Package ‘haploR’

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**Type**  Package

**Title**  Query 'HaploReg', 'RegulomeDB'

**Version**  4.0.4

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**Description**  A set of utilities for querying

- 'HaploReg' [https://pubs.broadinstitute.org/mammals/haploreg/haploreg.php],
- 'RegulomeDB' [https://www.regulomedb.org/regulome-search/]

web-based tools. The package connects to

'HaploReg', 'RegulomeDB' 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**  7.1.1

**Suggests**  knitr, rmarkdown,openxlsx

**VignetteBuilder**  knitr

**Imports**  httr,XML,tibble,RUnit,plyr,DT,RCurl,RJSONIO

**Depends**  R (>= 3.4.0)

**Encoding**  UTF-8

**License**  GPL-3

**NeedsCompilation**  no

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**Repository**  CRAN

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**R topics documented:**

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**as.num**

*Converts vector of strings to numeric vector*

**Description**

Converts vector of strings to numeric vector.

**Usage**

```r
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**

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

---

**getExtendedView**

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

**Description**

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

**Usage**

```r
getExtendedView(snp, url = HaploR.settings["extended.view.url"])
```
getStudyList

Arguments

snp A SNP of interest.

Value

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

Examples

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

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

Description

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

Usage

generateStudyList(url = Haploreg.settings[["study.url"]])

Arguments


Value

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

Examples

studies <- generateStudyList()
studies
queryHaploreg

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

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.
genotypes 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>
timeout A timeout parameter for curl. Default: 100
queryRegulome

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

Description

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

Usage

queryRegulome(
  query = NULL,
  genomeAssembly = "GRCh37",
  limit = 1000,
  timeout = 100
)

Arguments

query Query (a vector of rsIDs or exact one query region in rsid or like "chr1:39492461-39492462").

genomeAssembly Genome assembly built: can be GRCh37 (default) or GRCh38.

limit It controls how many variants will be queried and returned for a large region. It can be a number (1000 by default) or "all". Please note that large number or "all" may get yourself hurt because you could get timeout or may even crash the server.

timeout A timeout parameter for httr::GET. Default: 100
Value

a data frame (table) OR a list with the following items: - query_coordinates - features - regulome_score - variants - nearby_snps, - assembly

Examples

data <- queryRegulome(c("rs4791078","rs10048158"))
head(data)

regulomeSearch

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

Description

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

Usage

regulomeSearch(
  query = NULL,
  genomeAssembly = NULL,
  limit = 1000,
  timeout = 100
)

regulomeSummary(
  query = NULL,
  limit = 1000,
  genomeAssembly = NULL,
  timeout = 100
)

Arguments

query Query (a vector of rsIDs).

genomeAssembly Genome assembly built: can be GRCh37 or GRCh38

limit It controls how many variants will be queried and returned for a large region. It can be a number (1000 by default) or "all". Please note that large number or "all" may get yourself hurt because you could get timeout or may even crash the server.

timeout A timeout parameter for http::GET. Default: 100
Value

- guery_coordinates
- features
- regulome_score
- variants
- nearby_snps
- assembly

A data frame (table)

Examples

```r
data <- regulomeSearch("rs4791078")
head(data)
data <- regulomeSummary(c("rs4791078","rs10048158"))
head(data)
```
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