

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 (<http://dgidb.genome.wustl.edu/>).

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LazyData TRUE

Imports jsonlite,httr,methods,graphics

Collate rDGIdbResult.R queryDGIdb.R plotInteractionsBySource.R
resourceVersions.R

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

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)

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

References

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

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 the as good as possible the web-interface.

Usage

```
queryDGIdb(genes,
  sourceDatabases = c("CIViC", "CancerCommons", "ChEMBL",
    "ClarityFoundationBiomarkers", "ClarityFoundationClinicalTrial",
    "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

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

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"))
```

rDGIdbFilters

Filter options for rDGIdb queries.

Description

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

Usage

`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)

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References

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. Nucleic Acids Research. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

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.

Author(s)

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References

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

See Also

[queryDGIdb](#), [rDGIdbFilters](#), [plotInteractionsBySource](#)

Examples

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

resourceVersions

Version numbers of DGIdb resources

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@bsse.ethz.ch>

See Also

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

Examples

```
resourceVersions()
```

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