

# Package ‘clustermole’

October 12, 2022

**Type** Package

**Title** Unbiased Single-Cell Transcriptomic Data Cell Type Identification

**Version** 1.1.0

**Description** Assignment of cell type labels to single-cell RNA sequencing (scRNA-seq) clusters is often a time-consuming process that involves manual inspection of the cluster marker genes complemented with a detailed literature search. This is especially challenging when unexpected or poorly described populations are present. The clustermole R package provides methods to query thousands of human and mouse cell identity markers sourced from a variety of databases.

**License** MIT + file LICENSE

**URL** <https://igordot.github.io/clustermole/>,  
<https://github.com/igordot/clustermole>

**BugReports** <https://github.com/igordot/clustermole/issues>

**Depends** R (>= 3.6)

**Imports** dplyr, GSEABase, GSVA (>= 1.26.0), magrittr, methods, rlang (>= 0.1.2), singscore, tibble, tidyr, utils

**Suggests** covr, knitr, prettydoc, rmarkdown, roxygen2, testthat (>= 2.1.0)

**biocViews**

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**NeedsCompilation** no

**Author** Igor Dolgalev [aut, cre]

**Maintainer** Igor Dolgalev <igor.dolgalev@nyumc.org>

**Repository** CRAN

**Date/Publication** 2021-01-26 06:40:02 UTC

## R topics documented:

clustermole_enrichment . . . . .	2
clustermole_markers . . . . .	3
clustermole_overlaps . . . . .	3
read_gmt . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

---

clustermole\_enrichment

*Cell types based on the expression of all genes*

---

### Description

Perform enrichment of cell type signatures based on the full gene expression matrix.

### Usage

```
clustermole_enrichment(expr_mat, species, method = "gsva")
```

### Arguments

expr_mat	Expression matrix (logCPMs, logFPKMs, or logTPMs) with genes as rows and clusters/populations/samples as columns.
species	Species: hs for human or mm for mouse.
method	Enrichment method: ssgsea, gsva, singscore, or all. The method to use for the estimation of gene set enrichment scores. The options are ssGSEA (Barbie et al, 2009), GSVA (Hänzelmann et al, 2013), singscore (Foroutan et al, 2018), or a combination of all three methods.

### Value

A data frame of enrichment results.

### References

Barbie, D., Tamayo, P., Boehm, J. et al. Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. *Nature* 462, 108–112 (2009). doi: [10.1038/nature08460](https://doi.org/10.1038/nature08460)

Hänzelmann, S., Castelo, R. & Guinney, J. GSVA: Gene set variation analysis for microarray and RNA-Seq data. *BMC Bioinformatics* 14, 7 (2013). doi: [10.1186/14712105147](https://doi.org/10.1186/14712105147)

Foroutan, M., Bhuva, D.D., Lyu, R. et al. Single sample scoring of molecular phenotypes. *BMC Bioinformatics* 19, 404 (2018). doi: [10.1186/s1285901824354](https://doi.org/10.1186/s1285901824354)

### Examples

```
# my_enrichment <- clustermole_enrichment(expr_mat = my_expr_mat, species = "hs")
```

---

clustermole\_markers    *Available cell type markers*

---

**Description**

Retrieve the full list of cell type markers in the clustermole database.

**Usage**

```
clustermole_markers(species = c("hs", "mm"))
```

**Arguments**

species            Species: hs for human or mm for mouse.

**Value**

A data frame of cell type markers (one gene per row).

**Examples**

```
markers <- clustermole_markers()
head(markers)
```

---

clustermole\_overlaps    *Cell types based on overlap of marker genes*

---

**Description**

Perform overrepresentation analysis for a set of genes compared to all cell type signatures.

**Usage**

```
clustermole_overlaps(genes, species)
```

**Arguments**

genes            A vector of genes.  
species           Species: hs for human or mm for mouse.

**Value**

A data frame of enrichment results with hypergeometric test p-values.

**Examples**

```
my_genes <- c("CD2", "CD3D", "CD3E", "CD3G", "TRAC", "TRBC2", "LTB")
my_overlaps <- clustermole_overlaps(genes = my_genes, species = "hs")
head(my_overlaps)
```

---

read_gmt	<i>Read a GMT file into a data frame</i>
----------	--

---

**Description**

Read a GMT file into a data frame

**Usage**

```
read_gmt(file, geneset_label = "celltype", gene_label = "gene")
```

**Arguments**

file	A connection object or a character string (can be a URL).
geneset_label	Column name for gene sets (first column of the GMT file) in the output data frame.
gene_label	Column name for genes (variable columns of the GMT file) in the output data frame.

**Value**

A data frame with gene sets as the first column and genes as the second column (one gene per row).

**Examples**

```
gmt <- "http://software.broadinstitute.org/gsea/msigdb/supplemental/scsig.all.v1.0.symbols.gmt"
gmt_tbl <- read_gmt(gmt)
head(gmt_tbl)
```

# Index

clustermole\_enrichment, 2

clustermole\_markers, 3

clustermole\_overlaps, 3

read\_gmt, 4