Package ‘SIMLR’

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Title SIMLR: Single-cell Interpretation via Multi-kernel LeaRning
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Imports parallel, Matrix, stats, methods,
Suggests BiocGenerics, BiocStyle, testthat, knitr, igraph, scran,
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 to 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. SIMLR is capable of separating known subpopulations more accurately in single-cell data sets than do existing dimension reduction methods. Additionally, SIMLR demonstrates high sensitivity and accuracy on high-throughput peripheral blood mononuclear cells (PBMC) data sets generated by the GemCode single-cell technology from 10x Genomics.

Encoding UTF-8
LazyData TRUE
License file LICENSE
URL https://github.com/BatzoglouLabSU/SIMLR
BugReports https://github.com/BatzoglouLabSU/SIMLR
biocViews Clustering, GeneExpression, Sequencing, SingleCell
RoxygenNote 5.0.1
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NeedsCompilation yes
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Description
eexample 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

Description
perform the SIMLR clustering algorithm

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

**Arguments**

- **X**: an (m x n) data matrix of gene expression measurements of individual cells or an object of class SCESet.
- **c**: number of clusters to be estimated over X.
- **n_dim**: number of dimensions.
- **k**: tuning parameter.
- **if.impute**: should I transpose the input data?
- **normalize**: should I normalize the input data?
- **cores.ratio**: 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**

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

**Description**

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

**Usage**

```r
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: p-values 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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