

R documentation

of ‘calculateEvalMetrics.Rd’

September 3, 2020

calculateEvalMetrics

Calculate evaluation metrics for bulk RNA-seq samples from test data.

Description

Calculate evaluation metrics for bulk RNA-seq samples from test data in order to know the performance of the model. By default, absolute error (AbsErr), proportional absolute error (ppAbsErr), squared error (SqrErr) and proportional squared error (ppSqrErr) are calculated for each test sample. Moreover, each one of these metrics are aggregated using their mean values by three criteria: each cell type (CellType), probability bins of 0.1 (pBin), number of different cell types present in the sample nMix and a combination of pBin and nMix (pBinNMix). Finally, the process is repeated only for bulk samples, removing single-cell profiles from the evaluation. Evaluation metrics are available in eval.stats.samples slot of DigitalDLSorterDNN object (trained.model of DigitalDLSorter object).

Usage

```
calculateEvalMetrics(object, metrics = c("MAE", "MSE"))
```

Arguments

object	DigitalDLSorter object with single.cell.final and DigitalDLSorterDNN slots.
metrics	Metrics used for evaluating the performance of the model. Mean absolute error (MAE) and mean squared error (MSE) by default.

Value

A [DigitalDLSorter](#) object with trained.model slot containing a DigitalDLSorterDNN object with eval.stats.samples slot.

See Also

[distErrorPlot](#) [corrExpPredPlot](#) [blandAltmanLehPlot](#) [barErrorPlot](#)

Examples

```
DDLSchung <- calculateEvalMetrics(  
  object = DDLSchung  
)
```

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