

# Package ‘clustifyr’

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**Title** Classifier for Single-cell RNA-seq Using Cell Clusters

**Version** 1.25.0

**Description** Package designed to aid in classifying cells from single-cell RNA sequencing data using external reference data (e.g., bulk RNA-seq, scRNA-seq, microarray, gene lists). A variety of correlation based methods and gene list enrichment methods are provided to assist cell type assignment.

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clustifyr-package	<i>clustifyr: Classifier for Single-cell RNA-seq Using Cell Clusters</i>
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### Description

Package designed to aid in classifying cells from single-cell RNA sequencing data using external reference data (e.g., bulk RNA-seq, scRNA-seq, microarray, gene lists). A variety of correlation based methods and gene list enrichment methods are provided to assist cell type assignment.

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### See Also

Useful links:

- <https://github.com/rnabioco/clustifyr>
- <https://rnabioco.github.io/clustifyr/>
- Report bugs at <https://github.com/rnabioco/clustifyr/issues>

---

append_genes	<i>Given a reference matrix and a list of genes, take the union of all genes in vector and genes in reference matrix and insert zero counts for all remaining genes.</i>
--------------	--

---

### Description

Given a reference matrix and a list of genes, take the union of all genes in vector and genes in reference matrix and insert zero counts for all remaining genes.

### Usage

```
append_genes(gene_vector, ref_matrix)
```

**Arguments**

gene\_vector      char vector with gene names  
 ref\_matrix        Reference matrix containing cell types vs. gene expression values

**Value**

Reference matrix with union of all genes

**Examples**

```
mat <- append_genes(
  gene_vector = human_genes_10x,
  ref_matrix = cbmc_ref
)
```

---

assess\_rank\_bias      *Find rank bias*

---

**Description**

Find rank bias

**Usage**

```
assess_rank_bias(
  avg_mat,
  ref_mat,
  query_genes = NULL,
  res,
  organism,
  plot_name = NULL,
  rds_name = NULL,
  expand_unassigned = FALSE
)
```

**Arguments**

avg\_mat            average expression matrix  
 ref\_mat            reference expression matrix  
 query\_genes        original vector of genes used to clustify  
 res                dataframe of idents, such as output of cor\_to\_call  
 organism            for GO term analysis, organism name: human - 'hsapiens', mouse - 'mmusculus'  
 plot\_name          name for saved pdf, if NULL then no file is written (default)  
 rds\_name            name for saved rds of rank\_diff, if NULL then no file is written (default)  
 expand\_unassigned    test all ref clusters for unassigned results

**Value**

pdf of ggplot object

**Examples**

```
## Not run:
avg <- average_clusters(
  pbmc_matrix_small,
  pbmc_meta$seurat_clusters
)
res <- clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  query_genes = pbmc_vargenes,
  cluster_col = "seurat_clusters"
)
top_call <- cor_to_call(
  res,
  metadata = pbmc_meta,
  cluster_col = "seurat_clusters",
  collapse_to_cluster = FALSE,
  threshold = 0.8
)
res_rank <- assess_rank_bias(
  avg,
  cbmc_ref,
  res = top_call
)

## End(Not run)
```

---

assign\_ident

*manually change idents as needed*

---

**Description**

manually change idents as needed

**Usage**

```
assign_ident(
  metadata,
  cluster_col = "cluster",
  ident_col = "type",
  clusters,
  idents
)
```

**Arguments**

metadata	column of ident
cluster_col	column in metadata containing cluster info
ident_col	column in metadata containing identity assignment
clusters	names of clusters to change, string or vector of strings
idents	new idents to assign, must be length of 1 or same as clusters

**Value**

new dataframe of metadata

---

average_clusters	<i>Average expression values per cluster</i>
------------------	--

---

**Description**

Average expression values per cluster

**Usage**

```
average_clusters(
  mat,
  metadata,
  cluster_col = "cluster",
  if_log = TRUE,
  cell_col = NULL,
  low_threshold = 0,
  method = "mean",
  output_log = TRUE,
  subclusterpower = 0,
  cut_n = NULL
)
```

**Arguments**

mat	expression matrix
metadata	data.frame or vector containing cluster assignments per cell. Order must match column order in supplied matrix. If a data.frame provide the cluster_col parameters.
cluster_col	column in metadata with cluster number
if_log	input data is natural log, averaging will be done on unlogged data
cell_col	if provided, will reorder matrix first
low_threshold	option to remove clusters with too few cells
method	whether to take mean (default), median, 10% truncated mean, or trimean, max, min
output_log	whether to report log results
subclusterpower	whether to get multiple averages per original cluster
cut_n	set on a limit of genes as expressed, lower ranked genes are set to 0, considered unexpressed

**Value**

average expression matrix, with genes for row names, and clusters for column names

**Examples**

```
mat <- average_clusters(  
  mat = pbmc_matrix_small,  
  metadata = pbmc_meta,  
  cluster_col = "classified",  
  if_log = FALSE  
)  
mat[1:3, 1:3]
```

---

binarize\_expr

*Binarize scRNAseq data*

---

**Description**

Binarize scRNAseq data

**Usage**

```
binarize_expr(mat, n = 1000, cut = 0)
```

**Arguments**

mat	single-cell expression matrix
n	number of top expressing genes to keep
cut	cut off to set to 0

**Value**

matrix of 1s and 0s

**Examples**

```
pbmc_avg <- average_clusters(  
  mat = pbmc_matrix_small,  
  metadata = pbmc_meta,  
  cluster_col = "classified"  
)  
  
mat <- binarize_expr(pbmc_avg)  
mat[1:3, 1:3]
```

---

build_atlas	<i>Function to combine records into single atlas</i>
-------------	--

---

**Description**

Function to combine records into single atlas

**Usage**

```
build_atlas(matrix_fns = NULL, genes_fn, matrix_objs = NULL, output_fn = NULL)
```

**Arguments**

matrix_fns	character vector of paths to study matrices stored as .rds files. If a named character vector, then the name will be added as a suffix to the cell type name in the final matrix. If it is not named, then the filename will be used (without .rds)
genes_fn	text file with a single column containing genes and the ordering desired in the output matrix
matrix_objs	Checks to see whether .rds files will be read or R objects in a local environment. A list of environmental objects can be passed to matrix_objs, and that names will be used, otherwise defaults to numbers
output_fn	output filename for .rds file. If NULL the matrix will be returned instead of saving

**Value**

Combined matrix with all genes given

**Examples**

```
pbmc_ref_matrix <- average_clusters(
  mat = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified",
  if_log = TRUE # whether the expression matrix is already log transformed
)
references_to_combine <- list(pbmc_ref_matrix, cbmc_ref)
atlas <- build_atlas(NULL, human_genes_10x, references_to_combine, NULL)
```

---

calculate_pathway_gsea	<i>Convert expression matrix to GSEA pathway scores (would take a similar place in workflow before average_clusters/binarize)</i>
------------------------	---

---

**Description**

Convert expression matrix to GSEA pathway scores (would take a similar place in workflow before average\_clusters/binarize)

**Usage**

```
calculate_pathway_gsea(  
  mat,  
  pathway_list,  
  n_perm = 1000,  
  scale = TRUE,  
  no_warnings = TRUE  
)
```

**Arguments**

mat	expression matrix
pathway_list	a list of vectors, each named for a specific pathway, or dataframe
n_perm	Number of permutation for fgsea function. Defaults to 1000.
scale	convert expr_mat into zscores prior to running GSEA?, default = FALSE
no_warnings	suppress warnings from gsea ties

**Value**

matrix of GSEA NES values, cell types as row names, pathways as column names

**Examples**

```
gl <- list(  
  "n" = c("PPBP", "LYZ", "S100A9"),  
  "a" = c("IGLL5", "GNLY", "FTL")  
)  
  
pbmc_avg <- average_clusters(  
  mat = pbmc_matrix_small,  
  metadata = pbmc_meta,  
  cluster_col = "classified"  
)  
  
calculate_pathway_gsea(  
  mat = pbmc_avg,  
  pathway_list = gl  
)
```

---

calc\_distance

*Distance calculations for spatial coord*

---

**Description**

Distance calculations for spatial coord

**Usage**

```
calc_distance(
  coord,
  metadata,
  cluster_col = "cluster",
  collapse_to_cluster = FALSE
)
```

**Arguments**

coord	dataframe or matrix of spatial coordinates, cell barcode as rownames
metadata	data.frame or vector containing cluster assignments per cell. Order must match column order in supplied matrix. If a data.frame provide the cluster_col parameters.
cluster_col	column in metadata with cluster number
collapse_to_cluster	instead of reporting min distance to cluster per cell, summarize to cluster level

**Value**

min distance matrix

**Examples**

```
cbs <- paste0("cb_", 1:100)

spatial_coords <- data.frame(
  row.names = cbs,
  X = runif(100),
  Y = runif(100)
)
group_ids <- sample(c("A", "B"), 100, replace = TRUE)
dist_res <- calc_distance(
  spatial_coords,
  group_ids
)
```

---

calc_similarity	<i>compute similarity</i>
-----------------	---------------------------

---

**Description**

compute similarity

**Usage**

```
calc_similarity(query_mat, ref_mat, compute_method, rm0 = FALSE, ...)
```

**Arguments**

query_mat	query data matrix
ref_mat	reference data matrix
compute_method	method(s) for computing similarity scores
rm0	consider 0 as missing data, recommended for per_cell
...	additional parameters

**Value**

matrix of numeric values

---

call_consensus	<i>get consensus calls for a list of cor calls</i>
----------------	--

---

**Description**

get consensus calls for a list of cor calls

**Usage**

```
call_consensus(list_of_res)
```

**Arguments**

list_of_res	list of call dataframes from cor_to_call_rank
-------------	---

**Value**

dataframe of cluster, new ident, and mean rank

**Examples**

```
res <- clustify(  
  input = pbmc_matrix_small,  
  metadata = pbmc_meta,  
  cluster_col = "classified",  
  ref_mat = cbmc_ref  
)  
  
res2 <- cor_to_call_rank(res, threshold = "auto")  
res3 <- cor_to_call_rank(res)  
call_consensus(list(res2, res3))
```

---

call_to_metadata	<i>Insert called ident results into metadata</i>
------------------	--

---

## Description

Insert called ident results into metadata

## Usage

```
call_to_metadata(  
  res,  
  metadata,  
  cluster_col,  
  per_cell = FALSE,  
  rename_prefix = NULL  
)
```

## Arguments

res	dataframe of idents, such as output of cor_to_call
metadata	input metadata with tsne or umap coordinates and cluster ids
cluster_col	metadata column, can be cluster or cellid
per_cell	whether the res dataframe is listed per cell
rename_prefix	prefix to add to type and r column names

## Value

new metadata with added columns

## Examples

```
res <- clustify(  
  input = pbmc_matrix_small,  
  metadata = pbmc_meta,  
  cluster_col = "classified",  
  ref_mat = cbmc_ref  
)  
  
res2 <- cor_to_call(res, cluster_col = "classified")  
  
call_to_metadata(  
  res = res2,  
  metadata = pbmc_meta,  
  cluster_col = "classified",  
  rename_prefix = "assigned"  
)
```

---

cbmc_m	<i>reference marker matrix from seurat citeseq CBMC tutorial</i>
--------	--

---

**Description**

reference marker matrix from seurat citeseq CBMC tutorial

**Usage**

```
cbmc_m
```

**Format**

An object of class `data.frame` with 3 rows and 13 columns.

**Source**

[https://satijalab.org/seurat/v3.0/multimodal\\_vignette.html#identify-differentially-expressed-pro](https://satijalab.org/seurat/v3.0/multimodal_vignette.html#identify-differentially-expressed-pro)

**See Also**

Other data: [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

cbmc_ref	<i>reference matrix from seurat citeseq CBMC tutorial</i>
----------	---

---

**Description**

reference matrix from seurat citeseq CBMC tutorial

**Usage**

```
cbmc_ref
```

**Format**

An object of class `matrix` (inherits from `array`) with 2000 rows and 13 columns.

**Source**

[https://satijalab.org/seurat/v3.0/multimodal\\_vignette.html#identify-differentially-expressed-pro](https://satijalab.org/seurat/v3.0/multimodal_vignette.html#identify-differentially-expressed-pro)

**See Also**

Other data: [cbmc\\_m](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

check_raw_counts	<i>Given a count matrix, determine if the matrix has been either log-normalized, normalized, or contains raw counts</i>
------------------	---

---

**Description**

Given a count matrix, determine if the matrix has been either log-normalized, normalized, or contains raw counts

**Usage**

```
check_raw_counts(counts_matrix, max_log_value = 50)
```

**Arguments**

counts\_matrix    Count matrix containing scRNA-seq read data  
max\_log\_value    Static value to determine if a matrix is normalized

**Value**

String either raw counts, log-normalized or normalized

**Examples**

```
check_raw_counts(pbmc_matrix_small)
```

---

clustify	<i>Compare scRNA-seq data to reference data.</i>
----------	--

---

**Description**

Compare scRNA-seq data to reference data.

**Usage**

```
clustify(input, ...)

## Default S3 method:
clustify(
  input,
  ref_mat,
  metadata = NULL,
  cluster_col = NULL,
  query_genes = NULL,
  n_genes = 1000,
  per_cell = FALSE,
  n_perm = 0,
  compute_method = "spearman",
  pseudobulk_method = "mean",
  verbose = TRUE,
```

```
    lookuptable = NULL,
    rm0 = FALSE,
    obj_out = TRUE,
    seurat_out = obj_out,
    vec_out = FALSE,
    rename_prefix = NULL,
    threshold = "auto",
    low_threshold_cell = 0,
    exclude_genes = c(),
    if_log = TRUE,
    organism = "hsapiens",
    plot_name = NULL,
    rds_name = NULL,
    expand_unassigned = FALSE,
    ...
)

## S3 method for class 'Seurat'
clustify(
  input,
  ref_mat,
  cluster_col = NULL,
  query_genes = NULL,
  n_genes = 1000,
  per_cell = FALSE,
  n_perm = 0,
  compute_method = "spearman",
  pseudobulk_method = "mean",
  use_var_genes = TRUE,
  dr = "umap",
  obj_out = TRUE,
  seurat_out = obj_out,
  vec_out = FALSE,
  threshold = "auto",
  verbose = TRUE,
  rm0 = FALSE,
  rename_prefix = NULL,
  exclude_genes = c(),
  metadata = NULL,
  organism = "hsapiens",
  plot_name = NULL,
  rds_name = NULL,
  expand_unassigned = FALSE,
  ...
)

## S3 method for class 'SingleCellExperiment'
clustify(
  input,
  ref_mat,
  cluster_col = NULL,
  query_genes = NULL,
```

```

per_cell = FALSE,
n_perm = 0,
compute_method = "spearman",
pseudobulk_method = "mean",
use_var_genes = TRUE,
dr = "umap",
obj_out = TRUE,
seurat_out = obj_out,
vec_out = FALSE,
threshold = "auto",
verbose = TRUE,
rm0 = FALSE,
rename_prefix = NULL,
exclude_genes = c(),
metadata = NULL,
organism = "hsapiens",
plot_name = NULL,
rds_name = NULL,
expand_unassigned = FALSE,
...
)

```

### Arguments

input	single-cell expression matrix or Seurat object
...	additional arguments to pass to compute_method function
ref_mat	reference expression matrix
metadata	cell cluster assignments, supplied as a vector or data.frame. If data.frame is supplied then cluster_col needs to be set. Not required if running correlation per cell.
cluster_col	column in metadata that contains cluster ids per cell. Will default to first column of metadata if not supplied. Not required if running correlation per cell.
query_genes	A vector of genes of interest to compare. If NULL, then common genes between the expr_mat and ref_mat will be used for comparison.
n_genes	number of genes limit for Seurat variable genes, by default 1000, set to 0 to use all variable genes (generally not recommended)
per_cell	if true run per cell, otherwise per cluster.
n_perm	number of permutations, set to 0 by default
compute_method	method(s) for computing similarity scores
pseudobulk_method	method used for summarizing clusters, options are mean (default), median, truncate (10% truncated mean), or trimean, max, min
verbose	whether to report certain variables chosen and steps
lookuptable	if not supplied, will look in built-in table for object parsing
rm0	consider 0 as missing data, recommended for per_cell
obj_out	whether to output object instead of cor matrix
seurat_out	output cor matrix or called seurat object (deprecated, use obj_out instead)
vec_out	only output a result vector in the same order as metadata

rename_prefix	prefix to add to type and r column names
threshold	identity calling minimum correlation score threshold, only used when obj_out = TRUE
low_threshold_cell	option to remove clusters with too few cells
exclude_genes	a vector of gene names to throw out of query
if_log	input data is natural log, averaging will be done on unlogged data
organism	for GO term analysis, organism name: human - 'hsapiens', mouse - 'mmusculus'
plot_name	name for saved pdf, if NULL then no file is written (default)
rds_name	name for saved rds of rank_diff, if NULL then no file is written (default)
expand_unassigned	test all ref clusters for unassigned results
use_var_genes	if providing a seurat object, use the variable genes (stored in seurat_object@var.genes) as the query_genes.
dr	stored dimension reduction

### Value

single cell object with identity assigned in metadata, or matrix of correlation values, clusters from input as row names, cell types from ref\_mat as column names

### Examples

```
# Annotate a matrix and metadata
clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  query_genes = pbmc_vargenes,
  cluster_col = "RNA_snn_res.0.5",
  verbose = TRUE
)

# Annotate using a different method
clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  query_genes = pbmc_vargenes,
  cluster_col = "RNA_snn_res.0.5",
  compute_method = "cosine"
)

# Annotate a SingleCellExperiment object
sce <- sce_pbmc()
clustify(
  sce,
  cbmc_ref,
  cluster_col = "clusters",
  obj_out = TRUE,
  per_cell = FALSE,
  dr = "umap"
)
```

```
)

# Annotate a Seurat object
so <- so_pbmc()
clustifyr(
  so,
  cbmc_ref,
  cluster_col = "seurat_clusters",
  obj_out = TRUE,
  per_cell = FALSE,
  dr = "umap"
)

# Annotate (and return) a Seurat object per-cell
clustifyr(
  input = so,
  ref_mat = cbmc_ref,
  cluster_col = "seurat_clusters",
  obj_out = TRUE,
  per_cell = TRUE,
  dr = "umap"
)
```

---

clustifyr\_methods      *Correlation functions available in clustifyr*

---

### **Description**

Correlation functions available in clustifyr

### **Usage**

```
clustifyr_methods
```

### **Format**

An object of class character of length 5.

### **Examples**

```
clustifyr_methods
```

---

clustifyr\_lists      *Main function to compare scRNA-seq data to gene lists.*

---

### **Description**

Main function to compare scRNA-seq data to gene lists.

**Usage**

```
clustify_lists(input, ...)  
  
## Default S3 method:  
clustify_lists(  
  input,  
  marker,  
  marker_inmatrix = TRUE,  
  metadata = NULL,  
  cluster_col = NULL,  
  if_log = TRUE,  
  per_cell = FALSE,  
  topn = 800,  
  cut = 0,  
  genome_n = 30000,  
  metric = "hyper",  
  output_high = TRUE,  
  lookuptable = NULL,  
  obj_out = TRUE,  
  seurat_out = obj_out,  
  vec_out = FALSE,  
  rename_prefix = NULL,  
  threshold = 0,  
  low_threshold_cell = 0,  
  verbose = TRUE,  
  input_markers = FALSE,  
  details_out = FALSE,  
  ...  
)  
  
## S3 method for class 'Seurat'  
clustify_lists(  
  input,  
  metadata = NULL,  
  cluster_col = NULL,  
  if_log = TRUE,  
  per_cell = FALSE,  
  topn = 800,  
  cut = 0,  
  marker,  
  marker_inmatrix = TRUE,  
  genome_n = 30000,  
  metric = "hyper",  
  output_high = TRUE,  
  dr = "umap",  
  obj_out = TRUE,  
  seurat_out = obj_out,  
  vec_out = FALSE,  
  threshold = 0,  
  rename_prefix = NULL,  
  verbose = TRUE,  
  details_out = FALSE,
```

```

    ...
)

## S3 method for class 'SingleCellExperiment'
clustify_lists(
  input,
  metadata = NULL,
  cluster_col = NULL,
  if_log = TRUE,
  per_cell = FALSE,
  topn = 800,
  cut = 0,
  marker,
  marker_inmatrix = TRUE,
  genome_n = 30000,
  metric = "hyper",
  output_high = TRUE,
  dr = "umap",
  obj_out = TRUE,
  seurat_out = obj_out,
  vec_out = FALSE,
  threshold = 0,
  rename_prefix = NULL,
  verbose = TRUE,
  details_out = FALSE,
  ...
)

```

### Arguments

input	single-cell expression matrix, Seurat object, or SingleCellExperiment
...	passed to matrixize_markers
marker	matrix or dataframe of candidate genes for each cluster
marker_inmatrix	whether markers genes are already in preprocessed matrix form
metadata	cell cluster assignments, supplied as a vector or dataframe. If dataframe is supplied then cluster_col needs to be set. Not required if running correlation per cell.
cluster_col	column in metadata with cluster number
if_log	input data is natural log, averaging will be done on unlogged data
per_cell	compare per cell or per cluster
topn	number of top expressing genes to keep from input matrix
cut	expression cut off from input matrix
genome_n	number of genes in the genome
metric	adjusted p-value for hypergeometric test, or jaccard index
output_high	if true (by default to fit with rest of package), -log10 transform p-value
lookuptable	if not supplied, will look in built-in table for object parsing
obj_out	whether to output object instead of cor matrix

seurat_out	output cor matrix or called seurat object (deprecated, use obj_out instead)
vec_out	only output a result vector in the same order as metadata
rename_prefix	prefix to add to type and r column names
threshold	identity calling minimum correlation score threshold, only used when obj_out = T
low_threshold_cell	option to remove clusters with too few cells
verbose	whether to report certain variables chosen and steps
input_markers	whether input is marker data.frame of 0 and 1s (output of pos_neg_marker), and uses alternate enrichment mode
details_out	whether to also output shared gene list from jaccard
dr	stored dimension reduction

### Value

matrix of numeric values, clusters from input as row names, cell types from marker\_mat as column names

### Examples

```
# Annotate a matrix and metadata

# Annotate using a different method
clustify_lists(
  input = pbmc_matrix_small,
  marker = cbmc_m,
  metadata = pbmc_meta,
  cluster_col = "classified",
  verbose = TRUE,
  metric = "jaccard"
)
```

---

clustify_nudge	<i>Combined function to compare scRNA-seq data to bulk RNA-seq data and marker list</i>
----------------	---

---

### Description

Combined function to compare scRNA-seq data to bulk RNA-seq data and marker list

### Usage

```
clustify_nudge(input, ...)

## Default S3 method:
clustify_nudge(
  input,
  ref_mat,
  marker,
  metadata = NULL,
```

```

cluster_col = NULL,
query_genes = NULL,
compute_method = "spearman",
weight = 1,
threshold = -Inf,
dr = "umap",
norm = "diff",
call = TRUE,
marker_inmatrix = TRUE,
mode = "rank",
obj_out = FALSE,
seurat_out = obj_out,
rename_prefix = NULL,
lookuptable = NULL,
...
)

## S3 method for class 'Seurat'
clustify_nudge(
  input,
  ref_mat,
  marker,
  cluster_col = NULL,
  query_genes = NULL,
  compute_method = "spearman",
  weight = 1,
  obj_out = TRUE,
  seurat_out = obj_out,
  threshold = -Inf,
  dr = "umap",
  norm = "diff",
  marker_inmatrix = TRUE,
  mode = "rank",
  rename_prefix = NULL,
  ...
)

```

### Arguments

input	express matrix or object
...	passed to matrixize_markers
ref_mat	reference expression matrix
marker	matrix of markers
metadata	cell cluster assignments, supplied as a vector or data.frame. If data.frame is supplied then cluster_col needs to be set.
cluster_col	column in metadata that contains cluster ids per cell. Will default to first column of metadata if not supplied. Not required if running correlation per cell.
query_genes	A vector of genes of interest to compare. If NULL, then common genes between the expr_mat and ref_mat will be used for comparison.
compute_method	method(s) for computing similarity scores

weight	relative weight for the gene list scores, when added to correlation score
threshold	identity calling minimum score threshold, only used when obj_out = T
dr	stored dimension reduction
norm	whether and how the results are normalized
call	make call or just return score matrix
marker_inmatrix	whether markers genes are already in preprocessed matrix form
mode	use marker expression pct or ranked cor score for nudging
obj_out	whether to output object instead of cor matrix
seurat_out	output cor matrix or called seurat object (deprecated, use obj_out)
rename_prefix	prefix to add to type and r column names
lookuptable	if not supplied, will look in built-in table for object parsing

### Value

single cell object, or matrix of numeric values, clusters from input as row names, cell types from ref\_mat as column names

### Examples

```
# Seurat
so <- so_pbmc()
clustify_nudge(
  input = so,
  ref_mat = cbmc_ref,
  marker = cbmc_m,
  cluster_col = "seurat_clusters",
  threshold = 0.8,
  obj_out = FALSE,
  mode = "pct",
  dr = "umap"
)

# Matrix
clustify_nudge(
  input = pbmc_matrix_small,
  ref_mat = cbmc_ref,
  metadata = pbmc_meta,
  marker = as.matrix(cbmc_m),
  query_genes = pbmc_vargenes,
  cluster_col = "classified",
  threshold = 0.8,
  call = FALSE,
  marker_inmatrix = FALSE,
  mode = "pct"
)
```

---

collapse\_to\_cluster     *From per-cell calls, take highest freq call in each cluster*

---

### Description

From per-cell calls, take highest freq call in each cluster

### Usage

```
collapse_to_cluster(res, metadata, cluster_col, threshold = 0)
```

### Arguments

res	dataframe of idents, such as output of cor_to_call
metadata	input metadata with tsne or umap coordinates and cluster ids
cluster_col	metadata column for cluster
threshold	minimum correlation coefficient cutoff for calling clusters

### Value

new metadata with added columns

### Examples

```
res <- clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified",
  ref_mat = cbmc_ref,
  per_cell = TRUE
)

res2 <- cor_to_call(res)

collapse_to_cluster(
  res2,
  metadata = pbmc_meta,
  cluster_col = "classified",
  threshold = 0
)
```

---

compare\_lists     *Calculate adjusted p-values for hypergeometric test of gene lists or jaccard index*

---

### Description

Calculate adjusted p-values for hypergeometric test of gene lists or jaccard index

**Usage**

```
compare_lists(
  bin_mat,
  marker_mat,
  n = 30000,
  metric = "hyper",
  output_high = TRUE,
  details_out = FALSE
)
```

**Arguments**

bin_mat	binarized single-cell expression matrix, feed in by_cluster mat, if desired
marker_mat	matrix or dataframe of candidate genes for each cluster
n	number of genes in the genome
metric	adjusted p-value for hypergeometric test, or jaccard index
output_high	if true (by default to fit with rest of package), -log10 transform p-value
details_out	whether to also output shared gene list from jaccard

**Value**

matrix of numeric values, clusters from expr\_mat as row names, cell types from marker\_mat as column names

**Examples**

```
pbmc_mm <- matrixize_markers(pbmc_markers)

pbmc_avg <- average_clusters(
  pbmc_matrix_small,
  pbmc_meta,
  cluster_col = "classified"
)

pbmc_avgb <- binarize_expr(pbmc_avg)

compare_lists(
  pbmc_avgb,
  pbmc_mm,
  metric = "spearman"
)
```

---

cor\_to\_call

*get best calls for each cluster*


---

**Description**

get best calls for each cluster

**Usage**

```
cor_to_call(  
  cor_mat,  
  metadata = NULL,  
  cluster_col = "cluster",  
  collapse_to_cluster = FALSE,  
  threshold = 0,  
  rename_prefix = NULL,  
  carry_r = FALSE  
)
```

**Arguments**

cor_mat	input similarity matrix
metadata	input metadata with tsne or umap coordinates and cluster ids
cluster_col	metadata column, can be cluster or cellid
collapse_to_cluster	if a column name is provided, takes the most frequent call of entire cluster to color in plot
threshold	minimum correlation coefficient cutoff for calling clusters
rename_prefix	prefix to add to type and r column names
carry_r	whether to include threshold in unassigned names

**Value**

dataframe of cluster, new ident, and r info

**Examples**

```
res <- clustify(  
  input = pbmc_matrix_small,  
  metadata = pbmc_meta,  
  cluster_col = "classified",  
  ref_mat = cbmc_ref  
)  
  
cor_to_call(res)
```

---

cor_to_call_rank	<i>get ranked calls for each cluster</i>
------------------	--

---

**Description**

get ranked calls for each cluster

**Usage**

```
cor_to_call_rank(
  cor_mat,
  metadata = NULL,
  cluster_col = "cluster",
  collapse_to_cluster = FALSE,
  threshold = 0,
  rename_prefix = NULL,
  top_n = NULL
)
```

**Arguments**

cor_mat	input similarity matrix
metadata	input metadata with tsne or umap coordinates and cluster ids
cluster_col	metadata column, can be cluster or cellid
collapse_to_cluster	if a column name is provided, takes the most frequent call of entire cluster to color in plot
threshold	minimum correlation coefficient cutoff for calling clusters
rename_prefix	prefix to add to type and r column names
top_n	the number of ranks to keep, the rest will be set to 100

**Value**

dataframe of cluster, new ident, and r info

**Examples**

```
res <- clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified",
  ref_mat = cbmc_ref
)

cor_to_call_rank(res, threshold = "auto")
```

---

cor_to_call_topn	<i>get top calls for each cluster</i>
------------------	---------------------------------------

---

**Description**

get top calls for each cluster

**Usage**

```
cor_to_call_topn(
  cor_mat,
  metadata = NULL,
  col = "cluster",
  collapse_to_cluster = FALSE,
  threshold = 0,
  topn = 2
)
```

**Arguments**

<code>cor_mat</code>	input similarity matrix
<code>metadata</code>	input metadata with tsne or umap coordinates and cluster ids
<code>col</code>	metadata column, can be cluster or cellid
<code>collapse_to_cluster</code>	if a column name is provided, takes the most frequent call of entire cluster to color in plot
<code>threshold</code>	minimum correlation coefficient cutoff for calling clusters
<code>topn</code>	number of calls for each cluster

**Value**

dataframe of cluster, new potential ident, and r info

**Examples**

```
res <- clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  query_genes = pbmc_vargenes,
  cluster_col = "classified"
)

cor_to_call_topn(
  cor_mat = res,
  metadata = pbmc_meta,
  col = "classified",
  collapse_to_cluster = FALSE,
  threshold = 0.5
)
```

---

cosine

*Cosine distance*


---

**Description**

Cosine distance

**Usage**

```
cosine(vec1, vec2)
```

**Arguments**

```
vec1      test vector
vec2      reference vector
```

**Value**

numeric value of cosine distance between the vectors

---

downrefs	<i>table of references stored in clustifyrdata</i>
----------	--

---

**Description**

table of references stored in clustifyrdata

**Usage**

```
downrefs
```

**Format**

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 9 rows and 6 columns.

**Source**

various packages

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

downsample_matrix	<i>downsample matrix by cluster or completely random</i>
-------------------	--

---

**Description**

downsample matrix by cluster or completely random

**Usage**

```
downsample_matrix(
  mat,
  n = 1,
  keep_cluster_proportions = TRUE,
  metadata = NULL,
  cluster_col = "cluster"
)
```

**Arguments**

mat	expression matrix
n	number per cluster or fraction to keep
keep_cluster_proportions	whether to subsample
metadata	data.frame or vector containing cluster assignments per cell. Order must match column order in supplied matrix. If a data.frame provide the cluster_col parameters.
cluster_col	column in metadata with cluster number

**Value**

new smaller mat with less cell\_id columns

**Examples**

```
set.seed(42)
mat <- downsample_matrix(
  mat = pbmc_matrix_small,
  metadata = pbmc_meta$classified,
  n = 10,
  keep_cluster_proportions = TRUE
)
mat[1:3, 1:3]
```

---

feature\_select\_PCA      *Returns a list of variable genes based on PCA*

---

**Description**

Extract genes, i.e. "features", based on the top loadings of principal components formed from the bulk expression data set

**Usage**

```
feature_select_PCA(
  mat = NULL,
  pcs = NULL,
  n_pcs = 10,
  percentile = 0.99,
  if_log = TRUE
)
```

**Arguments**

mat	Expression matrix. Rownames are genes, colnames are single cell cluster name, and values are average single cell expression (log transformed).
pcs	Precalculated pcs if available, will skip over processing on mat.
n_pcs	Number of PCs to selected gene loadings from. See the explore_PCA_corr.Rmd vignette for details.

percentile      Select the percentile of absolute values of PCA loadings to select genes from. E.g. 0.999 would select the top point 1 percent of genes with the largest loadings.

if\_log          whether the data is already log transformed

**Value**

vector of genes

**Examples**

```
feature_select_PCA(
  cbmc_ref,
  if_log = FALSE
)
```

---

file\_marker\_parse      *takes files with positive and negative markers, as described in garnett, and returns list of markers*

---

**Description**

takes files with positive and negative markers, as described in garnett, and returns list of markers

**Usage**

```
file_marker_parse(filename)
```

**Arguments**

filename          txt file to load

**Value**

list of positive and negative gene markers

**Examples**

```
marker_file <- system.file(
  "extdata",
  "hsPBMC_markers.txt",
  package = "clustifyr"
)

file_marker_parse(marker_file)
```

---

find_rank_bias	<i>Find rank bias</i>
----------------	-----------------------

---

**Description**

Find rank bias

**Usage**

```
find_rank_bias(avg_mat, ref_mat, query_genes = NULL)
```

**Arguments**

avg_mat	average expression matrix
ref_mat	reference expression matrix
query_genes	original vector of genes used to clustify

**Value**

list of matrix of rank diff values

**Examples**

```
avg <- average_clusters(
  mat = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified",
  if_log = FALSE
)

rankdiff <- find_rank_bias(
  avg,
  cbmc_ref,
  query_genes = pbmc_vargenes
)
```

---

gene_pct	<i>pct of cells in each cluster that express genelist</i>
----------	---

---

**Description**

pct of cells in each cluster that express genelist

**Usage**

```
gene_pct(matrix, genelist, clusters, returning = "mean")
```

**Arguments**

matrix	expression matrix
genelist	vector of marker genes for one identity
clusters	vector of cluster identities
returning	whether to return mean, min, or max of the gene pct in the gene list

**Value**

vector of numeric values

---

gene_pct_markerm	<i>pct of cells in every cluster that express a series of genelists</i>
------------------	---

---

**Description**

pct of cells in every cluster that express a series of genelists

**Usage**

```
gene_pct_markerm(matrix, marker_m, metadata, cluster_col = NULL, norm = NULL)
```

**Arguments**

matrix	expression matrix
marker_m	matrixized markers
metadata	data.frame or vector containing cluster assignments per cell. Order must match column order in supplied matrix. If a data.frame provide the cluster_col parameters.
cluster_col	column in metadata with cluster number
norm	whether and how the results are normalized

**Value**

matrix of numeric values, clusters from mat as row names, cell types from marker\_m as column names

**Examples**

```
gene_pct_markerm(
  matrix = pbmc_matrix_small,
  marker_m = cbmc_m,
  metadata = pbmc_meta,
  cluster_col = "classified"
)
```

---

get\_best\_match\_matrix *Function to make best call from correlation matrix*

---

**Description**

Function to make best call from correlation matrix

**Usage**

```
get_best_match_matrix(cor_mat)
```

**Arguments**

cor\_mat            correlation matrix

**Value**

matrix of 1s and 0s

---

get\_best\_str            *Function to make call and attach score*

---

**Description**

Function to make call and attach score

**Usage**

```
get_best_str(name, best_mat, cor_mat, carry_cor = TRUE)
```

**Arguments**

name            name of row to query  
best\_mat        binarized call matrix  
cor\_mat        correlation matrix  
carry\_cor       whether the correlation score gets reported

**Value**

string with ident call and possibly cor value

---

get\_common\_elements     *Find entries shared in all vectors*

---

**Description**

return entries found in all supplied vectors. If the vector supplied is NULL or NA, then it will be excluded from the comparison.

**Usage**

```
get_common_elements(...)
```

**Arguments**

...                    vectors

**Value**

vector of shared elements

---

get\_similarity             *Compute similarity of matrices*

---

**Description**

Compute similarity of matrices

**Usage**

```
get_similarity(
  expr_mat,
  ref_mat,
  cluster_ids,
  compute_method,
  pseudobulk_method = "mean",
  per_cell = FALSE,
  rm0 = FALSE,
  if_log = TRUE,
  low_threshold = 0,
  ...
)
```

**Arguments**

expr\_mat                single-cell expression matrix  
 ref\_mat                reference expression matrix  
 cluster\_ids            vector of cluster ids for each cell  
 compute\_method        method(s) for computing similarity scores

pseudobulk_method	method used for summarizing clusters, options are mean (default), median, truncate (10% truncated mean), or trimean, max, min
per_cell	run per cell?
rm0	consider 0 as missing data, recommended for per_cell
if_log	input data is natural log, averaging will be done on unlogged data
low_threshold	option to remove clusters with too few cells
...	additional parameters not used yet

**Value**

matrix of numeric values, clusters from expr\_mat as row names, cell types from ref\_mat as column names

---

get\_ucsc\_reference      *Build reference atlases from external UCSC cell browsers*

---

**Description**

Build reference atlases from external UCSC cell browsers

**Usage**

```
get_ucsc_reference(cb_url, cluster_col, ...)
```

**Arguments**

cb_url	URL of cellbrowser dataset (e.g. <a href="http://cells.ucsc.edu/?ds=cortex-dev">http://cells.ucsc.edu/?ds=cortex-dev</a> ). Note that the URL must contain the ds=dataset-name suffix.
cluster_col	annotation field for summarizing gene expression (e.g. clustering, cell-type name, samples, etc.)
...	additional args passed to average_clusters

**Value**

reference matrix

**Examples**

```
## Not run:

# many datasets hosted by UCSC have UMI counts in the expression matrix
# set if_log = FALSE if the expression matrix has not been natural log transformed

get_ucsc_reference(
  cb_url = "https://cells.ucsc.edu/?ds=evocell+mus-musculus+marrow",
  cluster_col = "Clusters", if_log = FALSE
)

get_ucsc_reference(
  cb_url = "http://cells.ucsc.edu/?ds=muscle-cell-atlas",
```

```

    cluster_col = "cell_annotation",
    if_log = FALSE
)

## End(Not run)

```

---

get\_unique\_column      *Generate a unique column id for a dataframe*

---

### Description

Generate a unique column id for a dataframe

### Usage

```
get_unique_column(df, id = NULL)
```

### Arguments

df	dataframe with column names
id	desired id if unique

### Value

character

---

get\_vargenes      *Generate variable gene list from marker matrix*

---

### Description

Variable gene list is required for clustify main function. This function parses variables genes from a matrix input.

### Usage

```
get_vargenes(marker_mat)
```

### Arguments

marker_mat	matrix or dataframe of candidate genes for each cluster
------------	---

### Value

vector of marker gene names

### Examples

```
get_vargenes(cbmc_m)
```

---

gmt_to_list	<i>convert gmt format of pathways to list of vectors</i>
-------------	--

---

**Description**

convert gmt format of pathways to list of vectors

**Usage**

```
gmt_to_list(  
  path,  
  cutoff = 0,  
  sep = "\thttp://www.broadinstitute.org/gsea/msigdb/cards/.*\t"  
)
```

**Arguments**

path	gmt file path
cutoff	remove pathways with less genes than this cutoff
sep	sep used in file to split path and genes

**Value**

list of genes in each pathway

**Examples**

```
gmt_file <- system.file(  
  "extdata",  
  "c2.cp.reactome.v6.2.symbols.gmt.gz",  
  package = "clustifyr"  
)  
  
gene.lists <- gmt_to_list(path = gmt_file)  
length(gene.lists)
```

---

human_genes_10x	<i>Vector of human genes for 10x cellranger pipeline</i>
-----------------	--

---

**Description**

Vector of human genes for 10x cellranger pipeline

**Usage**

```
human_genes_10x
```

**Format**

An object of class character of length 33514.

**Source**

<https://support.10xgenomics.com/single-cell-gene-expression/software/downloads/latest>

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

insert\_meta\_object      *more flexible metadata update of single cell objects*

---

**Description**

more flexible metadata update of single cell objects

**Usage**

```
insert_meta_object(  
  input,  
  new_meta,  
  type = class(input),  
  meta_loc = NULL,  
  lookuptable = NULL  
)
```

**Arguments**

input	input object
new_meta	new metadata table to insert back into object
type	look up predefined slots/loc
meta_loc	metadata location
lookuptable	if not supplied, will look in built-in table for object parsing

**Value**

new object with new metadata inserted

**Examples**

```
so <- so_pbmc()  
insert_meta_object(so, seurat_meta(so, dr = "umap"))
```

---

kl_divergence	<i>KL divergence</i>
---------------	----------------------

---

**Description**

Use package entropy to compute Kullback-Leibler divergence. The function first converts each vector's reads to pseudo-number of transcripts by normalizing the total reads to total\_reads. The normalized read for each gene is then rounded to serve as the pseudo-number of transcripts. Function entropy::KL.shrink is called to compute the KL-divergence between the two vectors, and the maximal allowed divergence is set to max\_KL. Finally, a linear transform is performed to convert the KL divergence, which is between 0 and max\_KL, to a similarity score between -1 and 1.

**Usage**

```
kl_divergence(vec1, vec2, if_log = FALSE, total_reads = 1000, max_KL = 1)
```

**Arguments**

vec1	Test vector
vec2	Reference vector
if_log	Whether the vectors are log-transformed. If so, the raw count should be computed before computing KL-divergence.
total_reads	Pseudo-library size
max_KL	Maximal allowed value of KL-divergence.

**Value**

numeric value, with additional attributes, of kl divergence between the vectors

---

make_comb_ref	<i>make combination ref matrix to assess intermixing</i>
---------------	--

---

**Description**

make combination ref matrix to assess intermixing

**Usage**

```
make_comb_ref(ref_mat, if_log = TRUE, sep = "_and_")
```

**Arguments**

ref_mat	reference expression matrix
if_log	whether input data is natural
sep	separator for name combinations

**Value**

expression matrix

**Examples**

```
ref <- make_comb_ref(  
  cbmc_ref,  
  sep = "_+_"  
)  
ref[1:3, 1:3]
```

---

**marker\_select***decide for one gene whether it is a marker for a certain cell type*

---

**Description**

decide for one gene whether it is a marker for a certain cell type

**Usage**

```
marker_select(row1, cols, cut = 1, compto = 1)
```

**Arguments**

row1            a numeric vector of expression values (row)  
cols            a vector of cell types (column)  
cut             an expression minimum cutoff  
compto          compare max expression to the value of next 1 or more

**Value**

vector of cluster name and ratio value

**Examples**

```
pbmc_avg <- average_clusters(  
  mat = pbmc_matrix_small,  
  metadata = pbmc_meta,  
  cluster_col = "classified",  
  if_log = FALSE  
)  
  
marker_select(  
  row1 = pbmc_avg["PPBP", ],  
  cols = names(pbmc_avg["PPBP", ])  
)
```

---

matrixize_markers	<i>Convert candidate genes list into matrix</i>
-------------------	---

---

## Description

Convert candidate genes list into matrix

## Usage

```
matrixize_markers(  
  marker_df,  
  ranked = FALSE,  
  n = NULL,  
  step_weight = 1,  
  background_weight = 0,  
  unique = FALSE,  
  metadata = NULL,  
  cluster_col = "classified",  
  remove_rp = FALSE  
)
```

## Arguments

marker_df	dataframe of candidate genes, must contain "gene" and "cluster" columns, or a matrix of gene names to convert to ranked
ranked	unranked gene list feeds into hyperp, the ranked gene list feeds into regular corr_coef
n	number of genes to use
step_weight	ranked genes are transformed into pseudo expression by descending weight
background_weight	ranked genes are transformed into pseudo expression with added weight
unique	whether to use only unique markers to 1 cluster
metadata	vector or dataframe of cluster names, should have column named cluster
cluster_col	column for cluster names to replace original cluster, if metadata is dataframe
remove_rp	do not include rps, rpl, rp1-9 in markers

## Value

matrix of unranked gene marker names, or matrix of ranked expression

## Examples

```
matrixize_markers(pbmc_markers)
```

---

`mouse_genes_10x`*Vector of mouse genes for 10x cellranger pipeline*

---

**Description**

Vector of mouse genes for 10x cellranger pipeline

**Usage**

```
mouse_genes_10x
```

**Format**

An object of class character of length 31017.

**Source**

<https://support.10xgenomics.com/single-cell-gene-expression/software/downloads/latest>

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

`not_pretty_palette`*black and white palette for plotting continuous variables*

---

**Description**

black and white palette for plotting continuous variables

**Usage**

```
not_pretty_palette
```

**Format**

An object of class character of length 9.

**Value**

vector of colors

---

object_data	<i>Function to access object data</i>
-------------	---------------------------------------

---

### Description

Function to access object data

### Usage

```
object_data(object, ...)  
  
## S3 method for class 'Seurat'  
object_data(object, slot, n_genes = 1000, ...)  
  
## S3 method for class 'SingleCellExperiment'  
object_data(object, slot, ...)
```

### Arguments

object	object after tsne or umap projections and clustering
...	additional arguments
slot	data to access
n_genes	number of genes limit for Seurat variable genes, by default 1000, set to 0 to use all variable genes (generally not recommended)

### Value

expression matrix, with genes as row names, and cell types as column names

### Examples

```
so <- so_pbmc()  
mat <- object_data(  
  object = so,  
  slot = "data"  
)  
mat[1:3, 1:3]  
sce <- sce_pbmc()  
mat <- object_data(  
  object = sce,  
  slot = "data"  
)  
mat[1:3, 1:3]
```

---

object_loc_lookup	<i>lookup table for single cell object structures</i>
-------------------	---

---

**Description**

lookup table for single cell object structures

**Usage**

```
object_loc_lookup()
```

**Value**

A list populated with standardized functions to access relevant data structures in multiple single cell data formats.

---

object_ref	<i>Function to convert labelled object to avg expression matrix</i>
------------	---

---

**Description**

Function to convert labelled object to avg expression matrix

**Usage**

```
object_ref(input, ...)

## Default S3 method:
object_ref(
  input,
  cluster_col = NULL,
  var_genes_only = FALSE,
  assay_name = NULL,
  method = "mean",
  lookuptable = NULL,
  if_log = TRUE,
  ...
)

## S3 method for class 'Seurat'
object_ref(
  input,
  cluster_col = NULL,
  var_genes_only = FALSE,
  assay_name = NULL,
  method = "mean",
  lookuptable = NULL,
  if_log = TRUE,
  ...
)
```

```

)

## S3 method for class 'SingleCellExperiment'
object_ref(
  input,
  cluster_col = NULL,
  var_genes_only = FALSE,
  assay_name = NULL,
  method = "mean",
  lookuptable = NULL,
  if_log = TRUE,
  ...
)

```

### Arguments

input	object after tsne or umap projections and clustering
...	additional arguments
cluster_col	column name where classified cluster names are stored in seurat meta data, cannot be "rn"
var_genes_only	whether to keep only var.genes in the final matrix output, could also look up genes used for PCA
assay_name	any additional assay data, such as ADT, to include. If more than 1, pass a vector of names
method	whether to take mean (default) or median
lookuptable	if not supplied, will look in built-in table for object parsing
if_log	input data is natural log, averaging will be done on unlogged data

### Value

reference expression matrix, with genes as row names, and cell types as column names

### Examples

```

so <- so_pbmc()
object_ref(
  so,
  cluster_col = "seurat_clusters"
)

```

---

overcluster

*Overcluster by kmeans per cluster*

---

### Description

Overcluster by kmeans per cluster

### Usage

```
overcluster(mat, cluster_id, power = 0.15)
```

**Arguments**

mat	expression matrix
cluster_id	list of ids per cluster
power	decides the number of clusters for kmeans

**Value**

new cluster\_id list of more clusters

**Examples**

```
res <- overcluster(
  mat = pbmc_matrix_small,
  cluster_id = split(colnames(pbmc_matrix_small), pbmc_meta$classified)
)
length(res)
```

---

overcluster_test	<i>compare clustering parameters and classification outcomes</i>
------------------	--

---

**Description**

compare clustering parameters and classification outcomes

**Usage**

```
overcluster_test(
  expr,
  metadata,
  ref_mat,
  cluster_col,
  x_col = "UMAP_1",
  y_col = "UMAP_2",
  n = 5,
  ngenes = NULL,
  query_genes = NULL,
  threshold = 0,
  do_label = TRUE,
  do_legend = FALSE,
  newclustering = NULL,
  combine = TRUE
)
```

**Arguments**

expr	expression matrix
metadata	metadata including cluster info and dimension reduction plotting
ref_mat	reference matrix
cluster_col	column of clustering from metadata
x_col	column of metadata for x axis plotting

y_col	column of metadata for y axis plotting
n	expand n-fold for over/under clustering
ngenes	number of genes to use for feature selection, use all genes if NULL
query_genes	vector, otherwise genes with be recalculated
threshold	type calling threshold
do_label	whether to label each cluster at median center
do_legend	whether to draw legend
newclustering	use kmeans if NULL on dr or col name for second column of clustering
combine	if TRUE return a single plot with combined panels, if FALSE return list of plots (default: TRUE)

**Value**

faceted ggplot object

**Examples**

```
set.seed(42)
overcluster_test(
  expr = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  cluster_col = "classified",
  x_col = "UMAP_1",
  y_col = "UMAP_2"
)
```

---

parse\_loc\_object      *more flexible parsing of single cell objects*

---

**Description**

more flexible parsing of single cell objects

**Usage**

```
parse_loc_object(
  input,
  type = class(input),
  expr_loc = NULL,
  meta_loc = NULL,
  var_loc = NULL,
  cluster_col = NULL,
  lookuptable = NULL
)
```

**Arguments**

input	input object
type	look up predefined slots/loc
expr_loc	function that extracts expression matrix
meta_loc	function that extracts metadata
var_loc	function that extracts variable genes
cluster_col	column of clustering from metadata
lookuptable	if not supplied, will use object_loc_lookup() for parsing.

**Value**

list of expression, metadata, vargenes, cluster\_col info from object

**Examples**

```
so <- so_pbmc()
obj <- parse_loc_object(so)
length(obj)
```

---

pbmc_markers	<i>Marker genes identified by Seurat from single-cell RNA-seq PBMCs.</i>
--------------	--

---

**Description**

Dataframe of markers from Seurat FindAllMarkers function

**Usage**

```
pbmc_markers
```

**Format**

An object of class `data.frame` with 2304 rows and 7 columns.

**Source**

[pbmc\_matrix] processed by Seurat

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

pbmc\_markers\_M3Drop     *Marker genes identified by M3Drop from single-cell RNA-seq PBMCs.*

---

**Description**

Selected features of 3k pbmcs from Seurat3 tutorial

**Usage**

```
pbmc_markers_M3Drop
```

**Format**

A data frame with 3 variables:

**Source**

[pbmc\_matrix] processed by [M3Drop]

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

pbmc\_matrix\_small     *Matrix of single-cell RNA-seq PBMCs.*

---

**Description**

Count matrix of 3k pbmcs from Seurat3 tutorial, with only var.features

**Usage**

```
pbmc_matrix_small
```

**Format**

A sparseMatrix with genes as rows and cells as columns.

**Source**

[https://satijalab.org/seurat/v3.0/pbmc3k\\_tutorial.html](https://satijalab.org/seurat/v3.0/pbmc3k_tutorial.html)

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#)

---

pbmc\_meta

*Meta-data for single-cell RNA-seq PBMCs.*

---

**Description**

Metadata, including umap, of 3k pbmcs from Seurat3 tutorial

**Usage**

pbmc\_meta

**Format**

An object of class `data.frame` with 2638 rows and 9 columns.

**Source**

[`pbmc_matrix`] processed by Seurat

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_vargenes](#)

---

pbmc\_vargenes

*Variable genes identified by Seurat from single-cell RNA-seq PBMCs.*

---

**Description**

Top 2000 variable genes from 3k pbmcs from Seurat3 tutorial

**Usage**

pbmc\_vargenes

**Format**

An object of class `character` of length 2000.

**Source**

[`pbmc_matrix`] processed by Seurat

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#)

---

percent_clusters	<i>Percentage detected per cluster</i>
------------------	--

---

**Description**

Percentage detected per cluster

**Usage**

```
percent_clusters(mat, metadata, cluster_col = "cluster", cut_num = 0.5)
```

**Arguments**

mat	expression matrix
metadata	data.frame with cells
cluster_col	column in metadata with cluster number
cut_num	binary cutoff for detection

**Value**

matrix of numeric values, with genes for row names, and clusters for column names

---

permute_similarity	<i>Compute a p-value for similarity using permutation</i>
--------------------	---

---

**Description**

Permute cluster labels to calculate empirical p-value

**Usage**

```
permute_similarity(  
  expr_mat,  
  ref_mat,  
  cluster_ids,  
  n_perm,  
  per_cell = FALSE,  
  compute_method,  
  pseudobulk_method = "mean",  
  rm0 = FALSE,  
  ...  
)
```

**Arguments**

expr_mat	single-cell expression matrix
ref_mat	reference expression matrix
cluster_ids	clustering info of single-cell data assume that genes have ALREADY BEEN filtered
n_perm	number of permutations
per_cell	run per cell?
compute_method	method(s) for computing similarity scores
pseudobulk_method	method used for summarizing clusters, options are mean (default), median, truncate (10% truncated mean), or trimean, max, min
rm0	consider 0 as missing data, recommended for per_cell
...	additional parameters

**Value**

matrix of numeric values

---

plot_best_call	<i>Plot best calls for each cluster on a tSNE or umap</i>
----------------	---

---

**Description**

Plot best calls for each cluster on a tSNE or umap

**Usage**

```
plot_best_call(
  cor_mat,
  metadata,
  cluster_col = "cluster",
  collapse_to_cluster = FALSE,
  threshold = 0,
  x = "UMAP_1",
  y = "UMAP_2",
  plot_r = FALSE,
  per_cell = FALSE,
  ...
)
```

**Arguments**

cor_mat	input similarity matrix
metadata	input metadata with tsne or umap coordinates and cluster ids
cluster_col	metadata column, can be cluster or cellid
collapse_to_cluster	if a column name is provided, takes the most frequent call of entire cluster to color in plot

threshold	minimum correlation coefficient cutoff for calling clusters
x	x variable
y	y variable
plot_r	whether to include second plot of cor eff for best call
per_cell	whether the cor_mat was generate per cell or per cluster
...	passed to plot_dims

**Value**

ggplot object, cells projected by dr, colored by cell type classification

**Examples**

```
res <- clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  query_genes = pbmc_vargenes,
  cluster_col = "classified"
)

plot_best_call(
  cor_mat = res,
  metadata = pbmc_meta,
  cluster_col = "classified"
)
```

---

plot_call	<i>Plot called clusters on a tSNE or umap, for each reference cluster given</i>
-----------	---

---

**Description**

Plot called clusters on a tSNE or umap, for each reference cluster given

**Usage**

```
plot_call(cor_mat, metadata, data_to_plot = colnames(cor_mat), ...)
```

**Arguments**

cor_mat	input similarity matrix
metadata	input metadata with tsne or umap coordinates and cluster ids
data_to_plot	colname of data to plot, defaults to all
...	passed to plot_dims

**Value**

list of ggplot object, cells projected by dr, colored by cell type classification

---

plot\_cor *Plot similarity measures on a tSNE or umap*

---

### Description

Plot similarity measures on a tSNE or umap

### Usage

```
plot_cor(
  cor_mat,
  metadata,
  data_to_plot = colnames(cor_mat),
  cluster_col = NULL,
  x = "UMAP_1",
  y = "UMAP_2",
  scale_legends = FALSE,
  ...
)
```

### Arguments

cor_mat	input similarity matrix
metadata	input metadata with per cell tsne or umap coordinates and cluster ids
data_to_plot	colname of data to plot, defaults to all
cluster_col	colname of clustering data in metadata, defaults to rownames of the metadata if not supplied.
x	metadata column name with 1st axis dimension. defaults to "UMAP_1".
y	metadata column name with 2nd axis dimension. defaults to "UMAP_2".
scale_legends	if TRUE scale all legends to maximum values in entire correlation matrix. if FALSE scale legends to maximum for each plot. A two-element numeric vector can also be passed to supply custom values i.e. c(0, 1)
...	passed to plot_dims

### Value

list of ggplot objects, cells projected by dr, colored by cor values

### Examples

```
res <- clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  query_genes = pbmc_vargenes,
  cluster_col = "classified"
)

plot_cor(
  cor_mat = res,
```

```

    metadata = pbmc_meta,
    data_to_plot = colnames(res)[1:2],
    cluster_col = "classified",
    x = "UMAP_1",
    y = "UMAP_2"
  )

```

---

plot\_cor\_heatmap

*Plot similarity measures on heatmap*


---

## Description

Plot similarity measures on heatmap

## Usage

```

plot_cor_heatmap(
  cor_mat,
  metadata = NULL,
  cluster_col = NULL,
  col = not_pretty_palette,
  legend_title = NULL,
  ...
)

```

## Arguments

cor_mat	input similarity matrix
metadata	input metadata with per cell tsne or umap coordinates and cluster ids
cluster_col	colname of clustering data in metadata, defaults to rownames of the metadata if not supplied.
col	color ramp to use
legend_title	legend title to pass to Heatmap
...	passed to Heatmap

## Value

complexheatmap object

## Examples

```

res <- clustify(
  input = pbmc_matrix_small,
  metadata = pbmc_meta,
  ref_mat = cbmc_ref,
  query_genes = pbmc_vargenes,
  cluster_col = "classified",
  per_cell = FALSE
)

plot_cor_heatmap(res)

```

---

plot\_dims

*Plot a tSNE or umap colored by feature.*


---

### Description

Plot a tSNE or umap colored by feature.

### Usage

```
plot_dims(
  data,
  x = "UMAP_1",
  y = "UMAP_2",
  feature = NULL,
  legend_name = "",
  c_cols = pretty_palette2,
  d_cols = NULL,
  pt_size = 0.25,
  alpha_col = NULL,
  group_col = NULL,
  scale_limits = NULL,
  do_label = FALSE,
  do_legend = TRUE,
  do_repel = TRUE
)
```

### Arguments

data	input data
x	x variable
y	y variable
feature	feature to color by
legend_name	legend name to display, defaults to no name
c_cols	character vector of colors to build color gradient for continuous values, defaults to <a href="#">pretty_palette</a>
d_cols	character vector of colors for discrete values. defaults to RColorBrewer paired palette
pt_size	point size
alpha_col	whether to refer to data column for alpha values
group_col	group by another column instead of feature, useful for labels
scale_limits	defaults to min = 0, max = max(data\$x), otherwise a two-element numeric vector indicating min and max to plot
do_label	whether to label each cluster at median center
do_legend	whether to draw legend
do_repel	whether to use ggrepel on labels

**Value**

ggplot object, cells projected by dr, colored by feature

**Examples**

```
plot_dims(
  pbmc_meta,
  feature = "classified"
)
```

---

plot_gene	<i>Plot gene expression on to tSNE or umap</i>
-----------	--

---

**Description**

Plot gene expression on to tSNE or umap

**Usage**

```
plot_gene(expr_mat, metadata, genes, cell_col = NULL, ...)
```

**Arguments**

expr_mat	input single cell matrix
metadata	data.frame with tSNE or umap coordinates
genes	gene(s) to color tSNE or umap
cell_col	column name in metadata containing cell ids, defaults to rownames if not supplied
...	additional arguments passed to [clustifyr::plot_dims()]

**Value**

list of ggplot object, cells projected by dr, colored by gene expression

**Examples**

```
genes <- c(
  "RP11-314N13.3",
  "ARF4"
)

plot_gene(
  expr_mat = pbmc_matrix_small,
  metadata = tibble::rownames_to_column(pbmc_meta, "rn"),
  genes = genes,
  cell_col = "rn"
)
```

---

plot_pathway_gsea	<i>plot GSEA pathway scores as heatmap, returns a list containing results and plot.</i>
-------------------	---

---

### Description

plot GSEA pathway scores as heatmap, returns a list containing results and plot.

### Usage

```
plot_pathway_gsea(
  mat,
  pathway_list,
  n_perm = 1000,
  scale = TRUE,
  topn = 5,
  returning = "both"
)
```

### Arguments

mat	expression matrix
pathway_list	a list of vectors, each named for a specific pathway, or dataframe
n_perm	Number of permutation for fgsea function. Defaults to 1000.
scale	convert expr_mat into zscores prior to running GSEA?, default = TRUE
topn	number of top pathways to plot
returning	to return "both" list and plot, or either one

### Value

list of matrix and plot, or just plot, matrix of GSEA NES values, cell types as row names, pathways as column names

### Examples

```
gl <- list(
  "n" = c("PPBP", "LYZ", "S100A9"),
  "a" = c("IGLL5", "GNLY", "FTL")
)

pbmc_avg <- average_clusters(
  mat = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified"
)

plot_pathway_gsea(
  pbmc_avg,
  gl,
  5
)
```

---

plot_rank_bias	<i>Query rank bias results</i>
----------------	--------------------------------

---

**Description**

Query rank bias results

**Usage**

```
plot_rank_bias(bias_df, organism = "hsapiens")
```

**Arguments**

bias_df	data.frame of rank diff matrix between cluster and reference cell types
organism	for GO term analysis, organism name: human - 'hsapiens', mouse - 'mmusculus'

**Value**

ggplot object of distribution and annotated GO terms

**Examples**

```
## Not run:
avg <- average_clusters(
  mat = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified",
  if_log = FALSE
)

rankdiff <- find_rank_bias(
  avg,
  cbmc_ref,
  query_genes = pbmc_vargenes
)

qres <- query_rank_bias(
  rankdiff,
  "CD14+ Mono",
  "CD14+ Mono"
)

g <- plot_rank_bias(
  qres
)

## End(Not run)
```

---

pos_neg_marker	<i>generate pos and negative marker expression matrix from a list/dataframe of positive markers</i>
----------------	---

---

**Description**

generate pos and negative marker expression matrix from a list/dataframe of positive markers

**Usage**

```
pos_neg_marker(mat)
```

**Arguments**

mat	matrix or dataframe of markers
-----	--------------------------------

**Value**

matrix of gene expression

**Examples**

```
m1 <- pos_neg_marker(cbmc_m)
```

---

pos_neg_select	<i>adapt clustify to tweak score for pos and neg markers</i>
----------------	--

---

**Description**

adapt clustify to tweak score for pos and neg markers

**Usage**

```
pos_neg_select(
  input,
  ref_mat,
  metadata,
  cluster_col = "cluster",
  cutoff_n = 0,
  cutoff_score = 0.5
)
```

**Arguments**

input	single-cell expression matrix
ref_mat	reference expression matrix with positive and negative markers(set expression at 0)
metadata	cell cluster assignments, supplied as a vector or data.frame. If data.frame is supplied then cluster_col needs to be set. Not required if running correlation per cell.

cluster_col	column in metadata that contains cluster ids per cell. Will default to first column of metadata if not supplied. Not required if running correlation per cell.
cutoff_n	expression cutoff where genes ranked below n are considered non-expressing
cutoff_score	positive score lower than this cutoff will be considered as 0 to not influence scores

**Value**

matrix of numeric values, clusters from input as row names, cell types from ref\_mat as column names

**Examples**

```
pn_ref <- data.frame(  
  "Myeloid" = c(1, 0.01, 0),  
  row.names = c("CD74", "clustifyr0", "CD79A")  
)  
  
pos_neg_select(  
  input = pbmc_matrix_small,  
  ref_mat = pn_ref,  
  metadata = pbmc_meta,  
  cluster_col = "classified",  
  cutoff_score = 0.8  
)
```

---

pretty\_palette

*Color palette for plotting continuous variables*

---

**Description**

Color palette for plotting continuous variables

**Usage**

```
pretty_palette
```

**Format**

An object of class character of length 6.

**Value**

vector of colors

---

pretty_palette2	<i>Color palette for plotting continuous variables, starting at gray</i>
-----------------	--

---

**Description**

Color palette for plotting continuous variables, starting at gray

**Usage**

```
pretty_palette2
```

**Format**

An object of class character of length 9.

**Value**

vector of colors

---

pretty_palette_ramp_d	<i>Expanded color palette ramp for plotting discrete variables</i>
-----------------------	--

---

**Description**

Expanded color palette ramp for plotting discrete variables

**Usage**

```
pretty_palette_ramp_d(n)
```

**Arguments**

n                    number of colors to use

**Value**

color ramp

---

query_rank_bias	<i>Query rank bias results</i>
-----------------	--------------------------------

---

**Description**

Query rank bias results

**Usage**

```
query_rank_bias(bias_list, id_mat, id_ref)
```

**Arguments**

bias_list	list of rank diff matrix between cluster and reference cell types
id_mat	name of cluster from average cluster matrix
id_ref	name of cell type in reference matrix

**Value**

data.frame rank diff values

**Examples**

```
avg <- average_clusters(
  mat = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified",
  if_log = FALSE
)

rankdiff <- find_rank_bias(
  avg,
  cbmc_ref,
  query_genes = pbmc_vargenes
)

qres <- query_rank_bias(
  rankdiff,
  "CD14+ Mono",
  "CD14+ Mono"
)
```

---

ref_feature_select	<i>feature select from reference matrix</i>
--------------------	---

---

**Description**

feature select from reference matrix

**Usage**

```
ref_feature_select(mat, n = 3000, mode = "var", rm.lowvar = TRUE)
```

**Arguments**

mat	reference matrix
n	number of genes to return
mode	the method of selecting features
rm.lowvar	whether to remove lower variation genes first

**Value**

vector of genes

**Examples**

```
pbmc_avg <- average_clusters(
  mat = pbmc_matrix_small,
  metadata = pbmc_meta,
  cluster_col = "classified"
)

ref_feature_select(
  mat = pbmc_avg[1:100, ],
  n = 5
)
```

---

ref_marker_select	<i>marker selection from reference matrix</i>
-------------------	---

---

**Description**

marker selection from reference matrix

**Usage**

```
ref_marker_select(mat, cut = 0.5, arrange = TRUE, compto = 1)
```

**Arguments**

mat	reference matrix
cut	an expression minimum cutoff
arrange	whether to arrange (lower means better)
compto	compare max expression to the value of next 1 or more

**Value**

dataframe, with gene, cluster, ratio columns

**Examples**

```
ref_marker_select(  
  cbmc_ref,  
  cut = 2  
)
```

---

reverse\_marker\_matrix *generate negative markers from a list of exclusive positive markers*

---

**Description**

generate negative markers from a list of exclusive positive markers

**Usage**

```
reverse_marker_matrix(mat)
```

**Arguments**

mat                    matrix or dataframe of markers

**Value**

matrix of gene names

**Examples**

```
reverse_marker_matrix(cbmc_m)
```

---

run\_clustifyr\_app        *Launch Shiny app version of clustifyr, may need to run install\_clustifyr\_app() at first time to install packages*

---

**Description**

Launch Shiny app version of clustifyr, may need to run install\_clustifyr\_app() at first time to install packages

**Usage**

```
run_clustifyr_app()
```

**Value**

instance of shiny app

**Examples**

```
## Not run:  
run_clustifyr_app()  
  
## End(Not run)
```

---

run_gsea	<i>Run GSEA to compare a gene list(s) to per cell or per cluster expression data</i>
----------	--

---

### Description

Use fgsea algorithm to compute normalized enrichment scores and pvalues for gene set overlap

### Usage

```
run_gsea(
  expr_mat,
  query_genes,
  cluster_ids = NULL,
  n_perm = 1000,
  per_cell = FALSE,
  scale = FALSE,
  no_warnings = TRUE
)
```

### Arguments

expr_mat	single-cell expression matrix or Seurat object
query_genes	A vector or named list of vectors of genesets of interest to compare via GSEA. If supplying a named list, then the gene set names will appear in the output.
cluster_ids	vector of cell cluster assignments, supplied as a vector with order that matches columns in expr_mat. Not required if running per cell.
n_perm	Number of permutation for fgsea function. Defaults to 1000.
per_cell	if true run per cell, otherwise per cluster.
scale	convert expr_mat into zscores prior to running GSEA?, default = FALSE
no_warnings	suppress warnings from gsea ties

### Value

dataframe of gsea scores (pval, NES), with clusters as rownames

---

sce_pbmc	<i>An example SingleCellExperiment object</i>
----------	---

---

### Description

An example SingleCellExperiment object

### Usage

```
sce_pbmc()
```

### Value

a SingleCellExperiment object populated with data from the [pbmc\\_matrix\\_small](#) scRNA-seq dataset, additionally annotated with cluster assignments.

---

seurat_meta	<i>Function to convert labelled seurat object to fully prepared metadata</i>
-------------	--

---

**Description**

Function to convert labelled seurat object to fully prepared metadata

**Usage**

```
seurat_meta(seurat_object, ...)

## S3 method for class 'Seurat'
seurat_meta(seurat_object, dr = "umap", ...)
```

**Arguments**

seurat_object	seurat_object after tsne or umap projections and clustering
...	additional arguments
dr	dimension reduction method

**Value**

dataframe of metadata, including dimension reduction plotting info

**Examples**

```
so <- so_pbmc()
m <- seurat_meta(so)
```

---

seurat_ref	<i>Function to convert labelled seurat object to avg expression matrix</i>
------------	--

---

**Description**

Function to convert labelled seurat object to avg expression matrix

**Usage**

```
seurat_ref(seurat_object, ...)

## S3 method for class 'Seurat'
seurat_ref(
  seurat_object,
  cluster_col = "classified",
  var_genes_only = FALSE,
  assay_name = NULL,
  method = "mean",
  subclusterpower = 0,
  if_log = TRUE,
  ...
)
```

**Arguments**

seurat_object	seurat_object after tsne or umap projections and clustering
...	additional arguments
cluster_col	column name where classified cluster names are stored in seurat meta data, cannot be "rn"
var_genes_only	whether to keep only var_genes in the final matrix output, could also look up genes used for PCA
assay_name	any additional assay data, such as ADT, to include. If more than 1, pass a vector of names
method	whether to take mean (default) or median
subclusterpower	whether to get multiple averages per original cluster
if_log	input data is natural log, averaging will be done on unlogged data

**Value**

reference expression matrix, with genes as row names, and cell types as column names

**Examples**

```
so <- so_pbmc()
ref <- seurat_ref(so, cluster_col = "seurat_clusters")
```

---

so\_pbmc

*An example Seurat object*


---

**Description**

An example Seurat object

**Usage**

```
so_pbmc()
```

**Value**

a Seurat object populated with data from the [pbmc\\_matrix\\_small](#) scRNA-seq dataset, additionally annotated with cluster assignments.

---

vector\_similarity      *Compute similarity between two vectors*

---

### Description

Compute the similarity score between two vectors using a customized scoring function. Two vectors may be from either scRNA-seq or bulk RNA-seq data. The lengths of `vec1` and `vec2` must match, and must be arranged in the same order of genes. Both vectors should be provided to this function after pre-processing, feature selection and dimension reduction.

### Usage

```
vector_similarity(vec1, vec2, compute_method, ...)
```

### Arguments

<code>vec1</code>	test vector
<code>vec2</code>	reference vector
<code>compute_method</code>	method to run i.e. <code>corr_coef</code>
<code>...</code>	arguments to pass to <code>compute_method</code> function

### Value

numeric value of desired correlation or distance measurement

---

`write_meta`      *Function to write metadata to object*

---

### Description

Function to write metadata to object

### Usage

```
write_meta(object, ...)

## S3 method for class 'Seurat'
write_meta(object, meta, ...)

## S3 method for class 'SingleCellExperiment'
write_meta(object, meta, ...)
```

### Arguments

<code>object</code>	object after tsne or umap projections and clustering
<code>...</code>	additional arguments
<code>meta</code>	new metadata dataframe

**Value**

object with newly inserted metadata columns

**Examples**

```
so <- so_pbmc()
obj <- write_meta(
  object = so,
  meta = seurat_meta(so)
)
sce <- sce_pbmc()
obj <- write_meta(
  object = sce,
  meta = object_data(sce, "meta.data")
)
```

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