Package ‘haploR’
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Type Package
Title Query ‘HaploReg’ and ‘RegulomeDB’
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Description A set of utilities for querying
 and ‘RegulomeDB’ <http://www.regulomedb.org> web-based tools. The package connects to
 ‘HaploReg’ or ‘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.
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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 = "http://archive.broadinstitute.org/mammals/haploreg/detail_v4.1.php?query=&id=")

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 = "http://archive.broadinstitute.org/mammals/haploreg/haploreg.php")

Arguments

Value

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

Examples

```r
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

```r
queryHaploreg(query = NULL, file = NULL, study = NULL, ldThresh = 0.8,
ldPop = "EUR", epi = "vanilla", cons = "siphy", genetypes = "gencode",
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()`.
- `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.
- `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.
queryRegulome

Description

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

Usage

```r
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. \url{https://genome.ucsc.edu/FAQ/FAQformat.html#format5.1}, gff - GFF (General Feature Format), see e.g. \url{https://genome.ucsc.edu/FAQ/FAQformat.html#format3}.
  Only full is currently supported.
- `url`: Regulome url address. Default: \url{http://www.regulomedb.org/results}
- `timeout`: A timeout parameter for curl. Default: 10
- `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

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