

Package ‘MapRtools’

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Title Tools for genetic mapping
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R topics documented:

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LL	<i>Log-likelihood for inbred line-derived mapping populations</i>
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Description

Log-likelihood for inbred line-derived mapping populations

Usage

LL(r, counts, pop.type)

Arguments

r	recombination frequency
counts	3x3 contingency table for haplotype dosages 0,1,2
pop.type	One of the following: "DH","BC","F2","RIL.self","RIL.sib"

Details

The argument counts can be constructed using the `table` function for two markers. Genotype coding must represent dosage of a founder haplotype. For BC populations, possible allele dosages are 0,1. For DH and RIL pops, it is 0,2. For F2 pops, it is 0,1,2.

Value

log-likelihood

MLEL

Max Likelihood Estimation of Linkage

Description

Max Likelihood Estimation of Linkage

Usage

```
MLEL(geno, pop.type, LOD, n.core = 1)
```

Arguments

geno	Matrix of haplotype dosages (markers x indiv)
pop.type	One of the following: "DH","BC","F2"
LOD	Logical, whether to return LOD (TRUE) or recomb freq (FALSE)
n.core	For parallel execution on multiple cores

Details

Can be used to estimate either the LOD score or recombination frequency, depending on the value of LOD. Genotype coding must represent dosage of a founder haplotype. For BC populations, possible allele dosages are 0,1. For DH and RIL pops, it is 0,2. For F2 pops, it is 0,1,2.

Value

Matrix with RF or LOD

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_square	<i>Plot square (dis)similarity matrix</i>
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Description

Plot square (dis)similarity matrix

Usage

```
plot_square(data, lims = NULL)
```

Arguments

data	squared correlation matrix
lims	numeric 3-vector with the low,mid,high points for the colors

Details

Can be used to plot squared correlation, recomb frequency, LOD and more. By default, *lims* equals (0,median,max)

plot_square

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Value

ggplot2 variable

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