Package: MultiK (via r-universe)

May 23, 2026

Type Package

Title Multi-Resolution Consensus Clustering for Single-Cell RNA-seq

Version 1.0.0

Description Identifies optimal cluster numbers in single-cell RNA-seq data through subsampling-based consensus clustering. MultiK performs repeated subsampling and clustering across multiple resolution parameters, then evaluates clustering stability using the Proportion of Ambiguous Clustering (PAC) metric. Statistical significance of cluster separability is assessed using SigClust.

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Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.3.3

URL `https://github.com/Zaoqu-Liu/MultiK`, `https://zaoqu-liu.github.io/MultiK`

BugReports `https://github.com/Zaoqu-Liu/MultiK/issues`

Depends R (>= 4.0.0)

Imports Seurat (>= 4.0.0), sigclust, ggplot2, cowplot, ggrepel, gridExtra, scales, stats, utils, methods, future, future.apply, parallel

Suggests testthat (>= 3.0.0), knitr, rmarkdown

VignetteBuilder knitr

Config/pak/sysreqs cmake libglpk-dev make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev python3 zlib1g-dev

Repository https://zaoqu-liu.r-universe.dev

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RemoteUrl https://github.com/Zaoqu-Liu/MultiK

RemoteRef main

RemoteSha 780a0075c89a81017655fd980eb72edd6a4cd934

Contents

`CalcSigClust` *Pairwise SigClust tests between clusters*

Description

Performs statistical significance testing for cluster separability using the SigClust method on all pairwise combinations of clusters.

Usage

```
CalcSigClust(seu, clusters, nsim = 100, nfeatures = 2000, cores = 1)
```

Arguments

`seu`	A Seurat object
`clusters`	Vector of cluster assignments
`nsim`	Number of simulations for SigClust. Default is 100
`nfeatures`	Number of variable features. Default is 2000
`cores`	Number of cores for parallel processing. Default is 1

Value

A symmetric matrix of p-values from pairwise SigClust tests. Diagonal elements are NA. P-values indicate significance of cluster separation.

`DiagMultiKPlot` *Diagnostic plots for optimal K selection*

Description

Generates three diagnostic plots from MultiK results: (1) Frequency distribution of K values (2) rPAC scores across K (3) Stability vs frequency trade-off plot

Usage

```
DiagMultiKPlot(ks, consensus)
```

Arguments

`ks`	Vector of K values from MultiK output
`consensus`	List of consensus matrices from MultiK output

Value

Combined ggplot object with 3 panels. Also prints optimal K to console.

`getClusters` *Extract cluster assignments for specified K values*

Description

Performs Seurat clustering and retrieves cluster assignments for the specified optimal K values.

Usage

```
getClusters(seu, optK, nPC = 30, k.param = 20, nfeatures = 2000)
```

Arguments

`seu`	A Seurat object
`optK`	Vector of target cluster numbers
`nPC`	Number of principal components. Default is 30
`k.param`	Number of nearest neighbors. Default is 20
`nfeatures`	Number of variable features. Default is 2000

Value

A list containing:

`clusters`	Matrix of cluster assignments (cells x K values)
`resolution`	Resolution parameters used for each K

`MultiK` *MultiK: Determine optimal cluster numbers via consensus clustering*

Description

Performs subsampling-based consensus clustering across multiple resolution parameters to identify robust cluster numbers in single-cell RNA-seq data.

Usage

```
MultiK(
  seu,
  resolution = seq(0.05, 2, 0.05),
  nPC = 30,
  reps = 100,
  pSample = 0.8,
  k.param = 20,
  nfeatures = 2000,
  seed = NULL,
  cores = 1
)
```

Arguments

`seu`	A Seurat object
`resolution`	Numeric vector of resolution parameters for Seurat clustering. Default is seq(0.05, 2, 0.05)
`nPC`	Number of principal components. Default is 30
`reps`	Number of subsampling iterations. Default is 100
`pSample`	Proportion of cells to subsample. Default is 0.8
`k.param`	Number of nearest neighbors for graph construction. Default is 20
`nfeatures`	Number of variable features to select. Default is 2000
`seed`	Random seed for reproducibility. Default is NULL
`cores`	Number of cores for parallel processing. Default is 1

Value

A list containing:

`k`	Vector of K values from all clustering runs
`clusters`	Clustering results for each K
`consensus`	Consensus matrix for each K

`p3cl` *Three Cell Line Mixture Dataset*

Description

A Seurat object containing single-cell RNA-seq data from a mixture of three cell lines (H2228, H1975, HCC827). This dataset is used for demonstrating the MultiK workflow.

Usage

```
p3cl
```

Format

A Seurat object with approximately 2,600 cells and the following structure:

assays RNA assay with count and normalized data

meta.data Cell metadata including cell line annotations

Source

Dong et al. 2019 (PMID: 31925417)

Examples

```
data(p3cl)
p3cl
```

`PlotSigClust` *Visualize SigClust results with dendrogram and heatmap*

Description

Generates a combined visualization showing: (1) Hierarchical clustering dendrogram of cluster centroids (2) Heatmap of pairwise SigClust p-values

Usage

```
PlotSigClust(seu, clusters, pval, nfeatures = 2000)
```

Arguments

`seu`	A Seurat object
`clusters`	Vector of cluster assignments
`pval`	P-value matrix from CalcSigClust
`nfeatures`	Number of variable features. Default is 2000

Details

Node shapes indicate statistical significance: - Filled circles: significant separation ($p < 0.05$) - Open circles: non-significant separation ($p >= 0.05$)

Value

Invisibly returns NULL; displays the combined plot

Index