R documentation

of 'loadFinalSCProfiles.Rd'

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`loadFinalSCProfiles` *Load final real scRNA-Seq data into a* `DigitalDLSorter` *object*

Description

Load scRNA-Seq data into a `DigitalDLSorter` from file stored on disk or from a `SingleCellExperiment` object. Provided data must be composed by three pieces of information:

- Single-cell counts: genes in rows and cells in columns.
- Cells metadata: with annotations (columns) for each cell (rows).
- Genes metadata with annotations (columns) for each gene (rows).

In the case that data is provided from files, `single.cell.real` argument must be a vector of three elements ordered so that the first file corresponds to counts, the second to cells metadata and the last to genes metadata. On the other hand, if data is provided as `SingleCellExperiment`, the object must contains single-cell counts in `assay` slot, cells metadata in `colData` slot and genes metadata in `rowData`.

Usage

```
loadFinalSCProfiles(
  single.cell.final,
  cell.ID.column = 1,
  gene.ID.column = 1,
  min.counts = 0,
  min.cells = 0,
  project = "DigitalDLSorterProject"
)
```

Arguments

`single.cell.final`
: If data is provided from files, `single.cell.real` must be a vector with three elements: single-cell counts, cells metadata and genes metadata. If data is provided from a `SingleCellExperiment` object, singlecell counts must be in `assay` slot, cells metadata in `colData` and genes metadata in `rowData`.

`cell.ID.column`
: Name or number of the column in cells.metadata corresponding with cell names in expression matrix.

`gene.ID.column`
: Name or number of the column in genes.metadata corresponding with the notation used for features/genes.

`min.counts`
: Minimum gene counts to filter (0 by default).

`min.cells`
: Minimum of cells with more than min.counts (0 by default).

`project`
: Name of the project for `DigitaDLSorter` object.

Details

#' The difference with `loadFinalSCProfiles` is that data loaded with this functions will be used for estimating ZINB-WaVE parameters and simulating new single-cell profiles in order to increase the signal of cell types. On the other side, `loadFinalSCProfiles` loads data on `single.cell.final` slot, so this scRNA-seq profiles will be used directly for simulating bulk samples. In this case, data must be enough cells for each cell type and enough cells for simulating bulk profiles.

See Also

`simSingleCellProfiles`

Examples

```
DDLSChung <- loadFinalSCProfiles(
  single.cell.real = sc.chung.breast,
  cell.ID.column = "Cell_ID",
  gene.ID.column = "external_gene_name",
  min.cells = 0,
  min.counts = 0,
  project = "Chung_example"
)
```

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