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`	`rowSums()`	Row sums	Calculates sums for each row
Base `R`	`colSums()`	Column sums	Calculates sums for each column
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> }`	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`	`geom_vline()`	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 **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`	`colData()`	Column Data	Extracts and stores cell-level metadata that describes features of the `SingleCellExperiment` object
`SingleCellExperiment`	`rowData()`	Row Data	Extracts and stores gene-level metadata that describes features of the `SingleCellExperiment` object
`SingleCellExperiment`	`logcounts()`	Log counts	Stores or extracts log-transformed single-cell experiment count data as an assay of the `SingleCellExperiment` object
`SingleCellExperiment`	`counts()`	Counts	Stores or extracts raw single-cell experiment count data as an assay 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`
		Compute	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-

`scran`	`computeSumFactors()`	Sum Factors	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
`scran`	`getTopHVGs()`	Get top highly variable genes	Identify variable genes in a `SingleCellExperiment` object, based on variance
`scran`	`modelGeneVar()`	model per gene variance	Model the per gene variance of a `SingleCellExperiment` object
`scran`	`findMarkers()`	Find marker genes	Find candidate marker genes for clusters of cells
`scater`	`addPerCellQC()`	Add per cell quality control	For a `SingleCellExperiment` object, calculate and add quality control per cell and store in `colData`
`scater`	`addPerFeatureQC()`	Add per feature quality control	For a `SingleCellExperiment` object, calculate and add quality control per feature (genes usually) and store in `rowData`
`scater`	`calculatePCA()`	Calculate PCA	Calculates principal components analysis on a `SingleCellExperiment` object

`scater`	calculateUMAP()	Calculate UMAP	Calculates uniform manifold approximate projection on a `SingleCellExperiment` object
`scater`	calculateTSNE()	Calculate t-SNE	Calculate t-stochastic neighbor embedding on a `SingleCellExperiment` object

`purrr`

Read the `purrr` documentation **here**.

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` documentation **here**

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
`dat`	`DataFrame()`	Data frame	Not to be confused with [`data.frame()` from Base R. This is a slightly different data frame-like object needed for storing information in `SingleCellExperiment` object's `colData()` .
`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`	`as_tibble()`	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
`salmon alevin`	Salmon Alevin	Runs the Alevin quantification from the command line