

Advanced 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.

You may also be interested in the following additional cheatsheets:

- Download the PDF for the [Introduction to R and Tidyverse](#)
- Download the PDF for the [Introduction to Single-Cell RNA sequencing cheatsheet](#)

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.

Please be aware that the documentation will generally provide information about the given function's most current version (or a recent version, depending on how often the documentation site is updated).

This will usually (but not always!) match what you have installed on your machine.

If you have a different version of R or other R packages, the documentation may differ from what you have installed.

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scater

Read the [scater package documentation](#), and a [vignette on its usage](#).

Library/Package	Piece of Code	What it's called	What it does
scater	<code>plotReducedDim()</code>	Plot reduced dimensions	Plot a given reduced dimension slot from a <code>SingleCellExperiment</code> object by its name
scater	<code>plotUMAP()</code>	Plot UMAP	Plot the "UMAP"-named reduced dimension slot from a <code>SingleCellExperiment</code> object
scater	<code>plotExpression()</code>	Plot expression	Plot expression values for all cells in a <code>SingleCellExperiment</code> object, using the <code>logcounts</code> assay by default

miQC

Read the [miQC package documentation](#), and a [vignette on its usage](#).

Library/Package	Piece of Code	What it's called	What it does
miQC	<code>mixtureModel()</code>	Mixture model	Fit a <code>miQC</code> mixture model to a <code>SingleCellExperiment</code> object for use in filtering
miQC	<code>filterCells()</code>	Filter cells	Filter cells from a <code>SingleCellExperiment</code> object based on a <code>miQC</code> model, returning a filtered <code>SingleCellExperiment</code> object
miQC	<code>plotMetrics()</code>	Plot metrics	Plot percent of mitochondrial reads against the number of unique genes found for each cell
miQC	<code>plotModel()</code>	Plot model	<code>miQC::plotMetrics()</code> with the <code>miQC</code> fitted model overlaid
miQC	<code>plotFiltering()</code>	Plot filtering	Plot percent of mitochondrial reads against the number of unique genes found, coloring points based on whether they will be filtered out or not

batchelor and harmony

Read the [batchelor package documentation](#), and a [vignette on its usage](#).

Read the [harmony package documentation](#), and a [vignette on its usage](#).

Library/Package	Piece of Code	What it's called	What it does
<code>batchelor</code>	<code>MultiBatchPCA()</code>	Multi-batch PCA	Perform PCA across multiple gene expression matrices, weighted by batch size
<code>batchelor</code>	<code>fastMNN()</code>	Fast mutual nearest neighbors correction	Perform integration on an SCE object with mutual nearest neighbors using the <code>fastMNN</code> algorithm, returning an SCE object with batch-corrected principal components
<code>harmony</code>	<code>HarmonyMatrix()</code>	Perform <code>harmony</code> integration on a matrix	Perform integration with <code>harmony</code> on either a matrix of principle components or gene expression, returning a matrix of batch-corrected principal components

`pheatmap` and `EnhancedVolcano`

Read the [pheatmap package documentation](#).

Read the [EnhancedVolcano package documentation](#), and [vignette on its usage](#).

Library/Package	Piece of Code	What it's called	What it does
<code>pheatmap</code>	<code>pheatmap()</code>	Pretty heatmap	Plot a (pretty!) clustered heatmap
<code>EnhancedVolcano</code>	<code>EnhancedVolcano()</code>	Enhanced volcano	Plot a volcano plot to visualize differential expression analysis results

`tidyverse` functions

`purrr` functions

Read the [purrr package documentation](#) and a [vignette on its usage](#), and download the [purrr package cheatsheet](#).

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>imap()</code>	imap	Apply a function across each element of list and its index/names; return a list
<code>purrr</code>	<code>map2()</code>	map2	Apply a function across each element of two lists at a time; return a list

Library/Package	Piece of Code	What it's called	What it does
<code>purrr</code>	<code>reduce()</code>	Reduce	Reduce a list to a single value by applying a given function

Note that `purrr::map()` functions can take advantage of R's new (as of version 4.1.0) [anonymous function syntax](#):

```
# One-line syntax:
\(x) function code goes here

# Multi-line syntax:
\(x) {
  function code goes
  inside the curly braces
}

# Example: Use an anonymous function with `purrr::map()`
# to get the colData's rownames for each SCE in `list_of_sce_objects`
purrr::map(
  list_of_sce_objects,
  \(x) rownames(colData(x))
)
```

ggplot2 functions

Read the [ggplot2 package documentation](#) and an [overall reference for ggplot2 functions](#), and download the [ggplot2 package cheatsheet](#).

Library/Package	Piece of Code	What it's called	What it does
<code>ggplot2</code>	<code>geom_bar()</code>	Barplot	Creates a barplot of counts for a given categorical variable when added as a layer to a <code>ggplot()</code> object
<code>ggplot2</code>	<code>scale_fill_brewer()</code>	Add brewer fill scale	Apply a Brewer "fill" color palette to a categorical variable in a <code>ggplot()</code> object
<code>ggplot2</code>	<code>guides()</code>	Guides	Function to customize legend ("guide") appearance
<code>ggplot2</code>	<code>facet_grid()</code>	Facet grid	Plot individual panels using specified variables to subset the data across rows and/or columns of a grid

Library/Package	Piece of Code	What it's called	What it does
ggplot2	vars()	Vars	Helper function to specify variables to <code>facet_grid()</code> or <code>facet_wrap()</code>
ggplot2	theme_bw()	Black and white theme	Display <code>ggplot</code> with gridlines but a white background
ggplot2	theme()	Theme	Customize elements of a <code>ggplot</code> plot theme
ggplot2	element_text()	Element text	Customize textual elements of a <code>ggplot</code> theme

`dplyr`, `tidyr`, `stringr`, and `tibble` functions

Read the full documentation and download cheatsheets (where available) for these `tidyverse` packages at the following links:

- [dplyr documentation](#) and [dplyr cheatsheet](#)
- [tidyr documentation](#) and [tidyr cheatsheet](#)
- [stringr documentation](#) and [stringr cheatsheet](#)
- [tibble documentation](#)

Library/Package	Piece of Code	What it's called	What it does
dplyr	pull()	Pull	Extract a single column from a data frame into a stand-alone vector
dplyr	count()	Count	Count the number of observations in each group of a data frame
dplyr	left_join()	Left join	Joins two data frames together, retaining only rows present in the first ("left") argument to the function
dplyr	relocate()	Relocate	Change column order in a data frame by relocating one or more columns
dplyr	case_when()	Case when	Return a value based on a set of <code>TRUE/FALSE</code> comparisons; a vectorized <code>if-else</code>
tidyr	pivot_longer()	Pivot longer	Convert a "wide" format data frame to a "long" format data frame

Library/Package	Piece of Code	What it's called	What it does
<code>tibble</code>	<code>as_tibble()</code>	As tibble	Convert an object to a tibble
<code>stringr</code>	<code>str_detect()</code>	String detect	Returns TRUE/FALSE if a string contains a given substring
<code>stringr</code>	<code>str_starts()</code>	String starts	Returns TRUE/FALSE if a string starts with a given substring

Seurat and SCE object conversion

Converting from Seurat to SCE

Converting from SCE to Seurat