

Package ‘SlimR’

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Title Adaptive Machine Learning-Powered, Context-Matching Tool for
Single-Cell and Spatial Transcriptomics Annotation

Description Annotates single-cell and spatial-transcriptomic (ST) data using context-matching marker datasets. It creates a unified marker list (`Markers_list``) from multiple sources: built-in curated databases ('Cellmarker2', 'PanglaoDB', 'scIBD', 'TCellSI', 'PC-TIT', 'PCTAM'), Seurat objects with cell labels, or user-provided Excel tables. SlimR first uses adaptive machine learning for parameter optimization, and then offers two automated annotation approaches: 'cluster-based' and 'per-cell'. Cluster-based annotation assigns one label per cluster, expression-based probability calculation, and AUC validation. Per-cell annotation assigns labels to individual cells using three scoring methods with adaptive thresholds and ratio-based confidence filtering, plus optional UMAP spatial smoothing, making it ideal for heterogeneous clusters and rare cell types. The package also supports semi-automated workflows with heatmaps, feature plots, and combined visualizations for manual annotation. For more details, see Kabacoff (2020, ISBN:9787115420572).

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URL <https://github.com/zhaoqing-wang/SlimR>

BugReports <https://github.com/zhaoqing-wang/SlimR/issues>

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`calculate_cluster_variability`*Calculate Cluster Variability (Use in package)*

Description

Measures the degree of separation between different cell clusters based on expression patterns.

Usage

```
calculate_cluster_variability(data.features, features)
```

Arguments

<code>data.features</code>	Data frame containing expression data and cluster labels
<code>features</code>	Feature names to include in analysis

Value

Numeric value representing cluster separation strength

See Also

Other Section_1_Functions_Use_in_Package: [calculate_expression\(\)](#), [calculate_expression_skewness\(\)](#), [calculate_probability\(\)](#), [compute_adaptive_parameters\(\)](#), [estimate_batch_effect\(\)](#), [extract_dataset_features\(\)](#)

`calculate_expression` *Counts average expression of gene set (Use in package)*

Description

Counts average expression of gene set (Use in package)

Usage

```
calculate_expression(  
  object,  
  features,  
  assay = NULL,  
  cluster_col = NULL,  
  colour_low = "white",  
  colour_high = "navy"  
)
```

Arguments

object	Enter a Seurat object.
features	Enter one or a set of markers.
assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = NULL".
cluster_col	Enter the meta.data column in the Seurat object to be annotated, such as "seurat_cluster". Default parameters use "cluster_col = NULL".
colour_low	Color for lowest expression level. (default = "white")
colour_high	Color for highest expression level. (default = "black")

Value

Average expression genes and relatied informations in the input "Seurat" object given "cluster_col" and given "features".

See Also

Other Section_1_Functions_Use_in_Package: [calculate_cluster_variability\(\)](#), [calculate_expression_skewness\(\)](#), [calculate_probability\(\)](#), [compute_adaptive_parameters\(\)](#), [estimate_batch_effect\(\)](#), [extract_dataset_features\(\)](#)

calculate_expression_skewness
<i>Calculate Expression Distribution Skewness (Use in package)</i>

Description

Computes the average skewness of gene expression distributions across all features.

Usage

```
calculate_expression_skewness(expression_matrix)
```

Arguments

expression_matrix	Matrix of expression values
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Value

Mean absolute skewness across all genes

See Also

Other Section_1_Functions_Use_in_Package: [calculate_cluster_variability\(\)](#), [calculate_expression\(\)](#), [calculate_probability\(\)](#), [compute_adaptive_parameters\(\)](#), [estimate_batch_effect\(\)](#), [extract_dataset_features\(\)](#)

`calculate_probability` *Calculate gene set expression and infer probabilities with control datasets (Use in package)*

Description

Calculate gene set expression and infer probabilities with control datasets (Use in package)

Usage

```
calculate_probability(
  object,
  features,
  assay = NULL,
  cluster_col = NULL,
  min_expression = 0.1,
  specificity_weight = 3
)
```

Arguments

<code>object</code>	Enter a Seurat object.
<code>features</code>	Enter one or a set of markers.
<code>assay</code>	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = NULL".
<code>cluster_col</code>	Enter the meta.data column in the Seurat object to be annotated, such as "seurat_cluster". Default parameters use "cluster_col = NULL".
<code>min_expression</code>	The <code>min_expression</code> parameter defines a threshold value to determine whether a cell's expression of a feature is considered "expressed" or not. It is used to filter out low-expression cells that may contribute noise to the analysis. Default parameters use "min_expression = 0.1".
<code>specificity_weight</code>	The <code>specificity_weight</code> parameter controls how much the expression variability (standard deviation) of a feature within a cluster contributes to its "specificity score." It amplifies or suppresses the impact of variability in the final score calculation. Default parameters use "specificity_weight = 3".

Value

Average expression of genes in the input "Seurat" object given "cluster_col" and given "features".

See Also

Other Section_1_Functions_Use_in_Package: [calculate_cluster_variability\(\)](#), [calculate_expression\(\)](#), [calculate_expression_skewness\(\)](#), [compute_adaptive_parameters\(\)](#), [estimate_batch_effect\(\)](#), [extract_dataset_features\(\)](#)

Cellmarker2	<i>Cellmarker2 dataset</i>
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Description

A dataset containing marker genes for different cell types from Cellmarker2

Usage

Cellmarker2

Format

A data frame with 8 columns:

Details

This dataset is used to filter and create a standardized marker list. The dataset can be filtered based on species, tissue class, tissue type, cancer type, and cell type to generate a list of marker genes for specific cell types.

Source

<http://117.50.127.228/CellMarker/>

See Also

Other Section_0_Database: [Cellmarker2_raw](#), [Cellmarker2_table](#), [Markers_list_PCTAM](#), [Markers_list_PCTIT](#), [Markers_list_TCellSI](#), [Markers_list_scIBD](#), [PanglaoDB](#), [PanglaoDB_raw](#), [PanglaoDB_table](#)

Cellmarker2_raw	<i>Cellmarker2 raw dataset</i>
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Description

A dataset containing marker genes for different cell types from Cellmarker2

Usage

Cellmarker2_raw

Format

A data frame with 20 columns contined in the Cellmarker2 database:

Details

This dataset is used to filter and create a standardized marker list. The dataset can be filtered based on species, tissue class, tissue type, cancer type, and cell type to generate a list of marker genes for specific cell types.

Source

<http://117.50.127.228/CellMarker/>

See Also

Other Section_0_Database: [Cellmarker2](#), [Cellmarker2_table](#), [Markers_list_PCTAM](#), [Markers_list_PCTIT](#), [Markers_list_TCellSI](#), [Markers_list_scIBD](#), [PanglaoDB](#), [PanglaoDB_raw](#), [PanglaoDB_table](#)

Cellmarker2_table	<i>Cellmarker2 table</i>
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Description

A dataset containing marker genes for different cell types from Cellmarker2

Usage

Cellmarker2_table

Format

A list contain different types like species, tissue_class, tissue_type, cancer_type, cell_type

Details

This list is used to choose filters for creation of standardized marker list.

Source

<http://117.50.127.228/CellMarker/>

See Also

Other Section_0_Database: [Cellmarker2](#), [Cellmarker2_raw](#), [Markers_list_PCTAM](#), [Markers_list_PCTIT](#), [Markers_list_TCellSI](#), [Markers_list_scIBD](#), [PanglaoDB](#), [PanglaoDB_raw](#), [PanglaoDB_table](#)

Celltype_Annotation *Annotate Seurat Object with SlimR Cell Type Predictions*

Description

This function assigns SlimR predicted cell types to a Seurat object based on cluster annotations, and stores the results in the meta.data slot.

Usage

```
Celltype_Annotation(
  seurat_obj,
  cluster_col,
  SlimR_anno_result,
  plot_UMAP = TRUE,
  annotation_col = "Cell_type_SlimR"
)
```

Arguments

<code>seurat_obj</code>	A Seurat object containing cluster information in meta.data.
<code>cluster_col</code>	Character string indicating the column name in meta.data that contains cluster IDs.
<code>SlimR_anno_result</code>	List generated by function <code>Celltype_Calculate()</code> which containing a data.frame in <code>\$Prediction_results</code> with: 1. <code>cluster_col</code> (Cluster identifiers (should match <code>cluster_col</code> in meta.data)) 2. <code>Predicted_cell_type</code> (Predicted cell types for each cluster).
<code>plot_UMAP</code>	logical(1); if TRUE, plot the UMAP with cell type annotations.
<code>annotation_col</code>	The location to write in 'meta.data' that contains the predicted cell type. (default = "Cell_type_SlimR")

Value

A Seurat object with updated meta.data containing the predicted cell types.

Note

If `plot_UMAP = TRUE`, this function will print a UMAP plot as a side effect.

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation_PerCell\(\)](#), [Celltype_Calculate\(\)](#), [Celltype_Calculate_PerCell\(\)](#), [Celltype_Verification\(\)](#), [Celltype_Verification_PerCell\(\)](#), [Parameter_Calculate\(\)](#), [percell_workflow](#)

Examples

```
## Not run:
sce <- Celltype_Annotation(seurat_obj = sce,
  cluster_col = "seurat_clusters",
  SlimR_anno_result = SlimR_anno_result,
  plot_UMAP = TRUE,
  annotation_col = "Cell_type_SlimR"
)

## End(Not run)
```

Celltype_annotation_Cellmarker2

Uses "marker_list" from Cellmarker2 for cell annotation

Description

Uses "marker_list" from Cellmarker2 for cell annotation

Usage

```
Celltype_annotation_Cellmarker2(
  seurat_obj,
  gene_list,
  species,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = NULL,
  min_counts = 1,
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy"
)
```

Arguments

seurat_obj	Enter the Seurat object with annotation columns such as "seurat_cluster" in meta.data to be annotated.
gene_list	Enter the standard "Marker_list" generated by the Cellmarker2 database for the SlimR package, generated by the "Markers_filter_Cellmarker2 ()" function.
species	This parameter selects the species "Human" or "Mouse" for standard gene format correction of markers entered by "Marker_list".
cluster_col	Enter annotation columns such as "seurat_cluster" in meta.data of the Seurat object to be annotated. Default parameters use "cluster_col = 'seurat_clusters'".

assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = "RNA"".
save_path	The output path of the cell annotation picture. Example parameters use "save_path = './SlimR/Celltype_annotation_Cellmarker2/'".
min_counts	The minimum number of counts of genes in "Marker_list" entered. This number represents the number of the same gene in the same species and the same location in the Cellmarker2 database used for annotation of this cell type. Default parameters use "min_counts = 1".
colour_low	Color for lowest expression level. (default = "white")
colour_high	Color for highest expression level. (default = "navy")
colour_low_mertic	Color for lowest mertic level. (default = "white")
colour_high_mertic	Color for highest mertic level. (default = "navy")

Value

The cell annotation picture is saved in "save_path".

See Also

Other Section_5_Other_Functions_Provided: [Celltype_annotation_Excel\(\)](#), [Celltype_annotation_PanglaoDB\(\)](#), [Celltype_annotation_Seurat\(\)](#)

Examples

```
## Not run:
Celltype_annotation_Cellmarker2(seurat_obj = sce,
  gene_list = Markers_list_Cellmarker2,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_annotation_Cellmarker2")
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
)

## End(Not run)
```

Celltype_Annotation_Combined

Uses "marker_list" to generate combined plot for cell annotation

Description

Uses "marker_list" to generate combined plot for cell annotation

Usage

```
Celltype_Annotation_Combined(
  seurat_obj,
  gene_list,
  species,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = NULL,
  colour_low = "white",
  colour_high = "navy"
)
```

Arguments

seurat_obj	Enter the Seurat object with annotation columns such as "seurat_cluster" in meta.data to be annotated.
gene_list	A list of cells and corresponding gene controls, the name of the list is cell type, and the first column of the list corresponds to markers. Lists can be generated using functions such as "Markers_filter_Cellmarker2 ()", "Markers_filter_PanglaoDB ()", "read_excel_markers ()", "read_seurat_markers ()", etc.
species	This parameter selects the species "Human" or "Mouse" for standard gene format correction of markers entered by "Marker_list".
cluster_col	Enter annotation columns such as "seurat_cluster" in meta.data of the Seurat object to be annotated. Default parameters use "cluster_col = 'seurat_clusters'".
assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = 'RNA'".
save_path	The output path of the cell annotation picture. Example parameters use "save_path = './SlimR/Celltype_annotation_Bar/'".
colour_low	Color for lowest expression level. (default = "white")
colour_high	Color for highest expression level. (default = "navy")

Value

The cell annotation picture is saved in "save_path".

See Also

Other Section_4_Semi_Automated_Annotation: [Celltype_Annotation_Features\(\)](#), [Celltype_Annotation_Heatmap\(\)](#)

Examples

```
## Not run:
Celltype_Annotation_Combined(seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_Annotation_Combined"),
  colour_low = "white",
  colour_high = "navy"
)

## End(Not run)
```

Celltype_annotation_Excel

Uses "marker_list" from Excel input for cell annotation

Description

Uses "marker_list" from Excel input for cell annotation

Usage

```
Celltype_annotation_Excel(
  seurat_obj,
  gene_list,
  species,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = NULL,
  metric_names = NULL,
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy"
)
```

Arguments

seurat_obj	Enter the Seurat object with annotation columns such as "seurat_cluster" in meta.data to be annotated.
------------	--

gene_list	Enter the standard "Marker_list" generated by the Excel files database for the SlimR package, generated by the "read_excel_markers()" function.
species	This parameter selects the species "Human" or "Mouse" for standard gene format correction of markers entered by "Marker_list".
cluster_col	Enter annotation columns such as "seurat_cluster" in meta.data of the Seurat object to be annotated. Default parameters use "cluster_col = "seurat_clusters"".
assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = 'RNA'".
save_path	The output path of the cell annotation picture. Example parameters use "save_path = './SlimR/Celltype_annotation_Excel/'".
metric_names	Change the row name for the input merts, not recommended unless necessary. (NULL is used as default parameter)
colour_low	Color for lowest expression level. (default = "white")
colour_high	Color for highest expression level. (default = "navy")
colour_low_mertic	Color for lowest mertic level. (default = "white")
colour_high_mertic	Color for highest mertic level. (default = "navy")

Value

The cell annotation picture is saved in "save_path".

See Also

Other Section_5_Other_Functions_Provided: [Celltype_annotation_Cellmarker2\(\)](#), [Celltype_annotation_PanglaoDE](#), [Celltype_annotation_Seurat\(\)](#)

Examples

```
## Not run:
Celltype_annotation_Excel(seurat_obj = sce,
  gene_list = Markers_list_Excel,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_annotation_Excel")
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
)

## End(Not run)
```

Celltype_Annotation_Features

Annotate cell types using features plot with different marker databases

Description

This function dynamically selects the appropriate annotation method based on the `gene_list_type` parameter. It supports marker databases from Cellmarker2, PanglaoDB, Seurat (via `FindAllMarkers`), or Excel files.

Usage

```
Celltype_Annotation_Features(
  seurat_obj,
  gene_list,
  gene_list_type = "Default",
  species = NULL,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = NULL,
  min_counts = 1,
  metric_names = NULL,
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
  ...
)
```

Arguments

<code>seurat_obj</code>	A valid Seurat object with cluster annotations in <code>meta.data</code> .
<code>gene_list</code>	A list of data frames containing marker genes and metrics. Format depends on <code>gene_list_type</code> : - Cellmarker2 : Generated by <code>Markers_filter_Cellmarker2()</code> . - PanglaoDB : Generated by <code>Markers_filter_PanglaoDB()</code> . - Seurat : Generated by <code>read_seurat_markers()</code> . - Excel : Generated by <code>read_excel_markers()</code> .
<code>gene_list_type</code>	Type of marker database to use. Be one of: "Cellmarker2", "PanglaoDB", "Seurat", or "Excel".
<code>species</code>	Species of the dataset: "Human" or "Mouse" for gene name standardization.
<code>cluster_col</code>	Column name in <code>meta.data</code> defining clusters (default: "seurat_clusters").
<code>assay</code>	Assay layer in the Seurat object (default: "RNA").
<code>save_path</code>	Directory to save output PNGs. Must be explicitly specified.
<code>min_counts</code>	Minimum number of counts for Cellmarker2 annotations (default: 1).
<code>metric_names</code>	Optional. Change the row name for the input mertics, not recommended unless necessary. (NULL is used as default parameter; used in "Seurat"/"Excel").

```

colour_low      Color for lowest expression level. (default = "white")
colour_high     Color for highest expression level. (default = "navy")
colour_low_mertic
                Color for lowest mertic level. (default = "white")
colour_high_mertic
                Color for highest mertic level. (default = "navy")
...            Additional parameters passed to the specific annotation function.

```

Value

Saves cell type annotation PNGs in save_path. Returns invisibly.

See Also

Other Section_4_Semi_Automated_Annotation: [Celltype_Annotation_Combined\(\)](#), [Celltype_Annotation_Heatmap\(\)](#)

Examples

```

## Not run:
# Example for Cellmarker2
Celltype_Annotation_Features(seurat_obj = sce,
  gene_list = Markers_list_Cellmarker2,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_annotation_Cellmarker2"),
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
)

# Example for PanglaoDB
Celltype_Annotation_Features(seurat_obj = sce,
  gene_list = Markers_list_panglaoDB,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_annotation_PanglaoDB")
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
)

# Example for Seurat marker list
Celltype_Annotation_Features(seurat_obj = sce,
  gene_list = Markers_list_Seurat,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",

```

```

    save_path = file.path(tempdir(), "SlimR_Celltype_annotation_Seurat")
    colour_low = "white",
    colour_high = "navy",
    colour_low_mertic = "white",
    colour_high_mertic = "navy",
  )

# Example for Excel marker list
Celltype_Annotation_Features(seurat_obj = sce,
  gene_list = Markers_list_Excel,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_annotation_Excel")
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
)

## End(Not run)

```

Celltype_Annotation_Heatmap

Uses "marker_list" to generate heatmap for cell annotation

Description

Uses "marker_list" to generate heatmap for cell annotation

Usage

```

Celltype_Annotation_Heatmap(
  seurat_obj,
  gene_list,
  species,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  min_expression = 0.1,
  specificity_weight = 3,
  colour_low = "navy",
  colour_high = "firebrick3"
)

```

Arguments

seurat_obj	Enter the Seurat object with annotation columns such as "seurat_cluster" in meta.data to be annotated.
------------	--

gene_list	A list of cells and corresponding gene controls, the name of the list is cell type, and the first column of the list corresponds to markers. Lists can be generated using functions such as "Markers_filter_Cellmarker2()", "Markers_filter_PanglaoDB()", "read_excel_markers()", "read_seurat_markers()", etc.
species	This parameter selects the species "Human" or "Mouse" for standard gene format correction of markers entered by "Marker_list".
cluster_col	Enter annotation columns such as "seurat_cluster" in meta.data of the Seurat object to be annotated. Default parameters use "cluster_col = 'seurat_clusters'".
assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = 'RNA'".
min_expression	The min_expression parameter defines a threshold value to determine whether a cell's expression of a feature is considered "expressed" or not. It is used to filter out low-expression cells that may contribute noise to the analysis. Default parameters use "min_expression = 0.1".
specificity_weight	The specificity_weight parameter controls how much the expression variability (standard deviation) of a feature within a cluster contributes to its "specificity score." It amplifies or suppresses the impact of variability in the final score calculation. Default parameters use "specificity_weight = 3".
colour_low	Color for lowest probability level in Heatmap visualization of probability matrix. (default = "navy")
colour_high	Color for highest probability level Heatmap visualization of probability matrix. (default = "firebrick3")

Value

The heatmap of the comparison between "cluster_col" in the Seurat object and the given gene set "gene_list" needs to be annotated.

See Also

Other Section_4_Semi_Automated_Annotation: [Celltype_Annotation_Combined\(\)](#), [Celltype_Annotation_Features\(\)](#)

Examples

```
## Not run:
Celltype_Annotation_Heatmap(seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  min_expression = 0.1,
  specificity_weight = 3,
  colour_low = "navy",
  colour_high = "firebrick3"
)

## End(Not run)
```

Celltype_annotation_PanglaoDB

Uses "marker_list" from PanglaoDB for cell annotation

Description

Uses "marker_list" from PanglaoDB for cell annotation

Usage

```
Celltype_annotation_PanglaoDB(
  seurat_obj,
  gene_list,
  species,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = NULL,
  metric_names = NULL,
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy"
)
```

Arguments

seurat_obj	Enter the Seurat object with annotation columns such as "seurat_cluster" in meta.data to be annotated.
gene_list	Enter the standard "Marker_list" generated by the PanglaoDB database for the SlimR package, generated by the "Markers_filter_PanglaoDB ()" function.
species	This parameter selects the species "Human" or "Mouse" for standard gene format correction of markers entered by "Marker_list".
cluster_col	Enter annotation columns such as "seurat_cluster" in meta.data of the Seurat object to be annotated. Default parameters use "cluster_col = 'seurat_clusters'".
assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = 'RNA'".
save_path	The output path of the cell annotation picture. Example parameters use "save_path = './SlimR/Celltype_annotation_PanglaoDB/'".
metric_names	Warning: Do not enter information. This parameter is used to check if "Marker_list" conforms to the PanglaoDB database output.
colour_low	Color for lowest expression level. (default = "white")
colour_high	Color for highest expression level. (default = "navy")
colour_low_mertic	Color for lowest mertic level. (default = "white")
colour_high_mertic	Color for highest mertic level. (default = "navy")

Value

The cell annotation picture is saved in "save_path".

See Also

Other Section_5_Other_Functions_Provided: [Celltype_annotation_Cellmarker2\(\)](#), [Celltype_annotation_Excel\(\)](#), [Celltype_annotation_Seurat\(\)](#)

Examples

```
## Not run:
Celltype_annotation_PanglaoDB(seurat_obj = sce,
  gene_list = Markers_list_panglaoDB,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_annotation_PanglaoDB")
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
)

## End(Not run)
```

Celltype_Annotation_PerCell

Annotate Seurat Object with Per-Cell SlimR Predictions

Description

This function assigns SlimR per-cell predicted cell types directly to individual cells in a Seurat object's meta.data slot.

Usage

```
Celltype_Annotation_PerCell(
  seurat_obj,
  SlimR_percell_result,
  plot_UMAP = TRUE,
  annotation_col = "Cell_type_PerCell_SlimR",
  plot_confidence = FALSE
)
```

Arguments

seurat_obj A Seurat object.
SlimR_perccell_result List generated by Celltype_Calculate_PerCell() containing Cell_annotations data.frame with Cell_barcode and Predicted_cell_type columns.
plot_UMAP Logical; if TRUE, plot the UMAP with cell type annotations. Default: TRUE.
annotation_col Column name to write in meta.data. Default: "Cell_type_PerCell_SlimR".
plot_confidence Logical; if TRUE, also plot a UMAP colored by confidence scores. Default: FALSE.

Value

A Seurat object with updated meta.data containing:

- annotation_col: Predicted cell type for each cell
- paste0(annotation_col, "_score"): Max score for each cell
- paste0(annotation_col, "_confidence"): Confidence score for each cell

Note

If plot_UMAP = TRUE, this function will print UMAP plot(s) as a side effect.

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation\(\)](#), [Celltype_Calculate\(\)](#), [Celltype_Calculate_PerCell\(\)](#), [Celltype_Verification\(\)](#), [Celltype_Verification_PerCell\(\)](#), [Parameter_Calculate\(\)](#), [perccell_workflow](#)

Examples

```
## Not run:
# Run per-cell annotation
result <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human"
)

# Annotate Seurat object
sce <- Celltype_Annotation_PerCell(
  seurat_obj = sce,
  SlimR_perccell_result = result,
  plot_UMAP = TRUE,
  annotation_col = "Cell_type_PerCell_SlimR"
)

## End(Not run)
```

Celltype_annotation_Seurat

Uses "marker_list" from Seurat object for cell annotation

Description

Uses "marker_list" from Seurat object for cell annotation

Usage

```
Celltype_annotation_Seurat(
  seurat_obj,
  gene_list,
  species,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = NULL,
  metric_names = NULL,
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy"
)
```

Arguments

seurat_obj	Enter the Seurat object with annotation columns such as "seurat_cluster" in meta.data to be annotated.
gene_list	Enter the standard "Marker_list" generated by the Seurat object database for the SlimR package, generated by the "read_seurat_markers()" function.
species	This parameter selects the species "Human" or "Mouse" for standard gene format correction of markers entered by "Marker_list".
cluster_col	Enter annotation columns such as "seurat_cluster" in meta.data of the Seurat object to be annotated. Default parameters use "cluster_col = 'seurat_clusters'".
assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = 'RNA'".
save_path	The output path of the cell annotation picture. Example parameters use "save_path = './SlimR/Celltype_annotation_Seurat/'".
metric_names	Change the row name for the input mertics, not recommended unless necessary. (NULL is used as default parameter)
colour_low	Color for lowest expression level. (default = "white")
colour_high	Color for highest expression level. (default = "navy")
colour_low_mertic	Color for lowest mertic level. (default = "white")
colour_high_mertic	Color for highest mertic level. (default = "navy")

Value

The cell annotation picture is saved in "save_path".

See Also

Other Section_5_Other_Functions_Provided: [Celltype_annotation_Cellmarker2\(\)](#), [Celltype_annotation_Excel\(\)](#), [Celltype_annotation_PanglaoDB\(\)](#)

Examples

```
## Not run:
Celltype_annotation_Seurat(seurat_obj = sce,
  gene_list = Markers_list_Seurat,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  save_path = file.path(tempdir(), "SlimR_Celltype_annotation_Seurat")
  colour_low = "white",
  colour_high = "navy",
  colour_low_mertic = "white",
  colour_high_mertic = "navy",
)

## End(Not run)
```

Celltype_Calculate	<i>Uses "marker_list" to calculate probability, prediction results, AUC and generate heatmap for cell annotation</i>
--------------------	--

Description

Uses "marker_list" to calculate probability, prediction results, AUC and generate heatmap for cell annotation

Usage

```
Celltype_Calculate(
  seurat_obj,
  gene_list,
  species,
  cluster_col = "seurat_clusters",
  assay = "RNA",
  min_expression = 0.1,
  specificity_weight = 3,
  threshold = 0.6,
  compute_AUC = TRUE,
  plot_AUC = TRUE,
```

```

    AUC_correction = FALSE,
    colour_low = "navy",
    colour_high = "firebrick3"
)

```

Arguments

seurat_obj	Enter the Seurat object with annotation columns such as "seurat_cluster" in meta.data to be annotated.
gene_list	A list of cells and corresponding gene controls, the name of the list is cell type, and the first column of the list corresponds to markers. Lists can be generated using functions such as "Markers_filter_Cellmarker2()", "Markers_filter_PanglaoDB()", "read_excel_markers()", "read_seurat_markers()", etc.
species	This parameter selects the species "Human" or "Mouse" for standard gene format correction of markers entered by "Marker_list".
cluster_col	Enter annotation columns such as "seurat_cluster" in meta.data of the Seurat object to be annotated. Default parameters use "cluster_col = 'seurat_clusters'".
assay	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = 'RNA'".
min_expression	The min_expression parameter defines a threshold value to determine whether a cell's expression of a feature is considered "expressed" or not. It is used to filter out low-expression cells that may contribute noise to the analysis. Default parameters use "min_expression = 0.1".
specificity_weight	The specificity_weight parameter controls how much the expression variability (standard deviation) of a feature within a cluster contributes to its "specificity score." It amplifies or suppresses the impact of variability in the final score calculation. Default parameters use "specificity_weight = 3".
threshold	This parameter refers to the normalized similarity between the "alternative cell type" and the "predicted cell type" in the returned results. (the default parameter is 0.6)
compute_AUC	Logical indicating whether to calculate AUC values for predicted cell types. AUC measures how well the marker genes distinguish the cluster from others. When TRUE, adds an AUC column to the prediction results. (default: TRUE)
plot_AUC	The logic indicates whether to draw an AUC curve for the predicted cell type. When TRUE, add an AUC_plot to result. (default: TRUE)
AUC_correction	Logical value controlling AUC-based correction. (default = FALSE) When set to TRUE: 1.Computes AUC values for candidate cell types. (probability > threshold) 2.Selects the cell type with the highest AUC as the final predicted type. 3.Records the selected type's AUC value in the "AUC" column.
colour_low	Color for lowest probability level in Heatmap visualization of probability matrix. (default = "navy")
colour_high	Color for highest probability level Heatmap visualization of probability matrix. (default = "firebrick3")

Value

A list containing:

- Expression_list: List of expression matrices for each cell type
- Proportion_list: List of proportion of expression for each cell type
- Expression_scores_matrix: Matrix of expression scores
- Probability_matrix: Matrix of normalized probabilities
- Prediction_results: Data frame with cluster annotations including:
 - cluster_col: Cluster identifier
 - Predicted_cell_type: Primary predicted cell type
 - AUC: Area Under the Curve value (when compute_AUC = TRUE)
 - Alternative_cell_types: Semi-colon separated alternative cell types
- Heatmap_plot: Heatmap visualization of probability matrix (pheatmap object). Can be displayed using print() or plot()
- AUC_plot: AUC visualization of Predicted cell type (ggplot object)
- AUC_list: The resulting list of AUC values calculated for genes in alternative cell types above the approximate threshold

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation\(\)](#), [Celltype_Annotation_PerCell\(\)](#), [Celltype_Calculate_PerCell\(\)](#), [Celltype_Verification\(\)](#), [Celltype_Verification_PerCell\(\)](#), [Parameter_Calculate\(\)](#), [percell_workflow](#)

Examples

```
## Not run:
SlimR_anno_result <- Celltype_Calculate(seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  cluster_col = "seurat_clusters",
  assay = "RNA",
  min_expression = 0.1,
  specificity_weight = 3,
  threshold = 0.6,
  compute_AUC = TRUE,
  plot_AUC = TRUE,
  AUC_correction = FALSE,
  colour_low = "navy",
  colour_high = "firebrick3"
)

## End(Not run)
```

Celltype_Calculate_PerCell*Per-cell annotation using marker expression and optional UMAP spatial smoothing*

Description

Unlike cluster-based annotation, this function assigns cell type labels to each individual cell based on marker gene expression profiles. Optionally uses UMAP coordinates to smooth predictions via k-nearest neighbor voting.

Usage

```
Celltype_Calculate_PerCell(
  seurat_obj,
  gene_list,
  species,
  assay = "RNA",
  method = c("weighted", "mean", "AUCell"),
  min_expression = 0.1,
  use_umap_smoothing = FALSE,
  umap_reduction = "umap",
  k_neighbors = 15,
  smoothing_weight = 0.3,
  min_score = "auto",
  min_confidence = 1.2,
  return_scores = FALSE,
  ncores = 1,
  chunk_size = 5000,
  verbose = TRUE
)
```

Arguments

seurat_obj	Seurat object with normalized expression data.
gene_list	A standardized marker list (same format as Celltype_Calculate).
species	"Human" or "Mouse" for gene name formatting.
assay	Assay to use (default: "RNA").
method	Scoring method: "AUCell" (rank-based), "mean" (average expression), or "weighted" (expression * detection weighted). Default: "weighted".
min_expression	Minimum expression threshold for detection. Default: 0.1.
use_umap_smoothing	Logical. If TRUE, apply k-NN smoothing using UMAP coordinates to improve annotation consistency. Default: FALSE.
umap_reduction	Name of UMAP reduction in Seurat object. Default: "umap".

k_neighbors	Number of neighbors for UMAP smoothing. Default: 15.
smoothing_weight	Weight for neighbor votes vs cell's own score (0-1). Higher values give more weight to neighbors. Default: 0.3.
min_score	Minimum score threshold to assign a cell type. Cells below this threshold are labeled "Unassigned". Default: "auto" which adaptively sets the threshold based on number of cell types ($1.5 / n_celltypes$). Set to a numeric value (e.g., 0.1) to use a fixed threshold.
min_confidence	Minimum confidence threshold. Cells with confidence below this value are labeled "Unassigned". Confidence is calculated as the ratio of max score to second-highest score. Default: 1.2 (max must be 20% higher than second). Set to 1.0 to disable confidence filtering.
return_scores	If TRUE, return full score matrix. Default: FALSE.
ncores	Number of cores for parallel processing. Default: 1.
chunk_size	Number of cells to process per chunk (memory optimization). Default: 5000.
verbose	Print progress messages. Default: TRUE.

Details

Scoring Methods:

"weighted" (recommended): Combines normalized expression with detection rate. For each cell and cell type: $score = \text{mean}(\text{expr}_i * \text{weight}_i)$ where weight_i is derived from the marker's specificity across the dataset.

"mean": Simple average of normalized marker expression. Fast but less discriminative for overlapping marker sets.

"AUCell": Rank-based scoring similar to AUCell package. For each cell, genes are ranked by expression, and the score is the proportion of marker genes in the top X% of expressed genes. Robust to technical variation.

UMAP Smoothing:

When `use_umap_smoothing = TRUE`, the function:

1. Computes initial per-cell scores
2. Finds k nearest neighbors in UMAP space for each cell
3. Smooths scores by weighted averaging with neighbors
4. Re-assigns cell types based on smoothed scores

This helps reduce noise and improve consistency of annotations within spatially coherent regions.

Value

A list containing:

- Cell_annotations: Data frame with Cell_barcode, Predicted_cell_type, Max_score, Confidence
- Cell_confidence: Numeric vector of confidence scores per cell
- Summary: Summary table of cell type counts and percentages

- Expression_list: List of mean expression matrices per cell type (for verification)
- Proportion_list: List of detection proportion matrices per cell type
- Prediction_results: Summary data frame with per-cell-type statistics
- Probability_matrix: Full cell $\times$ cell_type probability matrix (normalized)
- Raw_score_matrix: Full cell $\times$ cell_type raw score matrix (before normalization)
- Parameters: List of parameters used including adaptive thresholds
- Cell_scores: (if return_scores=TRUE) Same as Probability_matrix

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation\(\)](#), [Celltype_Annotation_PerCell\(\)](#), [Celltype_Calculate\(\)](#), [Celltype_Verification\(\)](#), [Celltype_Verification_PerCell\(\)](#), [Parameter_Calculate\(\)](#), [percell_workflow](#)

Examples

```
## Not run:
# Basic per-cell annotation
result <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  method = "weighted"
)

# Add annotations to Seurat object
sce$Cell_type_PerCell <- result$Cell_annotations$Predicted_cell_type

# With UMAP smoothing for more consistent annotations
result_smooth <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  use_umap_smoothing = TRUE,
  k_neighbors = 20,
  smoothing_weight = 0.3
)

## End(Not run)
```

Celltype_Verification *Perform cell type verification and generate the validation dotplot*

Description

This function performs verification of predicted cell types by selecting high log2FC and high expression proportion genes and generates and generate the validation dotplot.

Usage

```
Celltype_Verification(
  seurat_obj,
  SlimR_anno_result,
  assay = "RNA",
  gene_number = 5,
  colour_low = "white",
  colour_high = "navy",
  annotation_col = "Cell_type_SlimR"
)
```

Arguments

<code>seurat_obj</code>	A Seurat object containing single-cell data.
<code>SlimR_anno_result</code>	A list containing SlimR annotation results with: <code>Expression_list</code> - List of expression matrices for each cell type. <code>Prediction_results</code> - Data frame with cluster annotations.
<code>assay</code>	Enter the assay used by the Seurat object, such as "RNA". Default parameters use "assay = 'RNA'".
<code>gene_number</code>	Integer specifying number of top genes to select per cell type.
<code>colour_low</code>	Color for lowest expression level. (default = "white")
<code>colour_high</code>	Color for highest expression level. (default = "navy")
<code>annotation_col</code>	Character string specifying the column in meta.data to use for grouping.

Value

A ggplot object showing expression of top variable genes.

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation\(\)](#), [Celltype_Annotation_PerCell\(\)](#), [Celltype_Calculate\(\)](#), [Celltype_Calculate_PerCell\(\)](#), [Celltype_Verification_PerCell\(\)](#), [Parameter_Calculate\(\)](#), [percell_workflow](#)

Examples

```
## Not run:
Celltype_Verification(seurat_obj = sce,
  SlimR_anno_result = SlimR_anno_result,
  assay = "RNA",
  gene_number = 5,
  colour_low = "white",
  colour_high = "navy",
  annotation_col = "Cell_type_SlimR"
)

## End(Not run)
```

Celltype_Verification_PerCell

Verify per-cell annotations with marker expression dotplot

Description

This function verifies per-cell SlimR annotations by generating a dotplot showing marker gene expression across predicted cell types.

Usage

```
Celltype_Verification_PerCell(
  seurat_obj,
  SlimR_percell_result,
  assay = "RNA",
  gene_number = 5,
  colour_low = "white",
  colour_high = "navy",
  annotation_col = "Cell_type_PerCell_SlimR",
  min_cells = 10
)
```

Arguments

<code>seurat_obj</code>	A Seurat object with per-cell annotations.
<code>SlimR_percell_result</code>	A list from <code>Celltype_Calculate_PerCell()</code> containing <code>Expression_list</code> with marker genes per cell type.
<code>assay</code>	Assay to use. Default: "RNA".
<code>gene_number</code>	Number of top genes to show per cell type. Default: 5.
<code>colour_low</code>	Color for lowest expression. Default: "white".
<code>colour_high</code>	Color for highest expression. Default: "navy".
<code>annotation_col</code>	Column in meta.data with cell type annotations. Default: "Cell_type_PerCell_SlimR".
<code>min_cells</code>	Minimum number of cells required for a cell type to be included in the plot. Default: 10.

Value

A ggplot object showing marker gene expression dotplot.

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation\(\)](#), [Celltype_Annotation_PerCell\(\)](#), [Celltype_Calculate\(\)](#), [Celltype_Calculate_PerCell\(\)](#), [Celltype_Verification\(\)](#), [Parameter_Calculate\(\)](#), [percell_workflow](#)

Examples

```
## Not run:
# After running Celltype_Calculate_PerCell and Celltype_Annotation_PerCell
dotplot <- Celltype_Verification_PerCell(
  seurat_obj = sce,
  SlimR_perCell_result = result,
  gene_number = 5,
  annotation_col = "Cell_type_PerCell_SlimR"
)
print(dotplot)

## End(Not run)
```

```
compute_adaptive_parameters
```

Compute Adaptive Parameters Based on Dataset Features (Use in package)

Description

Calculates optimal min_expression, specificity_weight, and threshold parameters using continuous adaptive algorithms based on dataset characteristics.

Usage

```
compute_adaptive_parameters(dataset_features, n_celltypes = 50)
```

Arguments

dataset_features List of dataset characteristics from `extract_dataset_features()`

n_celltypes Expected number of cell types in marker database

Value

List containing min_expression, specificity_weight, threshold, and rationale

See Also

Other Section_1_Functions_Use_in_Package: [calculate_cluster_variability\(\)](#), [calculate_expression\(\)](#), [calculate_expression_skewness\(\)](#), [calculate_probability\(\)](#), [estimate_batch_effect\(\)](#), [extract_dataset_features\(\)](#)

estimate_batch_effect *Estimate Batch Effect Strength (Use in package)*

Description

Roughly estimates the potential impact of batch effects using available metadata.

Usage

```
estimate_batch_effect(seurat_obj, assay)
```

Arguments

seurat_obj	Seurat object
assay	Assay name

Value

Batch effect score (0 indicates no detectable batch effect)

See Also

Other Section_1_Functions_Use_in_Package: [calculate_cluster_variability\(\)](#), [calculate_expression\(\)](#), [calculate_expression_skewness\(\)](#), [calculate_probability\(\)](#), [compute_adaptive_parameters\(\)](#), [extract_dataset_features\(\)](#)

extract_dataset_features

*Extract Dataset Characteristics for Adaptive Parameter Calculation
(Use in package)*

Description

Computes various statistical features from single-cell data that are used as input for the parameter prediction model.

Usage

```
extract_dataset_features(  
  seurat_obj,  
  features,  
  assay = NULL,  
  cluster_col = NULL  
)
```

Arguments

seurat_obj	Seurat object
features	Features to analyze
assay	Assay name
cluster_col	Cluster column name

Value

List of dataset characteristics including expression statistics, variability measures, and cluster properties

See Also

Other Section_1_Functions_Use_in_Package: [calculate_cluster_variability\(\)](#), [calculate_expression\(\)](#), [calculate_expression_skewness\(\)](#), [calculate_probability\(\)](#), [compute_adaptive_parameters\(\)](#), [estimate_batch_effect\(\)](#)

Markers_filter_Cellmarker2

Create Marker_list from the Cellmarkers2 database

Description

Create Marker_list from the Cellmarkers2 database

Usage

```
Markers_filter_Cellmarker2(
  df,
  species = NULL,
  tissue_class = NULL,
  tissue_type = NULL,
  cancer_type = NULL,
  cell_type = NULL
)
```

Arguments

df	Standardized Cellmarkers2 database. It is read as data(Cellmarkers2) in the SlimR library.
species	Species information in Cellmarkers2 database. The default input is "Human" or "Mouse".The input can be retrieved by "Cellmarkers2_table". For more information,please refer to http://117.50.127.228/CellMarker/ on Cellmarkers2's official website.

tissue_class	Tissue_class information in Cellmarkers2 database. The input can be retrieved by "Cellmarkers2_table". For more information, please refer to http://117.50.127.228/CellMarker/ on Cellmarkers2's official website.
tissue_type	Tissue_type information in Cellmarkers2 database. The input can be retrieved by "Cellmarkers2_table". For more information, please refer to http://117.50.127.228/CellMarker/ on Cellmarkers2's official website.
cancer_type	Cancer_type information in Cellmarkers2 database. The input can be retrieved by "Cellmarkers2_table". For more information, please refer to http://117.50.127.228/CellMarker/ on Cellmarkers2's official website.
cell_type	Cell_type information in Cellmarkers2 database. The input can be retrieved by "Cellmarkers2_table". For more information, please refer to http://117.50.127.228/CellMarker/ on Cellmarkers2's official website.

Value

The standardized "Marker_list" in the SlimR package

See Also

Other Section_2_Standardized_Markers_List: [Markers_filter_PanglaoDB\(\)](#), [Read_excel_markers\(\)](#), [Read_seurat_markers\(\)](#)

Examples

```
Cellmarker2 <- SlimR::Cellmarker2
Markers_list_Cellmarker2 <- Markers_filter_Cellmarker2(
  Cellmarker2,
  species = "Human",
  tissue_class = "Intestine",
  tissue_type = NULL,
  cancer_type = NULL,
  cell_type = NULL
)
```

Markers_filter_PanglaoDB

Create Marker_list from the PanglaoDB database

Description

Create Marker_list from the PanglaoDB database

Usage

```
Markers_filter_PanglaoDB(df, species_input, organ_input)
```

Arguments

- df Standardized PanglaoDB database. It is read as data(PanglaoDB) in the SlimR library.
- species_input Species information in PanglaoDB database. The default input is "Human" or "Mouse".The input can be retrieved by "PanglaoDB_table". For more information,please refer to <https://panglaodb.se/> on PanglaoDB’s official website.
- organ_input Organ type information in the PanglaoDB database. The input can be retrieved by "PanglaoDB_table".For more information, please refer to <https://panglaodb.se/> on PanglaoDB’s official website.

Value

The standardized "Marker_list" in the SlimR package

See Also

Other Section_2_Standardized_Markers_List: [Markers_filter_Cellmarker2\(\)](#),[Read_excel_markers\(\)](#),
[Read_seurat_markers\(\)](#)

Examples

```
PanglaoDB <- SlimR::PanglaoDB
Markers_list_panglaoDB <- Markers_filter_PanglaoDB(
  PanglaoDB,
  species_input = 'Human',
  organ_input = 'GI tract'
)
```

Markers_list_PCTAM	<i>List of Macrophage subtype markers in the article "Macrophage diversity in cancer revisited in the era of single-cell omics"</i>
--------------------	---

Description

A dataset containing marker genes for different Macrophage subtypes from the article "Macrophage diversity in cancer revisited in the era of single-cell omics"

Usage

```
Markers_list_PCTAM
```

Format

A list with 7 tables.

Details

This list is a table of 7 types of Tumor-associated macrophages (TAMs) markers obtained from the article "Macrophage diversity in cancer revisited in the era of single-cell omics". The data source is "https://doi.org/10.1016/j.it.2022.04.008", and the reference literature is: Ruo-Yu Ma et al. (2022) [doi:10.1016/j.it.2022.04.008](https://doi.org/10.1016/j.it.2022.04.008).

Source

[doi:10.1016/j.it.2022.04.008](https://doi.org/10.1016/j.it.2022.04.008)

See Also

Other Section_0_Database: [Cellmarker2](#), [Cellmarker2_raw](#), [Cellmarker2_table](#), [Markers_list_PCTIT](#), [Markers_list_TCellSI](#), [Markers_list_scIBD](#), [PanglaoDB](#), [PanglaoDB_raw](#), [PanglaoDB_table](#)

Markers_list_PCTIT	<i>List of T cell subtype markers in the article "Pan-cancer single cell landscape of tumor-infiltrating T cells"</i>
--------------------	---

Description

A dataset containing marker genes for different T cell types from the article "Pan-cancer single cell landscape of tumor-infiltrating T cells"

Usage

Markers_list_PCTIT

Format

A list with 40 tables.

Details

This list is a table of 40 types of pan-cancer tumor-infiltrating T cell (PCTIT) markers obtained from the article "Pan-cancer single cell landscape of tumor-infiltrating T cells". The data source is "https://doi.org/10.1126/science.abe6474", and the reference literature is: L. Zheng et al. (2021) [doi:10.1126/science.abe6474](https://doi.org/10.1126/science.abe6474).

Source

[doi:10.1126/science.abe6474](https://doi.org/10.1126/science.abe6474)

See Also

Other Section_0_Database: [Cellmarker2](#), [Cellmarker2_raw](#), [Cellmarker2_table](#), [Markers_list_PCTAM](#), [Markers_list_TCellSI](#), [Markers_list_scIBD](#), [PanglaoDB](#), [PanglaoDB_raw](#), [PanglaoDB_table](#)

Markers_list_scIBD	List of cell type markers in the article scIBD
Description	
A dataset containing marker genes for different human intestine cell types from scIBD	
Usage	
Markers_list_scIBD	
Format	
A list with one hundred and one tables.	
Details	
This list is a table of 101 types of human intestine cell types markers obtained from scIBD. The article doi source is "https://doi.org/10.1038/s43588-023-00464-9", and the reference literature is: Nie et al. (2023) doi:10.1038/s43588-023-00464-9. Note: The 'Markers_list_scIBD' was generated using section 2.5.2 and the parameters 'sort_by = "logFC"' and 'gene_filter = 20' were set.	
Source	
doi:10.1038/s43588023004649	
See Also	
Other Section_0_Database: Cellmarker2 , Cellmarker2_raw , Cellmarker2_table , Markers_list_PCTAM , Markers_list_PCTIT , Markers_list_TCellSI , PanglaoDB , PanglaoDB_raw , PanglaoDB_table	
Markers_list_TCellSI	List of T cell subtype markers in the article TCellSI

Description

A dataset containing marker genes for different T cell subtypes from TCellSI

Usage

Markers_list_TCellSI

Format

A list with ten tables.

Details

This list is a table of 10 types of T cell markers obtained from TCellSI. The data source is "https://github.com/GuoBioinfoLab/" and the reference literature is: Yang et al. (2024) doi:10.1002/imt2.231.

Source

https://github.com/GuoBioinfoLab/TCellSI/

See Also

Other Section_0_Database: Cellmarker2, Cellmarker2_raw, Cellmarker2_table, Markers_list_PCTAM, Markers_list_PCTIT, Markers_list_scIBD, PanglaoDB, PanglaoDB_raw, PanglaoDB_table

PanglaoDB	PanglaoDB dataset
-----------	-------------------

Description

A dataset containing marker genes for different cell types from PanglaoDB

Usage

PanglaoDB

Format

A data frame with 9 columns:

Details

This dataset is used to filter and create a standardized marker list.'

Source

https://panglaodb.se/

See Also

Other Section_0_Database: Cellmarker2, Cellmarker2_raw, Cellmarker2_table, Markers_list_PCTAM, Markers_list_PCTIT, Markers_list_TCellSI, Markers_list_scIBD, PanglaoDB_raw, PanglaoDB_table

PanglaoDB_raw	<i>PanglaoDB raw dataset</i>
---------------	------------------------------

Description

A dataset containing marker genes for different cell types from PanglaoDB

Usage

PanglaoDB_raw

Format

A data frame with 14 columns contined in the PanglaoDB database:

Details

This dataset is used to filter and create a standardized marker list.'

Source

<https://panglaodb.se/>

See Also

Other Section_0_Database: [Cellmarker2](#), [Cellmarker2_raw](#), [Cellmarker2_table](#), [Markers_list_PCTAM](#), [Markers_list_PCTIT](#), [Markers_list_TCellSI](#), [Markers_list_scIBD](#), [PanglaoDB](#), [PanglaoDB_table](#)

PanglaoDB_table	<i>PanglaoDB table</i>
-----------------	------------------------

Description

A dataset containing marker genes for different cell types from PanglaoDB

Usage

PanglaoDB_table

Format

A list contain different types like species, organ, cell type.

Details

This list is used to choose filters for creation of standardized marker list.

Source

<https://panglaodb.se/>

See Also

Other Section_0_Database: [Cellmarker2](#), [Cellmarker2_raw](#), [Cellmarker2_table](#), [Markers_list_PCTAM](#), [Markers_list_PCTIT](#), [Markers_list_TCellSI](#), [Markers_list_scIBD](#), [PanglaoDB](#), [PanglaoDB_raw](#)

Parameter_Calculate *Adaptive Parameter Tuning for Single-Cell Data Annotation in SlimR*

Description

This function automatically determines optimal min_expression, specificity_weight, and threshold parameters for single-cell data analysis based on dataset characteristics using adaptive algorithms derived from empirical analysis of single-cell datasets.

Usage

```
Parameter_Calculate(
  seurat_obj,
  features = NULL,
  assay = NULL,
  cluster_col = NULL,
  n_celltypes = 50,
  verbose = TRUE
)
```

Arguments

seurat_obj	A Seurat object containing single-cell data
features	Character vector of feature names (genes) to analyze. If NULL, will use highly variable features from the Seurat object.
assay	Name of assay to use (default: default assay)
cluster_col	Column name in metadata containing cluster information
n_celltypes	Expected number of cell types in marker database (default: 50). Used for threshold recommendation calculation.
verbose	Whether to print progress messages (default: TRUE)

Value

A list containing:

- min_expression: Recommended expression threshold
- specificity_weight: Recommended specificity weight
- threshold: Recommended probability threshold for candidate selection
- dataset_features: Extracted dataset characteristics
- parameter_rationale: Explanation of parameter choices

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation\(\)](#), [Celltype_Annotation_PerCell\(\)](#), [Celltype_Calculate\(\)](#), [Celltype_Calculate_PerCell\(\)](#), [Celltype_Verification\(\)](#), [Celltype_Verification_PerCell\(\)](#), [percell_workflow](#)

Examples

```
## Not run:
SlimR_params <- Parameter_Calculate(
  seurat_obj = sce,
  features = c("CD3E", "CD4", "CD8A"),
  assay = "RNA",
  cluster_col = "seurat_clusters",
  n_celltypes = 98,
  verbose = TRUE
)

## End(Not run)
```

percell_workflow

Per-Cell Annotation Workflow Example

Description

Example workflow for using SlimR's per-cell annotation functions

Overview

The per-cell annotation workflow in SlimR provides an alternative to cluster-based annotation by scoring and labeling individual cells based on marker expression. This is useful when:

- Clusters contain mixed cell types
- You want finer-grained annotations
- Cell states exist on a continuum
- UMAP spatial context can improve annotation quality

Basic Workflow

```
# 1. Prepare your Seurat object (must have normalized data)
library(SlimR)
library(Seurat)

# 2. Create or load marker list
Markers_list <- Markers_filter_Cellmarker2(
  Cellmarker2,
  species = "Human",
```



```

    tissue_class = "Intestine"
  )

# 3. Run per-cell annotation
result <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  method = "weighted",          # "weighted", "mean", or "AUCell"
  min_expression = 0.1,
  min_score = 0.1,
  verbose = TRUE
)

# 4. Annotate Seurat object
sce <- Celltype_Annotation_PerCell(
  seurat_obj = sce,
  SlimR_percell_result = result,
  plot_UMAP = TRUE,
  plot_confidence = TRUE,
  annotation_col = "Cell_type_PerCell"
)

# 5. Verify annotations
dotplot <- Celltype_Verification_PerCell(
  seurat_obj = sce,
  SlimR_percell_result = result,
  gene_number = 5,
  annotation_col = "Cell_type_PerCell"
)
print(dotplot)

```

Advanced

UMAP Spatial Smoothing:

```

# Use UMAP coordinates to smooth predictions via k-NN
# This reduces noise and improves consistency in spatial regions

result_smooth <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  use_umap_smoothing = TRUE,
  k_neighbors = 20,          # Number of neighbors to consider
  smoothing_weight = 0.3,    # 30
  verbose = TRUE
)

```

```
# Compare smoothed vs unsmoothed
sce$Cell_type_Smooth <- result_smooth$Cell_annotations$Predicted_cell_type
sce$Cell_type_Raw <- result$Cell_annotations$Predicted_cell_type

DimPlot(sce, group.by = "Cell_type_Raw") |
  DimPlot(sce, group.by = "Cell_type_Smooth")
```

Scoring Methods Comparison

```
# Method 1: Weighted (recommended for most cases)
# Combines expression with marker specificity and detection rate
result_weighted <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  method = "weighted"
)

# Method 2: Mean (simple, fast)
# Just averages normalized marker expression
result_mean <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  method = "mean"
)

# Method 3: AUCell (rank-based, robust to batch effects)
# Scores based on proportion of markers in top 5
result_aucell <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  method = "AUCell"
)
```

Comparing Cluster vs Per-Cell Annotation

```
# Cluster-based annotation (original SlimR approach)
cluster_result <- Celltype_Calculate(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  cluster_col = "seurat_clusters"
)

sce <- Celltype_Annotation(
  seurat_obj = sce,
  cluster_col = "seurat_clusters",
```

```

    SlimR_anno_result = cluster_result,
    annotation_col = "Cell_type_Cluster"
)

# Per-cell annotation
percell_result <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human"
)

sce <- Celltype_Annotation_PerCell(
  seurat_obj = sce,
  SlimR_percell_result = percell_result,
  annotation_col = "Cell_type_PerCell"
)

# Compare
library(ggplot2)
library(patchwork)

p1 <- DimPlot(sce, group.by = "Cell_type_Cluster") +
  ggtitle("Cluster-based")
p2 <- DimPlot(sce, group.by = "Cell_type_PerCell") +
  ggtitle("Per-cell")

p1 | p2

# Check agreement
table(sce$Cell_type_Cluster, sce$Cell_type_PerCell)

```

Performance Optimization

```

# For large datasets, adjust chunk_size to manage memory
result <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",
  chunk_size = 10000, # Process 10k cells at a time
  verbose = TRUE
)

# For UMAP smoothing, install RANN for 10-100x speedup
# install.packages("RANN")

result_smooth <- Celltype_Calculate_PerCell(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human",

```

```

    use_umap_smoothing = TRUE,
    k_neighbors = 15
    # RANN will be used automatically if installed
  )

```

Accessing Results

```

# Cell-level annotations
head(result$Cell_annotations)
#   Cell_barcode Predicted_cell_type Max_score Confidence
# 1 AAACCTGAG... Enterocyte          0.85         0.62
# 2 AAACCTGCA... Goblet cell          0.72         0.45

# Summary statistics
result$Summary
#   Cell_type      Count Percentage
# 1 Enterocyte    5432    45.2
# 2 Goblet cell   2156    17.9

# Full probability matrix (if return_scores = TRUE)
result$Probability_matrix[1:5, 1:3]
#           Enterocyte Goblet_cell Stem_cell
# AAACCTGAG... 0.85         0.10         0.05

# Extract high-confidence cells
high_conf <- result$Cell_annotations$Cell_barcode[
  result$Cell_annotations$Confidence > 0.5
]

# Extract uncertain cells for manual review
uncertain <- result$Cell_annotations$Cell_barcode[
  result$Cell_annotations$Confidence < 0.2
]

```

See Also

Other Section_3_Automated_Annotation: [Celltype_Annotation\(\)](#), [Celltype_Annotation_PerCell\(\)](#), [Celltype_Calculate\(\)](#), [Celltype_Calculate_PerCell\(\)](#), [Celltype_Verification\(\)](#), [Celltype_Verification_PerCell\(\)](#), [Parameter_Calculate\(\)](#)

plot.pheatmap

Plot Method for pheatmap Objects

Description

This S3 method allows pheatmap objects (returned by `Celltype_Calculate()`) to be plotted using the generic `plot()` function. Without this method, attempting to use `plot()` on a pheatmap object results in an error.

Usage

```
## S3 method for class 'pheatmap'
plot(x, ...)
```

Arguments

x A pheatmap object, typically from `cluster_results$Heatmap_plot`

... Additional arguments (currently ignored)

Details

Pheatmap objects contain a `gtable` component that needs to be drawn using grid graphics. This method handles that automatically when `plot()` is called.

Alternative ways to display pheatmaps:

- `print(pheatmap_object)` - Works natively
- `plot(pheatmap_object)` - Works after loading SlimR
- `grid::grid.draw(pheatmap_object$gtable)` - Direct access

Value

Invisibly returns the input pheatmap object after displaying it

Examples

```
## Not run:
# After running Celltype_Calculate()
cluster_results <- Celltype_Calculate(
  seurat_obj = sce,
  gene_list = Markers_list,
  species = "Human"
)

# Now both of these work:
print(cluster_results$Heatmap_plot)
plot(cluster_results$Heatmap_plot)

## End(Not run)
```

Read_excel_markers *Create "Marker_list" from Excel files ".xlsx"*

Description

Create "Marker_list" from Excel files ".xlsx"

Usage

```
Read_excel_markers(path, has_colnames = TRUE)
```

Arguments

path	The path information of Marker files stored in ".xlsx" format. The Sheet name in the file is filled with cell type. The first line of each Sheet is the table head, the first column is filled with markers information, and the following column is filled with mertic information.
has_colnames	Logical value indicating whether the first row contains column names. If FALSE, the first column will be named "Markers" and subsequent columns will be named "Col1", "Col2", etc.

Value

The standardized "Marker_list" in the SlimR package.

See Also

Other Section_2_Standardized_Markers_List: [Markers_filter_Cellmarker2\(\)](#), [Markers_filter_PanglaoDB\(\)](#), [Read_seurat_markers\(\)](#)

Examples

```
## Not run:
Markers_list_Excel <- Read_excel_markers(
  "D:/Laboratory/Marker_load.xlsx"
)

## End(Not run)
```

Read_seurat_markers	Create "Marker_list" from Seurat object
---------------------	---

Description

Create "Marker_list" from Seurat object

Usage

```
Read_seurat_markers(
  df,
  sources = c("Seurat", "presto"),
  sort_by = "FSS",
  gene_filter = 20
)
```

Arguments

df	Dataframe generated by "FindAllMarkers" function, recommend to use parameter "group.by = "Cell_type"" and "only.pos = TRUE".
sources	Type of markers sources to use. Be one of: "Seurat" or "presto".
sort_by	Marker sorting parameter, for Seurat sources, select "avg_log2FC" or "p_val_adj" or "FSS" (Feature Significance Score, FSS, product value of log2FC and Expression ratio). Default parameters use "sort_by = 'FSS'".for presto sources, select "logFC" or "padj" or "FSS". Default parameters use "sort_by = 'FSS'".
gene_filter	The number of markers left for each cell type based on the "sort_by" parameter's level of difference. Default parameters use "gene_filter = 20"

Value

The standardized "Marker_list" in the SlimR package.

See Also

Other Section_2_Standardized_Markers_List: [Markers_filter_Cellmarker2\(\)](#), [Markers_filter_PanglaoDB\(\)](#), [Read_excel_markers\(\)](#)

Examples

```
## Not run:
# Example for Seurat sources markers
seurat_markers <- Seurat::FindAllMarkers(
  object = sce,
  group.by = "Cell_type",
  only.pos = TRUE)

Markers_list_Seurat <- Read_seurat_markers(seurat_markers,
  sources = "Seurat",
  sort_by = "avg_log2FC",
  gene_filter = 20
)

# Example for presto sources markers
seurat_markers <- dplyr::filter(
  presto::wilcoxauc(
    X = sce,
    group_by = "Cell_type",
    seurat_assay = "RNA"
  ),
  padj < 0.05, logFC > 0.5
)

Markers_list_Seurat <- Read_seurat_markers(seurat_markers,
  sources = "presto",
  sort_by = "logFC",
  gene_filter = 20
)
```

```
## End(Not run)
```


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