

Package ‘gMCPmini’

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Type Package

Title Graph Based Multiple Comparison Procedures (Mini Version)

Version 0.8-15

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Description

Selected Functions From gMCP package to support gsDesign and remove JAVA dependency. The package version is the same as the gMCP package version.

Depends R (>= 3.0.0),
methods

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.1.2

Suggests testthat (>= 3.0.0),
stats

Config/testthat/edition 3

R topics documented:

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|----------------|----------------------|
| BonferroniHolm | <i>Example Graph</i> |
|----------------|----------------------|

Description

Example Graph

Usage

BonferroniHolm(n, weights = rep(1/n, n))

gMCP

*Graph based Multiple Comparison Procedures***Description**

Performs a graph based multiple test procedure for a given graph and unadjusted p-values.

Usage

```
gMCP(
  graph,
  pvalues,
  test,
  correlation,
  alpha = 0.05,
  approxEps = TRUE,
  eps = 10-3,
  ...,
  upscale = ifelse(missing(test) && !missing(correlation) || !missing(test) && test ==
    "Bretz2011", TRUE, FALSE),
  useC = FALSE,
  verbose = FALSE,
  keepWeights = FALSE,
  adjPValues = TRUE
)
```

Arguments

| | |
|-------------|--|
| graph | A graph of class graphMCP . |
| pvalues | A numeric vector specifying the p-values for the graph based MCP. Note the assumptions in the details section for the parametric tests, when a correlation is specified. |
| test | Should be either "Bonferroni", "Simes" or "parametric". If not specified by default the Bonferroni-based test procedure is used if no correlation is specified or the algorithm from Bretz et al. 2011 if a correlation is specified. If test is set to "Simes" the weighted Simes test will be performed for each subset of hypotheses. |
| correlation | Optional correlation matrix. If the weighted Simes test is performed, it is checked whether type I error rate can be ensured and a warning is given if this is not the case. For parametric tests the p-values must arise from one-sided tests with multivariate normal distributed test statistics for which the correlation is (partially) known. In that case a weighted parametric closed test is performed (also see generatePvals). Unknown values can be set to NA. (See details for more information) |
| alpha | A numeric specifying the maximal allowed type one error rate. |
| approxEps | A boolean specifying whether epsilon values should be substituted with the value given in the parameter eps. |
| eps | A numeric scalar specifying a value for epsilon edges. |
| ... | Test specific arguments can be given here. |

| | |
|-------------|---|
| upscale | Logical. If upscale=FALSE then for each intersection of hypotheses (i.e. each subgraph) a weighted test is performed at the possibly reduced level alpha of $\text{sum}(w) \cdot \alpha$, where $\text{sum}(w)$ is the sum of all node weights in this subset. If upscale=TRUE all weights are upscaled, so that $\text{sum}(w)=1$. For backward compatibility the default value is TRUE if a the parameter test is missing, but parameter correlation is specified or if <code>test=="Bretz2011"</code> . |
| useC | Logical scalar. If TRUE neither adjusted p-values nor intermediate graphs are returned, but the calculation is sped up by using code written in C. THIS CODE IS NOT FOR PRODUCTIVE USE YET! If approxEps is FALSE and the graph contains epsilon edges, a warning is thrown and useC will be ignored. |
| verbose | Logical scalar. If TRUE verbose output is generated. |
| keepWeights | Logical scalar. If FALSE the weight of a node without outgoing edges is set to 0 if it is removed. Otherwise it keeps its weight. |
| adjPValues | Logical scalar. If FALSE no adjusted p-values will be calculated. Especially for the weighted Simes test this will result in significantly less calculations in most cases. |

Details

For the Bonferroni procedure the p-values can arise from any statistical test, but if you improve the test by specifying a correlation matrix, the following assumptions apply:

It is assumed that under the global null hypothesis $(\Phi^{-1}(1 - p_1), \dots, \Phi^{-1}(1 - p_m))$ follow a multivariate normal distribution with correlation matrix `correlation` where Φ^{-1} denotes the inverse of the standard normal distribution function.

For example, this is the case if p_1, \dots, p_m are the raw p-values from one-sided z-tests for each of the elementary hypotheses where the correlation between z-test statistics is generated by an overlap in the observations (e.g. comparison with a common control, group-sequential analyses etc.). An application of the transformation $\Phi^{-1}(1 - p_i)$ to raw p-values from a two-sided test will not in general lead to a multivariate normal distribution. Partial knowledge of the correlation matrix is supported. The correlation matrix has to be passed as a numeric matrix with elements of the form: `correlation[i, i] = 1` for diagonal elements, `correlation[i, j] = ρ_{ij}` , where ρ_{ij} is the known value of the correlation between $\Phi^{-1}(1 - p_i)$ and $\Phi^{-1}(1 - p_j)$ or NA if the corresponding correlation is unknown. For example `correlation[1,2]=0` indicates that the first and second test statistic are uncorrelated, whereas `correlation[2,3] = NA` means that the true correlation between statistics two and three is unknown and may take values between -1 and 1. The correlation has to be specified for complete blocks (ie.: if `cor(i,j)`, and `cor(i,j')` for $i \neq j \neq j'$ are specified then `cor(j,j')` has to be specified as well) otherwise the corresponding intersection null hypotheses tests are not uniquely defined and an error is returned.

For further details see the given references.

Value

An object of class `gMCPResult`, more specifically a list with elements

`graphs` list of graphs

`pvalues` p-values

`rejected` logical whether hypotheses could be rejected

`adjPValues` adjusted p-values

Author(s)

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References

Frank Bretz, Willi Maurer, Werner Brannath, Martin Posch: A graphical approach to sequentially rejective multiple test procedures. *Statistics in Medicine* 2009 vol. 28 issue 4 page 586-604. http://www.meduniwien.ac.at/fwf_adaptive/papers/bretz_2009_22.pdf

Bretz F., Posch M., Glimm E., Klinglmueller F., Maurer W., Rohmeyer K. (2011): Graphical approaches for multiple endpoint problems using weighted Bonferroni, Simes or parametric tests. *Biometrical Journal* 53 (6), pages 894-913, Wiley. <http://onlinelibrary.wiley.com/doi/10.1002/bimj.201000239/full>

Strassburger K., Bretz F.: Compatible simultaneous lower confidence bounds for the Holm procedure and other Bonferroni based closed tests. *Statistics in Medicine* 2008; 27:4914-4927.

Hommel G., Bretz F., Maurer W.: Powerful short-cuts for multiple testing procedures with special reference to gatekeeping strategies. *Statistics in Medicine* 2007; 26:4063-4073.

Guilbaud O.: Simultaneous confidence regions corresponding to Holm's stepdown procedure and other closed-testing procedures. *Biometrical Journal* 2008; 50:678-692.

See Also

[graphMCP](#) [graphNEL](#)

Examples

```
g <- BonferroniHolm(5)
gMCP(g, pvalues=c(0.01, 0.02, 0.04, 0.04, 0.7))
# Simple Bonferroni with empty graph:
g2 <- matrix2graph(matrix(0, nrow=5, ncol=5))
gMCP(g2, pvalues=c(0.01, 0.02, 0.04, 0.04, 0.7))
# With 'upscale=TRUE' equal to BonferroniHolm:
gMCP(g2, pvalues=c(0.01, 0.02, 0.04, 0.04, 0.7), upscale=TRUE)
```

matrix2graph

Matrix2Graph and Graph2Matrix

Description

Creates a graph of class [graphMCP](#) from a given transition matrix or vice versa.

Usage

```
matrix2graph(m, weights = rep(1/dim(m)[1], dim(m)[1]))

graph2matrix(graph)
```

Arguments

| | |
|---------|--|
| m | A transition matrix. |
| weights | A numeric for the initial weights. |
| graph | A graph of class <code>graphMCP</code> . |

Details

The hypotheses names are the row names or if these are NULL, the column names or if these are also NULL of type H1, H2, H3, ...

If the diagonal of the matrix is unequal zero, the values are ignored and a warning is given.

Value

A graph of class `graphMCP` with the given transition matrix for `matrix2graph`. The transition matrix of a `graphMCP` graph for `graph2matrix`.

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Examples

```
# Bonferroni-Holm:
m <- matrix(rep(1/3, 16), nrow=4)
diag(m) <- c(0, 0, 0, 0)
graph <- matrix2graph(m)
print(graph)
graph2matrix(graph)
```

rejectNode

Rejects a node/hypothesis and updates the graph accordingly.

Description

Rejects a node/hypothesis and updates the graph accordingly.

Usage

```
rejectNode(graph, node, upscale = FALSE, verbose = FALSE, keepWeights = FALSE)
```

Arguments

| | |
|---------|---|
| graph | A graph of class <code>graphMCP</code> or <code>entangledMCP</code> . |
| node | A character string specifying the node to reject. |
| upscale | Logical. If <code>upscale=TRUE</code> then the weights of all non-rejected nodes are scaled so that the sum is equal to 1. This forces <code>keepWeights=FALSE</code> to reduce confusion, since otherwise the sum of weights could become bigger than 1. |

| | |
|-------------|---|
| verbose | Logical scalar. If TRUE verbose output is generated during sequentially rejection steps. |
| keepWeights | Logical scalar. If FALSE the weight of a node without outgoing edges is set to 0 if it is removed. Otherwise it keeps its weight. |

Details

For details see the given references.

Value

An updated graph of class `graphMCP` or `entangledMCP`.

Author(s)

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References

Frank Bretz, Willi Maurer, Werner Brannath, Martin Posch: A graphical approach to sequentially rejective multiple test procedures. Statistics in Medicine 2009 vol. 28 issue 4 page 586-604. http://www.meduniwien.ac.at/fwf_adaptive/papers/bretz_2009_22.pdf

See Also

`graphMCP`

substituteEps

Substitute Epsilon

Description

Substitute Epsilon with a given value.

Usage

```
substituteEps(graph, eps = 10^(-3))
```

Arguments

| | |
|-------|---|
| graph | A graph of class <code>graphMCP</code> or class <code>entangledMCP</code> . |
| eps | A numeric scalar specifying a value for epsilon edges. |

Details

For details see the given references.

Value

A graph where all epsilons have been replaced with the given value.

Author(s)

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See Also

[graphMCP](#), [entangledMCP](#)

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