Package ‘PhitestR’

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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

Author Wei Vivian Li [aut, cre] (<`https://orcid.org/0000-0002-2087-2709`>)

Maintainer Wei Vivian Li <`vivian.li@rutgers.edu`>

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Contents

`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.

Author(s)

Wei Vivian Li, <`vivian.li@rutgers.edu`>

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