

Package ‘CITMIC’

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Type Package

Title Estimation of Cell Infiltration Based on Cell Crosstalk

Version 0.1.0

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Description A systematic biology tool was developed to identify cell infiltration via Individualized Cell-Cell interaction network. 'CITMIC' first constructed a weighted cell interaction network through integrating Cell-target interaction information, molecular function data from Gene Ontology (GO) database and gene transcriptomic data in 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.

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Encoding UTF-8

LazyData true

Depends R (>= 2.10)

Imports fastmatch, igraph, parallel, stats

RoxygenNote 7.2.3

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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 CITMIC

CITMIC

Description

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

Usage

```
CITMIC(GEP, damping=0.90)
```

Arguments

GEP	An example gene expression profile
damping	Restart the probability of the random-walk algorithm (default: 0.9).

Value

cell infiltration score

Examples

```
# Obtain the example data
GEP<-GetData_CITMIC("GEP")
# Run the function
lnScore<-CITMIC(GEP, damping=0.90)
```

 CITMIC_Data

An environment variable that includes some example data

Description

An environment variable that includes some example data. `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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