Package ‘StarBioTrek’
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Type Package
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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:

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For TCGA data get human pathway data and creates a matrix with the average of genes for each pathway.

**Description**

average creates a matrix with a summarized value for each pathway

**Usage**

```r
average(dataFilt, pathway)
```

**Arguments**

- `dataFilt` TCGA matrix
- `pathway` pathway data

**Value**

a matrix value for each pathway

**Examples**

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

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**

```r
ds_score_crtlk(dataFilt, pathway)
```
euc_dist_crtlk

Arguments

- dataFilt: TCGA matrix
- pathway: pathway data

Value

- a matrix value for each pathway

Examples

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

descr

Usage

euc_dist_crtlk(dataFilt, pathway)

Arguments

- dataFilt: TCGA matrix
- pathway: pathway data

Value

- a matrix value for each pathway

Examples

score_euc_dist<-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**

Get human KEGG pathway data and a gene expression matrix in order to obtain a matrix with the gene expression for only pathways given in input.

**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 (e.g. 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**

Get human KEGG pathway data and output of path_net in order to define the common genes.

**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)
matrix_plot

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)

path_net

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

Get human KEGG pathway data and a gene expression matrix we obtain a matrix with the gene expression for only pathways given in input.

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 (eg. 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
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
processing 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

Description

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

Usage

proc_path(mer)

Arguments

mer output for example of select_path_carb

Value
dataframe with human pathway data

SelectedSample

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

select_class(auc.df, cutoff)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>auc.df</td>
<td>list of AUC value</td>
</tr>
<tr>
<td>cutoff</td>
<td>cut-off for AUC value</td>
</tr>
</tbody>
</table>

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

st_dv(DataMatrix, pathway)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DataMatrix</td>
<td>TCGA matrix</td>
</tr>
<tr>
<td>pathway</td>
<td>pathway data</td>
</tr>
</tbody>
</table>
**svm_classification**

**Value**

a matrix value for each pathway

**Examples**

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

**Description**

svm class creates a list with auc value

**Usage**

```r
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**

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