

Bulk RNA-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. 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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Base R

Read the [Base R package documentation](#).

Library/Package	Piece of Code	What it's called	What it does
Base R	<code>list.files()</code>	List files	Produces a character vector of files or directories in the specified directory
Base R	<code>names()</code>	Names	Gets or sets the names of an object
Base R	<code>colnames()</code>	Column names	Gets or sets the column names of a matrix or data frame
Base R	<code>all.equal()</code>	All equal	Checks if two R objects are nearly equal
Base R	<code>attr()</code>	Object Attributes	Gets or sets the attributes of an object
Base R	<code>rowSums()</code>	Row Sums	Returns the sum of the rows in a numeric matrix-like object (i.e.. a matrix, data.frame, etc.)
Base R	<code>relevel()</code>	Relevel	Reorders the levels of a factor as specified
Base R	<code>summary()</code>	Object Summary	Returns a result summary of an object
Base R	<code>as.data.frame()</code>	Data Frame	Checks if an object is a data.frame, and transforms the object into one, if possible

DESeq2

Read the [DESeq2 package documentation](#), and the [package vignette by Love, Anders, and Huber](#).

Library/Package	Piece of Code	What it's called	What it does
DESeq2	<code>vst()</code>	Variance Stabilizing Transformation	Applies variance stabilizing transformation to data (log2-like scale)
DESeq2	<code>DESeqDataSet()</code>	DESeqDataSet constructor that can take a <code>SummarizedExperiment</code>	Creates a DESeqDataSet object
DESeq2	<code>DESeqDataSetFromMatrix()</code>	DESeqDataSet constructor	Creates a DESeqDataSet object from a matrix of count data
DESeq2	<code>DESeq()</code>	Differential Expression Analysis Based on the Negative Binomial Distribution	Estimates size factors, estimates dispersion, and performs negative binomial fitting and Wald statistics as steps in the default DESeq2 differential expression analysis
DESeq2	<code>plotPCA()</code>	PCA plot	Produces a principal component analysis plot for transformed data. It can be used to visually inspect the data, which might allow an analyst to identify batch effects.
DESeq2	<code>counts()</code>	Counts	Returns count matrix from <code>DESeqDataSet</code> object
DESeq2	<code>results()</code>	Results	Returns the results table from a DESeq2 analysis
DESeq2	<code>assay()</code>	Assay	Returns matrix from the <code>assay</code> slot of a <code>DESeqDataSet</code> object

FastQC and fastp

Read the [FastQC documentation](#) and the [fastp documentation](#).

Library/Package	Piece of Code	What it's called	What it does
fastp	<code>fastp</code>	FASTQ preprocessor	Preprocesses FASTQ files through adapter trimming, quality filtering, length filtering, and a number of additional options
FastQC	<code>fastqc</code>	FASTQC (Quality Control)	Performs quality control checks on raw sequence data and outputs a QC(quality control) report

ggplot2

Read the [ggplot2 package documentation](#), an [overall reference for ggplot2 functions](#), and a [vignette on the usage of the ggplot2 aesthetics](#). Additional vignettes are available from the "Articles" dropdown menu on this webpage.

Library/Package	Piece of Code	What it's called	What it does
ggplot2	<code>ggsave()</code>	GG Save	Saves the last plot in working directory
ggplot2	<code>last_plot()</code>	Last plot	Returns the last plot produced
ggplot2	<code>geom_point()</code>	Geom point	Creates a scatterplot (when added to the <code>ggplot()</code> function)
ggplot2	<code>labs(); xlab() ; ylab()</code>	X Axis Labels; Y Axis Labels	Modifies the plot labels, with specific functions for the x axis and y axis, respectively
ggplot2	<code>coord_fixed()</code>	Cartesian Coordinates with Fixed Aspect Ratio	Coerces the coordinates on the plot to represent a fixed specified ratio

tximeta and SummarizedExperiment

Read the [tximeta package documentation](#), and the [package vignette by Love *et al.*](#). Read the [SummarizedExperiment package documentation](#), and the [package vignette by Morgan *et al.*](#).

Library/Package	Piece of Code	What it's called	What it does
tximeta	<code>tximeta()</code>	tximeta	Imports transcript-level estimates, attaches transcriptome annotation, and returns a <code>SummarizedExperiment</code> object
tximeta	<code>makeLinkedTxome()</code>	Make Linked Transcriptome	Sets up transcriptome annotation to be used by the <code>tximeta()</code> function (Only necessary if <code>tximeta()</code> fails to find annotation, like for non-human, non-mouse species data)
tximeta	<code>summarizeToGene()</code>	Summarize to Gene	Takes a <code>SummarizedExperiment</code> that was set up by <code>tximeta</code> and summarizes transcript data to the gene-level
SummarizedExperiment	<code>rowData()</code> <code>colData()</code>	Col/Row Data	Accesses the row or column data from a <code>SummarizedExperiment</code> object
SummarizedExperiment	<code>assay()</code> <code>assayNames()</code>	Assay or AssayNames	Accesses the assay data or the names of the assays from <code>SummarizedExperiment</code> object

stringr, readr, dplyr, pheatmap

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
stringr	<code>word()</code>	Word	Extracts words from a character vector
readr	<code>write_rds()</code>	Write RDS	Writes data to a .RDS output file
dplyr	<code>pull()</code>	Pull	Extracts a variable (column) as a vector
pheatmap	<code>pheatmap()</code>	Pretty heatmap	Plots clustered heatmaps

Salmon

Read the [Salmon tool documentation](#).

Tool	Piece of Code	What it's called	What it does
Salmon	salmon index	Salmon index	Builds a transcriptome index which is required for Salmon quantification (from the command line)

Tool	Piece of Code	What it's called	What it does
Salmon	<code>salmon</code> <code>quant</code>	Salmon quantification	Runs Salmon's quantification of transcript expression (from the command line)

