

Package ‘scds’

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Type Package

Title In-Silico Annotation of Doublets for Single Cell RNA Sequencing Data

Version 1.0.0

Description In single cell RNA sequencing (scRNA-seq) data combinations of cells are sometimes considered a single cell (doublets). The scds package provides methods to annotate doublets in scRNA-seq data computationally.

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Encoding UTF-8

biocViews SingleCell, RNASeq, QualityControl, Preprocessing, Transcriptomics, GeneExpression, Sequencing, Software, Classification

RoxygenNote 6.1.1

Depends R (>= 3.6.0)

Imports Matrix, S4Vectors, SingleCellExperiment, SummarizedExperiment, xgboost, methods, stats

Suggests BiocStyle, knitr, rsvd, Rtsne, scater, cowplot

VignetteBuilder knitr

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bcds *Find doublets/multiplets in UMI scRNA-seq data;*

Description

Annotates doublets/multiplets using a binary classification approach to discriminate artificial doublets from original data.

Usage

```
bcds(sce, ntop = 500, srat = 1, verb = FALSE, retRes = FALSE,
     nmax = "tune", varImp = FALSE)
```

Arguments

sce	single cell experiment (SingleCellExperiment) object to analyze; needs counts in assays slot.
ntop	integer, indicating number of top variance genes to consider. Default: 500
srat	numeric, indicating ratio between original number of "cells" and simulated doublets; Default: 1
verb	progress messages. Default: FALSE
retRes	logical, should the trained classifier be returned? Default: FALSE
nmax	maximum number of training rounds; integer or "tune". Default: "tune"
varImp	logical, should variable (i.e., gene) importance be returned? Default: FALSE

Value

sce input sce object SingleCellExperiment with doublet scores added to colData as "bcds_score" column, and possibly more (details)

Examples

```
data("sce_chcl")
## create small data set using only 100 cells
sce_chcl_small = sce_chcl[, 1:100]
sce_chcl_small = bcds(sce_chcl_small)
```

cxds *Find doublets/multiplets in UMI scRNA-seq data;*

Description

Annotates doublets/multiplets using co-expression based approach

Usage

```
cxds(sce, ntop = 500, binThresh = 0, verb = FALSE, retRes = FALSE)
```

Arguments

sce	single cell experiment (SingleCellExperiment) object to analyze; needs counts in assays slot.
ntop	integer, indicating number of top variance genes to consider. Default: 500
binThresh	integer, minimum counts to consider a gene "present" in a cell. Default: 0
verb	progress messages. Default: FALSE
retRes	logical, whether to return gene pair scores & top-scoring gene pairs? Default: FALSE.

Value

sce input sce object SingleCellExperiment with doublet scores added to colData as "cxds_score" column.

Examples

```
data("sce_chcl")
## create small data set using only 100 cells
sce_chcl_small = sce_chcl[, 1:100]
sce_chcl_small = cxds(sce_chcl_small)
```

cxds_bcds_hybrid	<i>Find doublets/multiples in UMI scRNA-seq data;</i>
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Description

Annotates doublets/multiplets using the hybrid approach

Usage

```
cxds_bcds_hybrid(sce, cxds_args = NULL, bcds_args = NULL)
```

Arguments

sce	single cell experiment (SingleCellExperiment) object to analyze; needs counts in assays slot.
cxds_args	list, arguments for cxds function in list form. Default: NULL
bcds_args	list, arguments for bcds function in list form. Default: NULL

Value

sce input sce object SingleCellExperiment with doublet scores added to colData as "hybrid_score" column.

Examples

```
data("sce_chcl")
## create small data set using only 100 cells
sce_chcl_small = sce_chcl[, 1:100]
sce_chcl_small = cxds_bcds_hybrid(sce_chcl_small)
```

cxds_getTopPairs	<i>Extract top-scoring gene pairs from an SingleCellExperiment where cxds has been run</i>
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Description

Extract top-scoring gene pairs from an SingleCellExperiment where cxds has been run

Usage

```
cxds_getTopPairs(sce, n = 100)
```

Arguments

sce	single cell experiment to analyze; needs "counts" in assays slot.
n	integer. The number of gene pairs to extract. Default: 100

Value

matrix Matrix with two columns, each containing gene indexes for gene pairs (rows).

sce_chcl	<i>Example single cell experiment (SingleCellExperiment) object</i>
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Description

Example data set, created by randomly sampling genes and cells from a real data set (ch_cl, i.e., the cell lines data from https://satijalab.org/seurat/hashing_vignette.html). Contains raw counts in the counts assay slot.

Usage

```
sce_chcl
```

Format

a single cell experiment object (SingleCellExperiment) with raw counts in the counts in assays, and colData with experimental annotations.

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