

Package ‘MultNonParam’

January 20, 2025

Type Package

Title Multivariate Nonparametric Methods

Version 1.3.9

Date 2023-08-29

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Description A collection of multivariate nonparametric methods, selected in part to support an MS level course in nonparametric statistical methods. Methods include adjustments for multiple comparisons, implementation of multivariate Mann-Whitney-Wilcoxon testing, inversion of these tests to produce a confidence region, some permutation tests for linear models, and some algorithms for calculating exact probabilities associated with one- and two- stage testing involving Mann-Whitney-Wilcoxon statistics. Supported by grant NSF DMS 1712839. See Kolassa and Seifu (2013) <[doi:10.1016/j.acra.2013.03.006](https://doi.org/10.1016/j.acra.2013.03.006)>.

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LazyData true

Encoding UTF-8

NeedsCompilation yes

Depends R (>= 2.10), ICSNP

RoxygenNote 7.2.1

Repository CRAN

Date/Publication 2023-08-30 04:40:02 UTC

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MultNonParam-package *MultNonParam*

Description

A collection of nonparametric methods.

Author(s)

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- Stephane Jankowski

aov.P

One-way ANOVA using permutation tests

Description

aov.P uses permutation tests instead of classic theory tests to run a one-way or two-way ANOVA.

Usage

```
aov.P(dattab, treatment = NULL, be = NULL)
```

Arguments

dattab	The table on which the ANOVA has to be done, or a vector of responses.
treatment	If dattab is a table, ignored. If dattab is a vector, a vector of treatment labels.
be	If dattab is a table, ignored. If dattab is a vector, a vector of end points of blocks. In this case, blocks must form contiguous subvectors of dattab. If null, no blocking.

Details

The function calls a Fortran code to perform the permutation tests and the ANOVA. The function has to be applied directly on a cross-table of two variables.

Value

A list with fields pv, the p-value obtained with the permutation tests, and tot, the total number of permutations.

betatest

Permutation test of association

Description

Calculate the p-value for the test of association between two variables using the permutation method.

Usage

```
betatest(x, y)
```

Arguments

x	First vector to be associated.
y	First vector to be associated.

Value

p-value

Examples

```
#Example using data from plant Qn1 from the CO2 data set.^M
betatest(CO2[CO2$Plant=="Qn1",4],CO2[CO2$Plant=="Qn1",5])
```

dconcordant	<i>Calculate the probability atom of the count of concordant pairs among independent pairs of random variables.</i>
-------------	---

Description

Calculate the probability atom of the count of concordant pairs among independent pairs of random variables.

Usage

```
dconcordant(ss, nn)
```

Arguments

ss	Integer number of pairs
nn	number of pairs

Value

real probability

dmannwhitney	<i>Mann Whitney Probability Mass function</i>
--------------	---

Description

Calculates the Mann Whitney Probability Mass function recursively.

Usage

```
dmannwhitney(u, m, n)
```

Arguments

u	Statistic value
m	Group 1 size
n	Group 2 size

Value

Probability that the Mann-Whitney statistic takes the value u under H_0

ecdfcis *Confidence Intervals for Empirical Cumulative Distribution Functions*

Description

Confidence Intervals for Empirical Cumulative Distribution Functions

Usage

```
ecdfcis(data, alpha = 0.05, dataname = NA, exact = TRUE, newplot = TRUE)
```

Arguments

data	vector of observations
alpha	1-confidence level.
dataname	Name of variable for use in axis labeling
exact	logical value controlling whether confidence intervals are exact or asymptotic.
newplot	logical value controlling whether the estimate is added to an existing plot, or whether a new plot should be constructed.

exactquantileci *Exact Quantile Confidence Interval*

Description

Calculates exact quantile confidence intervals by inverting the generalization of the sign test.

Usage

```
exactquantileci(xvec, tau = 0.5, alpha = 0.05, md = 0)
```

Arguments

xvec	vector of observations
tau	quantile to be estimated. If this is a vector, separate intervals and tests for each value will be calculated.
alpha	1-confidence level.
md	null value of quantile

Value

A list with components `cis`, an array with two columns, representing lower and upper bounds, and a vector `pvals`, of p-values.

genscorestat	<i>Normal-theory two sample scorestatistic.</i>
--------------	---

Description

Calculates the p-value from the normal approximation to the permutation distribution of a two-sample score statistic.

Usage

```
genscorestat(scores, group, correct = 0)
```

Arguments

scores	scores of the data.
group	numeric or character vector of group identities.
correct	half the minimal distance between two potential values of the score statistic.

Value

Object of class htest containing the p-value.

higgins.fisher.kruskal.test	<i>Fisher's LSD method applied to the Kruskal-Wallis test</i>
-----------------------------	---

Description

This function applies a rank-based method for controlling experiment-wise error. Two hypothesis have to be respected: normality of the distribution and no ties in the data. The aim is to be able to detect, among k treatments, those who lead to significant differences in the values for a variable of interest.

Usage

```
higgins.fisher.kruskal.test(resp, grp, alpha = 0.05)
```

Arguments

resp	vector containing the values for the variable of interest.
grp	vector specifying in which group is each observation.
alpha	level of the test.

Details

First, the Kruskal-Wallis test is used to test the equality of the distributions of each treatment. If the test is significant at the level α , the method can be applied.

Value

A matrix with two columns. Each row indicates a combination of two groups that have significant different distributions.

References

J.J. Higgins, (2004), *Introduction to Modern Nonparametric Statistics*, Brooks/Cole, Cengage Learning.

kweffectsiz

Sample Size for the Kruskal-Wallis test.

Description

kweffectsiz approximates effect size for the Kruskal-Wallis test, using a chi-square approximation under the null, and a non-central chi-square approximation under the alternative. The noncentrality parameter is calculated using alternative means and the null variance structure.

Usage

```
kweffectsiz(
  totsamp,
  shifts,
  distname = c("normal", "logistic", "cauchy"),
  targetpower = 0.8,
  proportions = rep(1, length(shifts))/length(shifts),
  level = 0.05
)
```

Arguments

totsamp	sample size
shifts	The offsets for the various populations, under the alternative hypothesis. This is used for direction on input.
distname	The distribution of the underlying observations; normal and logistic are currently supported.
targetpower	The distribution of the underlying observations; normal and logistic are currently supported.
proportions	The proportions in each group.
level	The test level.

Details

The standard noncentral chi-square power formula, or Monte Carlo, is used.

Value

A list with components `power`, giving the power approximation, `ncp`, giving the noncentrality parameter, `cv`, giving the critical value, `probs`, giving the intermediate output from pairwise probability, and `expect`, the quantities summed before squaring in the noncentrality parameter.

Examples

```
#Calculate the effect size necessary to have the desired power .8 for a test
#with the level .5 with sample size 60, group centers 0, 1, and 2,
#normally distributed observations, evenly split among the three groups.
kweffectsize(60,c(0,1,2),"normal")
```

kwpower

Power for the Kruskal-Wallis test.

Description

kwpower approximates power for the Kruskal-Wallis test, using a chi-square approximation under the null, and a non-central chi-square approximation under the alternative. The noncentrality parameter is calculated using alternative means and the null variance structure.

Usage

```
kwpower(
  nreps,
  shifts,
  distname = c("normal", "cauchy", "logistic"),
  level = 0.05,
  mc = 0,
  taylor = FALSE
)
```

Arguments

nreps	The numbers in each group.
shifts	The offsets for the various populations, under the alternative hypothesis.
distname	The distribution of the underlying observations; normal, cauchy, and logistic are currently supported.
level	The test level.
mc	0 for asymptotic calculation, or positive for mc approximation.
taylor	logical determining whether Taylor series approximation is used for probabilities.

Details

The standard noncentral chi-square power formula, or Monte Carlo, is used.

Value

A list with components `power`, giving the power approximation, `ncp`, giving the noncentrality parameter, `cv`, giving the critical value, `probs`, giving the intermediate output from pairwise probability, and `expect`, the quantities summed before squaring in the noncentrality parameter.

Examples

```
#Calculate the power for the Kruskal Wallis test for normal observations,
#10 observations in each of three groups, with groups centered at 0, 1, 2.
#Level is 0.05 by default.
kwpower(rep(10,3),c(0,1,2),"normal")
```

kwsamplesize

Sample Size for the Kruskal-Wallis test.

Description

`kwsamplesize` approximates sample size for the Kruskal-Wallis test, using a chi-square approximation under the null, and a non-central chi-square approximation under the alternative. The noncentrality parameter is calculated using alternative means and the null variance structure.

Usage

```
kwsamplesize(
  shifts,
  distname = c("normal", "logistic", "cauchy"),
  targetpower = 0.8,
  proportions = rep(1, length(shifts))/length(shifts),
  level = 0.05,
  taylor = FALSE
)
```

Arguments

<code>shifts</code>	The offsets for the various populations, under the alternative hypothesis.
<code>distname</code>	The distribution of the underlying observations; normal and logistic are currently supported.
<code>targetpower</code>	The distribution of the underlying observations; normal and logistic are currently supported.
<code>proportions</code>	The proportions in each group.
<code>level</code>	The test level.
<code>taylor</code>	Logical flag forcing the approximation of exceedence probabilities using the first derivative at zero.

Details

The standard noncentral chi-square power formula, is used.

Value

A list with the total number of observations needed to obtain approximate power, as long as this number is split among groups according to argument proportion.

Examples

```
#Calculate the sample size necessary to detect differences among three
#groups with centers at 0,1,2, from normal observations, using a test of
#level 0.05 and power 0.80.
kwsamplesize(c(0,1,2),"normal")
```

mannwhitney.test	<i>Perform the Mann Whitney two-sample test</i>
------------------	---

Description

Perform the Mann Whitney two-sample test

Usage

```
mannwhitney.test(x, y, alternative = c("two.sided", "less", "greater"))
```

Arguments

x	A vector of values from the first sample.
y	A vector of values from the first sample.
alternative	Specification of alternative hypothesis.

Value

Test results of class htest

Examples

```
mannwhitney.test(rnorm(10),rnorm(10)+.5)
```

mood.median.test	<i>Mood's Median test, extended to odd sample sizes.</i>
------------------	--

Description

Test whether two samples come from the same distribution. This version of Mood's median test is presented for pedagogical purposes only. Many authors successfully argue that it is not very powerful. The name "median test" is a misnomer, in that the null hypothesis is equality of distributions, and not just equality of median. Exact calculations are not optimal for the odd sample size case.

Usage

```
mood.median.test(x, y, exact = FALSE)
```

Arguments

x	First data set.
y	Second data set.
exact	Indicator for whether the test should be done exactly or approximately.

Details

The exact case reduces to Fisher's exact test.

Value

The two-sided p-value.

nextp	<i>Next permutation</i>
-------	-------------------------

Description

Cycles through permutations of first argument

Usage

```
nextp(perm, b = 1)
```

Arguments

perm	indices to be permutedj
b	number to begin at. Set equal to 1.

Value

The next permutation

`page.test.unbalanced` *Perform Page test for unbalanced two-way design*

Description

Perform Page test for unbalanced two-way design

Usage

```
page.test.unbalanced(x, trt, blk, sides = 2)
```

Arguments

<code>x</code>	A vector of responses
<code>trt</code>	A vector of consecutive integers starting at 1 indicating treatment
<code>blk</code>	A vector of consecutive integers starting at 1 indicating block
<code>sides</code>	A single integer indicating sides. Defaults to 2.

Value

P-value for Page test.

Examples

```
page.test.unbalanced(rnorm(15), rep(1:3, 5), rep(1:5, rep(3, 5)))
```

`pairwiseprobabilities` *Pairwise probabilities of Exceedence*

Description

`pairwiseprobabilities` calculates probabilities of one variable exceeding another, where the variables are independent, and with identical distributions except for a location shift. This calculation is useful for power of Mann-Whitney-Wilcoxon, Jonckheere-Terpstra, and Kruskal-Wallis testing.

Usage

```
pairwiseprobabilities(
  shifts,
  distname = c("normal", "cauchy", "logistic"),
  taylor = FALSE
)
```

Arguments

shifts	The offsets for the various populations, under the alternative hypothesis.
distname	The distribution of the underlying observations; normal, cauchy, and logistic are currently supported.
taylor	Logical flag forcing the approximation of exceedence probabilities using a Taylor series.

Details

Probabilities of particular families must be calculated analytically.

Value

A matrix with as many rows and columns as there are shift parameters. Row i and column j give the probability of an observation from group j exceeding one from group i .

Examples

```
pairwiseprobabilities(c(0,1,2),"normal")
```

pconcordant	<i>Calculate the cumulative distribution of the count of concordant pairs among independent pairs of random variables.</i>
-------------	--

Description

Calculate the cumulative distribution of the count of concordant pairs among independent pairs of random variables.

Usage

```
pconcordant(ss, nn)
```

Arguments

ss	Integer number of pairs
nn	number of pairs

Value

real probability

 powerplot

Power Plot

Description

Plots powers for the Kruskal-Wallis test, via Monte Carlo and two approximations.

Usage

```
powerplot(
  numgrps = 3,
  thetadagger = NULL,
  nnvec = 5:30,
  nmc = 50000,
  targetpower = 0.8,
  level = 0.05
)
```

Arguments

numgrps	Number of groups to compare
thetadagger	Direction of effect
nnvec	vector of numbers per group.
nmc	Number of Monte Carlo trials
targetpower	Target power for test
level	level for test.

 probabilityderiv

Derivative of pairwise probabilities of Exceedence

Description

probabilityderiv calculates derivatives probabilities of one variable exceeding another, where the variables are independent, and with identical distributions except for a location shift, at the null hypothesis. This calculation is useful for power of Mann-Whitney-Wilcoxon, Jonckheere-Terpstra, and Kruskal-Wallis testing.

Usage

```
probabilityderiv(distname = c("normal", "cauchy", "logistic"))
```

Arguments

distname	The distribution of the underlying observations; normal and logistic are currently supported.
----------	---

Details

Probabilities of particular families must be calculated analytically, and then differentiated.

Value

The scalar derivative.

 probest

Stratified Multivariate Kawaguchi Koch Wang Estimators

Description

Function that return the estimators and their variance-covariance matrix calculated with the Kawaguchi - Koch - Wang method.

Usage

```
probest(ds, resp, grp, str = NULL, covs = NULL, delta = NA, correct = FALSE)
```

Arguments

ds	The data frame to be used.
resp	The vector of the response manifest variable. There can be more than one variable. It has to be the name of the variable as a character string.
grp	The vector of the variable that divides the population into groups. It has to be the name of the variable as a character string.
str	The vector of the variable used for the strata. It has to be the name of the variable as a character string.
covs	The covariates to be used in the model. It has to be the name of the variable as a character string.
delta	Offset for covariates.
correct	Should the variance estimator be corrected as in Chen and Kolassa?

Details

The function calls a Fortran code to calculate the estimators b and their variance-covariance matrix V_b

Value

A list with components b , the vector of adjusted estimates from the method, and V_b , the corresponding estimated covariance matrix.

References

A. Kawaguchi, G. G. Koch and X. Wang (2012), "Stratified Multivariate Mann-Whitney Estimators for the Comparison of Two Treatments with Randomization Based Covariance Adjustment", *Statistics in Biopharmaceutical Research* 3 (2) 217-231.

J. E. Kolassa and Y. Seifu (2013), Nonparametric Multivariate Inference on Shift Parameters, *Academic Radiology* 20 (7), 883-888.

Examples

```
# Breast cancer data from the MultNonParam package.
data(sotiriou)
attach(sotiriou)
#First simple plot of the data
plot(AGE,TUMOR_SIZE,pch=(recur+1),main="Age and Tumor Size",
     sub="Breast Cancer Recurrence Data",xlab="Age (years)",
     ylab="Tumor Size",col=c("blue","darkolivegreen"))
legend(31,8,legend=c("Not Recurrent","Recurrent"),
     pch=1:2,col=c("blue","darkolivegreen"))
#AGE and TUMOR_SIZE are the response variables, recur is used for the groups,
#TAMOXIFEN_TREATMENT for the stratum and ELSTON.ELLIS_GRADE is a covariate.
po<-probest(sotiriou,c("AGE","TUMOR_SIZE"),"recur",
            "TAMOXIFEN_TREATMENT","ELSTON.ELLIS_GRADE")
```

prostate

prostate

Description

221 prostate cancer patients are collected in this data set.

Format

- hosp : Hospital in which the patient is hospitalized.
- stage : stage of the cancer.
- gleason score : used to help evaluate the prognosis of the cancer.
- psa : prostate-specific antigen.
- age : age of the patient.
- advanced : boolean. TRUE if the cancer is advanced.

References

A. V. D'Amico, R. Whittington, S. B. Malkowicz, D. Schultz, K. Blank, G. A. Broderick, J. E. Tomaszewski, A. A. Renshaw, I. Kaplan, C. J. Beard, A. Wein (1998) , *Biochemical outcome after radical prostatectomy, external beam radiation therapy, or interstitial radiation therapy for clinically localized prostate cancer*, *JAMA : the journal of the American Medical Association* 280 969-74.

Examples

```
data(prostate)
attach(prostate)
plot(age,psa,main="Age and PSA",sub="Prostate Cancer Data",
      xlab="Age (years)",ylab="PSA")
```

qconcordant	<i>Calculate the quantiles of the count of concordant pairs among independent pairs of random variables.</i>
-------------	--

Description

Calculate the quantiles of the count of concordant pairs among independent pairs of random variables.

Usage

```
qconcordant(qq, nn, exact = TRUE)
```

Arguments

qq	Desired quantile
nn	number of pairs
exact	flag to trigger exact calculation when possible.

Value

Integer quantile

sensitivity.plot	<i>Compare the sensitivity of different statistics.</i>
------------------	---

Description

Compare the sensitivity of different statistics.

Usage

```
sensitivity.plot(y, sub, stats)
```

Arguments

y	vector of the data.
sub	subtitle for the plot.
stats	vector of functions to be plotted.

Details

To compare the sensitivity, outliers are added to the original data. The shift of each statistics due to the new value is measured and plotted.

 shiftcr

Nonparametric Confidence Region for a Vector Shift Parameter

Description

Inversion of a one-sample bivariate rank test is used to produce a confidence region. The region is constructed by building a grid of potential parameter values, evaluating the test statistic on each grid point, collecting the p-values, and then drawing the appropriate contour of the p-values. The grid is centered at the bivariate median of the data set.

Usage

```
shiftcr(xm, hpts = 50)
```

Arguments

xm	A two-column matrix of bivariate data whose two location parameters are to be estimated.
hpts	Controls the number of grid points, by constructing a grid of $2 \cdot \text{hpts} + 1$ on each side.

Value

nothing

 solvenpc

Noncentrality Parameter for a Given Level and Power

Description

This function calculates the noncentrality parameter required to give a test whose null distribution is central chi-square and whose alternative distribution is noncentral chi-square the required level and power.

Usage

```
solvenpc(df, level = 0.05, targetpower = 0.8)
```

Arguments

df	Common degrees of freedom for null and alternative distributions.
level	Level (that is, type I error rate) for the test.
targetpower	Desired power

Value

required noncentrality parameter.

Examples

```
solvencp(4)
```

sotiriou	<i>Breast cancer data set</i>
----------	-------------------------------

Description

187 breast cancer patients are collected in this data set.

Usage

```
data(sotiriou)
```

Format

A data set with the following variables

- AGE : Age of the patient
- TUMOR_SIZE : The size of the tumor, numeric variable
- recur : 1 if the patient has a recurrent breast cancer, 0 if it is not recurrent.
- ELSTON.ELLIS_GRADE : Elston Ellis grading system in order to classify the breast cancers. It can be a low, intermediate or high grade (high being the worst prognosis)
- TAMOXIFEN_TREATMENT : boolean. TRUE if the patient is treated with the Tamoxifen treatment.

Source

<https://gdoc.georgetown.edu/gdoc/>

References

S. Madhavan, Y. Gusev, M. Harris, D. Tanenbaum, R. Gauba, K. Bhuvaneshwar, A. Shinohara, K. Rosso, L. Carabet, L. Song, R. Riggins, S. Dakshanamurthy, Y. Wang, S. Byers, R. Clarke, L. Weiner (2011), *A systems medicine platform for personalized oncology*, Neoplasia 13.

C. Sotiriou, P. Wirapati, S. Loi, A. Harris, S. Fox, J. Smeds, H. Nordgren, P. Farmer, V. Praz, B. Haibe-Kains, C. Desmedt, D. Larsimont, F. Cardoso, H. Peterse, D. Nuyten, M. Buyse, M. Van de Vijver, J. Bergh, M. Piccart, M. Delorenzi (2006), *Gene expression profiling in breast cancer: understanding the molecular basis of histologic grade to improve prognosis*, Journal of the National Cancer Institute 98 262-72.

Examples

```
data(sotiriou)
plot(sotiriou$AGE, sotiriou$TUMOR_SIZE, pch=(sotiriou$recur+1),
     main="Age and Tumor Size",
     sub="Breast Cancer Recurrence Data",
     xlab="Age (years)", ylab="Tumor Size",
     col=c("blue", "darkolivegreen"))
legend(31, 8, legend=c("Not Recurrent", "Recurrent"), pch=1:2,
      col=c("blue", "darkolivegreen"))
```

symscorestat

Generalization of Wilcoxon signed rank test

Description

This function returns either exact or asymptotic p-values for score tests of the null hypothesis of univariate symmetry about 0.

Usage

```
symscorestat(y, scores = NULL, exact = F, sides = 1)
```

Arguments

y	Vector of data on which test will be run.
scores	Scores to be used for the test. Defaults to integers 1:length(y).
exact	Logical variable indicating whether the exact p-value should be calculate. Default is false.
sides	Integer; 1 for one sided test rejecting for large values of the statistic, and 2 for the two-sided test. Defaults to 1.

Details

The statistic considered here is the sum of scores corresponding to those entries in y that are positive. If `exact=T`, the function calls a Fortran code to cycle through all permutations. If `exact=F`, the expectation of the statistic is calculated as half the sum of the scores, the variance is calculated as one quarter the sum of squares of scores about their mean, and the statistic is compared to its approximating normal distribution.

Value

A list with components `pv`, the p-value obtained with the permutation tests, and `tot`, the total number of rearrangements of the data considered in calculating the p-value.

References

J.J. Higgins, (2004), *Introduction to Modern Nonparametric Statistics*, Brooks/Cole, Cengage Learning.

Examples

```
symscorestat(y=c(1,-2,3,-4,5),exact=TRUE)
```

 terpstra.test

Perform the Terpstra version of the multi-ordered-sample test

Description

Perform the Terpstra version of the multi-ordered-sample test

Usage

```
terpstra.test(x, g, alternative = c("two.sided", "less", "greater"))
```

Arguments

<code>x</code>	A vector of values from all samples.
<code>g</code>	A vector of group labels.
<code>alternative</code>	Specification of alternative hypothesis.

Value

Test results of class `hstest`

Examples

```
terpstra.test(rnorm(15),rep(1:3,5))
```

 terpstrapower

Power for the nonparametric Terpstra test for an ordered effect.

Description

terpstrapower approximates power for the one-sided Terpstra test, using a normal approximation with expectations under the null and alternative, and using the null standard deviation.

Usage

```
terpstrapower(
  nreps,
  shifts,
  distname = c("normal", "logistic"),
  level = 0.025,
  mc = 0
)
```

Arguments

nreps	The numbers in each group.
shifts	The offsets for the various populations, under the alternative hypothesis.
distname	The distribution of the underlying observations; normal and logistic are currently supported.
level	The test level.
mc	Zero indicates asymptotic calculation. Positive for MC calculation.

Details

The standard normal-theory power formula is used.

Value

A list with components power, giving the power approximation, expect, giving null and alternative expectations, var, giving the null variance, probs, giving the intermediate output from pairwiseprobability, and level.

Examples

```
terpstrapower(rep(10,3),c(0,1,2),"normal")
terpstrapower(c(10,10,10),0:2,"normal",mc=1000)
```

testve *Diagnosis for multivariate stratified Kawaguchi - Koch - Wang method*

Description

Diagnostic tool that verifies the normality of the estimates of the probabilities b with the Kawaguchi - Koch - Wang method. The diagnostic method is based on a Monte Carlo method.

Usage

```
testve(n, m, k, nsamp = 100, delta = 0, beta = 0, disc = 0)
```

Arguments

n	number of observations in the first group.
m	number of observations in the second group.
k	number of strata.
nsamp	The number of estimates that will be calculated. Must be enough to be sure that the results are interpretable.
delta	Offset that depends on group.
beta	Correlation between x and y .
disc	The Mann Whitney test is designed to handle continuous data, but this method applies to discretized data; <code>disc</code> adjusts the discreteness.

Details

This functions serves as a diagnosis to prove that the Kawaguchi - Koch - Wang method gives Gaussian estimates for b . It generates random data sets, to which the Mann Whitney test gets applied. y is the generated response variable and x the generated covariable related to y through a regression model.

Value

Nothing is returned. A QQ plot is drawn.

References

A. Kawaguchi, G. G. Koch and X. Wang (2012), "Stratified Multivariate Mann-Whitney Estimators for the Comparison of Two Treatments with Randomization Based Covariance Adjustment", *Statistics in Biopharmaceutical Research* 3 (2) 217-231.

J. E. Kolassa and Y. Seifu (2013), Nonparametric Multivariate Inference on Shift Parameters, *Academic Radiology* 20 (7), 883-888.

Examples

```
testve(10, 15, 3, 100, 0.4)
```

theil	<i>Perform the Theil nonparametric estimation and confidence interval for a slope parameter.</i>
-------	--

Description

Perform the Theil nonparametric estimation and confidence interval for a slope parameter.

Usage

```
theil(x, y, conf = 0.9)
```

Arguments

x	A vector of values of the explanatory variable.
y	A vector of values of the response variable.
conf	Level of confidence interval.

Value

A list with letters and numbers.

- est - An estimate, the median of pairwise slopes.
- ci - A vector of confidence interval endpoints.

Examples

```
a<-0:19;b<-a^2.5
theil(a,b)
```

tukey.kruskal.test	<i>Tukey HSD procedure</i>
--------------------	----------------------------

Description

Rank-based method for controlling experiment-wise error. Assume normality of the distribution for the variable of interest.

Usage

```
tukey.kruskal.test(resp, grp, alpha = 0.05)
```

Arguments

resp	vector containing the values for the variable of interest.
grp	vector specifying in which group is each observation.
alpha	level of the test.

Details

The original Tukey HSD procedure is supposed to be applied for equal sample sizes. However, the `tukey.kruskal.test` function performs the Tukey-Kramer procedure that works for unequal sample sizes.

Value

A logical vector for every combination of two groups. TRUE if the distribution in one group is significantly different from the distribution in the other group.

References

J.J. Higgins, (2004), *Introduction to Modern Nonparametric Statistics*, Brooks/Cole, Cengage Learning.

twosamplesurvps *Two Sample Omnibus Tests of Survival Curves*

Description

Returns the Kolmogorov-Smirnov and Anderson-Darling test statistics for two right-censored data sets.

Usage

```
twosamplesurvps(times, delta, grp, nmc = 10000, plotme = TRUE, exact = FALSE)
```

Arguments

<code>times</code>	Event and censoring times
<code>delta</code>	Indicator of event (1) or censoring (0).
<code>grp</code>	Variable that divides the population into groups.
<code>nmc</code>	Number of Monte Carlo samples for p value calculation
<code>plotme</code>	logical; indicates whether to plot or not.
<code>exact</code>	logical; indicates whether to use exhaustive enumeration of permutations or not.

Details

The function calls a Fortran code to calculate the estimators b and their variance-covariance matrix V_b

Value

A vector of length two, with the Kolmogorov-Smirnov and Anderson-Darling statistics.

Examples

```
twosamplesurvps(rexp(20), rbinom(20, 1, .5), rbinom(20, 1, .5))
```

twosamplesurvtests *Two Sample Omnibus Tests of Survival Curves*

Description

Returns the Kolmogorov-Smirnov and Anderson-Darling test statistics for two right-censored data sets.

Usage

```
twosamplesurvtests(times, delta, grp)
```

Arguments

times	Event and censoring times
delta	Indicator of event (1) or censoring (0).
grp	Variable that divides the population into groups.

Value

A vector of length two, with the Kolmogorov-Smirnov and Anderson-Darling statistics.

Examples

```
twosamplesurvtps(rexp(20), rbinom(20, 1, .5), rbinom(20, 1, .5))
```

util.jplot *Plot a curve, skipping bits where there is a large jump.*

Description

Plot a curve, skipping bits where there is a large jump.

Usage

```
util.jplot(x, y, ...)
```

Arguments

x	Ordinates to be plotted.
y	Abcissas to be plotted.
...	Arguments passed directly to plot.

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