

Package ‘MapRtools’

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Title Tools for genetic mapping
Version 0.12
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Description Tools for genetic mapping
Depends R (>= 3.5.0)
License GPL-3
LazyData true
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Imports ggplot2, scam
Suggests knitr, rmarkdown
VignetteBuilder knitr

R topics documented:

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plot_coverage	<i>Plot marker coverage of the genome</i>
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Description

Plot marker coverage of the genome

Usage

```
plot_coverage(map, limits = NULL)
```

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	<i>Visualize haplotype dosage</i>
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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	<i>Plot LD vs distance</i>
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Description

Plot LD vs distance

Usage

```
plot_LD(r2, map, max.pair = 10000, dof = 8)
```

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

List containing

- plot** ggplot object
- spline** data frame with fitted values for the spline

plot_r2	<i>Plot heatmap of LD</i>
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Description

Plot heatmap of LD (squared correlation)

Usage

```
plot_r2(r2)
```

Arguments

r2	squared correlation matrix
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Value

ggplot2 variable

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