Package ‘rDGIdb’

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Type Package

Title R Wrapper for DGIdb

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Author Thomas Thurnherr, Franziska Singer, Daniel J. Stekhoven, and Niko Beerenwinkel

Maintainer Thomas Thurnherr <thomas.thurnherr@bsse.ethz.ch>

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/).

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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

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NeedsCompilation no

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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@bsse.ethz.ch>

References


See Also

rDGIdbResult, queryDGIdb, rDGIdbFilters

Examples

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

Thomas Thurnherr <thomas.thurnherr@bsse.ethz.ch>

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)**

Thomas Thurnherr <thomas.thurnherr@bsse.ethz.ch>

**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**

```r
## 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)**

Thomas Thurnherr <thomas.thurnherr@bsse.ethz.ch>

**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)
```

<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.
resourceVersions

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@bsse.ethz.ch>

See Also

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

Examples

resourceVersions()
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