

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 wants 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 | 3 |
| af | 4 |
| aov1 | 5 |
| aov2 | 6 |
| aov3 | 7 |
| aspirinCHD | 9 |
| BEdata | 9 |
| bk | 10 |
| BY | 11 |

| | |
|-------------------------|----|
| CIest | 12 |
| Coll | 13 |
| CONTR | 14 |
| Cor.test | 15 |
| corFisher | 16 |
| cSS | 17 |
| CV | 18 |
| Diffogram | 18 |
| e1 | 19 |
| e2 | 20 |
| e3 | 21 |
| EMS | 21 |
| est | 22 |
| ESTM | 23 |
| estmb | 24 |
| G2SWEEP | 25 |
| geoCV | 26 |
| geoMean | 27 |
| GLM | 28 |
| is.cor | 29 |
| Kurtosis | 30 |
| KurtosisSE | 31 |
| LCL | 31 |
| lfit | 32 |
| lr | 33 |
| lr0 | 34 |
| LSM | 35 |
| Max | 36 |
| Mean | 37 |
| Median | 37 |
| Min | 38 |
| ModelMatrix | 39 |
| mtest | 40 |
| N | 41 |
| OR | 41 |
| ORcmh | 42 |
| ORinv | 43 |
| ORmn | 44 |
| ORmn1 | 46 |
| pB | 47 |
| Pcor.test | 48 |
| pD | 49 |
| PDIFF | 49 |
| pResD | 51 |
| QuartileRange | 51 |
| Range | 52 |
| RanTest | 53 |
| RD | 54 |

| | |
|-----------------------|-----------|
| RDinv | 55 |
| RDmn | 56 |
| RDmn1 | 57 |
| REG | 58 |
| regD | 60 |
| RR | 61 |
| RRinv | 62 |
| RRmn | 63 |
| RRmn1 | 64 |
| satt | 65 |
| ScoreCI | 66 |
| SD | 67 |
| SEM | 67 |
| Skewness | 68 |
| SkewnessSE | 69 |
| SLICE | 69 |
| SS | 70 |
| T3MS | 71 |
| T3test | 72 |
| tmtest | 73 |
| trimmedMean | 74 |
| tsum | 74 |
| tsum0 | 75 |
| tsum1 | 76 |
| tsum2 | 77 |
| tsum3 | 78 |
| TTEST | 79 |
| UCL | 80 |
| UNIV | 81 |
| vtest | 82 |
| WhiteTest | 83 |
| ztest | 84 |
| Index | 85 |

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 (\hat{y}) 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, CO2)
aov1(uptake ~ Plant + Type + Treatment + conc, CO2, BETA=TRUE)
aov1(uptake ~ Plant + Type + Treatment + conc, CO2, Resid=TRUE)
aov1(uptake ~ Plant + Type + Treatment + conc, CO2, 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 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 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 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

```
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 | <i>Beautify the output of knitr::kable</i> |
|----|--|

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   |
```

 BY

Analysis BY variable

Description

GLM, REG, aov1 etc. functions can be run by levels of a variable.

Usage

```
BY(FUN, Formula, Data, By, ...)
```

Arguments

FUN Function name to be called such as GLM, REG
 Formula a conventional formula for a linear model.

| | |
|------|--|
| Data | a <code>data.frame</code> to be analyzed |
| By | a variable name in the Data |
| ... | arguments to be passed to FUN function |

Details

This mimics SAS procedues' BY clause.

Value

a list of FUN function outputs. The names are after each level.

Author(s)

Kyun-Seop Bae `k@acr.kr`

Examples

```
BY(GLM, uptake ~ Treatment + as.factor(conc), C02, By="Type")
BY(REG, uptake ~ conc, C02, By="Type")
```

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 <code>data.frame</code> to be analyzed |
| Term | a factor name to be estimated |
| Contrast | a level vector. Level is alphabetically ordered by default. |
| <code>conf.level</code> | 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, CO2) # sum of square
GLM(uptake ~ Type, CO2) # 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

| | |
|------------|--------------------------|
| Data | a matrix or a data.frame |
| conf.level | 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
```

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 <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", 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)")
```

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

| | |
|-----|---|
| XpX | crossprod of a design or model matrix. This should have appropriate column names. |
| eps | 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

| | |
|------------------|---|
| <code>x</code> | an output of <code>ModelMatrix</code> |
| <code>eps</code> | 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](#)

G2SWEEP

Generalized inverse matrix of type 2, g2 inverse

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 |
| 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. |
| 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, C02)
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 *Number of observations*

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

OR *Odds Ratio of two groups*

Description

Odds Ratio between two groups

Usage

OR(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 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)
```

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")
```

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 *Inter-Quartile Range*

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

Range

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)
```

| | |
|-------|--|
| RDmn1 | <i>Risk Difference and Score CI between two groups without strata by the MN method</i> |
|-------|--|

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, $y1/n1$ |
| p2 | proportion from the second group, $y2/n2$ |
| RD | risk difference, $p1 - p2$ |
| 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 <code>data.frame</code> 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 <code>lfit</code> 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)
```

| | |
|-------|--|
| 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

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 | <i>Standard Error of Skewness</i> |
|------------|-----------------------------------|

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 | <i>F Test with Slice</i> |
|-------|--------------------------|

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

Test Type III SS using error term other than MSE

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 tem |
| 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 | <i>Independent two means test similar to t.test with summarized input</i> |
|--------|---|

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=F)
```

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 | <i>Table Summary 1 independent(x) variable</i> |
|-------|--|

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

| | |
|-------------------------|----------------------|
| <code>y</code> | a vector of numerics |
| <code>conf.level</code> | 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)
```

vtest

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

```
vtest(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, 5190, 8.9^2, 3529) # 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

| | |
|-------------------------|---|
| <code>m1</code> | mean of the first (test, active, experimental) group |
| <code>s1</code> | known standard deviation of the first group |
| <code>n1</code> | sample size of the first group |
| <code>m0</code> | mean of the second (reference, control, placebo) group |
| <code>s0</code> | known standard deviation of the second group |
| <code>n0</code> | sample size of the second group |
| <code>conf.level</code> | confidence level |
| <code>nullHypo</code> | 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
```

Index

* 2x2 Table

ORcmh, 42
ORmn, 44
ORmn1, 46
RD, 54
RDmn, 56
RDmn1, 57
RR, 61
RRmn, 63
RRmn1, 64

* Descriptive Statistics

UNIV, 81

* Meta-analysis

ORinv, 43
RDinv, 55
RRinv, 62

* Plot

pB, 47
pD, 49
pResD, 51

* Table Summary

tsum, 74
tsum0, 75
tsum1, 76
tsum2, 77
tsum3, 78

* datasets

aspirinCHD, 9
BEdata, 9

* t-test

mtest, 40
tmtest, 73
TTEST, 79
ztest, 84

af, 4
aov1, 5
aov2, 6
aov3, 7
aspirinCHD, 9

BEdata, 9
binom.test, 66
bk, 10
BY, 11

CIest, 12
Coll, 13
CONTR, 14, 17
Cor.test, 15
corFisher, 16
cSS, 15, 17
CV, 18

Diffogram, 18, 36, 50

e1, 19
e2, 20
e3, 21
EMS, 21
est, 22, 24
ESTM, 23, 23
estmb, 24
ESTMIMATE (ESTM), 23

G2SWEEP, 25, 25
geoCV, 26, 28
geoMean, 27, 27
GLM, 28

is.cor, 29

Kurtosis, 30, 31
KurtosisSE, 30, 31

LCL, 31
lfit, 26, 32, 71
lr, 33, 59
lr0, 34
LSM, 19, 35, 50

Max, 36

- Mean, [37](#)
- Median, [37](#)
- Min, [38](#)
- ModelMatrix, [26](#), [33](#), [39](#), [71](#)
- mtest, [40](#), [73](#), [80](#), [84](#)

- N, [41](#)

- OR, [41](#), [54](#), [61](#)
- ORcmh, [42](#), [44](#), [45](#), [55](#), [57](#), [62](#), [64](#)
- ORinv, [43](#), [43](#), [45](#), [55](#), [57](#), [62](#), [64](#)
- ORmn, [42–44](#), [44](#), [47](#), [54](#), [55](#), [57](#), [58](#), [61](#), [62](#), [64](#), [65](#)
- ORmn1, [42–45](#), [46](#), [54](#), [55](#), [57](#), [58](#), [61](#), [62](#), [64](#), [65](#)

- pB, [47](#)
- Pcor.test, [48](#)
- pD, [49](#)
- PDIFF, [19](#), [23](#), [36](#), [49](#)
- pResD, [51](#)
- prop.test, [66](#)

- QuartileRange, [51](#)

- Range, [52](#)
- RanTest, [53](#)
- RD, [42](#), [54](#), [61](#)
- RDinv, [43–45](#), [55](#), [57](#), [62](#), [64](#)
- RDmn, [42–45](#), [47](#), [54](#), [55](#), [56](#), [58](#), [61](#), [62](#), [64](#), [65](#)
- RDmn1, [42–45](#), [47](#), [54](#), [55](#), [57](#), [57](#), [61](#), [62](#), [64](#), [65](#)
- REG, [58](#)
- regD, [60](#)
- RR, [42](#), [54](#), [61](#)
- RRinv, [43–45](#), [55](#), [57](#), [62](#), [64](#)
- RRmn, [42–45](#), [47](#), [54](#), [55](#), [57](#), [58](#), [61](#), [62](#), [63](#), [65](#)
- RRmn1, [42–45](#), [47](#), [54](#), [55](#), [57](#), [58](#), [61](#), [62](#), [64](#), [64](#)

- sasLM (sasLM-package), [3](#)
- sasLM-package, [3](#)
- satt, [65](#)
- ScoreCI, [66](#)
- SD, [67](#)
- SEM, [67](#)
- Skewness, [68](#), [69](#)
- SkewnessSE, [68](#), [69](#)
- SLICE, [69](#)
- SS, [70](#)

- T3MS, [71](#)
- T3test, [72](#)

- tmtest, [40](#), [73](#), [80](#), [84](#)
- trimmedMean, [74](#)
- tsum, [74](#), [76–79](#)
- tsum0, [11](#), [75](#), [75](#), [77–79](#)
- tsum1, [11](#), [75](#), [76](#), [76](#), [78](#), [79](#)
- tsum2, [11](#), [75–77](#), [77](#), [79](#)
- tsum3, [11](#), [75–78](#), [78](#)
- TTEST, [40](#), [73](#), [79](#), [84](#)

- UCL, [32](#), [80](#)
- UNIV, [81](#)

- vtest, [82](#)

- WhiteTest, [83](#)

- ztest, [40](#), [73](#), [80](#), [84](#)