Package 'Qtlizer'

November 12, 2026

Title Comprehensive QTL annotation of GWAS results

Version 1.26.0

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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Author Matthias Munz [aut, cre] (ORCID:
<https://orcid.org/0000-0002-4728-3357>),
Julia Remes [aut]

Maintainer Matthias Munz <matthias.munz@gmx.de>

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`communicate` *URL building and request/response handling*

Description

URL building and request/response handling

Usage

```
communicate(q, corr, ld_method, n.tries = 2)
```

Arguments

`q`	The qtlizer query. Can either be a single string or a vector.
`corr`	Linkage disequilibrium based on 1000 Genomes Phase 3 European. Optional value between 0 and 1. Default value is NA.
`ld_method`	There are two methods. Default method is "r2". The other opportunity is to use "dprime".

Value

Data frame with results.

`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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vector_split *Splits vector v into n subvectors*

Description

Splits vector v into n subvectors

Usage

```
vector_split(v, n)
```

Arguments

v	input vector
n	number of subvectors

Value

List with subvectors.

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