Package ‘rDGIdb’

January 31, 2017

Type Package
Title R Wrapper for DGIdb
Version 1.0.0
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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 (http://dgidb.genome.wustl.edu/).
License MIT + file LICENSE
LazyData TRUE
Imports jsonlite,httr,methods,graphics
biocViews Software,ResearchField,Pharmacogenetics,Pharmacogenomics,FunctionalGenomics,WorkflowStep,Annotation
VignetteBuilder knitr
Suggests BiocStyle,knitr,testthat
Date 2016
NeedsCompilation no

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plotInteractionsBySource

Interactions by source

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)

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References


See Also

rDGIdbResult, queryDGIdb, rDGIdbFilters

Examples

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

**Query DGIdb using R**

**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**

```r
queryDGIdb(genes, 
sourceDatabases = c("CIViC", "CancerCommons", "ChEMBL", 
"ClearityFoundationBiomarkers", "ClearityFoundationClinicalTrial", 
"DoCM", "DrugBank", "GuideToPharmacologyInteractions", 
"MyCancerGenome", "MyCancerGenomeClinicalTrial", "PharmGKB", "TALC", 
"TEND", "TTD", "TdgClinicalTrial"), 
geneCategories = c("abc transporter", "b30_2 spry domain", 
"cell surface", "clinically actionable", "cytochrome p450", 
"DNA directed RNA polymerase", "DNA repair", "drug metabolism", 
"drug resistance", "druggable genome", "exchanger", 
"external side of plasma membrane", "fibrinogen", 
"g protein coupled receptor", "growth factor", "histone modification", 
"hormone activity", "ion channel", "kinase", "lipase", "lipid kinase", 
"methyl transferase", "myotubularin related protein phosphatase", 
"neutral zinc metallopeptidase", "nuclear hormone receptor", 
"phosphatidylinositol 3 kinase", "phospholipase", "protease", 
"protease inhibitor", "protein phosphatase", "pten family", 
"RNA directed DNA polymerase", "serine threonine kinase", 
"short chain dehydrogenase reductase", "thioredoxin", 
"transcription factor binding", "transcription factor complex", 
"transporter", "tumor suppressor", "tyrosine kinase", "unknown"), 
interactionTypes = c("activator", "adduct", "agonist", 
"allosteric modulator", "antagonist", "antibody", "antisense", 
"antisense oligonucleotide", "binder", "blocker", "chaperone", 
"cleavage", "cofactor", "competitive", "immunotherapy", "inducer", 
"inhibitor", "inhibitory allosteric modulator", "inverse agonist", 
"ligand", "modulator", "multitarget", "n/a", "negative modulator", 
"other/unknown", "partial agonist", "partial antagonist", 
"positive allosteric modulator", "potentiator", "product of", 
"stimulator", "suppressor", "vaccine")
)
```

**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 `sourceDatabases()`.
- **geneCategories**: A character vector of gene categories to be queried. To query for all gene categories, skip argument or use `geneCategories()`.
interactionTypes

A character vector of interaction types to be queried. To query for all interaction types, skip argument or use 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)

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References


See Also

rDGIdbResult, rDGIdbFilters, plotInteractionsBySource

Examples

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"))
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)

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References


See Also

`queryDGIdb`, `rDGIdbResult`, `plotInteractionsBySource`

Examples

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

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.

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### References


### See Also

`queryDGIdb`, `rDGIdbFilters`, `plotInteractionsBySource`

### Examples

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

### resourceVersion

<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.

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See Also

http://dgidb.genome.wustl.edu/sources

Examples

resourceVersions()
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