Package: CITMIC (via r-universe)

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Type Package

Title Estimation of Cell Infiltration Based on Cell Crosstalk

Version 0.1.1

Maintainer Junwei Han <`hanjunwei1981@163.com`>

Description A systematic biology tool was developed to identify cell infiltration via an Individualized Cell crosstalk network. 'CITMIC' first constructed a weighted cell crosstalk network by integrating Cell-target interaction information, biological process data from the Gene Ontology (GO) database, and gene transcriptomic data in a specific sample, and then, it used a network propagation algorithm on the network to identify cell infiltration for the sample. Ultimately, cell infiltration in the patient dataset was obtained by normalizing the centrality scores of the cells.

License GPL (>= 2)

Encoding UTF-8

LazyData true

Depends R (>= 2.10)

Imports fastmatch, igraph, parallel, stats

RoxygenNote 7.2.3

Suggests knitr, rmarkdown

VignetteBuilder knitr

Repository https://hanjunwei-lab.r-universe.dev

RemoteUrl https://github.com/hanjunwei-lab/citmic

RemoteRef HEAD

RemoteSha fc6ea713d92d876d1cc10c97307736a6c7c628bb

Contents

`CITMIC` *CITMIC*

Description

The function "CITMIC" is used to identify cell infiltration in tumor microenvironment by calculating intercellular crosstalk.

Usage

```
CITMIC(GEP,weighted = TRUE,base = 10,damping=0.90,cl.cores=1,cell.type=NULL)
```

Arguments

`GEP`	An example gene expression profile.
`weighted`	This parameter specifies whether to create a weighted graph for the cell crosstalk network. If null, an unweighted graph is created, and the elements of the adjacency matrix indicate the number of edges between vertices. If true, a weighted graph is created(default: TRUE).
`base`	Standardized log base of data for improving data distribution(default: 10).
`damping`	Restart the probability of the random-walk algorithm (default: 0.9).
`cl.cores`	The number of CPU cores applied to this task(default:1).
`cell.type`	Preset the relevant cell type (e.g. if the solid tumour tissue does not contain 'HSC', it is better to remove it when we preset it.)

Value

A data frame containing the cell infiltration score for each sample.

Examples

```
# Obtain the example data
GEP<-GetData_CITMIC("GEP")
# Run the function
lnScore<-CITMIC(GEP,weighted = TRUE,base = 10,damping=0.90,cl.cores=1,cell.type=NULL)
```

`CITMIC_Data` *An environment variable that includes some example data*

Description

matirx_cell_go_inter:A matrix of Jaccard score between cells and GOBP. matirx_cell_go_jaccard:A matrix consisting of genes shared by cells targets and GOBP. GEP:An example gene expression profile.

Usage

```
CITMIC_Data
```

Format

An environment variable

`GetData_CITMIC` *GetData_CITMIC*

Description

Get the example data

Usage

```
GetData_CITMIC(Data)
```

Arguments

`Data`	A character should be one of "GEP", "matrix_cell_go_inter", "matrix_cell_go_jaccard"

Value

Data

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