Package ‘StarBioTrek’

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Type Package

Title StarBioTrek

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Author Claudia Cava,
Isabella Castiglioni

Maintainer Claudia Cava <`claudia.cava@ibfm.cnr.it`>

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.

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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`

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R topics documented:

`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)
```

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)
```

`euc_dist_crtlk` *For TCGA data get human pathway data and creates a measure of cross-talk among pathways*

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_dista<-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 (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)
```

`IPPI` *Multilayer analysis Cava et al. BMC Genomics 2017*

Description

IPPI function takes as input pathway and network data in order to select genes with central role in that pathway. Please see Cava et al. 2017 BMC Genomics

Usage

```
IPPI(patha, netwa)
```

Arguments

`patha`	pathway matrix Please see example path for format
`netwa`	a dataframe Please see example path for format netw

Value

a list with driver genes for each pathway

Examples

```
DRIVER_SP<-IPPI(patha=path,netwa=netw)
```

`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

`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

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

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`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

```
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]))
```

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