

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. 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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msigdb

Read the [msigdb](#) documentation.

Library/Package	Piece of Code	What it's called	What it does
<code>msigdb</code>	<code>msigdb()</code>	Retrieve the MSigDB gene sets data frame	Retrieves the specified MSigDB dataset

AnnotationDbi

Read the [AnnotationDbi](#) package vignette (PDF).

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.

Library/Package	Piece of Code	What it's called	What it does
Base R	<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 <code>data.frame</code> with count data
Base R	<code>setdiff()</code>	Set difference	Returns the difference of two sets (e.g., vectors)

enrichplot

Read the [enrichplot package documentation \(PDF\)](#).

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

clusterProfiler

Read the [clusterProfiler package documentation \(PDF\)](#).

Library/Package	Piece of Code	What it's called	What it does
clusterProfiler	<code>enricher()</code>	Enricher	Performs a universal over-representation analysis for a given list of genes and gene sets or pathways
clusterProfiler	<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](#).

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

qusage

Read the [qusage package documentation](#).

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