

# Package ‘clustifyr’

July 4, 2022

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

**Version** 1.9.0

**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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**biocViews** SingleCell, Annotation, Sequencing, Microarray, GeneExpression

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

---

**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:  
avg2 <- 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"
  )
  call1 <- cor_to_call(
    res,
    metadata = pbmc_meta,
    cluster_col = "seurat_clusters",
    collapse_to_cluster = FALSE,
    threshold = 0.8
  )
  res_rank <- assess_rank_bias(
    avg2,
    cbmc_ref,
    res = call1
  )

  ## End(Not run)

```

---

assign\_ident

*manually change ids as needed*

---

### Description

manually change ids as needed

### Usage

```

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

```

### 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   |
| ids         | new ids 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`

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

---

### 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

|                           |   |
|---------------------------|---|
| <code>mat</code>          | expression matrix   |
| <code>pathway_list</code> | a list of vectors, each named for a specific pathway, or dataframe    |
| <code>n_perm</code>       | Number of permutation for fgsea function. Defaults to 1000.           |
| <code>scale</code>        | convert expr_mat into zscores prior to running GSEA?, default = FALSE |
| <code>no_warnings</code>  | 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 | <i>Distance calculations for spatial coord</i> |
|---------------|--|

---

### 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

```
dist_res <- calc_distance(
  s_small13@reductions$tsne@cell.embeddings,
  s_small13@meta.data$letter.idents
)
```

---

|                 |                           |
|-----------------|---------------------------|
| 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

*reference marker matrix from seurat citeseq CBMC tutorial*

---

## 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-proteins](https://satijalab.org/seurat/v3.0/multimodal_vignette.html#identify-differentially-expressed-proteins)

## See Also

Other data: `cbmc_ref`, `downrefs`, `human_genes_10x`, `mouse_genes_10x`, `object_loc_lookup`, `pbmc_markers_M3Drop`, `pbmc_markers`, `pbmc_matrix_small`, `pbmc_meta`, `pbmc_vargenes`, `s_small3`, `s_small`, `sce_small`

---

|          |   |
|----------|---|
| 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-proteins](https://satijalab.org/seurat/v3.0/multimodal_vignette.html#identify-differentially-expressed-proteins)

**See Also**

Other data: [cbmc\\_m](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

|                  |   |
|------------------|---|
| 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

*Compare scRNA-seq data to reference data.*

---

**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 = TRUE,  
  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,  
  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 = TRUE,  
  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,  
  ...  
)
```



```
    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",
    seurat_out = TRUE,
    obj_out = TRUE,
    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",
  seurat_out = TRUE,
  obj_out = TRUE,
  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 = "classified",
  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 = "classified",
  compute_method = "cosine"
)

# Annotate a Seurat object
clustify(
  s_small3,
  cbmc_ref,
  cluster_col = "RNA_snn_res.1",
  obj_out = TRUE,
  per_cell = FALSE,
  dr = "tsne"
)

# Annotate (and return) a Seurat object per-cell
clustify(
  input = s_small3,
  ref_mat = cbmc_ref,
  cluster_col = "RNA_snn_res.1",
  obj_out = TRUE,
```

```

    per_cell = TRUE,
    dr = "tsne"
  )

```

---

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
```

---

clustify\_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 = TRUE,
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",
  seurat_out = TRUE,
  obj_out = TRUE,
  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",
seurat_out = TRUE,
obj_out = TRUE,
vec_out = FALSE,
threshold = 0,
rename_prefix = NULL,
verbose = TRUE,
details_out = FALSE,
...
)

```

### Arguments

|                    |   |
|--------------------|---|
| input              | single-cell expression matrix or Seurat object  |
| ...                | 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 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 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,
```

```

    seurat_out = FALSE,
    threshold = -Inf,
    dr = "umap",
    norm = "diff",
    call = TRUE,
    marker_inmatrix = TRUE,
    mode = "rank",
    obj_out = FALSE,
    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,
  seurat_out = TRUE,
  obj_out = FALSE,
  threshold = -Inf,
  dr = "umap",
  norm = "diff",
  marker_inmatrix = TRUE,
  mode = "rank",
  rename_prefix = NULL,
  ...
)

```

### Arguments

|                |  |
|----------------|--|
| input          | express matrix or object   |
| ...            | passed to <code>matrixize_markers</code>   |
| 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 <code>cluster_col</code> 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 <code>expr_mat</code> and <code>ref_mat</code> 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 |
| seurat_out      | output cor matrix or called seurat object                                 |
| 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                            |
| 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

```
# Seurat3
clustify_nudge(
  input = s_small3,
  ref_mat = cbmc_ref,
  marker = cbmc_m,
  cluster_col = "RNA_snn_res.1",
  threshold = 0.8,
  seurat_out = FALSE,
  mode = "pct",
  dr = "tsne"
)

# 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 | <i>Calculate adjusted p-values for hypergeometric test of gene lists or jaccard index</i> |
|---------------|---|

---

### 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      *get ranked calls for each cluster*

---

## 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

|                     |   |
|---------------------|---|
| cor_mat             | input similarity matrix   |
| metadata            | input metadata with tsne or umap coordinates and cluster ids                                  |
| 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                                   |
| topn                | 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 | <i>Cosine distance</i> |
|--------|------------------------|

---

**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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

downsample\_matrix      *downsample matrix by cluster or completely random*

---

### 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 | <i>takes files with positive and negative markers, as described in garnett, and returns list of markers</i> |
|-------------------|---|

---

**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

*pct of cells in each cluster that express genelist*

---

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

---

### 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 cellbrowsers*

---

**Description**

Build reference atlases from external UCSC cellbrowsers

**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:  
get_ucsc_reference(cb_url = "http://cells.ucsc.edu/?ds=kidney-atlas%2Ffetal_immune",  
                  cluster_col = "celltype")  
  
## 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 | <i>Generate variable gene list from marker matrix</i> |
|--------------|---|

---

**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"  
)  
  
gl <- gmt_to_list(path = gmt_file)  
length(gl)
```

---

|                 |  |
|-----------------|--|
| 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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

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

```
## Not run:  
insert_meta_object(s_small3, seurat_meta(s_small3, dr = "tsne"))  
  
## End(Not run)
```

---

|               |                      |
|---------------|----------------------|
| 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 | <i>decide for one gene whether it is a marker for a certain cell type</i> |
|---------------|---|

---

**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 tranformed into pseudo expression by descending weight   |
| background_weight | ranked genes are tranformed 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 | <i>Vector of mouse genes for 10x cellranger pipeline</i> |
|-----------------|--|

---

**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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small13](#), [s\\_small](#), [sce\\_small](#)

---

|                    |   |
|--------------------|---|
| not_pretty_palette | <i>black and white palette for plotting continous variables</i> |
|--------------------|---|

---

**Description**

black and white palette for plotting continous 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

```
mat <- object_data(  
  object = s_small3,  
  slot = "data"  
)  
mat[1:3, 1:3]  
mat <- object_data(  
  object = sce_small,  
  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
```

**Format**

An object of class `data.frame` with 4 rows and 6 columns.

**Source**

various packages

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small13](#), [s\\_small](#), [sce\\_small](#)

---

|            |   |
|------------|---|
| 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

```

object_ref(
  s_small13,

```

```
    cluster_col = "RNA_snn_res.1"  
  )
```

---

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

*compare clustering parameters and classification outcomes*

---

### 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    | expression matrix location                                      |
| meta_loc    | metadata location   |
| var_loc     | variable genes location   |
| cluster_col | column of clustering from metadata                              |
| lookuptable | if not supplied, will look in built-in table for object parsing |

### Value

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

### Examples

```

obj <- parse_loc_object(s_small13)
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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

|                     |  |
|---------------------|--|
| pbmc_markers_M3Drop | <i>Marker genes identified by M3Drop from single-cell RNA-seq PBMCs.</i> |
|---------------------|--|

---

**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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

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](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [s\\_small3](#), [s\\_small](#), [sce\\_small](#)

---

percent\_clusters      *Percentage detected per cluster*

---

**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     *Compute a p-value for similarity using permutation*

---

### 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      *Plot best calls for each cluster on a tSNE or umap*

---

### 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 | <i>Plot similarity measures on heatmap</i> |
|------------------|--|

---

### 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

*Plot gene expression on to tSNE or umap*

---

**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 <code>[clustifyr::plot_dims()]</code>              |

**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**

```
g1 <- 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,
  g1,
  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 | <i>Color palette for plotting continuous variables</i> |
|----------------|--|

---

**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 *Expanded color palette ramp for plotting discrete variables*

---

**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        *Query rank bias results*

---

**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_small | <i>Small SingleCellExperiment object</i> |
|-----------|--|

---

**Description**

Small SingleCellExperiment object

**Usage**

```
sce_small
```

**Format**

An object of class SingleCellExperiment with 200 rows and 200 columns.

**Source**

["https://scrnaseq-public-datasets.s3.amazonaws.com/scater-objects/segerstolpe.rds"](https://scrnaseq-public-datasets.s3.amazonaws.com/scater-objects/segerstolpe.rds)

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small3](#), [s\\_small](#)

---

|             |  |
|-------------|--|
| 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**

```
m <- seurat_meta(s_small13)
```

---

|            |  |
|------------|--|
| 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**

```
ref <- seurat_ref(s_small13, cluster_col = "RNA_snn_res.1")
```

---

|         |                                       |
|---------|---------------------------------------|
| s_small | <i>Small clustered Seurat2 object</i> |
|---------|---------------------------------------|

---

**Description**

Small clustered Seurat2 object

**Usage**

```
s_small
```

**Format**

An object of class seurat of length 1.

**Source**

[pbmc\_small1] processed by seurat

**See Also**

Other data: [cbmc\\_m](#), [cbmc\\_ref](#), [downrefs](#), [human\\_genes\\_10x](#), [mouse\\_genes\\_10x](#), [object\\_loc\\_lookup](#), [pbmc\\_markers\\_M3Drop](#), [pbmc\\_markers](#), [pbmc\\_matrix\\_small](#), [pbmc\\_meta](#), [pbmc\\_vargenes](#), [s\\_small13](#), [sce\\_small](#)

---

|           |                                       |
|-----------|---------------------------------------|
| s_small13 | <i>Small clustered Seurat3 object</i> |
|-----------|---------------------------------------|

---

**Description**

Small clustered Seurat3 object

**Usage**

```
s_small13
```

**Format**

An object of class Seurat of length 1.

**Source**

[pbmc\_small] processed by Seurat

**See Also**

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

---

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**

|        |  |
|--------|--|
| object | object after tsne or umap projections and clustering |
| ...    | additional arguments                                 |
| meta   | new metadata dataframe                               |

**Value**

object with newly inserted metadata columns

**Examples**

```
obj <- write_meta(  
  object = s_small3,  
  meta = seurat_meta(s_small3)  
)  
obj <- write_meta(  
  object = sce_small,  
  meta = object_data(sce_small, "meta.data")  
)
```

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