Package ‘rDGIdb’

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Type Package
Title R Wrapper for DGIdb
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Description The rDGIdb package provides a wrapper for the Drug Gene Interaction Database (DGIdb). For simplicity, the wrapper query function and output resembles the user interface and results format provided on the DGIdb website (https://www.dgidb.org/).
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LazyData TRUE
Imports jsonlite,httr,methods,graphics
biocViews Software,ResearchField,Pharmacogenetics,Pharmacogenomics,FunctionalGenomics,WorkflowStep,Annotation
VignetteBuilder knitr
Suggests BiocStyle,knitr,testthat
Date 2020
NeedsCompilation no
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git_branch RELEASE_3_19
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plotInteractionsBySource

Description

Creates a plot to visualize the number of interactions per source.

Usage

plotInteractionsBySource(queryResult, ...)

Arguments

queryResult A rDGIdbResult object obtained from queryDGIdb.
... Other arguments passed to barplot.

Value

A plot is created on the current graphics device.

Author(s)

Thomas Thurnherr <thomas.thurnherr@gmail.com>

References


See Also

rDGIdbResult, queryDGIdb, rDGIdbFilters

Examples

queryResult <- queryDGIdb('KRAS')
plotInteractionsBySource(queryResult)
queryDGIdb

Description
Provides an interface to query DGIdb from within R using the DGIdb API. The function is implemented to reflect as good as possible the web-interface.

Usage
queryDGIdb(genes, 
  sourceDatabases = NULL, 
  geneCategories = NULL, 
  interactionTypes = NULL)

Arguments
- genes: A character vector of genes for which drug interactions are queried.
- sourceDatabases: A character vector of source databases to be queried. To query all available databases, skip argument or use NULL. To see available options, type sourceDatabases().
- geneCategories: A character vector of gene categories to be queried. To query for all gene categories, skip argument or use NULL. To see available options, type geneCategories().
- interactionTypes: A character vector of interaction types to be queried. To query for all interaction types, skip argument or use NULL. To see available options, type interactionTypes().

Details
Only the first argument (genes) is required, all other arguments are optional. When optional arguments are not provided, the query considers all available possibilities for optional arguments: sourceDatabases, geneCategories, and interactionTypes.

Value
A S4 object of type rDGIdbResult.

Author(s)
Thomas Thurnherr <thomas.thurnherr@gmail.com>

References
See Also

`rDGIdbResult, rDGIdbFilters, plotInteractionsBySource`

Examples

```r
genes <- c("XYZA", "TNF", "IL6", "IL8")
result <- queryDGIdb(genes = genes)

result <- queryDGIdb(genes = genes,
                      sourceDatabases = c("MyCancerGenome", "TEND", "TTD"),
                      geneCategories = "CELL SURFACE",
                      interactionTypes = c("activator", "inhibitor"))
```

---

**rDGIdbFilters**

*Filter options for rDGIdb queries.*

**Description**

The gene categories, interaction types, and source databases available to filter queries with `queryDGIdb`.

**Usage**

```r
geneCategories()

interactionTypes()

sourceDatabases()
```

**Value**

- `geneCategories` returns a character vector of available gene categories which can be used to filter DGIdb queries with `queryDGIdb`.
- `interactionTypes` returns a character vector of available interaction types which can be used to filter DGIdb queries with `queryDGIdb`.
- `sourceDatabases` returns a character vector of available source databases which can be used to filter DGIdb queries with `queryDGIdb`.

**Author(s)**

Thomas Thurnherr <thomas.thurnherr@gmail.com>

**References**

See Also

queryDGIdb, rDGIdbResult, plotInteractionsBySource

Examples

geneCategories()
interactionTypes()
sourceDatabases()
res <- queryDGIdb(genes = "AP1",
                 interactionTypes = NULL,
                 geneCategories = NULL,
                 sourceDatabases = NULL)

rDGIdbResult

Result object of a rDGIdb query

Description

S4 helper functions to access DGIdb results, formatted in a similar way as result tables on the DGIdb web interface.

Usage

## S4 method for signature 'rDGIdbResult'
resultSummary(object)

## S4 method for signature 'rDGIdbResult'
detailedResults(object)

## S4 method for signature 'rDGIdbResult'
byGene(object)

## S4 method for signature 'rDGIdbResult'
searchTermSummary(object)

Arguments

object

A rDGIdbResult object returned by queryDGIdb.

Value

resultSummary returns a data.frame that summarizes drug-gene interactions by the source(s) that reported them.
detailedResult returns a data.frame with search terms matching exactly one gene that has one or more drug interactions.
byGene returns a data.frame with drug interaction count and druggable categories associated with each gene.
searchTermSummary returns a data.frame that summarizes the attempt to map gene names supplied by the user to gene records in DGIdb.

Author(s)
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References

See Also
queryDGIdb, rDGIdbFilters, plotInteractionsBySource

Examples
genes <- c("XYZA", "TNF", "IL6", "IL8")
result <- queryDGIdb(genes = genes)
resultSummary(result)
detailedResults(result)
byGene(result)
searchTermSummary(result)

<table>
<thead>
<tr>
<th>resourceVersions</th>
<th>Version numbers of DGIdb resources</th>
</tr>
</thead>
</table>

Description
Prints the version numbers of all DGIdb resources.

Usage
resourceVersions()

Value
Returns a data.frame with two columns, the name and the version numbers of the resources.

Author(s)
Thomas Thurnherr <thomas.thurnherr@gmail.com>

See Also
http://dgidb.genome.wustl.edu/sources
Examples

    resourceVersions()
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