

# scRNA-seq Cheatsheet

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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>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          | <pre>&lt;-<br/>function(x)<br/>{ &lt;code&gt; }</pre> | 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 [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 | <code>SingleCellExperiment()</code> | Single Cell Experiment | Creates a SingleCellExperiment object  |
| SingleCellExperiment | <code>colData()</code>              | Column Data            | Extracts and stores cell-level metadata that describes features of the SingleCellExperiment object |
| SingleCellExperiment | <code>rowData()</code>              | Row Data               | Extracts and stores gene-level metadata that describes features of the SingleCellExperiment object |

| Library/Package      | Piece of Code                    | What it's called                | What it does  |
|----------------------|----------------------------------|---------------------------------|---|
| SingleCellExperiment | <code>logcounts()</code>         | Log counts                      | Stores or extracts log-transformed single-cell experiment count data as an assay of the <code>SingleCellExperiment</code> object  |
| SingleCellExperiment | <code>counts()</code>            | Counts                          | Stores or extracts raw single-cell experiment count data as an assay of the <code>SingleCellExperiment</code> object  |
| scrn                 | <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>  |
| scrn                 | <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 <code>scrn::normalize</code> function for the normalization of each cell's gene expression profile |
| scater               | <code>normalize()</code>         | Normalize                       | Returns the <code>SingleCellExperiment</code> object with normalized expression values for each cell, using the size factors stored in the object   |
| scrn                 | <code>getTopHVGs()</code>        | Get top highly variable genes   | Identify variable genes in a <code>SingleCellExperiment</code> object, based on variance  |
| scrn                 | <code>modelGeneVar()</code>      | model per gene variance         | Model the per gene variance of a <code>SingleCellExperiment</code> object   |
| scrn                 | <code>findMarkers()</code>       | Find marker genes               | Find candidate marker genes for clusters of cells   |
| scater               | <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>  |
| scater               | <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>   |
| scater               | <code>calculatePCA()</code>      | Calculate PCA                   | Calculates principal components analysis on a <code>SingleCellExperiment</code> object  |

| Library/Package | Piece of Code                | What it's called | What it does   |
|-----------------|------------------------------|------------------|--|
| scater          | <code>calculateUMAP()</code> | Calculate UMAP   | Calculates uniform manifold approximate projection on a <code>SingleCellExperiment</code> object |
| scater          | <code>calculateTSNE()</code> | Calculate TSNE   | Calculate t-stochastic neighbor embedding on a <code>SingleCellExperiment</code> object          |

## 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>dat</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>colorblindr</code> | <code>scale_color_okabeIto()</code> | OkabeIto Color Scale  | When added as a layer to a plot, makes the plot colorblind friendly  |
| <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 |