

Package ‘Qtlizer’

September 5, 2022

Title Comprehensive QTL annotation of GWAS results

Version 1.11.0

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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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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