Package ‘scMappR’

October 16, 2021

Title Single Cell Mapper
Version 1.0.7

Description
The single cell mapper (scMappR) R package contains a suite of bioinformatic tools that provide experimentally relevant cell-type specific information to a list of differentially expressed genes (DEG). The function `scMappR_and_pathway_analysis` reranks DEGs to generate cell-type specificity scores called cell-weighted fold-changes. Users input a list of DEGs, normalized counts, and a signature matrix into this function. scMappR then reweights bulk DEGs by cell-type specific expression from the signature matrix, cell-type proportions from RNA-seq deconvolution and the ratio of cell-type proportions between the two conditions to account for changes in cell-type proportion. With cwFold-changes calculated, scMappR uses two approaches to utilize cwFold-changes to complete cell-type specific pathway analysis. The `process_dgTMatrix_lists` function in the scMappR package contains an automated scRNA-seq processing pipeline where users input scRNA-seq count data, which is made compatible for scMappR and other R packages that analyze scRNA-seq data. We further used this to store hundreds up regularly updating signature matrices. The functions `tissue_by_celltype_enrichment`, `tissue_scMappR_internal`, and `tissue_scMappR_custom` combine these consistently processed scRNAseq count data with gene-set enrichment tools to allow for cell-type marker enrichment of a generic gene list (e.g. GWAS hits). Reference: Sokolowski, D.J., Faykoo-Martinez, M., Erdman, L., Hou, H., Chan, C., Zhu, H., Holmes, M.M., Goldenberg, A. and Wilson, M.D. (2021) Single-cell mapper (scMappR): using scRNA-seq to infer cell-type specificities of differentially expressed genes. NAR Genomics and Bioinformatics. 3(1). Iqab011. <doi:10.1093/nargab/ltqab011>.

Depends R (>= 4.0.0)
Imports ggplot2, pheatmap, graphics, Seurat, GSVA, stats, utils, downloader, pcaMethods, grDevices, gProfileR, limSolve, gprofiler2, pbapply, ADAPTS, reshape,

License GPL-3

URL

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1
Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Dustin Sokolowski [aut, cre],
      Mariela Faykoo-Martinez [aut],
      Lauren Erdman [aut],
      Houyun Hou [aut],
      Cadia Chan [aut],
      Helen Zhu [aut],
      Melissa Holmes [aut],
      Anna Goldenberg [aut],
      Michael Wilson [aut]

Maintainer Dustin Sokolowski <dustin.sokolowski@sickkids.ca>

Repository CRAN

Date/Publication 2021-10-16 14:20:02 UTC

R topics documented:

cellmarker_enrich ................................................. 3
coEnrich ......................................................... 4
compare_deconvolution_methods .................................. 5
cwFoldChange_evaluate .......................................... 7
DeconRNAseq_CRAN ................................................. 9
deconvolute_and_contextualize .................................. 10
extract_genes_cell ............................................... 12
generes_to_heatmap .............................................. 13
get_gene_symbol ............................................... 15
get_signature_matrices .......................................... 16
gmt .......................................................... 16
gProfiler_cellWeighted_Foldchange .............................. 17
gsva_cellIdentify .............................................. 18
heatmap_generation ............................................... 20
human_mouse_et_marker_enrich .................................. 21
make_TF_barplot .................................................. 22
pathway_enrich_internal ......................................... 24
PBMC_example ..................................................... 25
plotBP .......................................................... 26
POA_example ....................................................... 27
process dgTMatrix_lists ......................................... 28
process_from_count .............................................. 30
scMappR_and_pathway_analysis ................................ 32
scMappR_tissues .................................................. 34
seurat_to_generes ............................................... 35
single_gene_preferences ....................................... 36
sm ........................................................... 37
tissue_by_celitype_enrichment .................................. 38
cellmarker_enrich

Fisher’s Exact Cell-Type Identification.

Description

This function uses the CellMarker and Panglao datasets to identify cell-type differentially expressed genes.

Usage

cellmarker_enrich(
  gene_list,
  p_thresh,
  gmt = "cellmarker_list.Rdata",
  fixed_length = 13000,
  min_genes = 5,
  max_genes = 3000,
  isect_size = 3
)

Arguments

gene_list A character vector of gene symbols with the same designation (e.g. mouse symbol - mouse, human symbol - human) as the gene set database.
p_thresh The Fisher’s test cutoff for a cell-marker to be enriched.
gmt Either a path to an rda file containing an object called "gmt", which is a named list where each element of the list is a vector of gene symbols website for more detail on the file type (https://software.broadinstitute.org/cancer/software/gsea/wiki/index.php/Data_formats). The gmt list may also be inputted.
fixed_length Estimated number of genes in your background.
min_genes Minimum number of genes in the cell-type markers.
max_genes Maximum number of genes in the cell-type markers.
isect_size Number of genes in your list and the cell-type.

Details

Complete a Fisher’s exact test of an input list of genes against a gene set saved in an *.RData object. The RData object is storing a named list of genes called "gmt".
**Value**

cellmarker_enrich Gene set enrichment of cell-types on your inputted gene list.

**Examples**

data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
Signature <- POA_Rank_signature
rowname <- get_gene_symbol(Signature)
rownames(Signature) <- rowname$rowname
genes <- rownames(Signature)[1:100]
data(gmt)
enriched <- cellmarker_enrich(gene_list = genes, p_thresh = 0.05, gmt = gmt)

---

**coEnrich**

*Identify co-expressed cell-types*

**Description**

This function identifies genes with similar cell-type markers and if those markers are driving enrichment.

**Usage**

```r
coEnrich(
  sig, 
  gene_list_heatmap, 
  background_heatmap, 
  study_name, 
  outDir, 
  toSave = FALSE, 
  path = NULL 
)
```

**Arguments**

- `sig` A The number of combinations of significant cell-types to enrich.
- `gene_list_heatmap` Signature matrix of inputted genes in heatmap and the cell-type preferences – output of heatmap generation.
compare_deconvolution_methods

background_heatmap
Signature matrix of background matrix in heatmap and cell-type preferences – output of heatmap generation.

study_name
Name of the outputted table.

outDir
Name of the directory this table will be printed in.

toSave
Allow scMappR to write files in the current directory (T/F).

path
If toSave == TRUE, path to the directory where files will be saved.

Details
This function takes significantly enriched cell-types from the single CT_enrich before testing to see if the genes driving their enrichment are overlapping to a significant proportion using Fisher’s exact test. To save computational time and to not complete this with an incredible number of permutations, scMappR stops at overlapping 5 cell-types.

Value
coEnrich Enrichment of cell-types that are expressed by the same genes, up to 4 sets of cell-types.

Examples

# load in signature matrices
data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
sig <- get_gene_symbol(POA_Rank_signature)
Signature <- POA_Rank_signature
rownames(Signature) <- sig$rowname
genes <- rownames(Signature)[1:60]
heatmap_test <- tissue_scMappR_custom( genes, signature_matrix = Signature,
output_directory = "scMappR_test", toSave = FALSE)
group_preferences <- heatmap_test$group_celltype_preferences

Description
This function calculates cell-type proportions of an inputted bulk sample using DeconRNA-seq, WGCNA, and DCQ methods. Outputted cell-type proportions are then compared.
Usage

```r
compare_deconvolution_methods(
  count_file,
  signature_matrix,
  print_plot = FALSE,
  order_celltype = NULL,
  useWGCNA = TRUE
)
```

Arguments

- `count_file`: Normalized (CPM, TPM, RPKM) RNA-seq count matrix where rows are gene symbols and columns are individuals. Either the object itself or the path of a .tsv file.
- `signature_matrix`: Signature matrix (odds ratios) of cell-type specificity of genes. Either the object itself or a pathway to an .RData file containing an object named "wilcoxon_rank_mat_or" - generally internal.
- `print_plot`: Print the barplot of estimated cell-type proportions from each method into the R console (logical: TRUE/FALSE)
- `order_celltype`: Specify the order that cell-type are placed on the barplot. NULL = alphabetical, otherwise a character vector of cell-type labels (i.e. column names of the signature matrix).
- `useWGCNA`: Specify if WGCNA is installed = TRUE/FALSE.

Value

List with the following elements:

- `cellWeighted_Foldchange`: data frame of cellweightedFold-changes for each gene.
- `cellType_Proportions`: data frame of cell-type proportions from DeconRNA-seq.
- `leave_one_out_proportions`: data frame of average cell-type proportions for case and control when gene is removed.
- `processed_signature_matrix`: signature matrix used in final analysis.

Examples

```r
data(PBMC_example)
norm_counts <- PBMC_example$bulk_normalized
signature <- PBMC_example$odds_ratio_in
tst <- compare_deconvolution_methods(norm_counts, signature, FALSE,
  order_celltype = c("I_mono", "C_mono", "CD8_CM", "CD8_TE"),
```
cwFoldChange_evaluate

"B_SM", "B_NSM", "B_naive"), useWGCNA = FALSE)

cwFoldChange_evaluate  Measure cell-type specificity of cell-weighted Fold-changes

Description

This function normalizes cwFold-changes by each gene to help visualize the cell-type specificity of DEGs. It then tests if a cell-type has a large change in correlation from bulk DEGs. Finally, it identifies genes that may be specific to each cell-type.

Usage

cwFoldChange_evaluate(
  cwFC,
  celltype_prop,
  DEG_list,
  gene_cutoff = NULL,
  sd_cutoff = 3
)

Arguments

cwFC A matrix or data frame of cell-weighted fold-changes of DEGs. Rows are DEGs and columns are cell-types.

celltype_prop A matrix or data frame of cell-type proportions. Rows are different cell-types and columns are different samples. These cell-type proportions can come from any source (not just scMappR).

DEG_list An object with the first column as gene symbols within the bulk dataset (doesn’t have to be in signature matrix), second column is the adjusted p-value, and the third the log2FC path to a .tsv file containing this info is also acceptable.

gene_cutoff Additional cut-off of normalized cwFold-change to see if a gene is cut-off.

sd_cutoff Number of standard deviations or median absolute deviations to calculate outliers.

Details

cwFold-changes and re-normalized and re-processed to interrogate cell-type specificity at the level of the cell-type and at the level of the gene. At the level of the cell-type, cwFold-changes are correlated to bulk DEGs. The difference in rank between bulk DEGs and cwFold-changes are also compared. At the level of the gene, cwFold-changes are re-normalized so that each gene sums to 1. Normalization of their distributions are tested with a Shapiro test. Then, outlier cell-types for each gene are measured by testing for ‘sd_cutoff’’s mad or sd’s greater than the median or mean depending on if the cwFold-change is non-normally or normally distributed respectively. Cell-types considered outliers are then further filtered so their normalized cwFold-changes are greater than the cell-type proportions of that gene and ‘gene_cutoff’ if the user sets it.
Value

List with the following elements:

gene_level_investigation
data frame of genes showing the Euclidian distances between cwFold-change and null vector as well as if cwFold-changes are distributed.

celltype_level_investigation
data frame of Spearman’s and Pearson’s correlation between bulk DEGs and cwFold-changes.

cwFoldchange_vs_bulk_rank_change
data frame of the change in rank of DEG between the bulk fold-change and cwFold-change.

cwFoldChange_normalized
cwFold-change normalized such that each gene sums to 1.

cwFoldchange_gene_assigned
List of cell-types where genes are designated to cell-type specific differential expression.

cwFoldchange_gene_flagged_FP
Mapped cwFoldchanges that are flagged as false-positives. These are genes that are driven by the reciprocal ratio of cell-type proportions between case and control. These genes may be DE in a non-cell-type specific manner but are falsely assigned to cell-types with very large differences in proportion between condition.

Examples

data(PBMC_example)
bulk_DE_cors <- PBMC_example$bulk_DE_cors
bulk_normalized <- PBMC_example$bulk_normalized
odds_ratio_in <- PBMC_example$odds_ratio_in
case_grep <- "_female"
control_grep <- "_male"
max_proportion_change <- 10
print_plots <- FALSE
theSpecies <- "human"
toOut <- scMappR_and_pathway_analysis(bulk_normalized, odds_ratio_in, bulk_DE_cors, case_grep = case_grep, control_grep = control_grep, rda_path = "", max_proportion_change = 10, print_plots = TRUE, plot_names = "tst1", theSpecies = "human", output_directory = "tester", sig_matrix_size = 3000, up_and_downregulated = FALSE, internet = FALSE)

cwFC1 <- toOut$cellWeighted_Foldchange
prop1 <- toOut$cellType_Proportions
DE <- bulk_DE_cors
eval_test <- cwFoldChange_evaluate(cwFC1, prop1, DE)
Description

This function runs DeconRNAseq with default parameters such that it is compatible with CRAN and scMappR.

Usage

```r
DeconRNAseq_CRAN(
  datasets,
  signatures,
  proportions = NULL,
  checksig = FALSE,
  known.prop = FALSE,
  use.scale = TRUE,
  fig = FALSE
)
```

Arguments

datasets: Normalized RNA-seq dataset

signatures: Signature matrix of odds ratios

proportions: If cell-type proportion is already inputted - always NULL for scMappR

checksig: Check to see if plotting is significant - always false for scMappR

known.prop: If proportions were known - always false for scMappR

use.scale: Scale and center value - always TRUE for scMappR

fig: Make figures - always FALSE for scMappR

Details

This is the exact same function as the primary function in the Bioconductor package, DeconRNAseq (PMID: 23428642) except it is now compatible with CRAN packages.

Value

DeconRNAseq_CRAN Estimated cell-type proportions with DeconRNAseq.
Examples

data(PBMC_example)
bulk_DE_cors <- PBMC_example$bulk_DE_cors
bulk_normalized <- PBMC_example$bulk_normalized
odds_ratio_in <- PBMC_example$odds_ratio_in
out <- DeconRNAseq_CRAN(as.data.frame(bulk_normalized), as.data.frame(odds_ratio_in))

---

decovolute_and_contextualize

Generate cell weighted Fold-Changes (cwFold-changes)

Description
This function takes a count matrix, signature matrix, and differentially expressed genes (DEGs) before generating cwFold-changes for each cell-type.

Usage

deconvolute_and_contextualize(
  count_file,
  signature_matrix,
  DEG_list,
  case_grep,
  control_grep,
  max_proportion_change = -9,
  print_plots = T,
  plot_names = "scMappR",
  theSpecies = "human",
  FC_coef = T,
  sig_matrix_size = 3000,
  drop_unknown_celltype = TRUE,
  toSave = FALSE,
  path = NULL,
  deconMethod = "DeconRNASeq"
)

Arguments

count_file       Normalized (e.g. CPM, TPM, RPKM) RNA-seq count matrix where rows are gene symbols and columns are individuals. Either the matrix itself of class "matrix" or data.frame or a path to a tsv file containing these DEGs. The gene symbols in the count file, signature matrix, and DEG list must match.
**signature_matrix**

Signature matrix (fold-change ratios) of cell-type specificity of genes. Either the object itself or a pathway to an .RData file containing an object named "wilcoxon_rank_mat_or". We strongly recommend inputting the signature matrix directly.

**DEG_list**

An object with the first column as gene symbols within the bulk dataset (doesn’t have to be in signature matrix), second column is the adjusted P-value, and the third the log2FC. Path to a tsv file containing this info is also acceptable.

**case_grep**

Tag in the column name for cases (i.e. samples representing upregulated) OR an index of cases.

**control_grep**

Tag in the column name for control (i.e. samples representing downregulated) OR an index of cases.

**max_proportion_change**

Maximum cell-type proportion change. May be useful if a cell-type does not exist in one condition, thus preventing infinite values.

**print_plots**

Whether boxplots of the estimated CT proportion for the leave-one-out method of CT deconvolution should be printed (T/F).

**plot_names**

If plots are being printed, the pre-fix of their .pdf files.

**theSpecies**

Internal species designation to be passed from 'scMappR_and_pathway_analysis'. It only impacts this function if data are taken directly from the PanglaoDB database (i.e. not reprocessed by scMappR or the user).

**FC_coef**

Making cwFold-changes based on fold-change (TRUE) or rank := (-log10(Pval)) (FALSE) rank. After testing, we strongly recommend to keep true (T/F).

**sig_matrix_size**

Number of genes in signature matrix for cell-type deconvolution.

**drop_unknown_celltype**

Whether or not to remove "unknown" cell-types from the signature matrix (T/F).

**toSave**

Allow scMappR to write files in the current directory (T/F).

**path**

If toSave == TRUE, path to the directory where files will be saved.

**deconMethod**

Which RNA-seq deconvolution method to use to estimate cell-type proporitons. Options are "WGCNA", "DCQ", or "DeconRNAseq"

### Details

This function completes the pre-processing, normalization, and scaling steps in the scMappR algorithm before calculating cwFold-changes. cwFold-changes scales bulk fold-changes by the cell-type specificity of the gene, cell-type gene-normalized cell-type proportions, and the reciprocal ratio of cell-type proportions between the two conditions. cwFold-changes are generated for genes that are in both the count matrix and in the list of DEGs. It does not have to also be in the signature matrix. First, this function will estimate cell-type proportions with all genes included before estimating changes in cell-type proportion between case/control using a t-test. Then, it takes a leave-one-out approach to cell-type deconvolution such that estimated cell-type proportions are computed for every inputted DEG. Optionally, the differences between cell-type proportions before and after a gene is removed is plotted in boxplots. Then, for every gene, cwFold-changes are computed with the following formula (the example for upregulated genes) val <- cell-preferences * cell-type_proportion * cell-type_proportion_fold-change * sign*2^abs(gene_DE$log2fc). A matrix of cwFold-changes for all DEGs are returned.
extract_genes_cell

Value

List with the following elements:

- **cellWeighted_Foldchange**: data frame of cellweightedFold changes for each gene.
- **cellType_Proportions**: data frame of cell-type proportions from DeconRNA-seq.
- **leave_one_out_proportions**: data frame of average cell-type proportions for case and control when gene is removed.
- **processed_signature_matrix**: signature matrix used in final analysis.

Examples

```r
data(PBMC_example)
bulk_DE_cors <- PBMC_example$bulk_DE_cors
bulk_normalized <- PBMC_example$bulk_normalized
odds_ratio_in <- PBMC_example$odds_ratio_in
case_grep <- "_female"
control_grep <- "_male"
max_proportion_change <- 10
print_plots <- FALSE
theSpecies <- "human"
norm <- deconvolute_and_contextualize(bulk_normalized, odds_ratio_in, bulk_DE_cors,
case_grep = case_grep, control_grep = control_grep,
max_proportion_change = max_proportion_change,
print_plots = print_plots,
theSpecies = theSpecies, toSave = FALSE)
```

extract_genes_cell  Extract Markers

Description

Extracting cell-type markers from a signature matrix.

Usage

```r
extract_genes_cell(
  geneHeat,
  cellTypes = "ALL",
  val = 1,
  isMax = FALSE,
  isPvalue = FALSE
)
```
generes_to_heatmap

Arguments

geneHeat  The heatmap of ranks from your scRNA-seq dataset with your genes subsetted.
cellTypes  The cell-types that you’re interested in extracting. They need to be colnames (not case sensitive).
val  How associated a gene is with a particular cell type to include in your list - default is slightly associated.
isMax  If you are taking the single best CT marker (T/F) – TRUE not recommended.
isPvalue  If the signature matrix is raw p-value (T/F) – TRUE not recommended.

Details

This function takes a signature matrix and extracts cell-type markers above a p-value or fold-change threshold.

Value

extract_genes_cell A vector of genes above the threshold for each sample.

Examples

data(POA_example)
Signature <- POA_example$POA_Rank_signature
RowName <- get_gene_symbol(Signature)
rownames(Signature) <- RowName$rownames
# extract genes with a -log10(Padj > 1)
Signat <- extract_genes_cell(Signature)

Description

Convert a list of cell-type markers from FindMarkers in Seurat to a signature matrix defined by odds ratio and rank.
Usage

generes_to_heatmap(
  generes,
  species = "human",
  naming_preference = -9,
  rda_path = "",
  make_names = TRUE,
  internal = FALSE
)

Arguments

generes A list of cell-type markers with fold-changes and p-values (FindMarkers output in Seurat).
species The species of gene symbols, if not internal, "human" or "mouse".
naming_preference Likely cell-types given tissues (to be passed into human_mouse_ct_marker_enrich).
rda_path Path to output directory, if toSave is true.
make_names Identify names of cell-type markers using the Fisher's exact test method (T/F).
internal If this function is pre-processing from Panglao (T/F).

Details

Take a list of compiled differentially expressed genes from different cell-types, identify what the cell-types are using the Fisher's exact test, and then convert into a signature matrix for both the adjusted p-value and odds ratio.

Value

List with the following elements:

pVal A dataframe containing the signature matrix of ranks (-\log_{10}(\text{Padj}) \times \text{sign}(\text{fold-change})).
OR A dataframe containing the signature matrix of odds ratios.
cellname A vector of the cell-labels returned from the GSVA method.
topGenes the top 30 most expressed genes in each cell-type.

Examples

data(POA_example)
POA_generes <- POA_example$POA_generes
signature <- generes_to_heatmap(POA_generes, species = -9, make_names = FALSE)
get_gene_symbol

Internal – get gene symbol from Panglao.db assigned gene-names (symbol-ensembl).

Description

Internal – removes Ensembl signature appended to signature matrix from Panglao and figure out species by pre-fix Ensembl of the Ensembl ID that is appended to gene names.

Usage

gene_symbol(wilcoxon_rank_mat)

Arguments

wilcoxon_rank_mat
Matrix where row names are "GeneSymbol-Ensembl" (human or mouse).

Details

Internal: This function removes the ENGMUS/ENGS tag from Panglao created gene names (symbol-ENGS). From the ENSG/ENSMUS, this function determines if the species is mouse/human and returns the gene symbols.

Value

List with the following elements:

rowname Genes in the signature matrix excluding the ensemble name.
species "mouse" or "human" depending on appended ensembl symbols.

Examples

# load signature
data(POA_example)
POA_OR_signature <- POA_example$POA_OR_signature
symbols <- get_gene_symbol(POA_OR_signature)
get_signature_matrices

Get signature matrices.

Description

This function downloads and returns signature matrices and associated cell-type labels from the scMappR_data repo.

Usage

get_signature_matrices(type = "all")

Arguments

type a character vector that can be 'all', 'pVal', or 'OR'

Value

get_signature_matrices Returns the signature matrices currently stored in scMappR_Data. Associated cell-type labels from different methods for each signature matrix is also provided.

Examples

signatures <- get_signature_matrices(type = "all")

Description

Markers of 5 glial cell-types

Usage

data(gmt)
Format

A list with 5 character vectors, each containing genes.

- **Astrocytes_panglao** astrocyte markers identified by panglao
- **Schwann_panglao** Schwann markers identified by panglao
- **Bergmann_glia_panglao** Bergmann glia markers identified by panglao
- **Kupffer_panglao** Kupffer markers identified by panglao
- **Oligodendrocyte_progenitor_panglao** Oligodendrocyte progenitor markers identified by panglao

Details

A named list containing the cell-type markers of 5 glial cell types. Used for testing cell-type naming functions.

Examples

```r
data(gmt)
```

---

**gProfiler_cellWeighted_Foldchange**

*Pathway enrichment for cwFold-changes*

Description

This function runs through each list of cell weighted Fold changes (cwFold-changes) and completes both pathway and transcription factor (TF) enrichment.

Usage

```r
gProfiler_cellWeighted_Foldchange(
  cellWeighted_Foldchange_matrix,
  species,
  background,
  gene_cut,
  newGprofiler
)
```

Arguments

- **cellWeighted_Foldchange_matrix**
  Matrix of cell weighted Fold changes from the deconvolute_and_contextualize functions.
- **species**
  Human, mouse, or a name that is compatible with gProfileR (e.g. "mmusculus").
- **background**
  A list of background genes to test against.
- **gene_cut**
  The top number of genes in pathway analysis.
- **newGprofiler**
  Using gProfileR or gprofiler2, (T/F).
gsva_cellIdentify

Details

This function takes a matrix of cellWeighted_Foldchange and a species (human, mouse, or a character directly compatible with g:ProfileR). Before completing pathway analysis with g:ProfileR. Enriched pathways are stored in a list and returned.

Value

List with the following elements:

BP  gprofiler enrichment of biological pathways for each cell-type
TF  gprofiler enrichment of transcription factors for each cell-type.

Examples

```r
data(PBMC_example)

bulk_DE_cors <- PBMC_example$bulk_DE_cors
bulk_normalized <- PBMC_example$bulk_normalized
odds_ratio_in <- PBMC_example$odds_ratio_in

case_grep <- "_female"
control_grep <- "_male"
max_proportion_change <- 10
print_plots <- FALSE
theSpecies <- "human"

norm <- deconvolute_and_contextualize(bulk_normalized, odds_ratio_in,
  bulk_DE_cors, case_grep = case_grep,
  control_grep = control_grep,
  max_proportion_change = max_proportion_change,
  print_plots = print_plots,
  theSpecies = theSpecies)

background = rownames(bulk_normalized)
STVs <- gProfiler_cellWeighted_Foldchange(norm$cellWeighted_Foldchange, theSpecies,
  background, gene_cut = -9, newGprofiler = FALSE)
```

gsva_cellIdentify  Cell-type naming with GSVA

Description

This function computes the mean expression of every cell-type before predicting the most likely cell-type using the GSVA method.
Usage

gsva_cellIdentify(
  pbmc,
  theSpecies,
  naming_preference = -9,
  rda_path = "",
  toSave = FALSE
)

Arguments

pbmc Processed Seurat object without named cells.
theSpecies "human" or "mouse" – it will determine which species cell-type markers will originate from.
naming_preference Once top cell-type markers are identified, naming_preferences will then extract CT markers within a more appropriate tissue type.
rda_path Path to pre-computed cell-type .gmt files (rda objects).
toSave If scMappR is allowed to write files and directories.

Details

This function inputs a Seurat object and uses the average normalized expression of each gene in each cluster to identify cell-types using the GSVA method.

Value

List with the following elements:

cellMarker Most likely cell-types predicted from CellMarker database.
panglao Most likely cell-types predicted from Panglao database.
avg_expression Average expression of each gene in each cell-type.

Examples

data(sm)
toProcess <- list(example = sm)
tst1 <- process_from_count(toProcess, "testProcess", theSpecies = "mouse")
cellnames <- gsva_cellIdentify(tst1, theSpecies = "mouse",
                              naming_preference = "brain", rda_path = ")
heatmap_generation

Generate Heatmap

Description

This function takes an inputted signature matrix as well as a list of genes and overlaps them. Then, if there is overlap, it prints a heatmap or barplot (depending on the number of overlapping genes). Then, for every cell-type, genes considered over-represented are saved in a list.

Usage

heatmap_generation(
  genesIn,
  comp,
  reference,
  cex = 0.8,
  rd_path = "",
  cellTypes = "ALL",
  pVal = 0.01,
  isPval = TRUE,
  isMax = FALSE,
  isBackground = FALSE,
  which_species = "human",
  toSave = FALSE,
  path = NULL
)

Arguments

- `genesIn`: A list of gene symbols (all caps) to have their cell type enrichment.
- `comp`: The name of the comparison.
- `reference`: Path to signature matrix or the signature matrix itself.
- `cex`: The size of the genes in the column label for the heatmap.
- `rd_path`: The directory to RData files – if they are not in this directory, then the files will be downloaded.
- `cellTypes`: Colnames of the cell-types you will extract (passed to extract_genes_cell).
- `pVal`: The level of association a gene has within a cell type (passed to extract_genes_cell).
- `isPval`: If the signature matrix is raw p-value (T/F) – TRUE not recommended.
- `isMax`: If you are taking the single best CT marker (T/F) – TRUE not recommended.
- `isBackground`: If the heatmap is from the entire signature matrix or just the inputted gene list (T/F). isBackground == TRUE is used for internal.
- `which_species`: Species of gene symbols – "human" or "mouse".
- `toSave`: Allow scMappR to write files in the path directory (T/F).
- `path`: If toSave == TRUE, path to the directory where files will be saved.
**Value**

List with the following elements:

- **genesIn**: Vector of genes intersecting gene list and signature matrix.
- **genesNoIn**: Vector of inputted genes not in signature matrix.
- **geneHeat**: Signature matrix subsetted by inputted gene list
- **preferences**: Cell-markers mapping to cell-types.

**Examples**

```r
# load in signature matrices
data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
Signature <- POA_Rank_signature
rownames <- get_gene_symbol(Signature)
rownames(Signature) <- rowname$rownames
genes <- rownames(Signature)[1:100]
heatmap_test <- heatmap_generation(genesIn = genes, "scMappR_test",
                                 reference = Signature, which_species = "mouse")
```

---

**human_mouse_ct_marker_enrich**

*Consensus cell-type naming (Fisher’s Exact)*

**Description**

This function completes the Fisher’s exact test cell-type naming for all cell-types.

**Usage**

```r
human_mouse_ct_marker_enrich(
  gene_lists,
  theSpecies = "human",
  cell_marker_path = "",
  naming_preference = -9
)
```

**Arguments**

- **gene_lists**: A named list of vectors containing cell-type markers (mouse or human gene-symbols) which will be named as a cell-type via the Fisher’s exact test method.
- **theSpecies**: The species of the gene symbols: "human" or "mouse".
cell_marker_path
If local, path to cell-type marker rda files, otherwise, we will try to download
data files.

naming_preference
Either -9 if there is no expected cell-type or one of the categories from get_naming_preference_options().
This is useful if you previously have an idea of which cell-type you were going
to enrich.

Details
Fisher's exact test method of cell-type identification using the Panglao and CellMarker databases.
It extracts significant pathways (pFDR < 0.05). Then, if naming_preference != -9, it will extract the
enriched cell-types within the cell-types identified with the naming preferences option. Generally,
this method seems to be biased to cell-types with a greater number of markers.

Value
List with the following elements:

- cellTypes most likely marker for each cell-type from each database.
- marker_sets all enriched cell-types for each cluster from each dataset.

Examples

data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
Signature <- POA_Rank_signature
rowname <- get_gene_symbol(Signature)
rownames(Signature) <- rowname$rowname
genes <- rownames(Signature)[1:100]
enriched <- human_mouse_ct_marker_enrich(gene_lists = genes, theSpecies = "mouse",
  cell_marker_path = "", naming_preference = "brain")

make_TF_barplot
Plot g:profileR Barplot (TF)

Description
Make a barplot of the top transcription factors enriched by gprofileR.

Usage
make_TF_barplot(ordered_back_all_tf, top_tf = 5)
make_TF_barplot

Arguments

ordered_back_all_tf
Output of the gprofileR function.

top_tf
The number of transcription factors to be plotted.

Details

This function takes a gprofileR output and prints the top "top_tfs" most significantly enriched fdr adjusted p-values before plotting the rank of their p-values.

Value

make_TF_barplot A barplot of the number of "top_tf" tf names (not motifs), ranked by -log10(Pfdr).

Examples

data(POA_example)
POA_generes <- POA_example$POA.generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
Signature <- as.data.frame(POA_Rank_signature)
rowname <- get_gene_symbol(Signature)
rownames(Signature) <- rowname$rownname
ordered_back_all <- gprofiler2::gost(query = rowname$rownames[1:100], organism = "mmusculus",
ordered_query = TRUE, significant = TRUE, exclude_iea = FALSE, multi_query = FALSE,
measure_underrepresentation = FALSE, evcodes = FALSE, user_threshold = 0.05,
correction_method = "fdr", numeric_ns = "", sources = c("GO:BP", "KEGG", "REAC"))
ordered_back_all <- ordered_back_all$result
ordered_back_all <- ordered_back_all[ordered_back_all$term_size > 15 &
ordered_back_all$term_size < 2000 & ordered_back_all$intersection_size > 2,]
ordered_back_all_tf <- gprofiler2::gost(query = rowname$rownames[1:150], organism = "mmusculus",
ordered_query = TRUE, significant = TRUE, exclude_iea = FALSE, multi_query = FALSE,
measure_underrepresentation = FALSE, evcodes = FALSE, user_threshold = 0.05,
correction_method = "fdr", numeric_ns = "", sources = c("TF"))
ordered_back_all_tf <- ordered_back_all_tf$result
ordered_back_all_tf <- ordered_back_all_tf[ordered_back_all_tf$term_size > 15
& ordered_back_all_tf$term_size < 5000 & ordered_back_all_tf$intersection_size > 2,]
TF = ordered_back_all_tf
BP <- ordered_back_all
bp <- plotBP(BP)
tf <- make_TF_barplot(TF)
pathway_enrich_internal

**Description**

This function completes pathway enrichment of cellWeighted_Foldchanges and bulk gene list.

**Usage**

```r
pathway_enrich_internal(
  DEGs,
  theSpecies,
  scMappR_vals,
  background_genes,
  output_directory,
  plot_names,
  number_genes = -9,
  newGprofiler = FALSE,
  toSave = FALSE,
  path = NULL
)
```

**Arguments**

- **DEGs**: Differentially expressed genes (gene_name, padj, log2fc).
- **theSpecies**: Human, mouse, or a character that is compatible with g:ProfileR.
- **scMappR_vals**: cell weighted Fold-changes of differentially expressed genes.
- **background_genes**: A list of background genes to test against.
- **output_directory**: Path to the directory where files will be saved.
- **plot_names**: Names of output.
- **number_genes**: Number of genes to if there are many, many DEGs.
- **newGprofiler**: Whether to use g:ProfileR or gprofiler2 (T/F).
- **toSave**: Allow scMappR to write files in the current directory (T/F).
- **path**: If toSave == TRUE, path to the directory where files will be saved.

**Details**

Internal: Pathway analysis of differentially expressed genes (DEGs) and cell weighted Fold-changes (cellWeighted_Foldchanges) for each cell-type. Returns .RData objects of differential analysis as well as plots of the top bulk pathways. It is a wrapper for making barplots, bulk pathway analysis, and gProfiler_cellWeighted_Foldchange.
Value

List with the following elements:

- **BPs**: Enriched biological pathways for each cell-type.
- **TFs**: Enriched transcription factors for each cell-type.

Examples

```r
data(PBMC_example)
bulk_DE_cors <- PBMC_example$bulk_DE_cors
bulk_normalized <- PBMC_example$bulk_normalized
odds_ratio_in <- PBMC_example$odds_ratio_in
case_grep <- "_female"
control_grep <- "_male"
max_proportion_change <- 10
print_plots <- FALSE
theSpecies <- "human"
toOut <- scMappR_and_pathway_analysis(bulk_normalized, odds_ratio_in,
bulk_DE_cors, case_grep = case_grep,
control_grep = control_grep, rda_path = "",
max_proportion_change = 10, print_plots = TRUE,
plot_names = "tst1", theSpecies = "human",
output_directory = "tester",
sig_matrix_size = 3000, up_and_downregulated = FALSE,
internet = FALSE)
```

**PBMC_example**  

**PBMC_scMappR**

Description

Toy example of data where cell-weighted fold-changes and related downstream analyses can be completed.

Usage

```r
data(PBMC_example)
```

Format

A list containing three data frames, normalized count data, a signature matrix, and a list of differentially expressed genes.

- **bulk_normalized**: A 3231 x 9 matrix where rows are genes, columns are samples, and the matrix is filled with CPM normalized counts.
odds_ratio_in  A 2336 x 7 matrix where rows are genes, columns are cell-types and matrix is filled with the odds-ratio that a gene is in each cell-type.

bulk_DE_cors  A 59 x 3 matrix of sex-specific genes found between male and female PBMC samples (female biased = upregulated). row and rownames are genes, columns are gene name, FDR adjusted p-value, and log2 fold-change. DEGs were computed with DESeq2 and genes with a log2FC > 1 were kept.

Details

A named list called "PBMC_example" containing the count data, signature matrix, and DEGs. The count data and signature matrix are shortened to fit the size of the package and do not reflect biologically relevant data.

Examples

```r
data(PBMC_example)
```

---

plotBP  

*Plot gProfileR Barplot*

Description

Make a barplot of the top biological factors enriched by g:ProfileR.

Usage

```r
plotBP(ordered_back_all, top_bp = 10)
```

Arguments

- `ordered_back_all`  
  Output of the g:ProfileR function.
- `top_bp`  
  The number of pathways you want to plot.

Details

This function takes a gProfileR output and prints the top "top_bp" most significantly enriched FDR adjusted p-values before plotting the rank of their p-values.

Value

`plotBP`  
A barplot of the number of "top_bp" pathways, ranked by -log10(Pfdr).
Examples

```r
data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
Signature <- as.data.frame(POA_Rank_signature)
rowname <- get_gene_symbol(Signature)
rownames(Signature) <- rowname$rowname
ordered_back_all <- gprofiler2::gost(query = rowname$rowname[1:100], organism = "mmusculus",
ordered_query = TRUE, significant = TRUE, exclude_iea = FALSE, multi_query = FALSE,
measure_underrepresentation = FALSE, evcodes = FALSE, user_threshold = 0.05,
correction_method = "fdr", numeric_ns = "", sources = c("GO:BP", "KEGG", "REAC"))
ordered_back_all <- ordered_back_all[ordered_back_all$term_size > 15
& ordered_back_all$intersection_size > 2,]
ordered_back_all_tf <- gprofiler2::gost(query = rowname$rowname[1:150], organism = "mmusculus",
ordered_query = TRUE, significant = TRUE, exclude_iea = FALSE, multi_query = FALSE,
measure_underrepresentation = FALSE, evcodes = FALSE, user_threshold = 0.05,
correction_method = "fdr", numeric_ns = "", sources = c("TF"))
ordered_back_all_tf <- ordered_back_all_tf$result
ordered_back_all_tf <- ordered_back_all_tf[ordered_back_all_tf$term_size > 15
& ordered_back_all_tf$intersection_size > 2,]
TF <- ordered_back_all_tf
BP <- ordered_back_all
bp <- plotBP(BP)
lf <- make_TF_barplot(TF)
```

POA_example  

Preoptic_Area

Description

Toy data for tissue_scMappR_custom, tissue_scMappR_internal, generes_to_heatmap.

Usage

```r
data(POA_example)
```

Format

A list containing three objects: summary statistics of cell-type markers, a signature matrix of odds ratios, and a signature matrix of ranks.

**POA_generes** A list of 27 data frames containing (up to 30) cell-type markers. Each element of the list is a dataframe where rows are genes, and columns are p-value, log2FC, percentage of cells expressing gene in cell-type, percentage of cells expressing gene in other cell-types, and FDR adjusted p-value.
**POA.OR.signature**  A 266 x 27 matrix where rows are genes, columns are cell-types and matrix is filled with the odds-ratio that a gene is in each cell-type.

**POA.Rank.signature**  A 266 x 27 matrix of matrix where rows are genes, columns are cell-types and matrix is filled with the rank := -log10(P.fdr) that a gene is in each cell-type.

Details

A named list called POA_example (pre-optic area example) containing three objects, POA.generes: a list of truncated dataframes containing summary statistics for each cell-type marker, POA.OR.signature a truncated signature matrix of odds ratio's for cell-types in the POA, and POA.Rank_signature a truncated signature matrix of -log10(Padj) for cell-type markers in the POA.

Examples

```r
data(POA_example)
```

---

**process_dgTMAtrix_lists**

*Count Matrix To Signature Matrix*

---

**Description**

This function takes a list of count matrices, processes them, calls cell-types, and generates signature matrices.

**Usage**

```r
process_dgTMAtrix_lists(
  dgTMAtrix_list,
  name,
  species_name,
  naming_preference = -9,
  rda_path = "",
  panglao_set = FALSE,
  haveUMAP = FALSE,
  saveSCObject = FALSE,
  internal = FALSE,
  toSave = FALSE,
  path = NULL,
  use_sctransform = FALSE,
  test_ctname = "wilcox",
  genes_integrate = 2000,
  genes_include = FALSE
)
```
process_dgTMatrix_lists

Arguments

dgTMatrix_list  A list of matrices in the class of dgTMatrix object – sparse object – compatible with Seurat rownames should be of the same species for each.

name  The name of the outputted signature matrices, cell-type preferences, and Seurat objects if you choose to save them.

species_name  Mouse or human symbols, -9 if internal as Panglao objects have gene symbol and ensembl combined.

naming_preference  For cell-type naming, see if cell-types given the inputted tissues are more likely to be named within one of the categories. These categories are: "brain", "epithelial", "endothelial", "blood", "connective","eye", "epidermis", "Digestive", "Immune", "pancreas", "liver", "reproductive", "kidney", "respiratory".

rda_path  If saved, directory to where data from scMappR_data is downloaded.

panglao_set  If the inputted matrices are from Panglao (i.e. if they’re internal).

haveUMAP  Save the UMAPs - requires additional packages (see Seurat for details).

saveSCObject  Save the Seurat object as an RData object (T/F).

internal  Was this used as part of the internal processing of Panglao datasets (T/F).

toSave  Allow scMappR to write files in the current directory (T/F)

path  If toSave == TRUE, path to the directory where files will be saved.

use_sctransform  If you should use sctransform or the Normalize/VariableFeatures/ScaleData pipeline (T/F).

test_ctname  statistical test for calling CT markers – must be in Seurat

genes_integrate  The number of genes to include in the integration anchors feature when combining datasets.

genes_include  TRUE or FALSE – include 2000 genes in signature matrix or all matrix.

Details

This function is a one line wrapper to process count matrices into a signature matrix. It combines process_from_count, two methods of identifying cell-type identities (GSVA A and Fisher’s test). Then, it takes the output of cell-type markers and converts it into a signature matrix of p-value ranks and odds ratios. It saves the Seurat object (if chosen with saveSCObject), cell-type identities from GSVA (its own object), and the signature matrices. Cell-type marker outputs are also saved in the generes .RData list. This is a list of cell-types containing all of the cell-type markers found with the FindMarkers function. Names of the generes lists and the signature matrices are kept.

Value

List with the following elements:

wilcoxon_rank_mat_t  A dataframe containing the signature matrix of ranks (-log10(Padj) * sign(fold-change)).
wilcoxon_rank_mat_or
A dataframe containing the signature matrix of odds-ratios.

generes
All cell-type markers for each cell-type with p-value and fold changes.

cellLabel
matrix where each row is a cluster and each column provides information on the
cell-type. Columns provide info on the cluster from seurat, the cell-type label
from CellMarker and Panglao using the fisher’s exact test and GSVA, and the
top 30 markers per cluster.

Examples

data(sm)
toProcess <- list(example = sm)
tst1 <- process_dgTMatrix_lists(toProcess, name = "testPropcess", species_name = "mouse",
naming_preference = "eye", rda_path = "")

process_from_count  Count Matrix To Seurat Object

Description
This function processes a list of count matrices (same species/gene symbols in each list) and con-
verts them to a Seurat object.

Usage

process_from_count(
    countmat_list,
    name,
    theSpecies = -9,
    haveUmap = FALSE,
    saveALL = FALSE,
    panglao_set = FALSE,
    toSave = FALSE,
    path = NULL,
    use_sctransform = FALSE,
    genes_integrate = 2000,
    genes_include = FALSE
)

Arguments

countmat_list  A list of count matrices that will be integrated using the IntegrationAnchors
features they should have the same rownames. A dgCMatrix or matrix object is
also acceptable, and no samples will be integrated.
The function `process_from_count` takes a list of count matrices and returns a Seurat object of the count matrices integrated using Seurat v4 (and IntegrationAnchors feature). Different normalization features such as the SCTransform pipeline are also available in this function. Different options are used when the function is being ran internally (i.e., reprocessing count matrices from PanglaoDB) or if it is running from custom scRNA-seq data. Larger scRNA-seq datasets can take considerable amounts of memory and run-time. See Seurat for details.

**Details**

This function takes a list of count matrices and returns a Seurat object of the count matrices integrated using Seurat v4 (and IntegrationAnchors feature). Different normalization features such as the SCTransform pipeline are also available in this function. Different options are used when the function is being ran internally (i.e., reprocessing count matrices from PanglaoDB) or if it is running from custom scRNA-seq data. Larger scRNA-seq datasets can take considerable amounts of memory and run-time. See Seurat for details.

**Value**

`process_from_count` A processed and integrated Seurat object that has been scaled and clustered. It can be returned as an internal object or also stored as an RData object if necessary.

**Examples**

```r
data(sm)
toProcess <- list(example = sm)
tst1 <- process_from_count(toProcess, "testProcess", theSpecies = "mouse")
```
**scMappR_and_pathway_analysis**

Generate cellWeighted_Foldchanges, visualize, and enrich.

**Description**

This function generates cell weighted Fold-changes (cellWeighted_Foldchange), visualizes them in a heatmap, and completes pathway enrichment of cellWeighted_Foldchanges and the bulk gene list using g:ProfileR.

**Usage**

```r
scMappR_and_pathway_analysis(
  count_file,
  signature_matrix,
  DEG_list,
  case_grep,
  control_grep,
  rda_path = "",
  max_proportion_change = -9,
  print_plots = T,
  plot_names = "scMappR",
  theSpecies = "human",
  output_directory = "scMappR_analysis",
  sig_matrix_size = 3000,
  drop_unknown_celltype = TRUE,
  internet = TRUE,
  up_and_downregulated = FALSE,
  gene_label_size = 0.4,
  number_genes = -9,
  toSave = FALSE,
  newGprofiler = FALSE,
  path = NULL,
  deconMethod = "DeconRNASeq"
)
```

**Arguments**

- **count_file**
  Normalized (i.e. TPM, RPKM, CPM) RNA-seq count matrix where rows are gene symbols and columns are individuals. Inputted data should be a data.frame or matrix. A character vector to a tsv file where this data can be loaded is also acceptable. Gene symbols from the count file, signature matrix, and DEG list should all match (case sensitive, gene symbol or ensembl, etc.)

- **signature_matrix**
  Signature matrix: a gene by cell-type matrix populated with the fold-change of gene expression in cell-type marker "i" vs all other cell-types. Object should be a data.frame or matrix.
DEG_list  An object with the first column as gene symbols within the bulk dataset (doesn’t have to be in signature matrix), second column is the adjusted p-value, and the third the log2FC path to a .tsv file containing this info is also acceptable.

case_grep  A character representing what designates the "cases" (i.e. upregulated is 'case' biased) in the columns of the count file. A numeric vector of the index of "cases" is also acceptable. Tag in the column name for cases (i.e. samples representing upregulated) OR an index of cases.

control_grep  A character representing what designates the "control" (i.e. downregulated is 'control biased) in the columns of the count file. A numeric vector of the index of "control" is also acceptable. Tag in the column name for cases (i.e. samples representing upregulated) OR an index of cases.

rda_path  If downloaded, path to where data from scMappR_data is stored.

max_proportion_change  Maximum cell-type proportion change – may be useful if there are many rare cell-type. Alternatively, if a cell-type is only present in one condition but not the other, it will prevent possible infinite or 0 cwFold-changes.

print_plots  Whether boxplots of the estimated CT proportion for the leave-one-out method of CT deconvolution should be printed. The same name of the plots will be completed for top pathways.

plot_names  The prefix of plot pdf files.

theSpecies  human, mouse, or a species directly compatible with gProfileR (i.e. g:ProfileR).

output_directory  The name of the directory that will contain output of the analysis.

sig_matrix_size  Maximum number of genes in signature matrix for cell-type deconvolution.

drop_unknown_celltype  Whether or not to remove "unknown" cell-types from the signature matrix.

internet  Whether you have stable Wifi (T/F).

up_and_downregulated  Whether you are additionally splitting up/downregulated genes (T/F).

gene_label_size  The size of the gene label on the plot.

number_genes  The number of genes to cut-off for pathway analysis (good with many DEGs).

toSave  Allow scMappR to write files in the current directory (T/F).

newGprofiler  Whether to use gProfileR or gprofiler2 (T/F).

path  If toSave == TRUE, path to the directory where files will be saved.

deconMethod  Which RNA-seq deconvolution method to use to estimate cell-type proportions. Options are "WGCNA", "DCQ", or "DeconRNAseq"

Details

This function generates cellWeighted_Foldchanges for every cell-type (see deconvolute_and_contextualize), as well as accompanying data such as cell-type proportions with the DeconRNA-seq, WGCNA, or DCQ methods. Then, it generates heatmaps of all cellWeighted_Foldchanges, cellWeighted_Foldchanges
overlapping with the signature matrix, the entire signature matrix, the cell-type preference values from the signature matrix that overlap with inputted differentially expressed genes. Then, assuming there is available internet, it will complete gProfileR of the reordered cellWeighted_Foldchanges as well as a the ordered list of genes. This function is a wrapper for deconvolute_and_contextualize and pathway_enrich_internal and the primary function within the package.

Value

List with the following elements:

- **cellWeighted_Foldchanges**: Cellweighted Fold-changes for all differentially expressed genes.
- **paths**: Enriched biological pathways for each cell-type.
- **TFs**: Enriched TFs for each cell-type.

Examples

```r
data(PBMC_example)
bulk_DE_cors <- PBMC_example$bulk_DE_cors
bulk_normalized <- PBMC_example$bulk_normalized
odds_ratio_in <- PBMC_example$odds_ratio_in
case_grep <- "_female"
control_grep <- "_male"
max_proportion_change <- 10
print_plots <- FALSE
theSpecies <- "human"
toOut <- scMappR_and_pathway_analysis(bulk_normalized, odds_ratio_in,
bulk_DE_cors, case_grep = case_grep,
control_grep = control_grep, rda_path = "",
max_proportion_change = 10, print_plots = TRUE,
plot_names = "tst1", theSpecies = "human",
output_directory = "tester",
sig_matrix_size = 3000, up_and_downregulated = FALSE,
internet = FALSE)
```

Description

Tissues available in scMappR.

Usage

```r
data(scMappR_tissues)
```
seurat_to_generes

Format

A vector of tissue names available for tissue_scMappR_internal or to download and use in scMappR_and_pathway_analysis.

scMappR_tissues A list of 174 tissue names from PanglaoDB.

Details

A vector of tissues available in scMappR.

Examples

data(scMappR_tissues)

seurat_to_generes Identify all cell-type markers

Description

Takes processed Seurat matrix and identifies cell-type markers with FindMarkers in Seurat.

Usage

seurat_to_generes(pbmc, test = "wilcox")

Arguments

pbmc Processed Seurat object.
test statistical test for calling CT markers – must be in Seurat.

Details

Internal: This function runs the FindMarkers function from Seurat in a loop, will use the Seurat v2 or Seurat v3 object after identifying which Seurat object is inputted. It then takes the output of the FindMarkers and puts it in a list, returning it.

Value

seurat_to_generes A list of genes where their over-representation in the i’th cell-type is computed. Each element contains the gene name, adjusted p-value, and the log2Fold-Change of each gene being present in that cell-type.
single_gene_preferences

**Examples**

```r
data(sm)
toProcess <- list(example = sm)
tst1 <- process_from_count(toProcess, "testProcess", theSpecies = "mouse")
generes <- seurat_to_generes(tst1)
```

---

**single_gene_preferences**

*Single cell-type gene preferences*

---

**Description**

Measure enrichment of individual cell-types in a signature matrix.

Internal function as part of `tissue_scMappR_internal()`. This function takes genes preferentially expressed within a gene list, each cell-type and the background (i.e. all genes within the signature matrix) before completing the cell-type specific enrichment of the inputted gene list on each cell type. This function then returns a table describing the cell-type enrichments (p-value and odds ratio) of each cell-type.

**Usage**

```r
single_gene_preferences(
  hg_short,
  hg_full,
  study_name,
  outDir,
  toSave = FALSE,
  path = NULL
)
```

**Arguments**

- **hg_short**: A list with two objects: a "preferences" and a "genesIn". Preferences is a list of gene symbols over-represented in each cell-type and genesIn were all the inputted genes.
- **hg_full**: The same as `hg_short` but for every gene in the signature matrix.
- **study_name**: Name of output table.
- **outDir**: Directory where table is outputted.
- **toSave**: Allow scMappR to write files in the current directory (T/F).
- **path**: If `toSave` == TRUE, path to the directory where files will be saved.
Value

single_gene_preferences A gene-set enrichment table of individual cell-type enrichment.

Examples

```r
# load in signature matrices
data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA.OR_signature
POA_Rank_signature <- POA_example$POA.Rank_signature
sig <- get_gene_symbol(POA_Rank_signature)
Signature <- POA_Rank_signature
rownames(Signature) <- sig$rownname
genes <- rownames(Signature)[1:60]
heatmap_test <- tissue_scMappR_custom( genes, signature_matrix = Signature,
                                        output_directory = "scMappR_test", toSave = FALSE)
single_preferences <- heatmap_test$single_celltype_preferences
```

**sm**  

**single_cell_process**

Description

Example data for processing scRNA-seq count data with Seurat.

Usage

data(sm)

Format

A 752 x 236 matrix of class dgCMatrix where rows are genes and columns are cells. Data matrix is filled with counts detected from scRNAseq.

TCTCTAACACAGGCCT Barcode of one of the sequenced cells present. Each column is the count from a scRNA-seq dataset reprocessed by PanglaoDB.

Details

A dgCMatrix object containing count data for scRNA-seq processing.

Examples

data(sm)
tissue_by_celltype_enrichment

Description
This function uses a Fisher’s-exact-test to rank gene-set enrichment.

Usage

tissue_by_celltype_enrichment(
  gene_list,
  species,
  name = "CT_Tissue_example",
  p_thresh = 0.05,
  rda_path = "",
  isect_size = 3,
  return_gmt = FALSE
)

Arguments

gene_list
  A character vector of gene symbols with the same designation (e.g. mouse symbol - mouse, human symbol - human) as the gene set database.

species
  Species of cell-type marker to use (’human’ or ’mouse’).

name
  Name of the pdf to be printed.

p_thresh
  The Fisher’s test cut-off for a cell-marker to be enriched.

rda_path
  Path to a .rda file containing an object called ”gmt”. Either human or mouse cell-type markers split by experiment. If the correct file isn’t present they will be downloaded from https://github.com/wilsonlabgroup/scMappR_Data.

isect_size
  Number of genes in your list and the cell-type.

return_gmt
  Return .gmt file – recommended if downloading from online as it may have updated (T/F).

Details

Complete a Fisher’s-exact test of an input list of genes against one of the two curated tissue by cell-type marker datasets from scMappR.

Value

List with the following elements:

enriched
  Data frame of enriched cell-types from tissues.

gmt
  Cell-markers in enriched cell-types from tissues.
Examples

```r
data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
Signature <- POA_Rank_signature
rownames(Signature) <- rowname$rownames
rowname <- get_gene_symbol(Signature)
rownames(Signature) <- rowname$rownames
genes <- rownames(Signature)[1:100]
enriched <- tissue_by_celltype_enrichment(gene_list = genes,
species = "mouse", p_threshold = 0.05, isect_size = 3)
```

**tissue_scMappR_custom**  
*Gene List Visualization and Enrichment with Custom Signature Matrix*

**Description**
This function visualizes signature matrix, clusters subsetted genes, completes enrichment of individual cell-types and co-enrichment.

**Usage**
```
tissue_scMappR_custom(
  gene_list,
  signature_matrix,
  output_directory = "custom_test",
  toSave = FALSE,
  path = NULL,
  gene_cutoff = 1,
  is_pvalue = TRUE
)
```

**Arguments**
- `gene_list`: A list of gene symbols matching that of the `signature_matrix`. Any gene symbol is acceptable.
- `signature_matrix`: Pre-computed signature matrix with matching gene names.
- `output_directory`: Directory made containing output of functions.
- `toSave`: Allow scMappR to write files in the current directory (T/F).
path If toSave == TRUE, path to the directory where files will be saved.
gene_cutoff Value cut-off (generally rank := log10(Padj)) for a gene to be considered a marker.
is_pvalue If signature matrix is p-value before rank is applied (not recommended) (T/F).

Details

This function is roughly the same as tissue_scMappR_internal, however now there is a custom signature matrix. It generates a heatmap of the signature matrix and your inputted gene list, as well as single cell-type and co-celltype enrichment.

Value

List with the following elements:

background_heatmap Data frame of the entire gene by cell-type signature matrix inputted.
gene_list_heatmap Data frame of inputted signature matrix subsetted by input genes.
single_celltype_preferences Data frame of enriched cell-types.
group_celtype_preference Data frame of groups of cell-types enriched by the same genes.

Examples

# load in signature matrices
data(POA_example)
POA_generes <- POA_example$POA_generes
POA_OR_signature <- POA_example$POA_OR_signature
POA_Rank_signature <- POA_example$POA_Rank_signature
sig <- get_gene_symbol(POA_Rank_signature)
Signature <- POA_Rank_signature
rownames(Signature) <- sig$rowname
genes <- rownames(Signature)[1:60]
heatmap_test <- tissue_scMappR_custom( genes, signature_matrix = Signature,
                                      output_directory = "scMappR_test", toSave = FALSE)
tissue_scMappR_internal

Usage

tissue_scMappR_internal(
  gene_list,
  species,
  output_directory,
  tissue,
  rda_path = "",
  cluster = "Pval",
  genecex = 0.01,
  raw_pval = FALSE,
  path = NULL,
  toSave = FALSE,
  drop_unkown_celltype = FALSE
)

Arguments

gene_list A list of gene symbols, mouse or human.

species "mouse", "human" or ".9" if using a precomputed signature matrix.

output_directory If toSave = TRUE, the name of the output directory that would be built.

tissue Name of the tissue in "get_tissues".

rda_path Path to the .rda file containing all of the signature matrices.

cluster 'Pval' or 'OR' depending on if you want to cluster odds ratios or p-values of cell-type preferences.

genecex The size of the gene names of the rows in the heatmap.

raw_pval If the inputted signature matrix are raw (untransformed) p-values – recommended to generate rank first (T/F).

path If toSave == TRUE, path to the directory where files will be saved.

toSave Allow scMappR to write files in the current directory (T/F).

drop_unkown_celltype Whether or not to remove "unknown" cell-types from the signature matrix (T/F).

Details

This function takes a list of genes and a tissue that is contained in current signature matrices before and generating heatmaps of cell-type preferences. It then completes cell-type enrichment of each individual cell-type, then, if more than two cell-types are significantly enriched, co-enrichment of those enriched cell-types is then computed.

Value

List with the following elements:

background_heatmap Data frame of the entire gene by cell-type signature matrix inputted.
To Character.

Description

This function checks if your vector is not a character and if not, will convert it to a character.

Usage

tochr(x)

Arguments

x A character, factor or numeric vector.

Value

tochr Returns a character vector.
toNum

Examples

# vector of factors
fact <- factor(c("a", "b", "c", "d"))
# convert to character
char <- tochr(fact)

---

**toNum** To Numeric.

Description

This function checks if your vector is not a character and if it is, then converts it to a numeric.

Usage

toNum(x)

Arguments

- **x** A character, factor, or numeric vector.

Value

toNum Returns a numeric vector.

Examples

# vector of factors
fact <- factor(c("1", "2", "3", "4"))
# convert to numeric
num <- toNum(fact)
**topgenes_extract**

*Extract Top Markers*

**Description**

Internal – Extracts strongest cell-type markers from a Seurat object.

**Usage**

```
topgenes_extract(generes, padj = 0.05, FC = 1.5, topNum = 30)
```

**Arguments**

- `generes` A list of cell-type markers with fold-changes and p-values (FindMarkers output in Seurat).
- `padj` The p-value (FDR) cutoff.
- `FC` The fold-change cutoff.
- `topNum` The number of genes to extract.

**Details**

Internal, this function runs through a list of outputs from FindMarkers objects in Seurat and will extract genes past a padj and fold-change threshold. Then it extracts the topNum number of genes. If you have not used the FindMarkers function, then a list of summary statistics with fold-change designated by avg_logFC and p-val by p_val_adj.

**Value**

`topgenes_extract` Returns a list of character vectors with the top (topNum) of gene markers for each cell-type.

**Examples**

```r
# load generes object
data(POA_example)
topGenes <- topgenes_extract(POA_example$POA_generes)
```
two_method_pathway_enrichment

Description

Pathway analysis of each cell-type based on cell-type specificity and rank improvement by scMappR.

Usage

two_method_pathway_enrichment(
  DEG_list,
  theSpecies,
  scMappR_vals,
  background_genes = NULL,
  output_directory = "output",
  plot_names = "reweighted",
  number_genes = -9,
  newGprofiler = FALSE,
  toSave = FALSE,
  path = NULL
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEG_list</td>
<td>Differentially expressed genes (gene_name, padj, log2fc).</td>
</tr>
<tr>
<td>theSpecies</td>
<td>Human, mouse, or a character that is compatible with g:ProfileR.</td>
</tr>
<tr>
<td>scMappR_vals</td>
<td>cell weighted Fold-changes of differentially expressed genes.</td>
</tr>
<tr>
<td>background_genes</td>
<td>A list of background genes to test against. NULL assumes all genes in g:profileR gene set databases.</td>
</tr>
<tr>
<td>output_directory</td>
<td>Path to the directory where files will be saved.</td>
</tr>
<tr>
<td>plot_names</td>
<td>Names of output.</td>
</tr>
<tr>
<td>number_genes</td>
<td>Number of genes to if there are many, many DEGs.</td>
</tr>
<tr>
<td>newGprofiler</td>
<td>Whether to use g:ProfileR or gprofiler2 (T/F).</td>
</tr>
<tr>
<td>toSave</td>
<td>Allow scMappR to write files in the current directory (T/F).</td>
</tr>
<tr>
<td>path</td>
<td>If toSave == TRUE, path to the directory where files will be saved.</td>
</tr>
</tbody>
</table>

Details

This function re-ranks cwFoldChanges based on their absolute cell-type specificity scores (per-celltype) as well as their rank increase in cell-type specificity before completing an ordered pathway analysis. In the second method, only genes with a rank increase in cell-type specificity were included.
two_method_pathway_enrichment

Value

List with the following elements:

- `rank_increase` - A list containing the degree of rank change between bulk DE genes and cwFold-changes. Pathway enrichment and TF enrichment of these reranked genes.
- `non_rank_increase` - list of DFs containing the pathway and TF enrichment of cwFold-changes.

Examples

```r
# load data for scMappR
data(PBMC_example)
bulk_DE_cors <- PBMC_example$bulk_DE_cors
bulk_normalized <- PBMC_example$bulk_normalized
odds_ratio_in <- PBMC_example$odds_ratio_in
case_grep <- "_female"
control_grep <- "_male"
max_proportion_change <- 10
print_plots <- FALSE
theSpecies <- "human"

# calculate cwFold-changes
toOut <- scMappR_and_pathway_analysis(bulk_normalized, odds_ratio_in,
bulk_DE_cors, case_grep = case_grep,
control_grep = control_grep, rda_path = "",
max_proportion_change = 10, print_plots = TRUE,
plot_names = "tst1", theSpecies = "human",
output_directory = "tester",
sig_matrix_size = 3000, up_and_downregulated = FALSE,
internet = FALSE)

# complete pathway enrichment using both methods
twoOutFiles <- two_method_pathway_enrichment(bulk_DE_cors, "human",
scMappR_vals = toOut$cellWeighted_Foldchange, background_genes = rownames(bulk_normalized),
output_directory = "newfun_test", plot_names = "nonreranked_", toSave = FALSE)
```
# Index

* **datasets**
  - gmt, 16
  - PBMC_example, 25
  - POA_example, 27
  - scMappR_tissues, 34
  - sm, 37

- cellmarker_enrich, 3
- coEnrich, 4
- compare_deconvolution_methods, 5
- cwFoldChange_evaluate, 7

- DeconRNAseq_CRAN, 9
- deconvolute_and_contextualize, 10

- extract_genes_cell, 12

- genes_to_heatmap, 13
- get_gene_symbol, 15
- get_signature_matrices, 16
- gmt, 16
- gProfiler_cellWeighted_Foldchange, 17
- gsva_cellIdentify, 18

- heatmap_generation, 20
- human_mouse_ct_marker_enrich, 21

- make_TF_barplot, 22

- pathway_enrich_internal, 24
- PBMC_example, 25
- plotBP, 26
- POA_example, 27
- process_dgTMATRIX_lists, 28
- process_from_count, 30

- scMappR_and_pathway_analysis, 32
- scMappR_tissues, 34
- seurat_to_generes, 35
- single_gene_preferences, 36
- sm, 37

- tissue_by_celltype_enrichment, 38
- tissue_scMappR_custom, 39
- tissue_scMappR_internal, 40
- tochr, 42
- toNum, 43
- topgenes_extract, 44
- two_method_pathway_enrichment, 45