Package ‘SNPediaR’

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Title  Query data from SNPedia
Version  1.0.0
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Description  SNPediaR provides some tools for downloading and parsing data from the SNPedia web site <http://www.snpedia.com>. The implemented functions allow users to import the wiki text available in SNPedia pages and to extract the most relevant information out of them. If some information in the downloaded pages is not automatically processed by the library functions, users can easily implement their own parsers to access it in an efficient way.

Depends  R (>= 3.0.0)
License  GPL-2
LazyData  true

URL  https://github.com/genometra/SNPediaR

BugReports  https://github.com/genometra/SNPediaR/issues

Suggests  BiocStyle, knitr, rmarkdown, testthat

VignetteBuilder  knitr

Imports  RCurl, jsonlite

biocViews  SNP, VariantAnnotation

RoxygenNote  5.0.1

NeedsCompilation  no

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Extract information from downloaded SNPedia pages.

Description
SNPedia pages usually have a table in the right hand side which summarizes most relevant information in the page. This functions help extracting this kind of information for the given tags or rows.

Usage
\[
\text{extractTags} \ (x, \ tags) \\
\text{extractSnpTags} \ (x, \ tags) \\
\text{extractGenotypeTags} \ (x, \ tags)
\]

Arguments
- **x** a wiki page (single character vector)
- **tags** character vector of tags (row names) to be collected.

Details

extractTags is a general purpose function aimed to work at any page. extractSnpTags calls extractTags with a set of predefined tags suitable for SNP pages. extractGenotypeTags does the same for genotype pages.

This functions take a character vector of length one but return a vector with as many values as the tag list provided. They are devised to be used with sapply functions.

Notice that in SNPedia not all information presented in the HTML table is available in the JSON format retrieved by the R package. Risk information for instance needs to be collected from the genotype pages as it is not available in the JSON version of the SNP pages.

Value
A character vector with the value of each of the tags if available in the page and NA otherwise.

See Also
getPages, getCategoryElements

Examples

```r
res <- getPages (c("Rs1234", "Rs53576"))
t (sapply (res, extractSnpTags))

extractTags (res[[1]], tags = c("rsid", "Chromosome", "position"))

res <- getPages (c("Rs1234(A;A)", "Rs1234(A;C)","Rs1234(C;C)"))
t (sapply (res, extractGenotypeTags))

getPages (c("Rs1234(A;A)", "Rs1234(A;C)","Rs1234(C;C)"),
             wikiParseFunction = extractGenotypeTags)
```
getCategoryElements

getPages (c("Rs1234(A;A)" , "Rs1234(A;C)" , "Rs1234(C;C)") ,
wikiParseFunction = extractGenotypeTags,
tags = c("rsid", "allele1", "allele2"))

getDescription

Get all elements of a given category

Description

A function to get all page names of SNPedia tagged under the indicated category.

Usage

gETCHCATEGORYELEMENTS(category, verbose = FALSE, includeTemplates = FALSE,
limit, baseURL, format, query, continue)

Arguments

category The category to be used. Just one at a time.
verbose If TRUE some messages are provided.
includeTemplates If TRUE page templates are kept in the output.
limit The maximum number of items to be queried at a time.
baseURL SNPedia boots URL.
format Downloading format. Currently just JSON is available.
query The query to be iterated.
continue To be used in multi-page queries.

Details

A list of all available categories may be found at:
http://www.snpedia.com/index.php/Special:Categories

Most used categories are:

- Is_a_medical_condition
- Is_a_medical_condition
- Is_a_medicine
- Is_a_topic
- Is_a_snp
- In_dbSNP
- Is_a_genotype

Some template pages are included in their corresponding category. By default those will be removed. Set includeTemplates to TRUE if you want to keep them.

Parameters other than category and verbose are not intended for standard users.
getPages

Value
A character vector containing the names of the pages under the required category.

See Also
getPages, extractTags

Examples
res <- getCategoryElements(category = "Is_a_medical_condition")
head(res)

## Not run:
res <- getCategoryElements(category = "Is_a_snp")
## End(Not run)

getPages

Description
A function to download the (wiki) text content of a list of SNPedia pages.

Usage
getPages(titles, verbose = FALSE, limit = 50,
  wikiParseFunction = identity, baseURL, format, query, ...)

Arguments
titles Titles of the pages to be downloaded.
verbose If TRUE some messages are provided.
limit The maximum number of items to be queried at a time.
wikiParseFunction Function to be used to parse the wiki code at downloading time. Default is identity so the raw wiki text is provided.
baseURL SNPedia boots URL.
format Downloading format. Currently just JSON is available.
query The query to be iterated.
... any parameter to be pasted to the wikiParseFunction.

Details
JSON format is parsed to extract the wiki text returned by the function.
If the wikiParseFunction parameter is provided, parsing of the pages is done internally once each batch of pages is downloaded.
Pages do not need to be of the same class... but users may be aware of the type of pages they are queering, moreover when using their own wikiParseFunction.
Parameters baseURL, format and query are not intended for end users.
**Value**

A list containing the wiki content of the required pages or the formatted objects returned by the `wikiParseFunction` applied to each page.

**See Also**

`extractTags`, `getCategoryElements`

**Examples**

```r
res <- getPages(titles = "Rs1234")
res

res <- getPages(titles = c("Rs1234", "Rs1234(A;A)", "Rs1234(A;C)"))
res

myfun <- function(x) substring(x, 1, 5)
lapply(res, myfun)
res <- getPages(titles = c("Rs1234", "Rs1234(A;A)", "Rs1234(A;C)"),
wikiParseFunction = myfun)
res
```
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