Package ‘StarBioTrek’

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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
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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)
```

---

**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_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 (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,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 (e.g., 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
getHumanKEGGdata 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
- 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[k,1:2],pathway=path)
```

---

**Description**

svm class creates a list with auc value

**Usage**

```r
sicm_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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