Package 'SRGnet'

October 16, 2018

Title SRGnet: An R package for studying synergistic response to gene
mutations from transcriptomics data from transcriptomics data

Version 1.6.0

Description

We developed SRGnet to analyze synergistic regulatory mechanisms in transcriptome profiles that act to enhance the overall cell response to combination of mutations, drugs or environmental exposure. This package can be used to identify regulatory modules downstream of synergistic response genes, prioritize synergistic regulatory genes that may be potential intervention targets, and contextualize gene perturbation experiments.

Depends R (>= 3.3.1), EBcoexpress, MASS, igraph, pvclust (>= 2.0-0),
gbm (>= 2.1.1), limma, DMwR (>= 0.4.1), matrixStats, Hmisc

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 5.0.1.9000

biocViews Software, StatisticalMethod, Regression

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

1

Differentially_expressed_genes

> *List of differentially expressed genes in a murine colon cancer model under single and combined mutations of mp53 and Ras*

Description

List of differentially expressed genes measured in young adult mouse colonic epithelium (YAMC) in four conditions: bleo/Neo vector control, mu-tant p53-expressing (mp53), activated Ras-expressing, and both mutant genes (mp53/Ras) cells using Affymetrix GeneChip® Mouse Genome 430 2.0 Arrays (GSE9199) (PMC2613942).

Usage

```
Differentially_expressed_genes
```

Format

An object of class `data.frame` with 540 rows and 4 columns.

PLCRG

> *List of synergistic response genes in a murine colon cancer model under single and combined mutations of mp53 and Ras*

Description

List of differentially expressed and synergistic response genes measured in young adult mouse colonic epithelium (YAMC) in four conditions: bleo/Neo vector control, mu-tant p53-expressing (mp53), activated Ras-expressing, and both mutant genes (mp53/Ras) cells using Affymetrix GeneChip® Mouse Genome 430 2.0 Arrays (GSE9199) (PMC2613942).

Usage

```
PLCRG
```

Format

An object of class `data.frame` with 85 rows and 2 columns.

SRGnet *Synergistic response to gene mutations specific network*

Description

The "SRGnet" can be applied if user has transcriptomic profile, list of differentially expressed genes and synergistic response genes as inputs. The function can be ran in two mode of Slow or Fast. In fast mode, step of expectation maximization for estimation of hyperparameters is omitted. User can run the function in fast or slow mode by using the "F" or "S" as input of "SRGnet()" function, respectively [e.g. SRGnet("F")]. SRGnet returns the topology of SRMs network and ranked list of genes in network based on differential connectivity score, which can be found in home directory of package under title of "DC_score" and "Topology_of_integrated_network" as text files.

Usage

```
SRGnet(type_of_run)
```

Arguments

type_of_run   A character, "F": Fast or "S": Slow.

Author(s)

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Examples

```
{
data(Differentially_expressed_genes)
data(Transcriptomics)
data(PLCRG)
SRGnet("F") #Fast run
}
```

Transcriptomics *Murine colon cancer transcriptomics profile under single and combined mutations of mp53 and Ras*

Description

Young adult mouse colonic epithelium (YAMC) transcriptomics profile in four conditions: YAMC control, mu-tant p53-expressing (mp53), activated Ras-expressing, and both mutant genes (mp53/Ras) cells using Affymetrix GeneChip® Mouse Genome 430 2.0 Arrays (GSE9199) (PMC2613942).

Usage

```
Transcriptomics
```

Format

An object of class matrix with 475 rows and 40 columns.

Index