Package ‘haploR’

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Type Package

Title Query 'HaploReg', 'RegulomeDB'

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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,methods

Depends R (>= 3.4.0)

Encoding UTF-8

License GPL-3

NeedsCompilation no

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as.num  

Converts vector of strings to numeric vector

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

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

getExtendedView(snp, url = Haploreg.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

getStudyList

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

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

Arguments


Value

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

Examples

studies <- getStudyList()
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.

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>

timeout
A timeout parameter for curl. Default: 100
queryRegulome

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

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) with results similar to HaploReg uses.

Examples

```r
library(haploR)

data <- queryHaploreg(c("rs10048158","rs4791078"))
head(data)
```
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 httr::GET. Default: 100
Value

- query_coordinates
- features
- regulome_score
- variants
- nearby_snps
- assembly

a data frame (table)

Examples

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