

# 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, 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** 6.0.1

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average	<i>For TCGA data get human pathway data and creates a matrix with the average of genes for each pathway.</i>
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### 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)
```

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ds_score_crtlk	<i>For TCGA data get human pathway data and creates a measure of discriminating score among pathways</i>
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**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	<i>For TCGA data get human pathway data and creates a measure of cross-talk among pathways</i>
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**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	<i>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 .</i>
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---

**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	<i>Get human KEGG pathway data and output of path_net in order to define the common genes.</i>
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---

**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	<i>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 .</i>
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---

**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	<i>Get human KEGG pathway data and network data in order to define the common gene.</i>
----------	---

---

### 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	<i>Get human KEGG pathway data and a gene expression matrix we obtain a matrix with the gene expression for only pathways given in input</i>
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---

### 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	<i>Process matrix TCGA data after the selection of pairwise pathway</i>
----------------	---

---

**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	<i>Get human KEGG pathway data.</i>
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---

**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
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**Value**

dataframe with human pathway data



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SelectedSample	<i>Select the class of TCGA data</i>
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**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	<i>Select the class of TCGA data</i>
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**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	<i>Download data</i>
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### 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	<i>For TCGA data get human pathway data and creates a measure of standard deviations among pathways</i>
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---

### 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)
```

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svm\_classification      *SVM classification for each feature*

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**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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