independent(x) variables.

Usage

```
tsum2(d, y, l, u, e=c("Mean", "SD", "N"), h=NULL, ol="", ou="", rm.dup=TRUE,
      repl=list(c("length"), c("n")))
```

Arguments

d	a data.frame or matrix with colnames
y	y variable name. a continuous variable
l	x variable name to be shown on the left side
u	x variable name to be shown on the upper side
e	a vector of summarize function names
h	a vector of summarize function names for the horizontal subgroup. If NULL, it becomes the same as e argument.
ol	order of levels of left side x variable
ou	order of levels of upper side x variable
rm.dup	if TRUE, duplicated names of levels are specified on the first occurrence only.
repl	list of strings to replace after summarize. The length of list should be 2, and both should have the same length.

Details

A convenient summarization function for a continuous variable with two x variables; one on the left side, the other on the upper side.

Value

A data.frame of summarized values. Column names are from the levels of u. Row names are basically from the levels of l.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[tsum](#), [tsum0](#), [tsum1](#), [tsum3](#)

Examples

```
tsum2(CO2, "uptake", "Type", "Treatment")
tsum2(CO2, "uptake", "Type", "conc")
tsum2(CO2, "uptake", "Type", "Treatment",
      e=c("mean", "median", "sd", "min", "max", "length"),
      ou=c("chilled", "nonchilled"),
      repl=list(c("median", "length"), c("med", "n")))
```

tsum3

Table Summary 3 independent(x) variables

Description

Summarize a continuous dependent(y) variable with three independent(x) variables.

Usage

```
tsum3(d, y, l, u, e=c("Mean", "SD", "N"), h=NULL, o1="", o2="", ou="",
      rm.dup=TRUE, repl=list(c("length"), c("n")))
```

Arguments

d	a data.frame or matrix with colnames
y	y variable name. a continuous variable
l	a vector of two x variable names to be shown on the left side. The length should be 2.
u	x variable name to be shown on the upper side
e	a vector of summarize function names
h	a list of two vectors of summarize function names for the first and second horizontal subgroups. If NULL, it becomes the same as e argument.
o1	order of levels of 1st left side x variable
o2	order of levels of 2nd left side x variable

<code>ou</code>	order of levels of upper side x variable
<code>rm.dup</code>	if TRUE, duplicated names of levels are specified on the first occurrence only.
<code>repl</code>	list of strings to replace after summarize. The length of list should be 2, and both should have the same length.

Details

A convenient summarization function for a continuous variable with three x variables; two on the left side, the other on the upper side.

Value

A data.frame of summarized values. Column names are from the levels of u. Row names are basically from the levels of l.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[tsum](#), [tsum0](#), [tsum1](#), [tsum2](#)

Examples

```
tsum3(CO2, "uptake", c("Type", "Treatment"), "conc")
tsum3(CO2, "uptake", c("Type", "Treatment"), "conc",
      e=c("mean", "median", "sd", "min", "max", "length"),
      h=list(c("mean", "sd", "length"), c("mean", "length")),
      o1=c("chilled", "nonchilled"),
      repl=list(c("median", "length"), c("med", "n")))
```

TTEST

Independent two groups t-test comparable to PROC TTEST

Description

This is comparable to SAS PROC TTEST.

Usage

```
TTEST(x, y, conf.level=0.95)
```

Arguments

<code>x</code>	a vector of data from the first (test, active, experimental) group
<code>y</code>	a vector of data from the second (reference, control, placebo) group
<code>conf.level</code>	confidence level

Details

Caution on choosing the row to use in the output.

Value

The output format is comparable to SAS PROC TTEST.

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[mtest](#), [tmttest](#), [ztest](#)

Examples

```
TTEST(mtcars[mtcars$am==1, "mpg"], mtcars[mtcars$am==0, "mpg"])
```

UCL

Upper Confidence Limit

Description

The estimate of the upper bound of the confidence limit using t-distribution

Usage

```
UCL(y, conf.level=0.95)
```

Arguments

y	a vector of numerics
conf.level	confidence level

Details

It removes NA in the input vector.

Value

The estimate of the upper bound of the confidence limit using t-distribution

Author(s)

Kyun-Seop Bae k@acr.kr

Description

Returns descriptive statistics of a numeric vector.

Usage

```
UNIV(y, conf.level = 0.95)
```

Arguments

y	a numeric vector
conf.level	confidence level for confidence limit

Details

A convenient and comprehensive function for descriptive statistics. NA is removed during the calculation. This is similar to SAS PROC UNIVARIATE.

Value

nAll	count of all elements in the input vector
nNA	count of NA element
nFinite	count of finite numbers
Mean	mean excluding NA
SD	standard deviation excluding NA
CV	coefficient of variation in percent
SEM	standard error of the sample mean, the sample mean divided by nFinite
LowerCL	lower confidence limit of mean
UpperCL	upper confidence limit of mean
TrimmedMean	trimmed mean with trimming 1 - confidence level
Min	minimum value
Q1	first quartile value
Median	median value
Q3	third quartile value
Max	maximum value
Range	range of finite numbers. maximum - minimum
IQR	inter-quartile range type 2, which is SAS default
MAD	median absolute deviation

VarLL	lower confidence limit of variance
VarUL	upper confidence limit of variance
Skewness	skewness
SkewnessSE	standard error of skewness
Kurtosis	kurtosis
KurtosisSE	kurtosis
GeometricMean	geometric mean, calculated only when all given values are positive.
GeometricCV	geometric coefficient of variation in percent, calculated only when all given values are positive.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
UNIV(1h)
```

```
vttest
```

F-Test for the ratio of two groups' variances

Description

F-test for the ratio of two groups' variances. This is similar to var.test except using the summarized input.

Usage

```
vttest(v1, n1, v0, n0, ratio=1, conf.level=0.95)
```

Arguments

v1	sample variance of the first (test, active, experimental) group
n1	sample size of the first group
v0	sample variance of the second (reference, control, placebo) group
n0	sample size of the second group
ratio	value for the ratio of variances under null hypothesis
conf.level	confidence level

Details

For the confidence interval of one group, use UNIV function.

Value

The output format is very similar to var.test.

Author(s)

Kyun-Seop Bae k@acr.kr

Examples

```
vtest(10.5^2, 3529, 8.9^2, 5190) # NEJM 388;15 p1386
vtest(2.3^2, 13, 1.5^2, 11, conf.level=0.9) # Red book p240
```

WhiteTest

White's Model Specification Test

Description

This is shown in SAS PROC REG as the Test of First and Second Moment Specification.

Usage

```
WhiteTest(rx)
```

Arguments

rx a result of lm

Details

This is also called as White's general test for heteroskedasticity.

Value

Returns a direct test result by more complex theorem 2 , not by simpler corollary 1.

Author(s)

Kyun-Seop Bae k@acr.kr

References

White H. A Heteroskedasticity-Consistent Covariance Matrix Estimator and a Direct Test for Heteroskedasticity. *Econometrica* 1980;48(4):817-838.

Examples

```
WhiteTest(lm(mpg ~ disp, mtcars))
```

ztest *Test for the difference of two groups' means*

Description

This is similar to two groups t-test, but using standard normal (Z) distribution.

Usage

```
ztest(m1, s1, n1, m0, s0, n0, conf.level=0.95, nullHypo=0)
```

Arguments

m1	mean of the first (test, active, experimental) group
s1	known standard deviation of the first group
n1	sample size of the first group
m0	mean of the second (reference, control, placebo) group
s0	known standard deviation of the second group
n0	sample size of the second group
conf.level	confidence level
nullHypo	value for the difference of means under null hypothesis

Details

Use this only for known standard deviations (or variances) or very large sample sizes per group.

Value

The output format is very similar to t.test

Author(s)

Kyun-Seop Bae k@acr.kr

See Also

[mtest](#), [tmtest](#), [TTEST](#)

Examples

```
ztest(5.4, 10.5, 3529, 5.1, 8.9, 5190) # NEJM 388;15 p1386
```

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