R documentation

of 'simSingleCellProfiles.Rd'

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simSingleCellProfiles

Simulate new single-cell expression profiles using the estimated ZINB parameters.

Description

Simulate single-cell expression profiles by randomly sampling from a negative binomial distribution using ZINB parameters estimated by ZINB-WaVE model and introducing dropouts by sampling from a binomial distribution with ZINB-WaVE model estimated.

Usage

```
simSingleCellProfiles(
  object,
  cell.ID.column,
  cell.type.column,
  n.cells,
  verbose = TRUE
)
```

Arguments

object   DigitalDLSorter object with single.cell.real and zinb.params slots.

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

cell.type.column
                Name or number of the column in cells metadata corresponding with the cell type of each cell.

n.cells   Number of simulated cells generated by cell type (i.e. if you have 10 different cell types on your dataset, if n.cells = 100, then 1000 cell profiles will be simulated).

verbose   Show informative messages during the execution.

Details

Before this step, see estimateZinbwaveParams. As described in Torroja and Sanchez-Cabo, 2019, this function simulates a determined number of transcriptional profiles for each cell type provided by randomly sampling from a negative binomial distribution with μ and θ estimated parameters and introducing dropouts by sampling from a binomial distribution with pi probability. All paramteres are estimated from single-cell real data using estimateZinbwaveParams function. It uses the ZINB-WaVE model (Risso et al., 2018). For more details about the model, see estimateZinbwaveParams.

Value

A DigitalDLSorter object with single.cell.final slot containing a SingleCellExperiment object with the simulated single-cell profiles.

References

Risso, D., Perraudeau, F., Gribkova, S. et al. (2018). A general and flexible method for signal extraction from single-cell RNA-seq data. Nat Commun 9, 284. doi: 10.1038/s41467-017-02554-5.

Torroja, C. y Sánchez-Cabo, F. (2019). digitalDLSorter: A Deep Learning algorithm to quantify immune cell populations based on scRNA-Seq data. Frontiers in Genetics 10, 978. doi: 10.3389/fgene.2019.00978

See Also

estimateZinbwaveParams

Examples

```
DDLSChungSmall <- simSingleCellProfiles(
  object = DDLSChungSmall,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_type",
  n.cells = 10,
  verbose = TRUE
)
```

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