Package ‘onemap’

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Title  Construction of Genetic Maps in Experimental Crosses

Version  2.8.2

Description  Analysis of molecular marker data from model (backcrosses, F2 and recombinant inbred lines) and non-model systems (i.e. outcrossing species). For the later, it allows statistical analysis by simultaneously estimating linkage and linkage phases (genetic map construction) according to Wu et al. (2002) <doi:10.1006/tpbi.2002.1577>. All analysis are based on multipoint approaches using hidden Markov models.

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Author  Gabriel Margarido [aut], Marcelo Mollinari [aut], Cristiane Taniguti [ctb, cre], Getulio Ferreira [ctb], Rodrigo Amadeu [ctb], Karl Broman [ctb], Katharine Preedy [ctb, cph] (MDS ordering algorithm), Bastian Schiffthaler [ctb, cph] (HMM parallelization), Augusto Garcia [aut, ctb]

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Maintainer Cristiane Taniguti <chtaniguti@tamu.edu>
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add_marker

Creates a new sequence by adding markers.

Description

Creates a new sequence by adding markers from a predetermined one. The markers are added in the end of the sequence.

Usage

add_marker(input.seq, mrks)

Arguments

input.seq an object of class sequence.
mrks a vector containing the markers to be added from the sequence.

Value

An object of class sequence, which is a list containing the following components:

seq.num a vector containing the (ordered) indices of markers in the sequence, according to the input file.
seq.phases a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
seq.rf a vector with the recombination fractions between markers in the sequence. -1 means that there are no estimated recombination fractions.
seq.like log-likelihood of the corresponding linkage map.
data.name name of the object of class onemap with the raw data.
twopt name of the object of class rf_2pts with the 2-point analyses.

@author Marcelo Mollinari, <mmollina@usp.br>

See Also

drop_marker
add_redundants

Examples

```r
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
(LG1 <- make_seq(groups,1))
(LG.aug<-add_marker(LG1, c(4,7))
```

Add the redundant markers removed by create_data_bins function

Description

Add the redundant markers removed by create_data_bins function

Usage

```r
add_redundants(sequence, onemap.obj, bins)
```

Arguments

- `sequence`: object of class `sequence`
- `onemap.obj`: object of class `onemap.obj` before redundant markers were removed
- `bins`: object of class `onemap_bin`

Value

New sequence object of class `sequence`, which is a list containing the following components:

- `seq.num`: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- `seq.phases`: a vector with the linkage phases between markers in the sequence, in corresponding positions. `-1` means that there are no defined linkage phases.
- `seq.rf`: a vector with the recombination frequencies between markers in the sequence. `-1` means that there are no estimated recombination frequencies.
- `seq.like`: log-likelihood of the corresponding linkage map.
- `data.name`: object of class `onemap` with the raw data.
- `twopt`: object of class `rf_2pts` with the 2-point analyses.

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

See Also

`find_bins`
Bonferroni_alpha  
*Calculates individual significance level to be used to achieve a global alpha (with Bonferroni)*

**Description**

It shows the alpha value to be used in each chi-square segregation test, in order to achieve a given global type I error. To do so, it uses Bonferroni’s criteria.

**Usage**

```
Bonferroni_alpha(x, global.alpha = 0.05)
```

**Arguments**

- `x`: an object of class `onemap_segreg_test`
- `global.alpha`: the global alpha that

**Value**

the alpha value for each test (numeric)

**Examples**

```
data(onemap_example_bc) # Loads a fake backcross dataset installed with onemap
Chi <- test_segregation(onemap_example_bc) # Performs the chi-square test for all markers
print(Chi) # Shows the results of the Chi-square tests
Bonferroni_alpha (Chi) # Shows the individual alpha level to be used
```

---

check_data  
*Onemap object sanity check*

**Description**

Based on MAPpoly check_data_sanity function by Marcelo Mollinari

**Usage**

```
check_data(x)
```

**Arguments**

- `x`: an object of class `onemap`
**check_twopts**

**Value**

if consistent, returns 0. If not consistent, returns a vector with a number of tests, where TRUE indicates a failed test.

**Author(s)**

Cristiane Taniguti, <chtaniguti@tamu.edu>

**Examples**

```r
data(onemap_example_bc)
check_data(onemap_example_bc)
```

---

**Description**

Based on MAPpoly check_data_sanity function by Marcelo Mollinari

**Usage**

```r
check_twopts(x)
```

**Arguments**

- `x` an object of class onemap

**Value**

if consistent, returns 0. If not consistent, returns a vector with a number of tests, where TRUE indicates a failed test.

**Author(s)**

Cristiane Taniguti, <chtaniguti@tamu.edu>

**Examples**

```r
data(onemap_example_bc)
twopts <- rf_2pts(onemap_example_bc)
check_twopts(twopts)
```
**combine_onemap**

**Combine OneMap datasets**

**Description**

Merge two or more OneMap datasets from the same cross type. Creates an object of class `onemap`.

**Usage**

```r
combine_onemap(...)```

**Arguments**

...  

Two or more `onemap` dataset objects of the same cross type.

**Details**

Given a set of OneMap datasets, all from the same cross type (full-sib, backcross, F2 intercross or recombinant inbred lines obtained by self- or sib-mating), merges marker and phenotype information to create a single `onemap` object.

If sample IDs are present in all datasets (the standard new format), not all individuals need to be genotyped in all datasets - the merged dataset will contain all available information, with missing data elsewhere. If sample IDs are missing in at least one dataset, it is required that all datasets have the same number of individuals, and it is assumed that they are arranged in the same order in every dataset.

**Value**

An object of class `onemap`, i.e., a list with the following components:

- **geno**: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- **n.ind**: number of individuals.
- **n.mar**: number of markers.
- **segr.type**: a vector with the segregation type of each marker, as strings.
- **segr.type.num**: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- **input**: a string indicating that this is a combined dataset.
- **n.phe**: number of phenotypes.
- **pheno**: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.
compare

Author(s)
Gabriel R A Margarido, <gramarga@gmail.com>

References
Lincoln, S. E., Daly, M. J. and Lander, E. S. (1993) Constructing genetic linkage maps with MAP-
MAKER/EXP Version 3.0: a tutorial and reference manual. A Whitehead Institute for Biomedical

See Also
read_onemap and read_mapmaker.

Examples

```R
data("onemap_example_out")
data("vcf_example_out")
combined_data <- combine_onemap(onemap_example_out, vcf_example_out)
```

---

**compare**

*Compare all possible orders (exhaustive search) for a given sequence of markers*

**Description**
For a given sequence with \( n \) markers, computes the multipoint likelihood of all \( \frac{n!}{2} \) possible orders.

**Usage**
```r
compare(input.seq, n.best = 50, tol = 0.001, verbose = FALSE)
```

**Arguments**
- `input.seq`: an object of class sequence.
- `n.best`: the number of best orders to store in object (defaults to 50).
- `tol`: tolerance for the C routine, i.e., the value used to evaluate convergence.
- `verbose`: if FALSE (default), simplified output is displayed. if TRUE, detailed output is displayed.
Details

Since the number $n!$ is large even for moderate values of $n$, this function is to be used only for sequences with relatively few markers. If markers were genotyped in an outcross population, linkage phases need to be estimated and therefore more states need to be visited in the Markov chain; when segregation types are D1, D2 and C, computation can required a very long time (specially when markers linked in repulsion are involved), so we recomend to use this function up to 6 or 7 markers. For inbred-based populations, up to 10 or 11 markers can be ordered with this function, since linkage phase are known. The multipoint likelihood is calculated according to Wu et al. (2002b) (Eqs. 7a to 11), assuming that the recombination fraction is the same in both parents. Hidden Markov chain codes adapted from Broman et al. (2008) were used.

Value

An object of class `compare`, which is a list containing the following components:

- `best.ord`: a matrix containing the best orders.
- `best.ord.rf`: a matrix with recombination frequencies for the corresponding best orders.
- `best.ord.phase`: a matrix with linkage phases for the best orders.
- `best.ord.LOD`: a vector with LOD Score values for the best orders.
- `data.name`: name of the object of class onemap with the raw data.
- `twopt`: name of the object of class rf_2pts with the 2-point analyses.

Author(s)

Marcelo Mollinari, <mmollina@usp.br>

References


See Also

`marker_type` for details about segregation types and `make_seq`. 

create_dataframe_for_plot_outcross

Examples

```r
#outcrossing example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
markers <- make_seq(twopt,c(12,14,15,26,28))
(markers.comp <- compare(markers))
(markers.comp <- compare(markers,verbose=TRUE))

#F2 example
data(onemap_example_f2)
twopt <- rf_2pts(onemap_example_f2)
markers <- make_seq(twopt,c(17,26,29,30,44,46,55))
(markers.comp <- compare(markers))
(markers.comp <- compare(markers,verbose=TRUE))
```

**create_dataframe_for_plot_outcross**

Create a dataframe suitable for a ggplot2 graphic

**Description**

An internal function that prepares a dataframe suitable for drawing a graphic of raw data using ggplot2, i.e., a data frame with long format

**Usage**

`create_dataframe_for_plot_outcross(x)`

**Arguments**

- `x` an object of classes onemap and outcross, with data and additional information

**Value**

a dataframe
create_data_bins  

Description

Creates a new dataset based on onemap_bin object

Usage

create_data_bins(input.obj, bins)

Arguments

input.obj: an object of class onemap.

bins: an object of class onemap_bin.

Details

Given a onemap_bin object, creates a new data set where the redundant markers are collapsed into bins and represented by the marker with the lower amount of missing data among those on the bin.

Value

An object of class onemap, i.e., a list with the following components:

- geno: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- n.ind: number of individuals.
- n.mar: number of markers.
- segr.type: a vector with the segregation type of each marker, as strings.
- segr.type.num: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- input: the name of the input file.
- n.phe: number of phenotypes.
- pheno: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.
- error: matrix containing HMM emission probabilities

Author(s)

Marcelo Mollinari, <mmollina@usp.br>
create_depths_profile

See Also

find_bins

Examples

```r
data("onemap_example_f2")
(bins<-find_bins(onemap_example_f2, exact=FALSE))
onemap_bins <- create_data_bins(onemap_example_f2, bins)
```

create_depths_profile  Create database and ggplot graphic of allele reads depths

Description

Create database and ggplot graphic of allele reads depths

Usage

```r
create_depths_profile(
  onemap.obj = NULL,
  vcfR.object = NULL,
  vcf = NULL,
  parent1 = NULL,
  parent2 = NULL,
  vcf.par = "AD",
  recovering = FALSE,
  mks = NULL,
  inds = NULL,
  GTfrom = "onemap",
  alpha = 1,
  rds.file = "data.rds",
  y_lim = NULL,
  x_lim = NULL,
  verbose = TRUE
)
```

Arguments

- **onemap.obj** an object of class onemap.
- **vcfR.object** object of class vcfR;
- **vcf** path to VCF file.
- **parent1** a character specifying the first parent ID
- **parent2** a character specifying the second parent ID
- **vcf.par** the vcf parameter that store the allele depth information.
recovering logical. If TRUE, all markers in vcf are considere, if FALSE only those in onemap.obj

mks a vector of characters specifying the markers names to be considered or NULL to consider all markers

inds a vector of characters specifying the individual names to be considered or NULL to consider all individuals

GTfrom the graphic should contain the genotypes from onemap.obj or from the vcf? Specify using "onemap", "vcf" or "prob".

alpha define the transparency of the dots in the graphic

rds.file rds file name to store the data frame with values used to build the graphic

y_lim set scale limit for y axis

x_lim set scale limit for x axis

verbose If TRUE, print tracing information.

Value

an rds file and a ggplot graphic.

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

See Also

onemap_read_vcfR

create_probs Build genotype probabilities matrix for hmm

Description

The genotypes probabilities can be calculated considering a global error (default method) or considering a genotype error probability for each genotype. Furthermore, user can provide directly the genotype probability matrix.

Usage

create_probs(  input.obj = NULL,  global_error = NULL,  genotypes_errors = NULL,  genotypes_probs = NULL)
create_probs

Arguments

- **input.obj**: object of class onemap or onemap sequence
- **global_error**: an integer specifying the global error value
- **genotypes_errors**: a matrix with dimensions (number of individuals) x (number of markers) with genotypes errors values
- **genotypes_probs**: a matrix with dimensions (number of individuals) x (number of markers) with possible genotypes (i.e., a ab ba b) with four columns for F2 and outcrossing populations, and two for backcross and RILs).

Details

The genotype probability matrix has number of individuals x number of markers rows and four columns (or two if considering backcross or RILs populations), one for each possible genotype of the population. This format follows the one proposed by MAPpoly.

The genotype probabilities come from SNP calling methods. If you do not have them, you can use a global error or an error value for each genotype. The OneMap until 2.1 version have only the global error option.

Value

An object of class onemap, i.e., a list with the following components:

- **geno**: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- **n.ind**: number of individuals.
- **n.mar**: number of markers.
- **segr.type**: a vector with the segregation type of each marker, as strings.
- **segr.type.num**: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- **input**: the name of the input file.
- **n.phe**: number of phenotypes.
- **pheno**: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.
- **error**: matrix containing HMM emission probabilities

Author(s)

Cristiane Taniguti <chtaniguti@tamu.edu>
References


See Also

make_seq

Examples

data(onemap_example_out)
new.data <- create_probs(onemap_example_out, global_error = 10^-5)

draw_map

Draw a genetic map

draw_map

Description

Provides a simple draw of a genetic map.

Usage

draw_map(
  map.list,
  horizontal = FALSE,
  names = FALSE,
  grid = FALSE,
  cex.mrk = 1,
  cex.grp = 0.75
)

Arguments

map.list a map, i.e. an object of class sequence with a predefined order, linkage phases, recombination fraction and likelihood; also it could be a list of maps.
horizontal if TRUE, indicates that the map should be plotted horizontally. Default is FALSE
names if TRUE, displays the names of the markers. Default is FALSE
grid if TRUE, displays a grid in the background. Default is FALSE
cex.mrk the magnification to be used for markers.
cex.grp the magnification to be used for group axis annotation.

Value

figure with genetic map draw
**draw_map2**

**Author(s)**

Marcelo Mollinari, <mmollina@usp.br>

**Examples**

```r
#outcross example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
lgs<group(make_seq(twopt, "all"))
maps<vector("list", lgs$n.groups)
for(i in 1:lg$n.groups)
  maps[[i]]<- make_seq(order_seq(input.seq= make_seq(lgs,i),twopt.alg = "rcd"), "force")
draw_map(maps, grid=TRUE)
draw_map(maps, grid=TRUE, horizontal=TRUE)
```

**Description**

Provides a simple draw of a linkage map.

**Usage**

```r
draw_map2(
  ..., tag = NULL, id = TRUE, pos = TRUE, cex.label = NULL, main = NULL,
  group.names = NULL, centered = FALSE, y.axis = TRUE, space = NULL, col.group = NULL, col.mark = NULL, col.tag = NULL, output = NULL, verbose = TRUE)
)
```
Arguments

... map(s). Object(s) of class sequence and/or data.frame. If data.frame, it must have two columns: column 1: marker id; column 2: position (cM) (numeric).

tag name(s) of the marker(s) to highlight. If "all", all markers will be highlighted. Default is NULL.

id logical. If TRUE (default), shows name(s) of tagged marker(s).

pos logical. If TRUE (default), shows position(s) of tagged marker(s).

cex.label the magnification used for label(s) of tagged marker(s). If NULL (default), the cex will be automatically calculated to avoid overlapping.

main an overall title for the plot. Default is NULL.

group.names name(s) to identify the group(s). If NULL (default), the name(s) of the sequence(s) will be used.

centered logical. If TRUE, the group(s) will be aligned in the center. If FALSE (default), the group(s) will be aligned at the top.

y.axis logical. If TRUE (default), shows y axis. If centered = TRUE, the y axis will always be hidden.

space numerical. Spacing between groups. If NULL (default), the spacing will be automatically calculated to avoid overlapping.

col.group the color used for group(s).

col.mark the color used for marker(s).

col.tag the color used for highlighted marker(s) and its/theirs label(s).

output the name of the output file. The file format can be specified by adding its extension. Available formats: 'bmp', 'jpeg', 'png', 'tiff', 'pdf' and 'eps' (default).

verbose If TRUE, print tracing information.

Value
ggplot graphic with genetic map draw

Author(s)

Getulio Caixeta Ferreira, <getulio.caifer@gmail.com>

Examples

data("onemap_example_out")
twopt <- rf_2pts(onemap_example_out)
lg <- group(make_seq(twopt, "all"))
seq1 <- make_seq(order_seq(input_seq = make_seq(lg, 1), twopt.alg = "rcd"), "force")
seq2 <- make_seq(order_seq(input_seq = make_seq(lg, 2), twopt.alg = "rcd"), "force")
seq3 <- make_seq(order_seq(input_seq = make_seq(lg, 3), twopt.alg = "rcd"), "force")
draw_map2(seq1, seq2, seq3, tag = c("M1", "M2", "M3", "M4", "M5"),
output = paste0(tempfile(), ".png"))
**drop_marker**

Creates a new sequence by dropping markers.

**Description**

Creates a new sequence by dropping markers from a predetermined one.

**Usage**

\[
drop\_marker(input\_seq, mrks)
\]

**Arguments**

- **input.seq**: an object of class `sequence`.
- **mrks**: a vector containing the markers to be removed from the sequence.

**Value**

An object of class `sequence`, which is a list containing the following components:

- **seq.num**: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- **seq.phases**: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- **seq.rf**: a vector with the recombination fractions between markers in the sequence. -1 means that there are no estimated recombination fractions.
- **seq.like**: log-likelihood of the corresponding linkage map.
- **data.name**: name of the object of class `onemap` with the raw data.
- **twopt**: name of the object of class `rf_2pts` with the 2-point analyses.

@author Marcelo Mollinari, <mmollina@usp.br>

**See Also**

- `add_marker`

**Examples**

```r
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
(LG1 <- make_seq(groups,1))
(LG.aug<--drop_marker(LG1, c(10,14)))```

empty_onemap_obj

Produce empty object to avoid code break. Function for internal purpose.

Description

Produce empty object to avoid code break. Function for internal purpose.

Usage

empty_onemap_obj(vcf, P1, P2, cross)

Arguments

vcf object of class vcfR
P1 character with parent 1 ID
P2 character with parent 2 ID
cross type of cross. Must be one of: "outcross" for full-sibs; "f2 intercross" for an F2 intercross progeny; "f2 backcross"; "ri self" for recombinant inbred lines by self-mating; or "ri sib" for recombinant inbred lines by sib-mating.

Value

An empty object of class onemap, i.e., a list with the following components:

geno a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
n.ind number of individuals.
n.mar number of markers.
segr.type a vector with the segregation type of each marker, as strings.
segr.type.num a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
input the name of the input file.
n.phe number of phenotypes.
pheno a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>
**est_hmm_out**

Run HMM chains

**Usage**

```r
est_hmm_out(geno_R, error_R, type_R, phase_R, rf_R, verbose_R, tol_R)
```

**Arguments**

- `geno_R`: genotypes
- `error_R`: genotypes probabilities
- `type_R`: marker types
- `phase_R`: phase estimated by 2-pts
- `rf_R`: recombination fraction
- `verbose_R`: logical to display or not the procedure
- `tol_R`: EM algorithm tolerance

**Value**

A list containing the re-estimated vector of recombination fractions and the logarithm of the likelihood

---

**extract_depth**

Extract allele counts of progeny and parents of vcf file

**Description**

Uses vcfR package and onemap object to generates list of vectors with reference allele count and total counts for each marker and genotypes included in onemap object (only available for biallelic sites)

**Usage**

```r
extract_depth(
  vcfR.object = NULL,
  onemap.object = NULL,
  vcf.par = c("GQ", "AD", "DPR, PL", "GL"),
  parent1 = "P1",
  parent2 = "P2",
  f1 = "F1",
  recovering = FALSE
)
```
extract_depth

Arguments

vcfR.object  object output from vcfR package
onemap.object onemap object output from read_onemap, read_mapmaker or onemap_read_vcf function
vcf.par  vcf format field that contain allele counts informations, the implemented are: AD, DPR, GQ, PL, GL. AD and DPR return a list with allele depth information. GQ returns a matrix with error probability for each genotype. PL return a data.frame with genotypes probabilities for every genotype.
parent1  parent 1 identification in vcfR object
parent2  parent 2 identification in vcfR object
f1  if your cross type is f2, you must define the F1 individual
recovering  TRUE/FALSE, if TRUE evaluate all markers from vcf file, if FALSE evaluate only markers in onemap object

Value

list containing the following components:

palt  a matrix with parent 1 and 2 alternative allele counts.
pref  a matrix with parent 1 and 2 reference allele counts.
psize  a matrix with parent 1 and 2 total allele counts.
oalt  a matrix with progeny alternative allele counts.
oref  a matrix with progeny reference allele counts.
osize  a matrix with progeny total allele counts.
n.mks  total number of markers.
n.ind  total number of individuals in progeny.
inds  progeny individuals identification.
mks  markers identification.
onemap.object  same onemap.object inputed

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>
filter_2pts_gaps

Filter markers based on 2pts distance

Description

Filter markers based on 2pts distance

Usage

```r
filter_2pts_gaps(input.seq, max.gap = 10)
```

Arguments

- `input.seq`: object of class sequence with ordered markers
- `max.gap`: maximum gap measured in kosambi centimorgans allowed between adjacent markers. Markers that presents the defined distance between both adjacent neighbors will be removed.

Value

New sequence object of class sequence, which is a list containing the following components:

- `seq.num`: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- `seq.phases`: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- `seq.rf`: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- `seq.like`: log-likelihood of the corresponding linkage map.
- `data.name`: object of class onemap with the raw data.
- `twopt`: object of class rf_2pts with the 2-point analyses.

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>
filter_missing

Filter markers according with a missing data threshold

Description

Filter markers according with a missing data threshold

Usage

filter_missing(onemap.obj = NULL, threshold = 0.25, verbose = TRUE)

Arguments

- **onemap.obj**: an object of class *onemap*.
- **threshold**: a numeric from 0 to 1 to define the threshold of missing data allowed.
- **verbose**: A logical, if TRUE it output progress status information.

Value

An object of class *onemap*, i.e., a list with the following components:

- **geno**: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- **n.ind**: number of individuals.
- **n.mar**: number of markers.
- **segr.type**: a vector with the segregation type of each marker, as strings.
- **segr.type.num**: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- **input**: the name of the input file.
- **n.phe**: number of phenotypes.
- **pheno**: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.
- **error**: matrix containing HMM emission probabilities

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>
Examples

data(onemap_example_out)
filt_obj <- filter_missing(onemap_example_out, threshold=0.25)

filter_prob

Function filter genotypes by genotype probability

Description

Function filter genotypes by genotype probability

Usage

filter_prob(onemap.obj = NULL, threshold = 0.8, verbose = TRUE)

Arguments

- **onemap.obj**: an object of class onemap.
- **threshold**: a numeric from 0 to 1 to define the threshold for the probability of the called genotype (highest probability)
- **verbose**: If TRUE, print tracing information.

Value

An object of class onemap, i.e., a list with the following components:

- **geno**: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- **n.ind**: number of individuals.
- **n.mar**: number of markers.
- **segr.type**: a vector with the segregation type of each marker, as strings.
- **segr.type.num**: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- **input**: the name of the input file.
- **n.phe**: number of phenotypes.
- **pheno**: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.
- **error**: matrix containing HMM emission probabilities
Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

Examples

data(onemap_example_out)
filt_obj <- filter_prob(onemap_example_out, threshold=0.8)

find_bins

Allocate markers into bins

Description

Function to allocate markers with redundant information into bins. Within each bin, the pairwise recombination fraction between markers is zero.

Usage

find_bins(input.obj, exact = TRUE)

Arguments

input.obj an object of class onemap.
exact logical. If TRUE, it only allocates markers with the exact same information into bins, including missing data; if FALSE, missing data are not considered when allocating markers. In the latter case, the marker with the lowest amount of missing data is taken as the representative marker on that bin.

Value

An object of class onemap_bin, which is a list containing the following components:
bins a list containing the bins. Each element of the list is a table whose lines indicate the name of the marker, the bin in which that particular marker was allocated and the percentage of missing data. The name of each element of the list corresponds to the marker with the lower amount of missing data among those on the bin
n.mar total number of markers.
n.ind number individuals
exact.search logical; indicates if the search was performed with the argument exact=TRUE or exact=FALSE

Author(s)

Marcelo Mollinari, <mmollina@usp.br>
**generate_overlapping_batches**

Function to divide the sequence in batches with user defined size

**Description**

Function to divide the sequence in batches with user defined size

**Usage**

```r
generate_overlapping_batches(input.seq, size = 50, overlap = 15)
```

**Arguments**

- `input.seq`: an object of class `sequence`.
- `size`: The center size around which an optimum is to be searched.
- `overlap`: The desired overlap between batches.

**group**

Assign markers to linkage groups

**Description**

Identifies linkage groups of markers, using results from two-point (pairwise) analysis and the transitive property of linkage.

**Usage**

```r
group(input.seq, LOD = NULL, max.rf = NULL, verbose = TRUE)
```
Arguments

input.seq  an object of class sequence.
LOD       a (positive) real number used as minimum LOD score (threshold) to declare linkage.
max.rf    a real number (usually smaller than 0.5) used as maximum recombination fraction to declare linkage.
verbose  logical. If TRUE, current progress is shown; if FALSE, no output is produced.

Details

If the arguments specifying thresholds used to group markers, i.e., minimum LOD Score and maximum recombination fraction, are NULL (default), the values used are those contained in object input.seq. If not using NULL, the new values override the ones in object input.seq.

Value

Returns an object of class group, which is a list containing the following components:

data.name  name of the object of class onemap that contains the raw data.
twopt      name of the object of class rf.2ts used as input, i.e., containing information used to assign markers to linkage groups.
marnames  marker names, according to the input file.
n.mar     total number of markers.
LOD        minimum LOD Score to declare linkage.
max.rf     maximum recombination fraction to declare linkage.
n.groups  number of linkage groups found.
groups    number of the linkage group to which each marker is assigned.

Author(s)

Gabriel R A Margarido, <gramarga@gmail.com> and Marcelo Mollinari, <mmollina@usp.br>

References


See Also

rf_2pts and make_seq
Examples

```r
data(onemap_example_out)
twopts <- rf_2pts(onemap_example_out)

all.data <- make_seq(twopts, "all")
link_gr <- group(all.data)
link_gr
print(link_gr, details=FALSE) # omit the names of the markers
```

**Description**

Assign markers to preexisting linkage groups

Identifies linkage groups of markers combining input sequences objects with unlinked markers from rf_2pts object. The results from two-point (pairwise) analysis and the transitive property of linkage are used for grouping, as group function.

**Usage**

```r
group_seq(
  input.2pts,
  seqs = "CHROM",
  unlink.mks = "all",
  repeated = FALSE,
  LOD = NULL,
  max.rf = NULL,
  min_mks = NULL
)
```

**Arguments**

- **input.2pts**: an object of class rf_2pts.
- **seqs**: a list of objects of class sequence or the string "CHROM" if there is CHROM information available in the input data file.
- **unlink.mks**: a object of class sequence with the number of the markers to be grouped with the preexisting sequences defined by seqs parameter. Using the string "all", all remaining markers of the rf_2pts object will be tested.
- **repeated**: logical. If TRUE, markers grouped in more than one of the sequences are kept in the output sequences. If FALSE, they are removed of the output sequences.
- **LOD**: a (positive) real number used as minimum LOD score (threshold) to declare linkage.
- **max.rf**: a real number (usually smaller than 0.5) used as maximum recombination fraction to declare linkage.
- **min_mks**: integer defining the minimum number of markers that a provided sequence (seqs or CHROM) should have to be considered a group.
Details

If the arguments specifying thresholds used to group markers, i.e., minimum LOD Score and maximum recombination fraction, are NULL (default), the values used are those contained in object `input.2pts`. If not using NULL, the new values override the ones in object `input.2pts`.

Value

Returns an object of class `group_seq`, which is a list containing the following components:

- `data.name`: name of the object of class `onemap` that contains the raw data.
- `twopt`: name of the object of class `rf.2ts` used as input, i.e., containing information used to assign markers to linkage groups.
- `mk.names`: marker names, according to the input file.
- `input.seqs`: list with the numbers of the markers in each inputted sequence.
- `input.unlink.mks`: numbers of the unlinked markers in inputted sequence.
- `out.seqs`: list with the numbers of the markers in each outputted sequence.
- `n.unlinked`: number of markers that remained unlinked.
- `n.repeated`: number of markers which repeated in more than one group.
- `n.mar`: total number of markers evaluated.
- `LOD`: minimum LOD Score to declare linkage.
- `max.rf`: maximum recombination fraction to declare linkage.
- `sequences`: list of outputted sequences.
- `repeated`: list with the number of the markers that are repeated in each outputted sequence.
- `unlinked`: number of the markers which remained unlinked.

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

See Also

- `make_seq` and `group`

Examples

```r
data(onemap_example_out) # load OneMap's fake dataset for a outcrossing population
data(vcf_example_out) # load OneMap's fake dataset from a VCF file for a outcrossing population
comb_example <- combine_onemap(onemap_example_out, vcf_example_out) # Combine datasets
twopts <- rf_2pts(comb_example)

out_CHROM <- group_seq(twopts, seqs="CHROM", repeated=FALSE)
out_CHROM

seq1 <- make_seq(twopts, c(1,2,3,4,5,25,26))
```
```r
seq2 <- make_seq(twopts, c(8,18))
seq3 <- make_seq(twopts, c(4,16,21,24,29))

out_seqs <- group_seq(twopts, seqs=list(seq1,seq2,seq3))
out_seqs
```

### Description

Identifies linkage groups of markers using the results of two-point (pairwise) analysis and UPGMA method. Function adapted from MAPpoly package written by Marcelo Mollinari.

### Usage

```r
group_upgma(input.seq, expected.groups = NULL, inter = TRUE, comp.mat = FALSE)
```

### Arguments

- `input.seq`: an object of class `mappoly.rf.matrix`
- `expected.groups`: when available, inform the number of expected linkage groups (i.e. chromosomes) for the species
- `inter`: if TRUE (default), plots a dendrogram highlighting the expected groups before continue
- `comp.mat`: if TRUE, shows a comparison between the reference based and the linkage based grouping, if the sequence information is available (default = FALSE)

### Value

Returns an object of class `group`, which is a list containing the following components:

- `data.name`: the referred dataset name
- `hc.snp`: a list containing information related to the UPGMA grouping method
- `expected.groups`: the number of expected linkage groups
- `groups.snp`: the groups to which each of the markers belong
- `seq.vs.grouped.snp`: comparison between the genomic group information (when available) and the groups provided by `group_upgma`
- `LOD`: minimum LOD Score to declare linkage.
- `max.rf`: maximum recombination fraction to declare linkage.
- `t woott`: name of the object of class `rf.2ts` used as input, i.e., containing information used to assign markers to linkage groups.
Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>
Cristiane Taniguti <chtaniguti@tamu.edu>

References


Examples

data("vcf_example_out")
twopts <- rf_2pts(vcf_example_out)
input.seq <- make_seq(twopts, "all")
lgs <- group_upgma(input.seq, expected.groups = 3, comp.mat=TRUE, inter = FALSE)
plot(lgs)

haldane

Apply Haldane mapping function

Description

Apply Haldane mapping function

Usage

haldane(rcmb)

Arguments

rcmb vector of recombination fraction values

Value

vector with centimorgan values
**Description**

Apply Kosambi mapping function

**Usage**

kosambi(rcmb)

**Arguments**

rcmb  vector of recombination fraction values

**Value**

vector with centimorgan values

---

**LG3_comp**

Dataset needed for build Outcrossing vignette. It is the result from compare function exemplified there.

**Description**

Dataset needed for build Outcrossing vignette. It is the result from compare function exemplified there.

**Usage**

data("LG3_comp")

**Format**

List of 7 $ best.ord : int [1:51, 1:7] 43 43 22 7 7 7 7 7 ... $ best.ord.rf : num [1:51, 1:6] 0.13186 0.12343 0.12852 0.12034 0.00481 ... $ best.ord.phase: int [1:51, 1:6] 1 1 1 1 1 1 2 2 1 ... $ best.ord.like : num [1:51] -399 -399 -399 -399 -399 ... $ best.ord.LOD : num [1:51] 0 -0.0509 -0.1518 -0.2156 -0.2512 ... $ data.name :List of 11 ..$ geno : num [1:100, 1:52] 2 2 2 2 2 1 1 1 1 ... $ segr.type : chr [1:52] "B3.7" "D2.18" "D1.13" "A.4" ...

... attr(*, "dimnames")=List of 2 ..$ : chr [1:100] "IND1" "IND2" "IND3" "IND4" ... ..$ : chr [1:52] "M1" "M2" "M3" "M4" ...

...$ n.ind : int 100 ..$ n.mar : int 52 ..$ n.phe : num 3 ..$ pheno : num [1:100, 1:3] 43 12 18 34 14 12 53 22 13 ...

... attr(*, "dimnames")=List of 2 ..$ : NULL ..$ : NULL ..$ : chr [1:3] "Pheno1" "Pheno2" "Pheno3" ..$ CHROM : chr [1:52] NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA ... ..$ input : NULL ..$ error : num [1:5200, 1:4] 5e-06 5e-06 5e-06 5e-06 1e+00 1e+00 ... ..$ : NULL ..$...
make_seq

Create a sequence of markers based on other OneMap object types

Details

Outcrossing vignette uses it to save time to build itself.

Description

Makes a sequence of markers based on an object of another type.

Usage

make_seq(input.obj, arg = NULL, phase = NULL, data.name = NULL, twopt = NULL)

Arguments

input.obj  
an object of class onemap, rf_2pts, group, compare, try or order.

arg  
its value depends on the type of object input.obj. For a onemap object, arg must be a string corresponding to one of the reference sequences on which markers are anchored (usually chromosomes). This requires that CHROM information be available in the input data file. It can also be a vector of integers specifying which markers comprise the sequence. For an object rf_2pts, arg can be the string "all", resulting in a sequence with all markers in the raw data (generally
make_seq

done for grouping markers); otherwise, it must be a vector of integers specifying which markers comprise the sequence. For an object of class group, arg must be an integer specifying the group. For a compare object, arg is an integer indicating the corresponding order (arranged according to the likelihood); if NULL (default), the best order is taken. For an object of class try, arg must be an integer less than or equal to the length of the original sequence plus one; the sequence obtained will be that with the additional marker in the position indicated by arg. Finally, for an order object, arg is a string: "safe" means the order that contains only markers mapped with the provided threshold; "force" means the order with all markers.

phase its value is also dependent on the type of input.obj. For an rf_2pts or onemap object, phase can be a vector with user-defined linkage phases (its length is equal to the number of markers minus one); if NULL (default), other functions will try to find the best linkage phases. For example, if phase takes on the vector c(1,2,3,4), the sequence of linkage phases will be coupling/coupling, coupling/repulsion, repulsion/coupling and repulsion/repulsion for a sequence of five markers. If input.obj is of class compare or try, this argument indicates which combination of linkage phases should be chosen, for the particular order given by argument arg. In both cases, NULL (default) makes the best combination to be taken. If input.obj is of class, group, group.upgma or order, this argument has no effect.

data.name the object which contains the raw data. This does not have to be defined by the user: it is here for compatibility issues when calling make_seq from inside other functions.
twopt the object which contains the two-point information. This does not have to be defined by the user: it is here for compatibility issues when calling make_seq from inside other functions.

Value

An object of class sequence, which is a list containing the following components:

seq.num a vector containing the (ordered) indices of markers in the sequence, according to the input file.

seq.phases a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.

seq.rf a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.

seq.like log-likelihood of the corresponding linkage map.

data.name object of class onemap with the raw data.
twopt object of class rf_2pts with the 2-point analyses.

Author(s)

Gabriel Margarido, <gramarga@gmail.com>
References


See Also

compare, try_seq, order_seq and map.

Examples

data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)

all_mark <- make_seq(twopt, "all")
all_mark <- make_seq(twopt, 1:30) # same as above, for this data set
groups <- group(all_mark)
LG1 <- make_seq(groups, 1)
LG1.ord <- order_seq(LG1)
(LG1.final <- make_seq(LG1.ord)) # safe order
(LG1.final.all <- make_seq(LG1.ord, "force")) # forced order

markers <- make_seq(twopt, c(2, 3, 12, 14))
markers.comp <- compare(markers)
(base.map <- make_seq(markers.comp))
(base.map <- make_seq(markers.comp, 1, 1) # same as above
(extend.map <- try_seq(base.map, 30))
(base.map <- make_seq(extend.map, 5)) # fifth position is the best
```r
parallelization.type = "PSOCK",
global_error = NULL,
genotypes_errors = NULL,
genotypes_probs = NULL
)
```

**Arguments**

- `input.seq` an object of class `sequence`.
- `tol` tolerance for the C routine, i.e., the value used to evaluate convergence.
- `verbose` If TRUE, print tracing information.
- `rm_unlinked` When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and returns a vector with remaining marker numbers (useful for `mds_onemap` and `map_avoid_unlinked` functions).
- `phase_cores` number of computer cores to be used in analysis
- `parallelization.type` one of the supported cluster types. This should be either PSOCK (default) or FORK.
- `global_error` single value to be considered as error probability in HMM emission function
- `genotypes_errors` matrix individuals x markers with error values for each marker
- `genotypes_probs` table containing the probability distribution for each combination of marker x individual. Each line on this table represents the combination of one marker with one individual, and the respective probabilities. The table should contain four three columns (prob(AA), prob(AB) and prob(BB)) and individuals*markers rows.

**Details**

Markers are mapped in the order defined in the object `input.seq`. If this object also contains a user-defined combination of linkage phases, recombination frequencies and log-likelihood are estimated for that particular case. Otherwise, the best linkage phase combination is also estimated. The multipoint likelihood is calculated according to Wu et al. (2002b)(Eqs. 7a to 11), assuming that the recombination fraction is the same in both parents. Hidden Markov chain codes adapted from Broman et al. (2008) were used.

**Value**

An object of class `sequence`, which is a list containing the following components:

- `seq.num` a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- `seq.phases` a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- `seq.rf` a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
seq.like  log-likelihood of the corresponding linkage map.
data.name  name of the object of class onemap with the raw data.
twopt  name of the object of class rf_2pts with the 2-point analyses.

Author(s)

Adapted from Karl Broman (package 'qtl') by Gabriel R A Margarido, <gramarga@usp.br> and Marcelo Mollinari, <mmollina@gmail.com>, with minor changes by Cristiane Taniguti and Bastian Schiffthaler

References


See Also

*make_seq*

Examples

```r
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
markers <- make_seq(twopt,c(30,12,3,14,2)) # correct phases
map(markers)

markers <- make_seq(twopt,c(30,12,3,14,2),phase=c(4,1,4,3)) # incorrect phases
map(markers)
```
Simulated data from a F2 population

Description

Simulated data set from a F2 population.

Usage

```r
data("mapmaker_example_f2")
```

Format

The format is: List of 8 $ geno : num [1:200, 1:66] 1 3 2 2 1 0 3 1 1 3 ... - attr(*, "dimnames")=List of 2 ... $ : NULL ...$ : chr [1:66] "M1" "M2" "M3" "M4" ... $ n.ind : num 200 $ n.mar : num 66 $ segr.type : chr [1:66] "A.H.B" "C.A" "D.B" "C.A" ... $ segr.type.num: num [1:66] 1 3 2 3 2 1 3 2 1 ... $ input : chr "/home/cristiane/R/x86_64-pc-linux-gnu-library/3.4/onemap/extdata/mapmaker_example_f2.raw" $ n.phe : num 1 $ pheno : num [1:200, 1] 37.6 36.4 37.2 35.8 37.1 ... - attr(*, "dimnames")=List of 2 ...$ : chr "Trait_1" - attr(*, "class")= chr [1:2] "onemap" "f2"

Details

A total of 200 individuals were genotyped for 66 markers (36 co-dominant, i.e. a, ab or b and 30 dominant i.e. c or a and d or b) with 15% of missing data. There is one quantitative phenotype to show how to use onemap output as R\qtl and QTL Cartographer input. Also, it is used for the analysis in the tutorial that comes with OneMap.

Examples

```r
data(mapmaker_example_f2)

# perform two-point analyses
twopts <- rf_2pts(mapmaker_example_f2)
twopts
```

Repeat HMM if map find unlinked marker

Description

Repeat HMM if map find unlinked marker
map_avoid_unlinked

Usage

map_avoid_unlinked(
  input.seq,
  size = NULL,
  overlap = NULL,
  phase_cores = 1,
  tol = 1e-04,
  parallelization.type = "PSOCK",
  max.gap = FALSE,
  global_error = NULL,
  genotypes_errors = NULL,
  genotypes_probs = NULL
)

Arguments

input.seq object of class sequence
size The center size around which an optimum is to be searched
overlap The desired overlap between batches
phase_cores The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)
tol tolerance for the C routine, i.e., the value used to evaluate convergence.
parallelization.type one of the supported cluster types. This should be either PSOCK (default) or FORK.
max.gap the marker will be removed if it have gaps higher than this defined threshold in both sides
global_error single value to be considered as error probability in HMM emission function
genotypes_errors matrix individuals x markers with error values for each marker
genotypes_probs table containing the probability distribution for each combination of marker × individual. Each line on this table represents the combination of one marker with one individual, and the respective probabilities. The table should contain four three columns (prob(AA), prob(AB) and prob(BB)) and individuals*markers rows.

Value

An object of class sequence, which is a list containing the following components:

seq.num a vector containing the (ordered) indices of markers in the sequence, according to the input file.
seq.phases a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
map_overlapping_batches

Description

Apply the batch mapping algorithm using overlapping windows.

Usage

```r
map_overlapping_batches(
   input.seq,
   size = 50,
   overlap = 15,
   phase_cores = 1,
   verbose = FALSE,
   seeds = NULL,
   tol = 1e-04,
   rm_unlinked = TRUE,
   max.gap = FALSE,
   parallelization.type = "PSOCK"
)
```
Arguments

- **input.seq**: an object of class sequence.
- **size**: The center size around which an optimum is to be searched.
- **overlap**: The desired overlap between batches.
- **phase_cores**: The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)
- **verbose**: A logical, if TRUE its output progress status information.
- **seeds**: A vector of phase information used as seeds for the first batch.
- **tol**: tolerance for the C routine, i.e., the value used to evaluate convergence.
- **rm_unlinked**: When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and map is performed again.
- **max.gap**: the marker will be removed if it have gaps higher than this defined threshold in both sides.
- **parallelization.type**: one of the supported cluster types. This should be either PSOCK (default) or FORK.

Details

This algorithm implements the overlapping batch maps for high density marker sets. The mapping problem is reduced to a number of subsets (batches) which carry information forward in order to more accurately estimate recombination fractions and phasing. It is a adapted version of map.overlapping.batches function of BatchMap package. The main differences are that this onemap version do not have the option to reorder the markers according to ripple algorithm and, if the it finds markers that do not reach the linkage criterias, the algorithm remove the problematic marker and repeat the analysis. Than, the output map can have few markers compared with the input.seq.

Value

An object of class sequence, which is a list containing the following components:

- **seq.num**: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- **seq.phases**: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- **seq.rf**: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- **seq.like**: log-likelihood of the corresponding linkage map.
- **data.name**: name of the object of class outcross with the raw data.
- **twopt**: name of the object of class rf.2pts with the 2-point analyses.

See Also

- `pick_batch_sizes`, `map`
Perform map using background objects with only selected markers. It saves ram memory during the procedure. It is useful if dealing with many markers in total data set.

Usage

map_save_ram(
  input.seq,  # object of class sequence
  tol = 1e-04,  # tolerance for the C routine, i.e., the value used to evaluate convergence.
  verbose = FALSE,  # If TRUE, print tracing information.
  rm_unlinked = FALSE,  # When some pair of markers do not follow the linkage criteria, if TRUE one of the
  phase_cores = 1,  # markers is removed and returns a vector with remaining marker numbers (useful
  size = NULL,  # for mds_onemap and map_avoid_unlinked functions).
  overlap = NULL,  # The number of parallel processes to use when estimating the phase of a marker.
  parallelization.type = "PSOCK",  # (Should be no more than 4)
  max.gap = FALSE  # the marker will be removed if it have gaps higher than this defined threshold in
)

Arguments

input.seq  # object of class sequence
tol  # tolerance for the C routine, i.e., the value used to evaluate convergence.
verbose  # If TRUE, print tracing information.
rm_unlinked  # When some pair of markers do not follow the linkage criteria, if TRUE one of the
phase_cores  # markers is removed and returns a vector with remaining marker numbers (useful
size  # for mds_onemap and map_avoid_unlinked functions).
overlap  # The desired overlap between batches
parallelization.type  # one of the supported cluster types. This should be either PSOCK (default) or
max.gap  # FORK.

marker_type

Informs the segregation patterns of markers

Description

Informs the type of segregation of all markers from an object of class sequence. For outcross populations it uses the notation by Wu et al., 2002. For backcrosses, F2s and RILs, it uses the traditional notation from MAPMAKER i.e. AA, AB, BB, not AA and not BB.

Usage

marker_type(input.seq)

Arguments

input.seq an object of class sequence.

Details

The segregation types are (Wu et al., 2002):

<table>
<thead>
<tr>
<th>Type</th>
<th>Cross</th>
<th>Segregation</th>
</tr>
</thead>
<tbody>
<tr>
<td>A.1</td>
<td>ab x cd</td>
<td>1:1:1:1</td>
</tr>
<tr>
<td>A.2</td>
<td>ab x ac</td>
<td>1:1:1:1</td>
</tr>
<tr>
<td>A.3</td>
<td>ab x co</td>
<td>1:1:1:1</td>
</tr>
<tr>
<td>A.4</td>
<td>ao x bo</td>
<td>1:1:1:1</td>
</tr>
<tr>
<td>B1.5</td>
<td>ab x ao</td>
<td>1:2:1</td>
</tr>
<tr>
<td>B2.6</td>
<td>ao x ab</td>
<td>1:2:1</td>
</tr>
<tr>
<td>B3.7</td>
<td>ab x ab</td>
<td>1:2:1</td>
</tr>
<tr>
<td>C8</td>
<td>ao x ao</td>
<td>3:1</td>
</tr>
<tr>
<td>D1.9</td>
<td>ab x cc</td>
<td>1:1</td>
</tr>
<tr>
<td>D1.10</td>
<td>ab x aa</td>
<td>1:1</td>
</tr>
<tr>
<td>D1.11</td>
<td>ab x oo</td>
<td>1:1</td>
</tr>
<tr>
<td>D1.12</td>
<td>bo x aa</td>
<td>1:1</td>
</tr>
<tr>
<td>D1.13</td>
<td>ao x oo</td>
<td>1:1</td>
</tr>
<tr>
<td>D2.14</td>
<td>cc x ab</td>
<td>1:1</td>
</tr>
<tr>
<td>D2.15</td>
<td>aa x ab</td>
<td>1:1</td>
</tr>
<tr>
<td>D2.16</td>
<td>oo x ab</td>
<td>1:1</td>
</tr>
<tr>
<td>D2.17</td>
<td>aa x bo</td>
<td>1:1</td>
</tr>
<tr>
<td>D2.18</td>
<td>oo x ao</td>
<td>1:1</td>
</tr>
</tbody>
</table>

Value

data.frame with segregation types of all markers in the sequence are displayed on the screen.

Author(s)

Gabriel R A Margarido, <gramarga@gmail.com>
References


See Also

make_seq

Examples

```r
data(onemap_example_out)
twopts <- rf_2pts(onemap_example_out)
markers.ex <- make_seq(twopts,c(3,6,8,12,16,25))
marker_type(input.seq = markers.ex) # segregation type for some markers

data(onemap_example_f2)
twopts <- rf_2pts(onemap_example_f2)
all_mrk <- make_seq(twopts, "all")
lg1 <- group(all_mrk)
lg1 <- make_seq(lg1,1)
marker_type(lg1) # segregation type for linkage group 1
```

**mds_onemap**

*OneMap interface with MDSMap package with possibility of multi-point distances estimation*

**Description**

For a given sequence of markers, apply mds method described in Preedy and Hackett (2016) using MDSMap package to ordering markers and estimates the genetic distances with OneMap multipoint approach. Also gives MDSMap input file format for directly analysis in this package.

**Usage**

```r
mds_onemap(
    input.seq, 
    out.file = NULL, 
    p = NULL, 
    ispc = TRUE, 
    displaytext = FALSE, 
    weightfn = "lod2", 
    mapfn = "haldane", 
    ndim = 2, 
    rm_unlinked = TRUE, 
    size = NULL, 
    overlap = NULL,
```
phase_cores = 1,
tol = 1e-05,
HMM = TRUE,
parallelization.type = "PSOCK"
)

**Arguments**

input.seq  an object of class sequence

out.file  path to the generated MDSMap input file.

p  Integer - the penalty for deviations from the sphere - higher p forces points more closely onto a sphere.

ispc  Logical determining the method to be used to estimate the map. By default this is TRUE and the method of principal curves will be used. If FALSE then the constrained MDS method will be used.

displaytext  Shows markers names in analysis graphic view

weightfn  Character string specifying the values to use for the weight matrix in the MDS 'lod2' or 'lod'.

mapfn  Character string specifying the map function to use on the recombination fractions 'haldane' is default, 'kosambi' or 'none'.

ndim  number of dimensions to be considered in the multidimensional scaling procedure (default = 2)

rm_unlinked  When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and mds is performed again.

size  The center size around which an optimum is to be searched

overlap  The desired overlap between batches

phase_cores  The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)

tol  tolerance for the C routine, i.e., the value used to evaluate convergence.

HMM  logical defining if the HMM must be applied to estimate multipoint genetic distances

parallelization.type  one of the supported cluster types. This should be either PSOCK (default) or FORK.

**Details**

For better description about MDS method, see MDSMap package vignette.

**Value**

An object of class sequence, which is a list containing the following components:

seq.num  a vector containing the (ordered) indices of markers in the sequence, according to the input file.
seq.phases a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.

seq.rf a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.

data.name name of the object of class onemap with the raw data.

twopt name of the object of class rf_2pts with the 2-point analyses.

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

References


See Also

https://CRAN.R-project.org/package=MDSMap.

---

**Simulated data from a backcross population**

Description

Simulated data set from a backcross population.

Usage

data(onemap_example_bc)
Format

The format is: List of 10 $ geno : num [1:150, 1:67] 1 2 1 2 1 2 1 2 ... - attr(*, "dimnames")=List of 2 .. ..$ : chr [1:150] "ID1" "ID2" "ID3" "ID4" ... ..$ : chr [1:67] "M1" "M2" "M3" "M4" ... $ n.ind : int 150 $ n.mar : int 67 $ segr.type : chr [1:67] "A.H" "A.H" "A.H" "A.H" ... $ segr.type.num: logi [1:67] NA NA NA NA NA NA ... $ n.phe : int 1 $ pheno : num [1:150, 1] 40.8 39.5 37.9 34.2 38.9 ... ..- attr(*, "dimnames")=List of 2 .. ..$ : NULL .. ..$ : chr "Trait_1" $ CHROM : NULL $ POS : NULL $ input : chr "onemap_example_bc.raw" - attr(*, "class")= chr [1:2] "onemap" "backcross"

Details

A total of 150 individuals were genotyped for 67 markers with 15% of missing data. There is one quantitative phenotype to show how to use onemap output as R\texttt{qtl} input.

Author(s)

Marcelo Mollinari, <mmollina@usp.br>

See Also

\texttt{read_onemap} and \texttt{read_mapmaker}.

Examples

```r
data(onemap_example_bc)
# perform two-point analyses
twopts <- rf_2pts(onemap_example_bc)
twopts
```

---

onemap_example_f2

\textit{Simulated data from a F2 population}

Description

Simulated data set from a F2 population.

Usage

data("onemap_example_f2")

Format

The format is: List of 10 $ geno : num [1:200, 1:66] 1 3 2 2 1 0 3 1 3 ... - attr(*, "dimnames")=List of 2 .. ..$ : chr [1:200] "IND1" "IND2" "IND3" "IND4" ... ..$ : chr [1:66] "M1" "M2" "M3" "M4" ... $ n.ind : int 200 $ n.mar : int 66 $ segr.type : chr [1:66] "A.H.B" "C.A" "D.B" "C.A" ... $ segr.type.num: num [1:66] 1 3 2 3 3 2 1 3 2 1 ... $ n.phe : int 1 $ pheno : num [1:200, 1] 37.6 36.4 37.2 35.8 37.1 ... ..- attr(*, "dimnames")=List of 2 .. ..$ : NULL .. ..$ : chr "Trait_1" $ CHROM : NULL $ POS : NULL $ input : chr "/home/cristiane/R/x86_64-pc-linux-gnu-library/3.4/onemap/extdata/onemap_example_f2.raw" - attr(*, "class")= chr [1:2] "onemap" "f2"
Details

A total of 200 individuals were genotyped for 66 markers (36 co-dominant, i.e. a, ab or b and 30 dominant i.e. c or a and d or b) with 15% of missing data. There is one quantitative phenotype to show how to use onemap output as R\qt1 and QTL Cartographer input. Also, it is used for the analysis in the tutorial that comes with OneMap.

Examples

```r
data(onemap_example_f2)
plot(onemap_example_f2)
```

---

### onemap_example_out

*Data from a full-sib family derived from two outbred parents*

Description

Simulated data set for an outcross, i.e., an F1 population obtained by crossing two non-homozygous parents.

Usage

```r
data(onemap_example_out)
```

Format

An object of class onemap.

Details

A total of 100 F1 individuals were genotyped for 30 markers. The data currently contains only genotype information (no phenotypes). It is included to be used as a reference in order to understand how a data file needs to be. Also, it is used for the analysis in the tutorial that comes with OneMap.

Author(s)

Gabriel R A Margarido, <gramarga@gmail.com>

See Also

`read_onemap` for details about objects of class onemap.

Examples

```r
data(onemap_example_out)

# perform two-point analyses
twopts <- rf_2pts(onemap_example_out)
twopts
```
Simulated data from a RIL population produced by selfing.

Description

Simulated biallelic data set for an RI self population.

Usage

```r
data("onemap_example_riself")
```

Format

The format is:

```r
List of 10
$ geno : num [1:100, 1:68] 3 1 3 1 1 1 1 1 1 1 ... attr(*, "dimnames")=List
of 2
..$ : chr [1:100] "ID1" "ID2" "ID3" "ID4" ... ..$ : chr [1:68] "M1" "M2" "M3" "M4" ... $ n.ind : int 100 $ n.mar : int 68 $ segr.type : chr [1:68] "A.B" "A.B" "A.B" "A.B" ... $ segr.type.num: logi [1:68] NA NA NA NA NA NA ... $ n.phe : int 0 $ pheno : NULL $ CHROM : NULL $ POS : NULL $ input : chr "onemap_example_riself.raw" - attr(*, "class")= chr [1:2] "onemap" "riself"
```

Details

A total of 100 F1 individuals were genotyped for 68 markers. The data currently contains only genotype information (no phenotypes). It is included to be used as a reference in order to understand how a data file needs to be.

Author(s)

Cristiane Taniguti, <chtaniguti@usp.br>

See Also

- `read_onemap` for details about objects of class onemap.

Examples

```r
data(onemap_example_riself)
plot(onemap_example_riself)
```
onemap_read_vcfR

Convert vcf file to onemap object

Description

Converts data from a vcf file to onemap initial object, while identify the appropriate marker segregation patterns.

Usage

onemap_read_vcfR(
  vcf = NULL,
  vcfR.object = NULL,
  cross = c("outcross", "f2 intercross", "f2 backcross", "ri self", "ri sib"),
  parent1 = NULL,
  parent2 = NULL,
  f1 = NULL,
  only_biallelic = TRUE,
  output_info_rds = NULL,
  verbose = TRUE
)

Arguments

vcf string defining the path to VCF file;
vcfR.object object of class vcfR;
cross type of cross. Must be one of: "outcross" for full-sibs; "f2 intercross" for an F2 intercross progeny; "f2 backcross"; "ri self" for recombinant inbred lines by self-mating; or "ri sib" for recombinant inbred lines by sib-mating.
parent1 string specifying sample ID of the first parent. If f2 backcross population, define here the ID of the backcrossed parent.
parent2 string specifying sample ID of the second parent.
f1 string if you are working with f2 intercross or backcross populations you may have f1 parents in your vcf, specify its ID here
only_biallelic if TRUE (default) only biallelic markers are considered, if FALSE multiallelic markers are included.
output_info_rds define a name for the file with alleles information.
verbose A logical, if TRUE it output progress status information.

Details

Only biallelic SNPs and indels for diploid variant sites are considered.

Genotype information on the parents is required for all cross types. For full-sib progenies, both outbred parents must be genotyped. For backcrosses, F2 intercrosses and recombinant inbred lines,
the original inbred lines must be genotyped. Particularly for backcross progenies, the recurrent line must be provided as the first parent in the function arguments.

Marker type is determined based on parental genotypes. Variants for which parent genotypes cannot be determined are discarded.

Reference sequence ID and position for each variant site are also stored.

Value

An object of class onemap, i.e., a list with the following components:

- `geno` a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- `n.ind` number of individuals.
- `n.mar` number of markers.
- `segr.type` a vector with the segregation type of each marker, as strings.
- `segr.type.num` a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- `input` the name of the input file.
- `n.phe` number of phenotypes.
- `pheno` a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.
- `error` matrix containing HMM emission probabilities

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

See Also

- `read_onemap` for a description of the output object of class onemap.

Examples

```r
data <- onemap_read_vcfR(vcf=system.file("extdata/vcf_example_out.vcf.gz", package = "onemap"),
                          cross="outcross",
                          parent1=c("P1"),
                          parent2=c("P2"))
```
order_seq

Search for the best order of markers combining compare and try_seq functions

Description

For a given sequence of markers, this function first uses the compare function to create a framework for a subset of informative markers. Then, it tries to map remaining ones using the try_seq function.

Usage

order_seq(
  input.seq,
  n.init = 5,
  subset.search = c("twopt", "sample"),
  subset.n.try = 30,
  subset.THRES = 3,
  twopt.alg = c("rec", "rcd", "ser", "ug"),
  THRES = 3,
  touchdown = FALSE,
  tol = 0.1,
  rm_unlinked = FALSE,
  verbose = FALSE
)

Arguments

- **input.seq**: an object of class sequence.
- **n.init**: the number of markers to be used in the compare step (defaults to 5).
- **subset.search**: a character string indicating which method should be used to search for a subset of informative markers for the compare step. It is used for backcross, $F_2$ or RIL populations, but not for outcrosses. See the Details section.
- **subset.n.try**: integer. The number of times to repeat the subset search procedure. It is only used if subset.search=="sample". See the Details section.
- **subset.THRES**: numerical. The threshold for the subset search procedure. It is only used if subset.search=="sample". See the Details section.
- **twopt.alg**: a character string indicating which two-point algorithm should be used if subset.search=="twopt". See the Details section.
- **THRES**: threshold to be used when positioning markers in the try_seq step.
- **touchdown**: logical. If FALSE (default), the try_seq step is run only once, with the value of THRES. If TRUE, try_seq runs with THRES and then once more, with THRES-1. The latter calculations take longer, but usually are able to map more markers.
- **tol**: tolerance number for the C routine, i.e., the value used to evaluate convergence of the EM algorithm.
When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and returns a vector with remaining marker numbers (useful for mds_onemap and map_avoid_unlinked functions).

verbose
A logical, if TRUE its output progress status information.

Details
For outcrossing populations, the initial subset and the order in which remaining markers will be used in the try_seq step is given by the degree of informativeness of markers (i.e. markers of type A, B, C and D, in this order).

For backcrosses, F2s or RILs, two methods can be used for choosing the initial subset: i) "sample" randomly chooses a number of markers, indicated by n.init, and calculates the multipoint log-likelihood of the \(\frac{n\text{init}}{2}\) possible orders. If the LOD Score of the second best order is greater than subset.THRES, than it takes the best order to proceed with the try_seq step. If not, the procedure is repeated. The maximum number of times to repeat this procedure is given by the subset.n.try argument. ii) "twopt" uses a two-point based algorithm, given by the option "twopt.alg", to construct a two-point based map. The options are "rec" for RECORD algorithm, "rcd" for Rapid Chain Delineation, "ser" for Seriation and "ug" for Unidirectional Growth. Then, equally spaced markers are taken from this map. The "compare" step will then be applied on this subset of markers.

In both cases, the order in which the other markers will be used in the try_seq step is given by marker types (i.e. co-dominant before dominant) and by the missing information on each marker.

After running the compare and try_seq steps, which result in a "safe" order, markers that could not be mapped are "forced" into the map, resulting in a map with all markers positioned.

Value
An object of class order, which is a list containing the following components:

ord an object of class sequence containing the "safe" order.
mrk.unpos a vector with unpositioned markers (if they exist).
LOD.unpos a matrix with LOD-Scores for unmapped markers, if any, for each position in the "safe" order.
THRES the same as the input value, just for printing.
ord.all an object of class sequence containing the "forced" order, i.e., the best order with all markers.
data.name name of the object of class onemap with the raw data.
twopt name of the object of class rf_2pts with the 2-point analyses.

Author(s)
Gabriel R A Margarido, <gramarga@usp.br> and Marcelo Mollinari, <mmollina@gmail.com>
References


See Also

make_seq, compare and try_seq.

Examples

```r
#outcross example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG2 <- make_seq(groups,2)
LG2.ord <- order_seq(LG2, touchdown=TRUE)
LG2.ord
make_seq(LG2.ord) # get safe sequence
make_seq(LG2.ord,"force") # get forced sequence
```

parents_haplotypes

Generates data.frame with parents estimated haplotypes

Description

Generates data.frame with parents estimated haplotypes
Usage

```r
parents_haplotypes(..., group_names = NULL)
```

Arguments

- `...` objects of class sequence
- `group_names` vector of characters defining the group names

Value

data.frame with group ID (group), marker number (mk.number) and names (mk.names), position in centimorgan (dist) and parents haplotypes (P1_1, P1_2, P2_1, P2_2)

Author(s)

Getulio Caixeta Ferreira, <getulio.caifer@gmail.com>

Cristiane Taniguti, <chtaniguti@tamu.edu>

Examples

```r
data("onemap_example_out")
twopts <- rf_2pts(onemap_example_out)
lgl <- make_seq(twopts, 1:5)
lgl.map <- map(lgl)
parents_haplotypes(lgl.map)
```

Description

Based on the strategy propoused by Schiffthaler et al. the markers of a linkage group with pre-defined order are divided in user defined batches with overlap markers between them. Each batch runs in a different core which increase the speed of the genetic distances estimation. The distances and phases of the previous batch are considered to joint the batches. Also, it is possible to store the differences between the genetic distances between the overlaped markers as a measure of the process quality. In other words, if these differences are to too high, you can considered that divide the group in batch did not compromise the distance estimation.
Usage

```r
gemaptm(input.seq = NULL, 
cores = 3, 
overlap = 4, 
tol = 1e-04, 
avoid_link_errors = TRUE, 
export_diff = FALSE, 
verbose = TRUE)
```

Arguments

- `input.seq`: an object of class `sequence`.
- `cores`: an integer defining the number of cores to be used and also the number of batches generated.
- `overlap`: number of markers overlapping between batches.
- `tol`: tolerance for the C routine, i.e., the value used to evaluate convergence.
- `avoid_link_errors`: logical. If TRUE markers which do not reach the linkage criteria are removed of the sequence and the distances are automatically reestimated. If FALSE an error stops the algorithm it find these markers.
- `export_diff`: If TRUE also returns (in the first level of the list) the differences in genetic distances between overlaped markers.
- `verbose`: A logical, if TRUE its output progress status information.

Value

An object of class `sequence`, which is a list containing the following components:

- `seq.num`: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- `seq.phases`: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- `seq.rf`: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- `seq.like`: log-likelihood of the corresponding linkage map.
- `data.name`: name of the object of class `onemap` with the raw data.
- `twopt`: name of the object of class `rf_2pts` with the 2-point analyses.

Author(s)

Cristiane Taniguti <chtaniguti@tamu.edu>
References


See Also

map

---

**pick_batch_sizes**   Picking optimal batch size values

**Description**

Suggest an optimal batch size value for use in map_overlapping_batches

**Usage**

pick_batch_sizes(input.seq, size = 50, overlap = 15, around = 5)

**Arguments**

- **input.seq**: an object of class sequence.
- **size**: The center size around which an optimum is to be searched
- **overlap**: The desired overlap between batches
- **around**: The range around the center which is maximally allowed to be searched.

**Value**

An integer value for the size which most evenly divides batches. In case of ties, bigger batch sizes are preferred.

**Author(s)**

Bastian Schiffthaler, <bastian.schiffthaler@umu.se>

**See Also**

map_overlapping_batches

**Examples**

```r
LG <- structure(list(seq.num = seq(1,800)), class = "sequence")
batchsize <- pick_batch_sizes(LG, 50, 19)
```
plot.onemap

**Description**

Shows a heatmap (in ggplot2, a graphic of geom "tile") for raw data. Lines correspond to markers and columns to individuals. The function can plot a graph for all marker types, depending of the cross type (dominant/codominant markers, in all combinations). The function receives a onemap object of class onemap, reads information from genotypes from this object, converts it to a long dataframe format using function melt() from package reshape2() or internal function create_dataframe_for_plot_outcross(), converts numbers from the object to genetic notation (according to the cross type), then plots the graphic. If there is more than 20 markers, removes y labels For outcross populations, it can show all markers together, or it can split them according the segregation pattern.

**Usage**

```r
## S3 method for class 'onemap'
plot(x, all = TRUE, ...)
```

**Arguments**

- `x` an object of class onemap, with data and additional information
- `all` a TRUE/FALSE option to indicate if results will be plotted together (if TRUE) or splitted based on their segregation pattern. Only used for outcross populations.
- `...` currently ignored

**Value**

a ggplot graphic

**Examples**

```r
# library(ggplot2)
data(onemap_example_bc) # Loads a fake backcross dataset installed with onemap
plot(onemap_example_bc) # This will show you the graph

# You can store the graphic in an object, then save it with a number of properties
# For details, see the help of ggplot2's function ggsave()
g <- plot(onemap_example_bc)

data(onemap_example_f2) # Loads a fake backcross dataset installed with onemap
plot(onemap_example_f2) # This will show you the graph

# You can store the graphic in an object, then save it with a number of properties
# For details, see the help of ggplot2's function ggsave()
```
plot.onemap_progeny_haplotypes

Plots progeny haplotypes

Description

Figure is generated with the haplotypes for each selected individual. As a representation, the recombination breakpoints are here considered to be in the mean point of the distance between two markers. It is important to highlight that it did not reflects the exact breakpoint position, specially if the genetic map have low resolution.

Usage

```r
## S3 method for class 'onemap_progeny_haplotypes'
plot(
  x,
  col = NULL,
  position = "stack",
  show_markers = TRUE,
  main = "Genotypes",
  ncol = 4,
  ...)
```

Arguments

- `x` object of class onemap_progeny_haplotypes
- `col` Color of parentes' homologous.
- `position` "split" or "stack"; if "split" (default) the alleles' are plotted separately. if "stack" the parents' alleles are plotted together.
- `show_markers` logical; if TRUE, the markers (default) are plotted.
- `main` An overall title for the plot; default is NULL.
- `ncol` number of columns of the facet_wrap
- `...` currently ignored
**Value**

a ggplot graphic

**Author(s)**

Getulio Caixeta Ferreira, <getulio.caifer@gmail.com>
Cristiane Taniguti, <chtaniguti@tamu.edu>

**Examples**

```
data("onemap_example_out")
twopts <- rf_2pts(onemap_example_out)
lgl <- make_seq(twopts, 1:5)
lgl.map <- map(lgl)
plot(progeny_haplotypes(lgl.map))
```

---

**Description**

Plot recombination breakpoints counts for each individual

**Usage**

```r
## S3 method for class 'onemap_progeny_haplotypes_counts'
plot(x, by_homolog = FALSE, n.graphics = NULL, ncol = NULL, ...)
```

**Arguments**

- `x` object of class `onemap_progeny_haplotypes_counts`
- `by_homolog` logical, if TRUE plots counts by homolog (two for each individuals), if FALSE plots total counts by individual
- `n.graphics` integer defining the number of graphics to be plotted, they separate the individuals in different plots
- `ncol` integer defining the number of columns in plot
- `...` currently ignored

**Value**

a ggplot graphic
Examples

```r
data("onemap_example_out")
twopts <- rf_2pts(onemap_example_out)
lgl <- make_seq(twopts, 1:5)
lgl.map <- map(lgl)
prog.haplo <- progeny_haplotypes(lgl.map, most_likely = TRUE)
plot(progeny_haplotypes_counts(prog.haplo))
```

Description

Draw a graphic showing the p-values (re-scaled to -log10(p-values)) associated with the chi-square tests for the expected segregation patterns for all markers in a dataset. It includes a vertical line showing the threshold for declaring statistical significance if Bonferroni’s correction is considered, as well as the percentage of markers that will be discarded if this criterion is used.

Usage

```r
## S3 method for class 'onemap_segreg_test'
plot(x, order = TRUE, ...)
```

Arguments

- `x`:
  - an object of class `onemap_segreg_test` (produced by `onemap`’s function `test_segregation()`), i.e., after performing segregation tests
- `order`:
  - a variable to define if p-values will be ordered in the plot
- `...`:
  - currently ignored

Value

- a ggplot graphic

Examples

```r
data(onemap_example_bc) # load OneMap's fake dataset for a backcross population
BC.seg <- test_segregation(onemap_example_bc) # Applies chi-square tests
print(BC.seg) # Shows the results
plot(BC.seg) # Plot the graph, ordering the p-values
plot(BC.seg, order=FALSE) # Plot the graph showing the results keeping the order in the dataset

data(onemap_example_out) # load OneMap's fake dataset for an outcrossing population
```
plot_by_segreg_type

Out.seg <- test_segregation(onemap_example_out) # Applies chi-square tests
print(Out.seg) # Shows the results
plot(Out.seg) # Plot the graph, ordering the p-values
plot(Out.seg, order=FALSE) # Plot the graph showing the results keeping the order in the dataset

plot_by_segreg_type

Draw a graphic showing the number of markers of each segregation pattern.

Description

The function receives an object of class onemap. For outcrossing populations, it can show detailed information (all 18 possible categories), or a simplified version.

Usage

plot_by_segreg_type(x, subcateg = TRUE)

Arguments

x an object of class onemap
subcateg a TRUE/FALSE option to indicate if results will be plotted showing all possible categories (only for outcrossing populations)

Value

a ggplot graphic

Examples

data(onemap_example_out) #Outcrossing data
plot_by_segreg_type(onemap_example_out)
plot_by_segreg_type(onemap_example_out, subcateg=FALSE)

data(onemap_example_bc)
plot_by_segreg_type(onemap_example_bc)

data(mapmaker_example_f2)
plot_by_segreg_type(mapmaker_example_f2)
print.compare  

**Description**

print method for object class 'compare'

**Usage**

```r
## S3 method for class 'compare'
print(x, ...)
```

**Arguments**

- `x` object of class compare
- `...` currently ignored

**Value**

compare object description

print.onemap  

**Description**

Print method for object class 'onemap'

**Usage**

```r
## S3 method for class 'onemap'
print(x, ...)
```

**Arguments**

- `x` object of class onemap
- `...` currently ignored

**Value**

printed information about onemap object
print.onemap_bin

print method for object class 'onemap_bin'

Description

print method for object class 'onemap_bin'

Usage

```r
## S3 method for class 'onemap_bin'
print(x, ...)
```

Arguments

- **x** 
  object of class onemap_bin
- **...** 
  currently ignored

Value

No return value, called for side effects

print.onemap-segreg_test

Show the results of segregation tests

Description

It shows the results of Chisquare tests performed for all markers in a onemap object of cross type outcross, backcross, F2 intercross or recombinant inbred lines.

Usage

```r
## S3 method for class 'onemap-segreg_test'
print(x, ...)
```

Arguments

- **x** 
  an object of class onemap-segreg_test
- **...** 
  currently ignored

Value

a dataframe with marker name, H0 hypothesis, chi-square statistics, p-values, and
Examples

```r
data(onemap_example_out) # Loads a fake outcross dataset installed with onemap
Chi <- test_segregation(onemap_example_out) # Performs the chi-square test for all markers
print(Chi) # Shows the results
```

---

**print.order**

*Print order_seq object*

**Description**

Print order_seq object

**Usage**

```r
## S3 method for class 'order'
print(x, ...)
```

**Arguments**

- `x`: object of class `order_seq`
- `...`: currently ignored

**Value**

printed information about order_seq object

---

**print.sequence**

*Print method for object class 'sequence'*

**Description**

Print method for object class 'sequence'

**Usage**

```r
## S3 method for class 'sequence'
print(x, ...)
```

**Arguments**

- `x`: object of class `sequence`
- `...`: currently ignored
progeny_haplotypes  Generate data.frame with genotypes estimated by HMM and its probabilities

Description
Generate data.frame with genotypes estimated by HMM and its probabilities

Usage

progeny_haplotypes(..., ind = 1, group_names = NULL, most_likely = FALSE)

Arguments

...  Map(s) or list(s) of maps. Object(s) of class sequence.
ind  vector with individual index to be evaluated or "all" to include all individuals
group_names  Names of the groups.
most_likely  logical; if TRUE, the most likely genotype receive 1 and all the rest 0. If there are more than one most likely both receive 0.5. if FALSE (default) the genotype probability is plotted.

Value

a data.frame information: individual (ind) and marker ID, group ID (grp), position in centimorgan (pos), genotypes probabilities (prob), parents, and the parents homologs and the allele IDs.

Author(s)

Getulio Caixeta Ferreira, <getulio.caifer@gmail.com>
Cristiane Taniguti, <chtaniguti@tamu.edu>

Examples

data("onemap_example_out")
twopts <- rf_2pts(onemap_example_out)
lgl <- make_seq(twopts, 1:5)
lgl.map <- map(lgl)
progeny_haplotypes(lgl.map)
progeny_haplotypes_counts

*Plot number of breakpoints by individuals*

**Description**

Generate graphic with the number of breakpoints for each individual considering the most likely genotypes estimated by the HMM. Genotypes with the same probability for two genotypes are removed. By now, only available for outcrossing and F2 intercross.

**Usage**

```r
progeny_haplotypes_counts(x)
```

**Arguments**

- `x` object of class `onemap_progeny_haplotypes`

**Value**

A data frame with columns individuals ID (ind), group ID (grp), homolog (homolog) and counts of breakpoints.

**Examples**

```r
data("onemap_example_out")
twopts <- rf_2pts(onemap_example_out)
lgl <- make_seq(twopts, 1:5)
lgl.map <- map(lgl)
progeny_haplotypes_counts(progeny_haplotypes(lgl.map, most_likely = TRUE))
```

---

rcd

*Rapid Chain Delineation*

**Description**

Implements the marker ordering algorithm *Rapid Chain Delineation* (Doerge, 1996).
Usage

rcd(
  input.seq,
  LOD = 0,
  max.rf = 0.5,
  tol = 1e-04,
  rm_unlinked = TRUE,
  size = NULL,
  overlap = NULL,
  phase_cores = 1,
  hmm = TRUE,
  parallelization.type = "PSOCK",
  verbose = TRUE
)

Arguments

input.seq   an object of class sequence.
LOD         minimum LOD-Score threshold used when constructing the pairwise recombination fraction matrix.
max.rf      maximum recombination fraction threshold used as the LOD value above.
tol         tolerance for the C routine, i.e., the value used to evaluate convergence.
rm_unlinked When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and rcd is performed again.
size        The center size around which an optimum is to be searched
overlap     The desired overlap between batches
phase_cores The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)
hmm         logical defining if the HMM must be applied to estimate multipoint genetic distances
parallelization.type one of the supported cluster types. This should be either PSOCK (default) or FORK.
verbose     A logical, if TRUE it output progress status information.

Details

*Rapid Chain Delineation (RCD)* is an algorithm for marker ordering in linkage groups. It is not an exhaustive search method and, therefore, is not computationally intensive. However, it does not guarantee that the best order is always found. The only requirement is a matrix with recombination fractions between markers. Next is an excerpt from QTL Cartographer Version 1.17 Manual describing the *RCD* algorithm (Basten et al., 2005):

*The linkage group is initiated with the pair of markers having the smallest recombination fraction. The remaining markers are placed in a “pool” awaiting placement on the map. The linkage group is extended by adding markers from the pool of unlinked markers. Each terminal marker of the*
linkage group is a candidate for extension of the chain: The unlinked marker that has the smallest recombination fraction with either is added to the chain subject to the provision that the recombination fraction is statistically significant at a prespecified level. This process is repeated as long as markers can be added to the chain.

After determining the order with RCD, the final map is constructed using the multipoint approach (function map).

Value

An object of class sequence, which is a list containing the following components:

- seq.num: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- seq.phases: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- seq.rf: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- seq.like: log-likelihood of the corresponding linkage map.
- data.name: name of the object of class onemap with the raw data.
- twopt: name of the object of class rf_2pts with the 2-point analyses.

Author(s)

Gabriel R A Margarido, <gramarga@gmail.com>

References


See Also

make_seq, map

Examples

# outcross example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG1 <- make_seq(groups,1)
LG1.rcd <- rcd(LG1, hmm = FALSE)

#F2 example
data(onemap_example_f2)
twopt <- rf_2pts(onemap_example_f2)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG1 <- make_seq(groups,1)
LG1.rcd <- rcd(LG1, hmm = FALSE)
LG1.rcd

---

**read_mapmaker**

*Read data from a Mapmaker raw file*

**Description**
Imports data from a Mapmaker raw file.

**Usage**

```r
read_mapmaker(file = NULL, dir = NULL, verbose = TRUE)
```

**Arguments**

- `file` (the name of the input file which contains the data to be read).
- `dir` (directory where the input file is located).
- `verbose` (A logical, if TRUE it output progress status information).

**Details**

For details about MAPMAKER files see Lincoln et al. (1993). The current version supports backcross, F2s and RIL populations. The file can contain phenotypic data, but it will not be used in the analysis.

**Value**

An object of class onemap, i.e., a list with the following components:

- `geno` (a matrix with integers indicating the genotypes read for each marker in onemap fashion. Each column contains data for a marker and each row represents an individual.

MAPMAKER/EXP fashion, i.e., 1, 2, 3: AA, AB, BB, respectively; 3, 4: BB, not BB, respectively; 1, 5: AA, not AA, respectively. Each column contains data for a marker and each row represents an individual.

- `n.ind` (number of individuals).
n.mar  number of markers.
segr.type  a vector with the segregation type of each marker, as strings. Segregation
types were adapted from outcross segregation types, using the same notation.
For details see read_onemap.
segr.type.num  a vector with the segregation type of each marker, represented in a simplified
manner as integers. Segregation types were adapted from outcross segregation
types. For details see read_onemap.
input  the name of the input file.
n.phe  number of phenotypes.
pheno  a matrix with phenotypic values. Each column contains data for a trait and each
row represents an individual. Currently ignored.
error  matrix containing HMM emission probabilities

Author(s)
Adapted from Karl Broman (package qtl) by Marcelo Mollinari, <mmollina@usp.br>

References
experiments R package version 1.09-43
Lincoln, S. E., Daly, M. J. and Lander, E. S. (1993) Constructing genetic linkage maps with MAP-
MAKER/EXP Version 3.0: a tutorial and reference manual. A Whitehead Institute for Biomedical

See Also
mapmaker_example_bc and mapmaker_example_f2 raw files in the package source.

Examples

map_data <- read_mapmaker(file=system.file("extdata/mapmaker_example_f2.raw", package = "onemap"))
#Checking 'mapmaker_example_f2'
data(mapmaker_example_f2)
names(mapmaker_example_f2)
Usage

read_onemap(inputfile = NULL, dir = NULL, verbose = TRUE)

Arguments

inputfile  the name of the input file which contains the data to be read.
dir  directory where the input file is located.
verbose  A logical, if TRUE it output progress status information.

Details

The file format is similar to that used by MAPMAKER/EXP (Lincoln et al., 1993). The first line indicates the cross type and is structured as data type \{cross\}, where cross must be one of "outcross", "f2 intercross", "f2 backcross", "ri self" or "ri sib". The second line contains five integers: i) the number of individuals; ii) the number of markers; iii) an indicator variable taking the value 1 if there is CHROM information, i.e., if markers are anchored on any reference sequence, and 0 otherwise; iv) a similar 1/0 variable indicating whether there is POS information for markers; and v) the number of phenotypic traits.

The next line contains sample IDs, separated by empty spaces or tabs. Addition of this sample ID requirement makes it possible for separate input datasets to be merged.

Next comes the genotype data for all markers. Each new marker is initiated with a "*" (without the quotes) followed by the marker name, without any space between them. Each marker name is followed by the corresponding segregation type, which may be: "A.1", "A.2", "A.3", "A.4", "B1.5", "B2.6", "B3.7", "C.8", "D1.9", "D1.10", "D1.11", "D1.12", "D1.13", "D2.14", "D2.15", "D2.16", "D2.17" or "D2.18" (without quotes), for full-sibs [see marker_type and Wu et al. (2002) for details]. Other cross types have special marker types: "A.H" for backcrosses; "A.H.B" for F2 intercrosses; and "A.B" for recombinant inbred lines.

After the segregation type comes the genotype data for the corresponding marker. Depending on the segregation type, genotypes may be denoted by ac, ad, bc, bd, a, ba, b, bc, ab and o, in several possible combinations. To make things easier, we have followed exactly the notation used by Wu et al. (2002). Allowed values for backcrosses are a and ab; for F2 crosses they are a, ab and b; for RILs they may be a and b. Genotypes must be separated by a space. Missing values are denoted by "-".

If there is physical information for markers, i.e., if they are anchored at specific positions in reference sequences (usually chromosomes), this is included immediately after the marker data. These lines start with special keywords *CHROM and *POS and contain strings and integers, respectively, indicating the reference sequence and position for each marker. These also need to be separated by spaces.

Finally, if there is phenotypic data, it will be added just after the marker or CHROM/POS data. They need to be separated by spaces as well, using the same symbol for missing information.

The example directory in the package distribution contains an example data file to be read with this function. Further instructions can be found at the tutorial distributed along with this package.

Value

An object of class onemap, i.e., a list with the following components:
read_onemap

- **geno**: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.

- **n.ind**: number of individuals.

- **n.mar**: number of markers.

- **segr.type**: a vector with the segregation type of each marker, as strings.

- **segr.type.num**: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.

- **input**: the name of the input file.

- **n.phe**: number of phenotypes.

- **pheno**: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.

- **error**: matrix containing HMM emission probabilities

**Author(s)**

Gabriel R A Margarido, <gramarga@gmail.com>

**References**


**See Also**

- `combine_onemap`
- the example directory in the package source.

**Examples**

```r
outcr_data <- read_onemap(inputfile= system.file("extdata/onemap_example_out.raw", package= "onemap"))
```
Description

Implements the marker ordering algorithm *Recombination Counting and Ordering* (Van Os et al., 2005).

Usage

```r
record(
  input.seq,
  times = 10,
  LOD = 0,
  max.rf = 0.5,
  tol = 1e-04,
  rm_unlinked = TRUE,
  size = NULL,
  overlap = NULL,
  phase_cores = 1,
  hmm = TRUE,
  parallelization.type = "PSOCK",
  verbose = TRUE
)
```

Arguments

- `input.seq` an object of class `sequence`.
- `times` integer. Number of replicates of the RECORD procedure.
- `LOD` minimum LOD-Score threshold used when constructing the pairwise recombination fraction matrix.
- `max.rf` maximum recombination fraction threshold used as the LOD value above.
- `tol` tolerance for the C routine, i.e., the value used to evaluate convergence.
- `rm_unlinked` When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and record is performed again.
- `size` The center size around which an optimum is to be searched
- `overlap` The desired overlap between batches
- `phase_cores` The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)
- `hmm` logical defining if the HMM must be applied to estimate multipoint genetic distances
- `parallelization.type` one of the supported cluster types. This should be either PSOCK (default) or FORK.
- `verbose` A logical, if TRUE it output progress status information.
Details

Recombination Counting and Ordering (RECORD) is an algorithm for marker ordering in linkage groups. It is not an exhaustive search method and, therefore, is not computationally intensive. However, it does not guarantee that the best order is always found. The only requirement is a matrix with recombination fractions between markers.

After determining the order with RECORD, the final map is constructed using the multipoint approach (function map).

Value

An object of class sequence, which is a list containing the following components:

- seq.num: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- seq.phases: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- seq.rf: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- seq.like: log-likelihood of the corresponding linkage map.
- data.name: name of the object of class onemap with the raw data.
- twopt: name of the object of class rf_2pts with the 2-point analyses.

Author(s)

Marcelo Mollinari, <mmollina@usp.br>

References


See Also

make_seq and map

Examples

```r
# outcross example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG1 <- make_seq(groups,1)
LG1.rec <- record(LG1, hmm = FALSE)
```
## F2 example

```r
data(onemap_example_f2)
twopt <- rf_2pts(onemap_example_f2)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG1 <- make_seq(groups,1)
LG1.rec <- record(LG1, hmm = FALSE)
LG1.rec
```

---

**remove_inds**

Remove individuals from the onemap object

### Description

Remove individuals from the onemap object

### Usage

```r
remove_inds(onemap.obj, rm.ind)
```

### Arguments

- **onemap.obj**: object of class onemap
- **rm.ind**: vector of charaters with individuals names

### Value

An object of class onemap without the selected individuals, i.e., a list with the following components:

- **geno**: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- **n.ind**: number of individuals.
- **n.mar**: number of markers.
- **segr.type**: a vector with the segregation type of each marker, as strings.
- **segr.type.num**: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- **input**: the name of the input file.
- **n.phe**: number of phenotypes.
- **pheno**: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.
rf_2pts  

Two-point analysis between genetic markers

**Description**

Performs the two-point (pairwise) analysis proposed by Wu et al. (2002) between all pairs of markers.

**Usage**

```r
rf_2pts(input.obj, LOD = 3, max.rf = 0.5, verbose = TRUE, rm_mks = FALSE)
```

**Arguments**

- `input.obj`: an object of class `onemap`.
- `LOD`: minimum LOD Score to declare linkage (defaults to 3).
- `max.rf`: maximum recombination fraction to declare linkage (defaults to 0.50).
- `verbose`: logical. If TRUE, current progress is shown; if FALSE, no output is produced.
- `rm_mks`: logical. If TRUE the algorithm will remove the markers for which it found numerical problems to calculates the recombination fraction. The numerical problems can happens because of excess of missing data or segregation deviation.

**Details**

For `n` markers, there are

\[
\frac{n(n - 1)}{2}
\]

pairs of markers to be analyzed. Therefore, completion of the two-point analyses can take a long time.

**Value**

An object of class `rf_2pts`, which is a list containing the following components:

- `n.mar`: total number of markers.
- `LOD`: minimum LOD Score to declare linkage.
- `max.rf`: maximum recombination fraction to declare linkage.
- `input`: the name of the input file.
- `analysis`: an array with the complete results of the two-point analysis for each pair of markers.
**Note**

The thresholds used for LOD and max. rf will be used in subsequent analyses, but can be overridden.

**Author(s)**

Gabriel R A Margarido <gramarga@gmail.com> and Marcelo Mollinari <mmollina@usp.br>

**References**


**Examples**

```r
data(onemap_example_out)
twopts <- rf_2pts(onemap_example_out, LOD=3, max.rf=0.5)  # perform two-point analyses
twopts
print(twopts,c("M1","M2"))  # detailed results for markers 1 and 2
```

---

**rf_graph_table**

Plots pairwise recombination fractions and LOD Scores in a heatmap

**Description**

Plots a matrix of pairwise recombination fraction or LOD Scores using a color scale. Any value of the matrix can be easily accessed using an interactive plotly-html interface, helping users to check for possible problems.

**Usage**

```r
rf_graph_table(
  input.seq,
  graph.LOD = FALSE,
  main = NULL,
  inter = FALSE,
  html.file = NULL,
  mrk.axis = "numbers",
  lab.xy = NULL,
  n.colors = 4,
  display = TRUE
)
```
Arguments

input.seq an object of class sequence with a predefined order.

graph.LOD logical. If TRUE, displays the LOD heatmap, otherwise, displays the recombination fraction heatmap.

main character. The title of the plot.

inter logical. If TRUE, an interactive HTML graphic is plotted. Otherwise, a default graphic device is used.

html.file character naming the html file with iterative graphic.

mrk.axis character, "names" to display marker names in the axis, "numbers" to display marker numbers and "none" to display axis free of labels.

lab.xy character vector with length 2, first component is the label of x axis and second of the y axis.

n.colors integer. Number of colors in the pallete.

display logical. If inter TRUE and display TRUE interactive graphic is plotted in browser automatically when run the function

Details

The color scale varies from red (small distances or big LODs) to purple. When hover on a cell, a dialog box is displayed with some information about corresponding markers for that cell (line (y) \times column (x)). They are: i) the name of the markers; ii) the number of the markers on the data set; iii) the segregation types; iv) the recombination fraction between the markers and v) the LOD-Score for each possible linkage phase calculated via two-point analysis. For neighbor markers, the multipoint recombination fraction is printed; otherwise, the two-point recombination fraction is printed. For markers of type D1 and D2, it is impossible to calculate recombination fraction via two-point analysis and, therefore, the corresponding cell will be empty (white color). For cells on the diagonal of the matrix, the name, the number and the type of the marker are printed, as well as the percentage of missing data for that marker.

Value

a ggplot graphic

Author(s)

Rodrigo Amadeu, <rramadeu@gmail.com>

Examples

```r
# outcross example
data(onemap_example_out)
twop <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twop,"all")
groups <- group(all_mark)
LG1 <- make_seq(groups,1)
```
LG1.rcd <- rcd(LG1)
rf_graph_table(LG1.rcd, inter=FALSE)

##F2 example
data(onemap_example_f2)
twopt <- rf_2pts(onemap_example_f2)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)

##"pre-allocate" an empty list of length groups$n.groups (3, in this case)
maps.list<-vector("list", groups$n.groups)

for(i in 1:groups$n.groups){
  #create linkage group i
  LG.cur <- make_seq(groups,i)
  #ordering
  map.cur<-order_seq(LG.cur, subset.search = "sample")
  #assign the map of the i-th group to the maps.list
  maps.list[[i]]<-make_seq(map.cur, "force")
}

ripple_seq

---

**ripple_seq**

*Compares and displays plausible alternative orders for a given linkage group*

**Description**

For a given sequence of ordered markers, computes the multipoint likelihood of alternative orders, by shuffling subsets (windows) of markers within the sequence. For each position of the window, all possible \((ws)!\) orders are compared.

**Usage**

```r
ripple_seq(input.seq, ws = 4, ext.w = NULL, LOD = 3, tol = 0.1, verbose = TRUE)
```

**Arguments**

- `input.seq`: an object of class `sequence` with a predefined order.
- `ws`: an integer specifying the length of the window size (defaults to 4).
- `ext.w`: an integer specifying how many markers should be considered in the vicinity of the permuted window. If `ext.w=NULL` all markers in the sequence are considered. In this version, it is used only in backcross, F2 or RIL crosses.
- `LOD`: threshold for the LOD-Score, so that alternative orders with LOD less then or equal to this threshold will be displayed.
- `tol`: tolerance for the C routine, i.e., the value used to evaluate convergence.
- `verbose`: A logical, if TRUE it output progress status information.
Details

Large values for the window size make computations very slow, specially if there are many partially informative markers.

Value

This function does not return any value; it just produces text output to suggest alternative orders.

Author(s)

Gabriel R A Margarido, <gramarga@gmail.com> and Marcelo Mollinari, <mmollina@usp.br>

References


See Also

`make_seq`, `compare`, `try_seq` and `order_seq`.

Examples

```r
#Outcross example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
markers <- make_seq(twopt,c(27,16,20,4,19,21,23,9,24,29))
markers.map <- map(markers)
ripple_seq(markers.map)

#F2 example
data(onemap_example_f2)
twopt <- rf_2pts(onemap_example_f2)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
```
rm_dupli_mks

LG3 <- make_seq(groups,1)
LG3.ord <- order_seq(LG3, subset.search = "twopt", twopt.alg = "rcd", touchdown=TRUE)
LG3.ord
make_seq(LG3.ord) # get safe sequence
ord.1<-make_seq(LG3.ord,"force") # get forced sequence
ripple_seq(ord.1, ws=5)

---

**rm_dupli_mks**  
*Remove duplicated markers keeping the one with less missing data*

**Description**
Remove duplicated markers keeping the one with less missing data

**Usage**

```r
rm_dupli_mks(onemap.obj)
```

**Arguments**

- `onemap.obj`: object of class `onemap`

**Value**
An empty object of class `onemap`, i.e., a list with the following components:

- `geno`: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- `n.ind`: number of individuals.
- `n.mar`: number of markers.
- `segr.type`: a vector with the segregation type of each marker, as strings.
- `segr.type.num`: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- `input`: the name of the input file.
- `n.phe`: number of phenotypes.
- `pheno`: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.

**Author(s)**

Cristiane Taniguti, <chtaniguti@tamu.edu>
seeded_map

Construct the linkage map for a sequence of markers after seeding phases

Description

Estimates the multipoint log-likelihood, linkage phases and recombination frequencies for a sequence of markers in a given order using seeded phases.

Usage

```
seeded_map(
  input.seq,
  tol = 1e-04,
  phase_cores = 1,
  seeds,
  verbose = FALSE,
  rm_unlinked = FALSE,
  parallelization.type = "PSOCK"
)
```

Arguments

- `input.seq`: an object of class `sequence`.
- `tol`: tolerance for the C routine, i.e., the value used to evaluate convergence.
- `phase_cores`: The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)
- `seeds`: A vector given the integer encoding of phases for the first $N$ positions of the map
- `verbose`: A logical, if TRUE it output progress status information.
- `rm_unlinked`: When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and map is performed again.
- `parallelization.type`: one of the supported cluster types. This should be either PSOCK (default) or FORK.

Details

Markers are mapped in the order defined in the object `input.seq`. The best combination of linkage phases is also estimated starting from the first position not in the given seeds. The multipoint likelihood is calculated according to Wu et al. (2002b) (Eqs. 7a to 11), assuming that the recombination fraction is the same in both parents. Hidden Markov chain codes adapted from Broman et al. (2008) were used.
seeded_map

Value

An object of class sequence, which is a list containing the following components:

- **seq.num**: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- **seq.phases**: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- **seq.rf**: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- **seq.like**: log-likelihood of the corresponding linkage map.
- **data.name**: name of the object of class outcross with the raw data.
- **twopt**: name of the object of class rf_2pts with the 2-point analyses.

Author(s)

Adapted from Karl Broman (package 'qtl') by Gabriel R A Margarido, <gramarga@usp.br> and Marcelo Mollinari, <mmollina@gmail.com>. Modified to use seeded phases by Bastian Schiffthaler <bastian.schiffthaler@umu.se>

References


See Also

- **make_seq**

Examples

```r
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)

markers <- make_seq(twopt, c(30, 12, 3, 14, 2))
seeded_map(markers, seeds = c(4, 2))
```
**select_segreg**

Show markers with/without segregation distortion

**Description**

A function to show which marker have segregation distortion if Bonferroni’s correction is applied for the Chi-square tests of mendelian segregation.

**Usage**

```r
select_segreg(x, distorted = FALSE, numbers = FALSE, threshold = NULL)
```

**Arguments**

- `x` an object of class onemap_segreg_test
- `distorted` a TRUE/FALSE variable to show distorted or non-distorted markers
- `numbers` a TRUE/FALSE variable to show the numbers or the names of the markers
- `threshold` a number between 0 and 1 to specify the threshold (alpha) to be considered in the test. If NULL, it uses the threshold alpha = 0.05. Bonferroni correction is applied for multiple test correction.

**Value**

a vector with marker names or numbers, according to the option for "distorted" and "numbers"

**Examples**

```r
# Loads a fake backcross dataset installed with onemap
data(onemap_example_out)
# Performs the chi-square test for all markers
Chi <- test_segregation(onemap_example_out)
# To show non-distorted markers
select_segreg(Chi)
# To show markers with segregation distortion
select_segreg(Chi, distorted=TRUE)
# To show the numbers of the markers with segregation distortion
select_segreg(Chi, distorted=TRUE, numbers=TRUE)
```
Description

Extract marker number by name

Usage

```r
seq_by_type(sequence, mk_type)
```

Arguments

- `sequence`: object of class or sequence
- `mk_type`: vector of character with marker type to be selected

Value

New sequence object of class `sequence` with selected marker type, which is a list containing the following components:

- `seq.num`: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- `seq.phases`: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- `seq.rf`: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- `seq.like`: log-likelihood of the corresponding linkage map.
- `data.name`: object of class `onemap` with the raw data.
- `twopt`: object of class `rf_2pts` with the 2-point analyses.

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

See Also

- `make_seq`
seriation  Seriation

Description

Implements the marker ordering algorithm *Seriation* (Buetow & Chakravarti, 1987).

Usage

```r
seriation(
  input.seq,
  LOD = 0,
  max.rf = 0.5,
  tol = 1e-04,
  rm_unlinked = TRUE,
  size = NULL,
  overlap = NULL,
  phase_cores = 1,
  hmm = TRUE,
  parallelization.type = "PSOCK",
  verbose = TRUE
)
```

Arguments

- `input.seq`: an object of class `sequence`.
- `LOD`: minimum LOD-Score threshold used when constructing the pairwise recombination fraction matrix.
- `max.rf`: maximum recombination fraction threshold used as the LOD value above.
- `tol`: tolerance for the C routine, i.e., the value used to evaluate convergence.
- `rm_unlinked`: When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and ug is performed again.
- `size`: The center size around which an optimum is to be searched.
- `overlap`: The desired overlap between batches.
- `phase_cores`: The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)
- `hmm`: logical defining if the HMM must be applied to estimate multipoint genetic distances.
- `parallelization.type`: one of the supported cluster types. This should be either PSOCK (default) or FORK.
- `verbose`: A logical, if TRUE it output progress status information.
**Details**

*Seriation* is an algorithm for marker ordering in linkage groups. It is not an exhaustive search method and, therefore, is not computationally intensive. However, it does not guarantee that the best order is always found. The only requirement is a matrix with recombination fractions between markers.

NOTE: When there are too many pairs of markers with the same value in the recombination fraction matrix, it can result in ties during the ordination process and the Seriation algorithm may not work properly. This is particularly relevant for outcrossing populations with mixture of markers of type D1 and D2. When this occurs, the function shows the following error message: There are too many ties in the ordination process - please, consider using another ordering algorithm.

After determining the order with *Seriation*, the final map is constructed using the multipoint approach (function `map`).

**Value**

An object of class `sequence`, which is a list containing the following components:

- `seq.num`: a vector containing the (ordered) indices of markers in the sequence, according to the input file.
- `seq.phases`: a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
- `seq.rf`: a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
- `seq.like`: log-likelihood of the corresponding linkage map.
- `data.name`: name of the object of class `onemap` with the raw data.
- `twopt`: name of the object of class `rf_2pts` with the 2-point analyses.

**Author(s)**

Gabriel R A Margarido, <gramarga@gmail.com>

**References**


**See Also**

`make_seq`, `map`
Examples

## outcross example

data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG3 <- make_seq(groups,3)
LG3.ser <- seriation(LG3)

set_map_fun

Defines the default mapping function

Description

Defines the function that should be used to display the genetic map through the analysis.

Usage

set_map_fun(type = c("kosambi", "haldane"))

Arguments

type Indicates the function that should be used, which can be "kosambi" or "haldane"

Value

No return value, called for side effects


Author(s)

Marcelo Mollinari, <mmollina@usp.br>

References


See Also

kosambi and haldane
sort_by_pos

Sort markers in onemap object by their position in reference genome

Description
Sort markers in onemap object by their position in reference genome

Usage
sort_by_pos(onemap.obj)

Arguments
onemap.obj object of class onemap

Value
An object of class onemap, i.e., a list with the following components:

- geno: a matrix with integers indicating the genotypes read for each marker. Each column contains data for a marker and each row represents an individual.
- n.ind: number of individuals.
- n.mar: number of markers.
- segr.type: a vector with the segregation type of each marker, as strings.
- segr.type.num: a vector with the segregation type of each marker, represented in a simplified manner as integers, i.e. 1 corresponds to markers of type "A"; 2 corresponds to markers of type "B1.5"; 3 corresponds to markers of type "B2.6"; 4 corresponds to markers of type "B3.7"; 5 corresponds to markers of type "C.8"; 6 corresponds to markers of type "D1" and 7 corresponds to markers of type "D2". Markers for F2 intercrosses are coded as 1; all other crosses are left as NA.
- input: the name of the input file.
- n.phe: number of phenotypes.
- pheno: a matrix with phenotypic values. Each column contains data for a trait and each row represents an individual.

Author(s)
Cristiane Taniguti, <chtaniguti@tamu.edu>
**split_2pts**  
.Split rf_2pts object by markers

**Usage**

```r
split_2pts(twopts.obj, mks)
```

**Arguments**

- `twopts.obj`: object of class `rf_2pts`
- `mks`: markers names (vector of characters) or number (vector of integers) to be removed and added to a new `rf_2pts` object

**Value**

An object of class `rf_2pts` with only the selected markers, which is a list containing the following components:

- `n.mar`: total number of markers.
- `LOD`: minimum LOD Score to declare linkage.
- `max.rf`: maximum recombination fraction to declare linkage.

**Author(s)**

Cristiane Taniguti, `<chtaniguti@tamu.edu>`

---

**split_onemap**  
.Split onemap data sets

**Description**

 Receives one onemap object and a vector with markers names to be removed from the input onemap object and inserted in a new one. The output is a list containing the two onemap objects.

**Usage**

```r
split_onemap(onemap.obj = NULL, mks = NULL)
```

**Arguments**

- `onemap.obj`: object of class onemap
- `mks`: markers names (vector of characters) or number (vector of integers) to be removed and added to a new onemap object
suggest_lod

Value

a list containing in first level the original onemap object without the indicated markers and the second level the new onemap object with only the indicated markers

Description

It suggests a LOD Score for declaring statistical significance for two-point tests for linkage between all pairs of markers, considering that multiple tests are being performed.

Usage

suggest_lod(x)

Arguments

x an object of class sequence or onemap

Details

In a somehow naive approach, the function calculates the number of two-point tests that will be performed for all markers in the data set, and then using this to calculate the global alpha required to control type I error using Bonferroni’s correction.

From this global alpha, the corresponding quantile from the chi-square distribution is taken and then converted to LOD Score.

This can be seen as just an initial approximation to help users to select a LOD Score for two point tests.

Value

the suggested LOD to be used for testing linkage

Examples

data(onemap_example_bc) # Loads a fake backcross dataset installed with onemap
suggest_lod(onemap_example_bc) # An value that should be used to start the analysis
Description

Using OneMap internal function test_segregation_of_a_marker(), performs the Chi-square test to check if all markers in a dataset are following the expected segregation pattern, i.e., 1:1:1:1 (A), 1:2:1 (B), 3:1 (C) and 1:1 (D) according to OneMap’s notation.

Usage

test_segregation(x, simulate.p.value = FALSE)

Arguments

x: an object of class onemap, with data and additional information.

simulate.p.value: a logical indicating whether to compute p-values by Monte Carlo simulation.

Details

First, it identifies the correct segregation pattern and corresponding H0 hypothesis, and then tests it.

Value

an object of class onemap_segreg_test, which is a list with marker name, H0 hypothesis being tested, the chi-square statistics, the associated p-values and the % of individuals genotyped. To see the object, it is necessary to print it.

Examples

data(onemap_example_out) # Loads a fake outcross dataset installed with onemap
Chi <- test_segregation(onemap_example_out) # Performs the chi-square test for all markers
print(Chi) # Shows the results
Description

Applies the chi-square test to check if markers are following the expected segregation pattern, i.e., 1:1:1:1 (A), 1:2:1 (B), 3:1 (C) and 1:1 (D) according to OneMap’s notation. It does not use Yate’s correction.

Usage

test_segregation_of_a_marker(x, marker, simulate.p.value = FALSE)

Arguments

x  an object of class onemap, with data and additional information.
marker  the marker which will be tested for its segregation.
simulate.p.value  a logical indicating whether to compute p-values by Monte Carlo simulation.

Details

First, the function selects the correct segregation pattern, then it defines the H0 hypothesis, and then tests it, together with percentage of missing data.

Value

a list with the H0 hypothesis being tested, the chi-square statistics, the associated p-values, and the % of individuals genotyped.

Examples

data(onemap_example_bc) # Loads a fake backcross dataset installed with onemap
test_segregation_of_a_marker(onemap_example_bc,1)

data(onemap_example_out) # Loads a fake outcross dataset installed with onemap

test_segregation_of_a_marker(onemap_example_out,1)
try_seq

| try_seq | Try to map a marker into every possible position between markers in a given map |

Description

For a given linkage map, tries do add an additional unpositioned marker. This function estimates parameters for all possible maps including the new marker in all possible positions, while keeping the original linkage map unaltered.

Usage

try_seq(input.seq, mrk, tol = 0.1, pos = NULL, verbose = FALSE)

Arguments

- input.seq: an object of class `sequence` with a predefined order.
- mrk: the index of the marker to be tried, according to the input file.
- tol: tolerance for the C routine, i.e., the value used to evaluate convergence.
- pos: defines in which position the new marker `mrk` should be placed for the diagnostic graphic. If `NULL` (default), the marker is placed on the best position i.e. the one which results LOD = 0.00.
- verbose: if `FALSE` (default), simplified output is displayed. If `TRUE`, detailed output is displayed.

Value

An object of class `try`, which is a list containing the following components:

- `ord`: a list containing results for every linkage map estimated. These results include linkage phases, recombination frequencies and log-likelihoods.
- `LOD`: a vector with LOD-Scores for each position where the additional marker is placed. This Score is based on the best combination of linkage phases for each map.
- `try.ord`: a matrix with the orders of all linkage maps.
- `data.name`: name of the object of class `onemap` with the raw data.
- `twopt`: name of the object of class `rf_2pts` with the 2-point analyses.

Author(s)

Marcelo Mollinari, `<mmollina@usp.br>`
References


See Also

make_seq and compare.

Examples

```r
# outcrossing example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
markers <- make_seq(twopt, c(2, 3, 12, 14))
markers.comp <- compare(markers)
base.map <- make_seq(markers.comp, 1)

extend.map <- try_seq(base.map, 30)
print(extend.map, 5) # best position
print(extend.map, 4) # second best position
```

try_seq_by_seq

Run try_seq considering previous sequence

Description

It uses try_seq function repeatedly trying to positioned each marker in a vector of markers into a already ordered sequence. Each marker in the vector "markers" is kept in the sequence if the difference of LOD and total group size of the models with and without the marker are below the thresholds "lod.thr" and "cM.thr".
Usage

try_seq_by_seq(sequence, markers, cM.thr = 10, lod.thr = -10, verbose = TRUE)

Arguments

  sequence  object of class sequence with ordered markers
  markers   vector of integers defining the marker numbers to be inserted in the sequence
  cM.thr    number defining the threshold for total map size increase when inserting a single marker
  lod.thr   the difference of LODs between model before and after inserting the marker need to have value higher than the value defined in this argument
  verbose   A logical, if TRUE it output progress status information.

Value

An object of class sequence, which is a list containing the following components:

  seq.num    a vector containing the (ordered) indices of markers in the sequence, according to the input file.
  seq.phases a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.
  seq.rf     a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.
  seq.like   log-likelihood of the corresponding linkage map.
  data.name  name of the object of class onemap with the raw data.
  twopt      name of the object of class rf_2pts with the 2-point analyses.

---

ug  

Unidirectional Growth

Description

Implements the marker ordering algorithm Unidirectional Growth (Tan & Fu, 2006).

Usage

ug(
  input.seq,
  LOD = 0,
  max.rf = 0.5,
  tol = 1e-04,
  rm_unlinked = TRUE,
  size = NULL,
  overlap = NULL,


```
phase_cores = 1,
hmm = TRUE,
parallelization.type = "PSOCK",
verbose = TRUE
```

### Arguments

- **input.seq**
  - an object of class `sequence`.

- **LOD**
  - minimum LOD-Score threshold used when constructing the pairwise recombination fraction matrix.

- **max.rf**
  - maximum recombination fraction threshold used as the LOD value above.

- **tol**
  - tolerance for the C routine, i.e., the value used to evaluate convergence.

- **rm_unlinked**
  - When some pair of markers do not follow the linkage criteria, if TRUE one of the markers is removed and ug is performed again.

- **size**
  - The center size around which an optimum is to be searched

- **overlap**
  - The desired overlap between batches

- **phase_cores**
  - The number of parallel processes to use when estimating the phase of a marker. (Should be no more than 4)

- **hmm**
  - logical defining if the HMM must be applied to estimate multipoint genetic distances

- **parallelization.type**
  - one of the supported cluster types. This should be either PSOCK (default) or FORK.

- **verbose**
  - A logical, if TRUE it output progress status information.

### Details

**Unidirectional Growth (UG)** is an algorithm for marker ordering in linkage groups. It is not an exhaustive search method and, therefore, is not computationally intensive. However, it does not guarantee that the best order is always found. The only requirement is a matrix with recombination fractions between markers.

After determining the order with **UG**, the final map is constructed using the multipoint approach (function `map`).

### Value

An object of class `sequence`, which is a list containing the following components:

- **seq.num**
  - a vector containing the (ordered) indices of markers in the sequence, according to the input file.

- **seq.phases**
  - a vector with the linkage phases between markers in the sequence, in corresponding positions. -1 means that there are no defined linkage phases.

- **seq.rf**
  - a vector with the recombination frequencies between markers in the sequence. -1 means that there are no estimated recombination frequencies.

- **seq.like**
  - log-likelihood of the corresponding linkage map.
data.name  object of class onemap with the raw data.
twopt     object of class rf_2pts with the 2-point analyses.

Author(s)
Marcelo Mollinari, <mmollina@usp.br>

References

See Also
make_seq, map

Examples

```r
# outcross example
data(onemap_example_out)
twopt <- rf_2pts(onemap_example_out)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG1 <- make_seq(groups,1)
LG1.ug <- ug(LG1)

# F2 example
data(mapmaker_example_f2)
twopt <- rf_2pts(mapmaker_example_f2)
all_mark <- make_seq(twopt,"all")
groups <- group(all_mark)
LG1 <- make_seq(groups,1)
LG1.ug <- ug(LG1)
LG1.ug
```

vcf2raw

These functions are defunct and no longer available.

Description
These functions are defunct and no longer available.

Usage
vcf2raw()
Value

No return value, called for side effects

---

| vcf_example_bc | Data generated from VCF file with biallelic markers from a f2 backcross population |

Description

Simulated biallelic data set for an backcross population

Usage

data("vcf_example_bc")

Format

An object of class onemap.

Details

A total of 142 backcross individuals were genotyped with 25 markers. The data was generated from a VCF file. It contains chromosome and position informations for each marker. It is included to be used as a example in order to understand how to convert VCF file to OneMap input data with the functions vcf2raw and onemap_read_vcfR.

Author(s)

Cristiane Hayumi Taniguti, <chaytaniguti@gmail.com>

See Also

read_onemap for details about objects of class onemap.

Examples

data(vcf_example_bc)
plot(vcf_example_bc)
vcf_example_f2

Data generated from VCF file with biallelic markers from a f2 intercross population

Description

Simulated biallelic data set for an f2 population

Usage

data(vcf_example_f2)

Format

An object of class onemap.

Details

A total of 192 F2 individuals were genotyped with 25 markers. The data was generated from a VCF file. It contains chromosome and position informations for each marker. It is included to be used as a reference in order to understand how to convert VCF file to OneMap input data. Also, it is used for the analysis in the tutorial that comes with OneMap.

Author(s)

Cristiane Hayumi Taniguti, <chaytaniguti@gmail.com>

See Also

read_onemap for details about objects of class onemap.

Examples

data(vcf_example_f2)

# plot markers informations
plot(vcf_example_f2)
Description

Simulated biallelic data set for an outcross, i.e., an F1 population obtained by crossing two non-homozygous parents.

Usage

data(vcf_example_out)

Format

An object of class onemap.

Details

A total of 92 F1 individuals were genotyped with 27 markers. The data was generated from a VCF file. It contains chromosome and position informations for each marker. It is included to be used as a reference in order to understand how to convert VCF file to OneMap input data. Also, it is used for the analysis in the tutorial that comes with OneMap.

Author(s)

Cristiane Hayumi Taniguti, <chaytaniguti@gmail.com>

See Also

read_onemap for details about objects of class onemap.

Examples

data(vcf_example_out)

# plot markers informations
plot(vcf_example_out)
Data generated from VCF file with biallelic markers from a RIL population produced by selfing

Description

Simulated biallelic data set for an ril self population.

Usage

data("vcf_example_riself")

Format

The format is: List of 10 $ geno : num [1:92, 1:25] 3 3 1 3 1 3 1 3 1 ... - attr(*, "dimnames")=List of 2 .. ..$ : chr [1:92] "ID1" "ID3" "ID4" "ID5" ... ..$ : chr [1:25] "SNP16" "SNP12" "SNP17" "SNP10" ... $ n.ind : int 92 $ n.mar : int 25 $ segr.type : chr [1:25] "A.B" "A.B" "A.B" "A.B" ... $ segr.type.num: logi [1:25] NA NA NA NA NA NA ... $ n.phe : int 0 $ pheno : NULL $ CHROM : chr [1:25] "1" "1" "1" "1" "1" ... $ POS : int [1:25] 1791 6606 9001 11326 11702 15533 17151 18637 19146 19220 ... $ input : chr "vcf_example_riself.raw" - attr(*, "class")= chr [1:2] "onemap" "riself"

Details

A total of 92 rils individuals were genotyped with 25 markers. The data was generated from a VCF file. It contains chromosome and position informations for each marker. It is included to be used as an example in order to understand how to convert VCF file to OneMap input data with the functions vcf2raw and onemap_read_vcfR.

Author(s)

Cristiane Hayumi Taniguti, <chaytaniguti@gmail.com>

See Also

read_onemap for details about objects of class onemap.

Examples

data(vcf_example_riself)
plot(vcf_example_riself)
Write a genetic map to a file

Description
Write a genetic map to a file, base on a given map, or a list of maps. The output file can be used as an input to perform QTL mapping using the package R/qtl. It is also possible to create an output to be used with QTLCartographer program.

Usage
write_map(map.list, file.out)

Arguments
map.list             a map, i.e. an object of class sequence with a predefined order, linkage phases, recombination fraction and likelihood or a list of maps.
file.out             output map file.

Details
This function is available only for backcross, F2 and RILs.

Value
file with genetic map information


Author(s)
Marcelo Mollinari, <mmollina@usp.br>

References

Examples

data(mapmaker_example_f2)
twopt<-rf_2pts(mapmaker_example_f2)
lg<-group(make_seq(twopt, “all”))

#“pre-allocate” an empty list of length lg$n.groups (3, in this case)
maps.list<-vector(“list”, lg$n.groups)
for(i in 1:lg$n.groups){
    ##create linkage group i
    LG.cur <- make_seq(lg,i)
    ##ordering
    map.cur<-order_seq(LG.cur, subset.search = "sample")
    ##assign the map of the i-th group to the maps.list
    maps.list[[i]]<-make_seq(map.cur, "force")
    ##write maps.list to ".map" file
    write_map(maps.list, tempfile(fileext = ".map"))
}

write_onemap_raw

Convert onemap object to onemap raw file

Description

Converts onemap R object to onemap input file. The input file brings information about the mapping population: First line: cross type, it can be "outcrossing", "f2 intercross", "f2 backcross", "ri self" or "ri sib". Second line: number of individuals, number of markers, presence (1) or absence (0) of chromosome and position of the markers, and number of phenotypes measured. Third line: Individuals/sample names; Followed lines: marker name, marker type and genotypes. One line for each marker. Final lines: chromosome, position and phenotypes informations. See more about input file format at vignettes.

Usage

write_onemap_raw(onemap.obj = NULL, file.name = NULL)

Arguments

onemap.obj object of class `onemap`
file.name a character for the onemap raw file name. Default is "out.raw"

Value

a onemap input file

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

See Also

read_onemap for a description of the output object of class onemap.
Examples

```r
data(onemap_example_out)
write_onemap_raw(onemap_example_out, file.name = paste0(tempfile(), "\".raw\"))
```
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