Package 'DysPIA'

May 7, 2026

Type Package

Title Dysregulated Pathway Identification Analysis

Version 1.3

Date 2020-06-26

Maintainer Limei Wang <lemon619@gmail.com>

Description It is used to identify dysregulated pathways based on a pre-ranked gene pair list. A fast algorithm is used to make the computation really fast. The data in package 'DysPIAData' is needed.

License GPL (>= 2)

Depends R (>= 3.5.0), DysPIAData

Imports Rcpp (>= 1.0.4), BiocParallel, fastmatch, data.table, stats,parmigene

LinkingTo Rcpp

RoxygenNote 7.1.0

Encoding UTF-8

LazyData true

NeedsCompilation yes

Author Limei Wang [aut, cre], Jin Li [aut, ctb]

Repository CRAN

Date/Publication 2020-07-10 05:10:03 UTC

Contents

`calcDyspiaStat` *calcDyspiaStat: Calculates DysPIA statistics*

Description

Calculates DysPIA statistics for a given query gene pair set.

Usage

```
calcDyspiaStat(
  stats,
  selectedStats,
  DyspiaParam = 1,
  returnAllExtremes = FALSE,
  returnLeadingEdge = FALSE
)
```

Arguments

`stats`	Named numeric vector with gene pair-level statistics sorted in decreasing order (order is not checked).
`selectedStats`	Indexes of selected gene pairs in the ‘stats‘ array.
`DyspiaParam`	DysPIA weight parameter (0 is unweighted, suggested value is 1).
`returnAllExtremes`	If TRUE return not only the most extreme point, but all of them. Can be used for enrichment plot.
`returnLeadingEdge`	If TRUE return also leading edge gene pairs.

Value

Value of DysPIA statistic if both returnAllExtremes and returnLeadingEdge are FALSE. Otherwise returns list with the folowing elements:

- res – value of DysPIA statistic
- tops – vector of top peak values of cumulative enrichment statistic for each gene pair;
- bottoms – vector of bottom peak values of cumulative enrichment statistic for each gene pair;
- leadingEdge – vector with indexes of leading edge gene pairs that drive the enrichment.

calcDyspiaStatCumulative

Calculates DysPIA statistic values for all the prefixes of a gene pair set

Description

Calculates DysPIA statistic values for all the prefixes of a gene pair set

Usage

```
calcDyspiaStatCumulative(stats, selectedStats, DyspiaParam)
```

Arguments

stats	Named numeric vector with gene pair-level statistics sorted in decreasing order (order is not checked)
selectedStats	indexes of selected gene pairs in a ‘stats‘ array
DyspiaParam	DysPIA weight parameter (0 is unweighted, suggested value is 1)

Value

Numeric vector of DysPIA statistics for all prefixes of selectedStats.

calcDyspiaStatCumulativeBatch

Calculates DysPIA statistic values for the gene pair sets

Description

Calculates DysPIA statistic values for the gene pair sets

Usage

```
calcDyspiaStatCumulativeBatch(
  stats,
  DyspiaParam,
  pathwayScores,
  pathwaysSizes,
  iterations,
  seed
)
```

Arguments

stats	Named numeric vector with gene pair-level statistics sorted in decreasing order (order is not checked).
DyspiaParam	DysPIA weight parameter (0 is unweighted, suggested value is 1).
pathwayScores	Vector with enrichment scores for the pathways in the database.
pathwaysSizes	Vector of pathway sizes.
iterations	Number of iterations.
seed	Seed vector

Value

List of DysPIA statistics for gene pair sets.

---

calEdgeCorScore_ESEA *calEdgeCorScore_ESE*

Description

Calculates differential Mutual information.

Usage

```
calEdgeCorScore_ESEA(
  dataset,
  class.labels,
  controlcharacter,
  casecharacter,
  background
)
```

Arguments

dataset	Matrix of gene expression values (rownames are genes, columnnames are samples).
class.labels	Vector of binary labels.
controlcharacter	Charactor of control in the class labels.
casecharacter	Charactor of case in the class labels.
background	Matrix of the edges' background.

Value

A vector of the aberrant correlation in phenotype P based on mutual information (MI) for each edge.

Examples

```
data(gene_expression_p53, class.labels_p53,sample_background)
ESEAscore_p53<-calEdgeCorScore_ESEA(gene_expression_p53, class.labels_p53,
 "WT", "MUT", sample_background)
```

`class.labels_p53` *Example vector of category labels.*

Description

The labels for the 50 cell lines in p53 data. Control group's label is 'WT', case group's label is 'MUT'.

Usage

```
data(class.labels_p53)
```

`DysGPS` *DysGPS: Calculates Dysregulated gene pair score (DysGPS) for each gene pair*

Description

Calculates Dysregulated gene pair score (DysGPS) for each gene pair. Two-sample Welch's T test of gene pairs between case and control samples. The package 'DysPIAData' including the background data is needed to be loaded.

Usage

```
DysGPS(
  dataset,
  class.labels,
  controlcharacter,
  casecharacter,
  background = combined_background
)
```

Arguments

dataset	Matrix of gene expression values (rownames are genes, columnnames are samples).
class.labels	Vector of category labels.
controlcharacter	Charactor of control group in the class labels.
casecharacter	Charactor of case group in the class labels.
background	Matrix of the gene pairs' background. The default is 'combined_background', which includes real pathway gene pairs and randomly producted gene pairs. The 'combined_background' was incluede in 'DysPIAData'.

Value

A vector of DysGPS for each gene pair.

Examples

```
data(gene_expression_p53, class.labels_p53,sample_background)
DysGPS_sample<-DysGPS(gene_expression_p53, class.labels_p53,
 "WT", "MUT", sample_background)
```

DysGPS_p53 *Example vector of DysGPS in p53 data.*

Description

The score vector of 164923 gene pairs from p53 dataset. It can be loaded from the example datasets of R-package 'DysPIA', and also can be obtained by running DysGPS(), details see DysGPS.R

Usage

```
data(DysGPS_p53)
```

DysPIA *DysPIA: Dysregulated Pathway Identification Analysis*

Description

Runs Dysregulated Pathway Identification Analysis (DysPIA).The package 'DysPIAData' including the background data is needed to be loaded.

Usage

```
DysPIA(
  pathwayDB = "kegg",
  stats,
  nperm = 10000,
  minSize = 15,
  maxSize = 1000,
  nproc = 0,
  DyspiaParam = 1,
  BPPARAM = NULL
)
```

Arguments

pathwayDB	Name of the pathway database (8 databases:reactome,kegg,biocarta,panther,pathbank,nci,smpdb,pharmgk The default value is "kegg".
stats	Named vector of CILP scores for each gene pair. Names should be the same as in pathways.
nperm	Number of permutations to do. Minimial possible nominal p-value is about 1/nperm. The default value is 10000.
minSize	Minimal size of a gene pair set to test. All pathways below the threshold are excluded. The default value is 15.
maxSize	Maximal size of a gene pair set to test. All pathways above the threshold are excluded. The default value is 1000.
nproc	If not equal to zero sets BPPARAM to use nproc workers (default = 0).
DyspiaParam	DysPIA parameter value, all gene pair-level status are raised to the power of 'DyspiaParam' before calculation of DysPIA enrichment scores.
BPPARAM	Parallelization parameter used in bplapply. Can be used to specify cluster to run. If not initialized explicitly or by setting 'nproc' default value 'bpparam()' is used.

Value

A table with DysPIA results. Each row corresponds to a tested pathway. The columns are the following:

- pathway – name of the pathway as in 'names(pathway)';
- pval – an enrichment p-value;
- padj – a BH-adjusted p-value;
- DysPS – enrichment score, same as in Broad DysPIA implementation;
- NDysPS – enrichment score normalized to mean enrichment of random samples of the same size;
- nMoreExtreme' – a number of times a random gene pair set had a more extreme enrichment score value;
- size – size of the pathway after removing gene pairs not present in 'names(stats)';
- leadingEdge – vector with indexes of leading edge gene pairs that drive the enrichment.

Examples

```
data(pathway_list,package="DysPIAData")
data(DysGPS_p53)
DyspiaRes_p53 <- DysPIA("kegg", DysGPS_p53, nperm = 100, minSize = 20, maxSize = 100)
```

DyspiaRes_p53 *Example list of DysPIA result in p53 data.*

Description

The list includes 81 pathway results from 'DisPIA.R' as an example used in 'DyspiaSig.R'.

Usage

```
data(DyspiaRes_p53)
```

DyspiaSig *DyspiaSig*

Description

Returns the significant summary of DysPIA results.

Usage

```
DyspiaSig(DyspiaRes, fdr)
```

Arguments

DyspiaRes	Table with results of running DysPIA().
fdr	Significant threshold of 'padj' (a BH-adjusted p-value).

Value

A list of significant DysPIA results, including correlation gain and correlation loss.

Examples

```
data(pathway_list,package="DysPIAData")
data(DyspiaRes_p53)
summary_p53 <- DyspiaSig(DyspiaRes_p53, 0.05)       # filter with padj<0.05
```

DyspiaSimpleImpl *DyspiaSimpleImpl*

Description

Runs dysregulated pathway identification analysis for preprocessed input data.

Usage

```
DyspiaSimpleImpl(
  pathwayScores,
  pathwaysSizes,
  pathwaysFiltered,
  leadingEdges,
  permPerProc,
  seeds,
  toKeepLength,
  stats,
  BPPARAM
)
```

Arguments

pathwayScores	Vector with enrichment scores for the pathways in the database.
pathwaysSizes	Vector of pathway sizes.
pathwaysFiltered	Filtered pathways.
leadingEdges	Leading edge gene pairs.
permPerProc	Parallelization parameter for permutations.
seeds	Seed vector
toKeepLength	Number of ‘pathways‘ that meet the condition for ‘minSize‘ and ‘maxSize‘.
stats	Named vector of gene pair-level scores. Names should be the same as in pathways of ‘pathwayDB‘.
BPPARAM	Parallelization parameter used in bplapply. Can be used to specify cluster to run. If not initialized explicitly or by setting ‘nproc‘ default value ‘bpparam()‘ is used.

Value

A table with DysPIA results. Each row corresponds to a tested pathway. The columns are the following:

- pathway – name of the pathway as in ‘names(pathway)‘;
- pval – an enrichment p-value;

- padj – a BH-adjusted p-value;
- DysPS – enrichment score, same as in Broad DysPIA implementation;
- NDysPS – enrichment score normalized to mean enrichment of random samples of the same size;
- nMoreExtreme‘ – a number of times a random gene pair set had a more extreme enrichment score value;
- size – size of the pathway after removing gene pairs not present in ‘names(stats)‘;
- leadingEdge – vector with indexes of leading edge gene pairs that drive the enrichment.

`gene_expression_p53` *Example matrix of gene expression value.*

Description

A dataset of transcriptional profiles from p53+ and p53 mutant cancer cell lines. It includes the normalized gene expression for 6385 genes in 50 samples. Rownames are genes, columnnames are samples.

Usage

```
data(gene_expression_p53)
```

`sample_background` *Example list of gene pair background.*

Description

The list of background was used in ”DysGPS.R’ and ’calEdgeCorScore_ESEA.R’ which is a part of the ’combined_background’ in ’DysPIAData’.

Usage

```
data(sample_background)
```

`setUpBPPARAM` *setUpBPPARAM*

Description

Sets up parameter BPPARAM value.

Usage

```
setUpBPPARAM(nproc = 0, BPPARAM = NULL)
```

Arguments

`nproc`	If not equal to zero sets BPPARAM to use nproc workers (default = 0).
`BPPARAM`	Parallelization parameter used in bplapply. Can be used to specify cluster to run. If not initialized explicitly or by setting ‘nproc‘ default value ‘bpparam()‘ is used.

Value

parameter BPPARAM value

Index