

Package ‘haploR’

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Type Package

Title Query 'HaploReg', 'RegulomeDB', 'LDlink'

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Description A set of utilities for querying 'HaploReg' <<http://archive.broadinstitute.org/mammals/haploreg/haploreg.php>>, 'RegulomeDB' <<http://www.regulomedb.org>>, and LDlink <<https://analysistools.nci.nih.gov/LDlink>> web-based tools. The package connects to 'HaploReg', 'RegulomeDB' and 'LDlink', searches and downloads results, without opening web pages, directly from R environment. Results are stored in a data frame that can be directly used in various kinds of downstream analyses.

RoxygenNote 6.0.1

Suggests knitr, rmarkdown, openxlsx

VignetteBuilder knitr

Imports httr, XML, tibble, RUnit, plyr, DT

Depends R (>= 3.4.0)

Encoding UTF-8

License GPL-3

NeedsCompilation no

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R topics documented:

as.num 2

getExtendedView	2
getStudyList	3
LDlink.LDmatrix	4
makeStylishLDmatrix	4
queryHaploreg	5
queryRegulome	6

Index	8
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as.num	<i>Converts vector of strings to numeric vector</i>
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Description

Converts vector of strings to numeric vector

Usage

```
as.num(x, na.strings = "NA")
```

Arguments

x	Input vector of strings.
na.strings	A string which represents NA. Default: "NA"

Value

A numeric vector

Examples

```
library(haploR)
as.num(c("1", "2", "X"), na.strings="X")
```

getExtendedView	<i>This function queries HaploReg web-based tool in order to Extended view for SNP of interest</i>
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Description

This function queries HaploReg web-based tool in order to Extended view for SNP of interest

Usage

```
getExtendedView(snp, url = Haploreg.settings[["extended.view.url"]])
```

Arguments

snp A SNP of interest.

url A url to HaploReg. Default: <http://pubs.broadinstitute.org/mammals/haploreg/detail_v4.1.php?query=&
Previously was: <[http://archive.broadinstitute.org/mammals/haploreg/detail_v4.1.php?query=&id="](http://archive.broadinstitute.org/mammals/haploreg/detail_v4.1.php?query=&id=)>

Value

A list of tables t1, t2, ..., etc depending on information contained in HaploReg database.

Examples

```
tables <- getExtendedView(snp="rs10048158")
tables
```

getStudyList	<i>This function queries HaploReg web-based tool in order to see a list of GWAS.</i>
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Description

This function queries HaploReg web-based tool in order to see a list of GWAS.

Usage

```
getStudyList(url = Haploreg.settings[["study.url"]])
```

Arguments

url A url to HaploReg. Default: <<http://pubs.broadinstitute.org/mammals/haploreg/haploreg.php>>
Previously was: <<http://archive.broadinstitute.org/mammals/haploreg/haploreg.php>>

Value

A list of studies. Each study is itself a list of two: name, id.

Examples

```
studies <- getStudyList()
studies
```

LDlink.LDmatrix *This function queries HaploReg web-based tool and returns results.*

Description

This function queries HaploReg web-based tool and returns results.

Usage

```
LDlink.LDmatrix(snps, population = "ALL")
```

Arguments

snps A list of snps (a vector of rsIDs, or a file, one SNP per line).
 population A particular genetic population. Default: ALL.

Value

A list of three:
 (1) raw LD r2 matrix;
 (3) raw LD D-prime matrix

Examples

```
library(haploR)
data <- LDlink.LDmatrix(c("rs10048158", "rs4791078"))
head(data)
```

makeStylishLDmatrix *This function queries HaploReg web-based tool and returns results.*

Description

This function queries HaploReg web-based tool and returns results.

Usage

```
makeStylishLDmatrix(ldmat, haploreg.url = Haploreg.settings[["base.url"]])
```

Arguments

ldmat A LDmatrix in which the first column should contain rdIDs
 haploreg.url URL to HaploReg project. Default: <<https://pubs.broadinstitute.org/mammals/haploreg/haploreg.php>>

Value

colored (fancy) matrix with LD gradient (an object of classes datatables, htmlwidget)

Examples

```
library(haploR)
data <- LDlink.LDmatrix(c("rs10048158", "rs4791078"))
head(data)
makeStylishLDmatrix(data$matrix.r2)
```

queryHaploreg	<i>This function queries HaploReg web-based tool and returns results.</i>
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Description

This function queries HaploReg web-based tool and returns results.

Usage

```
queryHaploreg(query = NULL, file = NULL, study = NULL, ldThresh = 0.8,
  ldPop = "EUR", epi = "vanilla", cons = "siphy", genetypes = "gencode",
  url = Haploreg.settings[["base.url"]], timeout = 100,
  encoding = "UTF-8", querySNP = FALSE, fields = NULL, verbose = FALSE)
```

Arguments

query	Query (a vector of rsIDs).
file	A text file (one refSNP ID per line).
study	A particular study. See function getHaploRegStudyList(...). Default: NULL.
ldThresh	LD threshold, r2 (select NA to only show query variants). Default: 0.8.
ldPop	1000G Phase 1 population for LD calculation. Can be: "AFR", "AMR", "ASN". Default: "EUR".
epi	Source for epigenomes. Possible values: vanilla for ChromHMM (Core 15-state model); imputed for ChromHMM (25-state model using 12 imputed marks); methyl for H3K4me1/H3K4me3 peaks; acetyl for H3K27ac/H3K9ac peaks. Default: vanilla.
cons	Mammalian conservation algorithm. Possible values: gerp for GERP, siphy for SiPhy-omega, both for both. Default: siphy.
genetypes	Show position relative to. Possible values: gencode for Gencode genes; refseq for RefSeq genes; both for both. Default: gencode.
url	HaploReg url address. Default: <https://pubs.broadinstitute.org/mammals/haploreg/haploreg.php> Previously was: <http://archive.broadinstitute.org/mammals/haploreg/haploreg.php>
timeout	A timeout parameter for curl. Default: 100
encoding	sets the encoding for correct retrieval web-page content. Default: UTF-8

querySNP	A flag indicating to return query SNPs only. Default: FALSE
fields	A set of fields to extract. Refer to the package vignette for available fields. Default: All.
verbose	Verbosing output. Default: FALSE.

Value

A data frame (table) with results similar to HaploReg uses.

Examples

```
library(haploR)
data <- queryHaploreg(c("rs10048158", "rs4791078"))
head(data)
```

queryRegulome	<i>This function queries RegulomeDB www.regulomedb.org web-based tool and returns results in a data frame.</i>
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Description

This function queries RegulomeDB www.regulomedb.org web-based tool and returns results in a data frame.

Usage

```
queryRegulome(query = NULL, format = "full",
  url = "http://www.regulomedb.org/results", timeout = 100,
  check_bad_snps = TRUE, verbose = FALSE)
```

Arguments

query	Query (a vector of rsIDs).
format	An output format. Can be on of the following: full - plain text, bed - BED (Browser Extensible Data) format, see e.g. < https://genome.ucsc.edu/FAQ/FAQformat.html#format5.1 >, gff - GFF (General Feature Format), see e.g. < https://genome.ucsc.edu/FAQ/FAQformat.html#format3 > Only full is currently supported.
url	Regulome url address. Default: < http://www.regulomedb.org/results >
timeout	A timeout parameter for <code>httr::POST</code> . Default: 100
check_bad_snps	Checks if all SNPs are annotated. Default: TRUE
verbose	Verbosing output. Default: FALSE.

Value

A list of two: (1) a data frame (table) and (2) a list of bad SNP IDs. Bad SNP ID are those IDs that were not found in 1000 Genomes Phase 1 data

Examples

```
data <- queryRegulome(c("rs4791078","rs10048158"))  
head(data[["res.table"]])  
head(data[["bad.snp.id"]])
```

Index

`as.num`, [2](#)

`getExtendedView`, [2](#)

`getStudyList`, [3](#)

`LDlink.LDmatrix`, [4](#)

`makeStylishLDmatrix`, [4](#)

`queryHaploreg`, [5](#)

`queryRegulome`, [6](#)