Package ‘SCIBER’

May 2, 2023

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
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R topics documented:

<table>
<thead>
<tr>
<th>HumanDC</th>
<th>2</th>
</tr>
</thead>
<tbody>
<tr>
<td>SCIBER</td>
<td>2</td>
</tr>
</tbody>
</table>

Index

1
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**


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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

```r
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