# Package 'EdgeticDriver'

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**Type** Package

**Title** Identification of edgetic driver mutations by integrating gene
 expression and protein interaction network

**Version** 0.1.0

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**Description** More about what it does (maybe more than one line)
 Use four spaces when indenting paragraphs within the Description.

**License** GPL>=2

**Encoding** UTF-8

**LazyData** true

**Imports** outliers,igraph

**RoxygenNote** 6.0.1

# R topics documented:

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EdgeticDys_both          *Get dysregulated edges in cancer*

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## Description

 Identify the dysregulated edges for each sample

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## Usage

```
#Identifying the dysregulated edges in both two conditions
Input.exp=GetExampleData(exampleData="Exp.input")
# view first rows of data
head(Input.exp)
#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 |

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| EdgeticDys_CN | *Identify the dysregulated network edges* |
|---|---|

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## Description

Identify the dysregulated edges for each sample

## Usage

```
#Identifying the dysregulated edges between cancer and normal samples
Input.exp=GetExampleData(exampleData="Exp.input")
# view first rows of data
head(Input.exp)
#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 dyregulated edges for each sample

| getEdgeticDriver | *Identify the edgetic driver mutations* |
| --- | --- |

## Description

Identify the driver mutations that perturbe 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")
# view first rows of data
head(Input.exp)
#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

| GetExampleData | *Load example datasets* |
| --- | --- |

## Description

The default example files

## Usage

```
#obtain the data for gene expression.
library(EdgeticDriver)
Input.exp=GetExampleData(exampleData="Exp.input")
view first rows of data
head(Input.exp)
#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

## Value

return the default datasets required by the users

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grubbs.flag    *Identify the outliers*

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## Description

Identify the outliers

## Usage

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

## Arguments

x           Vector
thr         significant level

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initialize_data    *Get the environment datasets*

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## Usage

```
initialize_data()
```

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