Package ‘StarBioTrek’

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Title StarBioTrek
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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.
License GPL (>= 3)
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LazyData true
URL https://github.com/claudiacava/StarBioTrek
BugReports https://github.com/claudiacava/StarBioTrek/issues
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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

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)

d_s_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)

Arguments

dataFilt : TCGA matrix
pathway : pathway data
**euc_dist_crtlk**

**Value**

a matrix value for each pathway

**Examples**

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

**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**

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

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**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
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 (eg.TCGA data)
  pathway pathway data as provided by getKEGGdata
**list_path_net**

**Value**

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

**Examples**

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

**Description**

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

**Usage**

```r
list_path_net(net_type, pathway)
```

**Arguments**

- `net_type` network data as provided by getNETdata
- `pathway` pathway data as provided by getKEGGdata

**Value**

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

**Examples**

```r
list_path<-list_path_net(net_type=netw,pathway=path)
```

---

**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**

```r
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 GE_matrix
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

proc_path

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

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

selected two labels from ID barcode

Usage

```r
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

```r
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
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

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
def_class<~svm_classification(TCGA_matrix=score_euc_dist,nfs=nf,
                                normal=colnames(norm[,1:10]),
                                tumour=colnames(tumo[,1:10]))
```
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