

Package ‘genefindr’

August 1, 2026

Title Rapid Gene Characterization Using Public Genomic Databases

Version 1.1.0

Description A user-friendly interface for characterizing gene function by disease type and tissue site, integrating curated data from publicly available genomic and proteomic databases to support candidate gene prioritization in experimental workflows.

Depends R (>= 4.1.0)

License GPL-3

Encoding UTF-8

RoxygenNote 8.0.0

Imports httr2, gtexr, ggplot2

URL <https://github.com/martincyd/genefindr>

BugReports <https://github.com/martincyd/genefindr/issues>

Suggests knitr, rmarkdown, spelling, DESeq2, S4Vectors, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

Author Cydnie Martin [aut, cre]

Maintainer Cydnie Martin <martincydenise@gmail.com>

Repository CRAN

Date/Publication 2026-08-01 18:50:02 UTC

Contents

findr	2
findr_from_deseq	2
findr_multi	4
findr_plot_genes	4

findr_plot_heatmap	5
findr_plot_sites	6
findr_sites_table	6

Index	8
--------------	----------

findr	<i>Characterize a gene using public genomic databases</i>
-------	---

Description

Characterize a gene using public genomic databases

Usage

```
findr(gene, disease = NULL, site = NULL)
```

Arguments

gene	Character. Gene symbol (e.g. "TP53")
disease	Character. Disease context (e.g. "alzheimer")
site	Character. Cancer site (e.g. "breast", "lung"). Can be a vector for multi-site comparison.

Value

Invisibly returns a data frame of results

Examples

```
findr("TP53", site = "breast")
```

findr_from_deseq	<i>Characterize top differentially expressed genes from a DESeq2 results object</i>
------------------	---

Description

Characterize top differentially expressed genes from a DESeq2 results object

Usage

```
findr_from_deseq(  
  deseql_results,  
  site = NULL,  
  disease = NULL,  
  n_top = 20,  
  padj_cutoff = 0.05,  
  min_lfc = 1,  
  direction = "both"  
)
```

Arguments

deseql_results	A DESeqResults object from DESeq2::results()
site	Character. Cancer site (e.g. "breast", "lung")
disease	Character. Disease context for non-cancer queries
n_top	Integer. Number of top genes to characterize (default 20)
padj_cutoff	Numeric. Adjusted p-value cutoff (default 0.05)
min_lfc	Numeric. Minimum absolute log2 fold change (default 1.0)
direction	Character. "up", "down", or "both" (default "both")

Value

A data frame of gene characterization results

Examples

```
library(DESeq2)  
fake_res <- data.frame(  
  baseMean = c(100, 200, 150),  
  log2FoldChange = c(2.5, -1.8, 3.1),  
  lfcSE = c(0.3, 0.4, 0.3),  
  stat = c(8.3, -4.5, 10.3),  
  pvalue = c(0.0001, 0.001, 0.00001),  
  padj = c(0.001, 0.01, 0.0001),  
  row.names = c("TP53", "BRCA1", "EGFR")  
)  
fake_deseq <- DESeq2::DESeqResults(S4Vectors::DataFrame(fake_res))  
findr_from_deseq(fake_deseq, site = "breast", n_top = 3)
```

findr_multi	<i>Characterize multiple genes using public genomic databases</i>
-------------	---

Description

Characterize multiple genes using public genomic databases

Usage

```
findr_multi(genes, disease = NULL, site = NULL, output = "print")
```

Arguments

genes	Character vector. Gene symbols (e.g. c("TP53", "BRCA1"))
disease	Character. Disease context
site	Character. Cancer site
output	Character. "print" or "table"

Value

Invisibly returns a data frame of results

Examples

```
findr_multi(c("TP53", "BRCA1"), site = "breast")
```

findr_plot_genes	<i>Plot gene association scores for multiple genes in a single disease context</i>
------------------	--

Description

Plot gene association scores for multiple genes in a single disease context

Usage

```
findr_plot_genes(results, title = NULL)
```

Arguments

results	A data frame returned by findr_multi() with output = "table"
title	Optional plot title

Value

A ggplot2 object

Examples

```
results <- findr_multi(c("TP53", "BRCA1", "MYC"), site = "breast", output = "table")
findr_plot_genes(results)
```

findr_plot_heatmap	<i>Plot a heatmap of gene association scores across multiple cancer sites</i>
--------------------	---

Description

Plot a heatmap of gene association scores across multiple cancer sites

Usage

```
findr_plot_heatmap(results, title = NULL)
```

Arguments

results	A data frame returned by findr_multi() with output = "table"
title	Optional plot title

Value

A ggplot2 object

Examples

```
if (interactive()) {
  results <- findr_multi(c("TP53", "BRCA1", "EGFR"),
                        site = c("breast", "lung", "colon"),
                        output = "table")
  findr_plot_heatmap(results)
}
```

findr_plot_sites	<i>Plot association scores for a single gene across multiple disease sites</i>
------------------	--

Description

Plot association scores for a single gene across multiple disease sites

Usage

```
findr_plot_sites(results, title = NULL)
```

Arguments

results	A data frame returned by findr_multi() with output = "table"
title	Optional plot title

Value

A ggplot2 object

Examples

```
if (interactive()) {  
  results <- findr_sites_table("TP53", sites = c("breast", "lung"))  
  findr_plot_sites(results)  
}
```

findr_sites_table	<i>Get gene characterization data across multiple cancer sites as a table</i>
-------------------	---

Description

Get gene characterization data across multiple cancer sites as a table

Usage

```
findr_sites_table(gene, sites)
```

Arguments

gene	Character. Gene symbol (e.g. "TP53")
sites	Character vector of cancer sites (e.g. c("breast", "lung", "colon"))

Value

A data frame with results for each site

Examples

```
results <- findr_sites_table("TP53", sites = c("breast", "lung"))  
findr_plot_sites(results)
```

Index

`findr`, [2](#)
`findr_from_deseq`, [2](#)
`findr_multi`, [4](#)
`findr_plot_genes`, [4](#)
`findr_plot_heatmap`, [5](#)
`findr_plot_sites`, [6](#)
`findr_sites_table`, [6](#)