

Package ‘rChEA3’

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Title R Client for the 'ChEA3' Transcription Factor Enrichment API

Version 1.0.1

Description Interface to the 'ChEA3' transcription factor enrichment API.

'ChEA3' integrates evidence from ChIP-seq, co-expression, and literature resources to prioritize transcription factors regulating a given set of genes. This package provides convenient R functions to query the API, retrieve ranked results across collections (including integrated scores), and standardize output for downstream analysis in R/Bioconductor workflows. See <<https://maayanlab.cloud/chea3/>> or Keenan (2019) <[doi:10.1093/nar/gkz446](https://doi.org/10.1093/nar/gkz446)> for further details.

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Encoding UTF-8

RoxygenNote 8.0.0

URL <https://github.com/ckntav/rChEA3>, <https://ckntav.github.io/rChEA3/>

BugReports <https://github.com/ckntav/rChEA3/issues>

Imports cli, crayon, dplyr, ggplot2, httr, jsonlite, lubridate, rlang, tidyselect, writexl

Depends R (>= 4.1.0)

LazyData true

Suggests knitr, readxl, rmarkdown, testthat (>= 3.0.0)

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a549_dex_downreg	<i>A549 Downregulated Genes (Dex)</i>
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Description

Example gene set of downregulated (repressed) genes in A549 cells after dexamethasone treatment. To keep the dataset small and suitable for examples and tests, only the first 15 downregulated gene symbols are included here.

Usage

```
a549_dex_downreg
```

Format

A character vector of length 15, containing HGNC gene symbols.

Details

The full list of differentially expressed genes (activated and repressed) is provided as Supplementary Table S3 in Tav *et al.* (2023). The raw Excel file can be downloaded directly from *Frontiers in Genetics*: https://www.frontiersin.org/api/v4/articles/1237092/file/Table_3.XLSX/1237092_supplementary-materials_tables_3_xlsx/1.

In this package, we subset the data to only the first 15 repressed genes, which are stored in the object a549_dex_downreg.

Source

Supplementary Table S3 from Tav *et al.* (2023).

References

Tav C, Fournier É, Fournier M, Khadangi F, Baguette A, Côté MC, Silveira MAD, Bérubé-Simard F-A, Bourque G, Droit A, Bilodeau S (2023). "Glucocorticoid stimulation induces regionalized gene responses within topologically associating domains." *Frontiers in Genetics*. doi:10.3389/fgene.2023.1237092

Examples

```
# Load dataset
data(a549_dex_downreg)
a549_dex_downreg
```

displayTopN

Print the top-n rows for each ChEA3 collection

Description

Print the top-n rows for each ChEA3 collection

Usage

```
displayTopN(
  results,
  n = 10,
  columns = c("Rank", "TF", "Scaled Rank", "Set_name", "Intersect", "Score",
             "FET p-value", "FDR", "Odds Ratio")
)
```

Arguments

results	A named list of data frames (the output of queryChEA3()).
n	Number of rows to show per table (default: 10).
columns	Optional character vector of column names to display (keeps intersection with what's present in each data frame).

Value

(Invisibly) a named list of data frames, each truncated to the first n rows (and columns if provided).

Examples

```
genes <- c("TP53", "MYC", "STAT3", "FOXO1", "BRCA1")
results <- queryChEA3(genes, verbose = FALSE)

# Display top 10 TFs from each collection
displayTopN(results)

# Display only top 5 with specific columns
displayTopN(results, n = 5, columns = c("Rank", "TF", "Score", "FDR"))
```

 exportResults

Export rChEA3 Results to Excel

Description

Write a rChEA3 results object (named list of data frames, one per collection) to an Excel workbook, with one sheet per collection.

Usage

```
exportResults(
  results,
  output_dir,
  output_file = "rChEA3_results",
  with_date = TRUE,
  verbose = TRUE
)
```

Arguments

results	A named list of data frames (e.g., the return of queryChEA3()), where each element corresponds to a ChEA3 collection (e.g., "Integrated-meanRank", "ENCODE-ChIP-seq", etc.). A single data frame is also accepted and will be written to one sheet.
output_dir	A string specifying the output directory. This parameter is required and has no default.
output_file	Base file name (without extension). Default: "rChEA3_results".
with_date	Logical; if TRUE, prepend today's date (ISO, YYYY-MM-DD) to the file name. Default: TRUE.
verbose	Logical; if TRUE, print the saved path. Default: TRUE.

Value

(Invisibly) the full path to the saved .xlsx file.

Examples

```
data(a549_dex_downreg)
results <- queryChEA3(genes = a549_dex_downreg, query_name = "test_a549_dex_downreg")
exportResults(results,
  output_dir = tempdir(),
  output_file = "rChEA3_results_a549_dex_downreg.xlsx")
```

queryChEA3

Query ChEA3 API for TF enrichment

Description

Sends a gene list to the ChEA3 web service to identify enriched transcription factors using multiple evidence sources. The gene list should consist of HGNC-approved gene symbols.

Usage

```
queryChEA3(
  genes,
  query_name = "rChEA3_query",
  verbose = TRUE,
  url = "https://maayanlab.cloud/chea3/api/enrich/"
)
```

Arguments

genes	Character vector of HGNC gene symbols.
query_name	Optional query name (default: "rChEA3_query").
verbose	Logical; if TRUE, print a grouped summary of available result collections (default: TRUE).
url	Character; full URL of the ChEA3 enrichment endpoint. Defaults to the public API at "https://maayanlab.cloud/chea3/api/enrich/". Override this to point at a local or self-hosted ChEA3 instance (see https://github.com/MaayanLab/chea3). The URL must include the full enrich/ path.

Value

A named list of data frames. Each element corresponds to a ChEA3 collection and contains an enrichment table with transcription factors and their statistics. The expected names are: c("Integrated-meanRank", "Integrated-topRank", "GTEx-Coexpression", "ARCHS4-Coexpression", "ENCODE-ChIP-seq", "ReMap-ChIP-seq", "Literature-ChIP-seq", "Enrichr-Queries").

Examples

```
results <- queryChEA3(c("SMAD9", "FOXO1", "MYC", "STAT1", "STAT3", "SMAD3"))
names(results)
head(results[["Integrated--meanRank"]])

# Querying a local ChEA3 server
# results <- queryChEA3(
#   c("SMAD9", "FOXO1", "MYC"),
#   url = "http://localhost:8080/chea3/api/enrich/"
# )
```

`saveViz`*Save a Visualization to File (PDF, PNG, or SVG)*

Description

This function saves a visualization object to a file in the specified format and directory. It supports visualizations generated by `chea3_visualizeRank()`, `ggplot2`, or any other plot object that can be rendered using `print()` inside a graphics device. Optionally, the current date (stored in the `today` variable) can be prepended to the filename.

Usage

```
saveViz(  
  viz,  
  output_dir,  
  output_file = "figure_rChEA3",  
  format = "pdf",  
  with_date = TRUE,  
  width = 8,  
  height = 5,  
  resolution = 300,  
  verbose = TRUE  
)
```

Arguments

<code>viz</code>	A visualization object typically created by <code>visualizeRank()</code> , but can also be a <code>ggplot2</code> plot or any other plot object printable with <code>print()</code> .
<code>output_dir</code>	A string specifying the output directory. This parameter is required and has no default.
<code>output_file</code>	A string specifying the base filename (without extension). Defaults to <code>"viz_rChEA3"</code> .
<code>format</code>	Output format. One of <code>"pdf"</code> , <code>"png"</code> , or <code>"svg"</code> . Defaults to <code>"pdf"</code> .
<code>with_date</code>	Logical (default <code>TRUE</code>). Whether to prepend the current date (from <code>today</code>) to the filename.
<code>width</code>	Width of the output file in inches. Default is 8.
<code>height</code>	Height of the output file in inches. Default is 5.
<code>resolution</code>	Resolution in DPI (only used for PNG). Default is 300.
<code>verbose</code>	Logical. If <code>TRUE</code> , print a message with the saved path. Default <code>TRUE</code> .

Value

The visualization is saved to a file on disk. Invisibly returns the full path to the saved file.

Examples

```
genes <- c("TP53", "MYC", "STAT3")
results <- queryChEA3(genes, verbose = FALSE)
meanRank_res <- results[["Integrated--meanRank"]]

# Create visualization
viz <- visualizeRank(meanRank_res)

# Save as PDF
saveViz(viz, output_dir = tempdir(), output_file = "chea3_results")

# Save as PNG with custom dimensions
saveViz(viz, output_dir = tempdir(), output_file = "chea3_results",
        format = "png", width = 10, height = 6)
```

today

Today's Date at Package Load Time

Description

This variable stores the current date (in "yyyymmdd" format) at the time the package is loaded. It is useful for reproducible filenames (e.g., in `saveViz()`), and is automatically set when the package is attached.

Usage

```
today
```

Format

A character string (e.g., "20250908").

Examples

```
# Print the date stored at package load
library(rChEA3)
today

# Use it in a filename
paste0(today, "_rChEA3_plot_meanRank.pdf")
```

visualizeRank	<i>Visualize top transcription factors (TFs) from ChEA3 results</i>
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Description

Create a bar plot of the most significant transcription factors from a ChEA3 result table. The y-axis can be based on FDR, FET p-value, or Score (for integrated results). Bars are ordered by rank (Rank = 1 at the top).

Usage

```
visualizeRank(
  df_result,
  y_metric = c("auto", "FDR", "FET p-value", "Score"),
  fdr_threshold = 0.05,
  p_threshold = 0.05,
  query_name = "myGeneList",
  title_plot = "rChEA3 results (transcription factor enrichment analysis)",
  top_n = 10,
  fill_color = "#7AAACE"
)
```

Arguments

df_result	A ChEA3 result data frame. Must contain at least columns: <ul style="list-style-type: none"> • TF (transcription factor symbol), • Rank (integer rank). Optionally: FDR, FET p-value, Score.
y_metric	Character; which metric to use on the y-axis. One of: <ul style="list-style-type: none"> • "auto" (default): use FDR if present, otherwise FET p-value, otherwise Score. • "FDR": use FDR (requires FDR column). • "FET p-value": use Fisher's exact test p-value (requires FET p-value column). • "Score": use Score (used in integrated meanRank/topRank).
fdr_threshold	Numeric; FDR cutoff for significance (default 0.05). Used only if y_metric = "FDR".
p_threshold	Numeric; p-value cutoff for significance (default 0.05). Used only if y_metric = "FET p-value".
query_name	Character; name of the input gene set, shown in the subtitle (default myGeneList)
title_plot	Character; main plot title (default rChEA3 results (transcription factor enrichment analysis))
top_n	Integer; number of TFs to display (default 10). The subtitle reports the total number of significant TFs, while only the top_n by rank are plotted.
fill_color	Character; fill color of the bars (default "#7AAACE").

Details

The plot subtitle automatically reports the number of *significant TFs* (after filtering by `fdr_threshold` or `p_threshold` when applicable), while `top_n` controls how many of those TFs are displayed. For integrated collections (Mean Rank and Top Rank), the subtitle shows a descriptive label instead of individual library names.

Value

A ggplot object.

Examples

```
# Example with integrated meanRank results
genes <- c("STAT3", "RELA", "MYC", "FOXO1", "TP53")
results <- queryChEA3(genes, verbose = FALSE)
meanRank_res <- results[["Integrated--meanRank"]]
visualizeRank(meanRank_res, y_metric = "Score", top_n = 15)

# Example with ChIP-seq results (FET p-value-based)
chip_res <- results[["ENCODE--ChIP-seq"]]
visualizeRank(chip_res, y_metric = "FET p-value")
```

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