Package ‘SC3’

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### ann

**Description**

Cell type annotations for data extracted from a publication by Yan et al.

**Usage**

```r
ann
```

**Format**

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

**Source**

[http://dx.doi.org/10.1038/nsmb.2660](http://dx.doi.org/10.1038/nsmb.2660)

Each row corresponds to a single cell from 'yan' dataset

### calculate_distance

**Description**

Distance between the cells, i.e. columns, in the input expression matrix are calculated using the Euclidean, Pearson and Spearman metrics to construct distance matrices.

**Usage**

```r
calculate_distance(data, method)
```

**Arguments**

- `data` : expression matrix
- `method` : one of the distance metrics: 'spearman', 'pearson', 'euclidean'

**Value**

distance matrix
calculate_stability  Calculate the stability index of the obtained clusters when changing \( k \)

**Description**

Stability index shows how stable each cluster is across the selected range of \( k \). The stability index varies between 0 and 1, where 1 means that the same cluster appears in every solution for different \( k \).

**Usage**

```r
calculate_stability(consensus, k)
```

**Arguments**

- `consensus` consensus item of the sc3 slot of an object of `SingleCellExperiment` class
- `k` number of clusters \( k \)

**Details**

Imagine a given cluster is split into \( N \) clusters when \( k \) is changed (all possible values of \( k \) are provided via `ks` argument in the main sc3 function). In each of the new clusters there are `given_cells` of the given cluster and also some `extra_cells` from other clusters. Then we define stability as follows:

\[
\frac{1}{ks * N^2} \sum \sum \frac{given\_cells}{given\_cells + extra\_cells}
\]

Where one \( N \) corrects for the number of clusters and the other \( N \) is a penalty for splitting the cluster. \( ks \) corrects for the range of \( k \).

**Value**

- a numeric vector containing a stability index of each cluster

---

consensus_matrix  Calculate consensus matrix

**Description**

Consensus matrix is calculated using the Cluster-based Similarity Partitioning Algorithm (CSPA). For each clustering solution a binary similarity matrix is constructed from the corresponding cell labels: if two cells belong to the same cluster, their similarity is 1, otherwise the similarity is 0. A consensus matrix is calculated by averaging all similarity matrices.
**Usage**

```r
consensus_matrix(clusts)
```

**Arguments**

- `clusts` : a matrix containing clustering solutions in columns

**Value**

- consensus matrix

---

**consmx**  
**Consensus matrix computation**

---

**Description**

Computes consensus matrix given cluster labels

**Usage**

```r
consmx(dat)
```

**Arguments**

- `dat` : a matrix containing clustering solutions in columns

---

**ED1**  
**Compute Euclidean distance matrix by rows**

---

**Description**

Used in consmx function

**Usage**

```r
ED1(x)
```

**Arguments**

- `x` : A numeric matrix.
ED2

Compute Euclidean distance matrix by columns

Description

Used in sc3-funcs.R distance matrix calculation and within the consensus clustering.

Usage

ED2(x)

Arguments

x A numeric matrix.

estkTW

Estimate the optimal k for k-means clustering

Description

The function finds the eigenvalues of the sample covariance matrix. It will then return the number of significant eigenvalues according to the Tracy-Widom test.

Usage

estkTW(dataset)

Arguments

dataset processed input expression matrix.

Value

an estimated number of clusters k
**get_auroc**

*Calculate the area under the ROC curve for a given gene.*

**Description**

For a given gene a binary classifier is constructed based on the mean cluster expression values (these are calculated using the cell labels). The classifier prediction is then calculated using the gene expression ranks. The area under the receiver operating characteristic (ROC) curve is used to quantify the accuracy of the prediction. A p-value is assigned to each gene by using the Wilcoxon signed rank test.

**Usage**

get_auroc(gene, labels)

**Arguments**

gene  
expression data of a given gene

labels  
cell labels corresponding to the expression values of the gene

---

**get_biolgy**

*Wrapper for calculating biological properties*

**Description**

Wrapper for calculating biological properties

**Usage**

get_biolgy(dataset, labels, regime)

**Arguments**

dataset  
expression matrix

labels  
cell labels corresponding clusters

regime  
defines what biological analysis to perform. "marker" for marker genes, "de" for differentially expressed genes and "outl" for outlier cells

**Value**

results of either
get_de_genes  

*Find differentially expressed genes*

**Description**

Differential expression is calculated using the non-parametric Kruskal-Wallis test. A significant p-value indicates that gene expression in at least one cluster stochastically dominates one other cluster. Note that the calculation of differential expression after clustering can introduce a bias in the distribution of p-values, and thus we advise to use the p-values for ranking the genes only.

**Usage**

```r
get_de_genes(dataset, labels)
```

**Arguments**

- `dataset` expression matrix
- `labels` cell labels corresponding to the columns of the expression matrix

**Value**

a numeric vector containing the differentially expressed genes and corresponding p-values

**Examples**

```r
d <- get_de_genes(yan[1:10,], as.numeric(ann[,1]))
head(d)
```

get_marker_genes  

*Calculate marker genes*

**Description**

Find marker genes in the dataset. The `get_auroc` is used to calculate marker values for each gene.

**Usage**

```r
get_marker_genes(dataset, labels)
```

**Arguments**

- `dataset` expression matrix
- `labels` cell labels corresponding clusters
**get_outl_cells**

**Value**

data.frame containing the marker genes, corresponding cluster indexes and adjusted p-values

**Examples**

```r
d <- get_marker_genes(yan[1:10,], as.numeric(ann[,1]))
d
```

---

**get_outl_cells**

*Find cell outliers in each cluster.*

**Description**

Outlier cells in each cluster are detected using robust distances, calculated using the minimum covariance determinant (MCD), namely using `covMcd`. The outlier score shows how different a cell is from all other cells in the cluster and it is defined as the differences between the square root of the robust distance and the square root of the 99.99

**Usage**

`get_outl_cells(dataset, labels)`

**Arguments**

- **dataset**: expression matrix
- **labels**: cell labels corresponding to the columns of the expression matrix

**Value**

a numeric vector containing the cell labels and corresponding outlier scores ordered by the labels

**Examples**

```r
d <- get_outl_cells(yan[1:10,], as.numeric(ann[,1]))
head(d)
```
get_processed_dataset  
*Get processed dataset used by SC3 clustering*

**Description**
Takes data from the logcounts slot, removes spike-ins and applies the gene filter.

**Usage**
```
get_processed_dataset(object)
```

**Arguments**
- **object**
  - an object of SingleCellExperiment class

markers_for_heatmap  
*Reorder and subset gene markers for plotting on a heatmap*

**Description**
Reorders the rows of the input data.frame based on the sc3_k_markers_clusts column and also keeps only the top 10 genes for each value of sc3_k_markers_clusts.

**Usage**
```
markers_for_heatmap(markers)
```

**Arguments**
- **markers**
  - a data.frame object with the following colnames: sc3_k_markers_clusts, sc3_k_markers_auroc, sc3_k_markers_padj.

norm_laplacian  
*Graph Laplacian calculation*

**Description**
Calculate graph Laplacian of a symmetric matrix

**Usage**
```
norm_laplacian(A)
```

**Arguments**
- **A**
  - symmetric matrix
organise_de_genes  
Get differentially expressed genes from an object of SingleCellExperiment class

Description
This function returns all marker gene columns from the phenoData slot of the input object corresponding to the number of clusters $k$. Additionally, it rearranges genes by the cluster index and order them by the area under the ROC curve value inside of each cluster.

Usage
organise_de_genes(object, k, p_val)

Arguments
- object: an object of SingleCellExperiment class
- k: number of cluster
- p_val: p-value threshold

organise_marker_genes  Get marker genes from an object of SingleCellExperiment class

Description
This function returns all marker gene columns from the phenoData slot of the input object corresponding to the number of clusters $k$. Additionally, it rearranges genes by the cluster index and order them by the area under the ROC curve value inside of each cluster.

Usage
organise_marker_genes(object, k, p_val, auroc)

Arguments
- object: an object of SingleCellExperiment class
- k: number of cluster
- p_val: p-value threshold
- auroc: area under the ROC curve threshold
prepare_for_svm  A helper function for the SVM analysis

Description

Defines train and study cell indeces based on the svm_num_cells and svm_train_indds input parameters

Usage

prepare_for_svm(N, svm_num_cells = NULL, svm_train_indds = NULL, svm_max)

Arguments

N number of cells in the input dataset
svm_num_cells number of random cells to be used for training
svm_train_indds indeces of cells to be used for training
svm_max define the maximum number of cells below which SVM is not run

Value

A list of indeces of the train and the study cells

reindex_clusters  Reindex cluster labels in ascending order

Description

Given an hclust object and the number of clusters k this function reindex the clusters inferred by cutree(hc, k)[hc$order], so that they appear in ascending order. This is particularly useful when plotting heatmaps in which the clusters should be numbered from left to right.

Usage

reindex_clusters(hc, k)

Arguments

hc an object of class hclust
k number of cluster to be inferred from hc

Examples

hc <- hclust(dist(USArrests), 'ave')
cutree(hc, 10)[hc$order]
reindex_clusters(hc, 10)[hc$order]
Run all steps of SC3 in one go

Description

This function is a wrapper that executes all steps of SC3 analysis in one go.

Usage

```r
sc3.SingleCellExperiment(object, ks, gene_filter, pct_dropout_min, pct_dropout_max, d_region_min, d_region_max, svm_num_cells, svm_train_inds, svm_max, n_cores, kmeans_nstart, kmeans_iter_max, k_estimator, biology, rand_seed)
```

```r
## S4 method for signature 'SingleCellExperiment'
sc3(object, ks = NULL, gene_filter = TRUE, pct_dropout_min = 10, pct_dropout_max = 90, d_region_min = 0.04, d_region_max = 0.07, svm_num_cells = NULL, svm_train_inds = NULL, svm_max = 5000, n_cores = NULL, kmeans_nstart = NULL, kmeans_iter_max = 1e+09, k_estimator = FALSE, biology = FALSE, rand_seed = 1)
```

Arguments

- **object**
  - an object of `SingleCellExperiment` class.

- **ks**
  - a range of the number of clusters $k$ used for SC3 clustering. Can also be a single integer.

- **gene_filter**
  - a boolean variable which defines whether to perform gene filtering before SC3 clustering.

- **pct_dropout_min**
  - if `gene_filter = TRUE`, then genes with percent of dropouts smaller than `pct_dropout_min` are filtered out before clustering.

- **pct_dropout_max**
  - if `gene_filter = TRUE`, then genes with percent of dropouts larger than `pct_dropout_max` are filtered out before clustering.

- **d_region_min**
  - defines the minimum number of eigenvectors used for kmeans clustering as a fraction of the total number of cells. Default is $0.04$. See SC3 paper for more details.

- **d_region_max**
  - defines the maximum number of eigenvectors used for kmeans clustering as a fraction of the total number of cells. Default is $0.07$. See SC3 paper for more details.

- **svm_num_cells**
  - number of randomly selected training cells to be used for SVM prediction. The default is NULL.

- **svm_train_inds**
  - a numeric vector defining indices of training cells that should be used for SVM training. The default is NULL.
**svm_max**
define the maximum number of cells below which SVM is not run.

**n_cores**
defines the number of cores to be used on the user's machine. If not set, 'SC3' will use all but one cores of your machine.

**kmeans_nstart**
#start parameter passed to `kmeans` function. Can be set manually. By default it is 1000 for up to 2000 cells and 50 for more than 2000 cells.

**kmeans_iter_max**
iter.max parameter passed to `kmeans` function.

**k_estimator**
boolean parameter, defines whether to estimate an optimal number of clusters k. If user has already defined the ks parameter the estimation does not affect the user’s parameter.

**biology**
boolean parameter, defines whether to compute differentially expressed genes, marker genes and cell outliers.

**rand_seed**
sets the seed of the random number generator. SC3 is a stochastic method, so setting the rand_seed to a fixed values can be used for reproducibility purposes.

---

**sc3_calc_biology**

**Calculate DE genes, marker genes and cell outliers.**

---

**Description**

This function calculates differentially expressed (DE) genes, marker genes and cell outliers based on the consensus SC3 clusterings.

**Usage**

```
sc3_calc_biology.SingleCellExperiment(object, ks, regime)
```

## S4 method for signature 'SingleCellExperiment'

```
sc3_calc_biology(object, ks = NULL, 
regime = NULL)
```

**Arguments**

- **object**
an object of SingleCellExperiment class

- **ks**
a continuous range of integers - the number of clusters k to be used for SC3 clustering. Can also be a single integer.

- **regime**
defines what biological analysis to perform. "marker" for marker genes, "de" for differentially expressed genes and "outl" for outlier cells
sc3_calc_consens

Details

DE genes are calculated using \texttt{get_de_genes}. Results of the DE analysis are saved as new columns in the \texttt{featureData} slot of the input object. The column names correspond to the adjusted p-values of the genes and have the following format: \texttt{sc3\_k\_de\_padj}, where \( k \) is the number of clusters.

Marker genes are calculated using \texttt{get_marker_genes}. Results of the marker gene analysis are saved as three new columns (for each \( k \)) to the \texttt{featureData} slot of the input object. The column names correspond to the SC3 cluster labels, to the adjusted p-values of the genes and to the area under the ROC curve and have the following format: \texttt{sc3\_k\_markers\_clusts}, \texttt{sc3\_k\_markers\_padj} and \texttt{sc3\_k\_markers\_auroc}, where \( k \) is the number of clusters.

Outlier cells are calculated using \texttt{get_outl_cells}. Results of the cell outlier analysis are saved as new columns in the \texttt{phenoData} slot of the input object. The column names correspond to the \( \log_2(\text{outlier\_score}) \) and have the following format: \texttt{sc3\_k\_log2\_outlier\_score}, where \( k \) is the number of clusters.

Additionally, \texttt{biology} item is added to the \texttt{sc3} slot and is set to \texttt{TRUE} indicating that the biological analysis of the dataset has been performed.

Value

an object of \texttt{SingleCellExperiment} class

Description

This function calculates consensus matrices based on the clustering solutions contained in the \texttt{kmeans} item of the \texttt{sc3} slot of the \texttt{metadata(object)}. It then creates and populates the \texttt{consensus} item of the \texttt{sc3} slot with consensus matrices, their hierarchical clusterings in \texttt{hclust} objects, and Silhouette indices of the clusters. It also removes the previously calculated \texttt{kmeans} clusterings from the \texttt{sc3} slot, as they are not needed for further analysis.

Usage

\begin{verbatim}
sc3_calc_consens.SingleCellExperiment(object)

## S4 method for signature 'SingleCellExperiment'
sc3_calc_consens(object)
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{object} \hspace{1cm} an object of \texttt{SingleCellExperiment} class
\end{itemize}

Details

Additionally, it also adds new columns to the \texttt{colData} slot of the input object. The column names correspond to the consensus cell labels and have the following format: \texttt{sc3\_k\_clusters}, where \( k \) is the number of clusters.
**Value**

an object of SingleCellExperiment class

---

**sc3_calc_dists**

*Calculate distances between the cells.*

**Description**

This function calculates distances between the cells. It creates and populates the following items of the sc3 slot of the metadata(object):

- distances - contains a list of distance matrices corresponding to Euclidean, Pearson and Spearman distances.

**Usage**

```r
sc3_calc_dists.SingleCellExperiment(object)
```

```r
## S4 method for signature 'SingleCellExperiment'
sc3_calc_dists(object)
```

**Arguments**

- `object` an object of SingleCellExperiment class

**Value**

an object of SingleCellExperiment class

---

**sc3_calc_transfs**

*Calculate transformations of the distance matrices.*

**Description**

This function transforms all distances items of the sc3 slot of the metadata(object) using either principal component analysis (PCA) or by calculating the eigenvectors of the associated graph Laplacian. The columns of the resulting matrices are then sorted in descending order by their corresponding eigenvalues. The first d columns (where $d = \max(\text{metadata}(\text{object})$\$\text{sc3}\$\$\text{n\_dim})$) of each transformation are then written to the transformations item of the sc3 slot. Additionally, this function also removes the previously calculated distances from the sc3 slot, as they are not needed for further analysis.
Usage

\[
\text{sc3\_calc\_transfs.\textit{SingleCellExperiment}}(\text{object})
\]

```r
## S4 method for signature 'SingleCellExperiment'
sc3_calc_transfs(object)
```

Arguments

- **object**: an object of \textit{SingleCellExperiment} class

Value

an object of \textit{SingleCellExperiment} class

---

**Description**

Uses Tracy-Widom theory on random matrices to estimate the optimal number of clusters \(k\). It creates and populates the \textit{k\_estimation} item of the \textit{sc3} slot of the \textit{metadata(object)}.

Usage

\[
\text{sc3\_estimate\_k.\textit{SingleCellExperiment}}(\text{object})
\]

```r
## S4 method for signature 'SingleCellExperiment'
sc3_estimate_k(object)
```

Arguments

- **object**: an object of \textit{SingleCellExperiment} class

Value

an estimated value of \(k\)
### sc3_export_results_xls

*Write SC3 results to Excel file*

**Description**

This function writes all SC3 results to an excel file.

**Usage**

```r
sc3_export_results_xls.SingleCellExperiment(object, filename)
```

#### S4 method for signature 'SingleCellExperiment'

```r
sc3_export_results_xls(object, filename = "sc3_results.xls")
```

**Arguments**

- `object`: an object of SingleCellExperiment class
- `filename`: name of the excel file, to which the results will be written

### sc3_interactive

*Opens SC3 results in an interactive session in a web browser.*

**Description**

Runs interactive shiny session of SC3 based on precomputed clusterings.

**Usage**

```r
sc3_interactive.SingleCellExperiment(object)
```

#### S4 method for signature 'SingleCellExperiment'

```r
sc3_interactive(object)
```

**Arguments**

- `object`: an object of SingleCellExperiment class

**Value**

Opens a browser window with an interactive shiny app and visualize all precomputed clusterings.
sc3_kmeans

sc3_kmeans kmeans clustering of cells.

Description
This function performs kmeans clustering of the matrices contained in the transformations item of the sc3 slot of the metadata(object). It then creates and populates the following items of the sc3 slot:

• kmeans - contains a list of kmeans clusterings.

Usage
sc3_kmeans.SingleCellExperiment(object, ks)

## S4 method for signature 'SingleCellExperiment'
sc3_kmeans(object, ks = NULL)

Arguments

object an object of SingleCellExperiment class

ks a continuous range of integers - the number of clusters k to be used for SC3 clustering. Can also be a single integer.

Value
an object of SingleCellExperiment class

sc3_plot_cluster_stability

Plot stability of the clusters

Description
Stability index shows how stable each cluster is across the selected range of ks. The stability index varies between 0 and 1, where 1 means that the same cluster appears in every solution for different k.

Usage
sc3_plot_cluster_stability.SingleCellExperiment(object, k)

## S4 method for signature 'SingleCellExperiment'
sc3_plot_cluster_stability(object, k)
**sc3_plot_de_genes**

*Plot expression of DE genes of the clusters identified by SC3 as a heatmap*

**Description**

SC3 plots gene expression profiles of the 50 genes with the lowest p-values.

**Arguments**

- `object`: an object of `SingleCellExperiment` class
- `k`: number of clusters

---

**sc3_plot_consensus**

*Plot consensus matrix as a heatmap*

**Description**

The consensus matrix is a NxN matrix, where N is the number of cells. It represents similarity between the cells based on the averaging of clustering results from all combinations of clustering parameters. Similarity 0 (blue) means that the two cells are always assigned to different clusters. In contrast, similarity 1 (red) means that the two cells are always assigned to the same cluster. The consensus matrix is clustered by hierarchical clustering and has a diagonal-block structure. Intuitively, the perfect clustering is achieved when all diagonal blocks are completely red and all off-diagonal elements are completely blue.

**Usage**

```r
sc3_plot_consensus(object, k, show_pdata = NULL)
```

**Arguments**

- `object`: an object of `SingleCellExperiment` class
- `k`: number of clusters
- `show_pdata`: a vector of colnames of the pData(object) table. Default is NULL. If not NULL will add pData annotations to the columns of the output matrix

---

**sc3_plot_de_genes**

*Plot expression of DE genes of the clusters identified by SC3 as a heatmap*
**Usage**

```r
sc3_plot_de_genes.SingleCellExperiment(object, k, p.val, show_pdata)
```

## S4 method for signature 'SingleCellExperiment'

```r
sc3_plot_de_genes(object, k, p.val = 0.01,
show_pdata = NULL)
```

**Arguments**

- `object`: an object of `SingleCellExperiment` class
- `k`: number of clusters
- `p.val`: significance threshold used for the DE genes
- `show_pdata`: a vector of colnames of the `pData(object)` table. Default is `NULL`. If not `NULL` will add pData annotations to the columns of the output matrix

---

**Description**

The expression panel represents the original input expression matrix (cells in columns and genes in rows) after the gene filter. Genes are clustered by kmeans with `k = 100` (dendrogram on the left) and the heatmap represents the expression levels of the gene cluster centers after log2-scaling.

---

**Usage**

```r
sc3_plot_expression.SingleCellExperiment(object, k, show_pdata)
```

## S4 method for signature 'SingleCellExperiment'

```r
sc3_plot_expression(object, k,
show_pdata = NULL)
```

**Arguments**

- `object`: an object of `SingleCellExperiment` class
- `k`: number of clusters
- `show_pdata`: a vector of colnames of the `pData(object)` table. Default is `NULL`. If not `NULL` will add pData annotations to the columns of the output matrix
sc3_plot_markers

Plot expression of marker genes identified by SC3 as a heatmap.

Description

By default the genes with the area under the ROC curve (AUROC) > 0.85 and with the p-value < 0.01 are selected and the top 10 marker genes of each cluster are visualized in this heatmap.

Usage

sc3_plot_markers.SingleCellExperiment(object, k, auroc, p.val, show_pdata)

## S4 method for signature 'SingleCellExperiment'
sc3_plot_markers(object, k, auroc = 0.85, p.val = 0.01, show_pdata = NULL)

Arguments

- object: an object of 'SingleCellExperiment' class
- k: number of clusters
- auroc: area under the ROC curve
- p.val: significance threshold used for the DE genes
- show_pdata: a vector of colnames of the pData(object) table. Default is NULL. If not NULL will add pData annotations to the columns of the output matrix

sc3_plot_silhouette

Plot silhouette indexes of the cells

Description

A silhouette is a quantitative measure of the diagonality of the consensus matrix. An average silhouette width (shown at the bottom left of the silhouette plot) varies from 0 to 1, where 1 represents a perfectly block-diagonal consensus matrix and 0 represents a situation where there is no block-diagonal structure. The best clustering is achieved when the average silhouette width is close to 1.

Usage

sc3_plot_silhouette.SingleCellExperiment(object, k)

## S4 method for signature 'SingleCellExperiment'
sc3_plot_silhouette(object, k)
**sc3_prepare**

**Arguments**

- **object**: an object of 'SingleCellExperiment' class
- **k**: number of clusters

---

**Prepare the SingleCellExperiment object for SC3 clustering.**

**Description**

This function prepares an object of SingleCellExperiment class for SC3 clustering. It creates and populates the following items of the sc3 slot of the metadata(object):

- **kmeans_iter_max**: the same as the kmeans_iter_max argument.
- **kmeans_nstart**: the same as the kmeans_nstart argument.
- **n_dim**: contains numbers of the number of eigenvectors to be used in kmeans clustering.
- **rand_seed**: the same as the rand_seed argument.
- **svm_train_inds**: if SVM is used this item contains indexes of the training cells to be used for SC3 clustering and further SVM prediction.
- **svm_study_inds**: if SVM is used this item contains indexes of the cells to be predicted by SVM.
- **n_cores**: the same as the n_cores argument.

**Usage**

```r
sc3_prepare.SingleCellExperiment(object, gene_filter, pct_dropout_min, pct_dropout_max, d_region_min, d_region_max, svm_num_cells, svm_train_inds, svm_max, n_cores, kmeans_nstart, kmeans_iter_max, rand_seed)
```

```r
sc3_prepare(object, gene_filter = TRUE, pct_dropout_min = 10, pct_dropout_max = 90, d_region_min = 0.04, d_region_max = 0.07, svm_num_cells = NULL, svm_train_inds = NULL, svm_max = 5000, n_cores = NULL, kmeans_nstart = NULL, kmeans_iter_max = 1e+09, rand_seed = 1)
```

**Arguments**

- **object**: an object of SingleCellExperiment class.
- **gene_filter**: a boolean variable which defines whether to perform gene filtering before SC3 clustering.
- **pct_dropout_min**: if gene_filter = TRUE, then genes with percent of dropouts smaller than pct_dropout_min are filtered out before clustering.
pct_dropout_max

if gene_filter = TRUE, then genes with percent of dropouts larger than pct_dropout_max are filtered out before clustering.

d_region_min
defines the minimum number of eigenvectors used for kmeans clustering as a fraction of the total number of cells. Default is 0.04. See SC3 paper for more details.

d_region_max
defines the maximum number of eigenvectors used for kmeans clustering as a fraction of the total number of cells. Default is 0.07. See SC3 paper for more details.

svm_num_cells

the number of randomly selected training cells to be used for SVM prediction. The default is NULL.

svm_train_inds

a numeric vector defining indeces of training cells that should be used for SVM training. The default is NULL.

svm_max

define the maximum number of cells below which SVM is not run.

n_cores

defines the number of cores to be used on the user’s machine. If not set, ‘SC3’ will use all but one cores of your machine.

kmeans_nstart

nstart parameter passed to kmeans function. Default is 1000 for up to 2000 cells and 50 for more than 2000 cells.

kmeans_iter_max

iter.max parameter passed to kmeans function. Default is 1e+09.

rand_seed

sets the seed of the random number generator. SC3 is a stochastic method, so setting the rand_seed to a fixed values can be used for reproducibility purposes.

Value

an object of SingleCellExperiment class

Usage

sc3_run_svm.SingleCellExperiment(object, ks)

## S4 method for signature 'SingleCellExperiment'
sc3_run_svm(object, ks = NULL)
support_vector_machines

Arguments

object: an object of SingleCellExperiment class
ks: a continuous range of integers - the number of clusters k to be used for SC3 clustering. Can also be a single integer.

Details

Results are written to the sc3_k_clusters columns to the colData slot of the input object, where k is the number of clusters.

Value

an object of SingleCellExperiment class

support_vector_machines

Run support vector machines (SVM) prediction

Description

Train an SVM classifier on a training dataset (train) and then classify a study dataset (study) using the classifier.

Usage

support_vector_machines(train, study, kern)

Arguments

train: training dataset with colnames, corresponding to training labels
study: study dataset
kern: kernel to be used with SVM

Value

classification of the study dataset
transformation

---

tmult \hspace{2cm} \textit{Matrix left-multiplied by its transpose}

\underline{Description}

Given matrix A, the procedure returns A'A.

\underline{Usage}

tmult(x)

\underline{Arguments}

x \hspace{1cm} \text{Numeric matrix.}

---

transformation \hspace{2cm} \textit{Distance matrix transformation}

\underline{Description}

All distance matrices are transformed using either principal component analysis (PCA) or by calculating the eigenvectors of the graph Laplacian (Spectral). The columns of the resulting matrices are then sorted in descending order by their corresponding eigenvalues.

\underline{Usage}

transformation(dists, method)

\underline{Arguments}

dists \hspace{1cm} \text{distance matrix}

method \hspace{1cm} \text{transformation method: either 'pca' or 'laplacian'}

\underline{Value}

transformed distance matrix
**Description**

Single cell RNA-Seq data extracted from a publication 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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