

Package ‘eMutPath’

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Type Package

Title eMutPath (edge-based mutation prioritization based on network
perturbation paths)

Version 0.1.0

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Description Identification of edgetic driver mutations by integrating gene
expression and protein interaction network or functional pathways.

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports outliers,igraph,stats,utils

RoxygenNote 6.0.1

NeedsCompilation no

R topics documented:

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EdgeticDys_both

Get dysregulated edges in cancer

Description

Identify the dysregulated edges for each sample

Usage

```
#Identifying the dysregulated edges in both two conditions
Input.exp=GetExampleData(exampleData="Exp.input")
#obtain the sample label
Cancer_s=GetExampleData(exampleData="Cancer_s")
Normal_s=GetExampleData(exampleData="Normal_s")
#obtain the protein interaction network
Network=GetExampleData(exampleData="network")
#identify the dysregulated edges
DysCN=EdgeticDys_CN(Input.exp,Network,thr=0.01)
Input.exp=Input.exp[,Cancer_s]
DysC=EdgeticDys_CN(Input.exp,Network,thr=0.01)
Dys.net=EdgeticDys_both(DysCN,DysC)
```

Arguments

DysCN	The dysregulated network in cancer vs normal
DysC	The dysregulated network for specific cancer sample

EdgeticDys_CN

Identify the dysregulated network edges

Description

Identify the dysregulated edges for each sample

Usage

```
#Identifying the dysregulated edges between cancer and normal samples
Input.exp=GetExampleData(exampleData="Exp.input")
#obtain the sample label
Cancer_s=GetExampleData(exampleData="Cancer_s")
Normal_s=GetExampleData(exampleData="Normal_s")
#obtain the protein interaction network
Network=GetExampleData(exampleData="network")
#identify the dysregulated edges
DysCN=EdgeticDys_CN(Input.exp,Network,thr=0.01)
```

Arguments

Input.exp	The gene expression matrix
Network	The protein interaction network
thr	The significant level for grubbs's test

Value

All.sam.dys The dysregulated edges for each sample

envData	<i>Get the envData</i>
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Description

Get the env data

getEdgeticDriver	<i>Identify the edgetic driver mutations</i>
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Description

Identify the driver mutations that perturb the protein interaction network

Usage

```
#Identifying the mutation mediated-dysregulated edges in both two conditions
#obtain the data for gene expression.
Input.exp=GetExampleData(exampleData="Exp.input")
#obtain the sample label
Cancer_s=GetExampleData(exampleData="Cancer_s")
Normal_s=GetExampleData(exampleData="Normal_s")
#obtain the protein interaction network
Network=GetExampleData(exampleData="network")
#obtain the mutation data
Mut=GetExampleData(exampleData="mut")
DysCN=EdgeticDys_CN(Input.exp,Network,thr=0.01)
Input.exp2=Input.exp[,Cancer_s]
DysC=EdgeticDys_CN(Input.exp2,Network,thr=0.01)
Dys.net=EdgeticDys_both(DysCN,DysC)
Driver.mut=getEdgeticDriver(Dys.net,Mut,alpha=0.05,n.sim=1000)
```

Arguments

Dysnet	Dysregulated network for samples
Mut	The mutation files for samples
alpha	The significance level
n.sim	The simulation times defined by users

Value

MutPPI the mutation perturbed PPIs in cancer samples

Getenvir	<i>Get the envir data</i>
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Description

Get the envir data

GetExampleData	<i>Load example datasets</i>
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Description

The default example files

Usage

```
#obtain the data for gene expression.
Input.exp=GetExampleData(exampleData="Exp.input")
#obtain the sample label
Cancer_s=GetExampleData(exampleData="Cancer_s")
Normal_s=GetExampleData(exampleData="Normal_s")
#obtain the protein interaction network
Network=GetExampleData(exampleData="network")
#obtain the mutation data
Mut=GetExampleData(exampleData="mut")
```

Arguments

exampleData	Indicate which type of default datasets to import
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Value

return the default datasets required by the users

grubbs.flag	<i>Identify the outliers</i>
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Description

Identify the outliers

Usage

```
grubbs.flag(x, thr)
```

Arguments

x	Vector
thr	significant level

`initialize_data`*Get the environment datasets*

Description

Get the envir data

Usage

```
initialize_data()
```

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