

# Package ‘SIMLR’

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**Title** Single-cell Interpretation via Multi-kernel LeaRning (SIMLR)

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**Depends** R (>= 4.0.0),

**Imports** parallel, Matrix, stats, methods, Rcpp, pracma, RcppAnnoy,  
RSpectra

**Suggests** BiocGenerics, BiocStyle, testthat, knitr, igraph

**Description** Single-cell RNA-seq technologies enable high throughput gene expression measurement of individual cells, and allow the discovery of heterogeneity within cell populations. Measurement of cell-to-cell gene expression similarity is critical for the identification, visualization and analysis of cell populations. However, single-cell data introduce challenges to conventional measures of gene expression similarity because of the high level of noise, outliers and dropouts. We develop a novel similarity-learning framework, SIMLR (Single-cell Interpretation via Multi-kernel LeaRning), which learns an appropriate distance metric from the data for dimension reduction, clustering and visualization.

**Encoding** UTF-8

**LazyData** TRUE

**License** file LICENSE

**URL** <https://github.com/BatzoglouLabSU/SIMLR>

**BugReports** <https://github.com/BatzoglouLabSU/SIMLR>

**biocViews** ImmunoOncology, Clustering, GeneExpression, Sequencing,  
SingleCell

**RoxygenNote** 7.1.1

**LinkingTo** Rcpp

**NeedsCompilation** yes

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/SIMLR>

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BuettnerFlorian	<i>test dataset for SIMLR</i>
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## Description

example dataset to test SIMLR from the work by Buettner, Florian, et al.

## Usage

```
data(BuettnerFlorian)
```

## Format

gene expression measurements of individual cells

## Value

list of 6: `in_X` = input dataset as an (m x n) gene expression measurements of individual cells, `n_clust` = number of clusters (number of distinct true labels), `true_labs` = ground true of cluster assignments for each of the `n_clust` clusters, `seed` = seed used to compute the results for the example, `results` = result by SIMLR for the inputs defined as described, `nmi` = normalized mutual information as a measure of the inferred clusters compared to the true labels

## Source

Buettner, Florian, et al. "Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells." *Nature biotechnology* 33.2 (2015): 155-160.

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CIMLR *This function has been removed and it is now provided by the CIMLR package, please refer to <https://github.com/danro9685/CIMLR>*

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### Description

perform the CIMLR clustering algorithm

### Usage

```
CIMLR(X, c, no.dim = NA, k = 10, cores.ratio = 1)
```

### Arguments

X	a list of multi-omic data each of which is an (m x n) data matrix of measurements of cancer patients
c	number of clusters to be estimated over X
no.dim	number of dimensions
k	tuning parameter
cores.ratio	ratio of the number of cores to be used when computing the multi-kernel

### Value

clusters the patients based on CIMLR and their similarities

### Examples

```
## Not run:
CIMLR(X = GliomasReduced$in_X, c = 3, cores.ratio = 0)

## End(Not run)
```

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CIMLR\_Estimate\_Number\_of\_Clusters

*This function has been removed and it is now provided by the CIMLR package, please refer to <https://github.com/danro9685/CIMLR>*

---

### Description

CIMLR\_Estimate\_Number\_of\_Clusters

### Usage

```
CIMLR_Estimate_Number_of_Clusters(all_data, NUMC = 2:5, cores.ratio = 1)
```

**Arguments**

<code>all_data</code>	is a list of multi-omic data each of which is an (m x n) data matrix of measurements of cancer patients
<code>NUMC</code>	vector of number of clusters to be considered
<code>cores.ratio</code>	ratio of the number of cores to be used when computing the multi-kernel

**Value**

a list of 2 elements: K1 and K2 with an estimation of the best clusters (the lower values the better) as discussed in the original paper of SIMLR

**Examples**

```
## Not run:
CIMLR_Estimate_Number_of_Clusters(GliomasReduced$in_X,
  NUMC = 2:5,
  cores.ratio = 0)

## End(Not run)
```

SIMLR

*SIMLR***Description**

perform the SIMLR clustering algorithm

**Usage**

```
SIMLR(
  X,
  c,
  no.dim = NA,
  k = 10,
  if.impute = FALSE,
  normalize = FALSE,
  cores.ratio = 1
)
```

**Arguments**

<code>X</code>	an (m x n) data matrix of gene expression measurements of individual cells or and object of class SCESet
<code>c</code>	number of clusters to be estimated over X
<code>no.dim</code>	number of dimensions
<code>k</code>	tuning parameter
<code>if.impute</code>	should I transpose the input data?
<code>normalize</code>	should I normalize the input data?
<code>cores.ratio</code>	ratio of the number of cores to be used when computing the multi-kernel

**Value**

clusters the cells based on SIMLR and their similarities

list of 8 elements describing the clusters obtained by SIMLR, of which y are the resulting clusters: y = results of k-means clusterings, S = similarities computed by SIMLR, F = results from network diffusion, ydata = data referring the the results by k-means, alphaK = clustering coefficients, execution.time = execution time of the present run, converge = iterative convergence values by T-SNE, LF = parameters of the clustering

**Examples**

```
SIMLR(X = BuettnerFlorian$in_X, c = BuettnerFlorian$n_clust, cores.ratio = 0)
```

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SIMLR\_Estimate\_Number\_of\_Clusters

*SIMLR Estimate Number of Clusters*

---

**Description**

estimate the number of clusters by means of two huristics as discussed in the SIMLR paper

**Usage**

```
SIMLR_Estimate_Number_of_Clusters(X, NUMC = 2:5, cores.ratio = 1)
```

**Arguments**

X	an (m x n) data matrix of gene expression measurements of individual cells
NUMC	vector of number of clusters to be considered
cores.ratio	ratio of the number of cores to be used when computing the multi-kernel

**Value**

a list of 2 elements: K1 and K2 with an estimation of the best clusters (the lower values the better) as discussed in the original paper of SIMLR

**Examples**

```
SIMLR_Estimate_Number_of_Clusters(BuettnerFlorian$in_X,
  NUMC = 2:5,
  cores.ratio = 0)
```

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SIMLR\_Feature\_Ranking *SIMLR Feature Ranking*

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### Description

perform the SIMLR feature ranking algorithm. This takes as input the original input data and the corresponding similarity matrix computed by SIMLR

### Usage

```
SIMLR_Feature_Ranking(A, X)
```

### Arguments

A	an (n x n) similarity matrix by SIMLR
X	an (m x n) data matrix of gene expression measurements of individual cells

### Value

a list of 2 elements: pvalues and ranking ordering over the n covariates as estimated by the method

### Examples

```
SIMLR_Feature_Ranking(A = BuettnerFlorian$results$S, X = BuettnerFlorian$in_X)
```

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SIMLR\_Large\_Scale *SIMLR Large Scale*

---

### Description

perform the SIMLR clustering algorithm for large scale datasets

### Usage

```
SIMLR_Large_Scale(X, c, k = 10, kk = 100, if.impute = FALSE, normalize = FALSE)
```

### Arguments

X	an (m x n) data matrix of gene expression measurements of individual cells or and object of class SCESet
c	number of clusters to be estimated over X
k	tuning parameter
kk	number of principal components to be assessed in the PCA
if.impute	should I transpose the input data?
normalize	should I normalize the input data?

**Value**

clusters the cells based on SIMLR Large Scale and their similarities

list of 8 elements describing the clusters obtained by SIMLR, of which y are the resulting clusters: y = results of k-means clusterings, S0 = similarities computed by SIMLR, F = results from the large scale iterative procedure, ydata = data referring the the results by k-means, alphaK = clustering coefficients, val = distances from the k-nearest neighbour search, ind = indeces from the k-nearest neighbour search, execution.time = execution time of the present run

**Examples**

```
resized = ZeiselAmit$in_X[, 1:340]
## Not run:
SIMLR_Large_Scale(X = resized, c = ZeiselAmit$n_clust, k = 5, kk = 5)

## End(Not run)
```

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ZeiselAmit

*test dataset for SIMLR large scale*

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**Description**

example dataset to test SIMLR large scale. This is a reduced version of the dataset from the work by Zeisel, Amit, et al.

**Usage**

```
data(ZeiselAmit)
```

**Format**

gene expression measurements of individual cells

**Value**

list of 6: in\_X = input dataset as an (m x n) gene expression measurements of individual cells, n\_clust = number of clusters (number of distinct true labels), true\_labs = ground true of cluster assignments for each of the n\_clust clusters, seed = seed used to compute the results for the example, results = result by SIMLR for the inputs defined as described, nmi = normalized mutual information as a measure of the inferred clusters compared to the true labels

**Source**

Zeisel, Amit, et al. "Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq." *Science* 347.6226 (2015): 1138-1142.

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