Package ‘StarBioTrek’

April 26, 2017

Type Package
Title StarBioTrek
Version 1.2.0
Date 02-08-2017
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Depends R (>= 3.3)
Imports SpidermiR, KEGGREST, org.Hs.eg.db, AnnotationDbi, e1071, ROCR, grDevices, igraph
Description This tool StarBioTrek presents some methodologies to measure pathway activity and cross-talk among pathways integrating also the information of network data.
License GPL (>= 3)
biocViews GeneRegulation, Network, Pathways, KEGG
Suggests BiocStyle, knitr, rmarkdown, testthat, devtools, roxygen2, qgraph, png, grid
VignetteBuilder knitr
LazyData true
URL https://github.com/claudiacava/StarBioTrek
BugReports https://github.com/claudiacava/StarBioTrek/issues
RoxygenNote 5.0.1
NeedsCompilation no

R topics documented:

average ................................................................. 2
ds_score_crtlk ...................................................... 2
euc_dist_crtlk ....................................................... 3
getKEGGdata ......................................................... 4
getNETdata .......................................................... 4
GE_matrix ........................................................... 5
list_path_net ........................................................ 5
average

Description
average creates a matrix with a summarized value for each pathway

Usage
average(dataFilt, pathway)

Arguments
- dataFilt: TCGA matrix
- pathway: pathway data

Value
a matrix value for each pathway

Examples
score_mean<-average(dataFilt=tumo[,1:2],path)

ds_score_crtlk

For TCGA data get human pathway data and creates a measure of discriminating score among pathways

Description
ds_score_crtlk creates a matrix with discriminating score for pathways

Usage
ds_score_crtlk(dataFilt, pathway)
**euc_dist_crtlk**

**Arguments**

- **dataFilt**: TCGA matrix
- **pathway**: pathway data

**Value**

a matrix value for each pathway

**Examples**

```r
cross_talk_st_dv<-ds_score_crtlk(dataFilt=tumo[,1:2],pathway=path)
```

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**Description**

euc_dist_crtlk creates a matrix with euclidean distance for pairwise pathways

**Usage**

euc_dist_crtlk(dataFilt, pathway)

**Arguments**

- **dataFilt**: TCGA matrix
- **pathway**: pathway data

**Value**

a matrix value for each pathway

**Examples**

```r
score_euc_distac<-euc_dist_crtlk(dataFilt=tumo[,1:2],path)
```
getKEGGdata

Get human KEGG pathway data.

Description

getKEGGdata creates a data frame with human KEGG pathway. Columns are the pathways and rows the genes inside those pathway.

Usage

getKEGGdata(KEGG_path)

Arguments

KEGG_path variable

Value
dataframe with human pathway data

Examples

path<-getKEGGdata(KEGG_path="Transcript")

getNETdata

Get network data.

Description

getNETdata creates a data frame with network data. Network category can be filtered among: physical interactions, co-localization, genetic interactions and shared protein domain.

Usage

getNETdata(network, organism = NULL)

Arguments

network variable. The user can use the following parameters based on the network types to be used. PHint for Physical_interactions, COloc for Co-localization, GENint for Genetic_interactions and SHpd for Shared_protein_domains

organism organism==NULL default value is homo sapiens

Value
dataframe with gene-gene (or protein-protein interactions)

Examples

organism="Saccharomyces_cerevisiae"
netw<-getNETdata(network="SHpd",organism)
GE_matrix

Description

GE_matrix creates a matrix of gene expression for pathways given by the user.

Usage

GE_matrix(DataMatrix, pathway)

Arguments

DataMatrix  gene expression matrix (eg.TCGA data)
pathway    pathway data as provided by getKEGGdata

Value

a matrix for each pathway (gene expression level belong to that pathway)

Examples

list_path_gene<-GE_matrix(DataMatrix=tumo[,1:2],pathway=path)

list_path_net

Description

list_path_net creates a list of interacting genes for each human pathway.

Usage

list_path_net(lista_net, pathway)

Arguments

lista_net  output of path_net
pathway    pathway data as provided by getKEGGdata

Value

a list of genes for each pathway (interacting genes belong to that pathway)

Examples

lista_netw<-path_net(pathway=path,data=netw)
list_path<-list_path_net(lista_net=lista_netw,pathway=path)
Get human KEGG pathway data and a gene expression matrix in order to obtain a matrix with the mean gene expression for only pathways given in input.

Description
GE_matrix creates a matrix of mean gene expression for pathways given by the user.

Usage
matrix_plot(DataMatrix, pathway)

Arguments
DataMatrix gene expression matrix (eg. TCGA data)
pathway pathway data as provided by getKEGGdata

Value
a matrix for each pathway (mean gene expression level belong to that pathway)

Examples
list_path_plot<-matrix_plot(DataMatrix=tumo[,1:2],pathway=path)

Get human KEGG pathway data and network data in order to define the common gene.

Description
path_net creates a list of network data for each human pathway. The network data will be generated when interacting genes belong to that pathway.

Usage
path_net(pathway, data)

Arguments
pathway pathway data as provided by getKEGGdata
data network data as provided by getNETdata

Value
a list of network data for each pathway (interacting genes belong to that pathway)

Examples
lista_net<-path_net(pathway=path, data=netw)
plotting_cross_talk

Description

`plotting_matrix` creates a matrix of gene expression for pathways given by the user.

Usage

`plotting_cross_talk(DataMatrix, pathway, path_matrix)`

Arguments

- `DataMatrix`: gene expression matrix (e.g., TCGA data)
- `pathway`: pathway data as provided by `getKEGGdata`
- `path_matrix`: output of the function `matrix_plot`

Value

A plot for pathway cross talk

Examples

```r
mt<-plotting_cross_talk(DataMatrix=tumo[,1:2],pathway=path,path_matrix=list_path_plot)
```

process_matrix

Process matrix TCGA data after the selection of pairwise pathway

Description

`process_matrix` processes gene expression matrix

Usage

`process_matrix(measure, list_perf)`

Arguments

- `measure`: matrix with measure of cross-talk among pathways
- `list_perf`: output of the function `select_class`

Value

A gene expression matrix for case study 1


**SelectedSample**

Select the class of TCGA data

**Description**

select two labels from ID barcode

**Usage**

`SelectedSample(Dataset, typesample)`

**Arguments**

- **Dataset**
  - gene expression matrix
- **typesample**
  - the labels of the samples (e.g. tumor,normal)

**Value**

a gene expression matrix of the samples with specified label

**Examples**

`tumo<-SelectedSample(Dataset=Data_CANCER_normUQ_filt,typesample="tumor")[,2]`
**select_class**

*Select the class of TCGA data*

**Description**

select two labels from ID barcode

**Usage**

```r
select_class(auc.df, cutoff)
```

**Arguments**

- `auc.df`: list of AUC value
- `cutoff`: cut-off for AUC value

**Value**

a gene expression matrix with only pairwise pathway with a particular cut-off

**StarBioTrek**

*Download data*

**Description**

StarBioTrek allows you to Download data of samples from StarBioTrek

**Details**

The functions you’re likely to need from **StarBioTrek** is `path_star` Otherwise refer to the vignettes to see how to format the documentation.

**st_dv**

*For TCGA data get human pathway data and creates a measure of standard deviations among pathways*

**Description**

st_dv creates a matrix with standard deviation for pathways

**Usage**

```r
st_dv(DataMatrix, pathway)
```

**Arguments**

- `DataMatrix`: TCGA matrix
- `pathway`: pathway data
svm_classification

Value
a matrix value for each pathway

Examples
stand_dev<-st_dv(DataMatrix=tumo[,1:2],pathway=path)

svm_classification SVM classification for each feature

Description
svm class creates a list with auc value

Usage
svm_classification(TCGA_matrix, tumour, normal, nfs)

Arguments
TCGA_matrix gene expression matrix
tumour barcode samples for a class
normal barcode samples for another class
nfs nfs split data into a training and test set

Value
a list with AUC value for pairwise pathway

Examples
nf <- 60
res_class<-svm_classification(TCGA_matrix=score_euc_dist,nfs=nf,
normal=colnames(norm[,1:10]),tumour=colnames(tumo[,1:10]))
Index

average, 2

ds_score_crtlk, 2

euc_dist_crtlk, 3

GE_matrix, 5
getKEGGdata, 4
getNETdata, 4

list_path_net, 5

matrix_plot, 6

path_net, 6
plotting_cross_talk, 7
proc_path, 8
process_matrix, 7

select_class, 9
SelectedSample, 8
st_dv, 9
StarBioTrek, 9
StarBioTrek-package (StarBioTrek), 9
svm_classification, 10