

Package ‘SPC’

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Type Package

Title The statistical parametric connectome.

Version 1.0

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Description Converts p-values to relaxed p-values in presence of positive dependence.

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SPC-package	<i>The Statistical Parametric Connectome</i>
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Description

Convert p-values to relaxed p-values. This function is recommended in presence of positive dependence.

Details

Package: SPC
Type: Package
Version: 1.0
Author: Djalel-Eddine Meskaldji
Date: 2014-12-01
License: GPL-2

Convert p-values to relaxed p-values via the relaxPvalues function. This function is recommended in presence of positive dependence.

Author(s)

Djalel-Eddine Meskaldji

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References

NeuroImage paper: Improved statistical evaluation of group differences in connectomes by screening-filtering strategy with application to study maturation of brain connections between childhood and adolescence. Meskaldji et al.

Examples

```
# Simulate p-values
p_values=1-pnorm(c(rnorm(20, 3), rnorm(80)))

# Simulate SubregionsIndices
SubregionsIndices=sample(1:10, 100, replace=TRUE)

relaxPvalues(p_values, labels = NULL, SubregionsIndices,
alpha1 = 0.05, alpha2 = 0.05, procedure = "bonferroni",
strategy = "Standard method")

relaxPvalues(p_values, labels = NULL, SubregionsIndices,
alpha1 = 0.05, alpha2 = 0.05, procedure = "fdr",
strategy = "Both")

relaxPvalues(p_values, labels = NULL, SubregionsIndices,
alpha1 = 0.05, alpha2 = 0.05, procedure = "fdr",
strategy = "HTSF")
```

computeK

Compute relaxation coefficient.

Description

Compute relaxation coefficient.

Usage

```
computeK(alpha, m, si, scores, ui)
```

Arguments

alpha	Global type I error.
m	Number of substes.
si	Average subset size.
scores	Z-scores.
ui	Screening threshold.

Author(s)

Djalel-Eddine Meskaldji

References

NeuroImage paper: Improved statistical evaluation of group differences in connectomes by screening-filtering strategy with application to study maturation of brain connections between childhood and adolescence. Meskaldji et al.

Examples

```
alpha=0.05; m=50; si=10
scores=c(rnorm(100, 3), rnorm(400))
computeK(alpha, m, si, scores, ui=qnorm(1-alpha))
computeK(alpha, m, si, scores, ui=qnorm(1-alpha/m))
```

relaxPvalues

*Convert p-values to relaxed p-values.***Description**

Convert p-values to relaxed p-values. This function is recommended in presence of positive dependence.

Usage

```
relaxPvalues(p_values, labels = NULL, SubregionsIndices, alpha1 = 0.05, alpha2 = 0.05,
procedure = "bonferroni", strategy = "Standard method")
```

Arguments

p_values	Original p-values.
labels	Labels corresponding to p-values.
SubregionsIndices	A vector indicating subsets in which p-values belong to.
alpha1	Screening threshold.
alpha2	Global type I error.
procedure	The multiple testing procedure to correct for multiplicity. Possible values are "bonferroni", "fdr", "BH" and "BY".
strategy	Indicates which strategy to use: "Standard method", "HTSF", "STSF" or "Both".

Author(s)

Djalel-Eddine Meskaldji

References

NeuroImage paper: Improved statistical evaluation of group differences in connectomes by screening-filtering strategy with application to study maturation of brain connections between childhood and adolescence. Meskaldji et al.

Examples

```
# Simulate p-values
p_values=1-pnorm(c(rnorm(20, 3), rnorm(80)))

# Simulate SubregionsIndices
SubregionsIndices=sample(1:10, 100, replace=TRUE)

relaxPvalues(p_values, labels = NULL, SubregionsIndices,
alpha1 = 0.05, alpha2 = 0.05, procedure = "bonferroni",
strategy = "Standard method")

relaxPvalues(p_values, labels = NULL, SubregionsIndices,
alpha1 = 0.05, alpha2 = 0.05, procedure = "fdr",
strategy = "Standard method")

relaxPvalues(p_values, labels = NULL, SubregionsIndices,
alpha1 = 0.05, alpha2 = 0.05, procedure = "fdr",
strategy = "Both")

results=relaxPvalues(p_values, labels = NULL, SubregionsIndices,
alpha1 = 0.05, alpha2 = 0.05, procedure = "fdr",
strategy = "Both")

print(results) # to visualize the results.
save.data.path=~"/modified_p.values.csv" # set your own path.
write.csv(results, save.data.path) # to save the results
```

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