

scRNA-seq Cheatsheet

The tables below consist of valuable functions or commands that will help you through this module.

Each table represents a different library/tool and its corresponding commands.

Please note that these tables are not intended to tell you all the information you need to know about each command.

The hyperlinks found in each piece of code will take you to the documentation for further information on the usage of each command. Please be aware that the documentation will generally provide information about the given function's most current version (or a recent version, depending on how often the documentation site is updated). This will usually (but not always!) match what you have installed on your machine. If you have a different version of R or other R packages, the documentation may differ from what you have installed.

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Base R

Read the Base [R documentation](#).

Library/Package	Piece of Code	What it's called	What it does
Base R	<code>rowSums(.)</code>	Row sums	Calculates sums for each row
Base R	<code>colSums(.)</code>	Column sums	Calculates sums for each column
Base R	<code>t(.)</code>	Transpose	Returns the transpose of a matrix or data frame
Base R	<code>prcomp(.)</code>	Principal Components Analysis	Executes a principal components analysis on specified matrix or data frame
Base R	<code><-function(x) { <code> }</code>	Function	Creates a function that would take the defined parameters as input and execute the commands within the curly braces

Salmon and alevinQC

Read the command-line tool [Salmon documentation](#).

Read the R package [alevinQC documentation](#).

Software/package	Piece of Code	What it's called	What it does
Salmon	<code>salmon alevin</code>	Salmon Alevin	Runs the Alevin quantification from the command line
<code>alevinQC</code>	<code>alevinQCReport(.)</code>	Alevin QC Report	Produces a QC (quality check) report from the <code>salmon alevin</code> output

SingleCellExperiment, txmimeta, and DropletUtils

Read the [SingleCellExperiment package documentation \(and e-book\)](#), and a [vignette on its usage](#).

Note that some of the `SingleCellExperiment` functions link to documentation from other packages like `SummarizedExperiment` or `ExperimentSubset`. In fact, `SingleCellExperiment` objects are based around existing Bioconductor functions in those packages, so the function usage is equivalent!

Read the [txmimeta package documentation](#), and a [vignette on its usage](#).

Read the [DropletUtils package documentation](#).

Library/Package	Piece of Code	What it's called	What it does
<code>SingleCellExperiment</code>	SingleCellExperiment(.)	Single Cell Experiment	Creates a <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	colData(.)	Column Data	Extracts and stores cell-level metadata that describes features of the <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	rowData(.)	Row Data	Extracts and stores gene-level metadata that describes features of the <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	assay(.)	Assay	Extracts and stores a given assay from a <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	assayNames(.)	Assay names	Returns a vector of the names of all assays in a <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	logcounts(.)	Log counts	Extracts and stores log-transformed single-cell experiment count data as an assay of the <code>SingleCellExperiment</code>

			object
<code>SingleCellExperiment</code>	<code>counts()</code>	Counts	Extracts and stores raw single-cell experiment count data as an assay of the <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code>reducedDim()</code>	Reduced dim	Extracts or stores a given reduced dimension from a <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code>reducedDimNames()</code>	Reduced dim names	Returns a vector of the names of all reduced dimensions in a <code>SingleCellExperiment</code> object
<code>S4Vectors</code>	<code>DataFrame()</code>	Data frame	Not to be confused with <code>data.frame()</code> from Base R. This is a slightly different data frame-like object needed for storing information in <code>SingleCellExperiment</code> object's <code>colData</code> slot.
<code>tximeta</code>	<code>tximeta()</code>	Transcript Quantification Import with Automatic Metadata	Load a directory of results produced by Salmon/or alevin output, including the associated metadata
<code>DropletUtils</code>	<code>read10xCounts()</code>	Read 10x counts	Load data from a 10x Genomics experiment into R
<code>DropletUtils</code>	<code>emptyDrops()</code>	Empty drops	Use the overall gene expression patterns in the sample to identify empty droplets
<code>DropletUtils</code>	<code>emptyDropsCellRanger()</code>	Empty drops Cell Ranger	Use an approach analogous to Cell Ranger's algorithm to identify empty droplets

scrn and scater

Read the [scrn package documentation](#), and a [vignette on its usage](#).

Read the [scater package documentation](#), and a [vignette on its usage](#).

Library/Package	Piece of Code	What it's called	What it does
scrn	quickCluster()	Quick Clustering	Groups similar cells into clusters which are stored in the <code>SingleCellExperiment</code> object and are used for the calculation of size factors by <code>scrn::computeSumFactors</code>
scrn	computeSumFactors()	Compute Sum Factors	Returns a numeric vector of computed sum factors for each cell cluster stored in the <code>SingleCellExperiment</code> object. The cluster-based size factors are deconvolved into cell-based size factors that are stored in the <code>SingleCellExperiment</code> object and used by the <code>scrn::normalize</code> function for the normalization of each cell's gene expression profile
scrn	getTopHVGs()	Get top highly variable genes	Identify variable genes in a <code>SingleCellExperiment</code> object, based on variance
scrn	modelGeneVar()	model per gene variance	Model the per gene variance of a <code>SingleCellExperiment</code> object
scrn	findMarkers()	Find marker genes	Find candidate marker genes for clusters of cells
			Returns the <code>SingleCellExperiment</code>

scater	logNormCounts()	Normalize log counts	object with normalized expression values for each cell, using the size factors stored in the object
scater	addPerCellQC()	Add per cell quality control	For a <code>SingleCellExperiment</code> object, calculate and add quality control per cell and store in <code>colData</code>
scater	addPerFeatureQC()	Add per feature quality control	For a <code>SingleCellExperiment</code> object, calculate and add quality control per feature (genes usually) and store in <code>rowData</code>
scater	calculatePCA()	Calculate PCA	Calculates principal components analysis on a <code>SingleCellExperiment</code> object, returning a PCA matrix
scater	runPCA()	Run PCA	Calculates principal components analysis on a <code>SingleCellExperiment</code> object, returning an SCE object with a PCA reduced dimension
scater	calculateUMAP()	Calculate UMAP	Calculates uniform manifold approximate projection on a <code>SingleCellExperiment</code> object, returning a UMAP matrix
scater	runUMAP()	Run UMAP	Calculates uniform manifold approximate projection on a <code>SingleCellExperiment</code> object, returning an SCE object with a UMAP reduced dimension
scater	calculateTSNE()	Calculate t-SNE	Calculates t-stochastic neighbor embedding on a <code>SingleCellExperiment</code> object, returning an SCE object with a TSNE reduced dimension
		Calculate	Calculates t-stochastic neighbor embedding on a

scater	runTSNE(.)	UMAP	SingleCellExperiment object, returning a t-SNE matrix
scater	plotReducedDim(.)	Plot reduced dimensions	Plot a given reduced dimension slot from a SingleCellExperiment object by its name
scater	plotPCA(.)	Plot PCA	Plot the "PCA"-named reduced dimension slot from a SingleCellExperiment object
scater	plotUMAP(.)	Plot UMAP	Plot the "UMAP"-named reduced dimension slot from a SingleCellExperiment object

`purrr`, `stringr`, and `tibble`

Read the [purrr package documentation](#).

Read the [stringr package documentation](#).

Read the [tibble package documentation](#).

Library/Package	Piece of Code	What it's called	What it does
<code>purrr</code>	map(.)	map	Apply a function across each element of list; return a list
<code>purrr</code>	map_df(.)	map df	Apply a function across each element of list; return a data frame
<code>purrr</code>	imap(.)	imap	Apply a function across each element of list and its index/names
<code>stringr</code>	str_remove(.)	String remove	Remove matched string patterns
<code>tibble</code>	as_tibble(.)	As tibble	Coerce <code>data.frame</code> or matrix to a tibble

Note that `purrr::map()` functions can take advantage of R's new (as of version 4.1.0) [anonymous function syntax](#):

```
# One-line syntax:
\(x) # function code goes here #

# Multi-line syntax:
\(x) {
  # function code goes      #
  # inside the curly braces #
}

# Example: Use an anonymous function with `purrr::map()`
# to get the colData's rownames for each SCE in `list_of_sce_objects`
purrr::map(
  list_of_sce_objects,
  \(x) rownames(colData(x))
)
```


bluster

Read the [bluster package documentation](#) and [this vignette](#) on its usage.

Library/Package	Piece of Code	What it's called	What it does
bluster	clusterRows()	Cluster rows of a matrix	Perform clustering using a variety of algorithms on a matrix-like object
bluster	KmeansParam()	K-means clustering parameters	Set up parameters to run clustering using <code>kmeans()</code> within <code>bluster::clusterRows()</code>
bluster	NNGraphParam()	Graph-based clustering parameters	Set up parameters for nearest-neighbor (NN) graph-based clustering algorithms within <code>bluster::clusterRows()</code>

SingleR

Read the [SingleR package documentation](#), and an [e-book on its usage](#).

Library/Package	Piece of Code	What it's called	What it does
SingleR	trainSingleR()	Train the SingleR classifier	Build a <code>SingleR</code> classifier model object from an annotated reference dataset
SingleR	classifySingleR()	Classify cells with SingleR	Use a <code>SingleR</code> model object to assign cell types to the cells in an <code>SCE</code> object
SingleR	SingleR()	Annotate scRNA-seq data	Combines <code>trainSingleR()</code> and <code>classifySingleR()</code> to assign cell types to an <code>SCE</code> object from an annotated reference dataset

