

Package: qtl2browse (via r-universe)

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Version 0.1-2

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Title Genetics Genome Browser

Description Plot genome scan results with the Genetics Genome Browser:
fast, lightweight, powered by purescript.

Author Karl W Broman [aut, cre]
(<https://orcid.org/0000-0002-4914-6671>), Christian Fischer
[aut]

Maintainer Karl W Broman <broman@wisc.edu>

Depends R (>= 3.1.0)

Imports utils, jsonlite (>= 0.9.17), qtl2 (>= 0.18)

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URL <https://github.com/rqtl/qtl2browse>, <https://kbroman.org/qtl2/>

BugReports <https://github.com/rqtl/qtl2browse/issues>

LazyData true

Encoding UTF-8

ByteCompile true

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Remotes rqtl/qtl2

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Repository <https://rqtl.r-universe.dev>

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Description

Use the genetics genome browser to browse QTL mapping results

Usage

```
browse(scan1output, map, lodcolumn = 1, min_lod = 0, dir = NULL)
```

Arguments

scan1output	Genome scan output, as from <code>qt12::scan1()</code>
map	Corresponding physical map (in Mbp), as a list of chromosomes that are each a vector of marker positions. Can also be a data frame of SNP information, with columns chr, pos, and snp_id.
lodcolumn	LOD score column to plot (a numeric index, or a character string for a column name). Only one value allowed.
min_lod	Minimum LOD score to show; values below this are omitted.
dir	Optional directory to contain the results. If not provided, a temporary directory is created.

Value

File location (hidden).

Examples

```
## Not run:
library(qt12)
recla <- read_cross2(paste0("https://raw.githubusercontent.com/rqt1/",
                           "qt12data/master/DO_Recla/recla.zip"))

gmap <- insert_pseudomarkers(recla$gmap, step=0.2, stepwidth="max")
pmap <- interp_map(gmap, recla$gmap, recla$pmap)
pr <- calc_genoprob(recla, gmap, error_prob=0.002,
                  map_function="c-f", cores=2)
apr <- genoprob_to_alleleprob(pr)

k <- calc_kinship(apr, "loco", cores=2)

out <- scan1(apr, recla$pheno[, "HP_latency"], k, cores=2)

library(qt12browse)
browse(out, pmap)

## End(Not run)
```

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