

Package ‘PhitestR’

August 3, 2021

Type Package

Title Analyzing the Heterogeneity of Single-Cell Populations

Version 0.1.0

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, Seurat

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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 phitest

The generic function for the Phitest method

Description

Phitest for analyzing the heterogeneity of single-cell populations

Usage

```
phitest(object, ...)
```

Arguments

object	An object of single-cell data
...	Other parameters to be passed to the function.

Value

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

Author(s)

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 phitest.matrix

Applying the Phitest method with a count matrix

Description

Phitest for analyzing the heterogeneity of single-cell populations

Usage

```
## S3 method for class 'matrix'
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 <code>min.cell</code> cells are filtered out.

Value

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

Author(s)

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`phitest.Seurat`*Applying the Phitest method with a Seurat object*

Description

Phitest for analyzing the heterogeneity of single-cell populations

Usage

```
## S3 method for class 'Seurat'  
phitest(object, ncores = 1, min.cell = 10)
```

Arguments

<code>object</code>	A Seurat object.
<code>ncores</code>	Number of cores used for parallel computation.
<code>min.cell</code>	An integer specifying a threshold to filter genes. Genes expressed in fewer than <code>min.cell</code> cells are filtered out.

Value

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

Author(s)

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