

# Package ‘npGSEA’

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**Type** Package

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

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**Author** Jessica Larson and Art Owen

**Maintainer** Jessica Larson <larson.jess@gmail.com>

**Imports** Biobase, methods, BiocGenerics, graphics, stats

**Suggests** ALL, genefilter, limma, hgu95av2.db, ReportingTools, BiocStyle

**Depends** GSEABase (>= 1.24.0)

**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.

**License** Artistic-2.0

**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 freedom 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	<i>Determines the incidence of a gene set in a list of genes.</i>
--------------	-------------------------------------------------------------------

---

**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)
```

### 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 npGSEAResultNorm, npGSEAResultBeta, npGSEAResultChiSq, npGSEAResultNormCollection, npGSEAResultBetaCollection, or npGSEAResultChiSqCollection

**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 = "npGSEAResultChiS  
These methods display the corresponding statistics (linear or quadratic)for the npGSEA anal-  
ysis 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, 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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