

Package ‘PhitestR’

October 12, 2022

Type Package

Title Analyzing the Heterogeneity of Single-Cell Populations

Version 0.2.0

Description A bioinformatics method developed for analyzing the heterogeneity of single-cell populations. Phitest provides an objective and automatic method to evaluate the performance of clustering and quality of cell clusters.

License GPL-3

Encoding UTF-8

RoxygenNote 7.1.1

Imports parallel, fitdistrplus

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

phitest 2

Index 3

phitest

Applying the Phitest method to a count matrix

Description

Phitest for analyzing the heterogeneity of single-cell populations

Usage

```
phitest(object, label, ncores = 1, min.cell = 10)
```

Arguments

| | |
|----------|---|
| object | A matrix of single-cell UMI counts (rows for genes and columns for cells). |
| label | A character or numeric vector of cluster labels. Length should be the same as cell number and order should match the order in object. |
| ncores | Number of cores used for parallel computation. |
| min.cell | An integer specifying a threshold to filter genes. Genes expressed in fewer than min.cell cells are filtered out. |

Value

A list of two elements: pval contains the P values, and par contains the estimated parameters.

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Index

phitest, [2](#)