Package ‘SCIBER’

May 7, 2026

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.

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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

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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

- `input_batches` A list contains all the pre-processed matrices with dimension of n_genes*n_cells.
- `ref_index` The index of the reference batch in the object "input_batches"
- `batches_meta_data` 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.
- `omega` A list of proportion of matched clusters or a single value between 0 and 1 applied to all query batches.
- `h_fisher` The number of marker genes used for Fisher exact test.
- `n_core` Specify the number of cores otherwise use all the available cores.
- `seed` random seed.
- `k` Number of clusters used for K-means. If not provided, the default is k = the square root of 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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