Package 'webQueries'

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Type Package

Title NCBI Queries for Gene and Protein Annotations.

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Description Retrieve gene and protein annotations from NCBI,
given HUGO symbols or ids (entrezgene and Uniprot are supported).

License Artistic-2.0

biocViews Annotation,GenomeAnnotation

Imports XML,Hmisc

Suggests RUnit,knitr,BiocGenerics

VignetteBuilder knitr

R topics documented:

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webQueries-package   *Querying NCBI for Gene and/or Protein Annotations.*

Description

This function simply constructs an appropriate link to query the NCBI databases, using E-utilities.
See note. HUGO symbols or official ids are supported.
Information is extracted from the returned xml file, using xpathApply from XLM package.

Details

Package:	webQueries
Type:	Package
Version:	0.98.0
Date:	2015-03-15
License:	Artistic-2.0

This function simply constructs an appropriate link to query the NCBI databases, using E-utilities. Information is extracted from the returned xml file.

Note

See [Introduction to the E-utilities](#) for more details.
runQuery only supports queries sent to "gene", "protein" , and "snp" databases.

Author(s)

Frederic Commo <frederic.commo@gustaveroussy.fr>

Examples

```
## Not run:
# Querying the gene database using HUGO symbol or entrezgene id
runQuery("erbb2", "gene")
runQuery(2064, "gene", bySymbol = FALSE)

# Querying the Protein database
runQuery("erbb2", "protein")
runQuery("P04626", "protein", bySymbol = FALSE)

# Querying the SNP database
runQuery("erbb2", "snp")
runQuery(2064, "snp", bySymbol = FALSE)

# Multiple queries
ids <- c("egfr", "erbb2", "fgfr1")
annots <- lapply(ids, function(id) runQuery(id, "gene") )
annots <- do.call(rbind, annots)
annots

## End(Not run)
```

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runQuery   *Retrieve NCBI annotations through Web Queries*

Description

This function simply constructs an appropriate link to query the NCBI databases, using E-utilities. See note. HUGO symbols or official ids are supported.
Information is extracted from the returned xml file, using [xpathApply](#) from XLM package.

Usage

```
runQuery(symbol, db, bySymbol = TRUE, ktries = 10)
```

Arguments

symbol	: character or numeric. geneId can be either a valid HUGO symbol (not case sensitive), or an entrezgene id. See note.
db	: string. The NCBI database to query. "gene", "protein", and "snp" are supported.
bySymbol	: logical. Must be set to TRUE when a HUGO symbols is used.
ktries	: numeric. The number of retries when connexion errors occur. Default is 10.

Value

A vector of values.

Note

See Introduction to the E-utilities for more details.
runQuery only supports queries sent to "gene", "protein" , and "snp" databases.

Author(s)

Frederic Commo

Examples

```
# Querying the gene database using HUGO symbol or entrezgene id
## Not run:
runQuery("erbb2", "gene")
runQuery(2064, "gene", bySymbol = FALSE)

# Querying the Protein database
runQuery("erbb2", "protein")
runQuery("P04626", "protein", bySymbol = FALSE)

# Querying the SNP database
runQuery("erbb2", "snp")
runQuery(2064, "snp", bySymbol = FALSE)

# Multiple queries
ids <- c("egfr", "erbb2", "fgfr1")
annots <- lapply(ids, function(id) runQuery(id, "gene") )
annots <- do.call(rbind, annots)
annots

## End(Not run)
```

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