

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.

Base R

Read the Base R documentation [here](#).

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

ggplot2

Read the ggplot2 documentation [here](#).

Library/Package	Piece of Code	What it's called	What it does
ggplot2	<code>geom_vline(.)</code>	geom vertical line	Adds ggplot2 layer with a vertical line plotted

scran, scater, SingleCellExperiment

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

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

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

		What it's	
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Library/Package	Piece of Code	called	What it does
<code>SingleCellExperiment</code>	<code>SingleCellExperiment(.)</code>	Single Cell Experiment	Creates a <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code>colData(.)</code>	Column Data	Extracts and stores cell-level metadata that describes features of the <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code>rowData(.)</code>	Row Data	Extracts and stores gene-level metadata that describes features of the <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code>logcounts(.)</code>	Log counts	Stores or extracts log-transformed single-cell experiment count data as an assay of the <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code>counts(.)</code>	Counts	Stores or extracts raw single-cell experiment count data as an assay of the <code>SingleCellExperiment</code> object
<code>scrn</code>	<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>scrn::computeSumFactors</code>
<code>scrn</code>	<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

			<p>object and used by the <code>scrn::normalize</code> function for the normalization of each cell's gene expression profile</p>
<code>scrn</code>	<code>getTopHVGs()</code>	Get top highly variable genes	Identify variable genes in a <code>SingleCellExperiment</code> object, based on variance
<code>scrn</code>	<code>modelGeneVar()</code>	model per gene variance	Model the per gene variance of a <code>SingleCellExperiment</code> object
<code>scrn</code>	<code>findMarkers()</code>	Find marker genes	Find candidate marker genes for clusters of cells
<code>scater</code>	<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
<code>scater</code>	<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>
<code>scater</code>	<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>
<code>scater</code>	<code>calculatePCA()</code>	Calculate PCA	Calculates principal components analysis on a <code>SingleCellExperiment</code> object
<code>scater</code>	<code>calculateUMAP()</code>	Calculate UMAP	Calculates uniform manifold approximate projection on a <code>SingleCellExperiment</code> object
<code>scater</code>	<code>calculateTSNE()</code>	Calculate t-SNE	Calculate t-stochastic neighbor embedding on a <code>SingleCellExperiment</code> object

		SNE	SingleCellExperiment object
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purrr

Read the `purrr` documentation [here](#).

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

stringr

Read the `stringr` documentation [here](#).

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

Salmon

Read the Salmon documentation [here](#).

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