Package 'MapRtools'

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Title Tools for genetic mapping
Version 0.11
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Description Tools for genetic mapping
Depends R (>= $3.5.0$)
License GPL-3
LazyData true
RoxygenNote 7.1.1
Encoding UTF-8
Imports ggplot2, scam
Suggests knitr, rmarkdown
VignetteBuilder knitr
R topics documented:
plot_coverage plot_haplo plot_LD plot_r2
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plot_coverage Plot marker coverage of the genome
Description
Plot marker coverage of the genome
Usage
<pre>plot_coverage(map, limits = NULL)</pre>
,
1

2 plot_haplo

Arguments

map data frame with columns chrom & position

limits optional data frame with columns chrom & position, with the maximum length

for each chromosome

Details

If limits not provided, then the maximum values in map are used.

Value

ggplot2 variable

plot_haplo

Visualize haplotype dosage

Description

Visualize haplotype dosage in diploid biparental population from two inbreds

Usage

```
plot_haplo(geno, map)
```

Arguments

geno matrix of haplotype dosages (markers x indiv)

map data frame with 3 columns (marker, chrom, position)

Details

Input matrix geno should have rownames attribute that matches marker names in the first column of map.

Value

ggplot object

plot_LD 3

plot_LD

Plot LD vs distance

Description

Plot LD vs distance

Usage

```
plot_LD(r2, map, max.pair = 10000, dof = 5)
```

Arguments

r2 squared correlation matrix

map data frame with 3 columns (marker, chrom, position)

max.pair maximum number of r2 pairs for the spline

dof degrees of freedom for the spline

Details

A monotone decreasing, convex spline is fit using R package scam. The input matrix r2 should have rownames attribute that matches marker names in the first column of map.

Value

ggplot object

plot_r2

Plot heatmap of LD

Description

Plot heatmap of LD (squared correlation)

Usage

```
plot_r2(r2)
```

Arguments

r2 squared correlation matrix

Value

ggplot2 variable

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