Package 'mappoly'

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Type Package

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Description Constructs genetic linkage maps in autopolyploid full-sib populations. Uses pairwise recombination fraction estimation as the first source of information to sequentially position allelic variants in specific homologous chromosomes. For situations where pairwise analysis has limited power, the algorithm relies on the multilocus likelihood obtained through a hidden Markov model (HMM). Methods are described in Mollinari and Garcia (2019) <doi:10.1534/g3.119.400378> and Mollinari et al. (2020) <doi:10.1534/g3.119.400620>.

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Contents

add_marker 4
cache_counts_twopt 7
calc_genoprob 8
calc_genoprob_dist 9
calc_genoprob_error 10
calc_genoprob_single_parent 12
calc_homologprob 13
calc_prefpair_profiles 14
check_data_sanity 15
compare_maps 16
cross_simulate 16
detect_info_par 18
drop_marker 18
edit_order 19
elim_redundant 20
est_full_hmm_with_global_error 21
est_full_hmm_with_prior_prob 23
est_pairwise_rf 25
est_pairwise_rf2 27
est_rf_hmm 28
est_rf_hmm_sequential 31

export_data_to_polymapR . . . 34
export_map_list . . . 34
export_qtlpoly . . . 35
extract_map . . . 36
filter_aneuploid . . . 36
filter_individuals . . . 37
filter_missing . . . 38
filter_segregation . . . 39
find_blocks . . . 40
framework_map . . . 42
genetic-mapping-functions . . . 43
get_genomic_order . . . 45
get_submap . . . 45
get_tab_mrks . . . 47
group_mappoly . . . 48
hexafake . . . 49
hexafake.geno.dist . . . 50
import_data_from_polymapR . . . 51
import_from_updog . . . 52
import_phased_maplist_from_polymapR . . . 54
loglike_hmm . . . 55
make_mat_mappoly . . . 56
make_pairs_mappoly . . . 57
make_seq_mappoly . . . 58
maps.hexafake . . . 60
mds_mappoly . . . 60
merge_datasets . . . 62
merge_maps . . . 64
plot.mappoly.homoprob . . . 66
plot.mappoly.prefpair.profiles . . . 67
plot_genome_vs_map . . . 68
plot_GIC . . . 69
plot_mappoly.map2 . . . 69
plot_map_list . . . 70
plot_mrk_info . . . 71
plot_progeny_dosage_change . . . 71
read_fitpoly . . . 73
read_geno . . . 75
read_geno_csv . . . 78
read_geno_prob . . . 80
read_vcf . . . 82
reest_rf . . . 85
rev_map . . . 86
rf_list_to_matrix . . . 87
rf_snp_filter . . . 89
segreg_poly . . . 90
sim_homologous . . . 91
solcap.dose.map . . . 92

solcap.err.map 93
solcap.mds.map 93
solcap.prior.map 94
split_and_rephase 94
summary_maps 96
tetra.solcap 96
tetra.solcap.geno.dist 97
update_framework_map 98
update_map 100

Index **101**

`add_marker` *Add a single marker to a map*

Description

Creates a new map by adding a marker in a given position in a pre-built map.

Usage

```
add_marker(
  input.map,
  mrk,
  pos,
  rf.matrix,
  genoprob = NULL,
  phase.config = "best",
  tol = 0.001,
  extend.tail = NULL,
  r.test = NULL,
  verbose = TRUE
)
```

Arguments

`input.map`	an object of class `mappoly.map`
`mrk`	the name of the marker to be inserted
`pos`	the name of the marker after which the new marker should be added. One also can inform the numeric position (between markers) were the new marker should be added. To insert a marker at the beginning of a map, use `pos = 0`
`rf.matrix`	an object of class `mappoly.rf.matrix` containing the recombination fractions and the number of homologues sharing alleles between pairwise markers on `input.map`. It is important that `shared.alleles = TRUE` in function `rf_list_to_matrix` when computing `rf.matrix`.
`genoprob`	an object of class `mappoly.genoprob` containing the genotype probabilities for all marker positions on `input.map`

phase.config	which phase configuration should be used. "best" (default) will choose the maximum likelihood configuration
tol	the desired accuracy (default = 10e-04)
extend.tail	the length of the chain's tail that should be used to calculate the likelihood of the map. If NULL (default), the function uses all markers positioned.
r.test	for internal use only
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Details

add_marker splits the input map into two sub-maps to the left and the right of the given position. Using the genotype probabilities, it computes the log-likelihood of all possible linkage phases under a two-point threshold inherited from function rf_list_to_matrix.

Value

A list of class mappoly.map with two elements:

i) info: a list containing information about the map, regardless of the linkage phase configuration:

ploidy	the ploidy level
n.mrk	number of markers
seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
mrk.names	the names of markers in the map
seq.dose.p1	a vector containing the dosage in parent 1 for all markers in the map
seq.dose.p2	a vector containing the dosage in parent 2 for all markers in the map
chrom	a vector indicating the sequence (usually chromosome) each marker belongs as informed in the input file. If not available, chrom = NULL
genome.pos	physical position (usually in megabase) of the markers into the sequence
seq.ref	reference base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
seq.alt	alternative base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
chisq.pval	a vector containing p-values of the chi-squared test of Mendelian segregation for all markers in the map
data.name	name of the dataset of class mappoly.data
ph.thres	the LOD threshold used to define the linkage phase configurations to test

ii) a list of maps with possible linkage phase configuration. Each map in the list is also a list containing

seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
seq.rf	a vector of size (n.mrk - 1) containing a sequence of recombination fraction between the adjacent markers in the map
seq.ph	linkage phase configuration for all markers in both parents
loglike	the hmm-based multipoint likelihood

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

Examples

```
sub.map <- get_submap(maps.hexafake[[1]], 1:20, reestimate.rf = FALSE)
plot(sub.map, mrk.names = TRUE)
s <- make_seq_mappoly(hexafake, sub.map$info$mrk.names)
tpt <- est_pairwise_rf(s)
rf.matrix <- rf_list_to_matrix(input.twopt = tpt,
                               thresh.LOD.ph = 3,
                               thresh.LOD.rf = 3,
                               shared.alleles = TRUE)
###### Removing marker "M_1" (first) #######
mrk.to.remove <- "M_1"
input.map <- drop_marker(sub.map, mrk.to.remove)
plot(input.map, mrk.names = TRUE)
## Computing conditional probabilities using the resulting map
genoprob <- calc_genoprob(input.map)
res.add.M_1 <- add_marker(input.map = input.map,
                          mrk = "M_1",
                          pos = 0,
                          rf.matrix = rf.matrix,
                          genoprob = genoprob,
                          tol = 10e-4)
 plot(res.add.M_1, mrk.names = TRUE)
 best.phase <- res.add.M_1$maps[[1]]$seq.ph
 names.id <- names(best.phase$P)
 plot_compare_haplotypes(ploidy = 6,
                         hom.allele.p1 = best.phase$P[names.id],
                         hom.allele.q1 = best.phase$Q[names.id],
                         hom.allele.p2 = sub.map$maps[[1]]$seq.ph$P[names.id],
                         hom.allele.q2 = sub.map$maps[[1]]$seq.ph$Q[names.id])

###### Removing marker "M_10" (middle or last) #######
mrk.to.remove <- "M_10"
input.map <- drop_marker(sub.map, mrk.to.remove)
plot(input.map, mrk.names = TRUE)
# Computing conditional probabilities using the resulting map
genoprob <- calc_genoprob(input.map)
res.add.M_10 <- add_marker(input.map = input.map,
                          mrk = "M_10",
                          pos = "M_9",
                          rf.matrix = rf.matrix,
                          genoprob = genoprob,
                          tol = 10e-4)
 plot(res.add.M_10, mrk.names = TRUE)
 best.phase <- res.add.M_10$maps[[1]]$seq.ph
 names.id <- names(best.phase$P)
 plot_compare_haplotypes(ploidy = 6,
                         hom.allele.p1 = best.phase$P[names.id],
                         hom.allele.q1 = best.phase$Q[names.id],
```

```
                        hom.allele.p2 = sub.map$maps[[1]]$seq.ph$P[names.id],
                        hom.allele.q2 = sub.map$maps[[1]]$seq.ph$Q[names.id])
```

`cache_counts_twopt` *Frequency of genotypes for two-point recombination fraction estimation*

Description

Returns the frequency of each genotype for two-point reduction of dimensionality. The frequency is calculated for all pairwise combinations and for all possible linkage phase configurations.

Usage

```
cache_counts_twopt(
  input.seq,
  cached = FALSE,
  cache.prev = NULL,
  ncpus = 1L,
  verbose = TRUE,
  joint.prob = FALSE
)
```

Arguments

`input.seq`	an object of class `mappoly.sequence`
`cached`	If `TRUE`, access the counts for all linkage phase configurations in a internal file (default = FALSE)
`cache.prev`	an object of class `cache.info` containing pre-computed genotype frequencies, obtained with `cache_counts_twopt` (optional, default = NULL)
`ncpus`	Number of parallel processes to spawn (default = 1)
`verbose`	If `TRUE` (default), print the linkage phase configurations. If `cached = TRUE`, nothing is printed, since all linkage phase configurations will be cached.
`joint.prob`	If `FALSE` (default), returns the frequency of genotypes for transition probabilities (conditional probabilities). If `TRUE` returns the frequency for joint probabilities. The latter is especially important to compute the Fisher's Information for a pair of markers.

Value

An object of class `cache.info` which contains one (conditional probabilities) or two (both conditional and joint probabilities) lists. Each list contains all pairs of dosages between parents for all markers in the sequence. The names in each list are of the form 'A-B-C-D', where: A represents the dosage in parent 1, marker k; B represents the dosage in parent 1, marker k+1; C represents the dosage in parent 2, marker k; and D represents the dosage in parent 2, marker k+1. For each list,

the frequencies were computed for all possible linkage phase configurations. The frequencies for each linkage phase configuration are distributed in matrices whose names represents the number of homologous chromosomes that share alleles. The rows on these matrices represents the dosages in markers k and k+1 for an individual in the offspring. See Table 3 of S3 Appendix in Mollinari and Garcia (2019) for an example.

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu> with updates by Gabriel Gesteira, <gdesiqu@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
all.mrk <- make_seq_mappoly(tetra.solcap, 1:20)
## local computation
counts <- cache_counts_twopt(all.mrk, ncpus = 1)
## load from internal file or web-stored counts (especially important for high ploidy levels)
counts.cached <- cache_counts_twopt(all.mrk, cached = TRUE)
```

---

calc_genoprob *Compute conditional probabilities of the genotypes*

Description

Conditional genotype probabilities are calculated for each marker position and each individual given a map.

Usage

```
calc_genoprob(input.map, step = 0, phase.config = "best", verbose = TRUE)
```

Arguments

input.map	An object of class mappoly.map
step	Maximum distance (in cM) between positions at which the genotype probabilities are calculated, though for step = 0, probabilities are calculated only at the marker locations.
phase.config	which phase configuration should be used. "best" (default) will choose the phase configuration associated with the maximum likelihood
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced

Value

An object of class 'mappoly.genoprob' which has two elements: a tridimensional array containing the probabilities of all possible genotypes for each individual in each marker position; and the marker sequence with it's recombination frequencies

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## tetraploid example
probs.t <- calc_genoprob(input.map = solcap.dose.map[[1]],
                         verbose = TRUE)
probs.t
## displaying individual 1, 36 genotypic states
## (rows) across linkage group 1 (columns)
image(t(probs.t$probs[,,1]))
```

`calc_genoprob_dist` *Compute conditional probabilities of the genotypes using probability distribution of dosages*

Description

Conditional genotype probabilities are calculated for each marker position and each individual given a map. In this function, the probabilities are not calculated between markers.

Usage

```
calc_genoprob_dist(
  input.map,
  dat.prob = NULL,
  phase.config = "best",
  verbose = TRUE
)
```

Arguments

input.map	An object of class mappoly.map
dat.prob	an object of class mappoly.data containing the probability distribution of the genotypes
phase.config	which phase configuration should be used. "best" (default) will choose the phase configuration with the maximum likelihood
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Value

An object of class 'mappoly.genoprob' which has two elements: a tridimensional array containing the probabilities of all possible genotypes for each individual in each marker position; and the marker sequence with it's recombination frequencies

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## tetraploid example
probs.t <- calc_genoprob_dist(input.map = solcap.prior.map[[1]],
                          dat.prob = tetra.solcap.geno.dist,
                          verbose = TRUE)
probs.t
## displaying individual 1, 36 genotypic states
## (rows) across linkage group 1 (columns)
image(t(probs.t$probs[,,1]))
```

---

calc_genoprob_error *Compute conditional probabilities of the genotypes using global error*

Description

Conditional genotype probabilities are calculated for each marker position and each individual given a map.

Usage

```
calc_genoprob_error(
  input.map,
  step = 0,
  phase.config = "best",
  error = 0.01,
  th.prob = 0.95,
  restricted = TRUE,
  verbose = TRUE
)
```

Arguments

input.map	An object of class mappoly.map
step	Maximum distance (in cM) between positions at which the genotype probabilities are calculated, though for step = 0, probabilities are calculated only at the marker locations.
phase.config	which phase configuration should be used. "best" (default) will choose the maximum likelihood configuration
error	the assumed global error rate (default = 0.01)
th.prob	the threshold for using global error or genotype probability distribution contained in the dataset (default = 0.95)
restricted	if TRUE (default), restricts the prior to the possible classes under Mendelian non double-reduced segregation given the parental dosages
verbose	if TRUE (default), current progress is shown; if FALSE, no output is produced

Value

An object of class 'mappoly.genoprob' which has two elements: a tridimensional array containing the probabilities of all possible genotypes for each individual in each marker position; and the marker sequence with it's recombination frequencies

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
probs.error <- calc_genoprob_error(input.map = solcap.err.map[[1]],
                                   error = 0.05,
                                   verbose = TRUE)
```

`calc_genoprob_single_parent` *Compute conditional probabilities of the genotype (one informative parent)*

Description

Conditional genotype probabilities are calculated for each marker position and each individual given a map

Usage

```
calc_genoprob_single_parent(
  input.map,
  step = 0,
  info.parent = 1,
  uninfo.parent = 2,
  global.err = 0,
  phase.config = "best",
  verbose = TRUE
)
```

Arguments

`input.map`	An object of class `mappoly.map` (with exceptions)
`step`	Maximum distance (in cM) between positions at which the genotype probabilities are calculated, though for step = 0, probabilities are calculated only at the marker locations.
`info.parent`	index for informative parent
`uninfo.parent`	index for uninformative parent
`global.err`	the assumed global error rate (default = 0.0)
`phase.config`	which phase configuration should be used. "best" (default) will choose the phase configuration associated with the maximum likelihood
`verbose`	if `TRUE` (default), current progress is shown; if `FALSE`, no output is produced

Value

An object of class 'mappoly.genoprob' which has two elements: a tridimensional array containing the probabilities of all possible genotypes for each individual in each marker position; and the marker sequence with it's recombination frequencies

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## tetraploid example
s <- make_seq_mappoly(tetra.solcap, 'seq12', info.parent = "p1")
tpt <- est_pairwise_rf(s)
map <- est_rf_hmm_sequential(input.seq = s,
                             twopt = tpt,
                              start.set = 10,
                              thres.twopt = 10,
                              thres.hmm = 10,
                              extend.tail = 4,
                              info.tail = TRUE,
                              sub.map.size.diff.limit = 8,
                              phase.number.limit = 4,
                              reestimate.single.ph.configuration = TRUE,
                              tol = 10e-2,
                              tol.final = 10e-3)
plot(map)
probs <- calc_genoprob_single_parent(input.map = map,
                                     info.parent = 1,
                                     uninfo.parent = 2,
                                     step = 1)
probs
## displaying individual 1, 6 genotypic states
## (rows) across linkage group 1 (columns)
image(t(probs$probs[,,2]))
```

`calc_homologprob` *Homolog probabilities*

Description

Compute homolog probabilities for all individuals in the full-sib population given a map and conditional genotype probabilities.

Usage

```
calc_homologprob(input.genoprobs, verbose = TRUE)
```

Arguments

`input.genoprobs`	an object of class `mappoly.genoprob`
`verbose`	if `TRUE` (default), the current progress is shown; if `FALSE`, no output is produced

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari M., Olukolu B. A., Pereira G. da S., Khan A., Gemenet D., Yencho G. C., Zeng Z-B. (2020), Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400620

Examples

```
## tetraploid example
w1 <- calc_genoprob(solcap.dose.map[[1]])
h.prob <- calc_homologprob(w1)
print(h.prob)
plot(h.prob, ind = 5, use.plotly = FALSE)
## using error modeling (removing noise)
w2 <- calc_genoprob_error(solcap.err.map[[1]])
h.prob2 <- calc_homologprob(w2)
print(h.prob2)
plot(h.prob2, ind = 5, use.plotly = FALSE)
```

---

calc_prefpair_profiles

Preferential pairing profiles

Description

Given the genotype conditional probabilities for a map, this function computes the probability profiles for all possible homolog pairing configurations in both parents.

Usage

```
calc_prefpair_profiles(input.genoprobs, verbose = TRUE)
```

Arguments

input.genoprobs	an object of class mappoly.genoprob
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu> and Guilherme Pereira, <g.pereira@cgiar.org>

References

Mollinari M., Olukolu B. A., Pereira G. da S., Khan A., Gemenet D., Yencho G. C., Zeng Z-B. (2020), Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400620

Examples

```
## tetraploid example
w1 <- lapply(solcap.dose.map[1:12], calc_genoprob)
x1 <- calc_prefpair_profiles(w1)
print(x1)
plot(x1)
```

`check_data_sanity` *Data sanity check*

Description

Checks the consistency of a dataset

Usage

```
check_data_sanity(x)
```

Arguments

`x`	an object of class `mappoly.data`

Value

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

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
check_data_sanity(tetra.solcap)
```

compare_maps *Compare a list of maps*

Description

Compare lengths, density, maximum gaps and log likelihoods in a list of maps. In order to make the maps comparable, the function uses the intersection of markers among maps.

Usage

```
compare_maps(...)
```

Arguments

...	a list of objects of class mappoly.map

Value

A data frame where the lines correspond to the maps in the order provided in input list list

cross_simulate *Simulate an autopolyploid full-sib population*

Description

Simulate an autopolyploid full-sib population with one or two informative parents under random chromosome segregation.

Usage

```
cross_simulate(
  parental.phases,
  map.length,
  n.ind,
  draw = FALSE,
  file = "output.pdf",
  prefix = NULL,
  seed = NULL,
  width = 12,
  height = 6,
  prob.P = NULL,
  prob.Q = NULL
)
```

Arguments

parental.phases	a list containing the linkage phase information for both parents
map.length	the map length
n.ind	number of individuals in the offspring
draw	if TRUE, draws a graphical representation of the parental map, including the linkage phase configuration, in a pdf output (default = FALSE)
file	name of the output file. It is ignored if draw = TRUE
prefix	prefix used in all marker names.
seed	random number generator seed (default = NULL)
width	the width of the graphics region in inches (default = 12)
height	the height of the graphics region in inches (default = 6)
prob.P	a vector indicating the proportion of preferential pairing in parent P (currently ignored)
prob.Q	a vector indicating the proportion of preferential pairing in parent Q (currently ignored)

Details

parental.phases.p and parental.phases.q are lists of vectors containing linkage phase configurations. Each vector contains the numbers of the homologous chromosomes in which the alleles are located. For instance, a vector containing $(1, 3, 4)$ means that the marker has three doses located in the chromosomes 1, 3 and 4. For zero doses, use 0. For more sophisticated simulations, we strongly recommend using PedigreeSim V2.0 https://github.com/PBR/pedigreeSim

Value

an object of class mappoly.data. See read_geno for more information

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
h.temp <- sim_homologous(ploidy = 6, n.mrk = 20)
fake.poly.dat <- cross_simulate(h.temp, map.length = 100, n.ind = 200)
plot(fake.poly.dat)
```

detect_info_par *Detects which parent is informative*

Description

Detects which parent is informative

Usage

```
detect_info_par(x)
```

Arguments

x	an object of class mappoly.sequence or mappoly.map

drop_marker *Remove markers from a map*

Description

This function creates a new map by removing markers from an existing one.

Usage

```
drop_marker(input.map, mrk, verbose = TRUE)
```

Arguments

input.map	an object of class mappoly.map
mrk	a vector containing markers to be removed from the input map, identified by their names or positions
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Value

an object of class mappoly.map

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

Examples

```
sub.map <- get_submap(maps.hexafake[[1]], 1:50, reestimate.rf = FALSE)
plot(sub.map, mrk.names = TRUE)
mrk.to.remove <- c("M_1", "M_23", "M_34")
red.map <- drop_marker(sub.map, mrk.to.remove)
plot(red.map, mrk.names = TRUE)
```

`edit_order` *Edit sequence ordered by reference genome positions comparing to another set order*

Description

Edit sequence ordered by reference genome positions comparing to another set order

Usage

```
edit_order(input.seq, invert = NULL, remove = NULL)
```

Arguments

`input.seq`	object of class mappoly.sequence with alternative order (not genomic order)
`invert`	vector of marker names to be inverted
`remove`	vector of marker names to be removed

Value

object of class `mappoly.edit.order`: a list containing vector of marker names ordered according to editions ('edited_order'); vector of removed markers names ('removed'); vector of inverted markers names ('inverted').

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

Examples

```
dat <- filter_segregation(tetra.solcap, inter = FALSE)
seq_dat <- make_seq_mappoly(dat)
seq_chr <- make_seq_mappoly(seq_dat, arg = seq_dat$seq.mrk.names[which(seq_dat$chrom=="1")])

tpt <- est_pairwise_rf(seq_chr)
seq.filt <- rf_snp_filter(tpt, probs = c(0.05, 0.95))
mat <- rf_list_to_matrix(tpt)
mat2 <- make_mat_mappoly(mat, seq.filt)

seq_test_mds <- mds_mappoly(mat2)
```

```
seq_mds <- make_seq_mappoly(seq_test_mds)
edit_seq <- edit_order(input.seq = seq_mds)
```

`elim_redundant` *Eliminate redundant markers*

Description

Eliminate markers with identical dosage information for all individuals.

Usage

```
elim_redundant(input.seq, data = NULL)
```

Arguments

`input.seq`	an object of class `mappoly.sequence`
`data`	name of the dataset that contains sequence markers (optional, default = NULL)

Value

An object of class `mappoly.unique.seq` which is a list containing the following components:

`unique.seq`	an object of class `mappoly.sequence` with the redundant markers removed
`kept`	a vector containing the name of the informative markers
`eliminated`	a vector containing the name of the non-informative (eliminated) markers

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>, with minor modifications by Gabriel Gesteira, <gdesiqu@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
all.mrk <- make_seq_mappoly(hexafake, 'all')
red.mrk <- elim_redundant(all.mrk)
plot(red.mrk)
unique.mrks <- make_seq_mappoly(red.mrk)
```

`est_full_hmm_with_global_error` *Re-estimate genetic map given a global genotyping error*

Description

This function considers a global error when re-estimating a genetic map using Hidden Markov models. Since this function uses the whole transition space in the HMM, its computation can take a while, especially for hexaploid maps.

Usage

```
est_full_hmm_with_global_error(
  input.map,
  error = NULL,
  tol = 0.001,
  restricted = TRUE,
  th.prob = 0.95,
  verbose = FALSE
)
```

Arguments

`input.map`	an object of class `mappoly.map`
`error`	the assumed global error rate (default = NULL)
`tol`	the desired accuracy (default = 10e-04)
`restricted`	if `TRUE` (default), restricts the prior to the possible classes under Mendelian, non double-reduced segregation given dosage of the parents
`th.prob`	the threshold for using global error or genotype probability distribution if present in the dataset (default = 0.95)
`verbose`	if `TRUE`, current progress is shown; if `FALSE` (default), no output is produced

Value

A list of class `mappoly.map` with two elements:

i) info: a list containing information about the map, regardless of the linkage phase configuration:

`ploidy`	the ploidy level
`n.mrk`	number of markers
`seq.num`	a vector containing the (ordered) indices of markers in the map, according to the input file
`mrk.names`	the names of markers in the map
`seq.dose.p1`	a vector containing the dosage in parent 1 for all markers in the map
`seq.dose.p2`	a vector containing the dosage in parent 2 for all markers in the map

chrom	a vector indicating the sequence (usually chromosome) each marker belongs as informed in the input file. If not available, chrom = NULL
genome.pos	physical position (usually in megabase) of the markers into the sequence
seq.ref	reference base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
seq.alt	alternative base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
chisq.pval	a vector containing p-values of the chi-squared test of Mendelian segregation for all markers in the map
data.name	name of the dataset of class mappoly.data
ph.thres	the LOD threshold used to define the linkage phase configurations to test

ii) a list of maps with possible linkage phase configuration. Each map in the list is also a list containing

seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
seq.rf	a vector of size (n.mrk - 1) containing a sequence of recombination fraction between the adjacent markers in the map
seq.ph	linkage phase configuration for all markers in both parents
loglike	the hmm-based multipoint likelihood

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
submap <- get_submap(solcap.dose.map[[1]], mrk.pos = 1:20, verbose = FALSE)
err.submap <- est_full_hmm_with_global_error(submap,
                                             error = 0.01,
                                             tol = 10e-4,
                                             verbose = TRUE)
err.submap
plot_map_list(list(dose = submap, err = err.submap),
              title = "estimation procedure")
```

`est_full_hmm_with_prior_prob` *Re-estimate genetic map using dosage prior probability distribution*

Description

This function considers dosage prior distribution when re-estimating a genetic map using Hidden Markov models

Usage

```
est_full_hmm_with_prior_prob(
  input.map,
  dat.prob = NULL,
  phase.config = "best",
  tol = 0.001,
  verbose = FALSE
)
```

Arguments

`input.map`	an object of class `mappoly.map`
`dat.prob`	an object of class `mappoly.data` containing the probability distribution of the genotypes
`phase.config`	which phase configuration should be used. "best" (default) will choose the maximum likelihood configuration
`tol`	the desired accuracy (default = 10e-04)
`verbose`	if `TRUE`, current progress is shown; if `FALSE` (default), no output is produced

Value

A list of class `mappoly.map` with two elements:

i) info: a list containing information about the map, regardless of the linkage phase configuration:

`ploidy`	the ploidy level
`n.mrk`	number of markers
`seq.num`	a vector containing the (ordered) indices of markers in the map, according to the input file
`mrk.names`	the names of markers in the map
`seq.dose.p1`	a vector containing the dosage in parent 1 for all markers in the map
`seq.dose.p2`	a vector containing the dosage in parent 2 for all markers in the map
`chrom`	a vector indicating the sequence (usually chromosome) each marker belongs as informed in the input file. If not available, `chrom = NULL`
`genome.pos`	physical position (usually in megabase) of the markers into the sequence

seq.ref	reference base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
seq.alt	alternative base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
chisq.pval	a vector containing p-values of the chi-squared test of Mendelian segregation for all markers in the map
data.name	name of the dataset of class mappoly.data
ph.thres	the LOD threshold used to define the linkage phase configurations to test

ii) a list of maps with possible linkage phase configuration. Each map in the list is also a list containing

seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
seq.rf	a vector of size (n.mrk - 1) containing a sequence of recombination fraction between the adjacent markers in the map
seq.ph	linkage phase configuration for all markers in both parents
loglike	the hmm-based multipoint likelihood

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
submap <- get_submap(solcap.dose.map[[1]], mrk.pos = 1:20, verbose = FALSE)
prob.submap <- est_full_hmm_with_prior_prob(submap,
                                            dat.prob = tetra.solcap.geno.dist,
                                            tol = 10e-4,
                                            verbose = TRUE)
prob.submap
plot_map_list(list(dose = submap, prob = prob.submap),
              title = "estimation procedure")
```

`est_pairwise_rf` *Pairwise two-point analysis*

Description

Performs the two-point pairwise analysis between all markers in a sequence. For each pair, the function estimates the recombination fraction for all possible linkage phase configurations and associated LOD Scores.

Usage

```
est_pairwise_rf(
  input.seq,
  count.cache = NULL,
  count.matrix = NULL,
  ncpus = 1L,
  mrk.pairs = NULL,
  n.batches = 1L,
  est.type = c("disc", "prob"),
  verbose = TRUE,
  memory.warning = TRUE,
  parallelization.type = c("PSOCK", "FORK"),
  tol = .Machine$double.eps^0.25,
  ll = FALSE
)
```

Arguments

`input.seq`	an object of class `mappoly.sequence`
`count.cache`	an object of class `cache.info` containing pre-computed genotype frequencies, obtained with `cache_counts_twopt`. If `NULL` (default), genotype frequencies are internally loaded.
`count.matrix`	similar to `count.cache`, but in matrix format. Mostly for internal use.
`ncpus`	Number of parallel processes (cores) to spawn (default = 1)
`mrk.pairs`	a matrix of dimensions 2*N, containing N pairs of markers to be analyzed. If `NULL` (default), all pairs are considered
`n.batches`	deprecated. Not available on MAPpoly 0.3.0 or higher
`est.type`	Indicates whether to use the discrete ("disc") or the probabilistic ("prob") dosage scoring when estimating the two-point recombination fractions.
`verbose`	If `TRUE` (default), current progress is shown; if `FALSE`, no output is produced
`memory.warning`	if `TRUE`, prints a memory warning if the number of markers is greater than 10000 for ploidy levels up to 4, and 3000 for ploidy levels > 4.
`parallelization.type`	one of the supported cluster types. This should be either PSOCK (default) or FORK.

tol	the desired accuracy. See optimize() for details
ll	will return log-likelihood instead of LOD scores. (for internal use)

Value

An object of class mappoly.twopt which is a list containing the following components:

data.name Name of the object of class mappoly.data containing the raw data.

n.mrk Number of markers in the sequence.

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

pairwise A list of size choose(length(input.seq$seq.num), 2), where each element is a matrix. The rows are named in the format x-y, where x and y indicate how many homologues share the same allelic variant in parents P and Q, respectively (see Mollinari and Garcia, 2019 for notation). The first column indicates the LOD Score for the most likely linkage phase configuration. The second column shows the estimated recombination fraction for each configuration, and the third column indicates the LOD Score for comparing the likelihood under no linkage (r = 0.5) with the estimated recombination fraction (evidence of linkage).

chisq.pval.thres Threshold used to perform the segregation tests.

chisq.pval P-values associated with the performed segregation tests.

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## Tetraploid example (first 50 markers)
all.mrk <- make_seq_mappoly(tetra.solcap, 1:50)
red.mrk <- elim_redundant(all.mrk)
unique.mrks <- make_seq_mappoly(red.mrk)
all.pairs <- est_pairwise_rf(input.seq = unique.mrks,
                             ncpus = 1,
                             verbose = TRUE)
 all.pairs
 plot(all.pairs, 20, 21)
 mat <- rf_list_to_matrix(all.pairs)
 plot(mat)
```

`est_pairwise_rf2` *Pairwise two-point analysis - RcppParallel version*

Description

Performs the two-point pairwise analysis between all markers in a sequence. For each pair, the function estimates the recombination fraction for all possible linkage phase configurations and associated LOD Scores.

Usage

```
est_pairwise_rf2(
  input.seq,
  ncpus = 1L,
  mrk.pairs = NULL,
  verbose = TRUE,
  tol = .Machine$double.eps^0.25
)
```

Arguments

`input.seq`	an object of class `mappoly.sequence`
`ncpus`	Number of parallel processes (cores) to spawn (default = 1)
`mrk.pairs`	a matrix of dimensions 2*N, containing N pairs of markers to be analyzed. If `NULL` (default), all pairs are considered
`verbose`	If `TRUE` (default), current progress is shown; if `FALSE`, no output is produced
`tol`	the desired accuracy. See `optimize()` for details

Details

Differently from est_pairwise_rf this function returns only the values associated to the best linkage phase configuration.

Value

An object of class `mappoly.twopt2`

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## Tetraploid example
all.mrk <- make_seq_mappoly(tetra.solcap, 100:200)
all.pairs <- est_pairwise_rf2(input.seq = all.mrk, ncpus = 2)
m <- rf_list_to_matrix(all.pairs)
plot(m, fact = 2)
```

`est_rf_hmm` *Multipoint analysis using Hidden Markov Models in autopolyploids*

Description

Performs the multipoint analysis proposed by *Mollinari and Garcia (2019)* in a sequence of markers

Usage

```
est_rf_hmm(
  input.seq,
  input.ph = NULL,
  thres = 0.5,
  twopt = NULL,
  verbose = FALSE,
  tol = 1e-04,
  est.given.0.rf = FALSE,
  reestimate.single.ph.configuration = TRUE,
  high.prec = TRUE
)

## S3 method for class 'mappoly.map'
print(x, detailed = FALSE, ...)

## S3 method for class 'mappoly.map'
plot(
  x,
  left.lim = 0,
  right.lim = Inf,
  phase = TRUE,
  mrk.names = FALSE,
  cex = 1,
  config = "best",
  P = "Parent 1",
  Q = "Parent 2",
  xlim = NULL,
  ...
)
```

Arguments

input.seq	an object of class mappoly.sequence
input.ph	an object of class two.pts.linkage.phases. If not available (default = NULL), it will be computed
thres	LOD Score threshold used to determine if the linkage phases compared via two-point analysis should be considered. Smaller values will result in smaller number of linkage phase configurations to be evaluated by the multipoint algorithm.
twopt	an object of class mappoly.twopt containing two-point information
verbose	if TRUE, current progress is shown; if FALSE (default), no output is produced
tol	the desired accuracy (default = 1e-04)
est.given.0.rf	logical. If TRUE returns a map forcing all recombination fractions equals to 0 (1e-5, for internal use only. Default = FALSE)
reestimate.single.ph.configuration	logical. If TRUE returns a map without re-estimating the map parameters for cases where there is only one possible linkage phase configuration. This argument is intended to be used in a sequential map construction
high.prec	logical. If TRUE (default) uses high precision long double numbers in the HMM procedure
x	an object of the class mappoly.map
detailed	logical. if TRUE, prints the linkage phase configuration and the marker position for all maps. If FALSE (default), prints a map summary
...	currently ignored
left.lim	the left limit of the plot (in cM, default = 0).
right.lim	the right limit of the plot (in cM, default = Inf, i.e., will print the entire map)
phase	logical. If TRUE (default) plots the phase configuration for both parents
mrk.names	if TRUE, marker names are displayed (default = FALSE)
cex	The magnification to be used for marker names
config	should be 'best' or the position of the configuration to be plotted. If 'best', plot the configuration with the highest likelihood
P	a string containing the name of parent P
Q	a string containing the name of parent Q
xlim	range of the x-axis. If xlim = NULL (default) it uses the map range.

Details

This function first enumerates a set of linkage phase configurations based on two-point recombination fraction information using a threshold provided by the user (argument thresh). After that, for each configuration, it reconstructs the genetic map using the HMM approach described in Mollinari and Garcia (2019). As result, it returns the multipoint likelihood for each configuration in form of LOD Score comparing each configuration to the most likely one. It is recommended to use a small number of markers (e.g. 50 markers for hexaploids) since the possible linkage phase combinations bounded only by the two-point information can be huge. Also, it can be quite sensible to small changes in 'thresh'. For a large number of markers, please see est_rf_hmm_sequential.

Value

A list of class mappoly.map with two elements:

i) info: a list containing information about the map, regardless of the linkage phase configuration:

ploidy	the ploidy level
n.mrk	number of markers
seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
mrk.names	the names of markers in the map
seq.dose.p1	a vector containing the dosage in parent 1 for all markers in the map
seq.dose.p2	a vector containing the dosage in parent 2 for all markers in the map
chrom	a vector indicating the sequence (usually chromosome) each marker belongs as informed in the input file. If not available, chrom = NULL
genome.pos	physical position (usually in megabase) of the markers into the sequence
seq.ref	reference base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
seq.alt	alternative base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
chisq.pval	a vector containing p-values of the chi-squared test of Mendelian segregation for all markers in the map
data.name	name of the dataset of class mappoly.data
ph.thres	the LOD threshold used to define the linkage phase configurations to test

ii) a list of maps with possible linkage phase configuration. Each map in the list is also a list containing

seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
seq.rf	a vector of size (n.mrk - 1) containing a sequence of recombination fraction between the adjacent markers in the map
seq.ph	linkage phase configuration for all markers in both parents
loglike	the hmm-based multipoint likelihood

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. https://doi.org/10.1534/g3.119.400378

`est_rf_hmm_sequential` *Multipoint analysis using Hidden Markov Models: Sequential phase elimination*

Description

Performs the multipoint analysis proposed by *Mollinari and Garcia (2019)* in a sequence of markers removing unlikely phases using sequential multipoint information.

Usage

```
est_rf_hmm_sequential(
  input.seq,
  twopt,
  start.set = 4,
  thres.twopt = 5,
  thres.hmm = 50,
  extend.tail = NULL,
  phase.number.limit = 20,
  sub.map.size.diff.limit = Inf,
  info.tail = TRUE,
  reestimate.single.ph.configuration = FALSE,
  tol = 0.1,
  tol.final = 0.001,
  verbose = TRUE,
  detailed.verbose = FALSE,
  high.prec = FALSE
)
```

Arguments

`input.seq`	an object of class `mappoly.sequence`
`twopt`	an object of class `mappoly.twopt` containing the two-point information
`start.set`	number of markers to start the phasing procedure (default = 4)
`thres.twopt`	the LOD threshold used to determine if the linkage phases compared via two-point analysis should be considered for the search space reduction (A.K.A. η in *Mollinari and Garcia (2019)*, default = 5)
`thres.hmm`	the LOD threshold used to determine if the linkage phases compared via hmm analysis should be evaluated in the next round of marker inclusion (default = 50)
`extend.tail`	the length of the chain's tail that should be used to calculate the likelihood of the map. If `NULL` (default), the function uses all markers positioned. Even if `info.tail = TRUE`, it uses at least `extend.tail` as the tail length
`phase.number.limit`	the maximum number of linkage phases of the sub-maps defined by arguments `info.tail` and `extend.tail`. Default is 20. If the size exceeds this limit, the marker will not be inserted. If `Inf`, then it will insert all markers.

`sub.map.size.diff.limit`
: the maximum accepted length difference between the current and the previous sub-map defined by arguments `info.tail` and `extend.tail`. If the size exceeds this limit, the marker will not be inserted. If `NULL`(default), then it will insert all markers.

`info.tail`
: if `TRUE` (default), it uses the complete informative tail of the chain (i.e. number of markers where all homologous ($ploidyx2$) can be distinguished) to calculate the map likelihood

`reestimate.single.ph.configuration`
: logical. If `FALSE` (default) returns a map without re-estimating the map parameters in cases where there are only one possible linkage phase configuration

`tol`
: the desired accuracy during the sequential phase (default = 10e-02)

`tol.final`
: the desired accuracy for the final map (default = 10e-04)

`verbose`
: If `TRUE` (default), current progress is shown; if `FALSE`, no output is produced

`detailed.verbose`
: If `TRUE`, the expansion of the current submap is shown;

`high.prec`
: logical. If `TRUE` uses high precision (long double) numbers in the HMM procedure implemented in C++, which can take a long time to perform (default = FALSE)

Details

This function sequentially includes markers into a map given an ordered sequence. It uses two-point information to eliminate unlikely linkage phase configurations given `thres.twopt`. The search is made within a window of size `extend.tail`. For the remaining configurations, the HMM-based likelihood is computed and the ones that pass the HMM threshold (`thres.hmm`) are eliminated.

Value

A list of class `mappoly.map` with two elements:

i) info: a list containing information about the map, regardless of the linkage phase configuration:

`ploidy`
: the ploidy level

`n.mrk`
: number of markers

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

`mrk.names`
: the names of markers in the map

`seq.dose.p1`
: a vector containing the dosage in parent 1 for all markers in the map

`seq.dose.p2`
: a vector containing the dosage in parent 2 for all markers in the map

`chrom`
: a vector indicating the sequence (usually chromosome) each marker belongs as informed in the input file. If not available, `chrom` = `NULL`

`genome.pos`
: physical position (usually in megabase) of the markers into the sequence

`seq.ref`
: reference base used for each marker (i.e. A, T, C, G). If not available, `seq.ref` = `NULL`

seq.alt	alternative base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
chisq.pval	a vector containing p-values of the chi-squared test of Mendelian segregation for all markers in the map
data.name	name of the dataset of class mappoly.data
ph.thres	the LOD threshold used to define the linkage phase configurations to test

ii) a list of maps with possible linkage phase configuration. Each map in the list is also a list containing

seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
seq.rf	a vector of size (n.mrk - 1) containing a sequence of recombination fraction between the adjacent markers in the map
seq.ph	linkage phase configuration for all markers in both parents
loglike	the hmm-based multipoint likelihood

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
mrk.subset <- make_seq_mappoly(hexafake, 1:20)
red.mrk <- elim_redundant(mrk.subset)
unique.mrks <- make_seq_mappoly(red.mrk)
subset.pairs <- est_pairwise_rf(input.seq = unique.mrks,
                                ncpus = 1,
                                verbose = TRUE)
subset.map <- est_rf_hmm_sequential(input.seq = unique.mrks,
                                    thres.twopt = 5,
                                    thres.hmm = 10,
                                    extend.tail = 10,
                                    tol = 0.1,
                                    tol.final = 10e-3,
                                    phase.number.limit = 5,
                                    twopt = subset.pairs,
                                    verbose = TRUE)
 print(subset.map, detailed = TRUE)
 plot(subset.map)
 plot(subset.map, left.lim = 0, right.lim = 1, mrk.names = TRUE)
 plot(subset.map, phase = FALSE)

 ## Retrieving simulated linkage phase
```

```
ph.P <- maps.hexafake[[1]]$maps[[1]]$seq.ph$P
ph.Q <- maps.hexafake[[1]]$maps[[1]]$seq.ph$Q
## Estimated linkage phase
ph.P.est <- subset.map$maps[[1]]$seq.ph$P
ph.Q.est <- subset.map$maps[[1]]$seq.ph$Q
compare_haplotypes(ploidy = 6, h1 = ph.P[names(ph.P.est)], h2 = ph.P.est)
compare_haplotypes(ploidy = 6, h1 = ph.Q[names(ph.Q.est)], h2 = ph.Q.est)
```

`export_data_to_polymapR` *Export data to* `polymapR`

Description

See examples at https://rpubs.com/mmollin/tetra_mappoly_vignette.

Usage

```
export_data_to_polymapR(data.in)
```

Arguments

`data.in`	an object of class `mappoly.data`

Value

a dosage `matrix`

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

`export_map_list` *Export a genetic map to a CSV file*

Description

Function to export genetic linkage map(s) generated by `MAPpoly`. The map(s) should be passed as a single object or a list of objects of class `mappoly.map`.

Usage

```
export_map_list(map.list, file = "map_output.csv")
```

Arguments

map.list	A list of objects or a single object of class mappoly.map
file	either a character string naming a file or a connection open for writing. "" indicates output to the console.

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
export_map_list(solcap.err.map[[1]], file = "")
```

---

export_qtlpoly *Export to QTLpoly*

Description

Compute homolog probabilities for all individuals in the full-sib population given a map and conditional genotype probabilities, and exports the results to be used for QTL mapping in the QTLpoly package.

Usage

```
export_qtlpoly(input.genoprobs, verbose = TRUE)
```

Arguments

input.genoprobs	an object of class mappoly.genoprob
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari M., Olukolu B. A., Pereira G. da S., Khan A., Gemenet D., Yencho G. C., Zeng Z-B. (2020), Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400620

Examples

```
## tetraploid example
w1 <- calc_genoprob(solcap.dose.map[[1]])
h.prob <- export_qtlpoly(w1)
```

`extract_map` *Extract the maker position from an object of class 'mappoly.map'*

Description

Extract the maker position from an object of class 'mappoly.map'

Usage

```
extract_map(input.map, phase.config = "best")
```

Arguments

`input.map`	An object of class `mappoly.map`
`phase.config`	which phase configuration should be used. "best" (default) will choose the maximum likelihood configuration

Examples

```
x <- maps.hexafake[[1]]$info$genome.pos/1e6
y <- extract_map(maps.hexafake[[1]])
plot(y~x, ylab = "Map position (cM)", xlab = "Genome Position (Mbp)")
```

`filter_aneuploid` *Filter aneuploid chromosomes from progeny individuals*

Description

Filter aneuploid chromosomes from progeny individuals

Usage

```
filter_aneuploid(input.data, aneuploid.info, ploidy, rm_missing = TRUE)
```

Arguments

input.data	name of input object (class mappoly.data)
aneuploid.info	data.frame with ploidy information by chromosome (columns) for each individual in progeny (rows). The chromosome and individuals names must match the ones in the file used as input in mappoly.
ploidy	main ploidy
rm_missing	remove also genotype information from chromosomes with missing data (NA) in the aneuploid.info file

Value

object of class mappoly.data

Author(s)

Cristiane Taniguti, <chtaniguti@tamu.edu>

Examples

```
  aneuploid.info <- matrix(4, nrow=tetra.solcap$n.ind, ncol = 12)
  set.seed(8080)
aneuploid.info[sample(1:length(aneuploid.info), round((4*length(aneuploid.info))/100),0)] <- 3
aneuploid.info[sample(1:length(aneuploid.info), round((4*length(aneuploid.info))/100),0)] <- 5

  colnames(aneuploid.info) <- paste0(1:12)
  aneuploid.info <- cbind(inds = tetra.solcap$ind.names, aneuploid.info)

  filt.dat <- filter_aneuploid(input.data = tetra.solcap,
  aneuploid.info = aneuploid.info, ploidy = 4)
```

---

filter_individuals *Filter out individuals*

Description

This function removes individuals from the data set. Individuals can be user-defined or can be accessed via interactive kinship analysis.

Usage

```
filter_individuals(
  input.data,
  ind.to.remove = NULL,
  inter = TRUE,
  type = c("Gmat", "PCA"),
  verbose = TRUE
)
```

Arguments

input.data	name of input object (class mappoly.data)
ind.to.remove	individuals to be removed. If NULL it opens an interactive graphic to proceed with the individual selection
inter	if TRUE, expects user-input to proceed with filtering
type	A character string specifying the procedure to be used for detecting outlier offspring. Options include "Gmat", which utilizes the genomic kinship matrix, and "PCA", which employs principal component analysis on the dosage matrix. coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman": can be abbreviated.
verbose	if TRUE (default), shows the filtered out individuals

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

---

filter_missing *Filter missing genotypes*

Description

Excludes markers or individuals based on their proportion of missing data.

Usage

```
filter_missing(
  input.data,
  type = c("marker", "individual"),
  filter.thres = 0.2,
  inter = TRUE
)
```

Arguments

input.data	an object of class mappoly.data.
type	one of the following options: 1. "marker": filter out markers based on their percentage of missing data (default). 2. "individual": filter out individuals based on their percentage of missing data. Please notice that removing individuals with certain amount of data can change some marker parameters (such as depth), and can also change the estimated genotypes for other individuals. So, be careful when removing individuals.
filter.thres	maximum percentage of missing data (default = 0.2).
inter	if TRUE, expects user-input to proceed with filtering.

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>.

Examples

```
plot(tetra.solcap)
dat.filt.mrk <- filter_missing(input.data = tetra.solcap,
                               type = "marker",
                               filter.thres = 0.1,
                               inter = TRUE)
plot(dat.filt.mrk)
```

---

filter_segregation *Filter markers based on chi-square test*

Description

This function filter markers based on p-values of a chi-square test. The chi-square test assumes that markers follow the expected segregation patterns under Mendelian inheritance, random chromosome bivalent pairing and no double reduction.

Usage

```
filter_segregation(input.obj, chisq.pval.thres = NULL, inter = TRUE)
```

Arguments

input.obj	name of input object (class mappoly.data)
chisq.pval.thres	p-value threshold used for chi-square tests (default = Bonferroni aproximation with global alpha of 0.05, i.e., 0.05/n.mrk)
inter	if TRUE (default), plots distorted vs. non-distorted markers

Value

An object of class mappoly.chitest.seq which contains a list with the following components:

keep	markers that follow Mendelian segregation pattern
exclude	markers with distorted segregation
chisq.pval.thres	threshold p-value used for chi-square tests
data.name	input dataset used to perform the chi-square tests

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

Examples

```
mrks.chi.filt <- filter_segregation(input.obj = tetra.solcap,
                                    chisq.pval.thres = 0.05/tetra.solcap$n.mrk,
                                    inter = TRUE)
seq.init <- make_seq_mappoly(mrks.chi.filt)
```

`find_blocks` *Allocate markers into linkage blocks*

Description

Function to allocate markers into linkage blocks. This is an EXPERIMENTAL FUNCTION and should be used with caution.

Usage

```
find_blocks(
  input.seq,
  clustering.type = c("rf", "genome"),
  rf.limit = 1e-04,
  genome.block.threshold = 10000,
  rf.mat = NULL,
  ncpus = 1,
  ph.thres = 3,
  phase.number.limit = 10,
  error = 0.05,
  verbose = TRUE,
  tol = 0.01,
  tol.err = 0.001
)
```

Arguments

`input.seq`	an object of class `mappoly.sequence`.
`clustering.type`	if `'rf'`, it uses UPGMA clusterization based on the recombination fraction matrix to assemble blocks. Linkage blocks are assembled by cutting the clusterization tree at `rf.limit`. If `'genome'`, it splits the marker sequence at neighbor markers morre than `'genome.block.threshold'` apart.
`rf.limit`	the maximum value to consider linked markers in case of `'clustering.type = rf'`
`genome.block.threshold`	the threshold to assume markers are in the same linkage block. to be considered when allocating markers into blocks in case of `'clustering.type = genomee'`
`rf.mat`	an object of class `mappoly.rf.matrix`.

ncpus	Number of parallel processes to spawn
ph.thres	the threshold used to sequentially phase markers. Used in thres.twopt and thres.hmm. See est_rf_hmm_sequential for details.
phase.number.limit	the maximum number of linkage phases of the sub-maps. The default is 10. See est_rf_hmm_sequential for details.
error	the assumed global genotyping error rate. If NULL (default) it does not include an error in the block estimation.
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced.
tol	tolerance for the C routine, i.e., the value used to evaluate convergence.
tol.err	tolerance for the C routine, i.e., the value used to evaluate convergence, including the global genotyping error in the model.

Value

a list containing 1: a list of blocks in form of mappoly.map objects; 2: a vector containing markers that were not included into blocks.

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

Examples

```
## Not run:
## Selecting 50 markers in chromosome 5
s5 <- make_seq_mappoly(tetra.solcap, "seq5")
s5 <- make_seq_mappoly(tetra.solcap, s5$seq.mrk.names[1:50])
tpt5 <- est_pairwise_rf(s5)
m5 <- rf_list_to_matrix(tpt5, 3, 3)
fb.rf <- find_blocks(s5, rf.mat = m5, verbose = FALSE, ncpus = 2)
bl.rf <- fb.rf$blocks
plot_map_list(bl.rf)

## Merging resulting maps
map.merge <- merge_maps(bl.rf, tpt5)
plot(map.merge, mrk.names = T)

## Comparing linkage phases with pre assembled map
id <- na.omit(match(map.merge$info$mrk.names, solcap.err.map[[5]]$info$mrk.names))
map.orig <- get_submap(solcap.err.map[[5]], mrk.pos = id)
p1.m<-map.merge$maps[[1]]$seq.ph$P
p2.m<-map.merge$maps[[1]]$seq.ph$Q
names(p1.m) <- names(p2.m) <- map.merge$info$mrk.names
p1.o<-map.orig$maps[[1]]$seq.ph$P
p2.o<-map.orig$maps[[1]]$seq.ph$Q
names(p1.o) <- names(p2.o) <- map.orig$info$mrk.names
n <- intersect(names(p1.m), names(p1.o))
plot_compare_haplotypes(4, p1.o[n], p2.o[n], p1.m[n], p2.m[n])
```

```
  ### Using genome
  fb.geno <- find_blocks(s5, clustering.type = "genome", genome.block.threshold = 10^4)
  plot_map_list(fb.geno$blocks)
  splt <- lapply(fb.geno$blocks, split_mappoly, 1)
  plot_map_list(splt)

## End(Not run)
```

`framework_map` *Design linkage map framework in two steps: i) estimating the recombination fraction with HMM approach for each parent separately using only markers segregating individually (e.g. map 1 - P1:3 x P2:0, P1: 2x4; map 2 - P1:0 x P2:3, P1:4 x P2:2); ii) merging both maps and re-estimate recombination fractions.*

Description

Design linkage map framework in two steps: i) estimating the recombination fraction with HMM approach for each parent separately using only markers segregating individually (e.g. map 1 - P1:3 x P2:0, P1: 2x4; map 2 - P1:0 x P2:3, P1:4 x P2:2); ii) merging both maps and re-estimate recombination fractions.

Usage

```
framework_map(
  input.seq,
  twopt,
  start.set = 10,
  thres.twopt = 10,
  thres.hmm = 30,
  extend.tail = 30,
  inflation.lim.p1 = 5,
  inflation.lim.p2 = 5,
  phase.number.limit = 10,
  tol = 0.01,
  tol.final = 0.001,
  verbose = TRUE,
  method = "hmm"
)
```

Arguments

`input.seq`	object of class `mappoly.sequence`
`twopt`	object of class `mappoly.twopt`
`start.set`	number of markers to start the phasing procedure (default = 4)
`thres.twopt`	the LOD threshold used to determine if the linkage phases compared via two-point analysis should be considered for the search space reduction (default = 5)

`thres.hmm` the LOD threshold used to determine if the linkage phases compared via hmm analysis should be evaluated in the next round of marker inclusion (default = 50)

`extend.tail` the length of the chain's tail that should be used to calculate the likelihood of the map. If NULL (default), the function uses all markers positioned. Even if info.tail = TRUE, it uses at least extend.tail as the tail length

`inflation.lim.p1`
the maximum accepted length difference between the current and the previous parent 1 sub-map defined by arguments info.tail and extend.tail. If the size exceeds this limit, the marker will not be inserted. If NULL(default), then it will insert all markers.

`inflation.lim.p2`
same as 'inflation.lim.p1' but for parent 2 sub-map.

`phase.number.limit`
the maximum number of linkage phases of the sub-maps defined by arguments info.tail and extend.tail. Default is 20. If the size exceeds this limit, the marker will not be inserted. If Inf, then it will insert all markers.

`tol` the desired accuracy during the sequential phase of each parental map (default = 10e-02)

`tol.final` the desired accuracy for the final parental map (default = 10e-04)

`verbose` If TRUE (default), current progress is shown; if FALSE, no output is produced

`method` indicates whether to use 'hmm' (Hidden Markov Models), 'ols' (Ordinary Least Squares) to re-estimate the recombination fractions while merging the parental maps (default:hmm)

Value

list containing three `mappoly.map` objects:1) map built with markers with segregation information from parent 1; 2) map built with markers with segregation information from parent 2; 3) maps in 1 and 2 merged

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu> with documentation and minor modifications by Cristiane Taniguti <chtaniguti@tamu.edu>

---

genetic-mapping-functions

Genetic Mapping Functions

Description

These functions facilitate the conversion between recombination fractions (r) and genetic distances (d) using various mapping models. The functions starting with 'mf_' convert recombination fractions to genetic distances, while those starting with 'imf_' convert genetic distances back into recombination fractions.

Usage

```
mf_k(d)

mf_h(d)

mf_m(d)

imf_k(r)

imf_h(r)

imf_m(r)
```

Arguments

d	Numeric or numeric vector, representing genetic distances in centiMorgans (cM) for direct functions (mf_k, mf_h, mf_m).
r	Numeric or numeric vector, representing recombination fractions for inverse functions (imf_k, imf_h, imf_m).

Details

The 'mf_' prefixed functions apply different models to convert recombination fractions into genetic distances:

- `mf_k`: Kosambi mapping function.
- `mf_h`: Haldane mapping function.
- `mf_m`: Morgan mapping function.

The 'imf_' prefixed functions convert genetic distances back into recombination fractions:

- `imf_k`: Inverse Kosambi mapping function.
- `imf_h`: Inverse Haldane mapping function.
- `imf_m`: Inverse Morgan mapping function.

References

Kosambi, D.D. (1944). The estimation of map distances from recombination values. Ann Eugen., 12, 172-175. Haldane, J.B.S. (1919). The combination of linkage values, and the calculation of distances between the loci of linked factors. J Genet, 8, 299-309. Morgan, T.H. (1911). Random segregation versus coupling in Mendelian inheritance. Science, 34(873), 384.

get_genomic_order *Get the genomic position of markers in a sequence*

Description

This functions gets the genomic position of markers in a sequence and return an ordered data frame with the name and position of each marker

Usage

```
get_genomic_order(input.seq, verbose = TRUE)

## S3 method for class 'mappoly.geno.ord'
print(x, ...)

## S3 method for class 'mappoly.geno.ord'
plot(x, ...)
```

Arguments

input.seq	a sequence object of class mappoly.sequence
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced
x	an object of the class mappoly.geno.ord
...	currently ignored

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

Examples

```
s1 <- make_seq_mappoly(tetra.solcap, "all")
o1 <- get_genomic_order(s1)
plot(o1)
s.geno.ord <- make_seq_mappoly(o1)
```

get_submap *Extract sub-map from map*

Description

Given a pre-constructed map, it extracts a sub-map for a provided sequence of marker positions. Optionally, it can update the linkage phase configurations and respective recombination fractions.

Usage

```
get_submap(
  input.map,
  mrk.pos,
  phase.config = "best",
  reestimate.rf = TRUE,
  reestimate.phase = FALSE,
  thres.twopt = 5,
  thres.hmm = 3,
  extend.tail = 50,
  tol = 0.1,
  tol.final = 0.001,
  use.high.precision = FALSE,
  verbose = TRUE
)
```

Arguments

input.map	An object of class mappoly.map
mrk.pos	positions of the markers that should be considered in the new map. This can be in any order
phase.config	which phase configuration should be used. "best" (default) will choose the configuration associated with the maximum likelihood
reestimate.rf	logical. If TRUE (default) the recombination fractions between markers are re-estimated
reestimate.phase	logical. If TRUE, the linkage phase configurations are re-estimated (default = FALSE)
thres.twopt	the LOD threshold used to determine if the linkage phases compared via two-point analysis should be considered (default = 5)
thres.hmm	the threshold used to determine if the linkage phases compared via hmm analysis should be considered (default = 3)
extend.tail	the length of the tail of the chain that should be used to calculate the likelihood of the linkage phases. If info.tail = TRUE, the function uses at least extend.tail as the length of the tail (default = 50)
tol	the desired accuracy during the sequential phase (default = 0.1)
tol.final	the desired accuracy for the final map (default = 10e-04)
use.high.precision	logical. If TRUE uses high precision (long double) numbers in the HMM procedure implemented in C++, which can take a long time to perform (default = FALSE)
verbose	If TRUE (default), current progress is shown; if FALSE, no output is produced

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
 ## selecting the six first markers in linkage group 1
 ## re-estimating the recombination fractions and linkage phases
 submap1.lg1 <- get_submap(input.map = maps.hexafake[[1]],
                       mrk.pos = 1:6, verbose = TRUE,
                       reestimate.phase = TRUE,
                       tol.final = 10e-3)
## no recombination fraction re-estimation: first 20 markers
 submap2.lg1 <- get_submap(input.map = maps.hexafake[[1]],
                       mrk.pos = 1:20, reestimate.rf = FALSE,
                       verbose = TRUE,
                       tol.final = 10e-3)
plot(maps.hexafake[[1]])
plot(submap1.lg1, mrk.names = TRUE, cex = .8)
plot(submap2.lg1, mrk.names = TRUE, cex = .8)
```

`get_tab_mrks` *Get table of dosage combinations*

Description

Internal function

Usage

```
get_tab_mrks(x)
```

Arguments

`x`	an object of class `mappoly.map`

Author(s)

Gabriel Gesteira, <gdesiqu@ncsu.edu>

group_mappoly *Assign markers to linkage groups*

Description

Identifies linkage groups of markers using the results of two-point (pairwise) analysis.

Usage

```
group_mappoly(
  input.mat,
  expected.groups = NULL,
  inter = TRUE,
  comp.mat = FALSE,
  LODweight = FALSE,
  verbose = TRUE
)
```

Arguments

input.mat	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 chromosome information is available (default = FALSE)
LODweight	if TRUE, clusterization is weighted by the square of the LOD Score
verbose	logical. If TRUE (default), current progress is shown; if FALSE, no output is produced

Value

Returns an object of class mappoly.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_mappoly
chisq.pval.thres	the threshold used on the segregation test when reading the dataset
chisq.pval	the p-values associated with the segregation test for all markers in the sequence

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## Getting first 20 markers from two linkage groups
all.mrk <- make_seq_mappoly(hexafake, c(1:20,601:620))
red.mrk <- elim_redundant(all.mrk)
unique.mrks <- make_seq_mappoly(red.mrk)
counts <- cache_counts_twopt(unique.mrks, cached = TRUE)
all.pairs <- est_pairwise_rf(input.seq = unique.mrks,
                             count.cache = counts,
                             ncpus = 1,
                             verbose = TRUE)

## Full recombination fraction matrix
mat.full <- rf_list_to_matrix(input.twopt = all.pairs)
plot(mat.full, index = FALSE)

lgs <- group_mappoly(input.mat = mat.full,
                     expected.groups = 2,
                     inter = TRUE,
                     comp.mat = TRUE, #this data has physical information
                     verbose = TRUE)
lgs
plot(lgs)
```

---

hexafake *Simulated autohexaploid dataset.*

Description

A dataset of a hypothetical autohexaploid full-sib population containing three homology groups

Usage

```
hexafake
```

Format

An object of class `mappoly.data` which contains a list with the following components:

plody ploidy level = 6

n.ind number individuals = 300

n.mrk total number of markers = 1500

ind.names the names of the individuals

mrk.names the names of the markers

dosage.p1 a vector containing the dosage in parent P for all `n.mrk` markers

dosage.p2 a vector containing the dosage in parent Q for all `n.mrk` markers

chrom a vector indicating the chromosome each marker belongs. Zero indicates that the marker was not assigned to any chromosome

genome.pos Physical position of the markers into the sequence

geno.dose a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by `ploidy_level + 1 = 7`

n.phen There are no phenotypes in this simulation

phen There are no phenotypes in this simulation

chisq.pval vector containing p-values for all markers associated to the chi-square test for the expected segregation patterns under Mendelian segregation

---

`hexafake.geno.dist` *Simulated autohexaploid dataset with genotype probabilities.*

Description

A dataset of a hypothetical autohexaploid full-sib population containing three homology groups. This dataset contains the probability distribution of the genotypes and 2% of missing data, but is essentially the same dataset found in `hexafake`

Usage

```
hexafake.geno.dist
```

Format

An object of class `mappoly.data` which contains a list with the following components:

ploidy ploidy level = 6

n.ind number individuals = 300

n.mrk total number of markers = 1500

ind.names the names of the individuals

mrk.names the names of the markers

dosage.p1 a vector containing the dosage in parent P for all `n.mrk` markers

dosage.p2 a vector containing the dosage in parent Q for all `n.mrk` markers

chrom a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence

genome.pos Physical position of the markers into the sequence

prob.thres = 0.95 probability threshold to associate a marker call to a dosage. Markers with maximum genotype probability smaller than 'prob.thres' are considered as missing data for the dosage calling purposes

geno a data.frame containing the probability distribution for each combination of marker and offspring. The first two columns represent the marker and the offspring, respectively. The remaining elements represent the probability associated to each one of the possible dosages

geno.dose a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by `ploidy_level + 1 = 7`

n.phen There are no phenotypes in this simulation

phen There are no phenotypes in this simulation

`import_data_from_polymapR`

Import data from polymapR

Description

Function to import datasets from polymapR.

Usage

```
import_data_from_polymapR(
  input.data,
  ploidy,
  parent1 = "P1",
  parent2 = "P2",
  input.type = c("discrete", "probabilistic"),
  prob.thres = 0.95,
  pardose = NULL,
  offspring = NULL,
  filter.non.conforming = TRUE,
  verbose = TRUE
)
```

Arguments

`input.data`	a `polymapR` dataset
`ploidy`	the ploidy level
`parent1`	a character string containing the name (or pattern of genotype IDs) of parent 1

parent2	a character string containing the name (or pattern of genotype IDs) of parent 2
input.type	Indicates whether the input is discrete ("disc") or probabilistic ("prob")
prob.thres	threshold probability to assign a dosage to offspring. If the probability is smaller than thresh.parent.geno, the data point is converted to 'NA'.
pardose	matrix of dimensions (n.mrk x 3) containing the name of the markers in the first column, and the dosage of parents 1 and 2 in columns 2 and 3. (see polymapR vignette)
offspring	a character string containing the name (or pattern of genotype IDs) of the offspring individuals. If NULL (default) it considers all individuals as offsprings, except parent1 and parent2.
filter.non.conforming	if TRUE exclude samples with non expected genotypes under no double reduction. Since markers were already filtered in polymapR, the default is FALSE.
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Details

See examples at https://rpubs.com/mmollin/tetra_mappoly_vignette.

Author(s)

Marcelo Mollinari <mmollin@ncsu.edu>

References

Bourke PM et al: (2019) PolymapR — linkage analysis and genetic map construction from F1 populations of outcrossing polyploids. _Bioinformatics_ 34:3496–3502. doi:10.1093/bioinformatics/bty1002

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

---

import_from_updog *Import from updog*

Description

Read objects with information related to genotype calling in polyploids. Currently this function supports output objects created with the updog (output of multidog function) package. This function creates an object of class mappoly.data

Usage

```
import_from_updog(
  object,
  prob.thres = 0.95,
  filter.non.conforming = TRUE,
  chrom = NULL,
  genome.pos = NULL,
  verbose = TRUE
)
```

Arguments

object	the name of the object of class multidog
prob.thres	probability threshold to associate a marker call to a dosage. Markers with maximum genotype probability smaller than 'prob.thres' are considered as missing data for the dosage calling purposes
filter.non.conforming	if TRUE (default) exclude samples with non expected genotypes under random chromosome pairing and no double reduction
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	vector with physical position of the markers into the sequence
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Value

An object of class mappoly.data which contains a list with the following components:

ploidy	ploidy level
n.ind	number individuals
n.mrk	total number of markers
ind.names	the names of the individuals
mrk.names	the names of the markers
dosage.p1	a vector containing the dosage in parent P for all n.mrk markers
dosage.p2	a vector containing the dosage in parent Q for all n.mrk markers
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	physical position of the markers into the sequence
prob.thres	probability threshold to associate a marker call to a dosage. Markers with maximum genotype probability smaller than 'prob.thres' were considered as missing data in the 'geno.dose' matrix
geno.dose	a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by ploidy_level + 1

geno	a data.frame containing the probability distribution for each combination of marker and offspring. The first two columns represent the marker and the offspring, respectively. The remaining elements represent the probability associated to each one of the possible dosages. Missing data are converted from NA to the expected segregation ratio using function segreg_poly
n.phen	number of phenotypic traits
phen	a matrix containing the phenotypic data. The rows correspond to the traits and the columns correspond to the individuals
chisq.pval	a vector containing p-values related to the chi-squared test of Mendelian segregation performed for all markers

Author(s)

Gabriel Gesteira, <gdesiqu@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
if(requireNamespace("updog", quietly = TRUE)){
library("updog")
data("uitdewilligen")
mout = multidog(refmat = t(uitdewilligen$refmat),
                sizemat = t(uitdewilligen$sizemat),
                ploidy = uitdewilligen$ploidy,
                model = "f1",
                p1_id = colnames(t(uitdewilligen$sizemat))[1],
                p2_id = colnames(t(uitdewilligen$sizemat))[2],
                nc = 2)
mydata = import_from_updog(mout)
mydata
plot(mydata)
}
```

---

import_phased_maplist_from_polymapR

Import phased map list from polymapR

Description

Function to import phased map lists from polymapR

Usage

```
import_phased_maplist_from_polymapR(maplist, mappoly.data, ploidy = NULL)
```

Arguments

maplist	a list of phased maps obtained using function create_phased_maplist from package polymapR
mappoly.data	a dataset used to obtain maplist, converted into class mappoly.data
ploidy	the ploidy level

Details

See examples at https://rpubs.com/mmollin/tetra_mappoly_vignette.

Author(s)

Marcelo Mollinari <mmollin@ncsu.edu>

References

Bourke PM et al: (2019) PolymapR — linkage analysis and genetic map construction from F1 populations of outcrossing polyploids. _Bioinformatics_ 34:3496–3502. doi:10.1093/bioinformatics/bty1002

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

---

loglike_hmm *Multipoint log-likelihood computation*

Description

Update the multipoint log-likelihood of a given map using the method proposed by *Mollinari and Garcia (2019)*.

Usage

```
loglike_hmm(input.map, input.data = NULL, verbose = FALSE)
```

Arguments

input.map	An object of class mappoly.map
input.data	An object of class mappoly.data, which was used to generate input.map
verbose	If TRUE, map information is shown; if FALSE(default), no output is produced

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
hexa.map <- loglike_hmm(maps.hexafake[[1]])
hexa.map
```

`make_mat_mappoly` *Subset recombination fraction matrices*

Description

Get a subset of an object of class `mappoly.rf.matrix`, i.e. recombination fraction and LOD score matrices based in a sequence of markers.

Usage

```
make_mat_mappoly(input.mat, input.seq)
```

Arguments

`input.mat`	an object of class `mappoly.rf.matrix`
`input.seq`	an object of class `mappoly.sequence`, with a sequence of markers contained in `input.mat`

Value

an object of class `mappoly.rf.matrix`, which is a subset of `'input.mat'`. See `rf_list_to_matrix` for details

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
# sequence with 20 markers
mrk.seq <- make_seq_mappoly(hexafake, 1:20)
mrk.pairs <- est_pairwise_rf(input.seq = mrk.seq,
                             verbose = TRUE)
## Full recombination fraction matrix
mat <- rf_list_to_matrix(input.twopt = mrk.pairs)
plot(mat)
## Matrix subset
id <- make_seq_mappoly(hexafake, 1:10)
mat.sub <- make_mat_mappoly(mat, id)
plot(mat.sub)
```

---

make_pairs_mappoly *Subset pairwise recombination fractions*

Description

Get a subset of an object of class `mappoly.twopt` or `mappoly.twopt2` (i.e. recombination fraction) and LOD score statistics for all possible linkage phase combinations based on a sequence of markers.

Usage

```
make_pairs_mappoly(input.twopt, input.seq)
```

Arguments

`input.twopt`	an object of class `mappoly.twopt`
`input.seq`	an object of class `mappoly.sequence`, with a sequence of markers contained in `input.twopt`

Value

an object of class `mappoly.twopt` which is a subset of `input.twopt`. See `est_pairwise_rf` for details

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## selecting some markers along the genome
some.mrk <- make_seq_mappoly(hexafake, seq(1, 1500, 30))
all.pairs <- est_pairwise_rf(input.seq = some.mrk)
mat.full <- rf_list_to_matrix(input.twopt = all.pairs)
plot(mat.full)

## selecting two-point information for chromosome 1
mrks.1 <- make_seq_mappoly(hexafake, names(which(some.mrk$chrom == 1)))
p1 <- make_pairs_mappoly(input.seq = mrks.1, input.twopt = all.pairs)
m1 <- rf_list_to_matrix(input.twopt = p1)
plot(m1, main.text = "LG1")
```

`make_seq_mappoly` *Create a Sequence of Markers*

Description

Constructs a sequence of markers based on an object belonging to various specified classes. This function is versatile, supporting multiple input types and configurations for generating marker sequences.

Usage

```
make_seq_mappoly(
  input.obj,
  arg = NULL,
  data.name = NULL,
  info.parent = c("all", "p1", "p2"),
  genomic.info = NULL
)

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

## S3 method for class 'mappoly.sequence'
plot(x, ...)
```

Arguments

`input.obj`	An object belonging to one of the specified classes: `mappoly.data`, `mappoly.map`, `mappoly.sequence`, `mappoly.group`, `mappoly.unique.seq`, `mappoly.pcmap`, `mappoly.pcmap3d`, `mappoly.geno.ord`, or `mappoly.edit.order`.
`arg`	Specifies the markers to include in the sequence, accepting several formats: a string 'all' for all markers; a string or vector of strings 'seqx' where x is the sequence number (0 for unassigned markers); a vector of integers indicating

	specific markers; or a vector of integers representing linkage group numbers if `input.obj` is of class `mappoly.group`. For certain classes (`mappoly.pcmap`, `mappoly.pcmap3d`, `mappoly.unique.seq`, or `mappoly.geno.ord`), `arg` can be `NULL`.
`data.name`	Name of the `mappoly.data` class object.
`info.parent`	Selection criteria based on parental information: `'all'` for all dosage combinations, `'P1'` for markers informative in parent 1, or `'P2'` for markers informative in parent 2. Default is `'all'`.
`genomic.info`	Optional and applicable only to `mappoly.group` objects. Specifies the use of genomic information in sequence creation. With `NULL` (default), all markers defined by the grouping function are included. Numeric values indicate the use of specific sequences from genomic information, aiming to match the maximum number of markers with the group. Supports single values or vectors for multiple sequence consideration.
`x`	An object of class `mappoly.sequence`.
`...`	Currently ignored.

Value

Returns an object of class ‘mappoly.sequence‘, comprising:

`"seq.num"`	Ordered vector of marker indices according to the input.
`"seq.phases"`	List of linkage phases between markers; -1 for undefined phases.
`"seq.rf"`	Vector of recombination frequencies; -1 for not estimated frequencies.
`"loglike"`	Log-likelihood of the linkage map.
`"data.name"`	Name of the ‘mappoly.data‘ object with raw data.
`"twopt"`	Name of the ‘mappoly.twopt‘ object with 2-point analyses; -1 if not computed.

Author(s)

Marcelo Mollinari <mmollin@ncsu.edu>, with modifications by Gabriel Gesteira <gdesiqu@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019). Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models. _G3: Genes|Genomes|Genetics_, doi:10.1534/g3.119.400378.

Examples

```
all.mrk <- make_seq_mappoly(hexafake, 'all')
seq1.mrk <- make_seq_mappoly(hexafake, 'seq1')
plot(seq1.mrk)
some.mrk.pos <- c(1,4,28,32,45)
some.mrk.1 <- make_seq_mappoly(hexafake, some.mrk.pos)
plot(some.mrk.1)
```

---

maps.hexafake *Resulting maps from* hexafake

Description

A list containing three linkage groups estimated using the procedure available in [MAPpoly's tutorial](https://mmollina.github.io/MAPpoly/#estimating_the_map_for_a_given_order)

Usage

```
maps.hexafake
```

Format

A list containing three objects of class `mappoly.map`, each one representing one linkage group in the simulated data.

---

mds_mappoly *Estimates loci position using Multidimensional Scaling*

Description

Estimates loci position using Multidimensional Scaling proposed by *Preedy and Hackett (2016)*. The code is an adaptation from the package `MDSmap`, available under GNU GENERAL PUBLIC LICENSE, Version 3, at https://CRAN.R-project.org/package=MDSMap

Usage

```
mds_mappoly(
  input.mat,
  p = NULL,
  n = NULL,
  ndim = 2,
  weight.exponent = 2,
  verbose = TRUE
)

## S3 method for class 'mappoly.pcmap'
print(x, ...)

## S3 method for class 'mappoly.pcmap3d'
print(x, ...)
```

Arguments

input.mat	an object of class mappoly.input.matrix
p	integer. The smoothing parameter for the principal curve. If NULL (default) this will be done using the leave-one-out cross validation
n	vector of integers or strings containing loci to be omitted from the analysis
ndim	number of dimensions to be considered in the multidimensional scaling procedure (default = 2)
weight.exponent	the exponent that should be used in the LOD score values to weight the MDS procedure (default = 2)
verbose	if TRUE (default), display information about the analysis
x	an object of class mappoly.mds
...	currently ignored

Value

A list containing:

M	the input distance map
sm	the unconstrained MDS results
pc	the principal curve results
distmap	a matrix of pairwise distances between loci where the columns are in the estimated order
locimap	a data frame of the loci containing the name and position of each locus in order of increasing distance
length	integer giving the total length of the segment
removed	a vector of the names of loci removed from the analysis
scale	the scaling factor from the MDS
locikey	a data frame showing the number associated with each locus name for interpreting the MDS configuration plot
confplotno	a data frame showing locus name associated with each number on the MDS configuration plots

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu> mostly adapted from MDSmap codes, written by Katharine F. Preedy, <katharine.preedy@bioss.ac.uk>

References

Preedy, K. F., & Hackett, C. A. (2016). A rapid marker ordering approach for high-density genetic linkage maps in experimental autotetraploid populations using multidimensional scaling. _Theoretical and Applied Genetics_, 129(11), 2117-2132. doi:10.1007/s0012201627618

Examples

```
s1 <- make_seq_mappoly(hexafake, 1:20)
t1 <- est_pairwise_rf(s1, ncpus = 1)
m1 <- rf_list_to_matrix(t1)
o1 <- get_genomic_order(s1)
s.go <- make_seq_mappoly(o1)
plot(m1, ord = s.go$seq.mrk.names)
mds.ord <- mds_mappoly(m1)
plot(mds.ord)
so <- make_seq_mappoly(mds.ord)
plot(m1, ord = so$seq.mrk.names)
plot(so$seq.num ~ I(so$genome.pos/1e6),
     xlab = "Genome Position",
     ylab = "MDS position")
```

---

merge_datasets *Merge datasets*

Description

This function merges two datasets of class `mappoly.data`. This can be useful when individuals of a population were genotyped using two or more techniques and have datasets in different files or formats. Please notice that the datasets should contain the same number of individuals and they must be represented identically in both datasets (e.g. `Ind_1` in both datasets, not `Ind_1` in one dataset and `ind_1` or `Ind.1` in the other).

Usage

```
merge_datasets(dat.1 = NULL, dat.2 = NULL)
```

Arguments

`dat.1`	the first dataset of class `mappoly.data` to be merged
`dat.2`	the second dataset of class `mappoly.data` to be merged (default = NULL); if `dat.2 = NULL`, the function returns `dat.1` only

Value

An object of class `mappoly.data` which contains all markers from both datasets. It will be a list with the following components:

`ploidy`	ploidy level
`n.ind`	number individuals
`n.mrk`	total number of markers
`ind.names`	the names of the individuals
`mrk.names`	the names of the markers

dosage.p1	a vector containing the dosage in parent P for all n.mrk markers
dosage.p2	a vector containing the dosage in parent Q for all n.mrk markers
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	Physical position of the markers into the sequence
seq.ref	if one or both datasets originated from read_vcf, it keeps reference alleles from sequencing platform, otherwise is NULL
seq.alt	if one or both datasets originated from read_vcf, it keeps alternative alleles from sequencing platform, otherwise is NULL
all.mrk.depth	if one or both datasets originated from read_vcf, it keeps marker read depths from sequencing, otherwise is NULL
prob.thres	(unused field)
geno.dose	a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by ploidy_level + 1
geno	if both datasets contain genotype distribution information, the final object will contain 'geno'. This is set to NULL otherwise
nphen	(0)
phen	(NULL)
chisq.pval	a vector containing p-values related to the chi-squared test of Mendelian segregation performed for all markers in both datasets
kept	if elim.redundant = TRUE when reading any dataset, holds all non-redundant markers
elim.correspondence	if elim.redundant = TRUE when reading any dataset, holds all non-redundant markers and its equivalence to the redundant ones

Author(s)

Gabriel Gesteira, <gdesiqu@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## Loading a subset of SNPs from chromosomes 3 and 12 of sweetpotato dataset
## (SNPs anchored to Ipomoea trifida genome)
dat <- NULL
for(i in c(3, 12)){
  cat("Loading chromosome", i, "...\n")
    tempfl <- tempfile(pattern = paste0("ch", i), fileext = ".vcf.gz")
    x <- "https://github.com/mmollina/MAPpoly_vignettes/raw/master/data/sweet_sample_ch"
    address <- paste0(x, i, ".vcf.gz")
```

```
    download.file(url = address, destfile = tempfl)
    dattemp <- read_vcf(file = tempfl, parent.1 = "PARENT1", parent.2 = "PARENT2",
                        ploidy = 6, verbose = FALSE)
    dat <- merge_datasets(dat, dattemp)
  cat("\n")
}
dat
plot(dat)
```

`merge_maps` *Merge two maps*

Description

Estimates the linkage phase and recombination fraction between pre-built maps and creates a new map by merging them.

Usage

```
merge_maps(
  map.list,
  twopt,
  thres.twopt = 10,
  genoprob.list = NULL,
  thres.hmm = "best",
  tol = 1e-04
)
```

Arguments

`map.list`	a list of objects of class `mappoly.map` to be merged.
`twopt`	an object of class `mappoly.twopt` containing the two-point information for all pairs of markers present in the original maps
`thres.twopt`	the threshold used to determine if the linkage phases compared via two-point analysis should be considered for the search space reduction (default = 3)
`genoprob.list`	a list of objects of class `mappoly.genoprob` containing the genotype probabilities for the maps to be merged. If `NULL` (default), the probabilities are computed.
`thres.hmm`	the threshold used to determine which linkage phase configurations should be returned when merging two maps. If "best" (default), returns only the best linkage phase configuration. NOTE: if merging multiple maps, it always uses the "best" linkage phase configuration at each block insertion.
`tol`	the desired accuracy (default = 10e-04)

Details

merge_maps uses two-point information, under a given LOD threshold, to reduce the linkage phase search space. The remaining linkage phases are tested using the genotype probabilities.

Value

A list of class mappoly.map with two elements:

i) info: a list containing information about the map, regardless of the linkage phase configuration:

ploidy	the ploidy level
n.mrk	number of markers
seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
mrk.names	the names of markers in the map
seq.dose.p1	a vector containing the dosage in parent 1 for all markers in the map
seq.dose.p2	a vector containing the dosage in parent 2 for all markers in the map
chrom	a vector indicating the sequence (usually chromosome) each marker belongs as informed in the input file. If not available, chrom = NULL
genome.pos	physical position (usually in megabase) of the markers into the sequence
seq.ref	reference base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
seq.alt	alternative base used for each marker (i.e. A, T, C, G). If not available, seq.ref = NULL
chisq.pval	a vector containing p-values of the chi-squared test of Mendelian segregation for all markers in the map
data.name	name of the dataset of class mappoly.data
ph.thres	the LOD threshold used to define the linkage phase configurations to test

ii) a list of maps with possible linkage phase configuration. Each map in the list is also a list containing

seq.num	a vector containing the (ordered) indices of markers in the map, according to the input file
seq.rf	a vector of size (n.mrk - 1) containing a sequence of recombination fraction between the adjacent markers in the map
seq.ph	linkage phase configuration for all markers in both parents
loglike	the hmm-based multipoint likelihood

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

Examples

```
#### Tetraploid example #####
map1 <- get_submap(solcap.dose.map[[1]], 1:5)
map2 <- get_submap(solcap.dose.map[[1]], 6:15)
map3 <- get_submap(solcap.dose.map[[1]], 16:30)
full.map <- get_submap(solcap.dose.map[[1]], 1:30)
s <- make_seq_mappoly(tetra.solcap, full.map$maps[[1]]$seq.num)
twopt <- est_pairwise_rf(input.seq = s)
merged.maps <- merge_maps(map.list = list(map1, map2, map3),
                          twopt = twopt,
                          thres.twopt = 3)
plot(merged.maps, mrk.names = TRUE)
plot(full.map, mrk.names = TRUE)
best.phase <- merged.maps$maps[[1]]$seq.ph
names.id <- names(best.phase$P)
compare_haplotypes(ploidy = 4, best.phase$P[names.id],
                   full.map$maps[[1]]$seq.ph$P[names.id])
compare_haplotypes(ploidy = 4, best.phase$Q[names.id],
                   full.map$maps[[1]]$seq.ph$Q[names.id])
```

`plot.mappoly.homoprob` *Plots mappoly.homoprob*

Description

Plots mappoly.homoprob

Usage

```
## S3 method for class 'mappoly.homoprob'
plot(
  x,
  stack = FALSE,
  lg = NULL,
  ind = NULL,
  use.plotly = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

`x`	an object of class `mappoly.homoprob`
`stack`	logical. If `TRUE`, probability profiles of all homologues are stacked in the plot (default = FALSE)
`lg`	indicates which linkage group should be plotted. If `NULL` (default), it plots the first linkage group. If `"all"`, it plots all linkage groups

ind	indicates which individuals should be plotted. It can be the position of the individuals in the dataset or it's name. If NULL (default), the function plots the first individual
use.plotly	if TRUE (default), it uses plotly interactive graphic
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced
...	unused arguments

`plot.mappoly.prefpair.profiles`
Plots mappoly.prefpair.profiles

Description

Plots mappoly.prefpair.profiles

Usage

```
## S3 method for class 'mappoly.prefpair.profiles'
plot(
  x,
  type = c("pair.configs", "hom.pairs"),
  min.y.prof = 0,
  max.y.prof = 1,
  thresh = 0.01,
  P1 = "P1",
  P2 = "P2",
  ...
)
```

Arguments

x	an object of class mappoly.prefpair.profiles
type	a character string indicating which type of graphic is plotted: "pair.configs" (default) plots the preferential pairing profile for the pairing configurations or "hom.pairs" plots the preferential pairing profile for the homolog pairs
min.y.prof	lower bound for y axis on the probability profile graphic (default = 0)
max.y.prof	upper bound for y axis on the probability profile graphic (default = 1)
thresh	threshold for chi-square test (default = 0.01)
P1	a string containing the name of parent P1
P2	a string containing the name of parent P2
...	unused arguments

plot_genome_vs_map *Physical versus genetic distance*

Description

This function plots scatterplot(s) of physical distance (in Mbp) versus the genetic distance (in cM). Map(s) should be passed as a single object or a list of objects of class `mappoly.map`.

Usage

```
plot_genome_vs_map(
  map.list,
  phase.config = "best",
  same.ch.lg = FALSE,
  alpha = 1/5,
  size = 3
)
```

Arguments

`map.list`	A list or a single object of class `mappoly.map`
`phase.config`	A vector containing which phase configuration should be plotted. If `'best'` (default), plots the configuration with the highest likelihood for all elements in `'map.list'`
`same.ch.lg`	Logical. If `TRUE` displays only the scatterplots between the chromosomes and linkage groups with the same number. Default is `FALSE`.
`alpha`	transparency factor for SNPs points
`size`	size of the SNP points

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
plot_genome_vs_map(solcap.mds.map, same.ch.lg = TRUE)
plot_genome_vs_map(solcap.mds.map, same.ch.lg = FALSE,
                   alpha = 1, size = 1/2)
```

plot_GIC *Genotypic information content*

Description

This function plots the genotypic information content given an object of class `mappoly.homoprob`.

Usage

```
plot_GIC(hprobs, P = "P1", Q = "P2")
```

Arguments

`hprobs`	an object of class `mappoly.homoprob`
`P`	a string containing the name of parent P
`Q`	a string containing the name of parent Q

Examples

```
w <- lapply(solcap.err.map[1:3], calc_genoprob)
h.prob <- calc_homologprob(w)
plot_GIC(h.prob)
```

plot_mappoly.map2 *Plot object mappoly.map2*

Description

Plot object mappoly.map2

Usage

```
plot_mappoly.map2(x)
```

Arguments

`x`	object of class `mappoly.map2`

plot_map_list *Plot a genetic map*

Description

This function plots a genetic linkage map(s) generated by MAPpoly. The map(s) should be passed as a single object or a list of objects of class mappoly.map.

Usage

```
plot_map_list(
  map.list,
  horiz = TRUE,
  col = "lightgray",
  title = "Linkage group"
)
```

Arguments

map.list	A list of objects or a single object of class mappoly.map
horiz	logical. If FALSE, the maps are plotted vertically with the first map to the left. If TRUE (default), the maps are plotted horizontally with the first at the bottom
col	a vector of colors for each linkage group. (default = 'lightgray') ggstyle produces maps using the default ggplot color palette.
title	a title (string) for the maps (default = 'Linkage group')

Value

A data.frame object containing the name of the markers and their genetic position

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## hexafake map
plot_map_list(maps.hexafake, horiz = FALSE)
plot_map_list(maps.hexafake, col = c("#999999", "#E69F00", "#56B4E9"))

## solcap map
```

```
plot_map_list(solcap.dose.map, col = "ggstyle")
plot_map_list(solcap.dose.map, col = "mp_pallet3", horiz = FALSE)
```

`plot_mrk_info` *Plot marker information*

Description

Plots summary statistics for a given marker.

Usage

```
plot_mrk_info(input.data, mrk)
```

Arguments

`input.data`	an object of class `mappoly.data`
`mrk`	marker name or position in the dataset

Examples

```
plot_mrk_info(tetra.solcap.geno.dist, 2680)
plot_mrk_info(tetra.solcap.geno.dist, "solcap_snp_c2_23828")
```

`plot_progeny_dosage_change` *Plot progeny dosage changes after HMM-based correction with a global error model*

Description

Computes genotype probabilities under a global genotyping error rate, derives homolog probabilities, compares the most likely HMM-implied dosages to the original dosage matrix, and plots which entries were unchanged, imputed (originally missing), or changed.

Usage

```
plot_progeny_dosage_change(
  map_list,
  error,
  verbose = TRUE,
  output_corrected = FALSE
)
```

Arguments

map_list	A non-empty list of objects of class mappoly.map.
error	Numeric scalar. Global genotyping error rate passed to calc_genoprob_error.
verbose	Logical. If TRUE (default), progress is printed by underlying routines; if FALSE, suppresses progress messages where supported.
output_corrected	Logical. If FALSE (default), the function only prints the plot and returns invisible(NULL). If TRUE, returns a matrix containing marker metadata columns followed by the corrected dosages (individuals in columns).

Details

Missing dosages in dat$geno.dose are assumed to be encoded as ploidy + 1. The function prints a heatmap-style ggplot2 tile plot and, optionally, returns a corrected dosage matrix with marker metadata.

The mappoly.data object is retrieved by name from map_list[[1]]$info$data.name. The function:

1. Runs calc_genoprob_error() for each map in map_list.
2. Computes homolog probabilities with calc_homologprob().
3. For each marker and individual, selects the ploidy most likely homologs and converts them to a dosage implied by the phased map.
4. Compares implied dosages to dat$geno.dose and summarizes the fraction of entries that were imputed (original missing) vs changed.
5. Produces a tile plot showing unchanged/imputed/changed cells.

Value

If output_corrected = FALSE, returns invisible(NULL) and prints a ggplot. If output_corrected = TRUE, returns a matrix with columns P1, P2, sequence, sequence_position, followed by one column per individual containing corrected dosages.

Author(s)

Jeekin Lau, with optimization by Cristiane Taniguti

See Also

calc_genoprob_error, calc_homologprob

Examples

```
## Not run:
x <- get_submap(solcap.err.map[[1]], 1:5, reestimate.rf = FALSE)

corrected_matrix <- plot_progeny_dosage_change(list(x), error = 0.05,
                                               output_corrected = TRUE)
```

```
## End(Not run)
```

`read_fitpoly` *Data Input in fitPoly format*

Description

Reads an external data file generated as output of `saveMarkerModels`. This function creates an object of class `mappoly.data`.

Usage

```
read_fitpoly(
  file.in,
  ploidy,
  parent1,
  parent2,
  offspring = NULL,
  filter.non.conforming = TRUE,
  elim.redundant = TRUE,
  parent.geno = c("joint", "max"),
  thresh.parent.geno = 0.95,
  prob.thres = 0.95,
  file.type = c("table", "csv"),
  verbose = TRUE
)
```

Arguments

`file.in`	a character string with the name of (or full path to) the input file
`ploidy`	the ploidy level
`parent1`	a character string containing the name (or pattern of genotype IDs) of parent 1
`parent2`	a character string containing the name (or pattern of genotype IDs) of parent 2
`offspring`	a character string containing the name (or pattern of genotype IDs) of the offspring individuals. If `NULL` (default) it considers all individuals as offsprings, except `parent1` and `parent2`.
`filter.non.conforming`	if `TRUE` (default) converts data points with unexpected genotypes (i.e. no double reduction) to 'NA'. See function `segreg_poly` for information on expected classes and their respective frequencies.
`elim.redundant`	logical. If `TRUE` (default), removes redundant markers during map construction, keeping them annotated to in order to include them in the final map.

parent.geno	indicates whether to use the joint probability 'joint' (default) or the maximum probability of multiple replicates (if available) to assign dosage to parents. If there is one observation per parent, both options will yield the same results.
thresh.parent.geno	threshold probability to assign a dosage to parents. If the probability is smaller than thresh.parent.geno, the marker is discarded.
prob.thres	threshold probability to assign a dosage to offspring. If the probability is smaller than prob.thres, the data point is converted to 'NA'.
file.type	indicates whether the characters in the input file are separated by 'white spaces' ("table") or by commas ("csv").
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Value

An object of class mappoly.data which contains a list with the following components:

ploidy	ploidy level
n.ind	number individuals
n.mrk	total number of markers
ind.names	the names of the individuals
mrk.names	the names of the markers
dosage.p1	a vector containing the dosage in parent P for all n.mrk markers
dosage.p2	a vector containing the dosage in parent Q for all n.mrk markers
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	Physical position of the markers into the sequence
seq.ref	NULL (unused in this type of data)
seq.alt	NULL (unused in this type of data)
all.mrk.depth	NULL (unused in this type of data)
geno.dose	a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by ploidy_level + 1
n.phen	number of phenotypic traits
phen	a matrix containing the phenotypic data. The rows correspond to the traits and the columns correspond to the individuals
kept	if elim.redundant = TRUE, holds all non-redundant markers
elim.correspondence	if elim.redundant = TRUE, holds all non-redundant markers and its equivalence to the redundant ones

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Voorrips, R.E., Gort, G. & Vosman, B. (2011) Genotype calling in tetraploid species from bi-allelic marker data using mixture models. _BMC Bioinformatics_. doi:10.1186/1471210512172

Examples

```
#### Tetraploid Example
ft <- "https://raw.githubusercontent.com/mmollina/MAPpoly_vignettes/master/data/fitpoly.dat"
tempfl <- tempfile()
download.file(ft, destfile = tempfl)
fitpoly.dat <- read_fitpoly(file.in = tempfl, ploidy = 4,
                            parent1 = "P1", parent2 = "P2",
                            verbose = TRUE)
print(fitpoly.dat, detailed = TRUE)
plot(fitpoly.dat)
plot_mrk_info(fitpoly.dat, 37)
```

---

read_geno *Data Input*

Description

Reads an external data file. The format of the file is described in the `Details` section. This function creates an object of class `mappoly.data`

Usage

```
read_geno(
  file.in,
  filter.non.conforming = TRUE,
  elim.redundant = TRUE,
  verbose = TRUE
)

## S3 method for class 'mappoly.data'
print(x, detailed = FALSE, ...)

## S3 method for class 'mappoly.data'
plot(x, thresh.line = 1e-05, ...)
```

Arguments

`file.in`	a character string with the name of (or full path to) the input file which contains the data to be read

filter.non.conforming	if TRUE (default) converts data points with unexpected genotypes (i.e. no double reduction) to 'NA'. See function segreg_poly for information on expected classes and their respective frequencies.
elim.redundant	logical. If TRUE (default), removes redundant markers during map construction, keeping them annotated to export to the final map.
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced
x	an object of class mappoly.data
detailed	if available, print the number of markers per sequence (default = FALSE)
...	currently ignored
thresh.line	position of a threshold line for p values of the segregation test (default = 10e-06)

Details

The first line of the input file contains the string ploidy followed by the ploidy level of the parents. The second and third lines contain the strings n.ind and n.mrk followed by the number of individuals in the dataset and the total number of markers, respectively. Lines number 4 and 5 contain the strings mrk.names and ind.names followed by a sequence of the names of the markers and the name of the individuals, respectively. Lines 6 and 7 contain the strings dosageP and dosageQ followed by a sequence of numbers containing the dosage of all markers in parent P and Q. Line 8, contains the string seq followed by a sequence of integer numbers indicating the chromosome each marker belongs. It can be any 'a priori' information regarding the physical distance between markers. For example, these numbers could refer to chromosomes, scaffolds or even contigs, in which the markers are positioned. If this information is not available for a particular marker, NA should be used. If this information is not available for any of the markers, the string seq should be followed by a single NA. Line number 9 contains the string seqpos followed by the physical position of the markers into the sequence. The physical position can be given in any unity of physical genomic distance (base pairs, for instance). However, the user should be able to make decisions based on these values, such as the occurrence of crossing overs, etc. Line number 10 should contain the string nphen followed by the number of phenotypic traits. Line number 11 is skipped (Usually used as a spacer). The next elements are strings containing the name of the phenotypic trait with no space characters followed by the phenotypic values. The number of lines should be the same number of phenotypic traits. NA represents missing values. The line number 12 + nphen is skipped. Finally, the last element is a table containing the dosage for each marker (rows) for each individual (columns). NA represents missing values.

Value

An object of class mappoly.data which contains a list with the following components:

ploidy	ploidy level
n.ind	number individuals
n.mrk	total number of markers
ind.names	the names of the individuals
mrk.names	the names of the markers
dosage.p1	a vector containing the dosage in parent P for all n.mrk markers

dosage.p2	a vector containing the dosage in parent Q for all n.mrk markers
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	Physical position of the markers into the sequence
seq.ref	NULL (unused in this type of data)
seq.alt	NULL (unused in this type of data)
all.mrk.depth	NULL (unused in this type of data)
geno.dose	a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by ploidy_level + 1
n.phen	number of phenotypic traits
phen	a matrix containing the phenotypic data. The rows correspond to the traits and the columns correspond to the individuals
kept	if elim.redundant = TRUE, holds all non-redundant markers
elim.correspondence	if elim.redundant = TRUE, holds all non-redundant markers and its equivalence to the redundant ones

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari M., Olukolu B. A., Pereira G. da S., Khan A., Gemenet D., Yencho G. C., Zeng Z-B. (2020), Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400620

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
#### Tetraploid Example
fl1 = "https://raw.githubusercontent.com/mmollina/MAPpoly_vignettes/master/data/SolCAP_dosage"
tempfl <- tempfile()
download.file(fl1, destfile = tempfl)
SolCAP.dose <- read_geno(file.in  = tempfl)
print(SolCAP.dose, detailed = TRUE)
plot(SolCAP.dose)
```

read_geno_csv *Data Input in CSV format*

Description

Reads an external comma-separated values (CSV) data file. The format of the file is described in the Details section. This function creates an object of class mappoly.data.

Usage

```
read_geno_csv(
  file.in,
  ploidy,
  filter.non.conforming = TRUE,
  elim.redundant = TRUE,
  verbose = TRUE
)
```

Arguments

file.in	a character string with the name of (or full path to) the input file containing the data to be read
ploidy	the ploidy level
filter.non.conforming	if TRUE (default) converts data points with unexpected genotypes (i.e. no double reduction) to 'NA'. See function segreg_poly for information on expected classes and their respective frequencies.
elim.redundant	logical. If TRUE (default), removes redundant markers during map construction, keeping them annotated to export to the final map.
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Details

This is an alternative and a somewhat more straightforward version of the function read_geno. The input is a standard CSV file where the rows represent the markers, except for the first row which is used as a header. The first five columns contain the marker names, the dosage in parents 1 and 2, the chromosome information (i.e. chromosome, scaffold, contig, etc) and the position of the marker within the sequence. The remaining columns contain the dosage of the full-sib population. A tetraploid example of such file can be found in the Examples section.

Value

An object of class mappoly.data which contains a list with the following components:

ploidy	ploidy level
n.ind	number individuals

n.mrk	total number of markers
ind.names	the names of the individuals
mrk.names	the names of the markers
dosage.p1	a vector containing the dosage in parent P for all n.mrk markers
dosage.p2	a vector containing the dosage in parent Q for all n.mrk markers
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	Physical position of the markers into the sequence
seq.ref	NULL (unused in this type of data)
seq.alt	NULL (unused in this type of data)
all.mrk.depth	NULL (unused in this type of data)
geno.dose	a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by ploidy_level + 1
n.phen	number of phenotypic traits
phen	a matrix containing the phenotypic data. The rows correspond to the traits and the columns correspond to the individuals
kept	if elim.redundant = TRUE, holds all non-redundant markers
elim.correspondence	if elim.redundant = TRUE, holds all non-redundant markers and its equivalence to the redundant ones

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>, with minor changes by Gabriel Gesteira, <gdesiqu@ncsu.edu>

References

Mollinari M., Olukolu B. A., Pereira G. da S., Khan A., Gemenet D., Yencho G. C., Zeng Z-B. (2020), Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400620

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
#### Tetraploid Example
ft = "https://raw.githubusercontent.com/mmollina/MAPpoly_vignettes/master/data/tetra_solcap.csv"
tempfl <- tempfile()
download.file(ft, destfile = tempfl)
SolCAP.dose <- read_geno_csv(file.in  = tempfl, ploidy = 4)
print(SolCAP.dose, detailed = TRUE)
plot(SolCAP.dose)
```

read_geno_prob *Data Input*

Description

Reads an external data file. The format of the file is described in the Details section. This function creates an object of class mappoly.data

Usage

```
read_geno_prob(
  file.in,
  prob.thres = 0.95,
  filter.non.conforming = TRUE,
  elim.redundant = TRUE,
  verbose = TRUE
)
```

Arguments

file.in	a character string with the name of (or full path to) the input file which contains the data to be read
prob.thres	probability threshold to associate a marker call to a dosage. Markers with maximum genotype probability smaller than prob.thres are considered as missing data for the dosage calling purposes (default = 0.95)
filter.non.conforming	if TRUE (default) converts data points with unexpected genotypes (i.e. no double reduction) to 'NA'. See function segreg_poly for information on expected classes and their respective frequencies.
elim.redundant	logical. If TRUE (default), removes redundant markers during map construction, keeping them annotated to export to the final map.
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Details

The first line of the input file contains the string ploidy followed by the ploidy level of the parents. The second and third lines contains the strings n.ind and n.mrk followed by the number of individuals in the dataset and the total number of markers, respectively. Lines number 4 and 5 contain the string mrk.names and ind.names followed by a sequence of the names of the markers and the name of the individuals, respectively. Lines 6 and 7 contain the strings dosageP and dosageQ followed by a sequence of numbers containing the dosage of all markers in parent P and Q. Line 8, contains the string seq followed by a sequence of integer numbers indicating the chromosome each marker belongs. It can be any 'a priori' information regarding the physical distance between markers. For example, these numbers could refer to chromosomes, scaffolds or even contigs, in which the markers are positioned. If this information is not available for a particular marker, NA should be used. If this information is not available for any of the markers, the string seq should be followed by a single

NA. Line number 9 contains the string seqpos followed by the physical position of the markers into the sequence. The physical position can be given in any unity of physical genomic distance (base pairs, for instance). However, the user should be able to make decisions based on these values, such as the occurrence of crossing overs, etc. Line number 10 should contain the string nphen followed by the number of phenotypic traits. Line number 11 is skipped (Usually used as a spacer). The next elements are strings containing the name of the phenotypic trait with no space characters followed by the phenotypic values. The number of lines should be the same number of phenotypic traits. NA represents missing values. The line number 12 + nphen is skipped. Finally, the last element is a table containing the probability distribution for each combination of marker and offspring. The first two columns represent the marker and the offspring, respectively. The remaining elements represent the probability associated with each one of the possible dosages. NA represents missing data.

Value

an object of class mappoly.data which contains a list with the following components:

ploidy	ploidy level
n.ind	number individuals
n.mrk	total number of markers
ind.names	the names of the individuals
mrk.names	the names of the markers
dosage.p1	a vector containing the dosage in parent P for all n.mrk markers
dosage.p2	a vector containing the dosage in parent Q for all n.mrk markers
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	physical position of the markers into the sequence
seq.ref	NULL (unused in this type of data)
seq.alt	NULL (unused in this type of data)
all.mrk.depth	NULL (unused in this type of data)
prob.thres	probability threshold to associate a marker call to a dosage. Markers with maximum genotype probability smaller than 'prob.thres' were considered as missing data in the 'geno.dose' matrix
geno.dose	a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by ploidy_level + 1
geno	a data.frame containing the probability distribution for each combination of marker and offspring. The first two columns represent the marker and the offspring, respectively. The remaining elements represent the probability associated to each one of the possible dosages. Missing data are converted from NA to the expected segregation ratio using function segreg_poly
n.phen	number of phenotypic traits
phen	a matrix containing the phenotypic data. The rows correspond to the traits and the columns correspond to the individuals
chisq.pval	a vector containing p-values related to the chi-squared test of Mendelian segregation performed for all markers

`kept` if elim.redundant = TRUE, holds all non-redundant markers

`elim.correspondence` if elim.redundant = TRUE, holds all non-redundant markers and its equivalence to the redundant ones

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari M., Olukolu B. A., Pereira G. da S., Khan A., Gemenet D., Yencho G. C., Zeng Z-B. (2020), Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400620

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
#### Tetraploid Example
ft = "https://raw.githubusercontent.com/mmollina/MAPpoly_vignettes/master/data/hexa_sample"
tempfl <- tempfile()
download.file(ft, destfile = tempfl)
SolCAP.dose.prob <- read_geno_prob(file.in  = tempfl)
print(SolCAP.dose.prob, detailed = TRUE)
plot(SolCAP.dose.prob)
```

---

read_vcf *Data Input VCF*

Description

Reads an external VCF file and creates an object of class `mappoly.data`

Usage

```
read_vcf(
  file.in,
  parent.1,
  parent.2,
  ploidy = NA,
  filter.non.conforming = TRUE,
  thresh.line = 0.05,
  min.gt.depth = 0,
  min.av.depth = 0,
```

```
  max.missing = 1,
  elim.redundant = TRUE,
  verbose = TRUE,
  read.geno.prob = FALSE,
  prob.thres = 0.95
)
```

Arguments

file.in	a character string with the name of (or full path to) the input file which contains the data (VCF format)
parent.1	a character string containing the name of parent 1
parent.2	a character string containing the name of parent 2
ploidy	the species ploidy (optional, it will be automatically detected)
filter.non.conforming	if TRUE (default) converts data points with unexpected genotypes (i.e. no double reduction) to 'NA'. See function segreg_poly for information on expected classes and their respective frequencies.
thresh.line	threshold used for p-values on segregation test (default = 0.05)
min.gt.depth	minimum genotype depth to keep information. If the genotype depth is below min.gt.depth, it will be replaced with NA (default = 0)
min.av.depth	minimum average depth to keep markers (default = 0)
max.missing	maximum proportion of missing data to keep markers (range = 0-1; default = 1)
elim.redundant	logical. If TRUE (default), removes redundant markers during map construction, keeping them annotated to export to the final map.
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced
read.geno.prob	If genotypic probabilities are available (PL field), generates a probability-based dataframe (default = FALSE).
prob.thres	probability threshold to associate a marker call to a dosage. Markers with maximum genotype probability smaller than prob.thres are considered as missing data for the dosage calling purposes (default = 0.95)

Details

This function can handle .vcf files versions 4.0 or higher. The ploidy can be automatically detected, but it is highly recommended that you inform it to check for mismatches. All individual and marker names will be kept as they are in the .vcf file.

Value

An object of class mappoly.data which contains a list with the following components:

ploidy	ploidy level
n.ind	number individuals
n.mrk	total number of markers

ind.names	the names of the individuals
mrk.names	the names of the markers
dosage.p1	a vector containing the dosage in parent P for all n.mrk markers
dosage.p2	a vector containing the dosage in parent Q for all n.mrk markers
chrom	a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence
genome.pos	Physical position of the markers into the sequence
seq.ref	Reference base used for each marker (i.e. A, T, C, G)
seq.alt	Alternative base used for each marker (i.e. A, T, C, G)
prob.thres	(unused field)
geno.dose	a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by ploidy_level + 1
geno	a dataframe containing all genotypic probabilities columns for each marker and individual combination (rows). Missing data are represented by ploidy_level + 1
nphen	(unused field)
phen	(unused field)
all.mrk.depth	DP information for all markers on VCF file
chisq.pval	a vector containing p-values related to the chi-squared test of Mendelian segregation performed for all markers
kept	if elim.redundant = TRUE, holds all non-redundant markers
elim.correspondence	if elim.redundant = TRUE, holds all non-redundant markers and its equivalence to the redundant ones

Author(s)

Gabriel Gesteira, <gdesiqu@ncsu.edu>

References

Mollinari M., Olukolu B. A., Pereira G. da S., Khan A., Gemenet D., Yencho G. C., Zeng Z-B. (2020), Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400620

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
## Hexaploid sweetpotato: Subset of chromosome 3
fl = "https://github.com/mmollina/MAPpoly_vignettes/raw/master/data/sweet_sample_ch3.vcf.gz"
tempfl <- tempfile(pattern = 'chr3_', fileext = '.vcf.gz')
download.file(fl, destfile = tempfl)
```

```
dat.dose.vcf = read_vcf(file = tempfl, parent.1 = "PARENT1", parent.2 = "PARENT2")
print(dat.dose.vcf)
plot(dat.dose.vcf)
```

`reest_rf` *Re-estimate the recombination fractions in a genetic map*

Description

This function re-estimates the recombination fractions between all markers in a given map.

Usage

```
reest_rf(
  input.map,
  input.mat = NULL,
  tol = 0.01,
  phase.config = "all",
  method = c("hmm", "ols", "wMDS_to_1D_pc"),
  weight = TRUE,
  verbose = TRUE,
  high.prec = FALSE,
  max.rf.to.break.EM = 0.5,
  input.mds = NULL
)
```

Arguments

`input.map`	An object of class `mappoly.map`
`input.mat`	An object of class `mappoly.rf.matrix`
`tol`	tolerance for determining convergence (default = 10e-03)
`phase.config`	which phase configuration should be used. "best" (default) will choose the maximum likelihood configuration
`method`	indicates whether to use `'hmm'` (Hidden Markov Models), `'ols'` (Ordinary Least Squares) or `'wMDS_to_1D_pc'` (weighted MDS followed by fitting a one dimensional principal curve) to re-estimate the recombination fractions.
`weight`	if `TRUE` (default), it uses the LOD scores to perform a weighted regression when the Ordinary Least Squares is chosen
`verbose`	if `TRUE` (default), current progress is shown; if `FALSE`, no output is produced
`high.prec`	logical. If `TRUE` uses high precision (long double) numbers in the HMM procedure implemented in C++, which can take a long time to perform (default = FALSE)
`max.rf.to.break.EM`	for internal use only.
`input.mds`	An object of class `mappoly.map`

Value

An updated object of class `mappoly.pcmap` whose order was used in the `input.map`

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Stam P (1993) Construction of integrated genetic-linkage maps by means of a new computer package: Joinmap. _Plant J_ 3:739–744 doi:10.1111/j.1365313X.1993.00739.x

---

`rev_map` *Reverse map*

Description

Provides the reverse of a given map.

Usage

```
rev_map(input.map)
```

Arguments

`input.map`	an object of class `mappoly.map`

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

Examples

```
plot_genome_vs_map(solcap.mds.map[[1]])
plot_genome_vs_map(rev_map(solcap.mds.map[[1]]))
```

`rf_list_to_matrix` *Recombination fraction list to matrix*

Description

Transforms the recombination fraction list contained in an object of class `mappoly.twopt` or `mappoly.twopt2` into a recombination fraction matrix

Usage

```
rf_list_to_matrix(
  input.twopt,
  thresh.LOD.ph = 0,
  thresh.LOD.rf = 0,
  thresh.rf = 0.5,
  ncpus = 1L,
  shared.alleles = FALSE,
  verbose = TRUE
)

## S3 method for class 'mappoly.rf.matrix'
print(x, ...)

## S3 method for class 'mappoly.rf.matrix'
plot(
  x,
  type = c("rf", "lod"),
  ord = NULL,
  rem = NULL,
  main.text = NULL,
  index = FALSE,
  fact = 1,
  ...
)
```

Arguments

`input.twopt`	an object of class `mappoly.twopt` or `mappoly.twopt2`
`thresh.LOD.ph`	LOD score threshold for linkage phase configurations (default = 0)
`thresh.LOD.rf`	LOD score threshold for recombination fractions (default = 0)
`thresh.rf`	the threshold used for recombination fraction filtering (default = 0.5)
`ncpus`	number of parallel processes (i.e. cores) to spawn (default = 1)
`shared.alleles`	if `TRUE`, computes two matrices (for both parents) indicating the number of homologues that share alleles (default = FALSE)
`verbose`	if `TRUE` (default), current progress is shown; if `FALSE`, no output is produced

x	an object of class mappoly.rf.matrix
...	currently ignored
type	type of matrix that should be printed. Can be one of the following: "rf", for recombination fraction or "lod" for LOD Score
ord	the order in which the markers should be plotted (default = NULL)
rem	which markers should be removed from the heatmap (default = NULL)
main.text	a character string as the title of the heatmap (default = NULL)
index	logical should the name of the markers be printed in the diagonal of the heatmap? (default = FALSE)
fact	positive integer. factor expressed as number of cells to be aggregated (default = 1, no aggregation)

Details

thresh_LOD_ph should be set in order to only select recombination fractions that have LOD scores associated to the linkage phase configuration higher than thresh_LOD_ph when compared to the second most likely linkage phase configuration.

Value

A list containing two matrices. The first one contains the filtered recombination fraction and the second one contains the information matrix

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
all.mrk <- make_seq_mappoly(hexafake, 1:20)
red.mrk <- elim_redundant(all.mrk)
unique.mrks <- make_seq_mappoly(red.mrk)
all.pairs <- est_pairwise_rf(input.seq = unique.mrks,
                             ncpus = 1,
                             verbose = TRUE)

## Full recombination fraction matrix
mat.full <- rf_list_to_matrix(input.twopt = all.pairs)
plot(mat.full)
plot(mat.full, type = "lod")
```

rf_snp_filter *Remove markers that do not meet a LOD criteria*

Description

Remove markers that do not meet a LOD and recombination fraction criteria for at least a percentage of the pairwise marker combinations. It also removes markers with strong evidence of linkage across the whole linkage group (false positive).

Usage

```
rf_snp_filter(
  input.twopt,
  thresh.LOD.ph = 5,
  thresh.LOD.rf = 5,
  thresh.rf = 0.15,
  probs = c(0.05, 1),
  diag.markers = NULL,
  mrk.order = NULL,
  ncpus = 1L,
  diagnostic.plot = TRUE,
  breaks = 100
)
```

Arguments

input.twopt	an object of class mappoly.twopt
thresh.LOD.ph	LOD score threshold for linkage phase configuration (default = 5)
thresh.LOD.rf	LOD score threshold for recombination fraction (default = 5)
thresh.rf	threshold for recombination fractions (default = 0.15)
probs	indicates the probability corresponding to the filtering quantiles. (default = c(0.05, 1))
diag.markers	A window where marker pairs should be considered. If NULL (default), all markers are considered.
mrk.order	marker order. Only has effect if 'diag.markers' is not NULL
ncpus	number of parallel processes (i.e. cores) to spawn (default = 1)
diagnostic.plot	if TRUE produces a diagnostic plot
breaks	number of cells for the histogram

Details

thresh.LOD.ph should be set in order to only select recombination fractions that have LOD scores associated to the linkage phase configuration higher than thresh_LOD_ph when compared to the second most likely linkage phase configuration. That action usually eliminates markers that are unlinked to the set of analyzed markers.

Value

A filtered object of class `mappoly.sequence`. See `make_seq_mappoly` for details

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu> with updates by Gabriel Gesteira, <gdesiqu@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
all.mrk <- make_seq_mappoly(hexafake, 1:20)
red.mrk <- elim_redundant(all.mrk)
unique.mrks <- make_seq_mappoly(red.mrk)
all.pairs <- est_pairwise_rf(input.seq = unique.mrks,
                             ncpus = 1,
                             verbose = TRUE)

## Full recombination fraction matrix
mat.full <- rf_list_to_matrix(input.twopt = all.pairs)
plot(mat.full)

## Removing disruptive SNPs
tpt.filt <- rf_snp_filter(all.pairs, 2, 2, 0.07, probs = c(0.15, 1))
p1.filt <- make_pairs_mappoly(input.seq = tpt.filt, input.twopt = all.pairs)
m1.filt <- rf_list_to_matrix(input.twopt = p1.filt)
plot(mat.full, main.text = "LG1")
plot(m1.filt, main.text = "LG1.filt")
```

---

segreg_poly *Polysomic segregation frequency*

Description

Computes the polysomic segregation frequency given a ploidy level and the dosage of the locus in both parents. It does not consider double reduction.

Usage

```
segreg_poly(ploidy, dP, dQ)
```

Arguments

ploidy	the ploidy level
dP	the dosage in parent P
dQ	the dosage in parent Q

Value

a vector containing the expected segregation frequency for all possible genotypic classes.

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Serang O, Mollinari M, Garcia AAF (2012) Efficient Exact Maximum a Posteriori Computation for Bayesian SNP Genotyping in Polyploids. _PLoS ONE_ 7(2): e30906.

Examples

```
# autohexaploid with two and three doses in parents P and Q,
# respectively
seg <- segreg_poly(ploidy = 6, dP = 2, dQ = 3)
barplot(seg, las = 2)
```

---

sim_homologous *Simulate homology groups*

Description

Simulate two homology groups (one for each parent) and their linkage phase configuration.

Usage

```
sim_homologous(ploidy, n.mrk, prob.dose = NULL, seed = NULL)
```

Arguments

ploidy	ploidy level. Must be an even number
n.mrk	number of markers
prob.dose	a vector indicating the proportion of markers for different dosage to be simulated (default = NULL)
seed	random number generator seed

Details

This function prevents the simulation of linkage phase configurations which are impossible to estimate via two point methods

Value

a list containing the following components:

`hom.allele.p`	a list of vectors containing linkage phase configurations. Each vector contains the numbers of the homologous chromosomes in which the alleles are located. For instance, a vector containing $(1, 3, 4)$ means that the marker has three doses located in the chromosomes 1, 3 and 4. For zero doses, use 0
`p`	contains the indices of the starting positions of the dosages, considering that the vectors contained in `p` are concatenated. Markers with no doses (zero doses are also considered)
`hom.allele.q`	Analogously to `hom.allele.p`
`q`	Analogously to `p`
`ploidy`	ploidy level

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
h.temp <- sim_homologous(ploidy = 6, n.mrk = 20)
```

`solcap.dose.map` *Resulting maps from* `tetra.solcap`

Description

A list containing 12 linkage groups estimated using genomic order and dosage call

Usage

```
solcap.dose.map
```

Format

A list containing 12 objects of class `mappoly.map`, each one representing one linkage group in the `tetra.solcap` dataset.

solcap.err.map *Resulting maps from* tetra.solcap

Description

A list containing 12 linkage groups estimated using genomic order, dosage call and global calling error

Usage

```
solcap.err.map
```

Format

A list containing 12 objects of class `mappoly.map`, each one representing one linkage group in the `tetra.solcap` dataset.

solcap.mds.map *Resulting maps from* tetra.solcap

Description

A list containing 12 linkage groups estimated using `mds_mappoly` order and dosage call

Usage

```
solcap.mds.map
```

Format

A list containing 12 objects of class `mappoly.map`, each one representing one linkage group in the `tetra.solcap` dataset.

solcap.prior.map *Resulting maps from* tetra.solcap.geno.dist

Description

A list containing 12 linkage groups estimated using genomic order and prior probability distribution

Usage

```
solcap.prior.map
```

Format

A list containing 12 objects of class mappoly.map, each one representing one linkage group in the tetra.solcap.geno.dist dataset.

split_and_rephase *Divides map in sub-maps and re-phase them*

Description

The function splits the input map in sub-maps given a distance threshold of neighboring markers and evaluates alternative phases between the sub-maps.

Usage

```
split_and_rephase(
  input.map,
  twopt,
  gap.threshold = 5,
  size.rem.cluster = 1,
  phase.config = "best",
  thres.twopt = 3,
  thres.hmm = "best",
  tol.merge = 0.001,
  tol.final = 0.001,
  verbose = TRUE
)
```

Arguments

input.map	an object of class mappoly.map
twopt	an object of class mappoly.twopt containing the two-point information for the markers contained in input.map

`gap.threshold` distance threshold of neighboring markers where the map should be spitted. The default value is 5 cM

`size.rem.cluster` the size of the marker cluster (in number of markers) from which the cluster should be removed. The default value is 1

`phase.config` which phase configuration should be used. "best" (default) will choose the maximum likelihood phase configuration

`thres.twopt` the threshold used to determine if the linkage phases compared via two-point analysis should be considered for the search space reduction (default = 3)

`thres.hmm` the threshold used to determine which linkage phase configurations should be returned when merging two maps. If "best" (default), returns only the best linkage phase configuration. NOTE: if merging multiple maps, it always uses the "best" linkage phase configuration at each block insertion.

`tol.merge` the desired accuracy for merging maps (default = 10e-04)

`tol.final` the desired accuracy for the final map (default = 10e-04)

`verbose` if `TRUE` (default), the current progress is shown; if `FALSE`, no output is produced

Value

An object of class `mappoly.map`

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu>

References

Mollinari, M., and Garcia, A. A. F. (2019) Linkage analysis and haplotype phasing in experimental autopolyploid populations with high ploidy level using hidden Markov models, _G3: Genes, Genomes, Genetics_. doi:10.1534/g3.119.400378

Examples

```
map <- get_submap(solcap.dose.map[[1]], 1:20, verbose = FALSE)
tpt <- est_pairwise_rf(make_seq_mappoly(map))
new.map <- split_and_rephase(map, tpt, 1, 1)
map
new.map
plot_map_list(list(old.map = map, new.map = new.map), col = "ggstyle")
```

summary_maps *Summary maps*

Description

This function generates a brief summary table of a list of mappoly.map objects

Usage

```
summary_maps(map.list, verbose = TRUE)
```

Arguments

map.list	a list of objects of class mappoly.map
verbose	if TRUE (default), the current progress is shown; if FALSE, no output is produced

Value

a data frame containing a brief summary of all maps contained in map.list

Author(s)

Gabriel Gesteira, <gdesiqu@ncsu.edu>

Examples

```
tetra.sum <- summary_maps(solcap.err.map)
tetra.sum
```

tetra.solcap *Autotetraploid potato dataset.*

Description

A dataset of the B2721 population which derived from a cross between two tetraploid potato varieties: Atlantic × B1829-5. The population comprises 160 offsprings genotyped with the SolCAP Infinium 8303 potato array. The original data set can be found in [The Solanaceae Coordinated Agricultural Project (SolCAP) webpage](http://solcap.msu.edu/potato_infinium.shtml) The dataset also contains the genomic order of the SNPs from the Solanum tuberosum genome version 4.03. The genotype calling was performed using the fitPoly R package.

Usage

```
tetra.solcap
```

Format

An object of class `mappoly.data` which contains a list with the following components:

ploidy ploidy level = 4

n.ind number individuals = 160

n.mrk total number of markers = 4017

ind.names the names of the individuals

mrk.names the names of the markers

dosage.p1 a vector containing the dosage in parent P for all `n.mrk` markers

dosage.p2 a vector containing the dosage in parent Q for all `n.mrk` markers

chrom a vector indicating the chromosome each marker belongs. Zero indicates that the marker was not assigned to any sequence

genome.pos Physical position of the markers into the sequence

geno.dose a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by `ploidy_level + 1 = 5`

n.phen There are no phenotypes in this simulation

phen There are no phenotypes in this simulation

chisq.pval vector containing p-values for all markers associated to the chi-square test for the expected segregation patterns under Mendelian segregation

---

`tetra.solcap.geno.dist`

Autotetraploid potato dataset with genotype probabilities.

Description

A dataset of the B2721 population which derived from a cross between two tetraploid potato varieties: Atlantic × B1829-5. The population comprises 160 offsprings genotyped with the SolCAP Infinium 8303 potato array. The original data set can be found in [The Solanaceae Coordinated Agricultural Project (SolCAP) webpage](http://solcap.msu.edu/potato_infinium.shtml) The dataset also contains the genomic order of the SNPs from the Solanum tuberosum genome version 4.03. The genotype calling was performed using the fitPoly R package. Although this dataset contains the probability distribution of the genotypes, it is essentially the same dataset found in `tetra.solcap`

Usage

```
tetra.solcap.geno.dist
```

Format

An object of class `mappoly.data` which contains a list with the following components:

ploidy ploidy level = 4

n.ind number individuals = 160

n.mrk total number of markers = 4017

ind.names the names of the individuals

mrk.names the names of the markers

dosage.p1 a vector containing the dosage in parent P for all `n.mrk` markers

dosage.p2 a vector containing the dosage in parent Q for all `n.mrk` markers

chrom a vector indicating which sequence each marker belongs. Zero indicates that the marker was not assigned to any sequence

genome.pos Physical position of the markers into the sequence

prob.thres = 0.95 probability threshold to associate a marker call to a dosage. Markers with maximum genotype probability smaller than 'prob.thres' are considered as missing data for the dosage calling purposes

geno a data.frame containing the probability distribution for each combination of marker and offspring. The first two columns represent the marker and the offspring, respectively. The remaining elements represent the probability associated to each one of the possible dosages

geno.dose a matrix containing the dosage for each markers (rows) for each individual (columns). Missing data are represented by `ploidy_level + 1 = 5`

n.phen There are no phenotypes in this simulation

phen There are no phenotypes in this simulation

---

update_framework_map *Add markers that are informative in both parents using HMM approach and evaluating difference in LOD and gap size*

Description

Add markers that are informative in both parents using HMM approach and evaluating difference in LOD and gap size

Usage

```
update_framework_map(
  input.map.list,
  input.seq,
  twopt,
  thres.twopt = 10,
  init.LOD = 30,
  verbose = TRUE,
  method = "hmm",
```

```
  input.mds = NULL,
  max.rounds = 50,
  size.rem.cluster = 2,
  gap.threshold = 4
)
```

Arguments

input.map.list	list containing three mappoly.map objects:1) map built with markers with segregation information from parent 1; 2) map built with markers with segregation information from parent 2; 3) maps in 1 and 2 merged
input.seq	object of class mappoly.sequence containing all markers for specific group
twopt	object of class mappoly.twopt
thres.twopt	the LOD threshold used to determine if the linkage phases compared via two-point analysis should be considered for the search space reduction (default = 5)
init.LOD	the LOD threshold used to determine if the marker will be included or not after hmm analysis (default = 30)
verbose	If TRUE (default), current progress is shown; if FALSE, no output is produced
method	indicates whether to use 'hmm' (Hidden Markov Models), 'ols' (Ordinary Least Squares) or 'wMDS_to_1D_pc' (weighted MDS followed by fitting a one dimensional principal curve) to re-estimate the recombination fractions after adding markers
input.mds	An object of class mappoly.map
max.rounds	integer defining number of times to try to fit the remaining markers in the sequence
size.rem.cluster	threshold for number of markers that must contain in a segment after a gap is removed to keep this segment in the sequence
gap.threshold	threshold for gap size

Value

object of class mappoly.map2

Author(s)

Marcelo Mollinari, <mmollin@ncsu.edu> with documentation and minor modifications by Cristiane Taniguti <chtaniguti@tamu.edu>

update_map *Update map*

Description

This function takes an object of class mappoly.map and checks for removed redundant markers in the original dataset. Once redundant markers are found, they are re-added to the map in their respective equivalent positions and another HMM round is performed.

Usage

```
update_map(input.maps, verbose = TRUE)
```

Arguments

input.maps	a single map or a list of maps of class mappoly.map
verbose	if TRUE (default), shows information about each update process

Value

an updated map (or list of maps) of class mappoly.map, containing the original map(s) plus redundant markers

Author(s)

Gabriel Gesteira, <gdesiqu@ncsu.edu>

Examples

```
orig.map <- solcap.err.map
up.map <- lapply(solcap.err.map, update_map)
summary_maps(orig.map)
summary_maps(up.map)
```

Index

∗ **analysis**
cache_counts_twopt, 7
∗ **datasets**
hexafake, 49
hexafake.geno.dist, 50
maps.hexafake, 60
solcap.dose.map, 92
solcap.err.map, 93
solcap.mds.map, 93
solcap.prior.map, 94
tetra.solcap, 96
tetra.solcap.geno.dist, 97
∗ **genetics**
genetic-mapping-functions, 43
∗ **two-point**
cache_counts_twopt, 7

add_marker, 4

cache_counts_twopt, *7*, 7, *25*
calc_genoprob, 8
calc_genoprob_dist, 9
calc_genoprob_error, 10, *72*
calc_genoprob_single_parent, 12
calc_homologprob, 13, *72*
calc_prefpair_profiles, 14
check_data_sanity, 15
compare_maps, 16
cross_simulate, 16

detect_info_par, 18
drop_marker, 18

edit_order, 19
elim_redundant, 20
est_full_hmm_with_global_error, 21
est_full_hmm_with_prior_prob, 23
est_pairwise_rf, 25, *57*
est_pairwise_rf2, 27
est_rf_hmm, 28
est_rf_hmm_sequential, *29*, 31, *41*
export_data_to_polymapR, 34
export_map_list, 34
export_qtlpoly, 35
extract_map, 36

filter_aneuploid, 36
filter_individuals, 37
filter_missing, 38
filter_segregation, 39
find_blocks, 40
framework_map, 42

genetic-mapping-functions, 43
get_genomic_order, 45
get_submap, 45
get_tab_mrks, 47
group_mappoly, 48

hexafake, 49, *50*, *60*
hexafake.geno.dist, 50

imf_h *(*genetic-mapping-functions*)*, 43
imf_k *(*genetic-mapping-functions*)*, 43
imf_m *(*genetic-mapping-functions*)*, 43
import_data_from_polymapR, 51
import_from_updog, 52
import_phased_maplist_from_polymapR, 54

loglike_hmm, 55

make_mat_mappoly, 56
make_pairs_mappoly, 57
make_seq_mappoly, 58, *90*
maps.hexafake, 60
mds_mappoly, 60, *93*
merge_datasets, 62
merge_maps, 64
mf_h *(*genetic-mapping-functions*)*, 43
mf_k *(*genetic-mapping-functions*)*, 43

mf_m *(genetic-mapping-functions)*, 43

plot.mappoly.data *(read_geno)*, 75
plot.mappoly.geno.ord
(get_genomic_order), 45
plot.mappoly.homoprob, 66
plot.mappoly.map *(est_rf_hmm)*, 28
plot.mappoly.prefpair.profiles, 67
plot.mappoly.rf.matrix
(rf_list_to_matrix), 87
plot.mappoly.sequence
(make_seq_mappoly), 58
plot_genome_vs_map, 68
plot_GIC, 69
plot_map_list, 70
plot_mappoly.map2, 69
plot_mrk_info, 71
plot_progeny_dosage_change, 71
print.mappoly.data *(read_geno)*, 75
print.mappoly.geno.ord
(get_genomic_order), 45
print.mappoly.map *(est_rf_hmm)*, 28
print.mappoly.pcmap *(mds_mappoly)*, 60
print.mappoly.pcmap3d *(mds_mappoly)*, 60
print.mappoly.rf.matrix
(rf_list_to_matrix), 87
print.mappoly.sequence
(make_seq_mappoly), 58

read_fitpoly, 73
read_geno, *17*, 75, *78*
read_geno_csv, 78
read_geno_prob, 80
read_vcf, 82
reest_rf, 85
rev_map, 86
rf_list_to_matrix, *4, 5*, *56*, 87
rf_snp_filter, 89

saveMarkerModels, *73*
segreg_poly, *54*, *73*, *76*, *78*, *80, 81*, *83*, 90
sim_homologous, 91
solcap.dose.map, 92
solcap.err.map, 93
solcap.mds.map, 93
solcap.prior.map, 94
split_and_rephase, 94
summary_maps, 96

tetra.solcap, *92, 93*, 96, *97*
tetra.solcap.geno.dist, *94*, 97

update_framework_map, 98
update_map, 100