

R documentation

of ‘estimateZinbwaveParams.Rd’

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estimateZinbwaveParams

Estimate parameters for ZINB-WaVE model for simulating new single-cell expression profiles.

Description

Estimate parameters for the ZINB-WaVE model from a real single-cell data set using ZINB-WaVE model.

Usage

```
estimateZinbwaveParams(  
  object,  
  cell.ID.column,  
  gene.ID.column,  
  cell.type.column,  
  cell.cov.columns,  
  gene.cov.columns,  
  set.type = "All",  
  threads = 1,  
  verbose = TRUE  
)
```

Arguments

object	DigitalDLSorter object with a <code>single.cell.real</code> slot.
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.
cell.type.column	Name or number of the column in cells metadata corresponding with cell type of each cell.

<code>cell.cov.columns</code>	Name or number of columns in cells metadata that will be used as covariates in the model during the estimation.
<code>gene.cov.columns</code>	Name or number of columns in genes metadata that will be used as covariates in the model during estimation.
<code>set.type</code>	Cell type to evaluate. 'All' by default.
<code>threads</code>	Number of threads used for the estimation. For setting the parallel environment BiocParallel package is used.
<code>verbose</code>	Show informative messages during the execution.

Details

ZINB-WaVE is a flexible model for zero-inflated count data. This function carries out the model fit to real single-cell data modeling Y_{ij} (the count of feature j for sample i) as a random variable following a zero-inflated negative binomial (ZINB) distribution. The estimated parameters will be used for the simulation of new single-cell expression profiles by sampling a negative binomial distribution and introducing dropouts from a binomial distribution. To do this, [DigitalDLSorter](#) uses `zinbEstimate` function from `splatter` package (Zappia et al., 2017), that is a wrapper around `zinbFit` function from `zinbwave` package (Risso et al., 2018). For more details about the model, see Risso et al., 2018.

Value

A `DigitalDLSorter` object with `zinb.params` slot containing a `ZinbParams` object. This object contains the estimated ZINB parameters from real single-cell data.

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: doi.org/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](https://doi.org/10.3389/fgene.2019.00978)
- Zappia, L., Phipson, B. y Oshlack, A. Splatter: simulation of single-cell RNA sequencing data. *Genome Biol.* 2017; 18: 174.

See Also

[simSingleCellProfiles](#)

Examples

```
## Not run:
DDLSClungSmall <- estimateZinbwaveParams(
  object = DDLSClungSmall,
  cell.ID.column = "Cell_ID",
  gene.ID.column = "external_gene_name",
  cell.type.column = "Cell_type",
  cell.cov.columns = c("Patient", "Sample_type"),
  gene.cov.columns = "gene_length",
  verbose = TRUE
```

)

End (Not run)

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