

R documentation

of 'deconvDigitalDLSorterObj.Rd'

September 3, 2020

deconvDigitalDLSorterObj

Deconvolute bulk gene expression samples (bulk RNA-Seq).

Description

Deconvolute bulk gene expression samples (bulk RNA-Seq) enumerating and quantifying the proportion of cell types present in a bulk sample. This function needs a `DigitalDLSorter` object with a trained DNN model (`trained.model` slot) and bulk samples for deconvoluting in `deconv.data` slot.

Usage

```
deconvDigitalDLSorterObj(  
  object,  
  name.data,  
  batch.size = 128,  
  normalize = TRUE,  
  simplify.set = NULL,  
  simplify.majority = NULL,  
  verbose = TRUE  
)
```

Arguments

<code>object</code>	<code>DigitalDLSorter</code> object with <code>trained.data</code> and <code>deconv.data</code> slots.
<code>name.data</code>	Name of the data store in <code>DigitalDLSorter</code> object. If it is not provided, the first data set will be used.
<code>batch.size</code>	Number of samples per gradient update. If unspecified, <code>batch.size</code> will default to 128.
<code>normalize</code>	Normalize data before deconvolution. <code>TRUE</code> by default.
<code>simplify.set</code>	List specifying which cell types should be compressed into a new label whose name will be the list item. See examples for details. The results are stored in a list with normal and <code>simpli.majority</code> results (if provided). The name of the element in the list is 'simpli.set'.

`simplify.majority` List specifying which cell types should be compressed into the cell types with greater proportion in each sample. Unlike `simplify.set`, it allows to maintain the complexity of the results while compressing the information, because it is not created a new label. The results are stored in a list with normal and `simpli.set` results (if provided). The name of the element in the list is '`simpli.majority`'.

`verbose` Show informative messages during the execution.

Details

This function is oriented for users that have trained a DNN model using their own data. If you want to use a pre-trained model, see [deconvDigitalDLSorter](#).

Value

A `data.frame` with samples (i) as rows and cell types (j) as columns. Each entry represents the proportion of j cell type in i sample.

References

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

[trainDigitalDLSorterModel](#) [DigitalDLSorter](#)

Examples

```
## simplify arguments
simplify <- list(Tumor = c("ER+", "HER2+", "ER+/HER2+", "TNBC"),
                Bcells = c("Bmem", "BGC"))

## all results are stored in DigitalDLSorter object
DDLSC Chung <- deconvDigitalDLSorterObj(
  object = DDLSC Chung,
  name.data = "TCGA.small",
  normalize = TRUE,
  simplify.set = simplify,
  simplify.majority = simplify
)
```

Index

deconvDigitalDLSorter, [2](#)
deconvDigitalDLSorterObj, [1](#)
DigitalDLSorter, [1](#), [2](#)

trainDigitalDLSorterModel, [2](#)
trained.model, [1](#)