Package ‘haploR’

November 1, 2017

Type Package
Title Query ‘HaploReg’ and ‘RegulomeDB’
Version 1.6.2
Date 2017-10-31
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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.
RoxygenNote 6.0.1
Suggests knitr, rmarkdown,openxlsx
VignetteBuilder knitr
Imports httr,XML,tibble,RUnit,plyr
Depends R (>= 3.3.2)
Encoding UTF-8
License GPL-3
NeedsCompilation no
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Repository CRAN
Date/Publication 2017-10-31 23:30:02 UTC

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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

queryHaploreg

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

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

Examples

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

queryRegulome

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

Description
This function queries RegulomeDB at 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 = 10L,
check_bad_snps = TRUE, verbose = FALSE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>query</td>
<td>Query (a vector of rsIDs).</td>
</tr>
<tr>
<td>format</td>
<td>An output format. Can be one of the following: full - plain text, bed - BED (Browser Extensible Data format), see e.g. <a href="https://genome.ucsc.edu/FAQ/FAQformat.html#format5.1">https://genome.ucsc.edu/FAQ/FAQformat.html#format5.1</a>, gff - GFF (General Feature Format), see e.g. <a href="https://genome.ucsc.edu/FAQ/FAQformat.html#format3">https://genome.ucsc.edu/FAQ/FAQformat.html#format3</a> Only full is currently supported.</td>
</tr>
<tr>
<td>url</td>
<td>Regulome url address. Default: <a href="http://www.regulomedb.org/results">http://www.regulomedb.org/results</a></td>
</tr>
<tr>
<td>timeout</td>
<td>A timeout parameter for curl. Default: 10</td>
</tr>
<tr>
<td>check_bad_snps</td>
<td>Checks if all SNPs are annotated. Default: TRUE</td>
</tr>
<tr>
<td>verbose</td>
<td>Verbosing output. Default: FALSE.</td>
</tr>
</tbody>
</table>

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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