Package 'MapRtools'

February 10, 2021

Title Tools for genetic mapping

Version 0.14

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:

LDbin   *Create marker bins based on LD*

Description

Create marker bins based on LD

Usage

```
LDbin(geno, r2.thresh = 0.99)
```

Arguments

geno	matrix of haplotype dosages (markers x indiv)
r2.thresh	threshold for binning

Details

Bins are created based on hierarchical clustering with `hclust` and `method='single'`, using $1 - r^2$ as the dissimilarity metric. The argument `r2.thresh` controls the height for cutting the dendrogram to create the bins. The marker with the least missing data for each bin is chosen to represent it.

Value

List containing

bins data frame with two columns: marker,bin

geno genotype matrix for the bins

r2 r2 matrix for the bins

LL   *Log-likelihood for inbred line-derived mapping populations*

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   *Plot marker coverage of the genome*

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	*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	*Plot LD vs distance*

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 *Plot square (dis)similarity matrix*

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)

Value

ggplot2 variable

Index