

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

SingleCellExperiment, scran, and scater

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 [scran 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
SingleCellExperiment	<code>SingleCellExperiment()</code>	Single Cell Experiment	Creates a <code>SingleCellExperiment</code> object
SingleCellExperiment	<code>colData()</code>	Column Data	Extracts and stores cell-level metadata that describes features of the <code>SingleCellExperiment</code> object

Library/Package	Piece of Code	What it's called	What it does
SingleCellExperiment	<code>rowData()</code>	Row Data	Extracts and stores gene-level metadata that describes features of the <code>SingleCellExperiment</code> object
SingleCellExperiment	<code>assay()</code>	Assay	Extracts and stores a given assay from a <code>SingleCellExperiment</code> object
SingleCellExperiment	<code>assayNames()</code>	Assay names	Returns a vector of the names of all assays in a <code>SingleCellExperiment</code> object
SingleCellExperiment	<code>logcounts()</code>	Log counts	Extracts and stores log-transformed single-cell experiment count data as an assay of the <code>SingleCellExperiment</code> object
SingleCellExperiment	<code>counts()</code>	Counts	Extracts and stores raw single-cell experiment count data as an assay of the <code>SingleCellExperiment</code> object
SingleCellExperiment	<code>reducedDim()</code>	Reduced dim	Extracts or stores a given reduced dimension from a <code>SingleCellExperiment</code> object
SingleCellExperiment	<code>reducedDimNames()</code>	Reduced dim names	Returns a vector of the names of all reduced dimensions in a <code>SingleCellExperiment</code> object
scran	<code>quickCluster()</code>	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>scran::computeSumFactors</code>

Library/Package	Piece of Code	What it's called	What it does
scrn	<code>computeSumFactors()</code>	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	<code>getTopHVGs()</code>	Get top highly variable genes	Identify variable genes in a <code>SingleCellExperiment</code> object, based on variance
scrn	<code>modelGeneVar()</code>	model per gene variance	Model the per gene variance of a <code>SingleCellExperiment</code> object
scrn	<code>findMarkers()</code>	Find marker genes	Find candidate marker genes for clusters of cells
scater	<code>logNormCounts()</code>	Normalize log counts	Returns the <code>SingleCellExperiment</code> object with normalized expression values for each cell, using the size factors stored in the object
scater	<code>addPerCellQC()</code>	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	<code>addPerFeatureQC()</code>	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>

Library/Package	Piece of Code	What it's called	What it does
scater	<code>calculatePCA()</code>	Calculate PCA	Calculates principal components analysis on a <code>SingleCellExperiment</code> object, returning a PCA matrix
scater	<code>runPCA()</code>	Run PCA	Calculates principal components analysis on a <code>SingleCellExperiment</code> object, returning an SCE object with a PCA reduced dimension
scater	<code>calculateUMAP()</code>	Calculate UMAP	Calculates uniform manifold approximate projection on a <code>SingleCellExperiment</code> object, returning a UMAP matrix
scater	<code>runUMAP()</code>	Run UMAP	Calculates uniform manifold approximate projection on a <code>SingleCellExperiment</code> object, returning an SCE object with a UMAP reduced dimension
scater	<code>calculateTSNE()</code>	Calculate t-SNE	Calculates t-stochastic neighbor embedding on a <code>SingleCellExperiment</code> object, returning an SCE object with a TSNE reduced dimension
scater	<code>runTSNE()</code>	Calculate UMAP	Calculates t-stochastic neighbor embedding on a <code>SingleCellExperiment</code> object, returning a t-SNE matrix
scater	<code>plotReducedDim()</code>	Plot reduced dimensions	Plot a given reduced dimension slot from a <code>SingleCellExperiment</code> object by its name
scater	<code>plotPCA()</code>	Plot PCA	Plot the "PCA"-named reduced dimension slot from a <code>SingleCellExperiment</code> object
scater	<code>plotUMAP()</code>	Plot UMAP	Plot the "UMAP"-named reduced dimension slot from a <code>SingleCellExperiment</code> object

purrr

Read the [purrr package documentation](#).

Library/Package	Piece of Code	What it's called	What it does
purrr	map()	map	Apply a function across each element of list; return a list
purrr	map_df()	map df	Apply a function across each element of list; return a data frame
purrr	imap()	imap	Apply a function across each element of list and its index/names

stringr

Read the [stringr package documentation](#).

Library/Package	Piece of Code	What it's called	What it does
stringr	str_remove()	String remove	Remove matched string patterns

alevinQC, colorblindr, Rtsne, tibble

Documentation for each of these packages can be accessed by clicking the package name in the table below.

Library/Package	Piece of Code	What it's called	What it does
alevinQC	alevinQCReport()	Alevin QC Report	Produces a QC (quality check) report from the alevin output
S4Vectors	DataFrame()	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> .
Rtsne	Rtsne()	T-Distributed Stochastic Neighbor Embedding using a Barnes-Hut Implementation	Reduces the dimensions of the specified matrix or data frame
tibble	as_tibble()	As tibble	Coerce <code>data.frame</code> or matrix to a tibble

Salmon

Read the [Salmon documentation](#).

Piece of Code	What it's called	What it does
<code>salmon alevin</code>	Salmon Alevin	Runs the Alevin quantification from the command line