Package ‘StarBioTrek’

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Type Package

Title StarBioTrek

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Depends R (>= 3.3)

Imports SpidermiR, KEGGREST, org.Hs.eg.db, AnnotationDbi, e1071, ROCR, grDevices

Description
This tool StarBioTrek presents some methodologies to measure pathway activity and cross-talk among pathways integrating also the information of network data.

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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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average  

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  

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**

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

**Arguments**

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

**Value**

a matrix value for each pathway

**Examples**

```r
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
ginetDATA(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 (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

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,net_type=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, net_type)

Arguments
pathway pathway data as provided by getKEGGdata
net_type 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, net_type=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 pathway.

Usage

proc_path(mer)

Arguments

mer output for example of select_path_carb

Value

dataframe with human pathway data

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
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
st_dv(DataMatrix, pathway)

Arguments
DataMatrix  TCGA matrix
pathway     pathway data
**Value**

a matrix value for each pathway

**Examples**

```r
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**

```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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