

Package ‘SCIBER’

July 21, 2025

Type Package

Title Single-Cell Integrator and Batch Effect Remover

Version 0.2.2

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

License MIT + file LICENSE

Encoding UTF-8

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

NeedsCompilation no

Author Dailin Gan [aut, cre] (ORCID: <<https://orcid.org/0000-0003-0535-1259>>),
Jun Li [aut]

Maintainer Dailin Gan <dgan@end.edu>

Repository CRAN

Date/Publication 2023-05-02 08:10:12 UTC

Contents

HumanDC	2
SCIBER	2
Index	4

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 <code>n_genes*n_cells</code> .
<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 <code>k = the square root of n_0</code> , where <code>n_0</code> 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)
```

Index

* **datasets**

HumanDC, [2](#)

HumanDC, [2](#)

SCIBER, [2](#)