Package 'pARI'

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Type Package

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Description Computes the All-Resolution Inference method in the permutation framework, i.e., simultaneous lower confidence bounds for the number of true discoveries. <doi:10.1002/sim.9725>.

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`criticalVector` *Critical vector*

Description

Compute critical vector curve.

Usage

```
criticalVector(pvalues, family = "simes", alpha = 0.05, lambda, delta = 1, m = NULL)
```

Arguments

`pvalues`	Matrix of pvalues with dimensions $m \times B$ used instead of the data matrix `X`. Default to `NULL`.
`family`	String character. Name of the family confidence envelope to compute the critical vector from `"simes"`, `"aorc"`, `"beta"`, `"higher.criticism"`, and `"power"`. Default to "simes".
`alpha`	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.
`lambda`	Numeric value. λ value computed by `lambdaOpt`. Default to 1.
`delta`	Numeric value. δ value. Please see the reference below. Default to 1.
`m`	Numeric value. Number of hypothesis. Default to `NULL`.

Value

Numeric vector. Critical vector curve with length m.

Author(s)

Angela Andreella

References

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine, 42(14), 2311-2340.

See Also

lambdaOpt

Examples

```
db <- simulateData(pi0 = 0.8, m = 100, n = 20, rho = 0)
out <- pARI::signTest(X = db)
pv <- cbind(out$pv, out$pv_H0)
cv <- criticalVector(pvalues = pv, family = "simes", lambda = 1)
plot(sort(pv[,1]), type = "l")
lines(cv)
```

---

dI *Lower bound for the number of true discoveries*

Description

Calculates 1-α lower confidence bound for the set-wise of false null hypotheses.

Usage

```
dI(ix, cv, pvalues, iterative, approx, ncomb, ...)
```

Arguments

ix	Numeric vector: set-wise hypotheses considered.
cv	Numeric vector: critical vector computed by criticalVector.
pvalues	If iterative = TRUE you must put here the matrix of p-values with dimensions $m \times B$ where m is the number of variables and B the number of permutations. Instead, if iterative = FALSE, you can put directly the vector of m observed p-values.
iterative	Boolean value. If iterative = TRUE, the iterative method is applied (computationally demanding). Default to FALSE. Please see the reference below.
approx	Boolean value. Default to TRUE. If you are analyzing high dimensional data, we suggest to put approx = TRUE to speed up the computation time. Please see the reference below.

ncomb	Numeric value. If approx = TRUE, you must decide how many random sub collections (level of approximation) considered. Default to 100.
...	Further arguments for the iterative approach, i.e., iterative = TRUE.

Value

Numeric value: the lower confidence bound for the number of true discoveries concerning the cluster ix specified.

Author(s)

Angela Andreella

References

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine, 42(14), 2311-2340.

Examples

```
db <- simulateData(pi0 = 0.7, m = 100, n = 20, rho = 0)
out <- signTest(X = db)
pv <- cbind(out$pv, out$pv_H0)
cv <- criticalVector(pvalues = pv, family = "simes", lambda = 0.1, alpha = 0.1)
dI(ix = c(1:100), cv = cv, pvalues = pv)
```

---

lambdaOpt *Lambda calibration*

Description

Computes the optimal lambda calibration parameter used in the critical vector criticalVector.

Usage

```
lambdaOpt(pvalues, family, alpha = 0.05, delta = 0, step.down = FALSE,
 max.step = 10, m = NULL)
```

Arguments

pvalues	Matrix of p-values with dimensions $m \times B$ where m is the number of variables and B the number of permutations used instead of the data matrix X. Default to NULL.
family	String character. Name of the family confidence envelope to compute the critical vector from "simes", "aorc", "beta", "higher.criticism", and "power". Default to "simes".

alpha	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.
delta	Numeric value. δ value. Please see the reference below. Default to 0.
step.down	Boolean value. Default to FALSE If you want to compute the lambda calibration parameter using the step-down approach put TRUE. Please see the reference below.
max.step	Numeric value. Default to 10. Maximum number of steps for the step down approach, so useful when step.down = TRUE.
m	Numeric value. Number of hypotheses. Default to NULL.

Value

Numeric value. λ parameter estimate.

Author(s)

Angela Andreella

References

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine, 42(14), 2311-2340.

See Also

criticalVector

Examples

```
db <- simulateData(pi0 = 0.8, m = 100, n = 20, rho = 0)
out <- signTest(X = db)
pv <- cbind(out$pv, out$pv_H0)
cv <- lambdaOpt(pvalues = pv, family = "simes", alpha = 0.05)
```

---

map_TDP *True Discovery Proportion brain map*

Description

Performs the True Discovery Proportion brain map.

Usage

```
map_TDP(ARIout,path,name,mask)
```

Arguments

ARIout	Output object by pARIbrain.
path	Character string. Path to save the NIfTI file. The path does not must end with /.
name	Character string. The name of the map NIfTI file that will be used.
mask	NIfTI file or character string. 3D array of logical values (i.e. TRUE/FALSE in/out of the brain). Alternatively it may be a (character) NIfTI file name. If mask=NULL, it is assumed that none of the voxels have to be excluded.

Value

The function write directly in the path specified the true discovery proportion NIfTI map with name specified in name.

Author(s)

Angela Andreella

---

pARI *Permutation-based All-Resolutions Inference*

Description

The main function for All-Resolutions Inference (ARI) method based on the critical vector constructed using the p-values permutation distribution. The function computes simultaneous lower bounds for the number of true discoveries for each set of hypotheses specified in ix controlling family-wise error rate at level alpha.

Usage

```
pARI(X= NULL, ix, alpha = 0.05, family = "simes", delta = 0, B = 1000, pvalues = NULL,
test.type = "one_sample", complete = FALSE, clusters = FALSE, iterative = FALSE,
approx = TRUE, ncomb = 100, step.down = FALSE, max.step = 10, ...)
```

Arguments

X	Data matrix where rows represent the m variables and columns the n observations.
ix	Numeric vector which expresses the set of hypotheses of interest. It can be a vector with length equals m indicating the corresponding cluster for each variable, (in this case, you must put clusters = TRUE), or a vector containing the position indices of the variables of interest if only one set/cluster of hypotheses is considered.
alpha	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.

family	String character. Name of the family confidence envelope to compute the critical vector from "simes", "aorc", "beta", "higher.criticism", and "power". Default to "simes".
delta	Numeric value. δ value. Please see the reference below. Default to 0.
B	Numeric value. Number of permutations, default to 1000.
pvalues	Matrix of p-values with dimensions $m \times B$ where m is the number of variables and B the number of permutations used instead of the data matrix X. Default to NULL.
test.type	Character string. Choose a type of tests among "one_sample", i.e., one-sample t-tests, or "two_samples", i.e., two-samples t-tests. Default "one_sample".
complete	Boolean value. If TRUE the sets of critical vectors and the raw p-values are returned. Default to FALSE.
clusters	Boolean value. If ix indicates many clusters/sets must be TRUE. Default @FALSE.
iterative	Boolean value. If iterative = TRUE, the iterative method is applied (computationally demanding). Default to FALSE. Please see the reference below.
approx	Boolean value. Default to TRUE. If you are analyzing high dimensional data, we suggest to put approx = TRUE to speed up the computation time. Please see the reference below.
ncomb	Numeric value. If approx = TRUE, you must decide how many random sub collections (level of approximation) considered. Default to 100.
step.down	Boolean value. Default to FALSE If you want to compute the lambda calibration parameter using the step-down approach put TRUE. Please see the reference below.
max.step	Numeric value. Default to 10. Maximum number of steps for the step down approach, so useful when step.down = TRUE.
...	Further arguments

Value

by default returns a list with the following objects:

discoveries lower bound for the number of true discoveries in the set selected

ix selected variables

If complete = TRUE the raw pvalues and cv critical vector are also returned.

Author(s)

Angela Andreella

References

For the general framework of All-Resolutions Inference see:

Goeman, Jelle J., and Aldo Solari. "Multiple testing for exploratory research." Statistical Science 26.4 (2011): 584-597.

For permutation-based All-Resolutions Inference see:

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine, 42(14), 2311-2340.

See Also

The type of tests implemented: `signTest` `permTest`.

Examples

```
datas <- simulateData(pi0 = 0.8, m = 1000, n = 30, power = 0.9, rho = 0,seed = 123)
out <- pARI(X = datas, ix = c(1:200),test.type = "one_sample")
out
```

`pARIbrain` *Permutation-based All-Resolutions Inference for brain imaging.*

Description

The main function for All-Resolutions Inference (ARI) method based on the critical vector constructed using the p-values permutation distribution. The function computes simultaneous lower bounds for the number of true discoveries for each set of hypotheses specified in `ix` controlling family-wise error rate at level `alpha`.

Usage

```
pARIbrain(copes, thr=NULL, mask=NULL, alpha=.05, clusters = NULL,
alternative = "two.sided", summary_stat=c("max", "center-of-mass"),
silent=FALSE, family = "simes", delta = 0, B = 1000, rand = FALSE,
iterative = FALSE, approx = TRUE, ncomb = 100, step.down = FALSE, max.step = 10, ...)
```

Arguments

`copes`	List of NIfTI file. The list of copes, i.e., contrasts maps, one for each subject used to compute the statistical tests.
`thr`	Numeric value. Threshold used to construct the cluster map. Default to `NULL`.
`mask`	NIfTI file or character string. 3D array of logical values (i.e. `TRUE/FALSE` in/out of the brain). Alternatively it may be a (character) NIfTI file name. If `mask=NULL`, it is assumed that none of the voxels have to be excluded.
`alpha`	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.
`clusters`	NIfTI file or character string. 3D array of cluster ids (0 when voxel does not belong to any cluster) or a (character) NIfTI file name. If `cluster=NULL` the cluster map is computed by the `cluster_threshold` function with threshold equals `thr`.

alternative	Character string. It refers to the alternative hypothesis, must be one of "two.sided" (default), "greater" or "lower".
summary_stat	Character string. Choose among =c("max", "center-of-mass").
silent	Boolean value. Default to FALSE. If TRUE the function prints the results.
family	String character. Name of the family confidence envelope to compute the critical vector from "simes", "aorc", "beta", "higher.criticism", and "power". Default to "simes".
delta	Numeric value. δ value. Please see the reference below. Default to 0.
B	Numeric value. Number of permutations, default to 1000.
rand	Boolean value. Default to FALSE. If rand = TRUE, the p-values are computed by rowRanks. Please see signTest
iterative	Boolean value. If iterative = TRUE, the iterative method is applied (computationally demanding). Default to FALSE. Please see the reference below.
approx	Boolean value. Default to TRUE. If you are analyzing high dimensional data, we suggest to put approx = TRUE to speed up the computation time. Please see the reference below.
ncomb	Numeric value. If approx = TRUE, you must decide how many random sub collections (level of approximation) considered. Default to 100.
step.down	Boolean value. Default to FALSE If you want to compute the lambda calibration parameter using the step-down approach put TRUE. Please see the reference below.
max.step	Numeric value. Default to 10. Maximum number of steps for the step down approach, so useful when step.down = TRUE.
...	further arguments. See signTest.

Value

A list with elements:

out Data.frame containing the size, the number of false null hypotheses, the number of true null hypotheses, the lower bound for the true discovery proportion, and other statistics for each cluster.

clusters Matrix describing the clusters analyzed.

Author(s)

Angela Andreella

References

For the general framework of All-Resolutions Inference see:

Goeman, Jelle J., and Aldo Solari. "Multiple testing for exploratory research." Statistical Science 26.4 (2011): 584-597.

For All-Resolutions Inference for functional Magnetic Resonance Imaging data see:

Rosenblatt, Jonathan D., et al. "All-resolutions inference for brain imaging." Neuroimage 181 (2018): 786-796.

For permutation-based All-Resolutions Inference see:

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine, 42(14), 2311-2340.

See Also

signTest, lambdaOpt, criticalVector

Examples

```
## Not run:
library(remotes)
install_github("angeella/fMRIdata")
library(fMRIdata)
data(Auditory_clusterTH3_2)
data(Auditory_copes)
data(Auditory_mask)
auditory_out <- pARIbrain(copes = Auditory_copes,
clusters = Auditory_clusterTH3_2, mask = Auditory_mask,
alpha = 0.05, silent = TRUE)
auditory_out$out

## End(Not run)
```

---

pARIgene *Permutation-based All-Resolutions Inference for Gene Expression Data*

Description

This function computes the lower bound for the number of true discoveries within each cluster (pathways) of Gene Expression Data.

Usage

```
pARIgene(X= NULL, pathways, alpha = 0.05, family = "simes", delta = 0,
B = 1000, test.type = "one_sample", complete = FALSE, iterative = FALSE,
approx = TRUE, ncomb = 100, step.down = FALSE, max.step = 10, ...)
```

Arguments

X	Data matrix where rows represent the m variables and columns the n observations.
pathways	List of pathways where names indicates the name of the pathway.

alpha	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.
family	String character. Name of the family confidence envelope to compute the critical vector from "simes", "aorc", "beta", "higher.criticism", and "power". Default to "simes".
delta	Numeric value. δ value. Please see the reference below. Default to 0.
B	Numeric value. Number of permutations, default to 1000.
test.type	Character string. Choose a type of tests among "one_sample", i.e., one-sample t-tests, or "two_samples", i.e., two-samples t-tests. Default "one_sample".
complete	Boolean value. If TRUE the sets of critical vectors and the raw p-values are returned. Default to FALSE.
iterative	Boolean value. If iterative = TRUE, the iterative method is applied (computationally demanding). Default to FALSE. Please see the reference below.
approx	Boolean value. Default to TRUE. If you are analyzing high dimensional data, we suggest to put approx = TRUE to speed up the computation time. Please see the reference below.
ncomb	Numeric value. If approx = TRUE, you must decide how many random sub collections (level of approximation) considered. Default to 100.
step.down	Boolean value. Default to FALSE If you want to compute the lambda calibration parameter using the step-down approach put TRUE. Please see the reference below.
max.step	Numeric value. Default to 10. Maximum number of steps for the step down approach, so useful when step.down = TRUE.
...	Further arguments

Value

by default returns a list with the following objects:

discoveries lower bound for the number of true discoveries in the set selected

ix selected variables

If complete = TRUE the raw pvalues and cv critical vector are also returned.

Author(s)

Angela Andreella

References

For the general framework of All-Resolutions Inference see:

Goeman, Jelle J., and Aldo Solari. "Multiple testing for exploratory research. " Statistical Science 26.4 (2011): 584-597.

For permutation-based All-Resolutions Inference see:

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine, 42(14), 2311-2340.

See Also

The type of tests implemented: `signTest` `permTest`.

`permTest` *Permutation Test*

Description

Performs permutation-based two-sample t-tests.

Usage

```
permTest(X, B = 1000, alternative = "two.sided", seed = NULL,
mask = NULL, rand = FALSE, label = NULL)
```

Arguments

`X`	Data matrix where rows represent the m variables and columns the n observations.
`B`	Numeric value. Number of permutations, default to 1000.
`alternative`	Character string. It refers to the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"lower"`.
`seed`	Integer value. If you want to specify the seed. Default to to `NULL`
`mask`	NIfTI file or character string. 3D array of logical values (i.e. `TRUE/FALSE` in/out of the brain). Alternatively it may be a (character) NIfTI file name. If `mask=NULL`, it is assumed that none of the voxels have to be excluded.
`rand`	Boolean value. Default to `FALSE`. If `rand = TRUE`, the p-values are computed by `rowRanks`.
`label`	Numeric/character vector. Labels of the observations, if `NULL` the columns's name are considered. Default to `NULL`.

Value

Returns a list with the following objects:

Test Vector with length equals m. Observed two-samples t-tests, one for each m variable

Test_H0 Matrix with dimensions $m \times B - 1$. Test statistics under the null hypothesis

pv Vector with length equals m. Observed p-values, one for each m variable

pv_H0 Matrix with dimensions $m \times B - 1$. p-values under the null hypothesis

Author(s)

Angela Andreella

Examples

```
X <- matrix(rnorm(100*20), ncol=20)
X[,1:10] <- X[,1:10] + rnorm(100*10, mean = 5)
out <- permTest(X = X, alternative = "two.sided", label = c(rep(1,10),rep(0,10)))
```

---

plotNullDistribution *Plot permutation p-values distribution*

Description

Create a plot of permutation-based p-values with corresponding specified critical vectors.

Usage

```
plotNullDistribution(P=NULL,family="simes",alpha = 0.05,
path = getwd(), name = "plot", delta = 0,
copes=NULL,mask=NULL, alternative = "two.sided", rand = FALSE, B = 1000)
```

Arguments

P	Matrix of p-values with dimensions $m \times B$ where m is the number of variables and B the number of permutations used instead of the data matrix X. Default to NULL.
family	String character. Name of the family confidence envelope to compute the critical vector from "simes", "aorc", "beta", "higher.criticism", and "power". Default to "simes". If more than one critical vector are considered, it must be a vector.
alpha	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.
path	Character string. Path to save the plot. The path does not must end with /. Default to getwd().
name	Character string. The name of file that will be used to save the plot. Default to "plot".
delta	Numeric value. δ value. Please see the reference below. Default to 0. If more than one critical vector are considered, delta must be a vector having length equals to the length of the vector specified in family.
copes	List of NIfTI file. The list of copes, i.e., contrasts maps, one for each subject used to compute the statistical tests.
mask	NIfTI file or character string. 3D array of logical values (i.e. TRUE/FALSE in/out of the brain). Alternatively it may be a (character) NIfTI file name. If mask=NULL, it is assumed that none of the voxels have to be excluded.
alternative	Character string. It refers to the alternative hypothesis, must be one of "two.sided" (default), "greater" or "lower".
rand	Boolean value. Default to FALSE. If rand = TRUE, the p-values are computed by rowRanks.
B	Numeric value. Number of permutations, default to 1000.

Value

Save a plot in path with name specified in name describing the p-values null distribution with critical value curve and observed p-values in red.

Author(s)

Angela Andreella

References

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine, 42(14), 2311-2340.

Examples

```
## Not run:
db <- simulateData(pi0 = 0.8, m = 100, n = 20, rho = 0)
out <- signTest(X = db)
pv <- cbind(out$pv, out$pv_H0)
plotNullDistribution(P = pv)

## End(Not run)
```

---

signTest *Permutatation-based one-sample t-tests*

Description

Performs sign-flipped one-sample t-tests.

Usage

```
signTest(X, B = 1000, alternative = "two.sided", seed = NULL, mask = NULL, rand = FALSE)
```

Arguments

X	Data matrix where rows represent the m variables and columns the n observations.
B	Numeric value. Number of permutations, default to 1000.
alternative	Character string. It refers to the alternative hypothesis, must be one of "two.sided" (default), "greater" or "lower".
seed	Integer value. If you want to specify the seed. Default to to NULL
mask	NIfTI file or character string. 3D array of logical values (i.e. TRUE/FALSE in/out of the brain). Alternatively it may be a (character) NIfTI file name. If mask=NULL, it is assumed that none of the voxels have to be excluded.
rand	Boolean value. Default to FALSE. If rand = TRUE, the p-values are computed by rowRanks.

Value

Returns a list with the following objects:

Test Vector with length equals m. Observed two-samples t-tests, one for each m variable

Test_H0 Matrix with dimensions $m \times B - 1$. Test statistics under the null hypothesis

pv Vector with length equals m. Observed p-values, one for each m variable

pv_H0 Matrix with dimensions $m \times B - 1$. p-values under the null hypothesis

Author(s)

Angela Andreella

Examples

```
X <- matrix(rnorm(100*20), ncol=20)
out <- signTest(X = X, alternative = "two.sided")
```

---

simulateData *simulate normal distributed data*

Description

Simulate normal distributed data.

Usage

```
simulateData(pi0,m,n, rho, seed = NULL, power = 0.8, alpha = 0.05)
```

Arguments

pi0	Numeric value in '[0,1]'. Proportion of true null hypothesis.
m	Numeric value. Number of variables.
n	Numeric value. Number of observations.
rho	Numeric value in '[0,1]'. Level of equi-correlation between pairs of variables.
seed	Integer value. If you want to specify the seed. Default to to NULL
power	Numeric value in '[0,1]'. Level of power. Default to 0.8.
alpha	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.

Value

Returns a matrix with dimensions $m \times n$.

Author(s)

Angela Andreella

`simulateSpatialData` *simulate normal distributed data*

Description

Simulate normal distributed data with spatial correlation structure

`theta` (θ) describes how rapidly the correlation declines with respect to the distance between two voxels. The three-dimensional coordinates of the voxels are defined as all combinations of vector $c = (1, \ldots, m1/3)$, then $\Sigma_\theta = \exp(-\theta K)$ where K is the matrix containing the euclidean distances between the three-dimensional coordinates' voxels. So, $m^{1/3}$ must be an integer value.

Usage

```
simulateSpatialData(pi0,m,n, theta, seed = NULL, power = 0.8, alpha = 0.05)
```

Arguments

`pi0`	Numeric value in '[0,1]'. Proportion of true null hypothesis.
`m`	Numeric value. Number of variables.
`n`	Numeric value. Number of observations.
`theta`	Numeric value in '[0,1]'. Level of correlation between pairs of variables. See details
`seed`	Integer value. If you want to specify the seed. Default to to `NULL`
`power`	Numeric value in '[0,1]'. Level of power. Default to 0.8.
`alpha`	Numeric value in '[0,1]'. α level to control the family-wise error rate. Default to 0.05.

Value

Returns a matrix with dimensions $m \times n$.

Author(s)

Angela Andreella

`Statmap` *Create Statistical Parametric Mapping (SPM)*

Description

Creates the statistical parametric mapping in NIfTI format.

Usage

```
Statmap(copes, alternative = "two.sided", path = getwd(),
name = "map", Pmap = FALSE, mask = NULL)
```

Arguments

`copes`	List of NIfTI file. The list of copes, i.e., contrasts maps, one for each subject used to compute the statistical tests.
`alternative`	Character string. It refers to the alternative hypothesis, must be one of `"two.sided"` (default), `"greater"` or `"lower"`.
`path`	Character string. Path to save the plot. The path does not must end with `/`. Default to `getwd()`.
`name`	Character string. The name of file that will be used to save the plot. Default to "map".
`Pmap`	Boolean value. If `TRUE` the SPM of the p-values is returned. Default to `FALSE`.
`mask`	NIfTI file or character string. 3D array of logical values (i.e. `TRUE/FALSE` in/out of the brain). Alternatively it may be a (character) NIfTI file name. If `mask=NULL`, it is assumed that none of the voxels have to be excluded.

Value

Save the Statistical Parametric Mapping Nifti file in `path` with name specified in `name`.

Author(s)

Angela Andreella

Examples

```
## Not run:
library(fMRIdata)
data(Auditory_copes)
data(Auditory_mask)
Statmap(copes = Auditory_copes, mask = Auditory_mask)

## End(Not run)
```

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