

Package: SCIBER (via r-universe)

August 24, 2024

Type Package

Title Single-Cell Integrator and Batch Effect Remover

Version 0.2.1

Description Remove batch effects by projecting query batches into the reference batch space.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

LazyData true

URL <https://github.com/RavenGan/SCIBER>

BugReports <https://github.com/RavenGan/SCIBER/issues>

Imports dplyr, parallel, stats

Depends R (>= 2.10)

Suggests knitr, rmarkdown, testthat (>= 3.0.0), cowplot, ggplot2, ggthemes, Matrix, uwot

Config/testthat/edition 3

VignetteBuilder knitr

Repository <https://ravengan.r-universe.dev>

RemoteUrl <https://github.com/ravengan/sciber>

RemoteRef HEAD

RemoteSha 372e4117a554031a8b7fc21afe6ae2fb38294d92

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HumanDC

Human dendritic cell gene expression and meta data

Description

A dataset human dendritic cells gene expression and corresponding meta data

Usage

HumanDC

Format

An object of class list of length 2.

Source

<https://pubmed.ncbi.nlm.nih.gov/28428369/>

SCIBER

Batch effect removal with SCIBER

Description

Batch effect removal with SCIBER

Usage

```
SCIBER(  
  input_batches,  
  ref_index = NULL,  
  batches_meta_data = NULL,  
  omega = 0.5,  
  h_fisher = 75,  
  n_core = parallel::detectCores(),  
  seed = 7,  
  k = NULL  
)
```

Arguments

<code>input_batches</code>	A list contains all the pre-processed matrices with dimension of $n_genes * n_cells$.
<code>ref_index</code>	The index of the reference batch in the object "input_batches"
<code>batches_meta_data</code>	A list contains the meta data for all the batches. The order should be consistent with that in "input_batches". Each meta data contains three columns, "cell_id", "cell_type", and "dataset". "dataset" indicates which batch the data comes from. The row names of meta data should match the column names of batch.
<code>omega</code>	A list of proportion of matched clusters or a single value between 0 and 1 applied to all query batches.
<code>h_fisher</code>	The number of marker genes used for Fisher exact test.
<code>n_core</code>	Specify the number of cores otherwise use all the available cores.
<code>seed</code>	random seed.
<code>k</code>	Number of clusters used for K-means. If not provided, the default is $k = \sqrt{n_0}$, where n_0 is the number of cells in the reference batch.

Value

A list which contains the reference and batch-effect-corrected batches. The order is the same as that in `input_batches`.

Examples

```
data(HumanDC)
exp <- HumanDC[["exp"]]
meta <- HumanDC[["metadata"]]
omega <- c()
omega[[1]] <- 0.5
res <- SCIBER(input_batches = exp, ref_index = 1,
batches_meta_data = meta, omega = omega, n_core = 1)
```

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* **datasets**

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