Package 'scToppR'

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Title API Wrapper for ToppGene

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Description scToppR provides an easy-to-use API wrapper for the ToppGene web platform, used for gene ontology and functional enrichment research. The package also integrates visualization tools, making it a convenient tool directly connecting ToppGene to code-based workflows in R. The tool can also easily save results into different formats.

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Contents

`scToppR-package` *scToppR: API Wrapper for ToppGene*

Description

scToppR provides an easy-to-use API wrapper for the ToppGene web platform, used for gene ontology and functional enrichment research. The package also integrates visualization tools, making it a convenient tool directly connecting ToppGene to code-based workflows in R. The tool can also easily save results into different formats.

Author(s)

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See Also

Useful links:

- https://github.com/BioinformaticsMUSC/scToppR
- Report bugs at https://github.com/BioinformaticsMUSC/scToppR

addToppData *Add toppData results to SingleCellExperiment or SummarizedExperiment metadata*

Description

A convenience function to store toppData enrichment results in the metadata slot of a SingleCellExperiment or SummarizedExperiment object. Results are stored directly under the specified slot name, with optional analysis parameters stored in a separate `slot_name_params` slot.

Usage

```
addToppData(
  sce,
  toppData_results,
  slot_name = "toppData",
  include_params = TRUE
)
```

Arguments

`sce`	A SingleCellExperiment or SummarizedExperiment object
`toppData_results`	A data.frame of toppData results from toppFun()
`slot_name`	Name for the metadata slot (default: "toppData")
`include_params`	Logical, whether to include analysis parameters and timestamp in a separate `slot_name_params` slot (default: TRUE)

Value

SingleCellExperiment or SummarizedExperiment object with toppData stored in metadata

Examples

```
library(airway)
data("airway")  # example SummarizedExperiment object
data("toppdata.airway")  # example toppData results
se_with_topp <- addToppData(airway, toppdata.airway)

# Access results directly
topp_results <- S4Vectors::metadata(se_with_topp)$toppData

# Access analysis parameters (if include_params = TRUE)
topp_params <- S4Vectors::metadata(se_with_topp)$toppData_params
```

addToppData *Add toppData results to SingleCellExperiment or SummarizedExperiment metadata*

Description

A convenience function to store toppData enrichment results in the metadata slot of a SingleCellExperiment or SummarizedExperiment object. Results are stored directly under the specified slot name, with optional analysis parameters stored in a separate `slot_name_params` slot.

Usage

```
addToppData(
  sce,
  toppData_results,
  slot_name = "toppData",
  include_params = TRUE
)
```

Arguments

`sce`	A SingleCellExperiment or SummarizedExperiment object
`toppData_results`	A data.frame of toppData results from toppFun()
`slot_name`	Name for the metadata slot (default: "toppData")
`include_params`	Logical, whether to include analysis parameters and timestamp in a separate `slot_name_params` slot (default: TRUE)

Value

SingleCellExperiment or SummarizedExperiment object with toppData stored in metadata

Examples

```
library(airway)
data("airway")  # example SummarizedExperiment object
data("toppdata.airway")  # example toppData results
se_with_topp <- addToppData(airway, toppdata.airway)

# Access results directly
topp_results <- S4Vectors::metadata(se_with_topp)$toppData

# Access analysis parameters (if include_params = TRUE)
topp_params <- S4Vectors::metadata(se_with_topp)$toppData_params
```

get_Entrez *Convert genes into Entrez format*

Description

Convert genes into Entrez format

Usage

```
get_Entrez(genes)
```

Arguments

genes	A list of genes

Value

a vector of genes in Entrez format

Examples

```
get_Entrez(genes = c("IFNG", "FOXP3"))
```

get_ToppCats *Get a vector of ToppFun categories*

Description

Get a vector of ToppFun categories

Usage

```
get_ToppCats()
```

Value

a vector

Examples

```
get_ToppCats()
```

ifnb.de *IFNB DE results*

Description

A dataframe of differentially expressed genes generated using the FindMarkers function for each cluster from the Kang 2018 IFNB dataset Created using the IFNB dataset from the SeuratData package

Usage

```
data("ifnb.de")
```

Format

A dataframe with 92,860 rows and 7 columns

p_val P values

avg_log2FC avg log 2 fc values

pct.1 percentage of cells expressing gene in group 1

pct.2 percentage of cells expressing gene in group 2

p_val_adj adjusted p-value (FDR)

cluster cell group name

gene gene name

Source

https://www.nature.com/articles/nbt.4042

ifnb.markers.df *IFNB Marker DF*

Description

A dataframe of 100 top markers for each class in 'seurat_annotations' column using presto::wilcoxauc() and presto::top_markers() Created using the IFNB dataset from the SeuratData package

Usage

```
data("ifnb.markers.df")
```

Format

A dataframe with 100 rows and 14 columns

rank rank of marker

B cell group name

B Activated cell group name

CD14 Mono cell group name

CD16 Mono cell group name

CD4 Memory T cell group name

CD4 Naive T cell group name

CD8 T cell group name

DC cell group name

Eryth cell group name

Mk cell group name

CNK cell group name

pDC cell group name

T activated cell group name

Source

https://www.nature.com/articles/nbt.4042

Kang HM, Subramaniam M, Targ S, et al. Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nat Biotechnol. 2018;36(1):89-94. doi:10.1038/nbt.4042

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ifnb.markers.list.CD8T

IFNB Marker DF

Description

A list of the 100 top markers for CD8 T cells in ifnb dataset using presto::wilcoxauc() and presto::top_markers() Created using the IFNB dataset from the SeuratData package

Usage

```
data("ifnb.markers.list.CD8T")
```

Format

A character vector with 100 genes

ifnb.markers.list.CD8T rank of marker

Source

https://www.nature.com/articles/nbt.4042

Kang HM, Subramaniam M, Targ S, et al. Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nat Biotechnol. 2018;36(1):89-94. doi:10.1038/nbt.4042

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pbmc.markers *PBMC markers*

Description

A dataframe of marker genes generated using the FindMarkers function for each cluster from the PBMC 3k dataset

Usage

```
data("pbmc.markers")
```

Format

A dataframe with 11,629 rows and 7 columns

p_val P values

avg_log2FC avg log 2 fc values

pct.1 percentage of cells expressing gene in group 1

pct.2 percentage of cells expressing gene in group 2

p_val_adj adjusted p-value (FDR)

cluster cell group name

gene gene name

Source

10X Genomics PBMC 3k dataset. Available from https://www.10xgenomics.com/resources/datasets/. Analysis following Seurat PBMC tutorial: https://satijalab.org/seurat/articles/pbmc3k_tutorial.html

toppBalloon *Create a balloon plot from toppdata results*

Description

This function creates balloon plots from ToppGene enrichment results. It accepts either a data.frame with toppData results, or a SummarizedExperiment/SingleCellExperiment object with toppData stored in the metadata.

Usage

```
toppBalloon(
  toppData,
  categories = NULL,
  balloons = 3,
  x_axis_text_size = 6,
  cluster_col = "Cluster",
  filename = "toppBalloon",
  save = FALSE,
  save_dir = tempdir(),
  height = 6,
  width = 8,
  slot_name = "toppData",
  ...
)
```

Arguments

toppData	A toppData results dataframe, SummarizedExperiment, or SingleCellExperiment object
categories	The topp categories to plot
balloons	Number of balloons per group to plot
x_axis_text_size	Size of the text on the x axis
cluster_col	The column name for clusters (default: "Cluster")
filename	Filename of the saved balloon plot
save	Save the balloon plot if TRUE
save_dir	Directory to save the balloon plot
height	Height of the saved balloon plot
width	Width of the saved balloon plot
slot_name	For SE/SCE objects, the metadata slot name containing toppData (default: "toppData")
...	Additional parameters for future use

Value

ggplot object or list of ggplot objects

Examples

```
data("toppdata.pbmc")

# With data.frame
toppBalloon(toppdata.pbmc, balloons = 3, save = FALSE)

# With SummarizedExperiment (if toppData stored in metadata)
# toppBalloon(se_object, categories = "GeneOntologyMolecularFunction")
```

---

toppdata.airway *toppData example using the airway dataset results*

Description

A dataframe of of sample toppData results created from the ifnb.de dataset using the toppFun() function

Usage

```
data("toppdata.airway")
```

Format

A dataframe with 902 rows and 14 columns

Category ToppGene category

ID ToppGene Term ID

Name ToppGene Term Name

PValue P value

QValueFDRBH adjusted p-value (FDR)

QValueFDRBY adjusted p-value (BY)

QValueBonferroni adjusted p-value (Bonferroni)

TotalGenes Total genes in background

GenesInTerm Genes in ToppGene Term

GenesInQuery Genes in submitted query

GenesInTermQuery Intersection of genes in Term and in Query

Source ToppGene result source

URL ToppGene associated URL

Cluster cell group name

Source

https://toppgene.cchmc.org

Generated using ToppGene API (https://toppgene.cchmc.org/). Chen J, Bardes EE, Aronow BJ, Jegga AG. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. Nucleic Acids Res. 2009;37(Web Server issue):W305-11. doi: 10.1093/nar/gkp427.

Himes, E. B, Jiang, X., Wagner, P., Hu, R., Wang, Q., Klanderman, B., Whitaker, M. R, Duan, Q., Lasky-Su, J., Nikolos, C., Jester, W., Johnson, M., Panettieri, A. R, Tantisira, G. K, Weiss, T. S, Lu, Q. (2014). "RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells." PLoS ONE, 9(6), e99625. http://www.ncbi.nlm.nih.gov/pubmed/24926665.

https://www.bioconductor.org/packages/release/data/experiment/html/airway.html

---

toppdata.ifnb *toppData example for ifnb.de*

Description

A dataframe of of sample toppData results created from the ifnb.de dataset using the toppFun() function

Usage

```
data("toppdata.ifnb")
```

Format

A dataframe with 12,227 rows and 14 columns

Category ToppGene category

ID ToppGene Term ID

Name ToppGene Term Name

PValue P value

QValueFDRBH adjusted p-value (FDR)

QValueFDRBY adjusted p-value (BY)

QValueBonferroni adjusted p-value (Bonferroni)

TotalGenes Total genes in background

GenesInTerm Genes in ToppGene Term

GenesInQuery Genes in submitted query

GenesInTermQuery Intersection of genes in Term and in Query

Source ToppGene result source

URL ToppGene associated URL

Cluster cell group name

Source

Generated using ToppGene API (https://toppgene.cchmc.org/). Chen J, Bardes EE, Aronow BJ, Jegga AG. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. Nucleic Acids Res. 2009;37(Web Server issue):W305-11. doi: 10.1093/nar/gkp427.

https://toppgene.cchmc.org

Kang HM, Subramaniam M, Targ S, et al. Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nat Biotechnol. 2018;36(1):89-94. doi:10.1038/nbt.4042

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toppdata.pbmc *toppData example*

Description

A dataframe of of sample toppData results created from the pbmc.markers dataset using the toppFun() function

Usage

```
data("toppdata.pbmc")
```

Format

A dataframe with 8,550 rows and 14 columns

Category ToppGene category

ID ToppGene Term ID

Name ToppGene Term Name

PValue P value

QValueFDRBH adjusted p-value (FDR)

QValueFDRBY adjusted p-value (BY)

QValueBonferroni adjusted p-value (Bonferroni)

TotalGenes Total genes in background

GenesInTerm Genes in ToppGene Term

GenesInQuery Genes in submitted query

GenesInTermQuery Intersection of genes in Term and in Query

Source ToppGene result source

URL ToppGene associated URL

Cluster cell group name

Source

https://toppgene.cchmc.org

Generated using ToppGene API (https://toppgene.cchmc.org/). Chen J, Bardes EE, Aronow BJ, Jegga AG. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. Nucleic Acids Res. 2009;37(Web Server issue):W305-11. doi: 10.1093/nar/gkp427.

10X Genomics PBMC 3k dataset. Available from https://www.10xgenomics.com/resources/datasets/. Analysis following Seurat PBMC tutorial: https://satijalab.org/seurat/articles/pbmc3k_tutorial.html

---

`toppFun` *Get results from ToppFun*

Description

The toppFun() function takes a data.frame or other tabular data structure and selects genes to use in querying ToppGene.

Usage

```
toppFun(
  input_data,
  type = "degs",
  topp_categories = NULL,
  cluster_col = "cluster",
  gene_col = "gene",
  p_val_col = "adj_p_val_col",
  logFC_col = "avg_logFC",
  direction_mode = "all",
  num_genes = 1000,
  pval_cutoff = 0.5,
  fc_cutoff = 0,
  fc_filter = "ALL",
  clusters = NULL,
  correction = "FDR",
  key_type = "SYMBOL",
  min_genes = 2,
  max_genes = 1500,
  max_results = 50,
  verbose = TRUE
)
```

Arguments

`input_data` A vector of markers or dataframe with columns as cluster labels

type	One of c("degs", "marker_list", or "marker_df). If "degs" is selected, the input_data is assumed to be a data.frame with logfoldchange, pvalue, and gene name columns. If "marker_list" is selected, input_data is assumed to be a list of genes with no other stats, and any thresholds pertaining to "degs" will be ignored. If "marker_df" is selected, the input_data is assumed to be a data.frame with columns as clusters/celltypes, and entries are lists of markers.
topp_categories	A string or vector with specific toppfun categories for the query
cluster_col	Column name for the groups of cells (e.g. cluster or celltype)
gene_col	Column name for genes (e.g. gene or feature)
p_val_col	Column name for the p-value or adjusted p-value (preferred)
logFC_col	Column name for the avg log FC column
direction_mode	One of c("all", "split"). Whether to use all genes in the pathway analysis, or to split by up and down regulated genes
num_genes	Number of genes per group to use for toppGene query
pval_cutoff	(adjusted) P-value cutoff for filtering differentially expressed genes
fc_cutoff	Avg log fold change cutoff for filtering differentially expressed genes
fc_filter	Include "ALL" genes, or only "UPREG" or "DOWNREG" for each cluster
clusters	Which clusters to include in toppGene query
correction	P-value correction method ("FDR" is "BH")
key_type	Gene name format
min_genes	Minimum number of genes to match in a query
max_genes	Maximum number of genes to match in a query
max_results	Maximum number of results per cluster
verbose	Verbosity setting, TRUE or FALSE

Details

The use of data from ToppGene is governed by their Terms of Use: https://toppgene.cchmc.org/navigation/termsofuse.jsp

Value

data.frame

Examples

```
data("ifnb.de")
toppData <- toppFun(ifnb.de,
    topp_categories = NULL,
    cluster_col = "celltype",
    gene_col = "gene",
    p_val_col = "p_val_adj",
    logFC_col = "avg_log2FC"
)
```

toppPlot *Create a dotplot from toppdata results*

Description

This function creates dotplots from ToppGene enrichment results. It accepts either a data.frame with toppData results, or a SummarizedExperiment/SingleCellExperiment object with toppData stored in the metadata.

Usage

```
toppPlot(
  toppData,
  category = NULL,
  clusters = NULL,
  cluster_col = "Cluster",
  p_val_adj = "QValueFDRBH",
  p_val_display = "FDR_BH",
  num_terms = 10,
  save = FALSE,
  save_dir = tempdir(),
  width = 8,
  height = 6,
  file_prefix = "toppPlot",
  combine = FALSE,
  ncols = 2,
  y_axis_text_size = 10,
  slot_name = "toppData",
  ...
)
```

Arguments

toppData	A toppData results dataframe, SummarizedExperiment, or SingleCellExperiment object
category	The topp categories to plot
clusters	The cluster(s) to plot
cluster_col	The column name for clusters (default: "Cluster")
p_val_adj	The P-value correction method: "BH", "Bonferroni", "BY", or "none"
p_val_display	If "log", display the p-value in terms of -log10(p_value)
num_terms	The number of terms from the toppData results to be plotted, per cluster
save	Whether to save the file automatically
save_dir	Directory to save file
width	width of the saved file (inches)

height	height of the saved file (inches)
file_prefix	file prefix if saving the plot - the cluster name is also added automatically
combine	If TRUE and multiple clusters selected, return a patchwork object of all plots; if FALSE return list of plots
ncols	If patchwork element returned, number of columns for subplots
y_axis_text_size	Size of the Y axis text - for certain categories, it's helpful to decrease this
slot_name	For SE/SCE objects, the metadata slot name containing toppData (default: "toppData")
...	Additional parameters for future use

Value

ggplot object or list of ggplot objects

Examples

```
data("toppdata.pbmc")

# With data.frame
toppPlot(toppdata.pbmc,
    category = "GeneOntologyMolecularFunction",
    clusters = 0,
    save = FALSE
)

# With SummarizedExperiment (if toppData stored in metadata)
# toppPlot(se_object, category = "GeneOntologyMolecularFunction")
```

---

toppSave *Save toppData results (optionally) split by celltype/cluster*

Description

Save toppData results (optionally) split by celltype/cluster

Usage

```
toppSave(
  toppData,
  filename = "toppData_results",
  save_dir = NULL,
  split = TRUE,
  format = "xlsx",
  cluster_col = "Cluster",
  verbose = TRUE
)
```

Arguments

toppData	Results from toppFun as a dataframe
filename	filename prefix for each split file
save_dir	the directory to save files
split	Boolean, whether to split the dataframe by celltype/cluster
format	Saved file format, one of c("xlsx", "csv", "tsv")
cluster_col	Column name for the groups of cells (e.g. cluster or celltype), usually "Cluster"
verbose	Verbosity setting, TRUE or FALSE

Value

A saved file

Examples

```
data("toppdata.ifnb")
toppSave(toppdata.ifnb,
    filename = "toppFun_results",
    save_dir = tempdir(),
    split = TRUE,
    format = "xlsx")
```

Index