Package: qtl2browse (via r-universe)

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Title Genetics Genome Browser

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

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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

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Remotes rqtl/qtl2

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`browse` *Browse QTL results*

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 `qtl2::scan1()`
`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

```
library(qtl2)
recla <- read_cross2(paste0("https://raw.githubusercontent.com/rqtl/",
                            "qtl2data/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=0)
apr <- genoprob_to_alleleprob(pr)

k <- calc_kinship(apr, "loco", cores=0)

out <- scan1(apr, recla$pheno[,"HP_latency"], k, cores=0)

library(qtl2browse)
browse(out, pmap)
```

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