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`	`source()`	Source	Reads input from a specified file or URL
Base `R`	`which()`	Which	Assesses an object logically and returns true indices of the object that are `TRUE`
Base `R`	`t()`	Transpose	Returns the transpose of a matrix or data frame
Base `R`	`prcomp()`	Principal Components Analysis	Executes a principal components analysis on specified matrix or data frame
Base `R`	`<-function(x) { <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
`ggplot2`	`qplot`	Quick Plot	Allows for the quick production of different types of plots when used in conjuction with layers created by other `ggplot2` functions
`ggplot2`	`geom_density()`	Geom Density	Displays a smoothed version of the `ggplot` or `qplot` based on the computed density estimate
`ggplot2`	`geom_vline()`	Vertical Line	Adds a vertical reference line to a `ggplot` or `qplot`
`ggplot2`	`theme_classic()`	Classic Theme	Displays `ggplot` or `qplot` without gridlines
`ggplot2`	`facet_wrap()`	Facet Wrap	Plots individual graphs using specified variables to subset the data
`ggplot2`	`ggtitle()`	GG Title	Sets the title of a `ggplot`

`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**.

In addition to the links above, Amezquita et al. is a useful paper on the single-cell analysis workflow involving the `SingleCellExperiment` object.

Library/Package	Piece of Code	What it's called	What it does
`SingleCellExperiment`	`SingleCellExperiment()`	Single Cell Experiment	Creates a `SingleCellExperiment` object
`SingleCellExperiment`	`logcounts()`	Logcounts	Stores or extracts log-transformed single-cell experiment count data as an assay of the `SingleCellExperiment` object
`SingleCellExperiment`	`rowData()`	Row Data	Extracts and stores gene-level metadata that describes features of the `SingleCellExperiment` object
`scran`	`quickCluster()`	Quick Clustering	Groups similar cells into clusters which are stored in the `SingleCellExperiment` object and are used for the calculation of size factors by `scran::computeSumFactors`
`scran`	`computeSumFactors()`	Compute Sum Factors	Returns a numeric vector of computed sum factors for each cell cluster stored in the `SingleCellExperiment` object. The cluster-based size factors are deconvolved into cell-based size factors that are stored in the `SingleCellExperiment` object and used by the `scran::normalize` function for the normalization of each cell's gene expression profile.
`scater`	`normalize()`	Normalize	Returns the `SingleCellExperiment` object with normalized expression values for each cell, using the size factors stored in the 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
`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 colorblind friendly
`Rtsne`	`Rtsne()`	T-Distributed Stochastic Neighbor Embedding using a Barnes-Hut Implementation	Reduces the dimensions of the specified matrix or data frame
`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)

Salmon

Read the Salmon documentation **here**.

Piece of Code	What it's called	What it does
`salmon alevin`	Salmon Alevin	Runs the Alevin quantification from the command line