

Package ‘MapRtools’

February 10, 2021

Title Tools for genetic mapping
Version 0.13
Author Jeffrey B. Endelman
Maintainer Jeffrey Endelman <endelman@wisc.edu>
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:

LL	1
MLEL	2
plot_coverage	3
plot_haplo	3
plot_LD	4
plot_square	4
Index	6

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

Description

Log-likelihood for inbred line-derived mapping populations

Usage

LL(r, counts, pop.type)

Arguments

<code>r</code>	recombination frequency
<code>counts</code>	3x3 contingency table for haplotype dosages 0,1,2
<code>pop.type</code>	One of the following: "DH","BC","F2"

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 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

<code>geno</code>	Matrix of haplotype dosages (markers x indiv)
<code>pop.type</code>	One of the following: "DH","BC","F2"
<code>LOD</code>	Logical, whether to return LOD (TRUE) or recomb freq (FALSE)
<code>n.core</code>	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 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>
---------------	---

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>
------------	-----------------------------------

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>
---------	----------------------------

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>
-------------	---

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

5

Value

ggplot2 variable

Index

LL, [1](#)

MLEL, [2](#)

plot_coverage, [3](#)

plot_haplo, [3](#)

plot_LD, [4](#)

plot_square, [4](#)