

Package ‘pARI’

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Type Package

Title Permutation-Based All-Resolutions Inference Method

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Description It computes the All-Resolution Inference method in the permutation framework, i.e., simultaneous lower confidence bounds for the number of true discoveries. <[arXiv:2012.00368](#)>.

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License GPL (>= 2)

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URL <https://github.com/angeella/pARI>

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criticalVector	<i>Critical vector</i>
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Description

Compute critical vector curve.

Usage

```
criticalVector(pvalues, family, alpha = 0.05, lambda, delta = 0, 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. Choose a family of confidence envelopes to compute the critical vector. from "simes", "aorc", "beta" and "higher.criticism".
alpha	numeric value in '[0,1]'. It expresses the alpha level to control the family-wise error rate. Default 0.05.
lambda	numeric value. λ value computed by <code>lambdaOpt</code> .
delta	numeric value. It expresses the delta value, please see the references. Default to 0.
m	numeric value. Number of hypothesis. Default @NULL.

Value

numeric vector. Critical vector curve with length m .

Author(s)

Angela Andreella

Examples

```
db <- simulateData(pi0 = 0.8, m = 100, n = 20, rho = 0)
out <- signTest(X = db)
pv <- cbind(out$pv, out$pv_H0)
cv <- criticalVector(pvalues = pv, family = "simes", lambda = 0.05)
plot(sort(pv[,1]), type = "l")
lines(cv)
```

dI

*Lower bound for the number of true discoveries***Description**

Calculates $(1-\alpha)$ lower confidence bounds for the set-wise of false null hypotheses.

Usage

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

Arguments

ix	numeric vector. It refers to the set-wise hypotheses considered.
cv	numeric vector. It refers to the critical vector computed by criticalVector .
pvalues	matrix of pvalues with dimensions $m \times B$.
iterative	Boolean value. If <code>iterative = TRUE</code> , the iterative method for improvement of confidence envelopes is applied. Default <code>@FALSE</code> .
approx	Boolean value. Default <code>@TRUE</code> . If you are treating high dimensional data, we suggest to put <code>approx = TRUE</code> to speed up the computation time. Default <code>@TRUE</code> .
ncomb	Numeric value. If <code>approx = TRUE</code> , you must decide how many random subcollections (level of approximation) considered. Default 100.
...	further arguments for the iterative approach, i.e., <code>iterative = TRUE</code> .

Value

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

Author(s)

Angela Andreella

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

lambdaOpt computes the optimal lambda calibration parameter used in the critical vector.

Usage

```
lambdaOpt(pvalues, family, alpha = 0.05, delta = 0, step.down = FALSE,
max.step = 10, 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. Choose a family of confidence envelopes to compute the critical vector from "simes", "aorc", "beta" and "higher.criticism".
alpha	numeric value in '[0,1]'. It expresses the alpha level to control the family-wise error rate. Default 0.05.
delta	numeric value. It expresses the delta value, please see the references. Default to 0.
step.down	Boolean value. Default @FALSE If you want to compute the lambda calibration parameter using the step-down approach put TRUE.
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 hypothesis. Default @NULL.

Value

numeric value. It expresses the lambda parameter estimate, please see package references.

Author(s)

Angela Andreella

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	<i>True Discovery Proportion brain map</i>
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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 non of the voxels have to be excluded.

Value

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

Author(s)

Angela Andreella

Description

The main function for All-Resolutions Inference (ARI) method based on critical vectors 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.

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

<code>X</code>	data matrix where rows represent the m variables and columns the n observations.
<code>ix</code>	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 <code>clusters = TRUE</code>), or a vector containing the position indices of the variables of interest if only one set/cluster of hypotheses is considered.
<code>alpha</code>	numeric value in $[0,1]$. It expresses the alpha level to control the family-wise error rate.
<code>family</code>	string character. Choose a family of confidence envelopes to compute the critical vector from "simes", "aorc", "beta" and "higher.criticism".# @param alpha alpha level.
<code>delta</code>	numeric value. It expresses the delta value, please see the references. Default to 0.
<code>B</code>	numeric value. Number of permutations, default to 1000.
<code>pvalues</code>	matrix of pvalues with dimensions $m \times B$ used instead of the data matrix X . Default to @NULL.
<code>test.type</code>	character string. Choose a type of tests among "one_sample", i.e., one-sample t-test, or "two_samples", i.e., two-samples t-tests. Default "one_sample".
<code>complete</code>	Boolean value. If TRUE the sets of critical vectors and the raw pvalues are returned. Default @FALSE.
<code>clusters</code>	Boolean value. If <code>ix</code> indicates many clusters/sets must be TRUE. Default @FALSE.
<code>iterative</code>	Boolean value. If <code>iterative = TRUE</code> , the iterative method for improvement of confidence envelopes is applied. Default @FALSE.
<code>approx</code>	Boolean value. Default @TRUE. If you are treating high dimensional data, we suggest to put <code>approx = TRUE</code> to speed up the computation time.

ncomb	Numeric value. If approx = TRUE, you must decide how many random subcollections (level of approximation) considered.
step.down	Boolean value. Default @FALSE If you want to compute the lambda calibration parameter using the step-down approach put TRUE.
max.step	Numeric value. Default to 10. Maximum number of steps for the step down approach, so useful when step.down = TRUE.
...	Futher parameters.

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 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, Angela, et al. "Permutation-based true discovery proportions for fMRI cluster analysis." *arXiv preprint arXiv:2012.00368* (2020).

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 brain imaging All-Resolutions Inference (ARI) method based on critical vectors 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.

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

copies	list of NIfTI file. The list of copies, 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 @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 non of the voxels have to be excluded.
alpha	numeric value in '[0,1]'. It expresses the alpha level to control the family-wise error rate. Default 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 <code>cluster_threshold</code> 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 @FALSE. If @TRUE the function prints the results.
family	string character. Choose a family of confidence envelopes to compute the critical vector from "simes", "aorc", "beta" and "higher.criticism".# @param alpha alpha level.
delta	numeric value. It expresses the delta value, please see the references. Default to 0.
B	numeric value. Number of permutations, default to 1000.
rand	Boolean value. Default @FALSE. If rand = TRUE, the p-values are computed by <code>rowRanks</code> .
iterative	Boolean value. If iterative = TRUE, the iterative method for improvement of confidence envelopes is applied. Default @FALSE.
approx	Boolean value. Default @TRUE. If you are treating high dimensional data, we suggest to put approx = TRUE to speed up the computation time.
ncomb	Numeric value. If approx = TRUE, you must decide how many random subcollections (level of approximation) considered.
step.down	Boolean value. Default @FALSE. If you want to compute the lambda calibration parameter using the step-down approach put @TRUE.
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 <code>signTest</code> .

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, Angela, et al. "Permutation-based true discovery proportions for fMRI cluster analysis." arXiv preprint arXiv:2012.00368 (2020).

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)
```

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

<code>X</code>	data matrix where rows represent the m variables and columns the n observations.
<code>B</code>	numeric value. Number of permutations, default to 1000.
<code>alternative</code>	character string. It refers to the alternative hypothesis, must be one of "two.sided" (default), "greater" or "lower".
<code>seed</code>	integer value. If you want to specify the seed. Default to @NULL
<code>mask</code>	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 non of the voxels have to be excluded.
<code>rand</code>	Boolean value. Default @FALSE. If rand = TRUE, the p-values are computed by rowRanks .
<code>label</code>	numeric/character vector. Labels of the observations, if NULL the columns's name are considered. Default @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 H_0 , - `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 H_0 .

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 pvalues 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 pvalues with dimensions $m \times B$ used instead of the data matrix X. Default to @NULL.
family	string character. Choose a family of confidence envelopes to compute the critical vector. from "simes", "aorc", "beta" and "higher.criticism". If more than one critical vector are considered, it must be a vector. Default "simes".
alpha	numeric value in '[0,1]'. It expresses the alpha level to control the family-wise error rate. Default 0.1.
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 name.
delta	numeric value. It expresses the delta value, please see the references. Default to 0. If more than one critical vector are considered, delta must be a vector having length equals to the length of critical vectors specified in family.
cofes	list of NIfTI file if P = NULL. The list of cofes, i.e., constrasts 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 non 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 @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 pvalues in red.

Author(s)

Angela Andreella

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

Permutation-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 @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 non of the voxels have to be excluded.
rand	Boolean value. Default @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 one-sample t-tests, one for each m variable, - Test_H0: matrix with dimensions $m \times B - 1$. Test statistics under H0, - 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 H0.

Author(s)

Angela Andreella

Examples

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

simulateData	<i>simulate normal distributed data</i>
--------------	-----------------------------------------

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 @NULL
power	numeric value in '[0,1]'. Level of power. Default 0.8.
alpha	numeric value in '[0,1]'. It expresses the alpha level to control the family-wise error rate. Default 0.05.

Value

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

Author(s)

Angela Andreella

Statmap	<i>Create Statistical Parametric Mapping (SPM)</i>
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Description

It creates the statistical parametric mapping in NIfTI format.

Usage

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

Arguments

copies	list of NIfTI file. The list of copies, 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 NIfTI file. The path does not must end with /.
name	character string. The name of the map NIfTI file that will be used.
Pmap	Boolean value. If TRUE the SPM of the pvalues is returned. Default @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 non 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

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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