

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 the true indices of the object
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</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>

scrn

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

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

Library/Package	Piece of Code	What it's called	What it does
<code>scrn</code>	<code>rowData(.)</code>	Row Data	Extracts and stores gene-level metadata. This function is also available in the <code>scater</code> package.
<code>scrn</code>	<code>quickCluster(.)</code>	Quick Clustering	Groups similar cells in clusters based on rank correlations in gene expression
<code>scrn</code>	<code>computeSumFactors(.)</code>	Compute Sum Factors	Returns a numeric vector of computed sum factors for each cell cluster in the object.

scater

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

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

Library/Package	Piece of Code	What it's called	What it does
<code>scater</code>	<code>normalize(.)</code>	Normalize	Returns the SingleCellExperiment object with its normalized expression values, using its sum factors and log transform
<code>scater</code>	<code>logcounts(.)</code>	Logcounts	Extracts or sets log transformed single cell experiment count data as an assay of the SingleCellExperiment object

alevinQC, **colorblindr**, **salmon**, **Rtsne**, **SingleCellExperiment**,
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
colorblindr	scale_color_okabeIto(.)	OkabeIto Color Scale	When added as a layer to a plot, makes the plot color-blind friendly
Salmon	salmon alevin	Salmon Alevin	Runs the Alevin quantification from the command line
Rtsne	Rtsne(.)	T-Distributed Stochastic Neighbor Embedding using a Barnes-Hut Implementation	Reduces the dimensions of the specified matrix or data frame
SingleCellExperiment	SingleCellExperiment(.)	Single Cell Experiment	Creates a Single Cell Experiment object
tibble	rownames_to_column(.)	Rownames to Column	Transforms the rownames of a data frame into a column (which is added to the start of the data frame)