

Package ‘CITMIC’

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Type Package

Title Estimation of Cell Infiltration Based on Cell Crosstalk

Version 0.1.3

Maintainer Junwei Han <hanjunwei1981@163.com>

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 7.3.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Junwei Han [aut, cre, cph],
Xilong Zhao [aut]

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Contents

CITMIC	2
CITMIC_Data	3
GetData_CITMIC	3

Index	4
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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,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 tumor tissue does not contain 'HSC', it is better to remove it when we preset it.). When cell.type = NULL, all 86 cell types from the evaluation project are used by default.

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	<i>An environment variable that includes some example data</i>
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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	<i>GetData_CITMIC</i>
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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

Index

* **datasets**

CITMIC_Data, [3](#)

CITMIC, [2](#)

CITMIC_Data, [3](#)

GetData_CITMIC, [3](#)