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

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

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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@gmail.com>

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 = 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

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)

Thomas Thurnherr <thomas.thurnherr@gmail.com>

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 = 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)

Thomas Thurnherr <thomas.thurnherr@gmail.com>

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@gmail.com>

See Also

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

Examples

```
resourceVersions()
```

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