

# Package ‘SC3’

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**Type** Package

**Title** Single-Cell Consensus Clustering

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**Description** A tool for unsupervised clustering and analysis of single cell RNA-Seq data.

**License** GPL-3

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ann	<i>Cell type annotations for data extracted from a publication by Yan et al.</i>
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**Description**

Cell type annotations for data extracted from a publication 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 a single cell from 'yan' dataset

---

calculate_distance	<i>Calculate a distance matrix</i>
--------------------	------------------------------------

---

**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**

```
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

```
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:

$$\frac{1}{ks * N^2} \sum_{ks} \sum_N \frac{given\_cells}{given\_cells + extra\_cells}$$

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

```
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**

consmx(dat)

**Arguments**

dat                a matrix containing clustering solutions in columns

---

ED1                *Compute Euclidean distance matrix by rows*

---

**Description**

Used in consmx function

**Usage**

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	<i>Estimate the optimal k for k-means clustering</i>
--------	--

---

**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	<i>Calculate the area under the ROC curve for a given gene.</i>
-----------	---

---

**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	<i>Wrapper for calculating biological properties</i>
------------	--

---

**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	<i>Find differentially expressed genes</i>
--------------	--

---

**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**

```
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**

```
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

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

### Arguments

dataset	expression matrix
labels	cell labels corresponding clusters

### Value

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

### Examples

```
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**

```
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 indices based on the `svm_num_cells` and `svm_train_inds` input parameters

### Usage

```
prepare_for_svm(N, svm_num_cells = NULL, svm_train_inds = NULL, svm_max)
```

### Arguments

<code>N</code>	number of cells in the input dataset
<code>svm_num_cells</code>	number of random cells to be used for training
<code>svm_train_inds</code>	indices of cells to be used for training
<code>svm_max</code>	define the maximum number of cells below which SVM is not run

### Value

A list of indices 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

<code>hc</code>	an object of class <code>hclust</code>
<code>k</code>	number of cluster to be inferred from <code>hc</code>

### Examples

```
hc <- hclust(dist(USArrests), 'ave')
cutree(hc, 10)[hc$order]
reindex_clusters(hc, 10)[hc$order]
```

sc3

*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**

```
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)
```

```
## 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	nstart parameter passed to <a href="#">kmeans</a> 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 <a href="#">kmeans</a> 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.

**Value**

an object of SingleCellExperiment class

---

sc3_calc_biology	<i>Calculate DE genes, marker genes and cell outliers.</i>
------------------	--

---

**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

**Details**

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

Marker genes are calculated using [get\\_marker\\_genes](#). Results of the marker gene analysis are saved as three new columns (for each k) to the 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: sc3\_k\_markers\_clusts, sc3\_k\_markers\_padj and sc3\_k\_markers\_auroc, where k is the number of clusters.

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

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

### Value

an object of `SingleCellExperiment` class

---

<code>sc3_calc_consens</code>	<i>Calculate consensus matrix.</i>
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---

### Description

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

### Usage

```
sc3_calc_consens.SingleCellExperiment(object)

## S4 method for signature 'SingleCellExperiment'
sc3_calc_consens(object)
```

### Arguments

`object`                    an object of `SingleCellExperiment` class

### Details

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

### Value

an object of `SingleCellExperiment` class

---

sc3_calc_dists	<i>Calculate distances between the cells.</i>
----------------	---

---

### 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

```
sc3_calc_dists.SingleCellExperiment(object)

## 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	<i>Calculate transformations of the distance matrices.</i>
------------------	--

---

### 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  $d = \max(\text{metadata}(\text{object})\$sc3\$n\_dim)$ ) 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

```
sc3_calc_transfs.SingleCellExperiment(object)

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

### Arguments

object            an object of SingleCellExperiment class

**Value**

an object of SingleCellExperiment class

---

sc3_estimate_k	<i>Estimate the optimal number of cluster k for a scRNA-Seq expression matrix</i>
----------------	---

---

**Description**

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

**Usage**

```
sc3_estimate_k.SingleCellExperiment(object)

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

**Arguments**

object            an object of SingleCellExperiment class

**Value**

an estimated value of k

---

sc3_export_results_xls	<i>Write SC3 results to Excel file</i>
------------------------	--

---

**Description**

This function writes all SC3 results to an excel file.

**Usage**

```
sc3_export_results_xls.SingleCellExperiment(object, filename)

## S4 method for signature 'SingleCellExperiment'
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	<i>Opens SC3 results in an interactive session in a web browser.</i>
-----------------	--

---

**Description**

Runs interactive shiny session of SC3 based on precomputed clusterings.

**Usage**

```
sc3_interactive.SingleCellExperiment(object)

## S4 method for signature 'SingleCellExperiment'
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	<i>kmeans clustering of cells.</i>
------------	------------------------------------

---

**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)
```

### 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

```
sc3_plot_consensus.SingleCellExperiment(object, k, show_pdata)
```

```
## S4 method for signature 'SingleCellExperiment'
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	<i>Plot expression of DE genes of the clusters identified by SC3 as a heatmap</i>
-------------------	---

---

### Description

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

### Usage

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

```
## S4 method for signature 'SingleCellExperiment'
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

---

sc3_plot_expression	<i>Plot expression matrix used for SC3 clustering as a heatmap</i>
---------------------	--

---

### 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 log<sub>2</sub>-scaling.

### Usage

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

```
## S4 method for signature 'SingleCellExperiment'
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)
```

### Arguments

object	an object of 'SingleCellExperiment' class
k	number of clusters

sc3\_prepare

*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**

```
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)
```

```
## S4 method for signature 'SingleCellExperiment'
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**

<code>object</code>	an object of <code>SingleCellExperiment</code> class.
<code>gene_filter</code>	a boolean variable which defines whether to perform gene filtering before SC3 clustering.
<code>pct_dropout_min</code>	if <code>gene_filter = TRUE</code> , then genes with percent of dropouts smaller than <code>pct_dropout_min</code> are filtered out before clustering.
<code>pct_dropout_max</code>	if <code>gene_filter = TRUE</code> , then genes with percent of dropouts larger than <code>pct_dropout_max</code> are filtered out before clustering.
<code>d_region_min</code>	defines the minimum number of eigenvectors used for kmeans clustering as a fraction of the total number of cells. Default is <code>0.04</code> . See SC3 paper for more details.
<code>d_region_max</code>	defines the maximum number of eigenvectors used for kmeans clustering as a fraction of the total number of cells. Default is <code>0.07</code> . 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 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 <a href="#">kmeans</a> function. Default is 1000 for up to 2000 cells and 50 for more than 2000 cells.
kmeans_iter_max	iter.max parameter passed to <a href="#">kmeans</a> 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

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sc3_run_svm	<i>Run the hybrid SVM approach.</i>
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**Description**

This method parallelize SVM prediction for each k (the number of clusters). Namely, for each k, [support\\_vector\\_machines](#) function is utilized to predict the labels of study cells. Training cells are selected using svm\_train\_inds item of the sc3 slot of the metadata(object).

**Usage**

```
sc3_run_svm.SingleCellExperiment(object, ks)

## S4 method for signature 'SingleCellExperiment'
sc3_run_svm(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.

**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

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`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**

<code>train</code>	training dataset with colnames, corresponding to training labels
<code>study</code>	study dataset
<code>kern</code>	kernel to be used with SVM

**Value**

classification of the study dataset

---

`tmult`*Matrix left-multiplied by its transpose*

---

**Description**

Given matrix  $A$ , the procedure returns  $A'A$ .

**Usage**

```
tmult(x)
```

**Arguments**

<code>x</code>	Numeric matrix.
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transformation	<i>Distance matrix transformation</i>
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**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.

**Usage**

```
transformation(dists, method)
```

**Arguments**

dists	distance matrix
method	transformation method: either 'pca' or 'laplacian'

**Value**

transformed distance matrix

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yan	<i>Single cell RNA-Seq data extracted from a publication by Yan et al.</i>
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**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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