Package 'PhitestR'

January 21, 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	*Appling 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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