Package ‘LncPath’

October 12, 2022

Type Package
Title Identifying the Pathways Regulated by LncRNA Sets of Interest
Version 1.1
Date 2018-09-26
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Description Identifies pathways synergistically regulated by the interested lncRNA(long non-coding RNA) sets based on a lncRNA-mRNA(messenger RNA) interaction network. 1) The lncRNA-mRNA interaction network was built from the protein-protein interactions and the lncRNA-mRNA co-expression relationships in 28 RNA-Seq data sets. 2) The interested lncRNAs can be mapped into networks as seed nodes and a random walk strategy will be performed to evaluate the rate of each coding genes influenced by the seed lncRNAs. 3) Pathways regulated by the lncRNA set will be evaluated by a weighted Kolmogorov-Smirnov statistic as an ES Score. 4) The p value and false discovery rate value will also be calculated through a permutation analysis. 5) The running score of each pathway can be plotted and the heat map of each pathway can also be plotted if an expression profile is provided. 6) The rank and scores of the gene list of each pathway can be printed.

Imports stats, graphics, utils, grDevices
Depends R (>= 3.2.1), igraph
Suggests Matrix, graph
License GPL (>= 2)
LazyData Yes
NeedsCompilation no
Repository CRAN
Date/Publication 2018-09-26 14:20:06 UTC

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**drawAHeatMap**

*Draw a heatmap for the genes of a pathway*

**Description**

Draw a heatmap for the genes of a certain pathway based on the expression profile user specified.

**Usage**

```r
drawAHeatMap(Result, Name, PCExpr, Labels)
```

**Arguments**

- **Result**
  A lncPath object come from the lncPath function.

- **Name**
  A string, the name of the pathway to be plot.

- **PCExpr**
  A data frame, the expression profile to be plotted.

- **Labels**
  A vector of 0 and 1, 0 indicates control and 1 indicates case.

**Details**

Draw a heatmap of the genes of a pathway based on the expression profile. The rows of heatmap are genes ranked by their weights and the columns of heatmap are samples ordered the same as the expression profile.

**Author(s)**

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

**References**

findSigGenes

Examples

```r
#--- Should be DIRECTLY executable !! ----
#-- ==> Define data, use random,
#-- or do help(data=index) for the standard data sets.

Result <- getExampleData("Result")
Profile <- getExampleData("Profile")
Labels <- getExampleData("Labels")
drawAHeatMap(Result, "KEGG_RIBOSOME", Profile, Labels)
```

findSigGenes

Find genes significantly differentially expressed between two conditions.

Description

For a given expression profile of two conditions, find the genes differentially expressed using T-test, fold change or SAM algorithm.

Usage

```r
findSigGenes(Expr, Label, Method = "tTest", Directed = TRUE,
FdrCut = 0.01, FDCut = 1)
```

Arguments

- **Expr**: A data frame, the expression profile to find differentially expressed genes, the rownames should be the ID of genes.
- **Label**: A vector of 0/1s, indicating the class of samples in the expression profile, 0 represents case, 1 represents control.
- **Method**: A string, specifying the method to calculate the differentially expressed genes, should be one of the "tTest"or"foldChange".
- **Directed**: Logical, if the the up or down regulated set should be distinguished.
- **FdrCut**: Numeric, the fdr cutoff for T test, can be ignored if not using t-test.
- **FDCut**: Numeric, the cutoff for fold change, can be ignored if not using fold change.

Details

For a given expression profile of two conditions, IncPath package provide two method to find differentially expressed genes: t-test and fold change. The row of the expression profile should be gene IDs and the column of the expression profile should be names of samples. Samples should be under two conditions and the label should be given as 0 and 1. For t-test, fold change and SAM, different threshold can be set for significant differentially expressed genes.
Value

A vector of strings, the IDs of differentially expressed genes.

Author(s)

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

References


Examples

```r
## Should be DIRECTLY executable !! ----
##-- ==> Define data, use random, 
##-- or do help(data=index) for the standard data sets.
Profile <- getExampleData("Profile")
Labels <- getExampleData("Labels")

SigGenes <- findSigGenes(Profile, Labels)
head(SigGenes)
```

Description

Gain insight into the detail of the genes in a certain pathway, including the ranks, weights and cumulative running scores of each gene.

Usage

geneSetDetail(Result, Name)

Arguments

- **Result**: A IncPath object come from the IncPath function.
- **Name**: A string, the name of the pathway to be print.

Details

List all the genes of pathways ranked by the weights. The table also contains the gene name, the rank of genes in the whole gene list, the cumulative ES score and whether the gene is in the core gene sets which contribute to the score of the pathway.
getExampleData  

**Value**  

A data frame, the rows are gene names and the columns are detail of genes including gene name, rank, weight, cumulative ES score and core enrichment.

**Author(s)**  

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

**References**  


**Examples**  

```r  
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

Result <- getExampleData("Result")
Detail <- geneSetDetail(Result, "KEGG_RIBOSOME")
head(Detail)
```

---

getExampleData  

*Get the example data*

**Description**  

Get the example data of LncPath package for little trials.

**Usage**  

```r  
getExampleData(ExampleData)
```

**Arguments**  

- **ExampleData**  
  A character, should be one of "SigLncs", "ExampleNet", "Labels", "Profile", "Result" and "Table".
Details

The function `getExampleData(ExampleData = "SigLncs")` obtains a vector of IncRNAs confirmed to be related with breast cancer. The function `getExampleData(ExampleData = "Profile")` obtains the expression profile as a data frame. The function `getExampleData(ExampleData = "Labels")` obtains a vector of 0/1s describing the class of samples in the expression profile. The function `getExampleData(ExampleData = "Result")` obtains a lncPath object come from the lncPath function. The function `getExampleData(ExampleData = "Table")` obtains a data frame as the summary of lncPath object. The function `getExampleData(ExampleData = "ExampleNet")` obtains a data frame as the edges of IncRNA-mRNA interaction net.

Author(s)

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

References


---

getNet

Get the background IncRNA-mRNA interaction network

Description

Get the background IncRNA-mRNA interaction network.

Usage

getNet()

Details

Get the background IncRNA-mRNA interaction network, it was built by intergrating an IncRNA-mRNA co-expression network and the protein-protein interaction network.

Author(s)

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

References

Examples

```r
## Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##-- or do help(data=index) for the standard data sets.
LncPathNet <- getNet();
```

---

**IncPath**

**Identify pathways synergisticly regulated by IncRNA sets.**

**Description**

Identify pathways synergisticly regulated by IncRNA sets by combining the random walk strategy and weighted Kolmogorov-Smirnov statistic based on a huge IncRNA-mRNA interaction network.

**Usage**

```r
IncPath(LncRNAList, Network, Weighted = TRUE, PathwayDataSet = "KEGG",
minPathSize = 15, maxPathSize = 500, nperm = 1000)
```

**Arguments**

- `LncRNAList`: A character vector, contains the user interested IncRNAs, the ID of IncRNAs should be the Ensembl ID.
- `Network`: A dataframe with two columns, describing the edges of the network to perform the random walk.
- `Weighted`: Logical, tell if a weighted analysis to be performed, see detail.
- `PathwayDataSet`: A character, tells which pathway database is to be used, should be one of "KEGG", "Reactome" and "BioCarta".
- `minPathSize`: An integer, the lower limit of the mapped genes in pathway.
- `maxPathSize`: An integer, the upper limit of the mapped genes in pathway.
- `nperm`: An integer, how many times of perturbation to be performed in the perturbation analysis.

**Details**

IncPath is the main function of IncPath package, it takes a list of interested IncRNAs and a IncRNA-mRNA interaction network as input. Then it maps the IncRNAs into the IncRNA-mRNA interaction network as seed nodes and performs a random walk strategy to evaluate the rate of nodes affected by the seed nodes. A weighted Kolmogorov-Smirnov statistic was finnally used to evaluate the pathways related to the IncRNA sets. If the Weighted parameter is set to TRUE, the scores of mRNAs generated from random walk will be treated as the weight in Kolmogorov-Smirnov statistic. If the Weighted parameter is set to FALSE, only the ranks of mRNAs will be taken into consideration. Now three pathway data sets are supported, includeing the KEGG, Reactome and BioCarta. And pathways with number of genes out of the limit will be filtered.
Value

A lncPath object, containing the details of each pathways: pathway ID, pathway name, number of genes, gene names, score of genes etc. It can be summarized by function by function lncPath2Table and can be visualized by function plotRunningES.

Author(s)

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

References


Examples

```r
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## get example data
SigLncs <- getExampleData("SigLncs")
head(SigLncs)

ExampleNet <- getExampleData("ExampleNet")
head(ExampleNet)

##run lncPath
Result <- lncPath(SigLncs, ExampleNet, Weighted = TRUE, PathwayDataSet = "KEGG", nperm = 100,
minPathSize = 0, maxPathSize = 500)

## Print to table
Table <- lncPath2Table(Result)
head(Table)
```

lncPath2Table

Simplify the lncPath object into table

Description

Simplify the LncPath object into a data frame, which describes the detail information of each pathway.

Usage

`lncPath2Table(Result)`
Arguments

Result  The lncPath object come from the lncPath function.

Details

The lncPath object come from the lncPath function may be too complicated for user to view. This function can simplify it into a data frame. Each row of the data frame describe the detail of one pathway, including informations of pathway name, number of genes in the pathway, enrichment scores, normalized enrichment scores, p value and false discovery rate.

Value

A data frame, rows are pathways and columns are details of each pathway.

Author(s)

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

References


Examples

```r
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
Result <- getExampleData("Result")
Table <- lncPath2Table(Result)
head(Table)
```

---

LncPathEnvir  The variables in the environment variable LncPathEnvir of the system

Description

The variables in the environment variable LncPathEnvir of the system.

Format

An environment variable
**Author(s)**

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---

**plotRunningES**

Visualize the Kolmogorov-Smirnov running score of pathway

---

**Description**

Visualize the Kolmogorov-Smirnov running score of each gene of a certain pathway

**Usage**

```
plotRunningES(Result, Name)
```

**Arguments**

- **Result**
  A lncPath object come from the lncPath function.
- **Name**
  A string, the name of the pathway to be plot.

**Details**

Plot the KS-statistic running score of certain pathway. The plot has three sections, the top section is a curve describes the cumulative ES score of pathway through all coding genes. The middle section contains signals telling which gene is in the pathway. The bottom section describes the weight distribution of genes.

**Author(s)**

Junwei Han <hanjunwei1981@163.com>, Zeguo Sun <zeguo.sun@163.com>

**References**


**Examples**

```r
## Should be DIRECTLY executable !! ----
##-- ==> Define data, use random, 
##-- or do help(data=index) for the standard data sets.

Result <- getExampleData("Result")
plotRunningES(Result, "KEGG_RIBOSOME")
```
**printSignifResult**

*Output the details of significant pathways*

**Description**

Export all of the significant pathways into a specified location.

**Usage**

```r
printSignifResult(Result, Threshold = 0.01, Path = ".", HeatPlot = FALSE, 
PCExpr = "", Labels = "", Top = 0)
```

**Arguments**

- **Result**: A lncPath object come from the lncPath function.
- **Threshold**: Numeric, the FDR threshold for selecting significant pathways.
- **Path**: String, the output directory.
- **HeatPlot**: Logical, should the heatmaps be plotted.
- **PCExpr**: A data frame, represents the expression profile of genes, the rownames must be gene names, must be set if HeatPlot is TRUE.
- **Labels**: A vector of 0 and 1, 0 indicates control and 1 indicates case.
- **Top**: An integer, indicates the number of the most significant pathways to be print, the Threshold will be ignored.

**Details**

For a result from the lncPath function, printSignifResult will output all the details of significant pathways. Significant pathways can be defined by the threshold user submit or by ranks. The detail of pathways contains the running score plot, the gene sets detail and the heatmap of each pathway. For heatmap plot, the corresponding expression profile is needed. Considering a lot of files will be output, the output directory can be specified.

**Author(s)**

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**References**

Examples

```r
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.
## Not run:
Result <- getExampleData("Result")
Profile <- getExampleData("Profile")
Labels <- getExampleData("Labels")
dir.create("Signif")
SignifReport(Result, Threshold = 0.01, Path = "Signif", HeatPlot = TRUE, Profile, Labels, Top = 30)

## End(Not run)
```
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