

Package ‘postHoc’

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Type Package

Title Tools for Post-Hoc Analysis

Version 0.1.3

Description Implements a range of facilities for post-hoc analysis and summarizing linear models, generalized linear models and generalized linear mixed models, including grouping and clustering via pairwise comparisons using graph representations and efficient algorithms for finding maximal cliques of a graph. Includes also non-parametric tools for post-hoc analysis. It has S3 methods for printing summarizing, and producing plots, line and barplots suitable for post-hoc analyses.

URL <https://tildeweb.au.dk/au33031/astatlab/software/posthoc>

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AllContrasts	<i>Constructs a matrix with all the contrasts for pairwise comparisons.</i>
--------------	---

Description

Constructs a matrix with all the contrasts for pairwise comparisons.

Usage

```
AllContrasts(n)
```

Arguments

n an integer number larger than 1 giving the number of contrasts defining the pairwise comparisons pairwise comparisons.

Details

This is an auxiliary function forming a contrast matrix of all possible. Generates an error if n is smaller than 2.

Value

a matrix of dimension $n(n-1)/2 \times n$.

Author(s)

Rodrigo Labouriau

Examples

```
AllContrasts(3)
```

ApproxWaldPvalues	<i>Wald approximation for the p-values of pairwise comparisons based on the design matrix</i>
-------------------	---

Description

Wald approximation for the p-values of pairwise comparisons based on the design matrix

Usage

```
ApproxWaldPvalues(Effects, CovMatrix, DesignMatrix, padjust = "fdr")
```

Arguments

Effects	a vector containing the effects
CovMatrix	the covariance matrix of the effects
DesignMatrix	design matrix
padjust	method for correcting for multiple testing as in the function p.adjust (default = "fdr", if NULL no adjustments is made)

Value

a vector of p-values.

Author(s)

Rodrigo Labouriau

barplot.PostHoc	<i>Barplot method for objects of class PostHoc</i>
-----------------	--

Description

Barplot method for objects of class PostHoc

Usage

```
## S3 method for class 'PostHoc'
barplot(
  height,
  col = "lightblue",
  labelsCol = "black",
  space2max = 0,
  UseGrouping = TRUE,
  ylim = NULL,
```

```

main = "",
ylab = "",
xlab = "",
lty = 1,
drawAxis = TRUE,
rightshift = 0,
additionalTextGrouping = "",
superpose = FALSE,
cex.grouping = 1,
cex.ticks = 0.1,
cex.lab = 1,
ylog = FALSE,
...
)

```

Arguments

<code>height</code>	an object of class <code>PostHoc</code> to be printed
<code>col</code>	the colour of the bars (default = "lightblue")
<code>labelsCol</code>	the colour of the bars (default = "black")
<code>space2max</code>	space between the upper limit of the confidence interval and the label
<code>UseGrouping</code>	should the grouping be added to the plots (default = TRUE)
<code>ylim</code>	range of the vertical axis
<code>main</code>	character with the title of the plot (default = "")
<code>ylab</code>	label of the vertical axis
<code>xlab</code>	label of the horizontal axis
<code>lty</code>	type of line
<code>drawAxis</code>	should the axis be drawn (default = TRUE)
<code>rightshift</code>	a number specifying a (small) right shift of the line
<code>additionalTextGrouping</code>	character vector with additional text to the grouping
<code>superpose</code>	should the graph be superposed to an existing graph (default = FALSE)
<code>cex.grouping</code>	size of the labels of groups
<code>cex.ticks</code>	size of the thicks defining the the limits of the confidence intervals
<code>cex.lab</code>	size of the labels
<code>ylog</code>	should the vertical axis be expressed in a logarithmic scale (default = FALSE)
<code>...</code>	parameters to be passed to the <code>barlot</code> function

Value

none

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment+0, data=DeIdentifiedExample)
GG <- posthoc(MM)
barplot(GG)
```

DeIdentifiedExample *A simple example for testing pairwise comparison methods*

Description

A simple example of data for testing pairwise comparison methods composed of a normally distributed response and a factor with 7 levels.

Usage

```
data("DeIdentifiedExample")
```

Format

A data frame with 70 observations on the following 2 variables.

Y a numeric vector containing a response variable

Treatment a factor with 7 levels A B C D E F G

Details

De identified real dataset for testing

Source

A real data set with altered names, so that the source (irrelevant in this context) cannot be identified.

Examples

```
data(DeIdentifiedExample)
str(DeIdentifiedExample)
```

ExtractCI	<i>Calculates the Wald or a parametric bootstrap confidence intervals for GLMs and GLMMs</i>
-----------	--

Description

posthoc is used to group or cluster the effects of linear, generalised linear and generalised linear mixed models according to significance of pairwise tests comparing the levels of the effects.

Usage

```
ExtractCI (Model, EffectIndices = NULL, EffectLabels = NULL,
          ParBootstrap = FALSE, Nboots = 999, digits = 4, coverage = 0.95,
          UpperBound = Inf, SignificanceLevel = 1-coverage,
          EffectsMatrix = NULL, Scale = 1.0, Location = 0.0,
          isBinomialModel = FALSE, BackTransform = TRUE)
```

Arguments

Model	a model of class lm, glm, glmerMod, lme or gls.
EffectIndices	a vector containing the indices of the effects to be analysed (default = NULL, indicating that all the levels are used).
EffectLabels	a character vector with the labels of the effects (default = NULL, which implies that the corresponding labels of the model coefficient are used).
ParBootstrap	logic flag indicating whether the confidence intervals should be calculated with parametric bootstrap (default is false, i.e. the Wald confidence interval is used).
Nboots	number of bootstrap samples used for the confidence interval. (default = 999).
digits	number of digits used when reporting the results
coverage	the coverage of the confidence intervals (default = 0.95)
UpperBound	an upper bound to the confidence intervals (default = Inf)
SignificanceLevel	the significance level of the pairwise comparisons (default = 0.05).
EffectsMatrix	matrix defining contrasts to be compared (bypasses the EffectIndices, default is NULL, meaning that standard inference is performed).
Scale	a scaling factor multiplying the output table (default = 1, i.e., no scaling is used).
Location	a location term added to the output table (default = 0, i.e., no location shift is performed).
isBinomialModel	a logical flag indicating whether the model is a binomial model different than the Bernoulli (default = FALSE, i.e. not a binomial model).
BackTransform	should the parameters and CIs be back transformed by applying the inverse link function (default = TRUE)

Details

Two possible methods for obtaining confidence intervals are available: Wald confidence intervals and parametric bootstrap confidence intervals.

Value

an object of (S3) class "PostHoc".

a matrix with three columns containing the effects, the lower bound and the upper bound of the confidence intervals for the effects.

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment+0, data=DeIdentifiedExample)
ExtractCI (MM)
```

FormGroupsClusters *Group effects given the pairwise p-values*

Description

Group effects given the pairwise p-values

Usage

```
FormGroupsClusters(  
  PvaluesMatrix,  
  CI = NULL,  
  Effects,  
  SignificanceLevel = 0.05,  
  UpperCase = FALSE,  
  RankLabels = TRUE,  
  PlotAdj = FALSE,  
  padjust = NULL,  
  CalcClusters = FALSE,  
  digits = 4  
)
```

Arguments

PvaluesMatrix a matrix containing the p-values of the comparisons of each possible pairs of effects in the lower triangle (excluding the diagonal)

CI	a matrix containing with three columns containint the effects, the lower limits and the upper limits of a confidence interval for the effects (default = NULL, indicating that no confidence intervals are available)
Effects	a vector containing the effects
SignificanceLevel	the significance level of the pairwise comparisons (default = 0.05)
UpperCase	should upper case letters be used for labelling the groups (default is FALSE)
RankLabels	should the labels of the grouping be sorted according to the value of the response (default=TRUE)
PlotAdj	should the associated graph be printed(default = FALSE)
padjust	method for correcting the p-values (before the calculations are performed) as in the function p.adjust (Default is NULL, indicating that no multiple testing corrections are used)
CalcClusters	should the clusters be calculated and displayed instead of grouping (Default is FALSE)
digits	number of digits in the output (default = 4)

Details

This is an auxiliar function forming a contrast matrix of all possible. Generates an error if n is smaller than 2. The function constructs, using the supplied matrix of p-values for all pairwise comparisossn, an undirected graph with vertices representing the levels of the effects, using the convention that two vertices are connected by an edge iff the p-value for testing equality the two vertices is larger than the prefixed significance level. The maximal cliques of this graph form the grouping of the levels of the effects.

Value

an object of (S3) class "PostHoc" with methods for print, summary, plot, barplot and lines defined. An object of class "PostHoc" contains the effects, grouping, the matrix of p-values of all pairwise comparisons, the graph (Gr) of adjacency, the confidence intervals of the effects, the significance levels, the number of digits to be used for printing, the list of maximal cliques of the graph Gr, the clusters (if calculated).

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment+0, data=DeIdentifiedExample)
GG <- posthoc(MM)
Effects <- coef(MM)
PvaluesMatrix <- GG$PvaluesMatrix
TT <- FormGroupsClusters(PvaluesMatrix = PvaluesMatrix, Effects = Effects)
plot(TT)
```

GroupClusterEffects *Group effects for GLMs and GLMMs*

Description

GroupClusterEffects is an alias of the function posthoc, temporarily kept for compatibility.

Usage

```
GroupClusterEffects (Model, EffectIndices = NULL, EffectLabels = NULL,
  EffectsMatrix = NULL, ParBootstrap = FALSE, Nboots = 999,
  SignificanceLevel = 0.05, UpperCase = FALSE,
  RankLabels = TRUE, WaldApproximation = FALSE,
  CalcClusters = FALSE, QUIET = TRUE, PlotAdj = FALSE,
  digits = 4, padjust = NULL, Scale = 1.0, Location = 0.0,
  isBinomialModel = FALSE, BackTransform = TRUE)
```

Arguments

Model	a model of class lm, glm, glmerMod, lme or gls.
EffectIndices	a vector containing the indices of the effects to be analysed (default = NULL, indicating that all the levels are used).
EffectLabels	a character vector with the labels of the effects (default = NULL, which implies that the corresponding labels of the model coefficient are used).
EffectsMatrix	matrix defining contrasts to be compared (bypasses the EffectIndices, default is NULL, meaning that standard inference is performed).
ParBootstrap	logic flag indicating whether the confidence intervals should be calculated with parametric bootstrap (default is false, i.e. the Wald confidence interval is used). Not implemented for objects of class lme.
Nboots	number of bootstrap samples used for the confidence interval. (default = 999).
SignificanceLevel	the significance level of the pairwise comparisons (default = 0.05).
UpperCase	should upper case letters be used for labelling the groups (default is FALSE).
RankLabels	should the labels of the grouping be sorted according to the value of the response (default=TRUE)
WaldApproximation	logic flag indicating whether a Wald approximated test should be used (default = FALSE).
CalcClusters	should the clusters be calculated and displayed instead of grouping (Default is FALSE)
QUIET	flag indicating whter the (large) output of the multcomp library should be temporarily re-directed (default = TRUE).
PlotAdj	should the associated graph be printed(default = FALSE).

<code>digits</code>	number of digits in the output (default = 4)
<code>padjust</code>	method for correcting the p-values (before the calculations are performed) as in the function <code>p.adjust</code> (Default is NULL, indicating that no multiple testing corrections are used)
<code>Scale</code>	a scaling factor multiplying the output table (default = 1, i.e., no scaling is used).
<code>Location</code>	a location term added to the output table (default = 0, i.e., no location shift is performed).
<code>isBinomialModel</code>	a logical flag indicating whether the model is a binomial model different than the Bernoulli (default = FALSE, i.e. not a binomial model).
<code>BackTransform</code>	should the effects and CIs be back transformed by applying the inverse link function (default = TRUE)

Details

The function constructs, using the supplied matrix of p-values for all pairwise comparisons, an undirected graph with vertices representing the levels of the effects, using the convention that two vertices are connected by an edge iff the p-value for testing equality of the two vertices is larger than the prefixed significance level. The maximal cliques of this graph form the grouping of the levels of the effects. The parameter `BackTransform`, indicating whether the effects and CIs should be back transformed using the inverse of the link function is incorporated in this version, but was not present in the original function `GroupClusterEffects`. Since the default of the parameter `BackTransform` is TRUE any conflict with the old function `GroupClusterEffect` is generated, but the new facility is implemented.

Perform post hoc analyses via pairwise comparisons of all the effect levels, or of a supplied subset of effects (using the parameter "EffectIndices") or even linear combinations of effects (using the parameter "EffectsMatrix"). Uses the syntax of the function `posthoc`, which differs slightly from the original syntax of `GroupClusterEffects`.

Value

an object of (S3) class "PostHoc" with methods for `print`, `summary`, `plot`, `barplot` and `lines` defined. An object of class "PostHoc" contains the effects, grouping, the matrix of p-values of all pairwise comparisons, the graph (`Gr`) of adjacency, the confidence intervals of the effects, the significance levels, the number of digits to be used for printing, the list of maximal cliques of the graph `Gr`, the clusters (if calculated).

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment+0, data=DeIdentifiedExample)
GG <- posthoc(MM)
print(GG)
```

`KruskalWallisAllPvalues`*Calculates all p-values of pairwise comparisons using a Kruskal-Wallis test*

Description

Calculates all p-values of pairwise comparisons using a Kruskal-Wallis test

Usage

```
KruskalWallisAllPvalues(y, g, padjust = "fdr")
```

Arguments

<code>y</code>	is a vector with the response
<code>g</code>	is a single classification factor
<code>padjust</code>	the method for adjusting for multiple comparisons following the convention of the functions <code>stats::p.adjust</code> (default = "fdr"), NULL or "none" does not adjust

Value

a vector with the p-values for comparing all the possible pairs.

Author(s)

Rodrigo Labouriau

Examples

```
KruskalWallisAllPvalues(y = DeIdentifiedExample$Y,  
                        g = DeIdentifiedExample$Treatment)
```

`lines.PostHoc`*Lines method for objects of class PostHoc*

Description

Lines method for objects of class PostHoc

Usage

```
## S3 method for class 'PostHoc'
lines(
  x,
  col = "black",
  labelsCol = "black",
  space2max = 0,
  UseGrouping = TRUE,
  ylim = NULL,
  main = "",
  ylab = "",
  xlab = "",
  lty = 1,
  drawAxis = TRUE,
  rightshift = 0,
  additionalTextGrouping = "",
  superpose = FALSE,
  cex.grouping = 1,
  cex.ticks = 0.1,
  cex.lab = 1,
  ylog = FALSE,
  ...
)
```

Arguments

<code>x</code>	an object of class <code>PostHoc</code> to be printed
<code>col</code>	the colour of the lines (default = "black")
<code>labelsCol</code>	the colour of the bars (default = "black")
<code>space2max</code>	space between the upper limit of the confidence interval and the label
<code>UseGrouping</code>	should the grouping be added to the plots (default = TRUE)
<code>ylim</code>	range of the vertical axis
<code>main</code>	character with the title of the plot (default = "")
<code>ylab</code>	label of the vertical axis
<code>xlab</code>	label of the horizontal axis
<code>lty</code>	type of line
<code>drawAxis</code>	should the axis be drawn (default = TRUE)
<code>rightshift</code>	a number specifying a (small) right shift of the line
<code>additionalTextGrouping</code>	character vector with additional text to the grouping
<code>superpose</code>	should the graph be superposed to an existing graph (default = FALSE)
<code>cex.grouping</code>	size of the labels of groups
<code>cex.ticks</code>	size of the ticks defining the the limits of the confidence intervals

<code>cex.lab</code>	size of the labels
<code>ylog</code>	should the vertical axis be expressed in a logarithmic scale (default = FALSE)
<code>...</code>	parameters to be passed to the function lines

Value

none

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment+0, data = DeIdentifiedExample)
GG <- posthoc(MM)
lines(GG)
```

MedianBootCI	<i>Confidence intervals for medians</i>
--------------	---

Description

Confidence intervals for medians

Usage

```
MedianBootCI(y, g, Nboots = 9999, Coverage = 0.95, digits = 4)
```

Arguments

<code>y</code>	is a vector with the response.
<code>g</code>	is a single classification factor.
<code>Nboots</code>	number of bootstrap samples (default = 9999).
<code>Coverage</code>	the coverage probability of the confidence interval.
<code>digits</code>	the number of digits (default = 4) (default = 0.95) "none" does not adjust

Value

a matrix with three columns, the median, the lower bound and the upper bound of the confidence interval and one row for each level of `g`.

Author(s)

Rodrigo Labouriau

Examples

```
MedianBootCI (y = DeIdentifiedExample$Y,  
              g = DeIdentifiedExample$Treatment)
```

plot.PostHoc	<i>Plot method for objects of class PostHoc</i>
--------------	---

Description

Plot method for objects of class PostHoc

Usage

```
## S3 method for class 'PostHoc'  
plot(x, y, ...)
```

Arguments

x	an object of class PostHoc to be printed.
y	an object of class PostHoc to be printed.
...	further arguments passed to or from other methods.

Value

none

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment + 0, data = DeIdentifiedExample)  
GG <- posthoc(MM)  
plot(GG)
```

 posthoc

Group effects for GLMs and GLMMs

Description

posthoc is used to group or cluster the effects of linear, generalised linear and generalised linear mixed models according to significance of pairwise tests comparing the levels of the effects.

Usage

```
posthoc (Model, EffectIndices = NULL, EffectLabels = NULL,
        EffectsMatrix = NULL, ParBootstrap = FALSE, Nboots = 999,
        SignificanceLevel = 0.05, UpperCase = FALSE,
        RankLabels = TRUE, WaldApproximation = FALSE,
        CalcClusters = FALSE, QUIET = TRUE, PlotAdj = FALSE,
        digits = 4, padjust = NULL, Scale = 1.0, Location = 0.0,
        isBinomialModel = FALSE, BackTransform = TRUE)
```

Arguments

Model	a model of class lm, glm, glmerMod, lme or gls.
EffectIndices	a vector containing the indices of the effects to be analysed (default = NULL, indicating that all the levels are used).
EffectLabels	a character vector with the labels of the effects (default = NULL, which implies that the corresponding labels of the model coefficient are used).
EffectsMatrix	matrix defining contrasts to be compared (bypasses the EffectIndices, default is NULL, meaning that standard inference is performed).
ParBootstrap	logic flag indicating whether the confidence intervals should be calculated with parametric bootstrap (default is false, i.e. the Wald confidence interval is used). Not implemented for objects of class lme.
Nboots	number of bootstrap samples used for the confidence interval. (default = 999).
SignificanceLevel	the significance level of the pairwise comparisons (default = 0.05).
UpperCase	should upper case letters be used for labelling the groups (default is FALSE).
RankLabels	should the labels of the grouping be sorted according to the value of the response (default=TRUE)
WaldApproximation	logic flag indicating whether a Wald approximated test should be used (default = FALSE).
CalcClusters	should the clusters be calculated and displayed instead of grouping (Default is FALSE)
QUIET	flag indicating whter the (large) output of the multcomp library should be temporarily re-directed (default = TRUE).

PlotAdj	should the associated graph be printed(default = FALSE).
digits	number of digits in the output (default = 4)
padjust	method for correcting the p-values (before the calculations are performed) as in the function p.adjust (Default is NULL, indicating that no multiple testing corrections are used)
Scale	a scaling factor multiplying the output table (default = 1, i.e., no scaling is used).
Location	a location term added to the output table (default = 0, i.e., no location shift is performed).
isBinomialModel	a logical flag indicating whether the model is a binomial model different than the Bernoulli (default = FALSE, i.e. not a binomial model).
BackTransform	should the parameters and CIs be back transformed by applying the inverse link function (default = TRUE)

Details

The function constructs, using the supplied matrix of p-values for all pairwise comparisons, an undirected graph with vertices representing the levels of the effects, using the convention that two vertices are connected by an edge iff the p-value for testing equality of the two vertices is larger than the prefixed significance level. The maximal cliques of this graph form the grouping of the levels of the effects.

Perform post hoc analyses via pairwise comparisons of all the effect levels, or of a supplied subset of effects (using the parameter "EffectIndices") or even linear combinations of effects (using the parameter "EffectsMatrix")

Value

an object of (S3) class "PostHoc" with methods for print, summary, plot, barplot and lines defined. An object of class "PostHoc" contains the effects, grouping, the matrix of p-values of all pairwise comparisons, the graph (Gr) of adjacency, the confidence intervals of the effects, the significance levels, the number of digits to be used for printing, the list of maximal cliques of the graph Gr, the clusters (if calculated).

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment+0, data=DeIdentifiedExample)
GG <- posthoc(MM)
print(GG)
```

 posthocKW

Post-hoc analysis based on the Kruskal-Wallis test

Description

posthocKW is used to group or cluster effects using the Kruskal-Wallis test for making a non-parametric based post-hoc analysis.

Usage

```
posthocKW (y, g, EffectIndices = NULL, EffectLabels = NULL,
           Nboots = 9999, SignificanceLevel = 0.05, UpperCase = FALSE,
           RankLabels = TRUE, CalcClusters = FALSE, PlotAdj = FALSE,
           digits = 4, padjust = NULL, Scale = 1.0, Location = 0.0)
```

Arguments

y	is a vector with the response.
g	is a single classification factor.
EffectIndices	a vector containing the indices of the effects to be analysed (default = NULL, indicating that all the levels are used).
EffectLabels	a character vector with the labels of the effects (default = NULL, which implies that the corresponding labels of the model coefficient are used).
Nboots	number of bootstrap samples used for the confidence interval. (default = 9999).
SignificanceLevel	the significance level of the pairwise comparisons (default = 0.05).
UpperCase	should upper case letters be used for labelling the groups (default is FALSE).
RankLabels	should the labels of the grouping be sorted according to the value of the response (default=TRUE)
CalcClusters	should the clusters be calculated and displayed instead of grouping (Default is FALSE)
PlotAdj	should the associated graph be printed(default = FALSE).
digits	number of digits in the output (default = 4)
padjust	method for correcting the p-values (before the calculations are performed) as in the function p.adjust (Default is NULL, indicating that no multiple testing corrections are used)
Scale	a scaling factor multiplying the output table (default = 1, i.e., no scaling is used).
Location	a location term added to the output table (default = 0, i.e., no location shift is performed).

Details

The function constructs, using Kruskal-Wallis rank sum tests all pairwise comparisons, an undirected graph with vertices representing the levels of the effects, using the convention that two vertices are connected by an edge iff the p-value for testing equality the two vertices is larger than the prefixed significance level. The maximal cliques of this graph form the grouping of the levels of the effects.

Value

an object of (S3) class "PostHoc" with methods for print, summary, plot, barplot and lines defined. An object of class "PostHoc" contains the effects, grouping, the matrix of p-values of all pairwise comparisons, the graph (Gr) of adjacency, the confidence intervals of the effects, the significance levels, the number of digits to be used for printing, the list of maximal cliques of the graph Gr, the clusters (if calculated).

Author(s)

Rodrigo Labouriau

Examples

```
print( posthocKW(DeIdentifiedExample$Y, DeIdentifiedExample$Treatment) )
```

print.PostHoc	<i>Print methods for objects of class PostHoc</i>
---------------	---

Description

Print methods for objects of class PostHoc

Usage

```
## S3 method for class 'PostHoc'
print(x, digits = 4, ...)
```

Arguments

x	an object of class PostHoc to be printed
digits	number of digits in the output (default = 4)
...	further arguments passed to or from other methods.

Value

a dataframe with two variables, Levels a factor containing the levels of the effects and ParameterCI which is a factor with the effects and the corresponding confidence intervals and the grouping combined in a character constructed in such a way that when printing this dataframe yields a table arranged in a suitable format.

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment + 0, data = DeIdentifiedExample)
GG <- posthoc(MM)
print(GG)
```

summary.PostHoc	<i>Summary method for objects of class PostHoc</i>
-----------------	--

Description

Summary method for objects of class PostHoc

Usage

```
## S3 method for class 'PostHoc'
summary(object, ...)
```

Arguments

object	an object of class PostHoc to be printed.
...	further arguments passed to or from other methods.

Value

a dataframe constructed in such a way that when printing this dataframe yields a table arranged in a suitable format. The summary, differently than the print method displays also the matrix of p-values of all the pairwise comparisons.

Author(s)

Rodrigo Labouriau

Examples

```
MM <- glm(Y ~ Treatment + 0, data = DeIdentifiedExample)
GG <- posthoc(MM)
summary(GG)
```

WaldPvalues	<i>Calculates a Wald approximation for the p-values of pairwise comparisons</i>
-------------	---

Description

Calculates a Wald approximation for the p-values of pairwise comparisons

Usage

```
WaldPvalues(Effects, CovMatrix, padjust = "fdr")
```

Arguments

Effects	a vector containing the effects
CovMatrix	the covariance matrix of the effects
padjust	method for correcting for multiple testing as in the function p.adjust (default = "fdr", if NULL no adjustments is made)

Value

a vector of p-values.

Author(s)

Rodrigo Labouriau

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