Package 'Qtlizer'

October 18, 2022

Title Comprehensive QTL annotation of GWAS results

Version 1.10.0

Description This R package provides access to the Qtlizer web server. Qtlizer annotates lists of common small variants (mainly SNPs) and genes in humans with associated changes in gene expression using the most comprehensive database of published quantitative trait loci (QTLs).

Depends R (>= 3.6.0)

License GPL-3

Encoding UTF-8

LazyData false

BugReports https://github.com/matmu/Qtlizer/issues

Imports httr, curl, GenomicRanges, stringi

Suggests BiocStyle, testthat, knitr, rmarkdown

RoxygenNote 6.1.1

VignetteBuilder knitr

biocViews GenomeWideAssociation, SNP, Genetics, LinkageDisequilibrium

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R topics documented:

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get_qtls   *Query Qtlizer*

Description

Query Qtlizer database for expression quantitative trait loci (eQTLs) in human.

Usage

```
get_qtls(query, corr = NA, max_terms = 5, ld_method = "r2",
  ref_version = "hg19", return_obj = "dataframe")
```

Arguments

query	The query consists of search terms and can be a single string or a vector. Qtlizer allows to query both variants (Rsid, ref_version:chr:pos) and genes (Symbol consisting of letters and numbers according to the HGNC guidelines). Minimum allowed term length is 2.
corr	Linkage disequilibrium based on 1000 Genomes Phase 3 European. If this optional value between 0 and 1 is set, the input variants are enriched for proxy variants passing the threshold. Default value is NA.
max_terms	Number of terms in a single HTTP request. Default value is 5. A large value can lead to a very large result set and a error by the database.
ld_method	There are two methods available: "r2" (default) and "dprime".
ref_version	Two possible versions are supported: hg19 (GRCh37) or hg38 (GRCh38). Default value is "hg19". This argument is only considered if a GenomicRanges::GRanges object is returned.
return_obj	The user can choose to get the QTL data to be returned as data frame or as a GenomicRanges::GRanges object. The default value is "dataframe".

Value

Data frame or GenomicRanges::GRanges object containing QTL data.

Examples

```
get_qtls("rs4284742")
get_qtls(c("rs4284742", "DEFA1"))
get_qtls("rs4284742,DEFA1")
get_qtls("rs4284742", return_obj="granges", ref_version="hg38")
get_qtls("rs4284742", corr=0.6)
```

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