

Pathway Analysis 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.

msigdb

Read the `msigdb` documentation [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>msigdb</code>	<code>msigdb()</code>	geom vertical line	Retrieves the specified MSigDB dataset

AnnotationDbi

Read the `AnnotationDbi` package vignette [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>AnnotationDbi</code>	<code>keytypes()</code>	Keytypes	Returns a character vector of column names/types of gene identifiers (e.g. <code>ENSEMBL</code>) available in an <code>AnnotationDbi</code> package.
<code>AnnotationDbi</code>	<code>mapIds()</code>	Mapped IDs	Extracts the mapped IDs for a set of gene identifiers. The types of gene identifiers (e.g. <code>ENSEMBL</code> or <code>ENTREZ</code>) are supplied to arguments: <code>keytype</code> (type of gene identifiers we are providing in the <code>keys</code> argument) and <code>column</code> (type of gene identifiers we want returned).

Base R

Read the Base `R` documentation [here](#).

Library/Package	Piece of Code	What it's called	What it does
Base <code>R</code>	<code>fisher.test()</code>	Fisher's Exact Test	Performs the Fisher's exact test for testing the null of independence of rows and columns for a given matrix or data.frame with count data

DESeq2

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

Library/Package	Piece of Code	What it's called	What it does
<code>DESeq2</code>	<code>results()</code>	Results	Returns the results table from a DESeq2 analysis
<code>DESeq2</code>	<code>lfcShrink()</code>	Shrink Log Fold Changes	Adds shrunken log2 fold changes to the results of a <code>DESeqDataSet</code> object
<code>DESeq2</code>	<code>resultsNames()</code>	Results Names	Returns the names of the estimated effects or coefficients of the <code>DESeq</code> model

enrichplot

Read the `enrichplot` package documentation [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>enrichplot</code>	<code>dotplot()</code>	Dot plot	Produces a dot plot for given enrichment results
<code>enrichplot</code>	<code>upsetplot()</code>	Upset plot	Produces an upset plot, which shows the overlapping genes between gene sets, for given enrichment results
<code>enrichplot</code>	<code>gseaplot()</code>	GSEA plot	Produces a plot visualization displaying the distribution of gene set and enrichment score

clusterProfiler

Read the `clusterProfiler` package documentation [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>clusterProfiler</code>	<code>enricher()</code>	Enricher	Performs a universal over-representation/enrichment analysis for a given genes of interest list
<code>clusterProfiler</code>	<code>GSEA()</code>	Gene Set Enrichment Analysis (GSEA)	Performs a universal gene set enrichment analysis on given preranked (sorted) named vector of statistics, where the names in the vector are gene identifiers of gene sets

GSVA

Read the `GSVA` package documentation [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>GSVA</code>	<code>gsva(.)</code>	Gene Set Variation Analysis (GSVA)	Estimates gene set variation analysis enrichment scores on given gene expression matrix

qusage

Read the `qusage` package documentation [here](#).

Library/Package	Piece of Code	What it's called	What it does
<code>qusage</code>	<code>read.gmt(.)</code>	Read in <code>.gmt</code> files	Reads in gene set information from <code>.gmt</code> files