

# 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.

## Base R

Read the Base R documentation [here](#)

Library/Package	Piece of Code	What it's called	What it does
Base R	<code>source()</code>	Source	Reads input from a specified file or URL
Base R	<code>which()</code>	Which	Assesses an object logically and returns true indices of the object that are <code>TRUE</code>
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>&lt;-function(x) { code }</code>	Create a function	Creates a function that would take the defined parameters as input and execute the commands within the curly braces

## ggplot2

Read the `ggplot2` package documentation [here](#).

A vignette on the usage of the `ggplot2` package can be found [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>ggplot2</code>	<code>qplot</code>	Quick Plot	Allows for the quick production of different types of plots when used in conjunction with layers created by other <code>ggplot2</code> functions
<code>ggplot2</code>	<code>geom_density()</code>	Geom Density	Displays a smoothed version of the <code>ggplot</code> or <code>qplot</code> based on the computed density estimate
<code>ggplot2</code>	<code>geom_vline()</code>	Vertical Line	Adds a vertical reference line to a <code>ggplot</code> or <code>qplot</code>
<code>ggplot2</code>	<code>theme_classic()</code>	Classic Theme	Displays <code>ggplot</code> or <code>qplot</code> without gridlines
<code>ggplot2</code>	<code>facet_wrap()</code>	Facet Wrap	Plots individual graphs using specified variables to subset the data
<code>ggplot2</code>	<code>ggtitle()</code>	GG Title	Sets the title of a <code>ggplot</code>

## 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 [here](#), and a vignette on its usage [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>scran</code>	<code><a href="#">quickCluster()</a></code>	Quick Clustering	Groups similar cells into clusters and normalizes these cells separately. The size factors are rescaled for comparison across clusters.
<code>scran</code>	<code><a href="#">computeSumFactors()</a></code>	Compute Sum Factors	Returns a numeric vector of computed sum factors for each cell cluster in the object. The cluster-based size factors are deconvolved into cell-based size factors for the normalization of each cell's gene expression profile. This is done to avoid errors that may result from bulk normalization methods.
<code>scater</code>	<code><a href="#">normalize()</a></code>	Normalize	Returns the <code>SingleCellExperiment</code> object with normalized expression values for each cell, using the appropriate size factor and log transformation
<code>SingleCellExperiment</code>	<code><a href="#">logcounts()</a></code>	Logcounts	Stores or extracts log transformed single cell experiment count data as an assay of the <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code><a href="#">SingleCellExperiment()</a></code>	Single Cell Experiment	Creates a <code>SingleCellExperiment</code> object
<code>SingleCellExperiment</code>	<code><a href="#">rowData()</a></code>	Row Data	Extracts and stores gene-level metadata that describes features of the <code>SingleCellExperiment</code> object

**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
<a href="#">alevinQC</a>	<a href="#">alevinQCReport(.)</a>	Alevin QC Report	Produces a QC (quality check) report from the alevin output
<a href="#">colorblindr</a>	<a href="#">scale_color_OkabeIto(.)</a>	OkabeIto Color Scale	When added as a layer to a plot, makes the plot color-blind friendly
<a href="#">Rtsne</a>	<a href="#">Rtsne(.)</a>	T-Distributed Stochastic Neighbor Embedding using a Barnes-Hut Implementation	Reduces the dimensions of the specified matrix or data frame
<a href="#">tibble</a>	<a href="#">rownames_to_column(.)</a>	Rownames to Column	Transforms the rownames of a data frame into a column (which is added to the start of the data frame)

## Salmon

Read the Salmon documentation [here](#).

Piece of Code	What it's called	What it does
<a href="#">salmon_alevin</a>	Salmon Alevin	Runs the Alevin quantification from the command line