

Package ‘npGSEA’

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Type Package

Title Permutation approximation methods for gene set enrichment analysis (non-permutation GSEA)

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Description Current gene set enrichment methods rely upon permutations for inference. These approaches are computationally expensive and have minimum achievable p-values based on the number of permutations, not on the actual observed statistics. We have derived three parametric approximations to the permutation distributions of two gene set enrichment test statistics. We are able to reduce the computational burden and granularity issues of permutation testing with our method, which is implemented in this package. npGSEA calculates gene set enrichment statistics and p-values without the computational cost of permutations. It is applicable in settings where one or many gene sets are of interest. There are also built-in plotting functions to help users visualize results.

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biocViews GeneSetEnrichment, Microarray, StatisticalMethod, Pathways

Collate 'getIncidence.R' 'miscFunctions.R' 'miscDataPrepFunctions.R'
'npGSEA.R' 'AllClasses.R' 'AllGenerics.R'
'npGSEAResultBeta-accessors.R' 'npGSEAResultChiSq-accessors.R'
'npGSEAResultNorm-accessors.R' 'npGSEAPlot-methods.R'
'show-methods.R' 'pValues-methods.R'

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alphaValue-methods *~~ Methods for Function alphaValue ~~*

Description

This function returns the corresponding alpha value for the reference beta distribution for the npGSEA analysis in the gene set in the given experiment. This method is applicable for only the beta approximation method.

Usage

```
alphaValue(object)
```

Arguments

object An object of type npGSEAResultBeta or npGSEAResultBetaCollection

Methods

signature(object = "npGSEAResultBeta") Returns the value for alpha for a npGSEAResultBeta object

signature(object = "npGSEAResultBetaCollection") Returns a list of the alpha values for a npGSEAResultBetaCollection objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultBeta-class](#)

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15, approx= "beta")
alphaValue(res)
```

betaHats-methods

~~ *Methods for Function betaHats* ~~

Description

This function returns the betaHats for all genes in the corresponding GeneSet in the given experiment, or a list of such vectors for each set in a GeneSetCollection. This corresponds to each gene's contribution to the test statistic. This method is applicable for all three approximation methods.

Usage

```
betaHats(object)
```

Arguments

object An object of type npGSEAResultNorm, npGSEAResultBeta, npGSEAResultChiSq, npGSEAResultNormCollection, npGSEAResultBetaCollection, or npGSEAResultChiSqCollection

Methods

signature(object = "npGSEAResultNorm") Returns the betaHats used for analysis to create a npGSEAResultNorm object

signature(object = "npGSEAResultBeta") Returns the betaHats used for analysis to create a npGSEAResultBeta object

signature(object = "npGSEAResultChiSq") Returns the betaHats used for analysis to create a npGSEAResultChiSq object

signature(object = "npGSEAResultNormCollection") Returns the betaHats used for analysis to create the npGSEAResultNormCollection objects (1 for each set)

signature(object = "npGSEAResultBetaCollection") Returns a list of the betaHats used for analysis to create the npGSEAResultBetaCollection objects (1 for each set)

signature(object = "npGSEAResultChiSqCollection") Returns a list of the betaHats used for analysis to create the npGSEAResultChiSqCollection objects (1 for each set)

See Also

[npGSEAResultNorm-class](#)

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
betaHats(res)
```

betaStat-methods

~~ *Methods for Function betaStat* ~~

Description

This function returns the corresponding beta statistic which is compared to the reference beta distribution for the npGSEA analysis in the gene set in the given experiment.

Usage

```
betaStat(object)
```

Arguments

object An object of type npGSEAResultBeta or npGSEAResultBetaCollection

Methods

signature(object = "npGSEAResultBeta") Returns the beta-statistic for a npGSEAResultBeta object

signature(object = "npGSEAResultBetaCollection") Returns a list of the beta-statistics for a npGSEAResultBetaCollection objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultBeta](#)-class

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15, approx= "beta")
betaStat(res)
```

betaValue-methods *~~ Methods for Function betaValue ~~*

Description

This function returns the corresponding beta value for the reference beta distribution for the npGSEA analysis in the gene set in the given experiment. This method is applicable for only the beta approximation method.

Usage

```
betaValue(object)
```

Arguments

object An object of type npGSEAResultBeta or npGSEAResultBetaCollection

Methods

`signature(object = "npGSEAResultBeta")` Returns the value for beta for a `npGSEAResultBeta` object

`signature(object = "npGSEAResultBetaCollection")` Returns a list of the beta values for a `npGSEAResultBetaCollection` objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultBeta](#)-class

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15, approx= "beta")
betaValue(res)
```

chiSqStat-methods

~~ *Methods for Function chiSqStat* ~~

Description

This function returns the chi-sq statistic (which is compared to a reference Chi-sq distribution) for the chi-sq approximation of npGSEA for a corresponding GeneSet or a list of these statistics for a GeneSetCollection. This method is applicable for only the chi-sq approximation method.

Usage

`chiSqStat(object)`

Arguments

`object` An object of type `npGSEAResultChiSq` or `npGSEAResultChiSqCollection`

Methods

`signature(object = "npGSEAResultChiSq")` Returns the chi-sq statistic for a `npGSEAResultChiSq` object

`signature(object = "npGSEAResultChiSqCollection")` Returns a list of the chi-sq statistics for a `npGSEAResultChiSqCollection` objects (1 for each set)

Author(s)

Jessica L. Larson

See Also[npGSEAResultChiSq-class](#)**Examples**

```

set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15, approx= "chiSq")
chiSqStat(res)

```

DF-methods

~~ Methods for Function DF ~~

Description

This function returns the degrees of freedom for the chi-sq approximation of a corresponding GeneSet or a list of degrees of freedom for a GeneSetCollection. This method is applicable for only the chi-sq approximation method.

Usage

```
DF(object)
```

Arguments

object An object of type npGSEAResultChiSq or npGSEAResultChiSqCollection

Methods

```
signature(object = "npGSEAResultChiSq") Returns the degrees of freedom for a npGSEAResultChiSq
object
signature(object = "npGSEAResultChiSqCollection") Returns a list of the degrees of free-
dom for a npGSEAResultChiSqCollection objects (1 for each set)
```

Author(s)

Jessica L. Larson

See Also[npGSEAResultChiSq-class](#)

Examples

```

set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15, approx= "chiSq")
DF(res)

```

geneSetName-methods *~~ Methods for Function geneSetName ~~*

Description

This function returns the name of the corresponding GeneSet or a list of names for a GeneSetCollection. This method is applicable for all three approximation methods.

Usage

```
geneSetName(object)
```

Arguments

object An object of type npGSEAResultNorm, npGSEAResultBeta, npGSEAResultChiSq, npGSEAResultNormCollection, npGSEAResultBetaCollection, or npGSEAResultChiSqCollection

Methods

```
signature(object = "npGSEAResultNorm") Returns a the name of the gene set from a npGSEAResultNorm
object
signature(object = "npGSEAResultBeta") Returns a the name of the gene set from a npGSEAResultBeta
object
signature(object = "npGSEAResultChiSq") Returns a the name of the gene set from a npGSEAResultChiSq
object
signature(object = "npGSEAResultNormCollection") Returns a list of the names of the gene
sets from a npGSEAResultNormCollection objects (1 for each set)
signature(object = "npGSEAResultBetaCollection") Returns a list of the names of the gene
sets from a npGSEAResultBetaCollection objects (1 for each set)
signature(object = "npGSEAResultChiSqCollection") Returns a list of the names of the gene
sets from a npGSEAResultChiSqCollection objects (1 for each set)

```

Author(s)

Jessica L. Larson

See Also

[npGSEAResultNorm](#)-class

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
geneSetName (res)
```

getIncidence

Determines the incidence of a gene set in a list of genes.

Description

Calculates the incidence of a gene set in an experiment

Usage

```
getIncidence(universeIDs, set)
```

Arguments

universeIDs	A vector containing the list of possible gene ids in the universe (or experiment).
set	A GeneSet object containing a set of genes of interest

Details

getIncidence returns an incidence vector of the location of the genes within a gene set in a list of genes in an experiment and vise-versa.

Value

A list of inSet and inExp. inSet is a vector with the same length as universeIDs. Each value of inSet is 1 if the gene is in the set and 0 otherwise. inExp is a vector with the same length as geneIds(set), the number of genes in the set. Each value of inExp is 1 if the gene is in universeIDs and 0 otherwise.

Author(s)

Jessica L. Larson and Art Owen

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

Examples

```
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
getIncidence(letters, geneSetABC15)
```

npGSEA	<i>Calculates an approximation of the permutation GSEA statistics and p-values</i>
--------	--

Description

This function calculates the permutation gene set enrichment analysis test statistic and p-value without actually running the permutation. We account for the covariance among the genes within the set and approximate the corresponding permutation distribution. For more details on the method see Larson and Owen (2014).

Usage

```
npGSEA(x, y, set, covars = NULL, approx = c("norm", "beta", "chiSq"), w = NULL, epsilonBetaAdj=TRUE, scaleXY=TRUE, uniVarX=TRUE)
```

Arguments

x	A matrix of expression data or an object of type ExpressionSet. The columns of x represent samples in a given experiment. The rows are genes. The names of each row (or featureNames of the eSet) must be of the same type (e.g., entrez ids) as the ids of the gene set.
y	A vector containing the treatment for each sample. The length of y must be more than 4 for the "chisq" approximation. Each treatment group must have at least two observations for all approximation methods. There can only be two treatment groups.
covars	A vector or matrix containing covariate(s) of interest, optional
set	A GeneSet object containing a set of genes of interest or a GeneSetCollection object containing a collection of GeneSets
approx	A string of either "norm" (default), "beta" or "chiSq". If "norm", the normal approximation to the non-permutation GSEA is calculated and returned. If "beta", the beta approximation is reported. If "chiSq", the Chi-squared approximation to the permutation GSEA is calculated.
w	A vector or list containing the weights of each gene in the set or sets, optional. If w is a list, the number of elements in the list must correspond to the number of gene sets in the collection.
epsilonBetaAdj	A boolean indicating whether or to not to use an epsilon adjusted p-value for the Beta approximation. When TRUE, this prevents observed p-values of 0. The default is TRUE.
scaleXY	A boolean indicating whether or to not to scale x and y. The default is TRUE.
uniVarX	A boolean indicating whether or to not to scale x to have unit variance. The default is TRUE.

Value

An object with the corresponding GSEA results. If `approx="norm"` an `npGSEAResultNorm` object is returned. If `approx="beta"` a `npGSEAResultBeta` object is returned. If `approx="chiSq"` a `npGSEAResultChiSq` object is returned. If `set` is a `GeneSetCollection` (i.e., multiple sets of interest), then the corresponding `npGSEAResultNormCollection`, `npGSEAResultBetaCollection`, or `npGSEAResultChiSqCollection` is returned.

Author(s)

Jessica L. Larson and Art Owen

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10), nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
```

npGSEAPlot-methods *~~ Methods for Function npGSEAPlot ~~*

Description

This function plots the reference distribution and the corresponding scaled statistic (Z, Beta, or Chi-sq) from the npGSEA analysis for a given `GeneSet`. This method is applicable for all three approximation methods.

Usage

```
npGSEAPlot(object)
```

Arguments

`object` An object of type `npGSEAResultNorm`, `npGSEAResultBeta`, or `npGSEAResultChiSq`

Methods

`signature(object = "npGSEAResultNorm")` Plots the Z-statistic for a `npGSEAResultNorm` object and the standard normal distribution

`signature(object = "npGSEAResultBeta")` Plots the beta statistic for a `npGSEAResultBeta` object and the corresponding reference beta distribution (with alpha and beta calculated from `npGSEA`).

`signature(object = "npGSEAResultChiSq")` Plots the beta statistic for a `npGSEAResultChiSq` object and the corresponding reference chi-squared distribution (with degrees of freedom calculated from `npGSEA`).

Author(s)

Jessica L. Larson

See Also

[npGSEAResultNorm-class](#)

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
##npGSEAPlot (res)
```

npGSEAResultBeta-class

Class "npGSEAResultBeta"

Description

Objects of this class store results from running `npGSEA` with the beta approximation.

Objects from the Class

Objects can be created by calls of `npGSEA`.

Slots

geneSetName: Object of class "character", the name of the geneSet

betaStat: Object of class "numeric", the test statistic, scaled to the corresponding beta distribution

ThatGw: Object of class "numeric", the test statistic for the set

varThatGw: Object of class "numeric", the variance of ThatGw
 alpha: Object of class "numeric", the alpha value
 beta: Object of class "numeric", the beta value
 pLeft: Object of class "numeric", the p-value for the left-side hypothesis
 pRight: Object of class "numeric", the p-value for the right-side hypothesis
 pTwoSided: Object of class "numeric", the p-value for the two-sided hypothesis
 xSet: Object of class "matrix", the centered and scaled x data for this set
 betaHats: Object of class "vector", the betaHats for each gene in this set

Author(s)

Jessica L. Larson

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

See Also

[npGSEAResultNorm](#)

Examples

```
showClass("npGSEAResultBeta")
```

```

npGSEAResultBetaCollection-class
      Class "npGSEAResultBetaCollection"
  
```

Description

Objects of this class store results from running npGSEA with the beta approximation with a GeneSetCollection. npGSEAResultBetaCollection objects contain a list of npGSEAResultBeta objects (one result for each GeneSet).

Objects from the Class

Objects can be created by calls of npGSEA.

Author(s)

Jessica L. Larson

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

See Also

[npGSEAResultNormCollection](#)

Examples

```
showClass("npGSEAResultBetaCollection")
```

```
npGSEAResultChiSq-class
      Class "npGSEAResultChiSq"
```

Description

Objects of this class store results from running npGSEA with the Chi-square approximation.

Objects from the Class

Objects can be created by calls of npGSEA.

Slots

geneSetName: Object of class "character", the name of the geneSet
 chiSqStat: Object of class "numeric", the test statistic, scaled to the corresponding chi-sq distribution
 ChatGw: Object of class "numeric", the test statistic for the set
 sigmaSq: Object of class "numeric", the variance
 DF: Object of class "numeric", the degrees of freedom
 pTwoSided: Object of class "numeric", the p-value for the two-sided hypothesis
 xSet: Object of class "matrix", the centered and scaled x data for this set
 betaHats: Object of class "vector", the betaHats for each gene in this set

Author(s)

Jessica L. Larson

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

See Also[npGSEAResultNorm](#)**Examples**

```
showClass("npGSEAResultChiSq")
```

npGSEAResultChiSqCollection-class

Class "npGSEAResultChiSqCollection"

Description

Objects of this class store results from running npGSEA with the Chi-square approximation with a GeneSetCollection. npGSEAResultChiSqCollection objects contain a list of npGSEAResultChiSq objects (one result for each GeneSet).

Objects from the Class

Objects can be created by calls of npGSEA.

Author(s)

Jessica L. Larson

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

See Also[npGSEAResultNormCollection](#)**Examples**

```
showClass("npGSEAResultChiSqCollection")
```

npGSEAResultNorm-class

Class "npGSEAResultNorm"

Description

Objects of this class store results from running npGSEA with the Gaussian approximation.

Objects from the Class

Objects can be created by calls of npGSEA.

Slots

geneSetName: Object of class "character", the name of the geneSet

zStat: Object of class "numeric", the test statistic, scaled to a standard normal

ThatGw: Object of class "numeric", the test statistic for the set

varThatGw: Object of class "numeric", the variance of ThatGw

pLeft: Object of class "numeric", the p-value for the left-side hypothesis

pRight: Object of class "numeric", the p-value for the right-side hypothesis

pTwoSided: Object of class "numeric", the p-value for the two-sided hypothesis

xSet: Object of class "matrix", the centered and scaled x data for this set

betaHats: Object of class "vector", the betaHats for each gene in this set

Author(s)

Jessica L. Larson

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

See Also

[npGSEAResultChiSq](#)

Examples

```
showClass("npGSEAResultNorm")
```

```
npGSEAResultNormCollection-class  
  Class "npGSEAResultNormCollection"
```

Description

Objects of this class store results from running npGSEA with the Gaussian approximation with a GeneSetCollection. npGSEAResultNormCollection objects contain a list of npGSEAResultNorm objects (one result for each GeneSet).

Objects from the Class

Objects can be created by calls of npGSEA.

Author(s)

Jessica L. Larson

References

Jessica L Larson and Art B Owen: Moment based gene set tests. BMC Bioinformatics 2015, 16:132. <http://www.biomedcentral.com/1471-2105/16/132>

See Also

[npGSEAResultChiSqCollection](#)

Examples

```
showClass("npGSEAResultNormCollection")
```

```
pLeft-methods      ~~ Methods for Function pLeft ~~
```

Description

This function returns the left-sided p-value for the corresponding GeneSet or a list of p-values for a GeneSetCollection. This method is only applicable for the normal and beta approximation methods.

Usage

```
pLeft(object)
```

Arguments

object An object of type npGSEAResultNorm, npGSEAResultBeta, npGSEAResultNormCollection, or npGSEAResultBetaCollection

Methods

signature(object = "npGSEAResultNorm") Returns a left-sided p-value for a npGSEAResultNorm object

signature(object = "npGSEAResultBeta") Returns a left-sided p-value for a npGSEAResultBeta object

signature(object = "npGSEAResultNormCollection") Returns a list of left-sided p-values for a npGSEAResultNormCollection objects (1 for each set)

signature(object = "npGSEAResultBetaCollection") Returns a list of left-sided p-values for a npGSEAResultBetaCollection objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultNorm](#)-class, [pRight](#)

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
pLeft (res)
```

pRight-methods

~~ *Methods for Function pRight* ~~

Description

This function returns the right-sided p-value for the corresponding GeneSet or a list of p-values for a GeneSetCollection. This method is only applicable for the normal and beta approximation methods.

Usage

pRight(object)

Arguments

object An object of type npGSEAResultNorm, npGSEAResultBeta, npGSEAResultNormCollection, or npGSEAResultBetaCollection

Methods

signature(object = "npGSEAResultNorm") Returns a right-sided p-value for a npGSEAResultNorm object

signature(object = "npGSEAResultBeta") Returns a right-sided p-value for a npGSEAResultBeta object

signature(object = "npGSEAResultNormCollection") Returns a list of right-sided p-values for a npGSEAResultNormCollection objects (1 for each set)

signature(object = "npGSEAResultBetaCollection") Returns a list of right-sided p-values for a npGSEAResultBetaCollection objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultNorm](#)-class, pLeft

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10), nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
pRight (res)
```

pTwoSided-methods

~~ *Methods for Function pTwoSided* ~~

Description

This function returns the two-sided p-value for the corresponding GeneSet or a list of p-values for a GeneSetCollection. This method is applicable for all three approximation methods.

Usage

pTwoSided(object)

Arguments

object An object of type npGSEAResultNorm, npGSEAResultBeta, npGSEAResultChiSq, npGSEAResultNormCollection, npGSEAResultBetaCollection, or npGSEAResultChiSqCollection

Methods

signature(object = "npGSEAResultNorm") Returns a two-sided p-value for a npGSEAResultNorm object

signature(object = "npGSEAResultBeta") Returns a two-sided p-value for a npGSEAResultBeta object

signature(object = "npGSEAResultChiSq") Returns a two-sided p-value for a npGSEAResultChiSq object

signature(object = "npGSEAResultNormCollection") Returns a list of left-sided p-values for a npGSEAResultNormCollection objects (1 for each set)

signature(object = "npGSEAResultBetaCollection") Returns a list of left-sided p-values for a npGSEAResultBetaCollection objects (1 for each set)

signature(object = "npGSEAResultChiSqCollection") Returns a list of two-sided p-values for a npGSEAResultChiSqCollection objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultNorm](#)-class, [pRight](#)

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10),nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
pTwoSided (res)
```

pValues-methods

~~ *Methods for Function pValues* ~~

Description

~~ Methods for function pValues ~~

Methods

```
signature(x = "npGSEAResultNorm"),signature(x = "npGSEAResultBeta"),signature(x = "npGSEAResultChiSq")
```

These methods display the corresponding p-values for the npGSEA analysis in the gene set in the given experiment.

Author(s)

Jessica L. Larson

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
pValues(res)
```

sigmaSq-methods

~~ Methods for Function sigmaSq ~~

Description

This function returns the corresponding variance of the statistic (linear or quadratic) from the npGSEA analysis for a given GeneSet, or a list of these variances for a given GeneSetCollection. This method is applicable for all three approximation methods.

Usage

```
sigmaSq(object)
```

Arguments

object An object of type npGSEAResultNorm, npGSEAResultBeta, npGSEAResultChiSq, npGSEAResultNormCollection, npGSEAResultBetaCollection, or npGSEAResultChiSqCollection

Methods

```
signature(object = "npGSEAResultNorm") Returns the variance of the linear statistic for a npGSEAResultNorm object
signature(object = "npGSEAResultBeta") Returns the variance of the linear statistic for a npGSEAResultBeta object
signature(object = "npGSEAResultChiSq") Returns the variance of the quadratic statistic for a npGSEAResultChiSq object
signature(object = "npGSEAResultNormCollection") Returns a list of the variances of the linear statistics for a npGSEAResultNormCollection objects (1 for each set)
```

`signature(object = "npGSEAResultBetaCollection")` Returns a list of the variances of the linear statistics for a `npGSEAResultBetaCollection` objects (1 for each set)

`signature(object = "npGSEAResultChiSqCollection")` Returns a list of the variances of the linear statistics for a `npGSEAResultChiSqCollection` objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultNorm](#)-class

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
sigmaSq(res)
```

stat-methods

~~ *Methods for Function stat* ~~

Description

This function returns the corresponding statistic (linear or quadratic) from the `npGSEA` analysis for a given `GeneSet`, or a list of these statistics for a given `GeneSetCollection`. This method is applicable for all three approximation methods.

Usage

```
stat(object)
```

Arguments

object	An object of type <code>npGSEAResultNorm</code> , <code>npGSEAResultBeta</code> , <code>npGSEAResultChiSq</code> , <code>npGSEAResultNormCollection</code> , <code>npGSEAResultBetaCollection</code> , or <code>npGSEAResultChiSqCollection</code>
--------	--

Methods

`signature(object = "npGSEAResultNorm")` Returns the linear statistic for a `npGSEAResultNorm` object

`signature(object = "npGSEAResultBeta")` Returns the linear statistic for a `npGSEAResultBeta` object

`signature(object = "npGSEAResultChiSq")` Returns the quadratic statistic for a `npGSEAResultChiSq` object

`signature(object = "npGSEAResultNormCollection")` Returns a list of the linear statistics for a `npGSEAResultNormCollection` objects (1 for each set)

`signature(object = "npGSEAResultBetaCollection")` Returns a list of the linear statistics for a `npGSEAResultBetaCollection` objects (1 for each set)

`signature(object = "npGSEAResultChiSqCollection")` Returns a list of the quadratic statistics for a `npGSEAResultChiSqCollection` objects (1 for each set)

Author(s)

Jessica L. Larson

See Also

[npGSEAResultNorm-class](#)

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
stat(res)
```

summary-methods

~~ *Methods for Function show in Package* **base** ~~

Description

~~ Methods for function show in package **base** ~~

Methods

`signature(x = "npGSEAResultNorm"),signature(x = "npGSEAResultBeta"),signature(x = "npGSEAResultChiSq")`
 These methods display the corresponding statistics (linear or quadratic) for the npGSEA analysis in the gene set in the given experiment.

Author(s)

Jessica L. Larson

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
res
```

xSet-methods

~~ Methods for Function xSet ~~

Description

This function returns the scaled and centered expression data for all genes in the corresponding GeneSet in the given experiment, or a list of such matrices for each set in a GeneSetCollection. This method is applicable for all three approximation methods.

Usage

```
xSet(object)
```

Arguments

object An object of type npGSEAResultNorm, npGSEAResultBeta, npGSEAResultChiSq, npGSEAResultNormCollection, npGSEAResultBetaCollection, or npGSEAResultChiSqCollection

Methods

`signature(object = "npGSEAResultNorm")` Returns the centered and scaled X matrix used for analysis to create a npGSEAResultNorm object

`signature(object = "npGSEAResultBeta")` Returns the centered and scaled X matrix used for analysis to create a npGSEAResultBeta object

`signature(object = "npGSEAResultChiSq")` Returns the centered and scaled X matrix used for analysis to create a npGSEAResultChiSq object

`signature(object = "npGSEAResultNormCollection")` Returns a list of centered and scaled X matrices used for analysis to create the npGSEAResultNormCollection objects (1 for each set)

`signature(object = "npGSEAResultBetaCollection")` Returns a list of centered and scaled X matrices used for analysis to create the npGSEAResultBetaCollection objects (1 for each set)

`signature(object = "npGSEAResultChiSqCollection")` Returns a list of centered and scaled X matrices used for analysis to create the npGSEAResultChiSqCollection objects (1 for each set)

See Also[npGSEAResultNorm](#)-class**Examples**

```

set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15)
head( xSet(res) )

```

zStat-methods

~~ *Methods for Function zStat* ~~**Description**

This function returns the Z-statistic (which is compared to a reference standard normal distribution) for the normal approximation of npGSEA for a corresponding GeneSet or a list of these statistics for a GeneSetCollection. This method is applicable for only the normal approximation method.

Usage

```
zStat(object)
```

Arguments

object An object of type npGSEAResultNorm or npGSEAResultNormCollection

Methods

signature(object = "npGSEAResultNorm") Returns the Z-statistic for a npGSEAResultNorm object

signature(object = "npGSEAResultNormCollection") Returns a list of the Z- statistics for a npGSEAResultNormCollection objects (1 for each set)

Author(s)

Jessica L. Larson

See Also[npGSEAResultNorm](#)-class

Examples

```
set.seed(15)
yFactor <- as.factor( c(rep("treated", 5), rep("control", 5)) )
xData <- matrix(data=rnorm(length(letters)*10) ,nrow=length(letters), ncol=10)
rownames(xData) <- letters
geneSetABC15 <- GeneSet(geneIds=letters[1:15], setName="setABC15")
res <- npGSEA(x = xData, y = yFactor, set = geneSetABC15, approx= "norm")
zStat(res)
```

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