

# Package ‘PhitestR’

July 21, 2025

**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] (ORCID:  
<<https://orcid.org/0000-0002-2087-2709>>)

**Maintainer** Wei Vivian Li <[vivian.li@rutgers.edu](mailto:vivian.li@rutgers.edu)>

**Repository** CRAN

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phitest

*Applying the Phitest method to a count matrix*

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**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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