

# Package ‘RCSL’

May 21, 2026

**Type** Package

**Title** Rank Constrained Similarity Learning for single cell RNA sequencing data

**Version** 1.21.0

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**Description** A novel clustering algorithm and toolkit RCSL (Rank Constrained Similarity Learning) to accurately identify various cell types using scRNA-seq data from a complex tissue. RCSL considers both lo-cal similarity and global similarity among the cells to discern the subtle differences among cells of the same type as well as larger differences among cells of different types. RCSL uses Spearman’s rank correlations of a cell’s expression vector with those of other cells to measure its global similar-ity, and adap-tively learns neighbour representation of a cell as its local similarity. The overall similar-ity of a cell to other cells is a linear combination of its global similarity and local similarity.

**URL** <https://github.com/QinglinMei/RCSL>

**Depends** R (>= 4.1)

**License** Artistic-2.0

**VignetteBuilder** knitr

**biocViews** SingleCell, Software, Clustering, DimensionReduction, RNASeq, Visualization, Sequencing

**Suggests** testthat, knitr, BiocStyle, rmarkdown, mclust, tidyverse, tinytex

**Imports** RcppAnnoy, igraph, NbClust, Rtsne, ggplot2(>= 3.4.0), methods, pracma, umap, grDevices, graphics, stats, Rcpp (>= 0.11.0), MatrixGenerics, SingleCellExperiment

**LazyData** TRUE

**Encoding** UTF-8

**RoxygenNote** 7.3.1

**NeedsCompilation** no

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

**git\_branch** devel

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ann

*Cell type annotations of ‘yan’ datasets by Yan et al.*

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### Description

Cell type annotations of ‘yan’ datasets by Yan et al.

### Usage

ann

### Format

An object of class `data.frame` with 90 rows and 1 columns.

### Source

<http://dx.doi.org/10.1038/nsmb.2660>

Each row corresponds to one cell of ‘yan’ dataset

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BDSM                      *Calculate the block-diagonal matrix  $B$   $\min_B \geq 0, B^*1=1, F^*F=I \| B - A \|_1 + r \| B \|^2 + 2 * \lambda * \text{trace}(F^*L^*F)$*

---

**Description**

Calculate the block-diagonal matrix  $B$   $\min_B \geq 0, B^*1=1, F^*F=I \| B - A \|_1 + r \| B \|^2 + 2 * \lambda * \text{trace}(F^*L^*F)$

**Usage**

BDSM(S, C)

**Arguments**

S                      the calculated initial similarity matrix S  
 C                      the estimated number of clusters C

**Value**

B block-diagonal matrix  
 y clustering results

**Examples**

```
gfData <- GenesFilter(yan)
res_SimS <- SimS(gfData)
C <- EstClusters(res_SimS$drData, res_SimS$S)
BDSM(res_SimS$S, C)
```

---

EProjSimplexdiag                      *Solve the problem:  $\min 1/2 * x^*L*x - x^*d$  s.t.  $x \geq 0, 1^*x=1$*

---

**Description**

Solve the problem:  $\min 1/2 * x^*L*x - x^*d$  s.t.  $x \geq 0, 1^*x=1$

**Usage**

EProjSimplexdiag(d, l)

**Arguments**

d                      matrix or vector  
 l                      matrix or vector

**Value**

x

---

EstClusters                      *Estimate the optimal number of clusters C for clustering*

---

**Description**

Estimate the optimal number of clusters C for clustering

**Usage**

```
EstClusters(drData, S)
```

**Arguments**

drData                      gene expression matrix after PCA processing  
 S                              the calculated similarity matrix S from "SimS"

**Value**

C the estimated number of clusters

**Examples**

```
gfData <- GenesFilter(yan)
res_SimS <- SimS(gfData)
EstClusters(res_SimS$drData, res_SimS$S)
```

---

EucDist                              *Solve the problem:  $\|A-B\|^2 = \|A\|^2 + \|B\|^2 - 2*A'*B$*

---

**Description**

Solve the problem:  $\|A-B\|^2 = \|A\|^2 + \|B\|^2 - 2*A'*B$

**Usage**

```
EucDist(A, B)
```

**Arguments**

A                              matrix or vector  
 B                              matrix or vector

**Value**

d matrix or vector

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GenesFilter	<i>Perform the step of gene filtering to normalizaed gene expression data</i>
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**Description**

Perform the step of gene filtering to normalizaed gene expression data

**Usage**

```
GenesFilter(data, gfRatio = 0.025)
```

**Arguments**

data	the normalized gene expression matrix
gfRatio	the ratio of genes filtering

**Value**

the gene expression matrix after genes filtering gfData

**Examples**

```
data(yan)
GenesFilter(yan)
```

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getLineage	<i>Infer the development lineage based on the clustering results from RCSL and the pseudotime</i>
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**Description**

Infer the development lineage based on the clustering results from RCSL and the pseudotime

**Usage**

```
getLineage(drData, clustRes, pseudoTime, simMeasure = "kendall")
```

**Arguments**

drData	preprocessed gene expression data (each column represent a cell)
clustRes	the clustering results identified by RCSL
pseudoTime	inferred by PlotPseudoTime() using the similarity matrix S and starting cell
simMeasure	the calculation method of measuring the cluster centers' similarity

**Value**

lineage the cell lineages connected all the cluster centers based on the clustering results from RCSL

**Examples**

```
gfData <- GenesFilter(yan)
TrueLabel <- ann$cell_type1
res_SimS <- SimS(gfData)
C <- EstClusters(res_SimS$drData, res_SimS$S)
res_BDSM <- BDSM(res_SimS$S, C)
Pseudo <- PlotPseudoTime(res_SimS$S, TrueLabel, startPoint=1)
getLineage(res_SimS$drData, res_BDSM$y, Pseudo$pseudoTime)
```

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NeigRepresent	<i>Calculate the neighbor representation of cells to the low-dimensional gene expression matrix</i>
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**Description**

Calculate the neighbor representation of cells to the low-dimensional gene expression matrix

**Usage**

```
NeigRepresent(
  drData,
  NN.method = "KNN",
  Dis.method = "Euclidean",
  LSH.TreeNum = 30,
  LSH.Dim = 500,
  LSH.Dis = "angular",
  neiRatio = 0.65
)
```

**Arguments**

drData	gene expression matrix after dimensionality reduced by PCA
NN.method	the method of finding neighbors
Dis.method	the distance metric in finding neighbors
LSH.TreeNum	the tree number of LSH
LSH.Dim	the dimension in LSH
LSH.Dis	the distance metric in LSH
neiRatio	ratio of the number of selected

**Value**

the similarity matrix measured by neighbor representation NR

**Examples**

```
gfData <- GenesFilter(yan)
res_SimS <- SimS(gfData)
NeigRepresent(res_SimS$drData)
```

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PlotMST	<i>Plot the visualization of constructed Minimum Spanning Tree based on the clustering results of RCSL</i>
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---

### Description

Plot the visualization of constructed Minimum Spanning Tree based on the clustering results of RCSL

### Usage

```
PlotMST(  
  drData,  
  clustRes,  
  TrueLabel,  
  dataName = "",  
  fontSize = 12,  
  VisualMethod = "umap"  
)
```

### Arguments

drData	preprocessed gene expression data
clustRes	the clustering results identified by RCSL
TrueLabel	the real cell types to color the dots in plot
dataName	the name of the data that will be showed in the plot
fontSize	the font size of the plot
VisualMethod	the method for 2D visualization including UMAP,t-SNE and PCA

### Value

MSTPlot ggplot object of the visualization of constructed MST

### Examples

```
gfData <- GenesFilter(yan)  
TrueLabel <- ann$cell_type1  
res_SimS <- SimS(gfData)  
C <- EstClusters(res_SimS$drData, res_SimS$S)  
res_BDSM <- BDSM(res_SimS$S, C)  
PlotMST(res_SimS$drData, res_BDSM$y, TrueLabel)
```

---

PlotPseudoTime	<i>Infer the pseudo-temporal ordering between the cell types using the distance from a cell type to the predefined starting cell type.</i>
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---

### Description

Infer the pseudo-temporal ordering between the cell types using the distance from a cell type to the predefined starting cell type.

### Usage

```
PlotPseudoTime(
  S,
  TrueLabel,
  startPoint,
  fontSize = 12,
  dataName = "",
  sim = TRUE
)
```

### Arguments

S	the similarity matrix calculated by SimS() function
TrueLabel	the real cell types used to indicate the vertical axis
startPoint	the position of the starting cell in the matrix
fontSize	the font size of the plot
dataName	the name of the data that will be showed in the plot
sim	indicate the input data is simialrity matrix or not

### Value

PstudoTime  
PseudoTimePlot ggplot object of the pseudo-temporal ordering of cells

### Examples

```
gfData <- GenesFilter(yan)
TrueLabel <- ann$cell_type1
res_SimS <- SimS(gfData)
PlotPseudoTime(res_SimS$S, TrueLabel, startPoint=1)
```

---

PlotTrajectory	<i>Infer the developmental trajectories based on the clustering results from RCSL</i>
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---

### Description

Infer the developmental trajectories based on the clustering results from RCSL

### Usage

```
PlotTrajectory(
  gfData,
  clustRes,
  TrueLabel,
  lineage,
  fontSize = 12,
  dataName = "",
  VisualMethod = "umap"
)
```

### Arguments

gfData	preprocessed gene expression data (each column represent a cell)
clustRes	the clustering results identified by RCSL
TrueLabel	the real cell types
lineage	the lineage obtained by getLineage()
fontSize	the size of font in the plot
dataName	the name of the data that will be showed in the plot
VisualMethod	the display method of 2-D visualization

### Value

TrajectoryPlot ggplot object of the inferred developmental trajectories

### Examples

```
gfData <- GenesFilter(yan)
TrueLabel <- ann$cell_type1
res_SimS <- SimS(gfData)
C <- EstClusters(res_SimS$drData, res_SimS$S)
res_BDSM <- BDSM(res_SimS$S, C)
Pseudo <- PlotPseudoTime(res_SimS$S, TrueLabel, startPoint=1)
Linea <- getLineage(res_SimS$drData, res_BDSM$y, Pseudo$pseudoTime)
PlotTrajectory(gfData, res_BDSM$y, TrueLabel, lineage=Linea)
```

---

RCSL

*Perform the RCSL program*

---

## Description

Perform the RCSL program

## Usage

```
RCSL(  
  data,  
  GF = TRUE,  
  gfRatio = 0.025,  
  pcRatio = 0.95,  
  NN.method = "KNN",  
  Dis.method = "Euclidean",  
  neiRatio = 0.65  
)
```

## Arguments

<code>data</code>	normalizaed gene expression matrix(each column represents a cell)
<code>GF</code>	should I need the gene filter step?
<code>gfRatio</code>	the ratio of the gene filter
<code>pcRatio</code>	the ratio between the variance of the
<code>NN.method</code>	the method of finding neighbors
<code>Dis.method</code>	the distance metric in finding neighbors
<code>neiRatio</code>	ratio of the number of selected

## Value

`gfData` gene expression matrix after genes filtering  
`B` block-diagonal matrix  
`C` estimated number of clusters  
`y` clustering results

## Examples

```
data(yan)  
data <- log2(yan+1)  
RCSL(yan[,1:20])
```

---

`SimS`*Calculate the initial similarity matrix*

---

**Description**

Calculate the initial similarity matrix

**Usage**

```
SimS(  
  data,  
  pcRatio = 0.95,  
  gamma = 0.8,  
  NN.method = "KNN",  
  Dis.method = "Euclidean",  
  LSH.TreeNum = 30,  
  LSH.Dim = 1000,  
  LSH.Dis = "angular",  
  neiRatio = 0.65  
)
```

**Arguments**

<code>data</code>	gene expression matrix after genes filtering
<code>pcRatio</code>	the ratio between the variance of the
<code>gamma</code>	the ratio of the global simialrity
<code>NN.method</code>	the method of finding neighbors
<code>Dis.method</code>	the distance metric in finding neighbors
<code>LSH.TreeNum</code>	the tree number of LSH
<code>LSH.Dim</code>	the dimension in LSH
<code>LSH.Dis</code>	the distance metric in LSH
<code>neiRatio</code>	ratio of the number of selected

**Value**

initial similarity matrix *S*  
gene expression matrix after PCA processing *drData*

**Examples**

```
gfData <- GenesFilter(yan)  
SimS(gfData)
```

---

TrajectoryAnalysis      *Trajectory analysis*

---

### Description

Trajectory analysis

### Usage

```
TrajectoryAnalysis(
  gfData,
  drData,
  S,
  clustRes,
  fontSize = 12,
  TrueLabel,
  startPoint,
  dataName = "",
  sim = TRUE,
  simMeasure = "kendall",
  VisualMethod = "umap"
)
```

### Arguments

gfData	preprocessed gene expression data (each column represent a cell)
drData	preprocessed gene expression data (each column represent a cell)
S	the similarity matrix calculated by SimS() function
clustRes	the clustering results identified by RCSL
fontSize	the size of font in the plot
TrueLabel	the real cell types used to indicate the vertical axis
startPoint	the position of the starting cell in the matrix
dataName	the name of the data that will be showed in the plot
sim	indicate the input data is simialrity matrix or not
simMeasure	the calculation method of measuring the cluster centers' similarity
VisualMethod	the display method of 2-D visualization

### Value

PseudoTimePlot, MSTPlot, TrajectoryPlot

### Examples

```
gfData <- GenesFilter(yan)
TrueLabel <- ann$cell_type1
res_SimS <- SimS(gfData)
C <- EstClusters(res_SimS$drData, res_SimS$S)
res_BDSM <- BDSM(res_SimS$S, C)
TrajectoryAnalysis(gfData, res_SimS$drData, res_SimS$S, res_BDSM$y,
  TrueLabel=TrueLabel, startPoint=1)
```

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yan

*A public scRNA-seq dataset by Yan et al.*

---

**Description**

A public scRNA-seq dataset by Yan et al.

**Usage**

yan

**Format**

An object of class `data.frame` with 20214 rows and 90 columns.

**Source**

<http://dx.doi.org/10.1038/nsmb.2660>

Columns represent cells, rows represent genes expression values.

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