

# Package ‘CITMIC’

January 20, 2025

**Type** Package

**Title** Estimation of Cell Infiltration Based on Cell Crosstalk

**Version** 0.1.2

**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** 7.3.2

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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

**Repository** CRAN

**Date/Publication** 2024-11-08 12:20:02 UTC

## Contents

CITMIC . . . . .	2
CITMIC_Data . . . . .	3
GetData_CITMIC . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

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

---

**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>
----------------	-----------------------

---

**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