Package: polyqtlR (via r-universe)

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Type Package

Title QTL Analysis in Autopolyploid Bi-Parental F1 Populations

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Description Quantitative trait loci (QTL) analysis and exploration of meiotic patterns in autopolyploid bi-parental F1 populations. For all ploidy levels, identity-by-descent (IBD) probabilities can be estimated. Significance thresholds, exploring QTL allele effects and visualising results are provided. For more background and to reference the package see <doi:10.1093/bioinformatics/btab574>.

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Contents

BLUE — *Calculate Best Linear Unbiased Estimates using linear mixed model from* nlme *package*

Description

Calculation of BLUEs from data frame of genotype names and phenotypes (assuming repeated measurements)

Usage

```
BLUE(data, model, random, genotype.ID)
```

Arguments

data	Data frame of genotype codes and corresponding phenotypes
model	The model specification of fixed terms, eg. Yield ~ Clones
random	The random component of the model (repeat structure, can be nested), eg. ~1 | Blocks if only Blocks are used
genotype.ID	The colname used to describe genotypes, e.g. "Clones"

Value

A data-frame with columns "geno" for the genotype names, and "blue" for the BLUEs.

Examples

```
data("Phenotypes_4x")
blue <- BLUE(data = Phenotypes_4x,model = pheno~geno,random = ~1|year,genotype.ID = "geno")
```

BLUEs.pheno — *Best Linear Unbiased Estimates of phenotype*

Description

Best Linear Unbiased Estimates of phenotype

Usage

```
BLUEs.pheno
```

Format

An object of class data.frame with 50 rows and 2 columns.

check_cofactors *Build a multi-QTL model using step-wise procedure of checking genetic co-factors.*

Description

The function check_cofactors initially fits all significant QTL positions as co-factors, both individually and in combination. Significance thresholds are re-estimated each time, yielding threshold-corrected LOD scores. If this leads to a change in the estimated position of QTL, or detection of subsequent peaks, a second round of co-factor inclusion is performed for all new QTL or novel QTL combinations. Finally, the multi-QTL model that maximises the individual significance of each QTL is returned as a data.frame. This can be directly passed to the function PVE to estimate the percentage variance explained by the full multi-QTL model and all possible sub-models. Note: this function estimates the most likely QTL positions by maximising the threshold-corrected LOD at QTL peaks. Non-additive interactions between QTL may be missed as a result. It is recommended to run a manual co-factor analysis as well, as described in the package vignette.

Usage

```
check_cofactors(
  IBD_list,
  Phenotype.df,
  genotype.ID,
  trait.ID,
  LOD_data = NULL,
  min_res = 20,
  test_full_model = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

IBD_list	List of IBD_probabilities as estimated using one of the various methods available (e.g. estimate_IBD).
Phenotype.df	A data.frame containing phenotypic values
genotype.ID	The colname of Phenotype.df that contains the population identifiers (F1 names) (must be a colname of Phenotype.df)
trait.ID	The colname of Phenotype.df that contains the response variable to use in the model (must be a colname of Phenotype.df)
LOD_data	Output of QTLscan function. Since v.0.1.0 this argument is optional - function will re-run a QTLscan if not provided. Indeed, it may be desirable to not specify LOD_data if argument test_full_model is TRUE, as this will first combine the best results using additive-effects or allelic interaction-effects models before searching for additional QTL.

`min_res` The minimum genetic distance (resolution) assumed possible to consider 2 linked QTL (on the same linkage group) as independent. By default a value of 20 cM is used. This is not to suggest that 20 cM is a realistic resolution in a practical mapping study, but it provides the function with a criterion to consider 2 significant QTL within this distance as one and the same. For this purpose, 20 cM seems a reasonable value to use. In practice, closely linked QTL will generally "explain" all the variation at nearby positions, making it unlikely to be able to disentangle their effects. QTL positions will vary slightly when co-factors are introduced, but again this variation is presumed not to exceed 20 cM either side.

`test_full_model`
By default `FALSE`, in which case the normal additive-effects model is used in `QTLscan`. If set to `TRUE`, then both the additive and full models are run for each genome-wide scan.

`verbose` Logical, by default `TRUE` - should progress messages be printed to the console?

`...` Option to pass extra arguments to `QTLscan`, for example specifying `ncores` for parallel processing, or changing the default settings of the permutation test (by default the number of permutations to perform = 1000 and alpha = 0.05). For a full list of options see the documentation of `QTLscan`.

Value

Data frame with the following columns:

LG Linkage group identifier

cM CentiMorgan position

deltaLOD The difference between the LOD score at the peak and the significance threshold (always positive, otherwise the QTL would not be significant)

CofactorID An identifier giving the co-factor model used in detecting the QTL (if no co-factors were included then `NA`). The co-factor model is described by concatenating all co-factor positions with a '+', so for example 1_10+4_20 would mean a co-factor model with 2 positions included as co-factors, namely 10 cM on linkage group 1 and 20 cM on linkage group 4.

Examples

```
data("IBD_4x","BLUEs.pheno","qtl_LODs.4x")
check_cofactors(IBD_list=IBD_4x,Phenotype.df=BLUEs.pheno,
genotype.ID="Geno",trait.ID="BLUE",LOD_data=qtl_LODs.4x)
```

---

convert_mappoly_to_phased.maplist

Function to extract the phased map from a mappoly.map object

Description

Convert MAPpoly.map object into a phased maplist, needed for IBD estimation

Usage

```
convert_mappoly_to_phased.maplist(mappoly_object)
```

Arguments

mappoly_object	An object of class 'mappoly.map', for example output of the function mappoly::est_rf_hmm_sequentia

Value

A phased.maplist, with linkage group names LG1 etc. Each list item is a data.frame with columns marker, position followed by the phased map, coded in 1 and 0 for presence/absence of SNP (alternative) allele on parental homologues (h) numbered 1:ploidy for parent 1 and ploidy + 1 : 2*ploidy for parent 2.

Examples

```
## Not run:
library("mappoly")
phased.maplist <- convert_mappoly_to_phased.maplist(maps.hexafake)

## End(Not run)
```

---

count_recombinations *Predict recombination breakpoints using IBD probabilities*

Description

The function count_recombinations returns a list of all predicted recombination breakpoints. The output can be passed using the argument recombination_data to the function visualiseHaplo, where the predicted breakpoints overlay the haplotypes. Alternatively, a genome-wide visualisation of the recombination landscape both per linkage group and per individual can be generated using the function plotRecLS, which can be useful in identifying problematic areas of the linkage maps, or problematic individuals in the population. Currently, recombination break-points are only estimated from bivalents in meiosis; any offspring resulting from a predicted multivalent is excluded from the analysis and will be returned with a NA value.

Usage

```
count_recombinations(IBD_list, plausible_pairing_prob = 0.3)
```

Arguments

IBD_list	List of IBD_probabilities as estimated using one of the various methods available (e.g. estimate_IBD).

plausible_pairing_prob
: The minimum probability of a pairing configuration needed to analyse an individual's IBD data. The default setting of 0.3 accommodates scenarios where e.g. two competing plausible pairing scenarios are possible. In such situations, both pairing configurations (also termed "valencies") would be expected to have a probability close to 0.5. Both are then considered, and the output contains the probability of both situations. These can then be used to generate a probabilistic recombination landscape. In some cases, it may not be possible to discern the pairing in one of the parents due to a lack of recombination (ie. full parental haplotypes were transmitted). In such cases, having a lower threshold here will allow more offspring to be analysed without affecting the quality of the predictions. If a more definite set of predictions is required, simply increase `plausible_pairing_prob` to eliminate such uncertainty. These individuals will then be returned with a `NA` value. In any case, it is always helpful to visualise the output using the function `visualiseHaplo`.

Value

A nested list corresponding to each linkage group. Within each LG, a list with 3 items is returned, specifying the `plausible_pairing_prob`, the `map` and the predicted `recombinations` in each individual in the mapping population. Per individual, all valencies with a probability greater than `plausible_pairing_prob` are returned, specifying both the `Valent_probability` and the best estimate of the cM position of the `recombination_breakpoints` involving pairs of homologues A, B, C etc. (in the order parent 1, parent 2). If no recombinations are predicted, a `NA` value is given instead.

Examples

```
data("IBD_4x")
recom.ls <- count_recombinations(IBD_4x)
```

---

estimate_GIC *Estimate the Genotypic Information Coefficient (GIC)*

Description

Function to estimate the GIC per homologue using IBD probabilities

Usage

```
estimate_GIC(IBD_list)
```

Arguments

`IBD_list`	List of IBD probabilities

Value

A nested list; each list element (per linkage group) contains the following items:

GIC : Matrix of GIC values estimated from the IBD probabilities

map : Integrated linkage map positions of markers used in IBD calculation

parental_phase : The parental marker phasing, coded in 1 and 0's

Examples

```
data("IBD_4x")
GIC_4x <- estimate_GIC(IBD_list = IBD_4x)
```

`estimate_IBD` *Generate IBD probabilities from marker genotypes and a phased linkage map*

Description

`estimate_IBD` is a function for creating identity-by-descent (IBD) probabilities. Two computational methods are offered: by default IBD probabilites are estimated using hidden Markov models, but a heuristic method based on Bourke et al. (2014) is also included. Basic input data for this function are marker genotypes (either discrete marker dosages (ie scores 0, 1, ..., ploidy representing the number of copies of the marker allele), or the probabilities of these dosages) and a phased linkage map. Details on each of the methods are included under `method`

Usage

```
estimate_IBD(
  input_type = "discrete",
  genotypes,
  phased_maplist,
  method = "hmm",
  remove_markers = NULL,
  ploidy,
  ploidy2 = NULL,
  parent1 = "P1",
  parent2 = "P2",
  individuals = "all",
  log = NULL,
  map_function = "haldane",
  bivalent_decoding = TRUE,
  error = 0.01,
  full_multivalent_hexa = FALSE,
  verbose = FALSE,
  ncores = 1,
  fix_threshold = 0.1,
  factor_dist = 1
)
```

Arguments

input_type	Can be either one of 'discrete' or 'probabilistic'. For the former (default), dosage_matrix must be supplied, while for the latter probgeno_df must be supplied. Note that probabilistic genotypes can only be accepted if the method is default ('hmm').
genotypes	Marker genotypes, either a 2d matrix of integer marker scores or a data.frame of dosage probabilities. Details are as follows: **discrete :** If input_type is 'discrete', genotypes is a matrix of marker dosage scores with markers in rows and individuals in columns. Both (marker) rownames and (individual or sample) colnames are needed. **probabilistic :** If input_type is 'probabilistic', genotypes is a data frame as read from the scores file produced by function saveMarkerModels of R package fitPoly, or alternatively, a data frame containing at least the following columns: **SampleName :** Name of the sample (individual) **MarkerName :** Name of the marker **P0 :** Probabilities of dosage score '0' **P1, P2... etc. :** Probabilities of dosage score '1' etc. (up to max offspring dosage, e.g. P4 for tetraploid population)
phased_maplist	A list of phased linkage maps, the output of polymapR::create_phased_maplist
method	The method used to estimate IBD probabilities, either "hmm" or "heur". By default, the Hidden Markov Model (hmm) method is used. This uses an approach developed by Zheng et al (2016), and implemented in the 'TetraOrigin' package. However, unlike the original TetraOrigin software, it does not re-estimate parental linkage phase, as this is assumed to have been generated during map construction. Alternatively, a heuristic algorithm can be employed (method = "heur"), providing computational efficiency at higher ploidy levels (hexaploid, octoploid etc.), but at the cost of some accuracy. If method = "hmm" is specified, only diploid, triploid, autotetraploid and autohexaploid populations are currently allowed, while method = "heur" caters for all possible ploidy levels. Furthermore, the argument bivalent_decoding can only be set to FALSE in the case of the 'hmm' method (i.e. allowing for the possibility of multivalent formation and double reduction).
remove_markers	Optional vector of marker names to remove from the maps. Default is NULL.
ploidy	Integer. Ploidy of the organism.
ploidy2	Optional integer, by default NULL. Ploidy of parent 2, if different from parent 1.
parent1	Identifier of parent 1, by default assumed to be "P1"
parent2	Identifier of parent 2, by default assumed to be "P2"
individuals	By default "all" offspring are included, but otherwise a subset can be selected, using a vector of offspring indexing numbers (1,2, etc.) according to their order in dosage_matrix
log	Character string specifying the log filename to which standard output should be written. If NULL log is send to stdout.

`map_function` Mapping function to use when converting map distances to recombination frequencies. Currently only `"haldane"` or `"kosambi"` are allowed.

`bivalent_decoding`
Option to consider only bivalent pairing during formation of gametes (ignored for diploid populations, as only bivalents possible there), by default `TRUE`

`error` The (prior) probability of errors in the offspring dosages, usually assumed to be small but non-zero

`full_multivalent_hexa`
Option to allow multivalent pairing in both parents at the hexaploid level, by default `FALSE`. Note that if `TRUE`, a very large available RAM may be required (>= 32Gb) to process the data.

`verbose` Logical, by default `TRUE`. Should progress messages be written?

`ncores` How many CPU cores should be used in the evaluation? By default 1 core is used.

`fix_threshold` If `method = "heur"`, the threshold to fix the IBD probabilities while correcting for the sum of probabilities.

`factor_dist` If `method = "heur"`, the factor by which to increase or decrease the recombination frequencies as calculated from the map distances.

Value

A list of IBD probabilities, organised by linkage group (as given in the input `phased_maplist`). Each list item is itself a list containing the following:

IBDtype The type of IBD; for this function only "genotypeIBD" are calculated.

IBDarray A 3d array of IBD probabilities, with dimensions marker, genotype-class and F1 individual.

map A 3-column data-frame specifying chromosome, marker and position (in cM)

parental_phase Phasing of the markers in the parents, as given in the input `phased_maplist`

marginal.likelihoods A list of marginal likelihoods of different valencies if method "hmm" was used, otherwise `NULL`

valency The predicted valency that maximised the marginal likelihood, per offspring. For method "heur", `NULL`

offspring Offspring names

biv_dec Logical, whether bivalent decoding was used in the estimation of the F1 IBD probabilities.

gap The size of the gap (in cM) used when interpolating the IBD probabilities. See function `spline_IBD` for details.

genocodes Ordered list of genotype codes used to represent different genotype classes.

pairing log likelihoods of each of the different pairing scenarios considered (can be used e.g. for post-mapping check of preferential pairing)

ploidy ploidy of parent 1

ploidy2 ploidy of parent 2

method The method used, either "hmm" (default) or "heur". See argument `method`

error The error prior used, if method "hmm" was used, otherwise `NULL`

References

- Durbin R, Eddy S, Krogh A, Mitchison G (1998) Biological sequence analysis: Probabilistic models of proteins and nucleic acids. Cambridge: Cambridge University Press.
- Hackett et al. (2013) Linkage analysis and QTL mapping using SNP dosage data in a tetraploid potato mapping population. PLoS One 8(5): e63939
- Zheng et al. (2016) Probabilistic multilocus haplotype reconstruction in outcrossing tetraploids. Genetics 203: 119-131
- Bourke P.M. (2014) QTL analysis in polyploids: Model testing and power calculations. Wageningen University (MSc thesis)

Examples

```
data("phased_maplist.4x", "SNP_dosages.4x")
estimate_IBD(phased_maplist=phased_maplist.4x,genotypes=SNP_dosages.4x,ploidy=4)
```

`exploreQTL` *Explore the possible segregation type of a QTL peak using Schwarz Information Criterion*

Description

Function to explore the possible segregation type at a QTL position using the Schwarz Information Criterion

Usage

```
exploreQTL(
  IBD_list,
  Phenotype.df,
  genotype.ID,
  trait.ID,
  linkage_group,
  LOD_data,
  cM = NULL,
  QTLconfig = NULL,
  plotBIC = TRUE,
  deltaBIC = 6,
  testAllele_Effects = TRUE,
  log = NULL
)
```

Arguments

`IBD_list`	List of IBD probabilities
`Phenotype.df`	A data.frame containing phenotypic values

`genotype.ID` The colname of `Phenotype.df` that contains the population identifiers (F1 names) (must be a colname of `Phenotype.df`)

`trait.ID` The colname of `Phenotype.df` that contains the response variable to use in the model (must be a colname of `Phenotype.df`)

`linkage_group` Numeric identifier of the linkage group being tested, based on the order of `IBD_list`. Only a single linkage group is allowed.

`LOD_data` Output of `QTLscan` function

`cM` By default `NULL`, in which case the position of maximum LOD score is taken as the position of interest. Otherwise, the cM position to be explored.

`QTLconfig` Nested list of homologue configurations and modes of action of QTL to be explored and compared, the output of `segMaker`. Note that a default List is available of all possible bi-allelic QTL if none is provided. Each list element is itself a list with components

homs : a vector of length at least 1, describing the proposed homologues the functional allele Q is on

mode : Vector of same length as `homs` with codes "a" for additive and "d" for dominant.

`plotBIC` Logical, with default `TRUE` - should the calculated BIC values be plotted?

`deltaBIC` Numeric, by default 6. Configurations within this distance of the minimum BIC are considered plausible.

`testAllele_Effects` Logical, with default `TRUE` - should the effects of the different alleles be tested using the most likely QTL configuration?

`log` Character string specifying the log filename to which standard output should be written. If `NULL` log is send to stdout.

Value

List with the following items:

linkage_group Linkage group of the QTL peak being explored

cM CentiMorgan position of the locus being explored

BIC Vector of BIC values corresponding to elements of `QTLconfig` provided for testing

Allele.effects Summary of the means and standard errors of groups with (+) and without(-) the specified allele combinations for the most likely QTLconfig if `testAllele_Effects = TRUE` (`NULL` otherwise).

genotype.means A one-column matrix of mean phenotype values of offspring classes, with rownames corresponding to the genotype class. If the probability of certain genotype classes is 0 (e.g. double reduction classes where no double reduction occurred), then the genotype mean for that class will be `NA`

Examples

```
data("IBD_4x","BLUEs.pheno","qtl_LODs.4x")
exploreQTL(IBD_list = IBD_4x,
           Phenotype.df = BLUEs.pheno,
           genotype.ID = "Geno",
           trait.ID = "BLUE",
           linkage_group = 1,
           LOD_data = qtl_LODs.4x)
```

---

findPeak *Function to find the position of maximum LOD on a particular linkage group*

Description

Given QTL output, this function returns the position of maximum LOD for a specified linkage group.

Usage

```
findPeak(LOD_data, linkage_group, verbose = TRUE)
```

Arguments

LOD_data	Output of QTLscan function.
linkage_group	Numeric identifier of the linkage group being tested, based on the order of IBD_list. Only a single linkage group is allowed.
verbose	Should messages be written to standard output? By default TRUE.

Examples

```
data("qtl_LODs.4x")
findPeak(LOD_data=qtl_LODs.4x,linkage_group=1)
```

---

findSupport *Function to find a LOD - x support interval around a QTL position*

Description

Given QTL output, this function returns the LOD - x support for a specified linkage group, taking the maximum LOD position as the desired QTL peak.

Usage

```
findSupport(LOD_data, linkage_group, LOD_support = 2)
```

Arguments

LOD_data	Output of QTLscan function.
linkage_group	Numeric identifier of the linkage group being tested, based on the order of IBD_list. Only a single linkage group is allowed.
LOD_support	The level of support around a QTL peak, by default 2 (giving a LOD - 2 support interval, the range of positions with a LOD score within 2 LOD units of the maximum LOD on that linkage group).

Examples

```
data("qtl_LODs.4x")
findSupport(LOD_data=qtl_LODs.4x,linkage_group=1)
```

GIC_4x *Genotypic Information Coefficient for example tetraploid*

Description

Genotypic Information Coefficient for example tetraploid

Usage

```
GIC_4x
```

Format

An object of class list of length 2.

IBD_4x *Identical by descent probabilities for example tetraploid*

Description

Identical by descent probabilities for example tetraploid

Usage

```
IBD_4x
```

Format

An object of class list of length 2.

`import_IBD` *Import IBD probabilities as estimated by TetraOrigin or PolyOrigin*

Description

Imports the IBD probability output of TetraOrigin (Mathematica software) or PolyOrigin (julia software) into the same format as natively-estimated IBD probabilities from the polyqtlR package.

Usage

```
import_IBD(
  method,
  folder = NULL,
  filename,
  bivalent_decoding = TRUE,
  error = 0.01,
  log = NULL
)
```

Arguments

`method`	The method used for IBD estimation, either "TO" for TetraOrigin or "PO" for PolyOrigin
`folder`	The path to the folder in which the Tetra/PolyOrigin (ie. TetraOrigin or PolyOrigin) output is contained, default is `NULL` if files are in working directory.
`filename`	If method = "TO", the (vector of) character filename stem(s) of the `.csv` file(s) containing the output of TetraOrigin (stem = without ".csv"). Should be in order according to LG/chromosome numbering. If method = "PO", then simply specify the PolyOrigin filename stem here (as the output is not split into separate linkage groups in PolyOrigin). A PolyOrigin file with name <filename>_polyancestry.csv and its corresponding log file <filename>.log will then be searched for.
`bivalent_decoding`	Logical, if method = "TO" you must specify `TRUE` if only bivalent pairing was allowed in TetraOrigin (in offspring deciding step), otherwise specify `FALSE` if multivalent pairing was also allowed. If method = "PO", this will be automatically detected, so no need to specify (will be ignored).
`error`	If method = "TO", the offspring error prior used in the offspring decoding step of TetraOrigin, by default assumed to be 0.01. For method = "PO", this is automatically read in.
`log`	Character string specifying the log filename to which standard output should be written. If `NULL` log is send to stdout.

Value

Returns a list with the following items:

`IBDtype` : Always "genotypeIBD" for the output of TetraOrigin

`IBDarray` : An array of IBD probabilities. The dimensions of the array are: markers, genotype classes and individuals.

`map` : Integrated linkage map positions of markers used in IBD calculation

`parental_phase` : The parental marker phasing as used by TetraOrigin, recoded in 1 and 0's

`marginal.likelihoods` : A list of marginal likelihoods of different valencies, currently `NULL`

`valency` : The predicted valency that maximised the marginal likelihood, per offspring. Currently `NULL`

`offspring` : Offspring names

`biv_dec` : Logical, the bivalent_decoding parameter specified.

`gap` : The gap size used in IBD interpolation if performed by `spline_IBD`. At this stage, `NULL`

`genocodes` : Ordered list of genotype codes used to represent different genotype classes.

`pairing` : log likelihoods of each of the different pairing scenarios considered (can be used e.g. for post-mapping check of preferential pairing)

`ploidy` : The ploidy of parent 1, by default assumed to be 4

`ploidy2` : The ploidy of parent 2, by default assumed to be 4

`method` : The method used, either "hmm_TO" (TetraOrigin) or "hmm_PO" (PolyOrigin)

`error` : The error prior used in the calculation in TetraOrigin, assumed to be 0.01

Examples

```
## Not run:
## These examples demonstrate the function call for both methods, but won't run without input files
## from either package, hence this call will normally result in an Error:
IBD_TO <- import_IBD(method = "TO", filename = paste0("test_LinkageGroup",1:5,"_Summary"),
bivalent_decoding = FALSE, error = 0.05)
## Equivalent call for PolyOrigin output:
IBD_PO <- import_IBD(method = "PO",filename = "test")

## End(Not run)
```

`impute_dosages` *Re-estimate marker dosages given IBD input estimated using a high error prior.*

Description

Function to correct marker dosage scores given a list of previously estimated IBD probabilities. This may prove useful to correct genotyping errors. Running the `estimate_IBD` function with a high error prior will result in suppressed predictions of double recombination events, associated with genotyping errors. By forcing the HMM to penalise double recombinations heavily, a smoothed haplotype landscape is achieved in which individual genotype observations are down-weighted. This smoothed output is then used to re-estimate marker dosages, dependent on (correct) parental scores. An alternative strategy is to use the function `maxL_IBD` over a range of error priors first, and use the resulting `$maxL_IBD` output as input here (as the `IBD_list`). In this case, set the argument `min_error_prior` to a low value (0.005 say) to avoid issues.

Usage

```
impute_dosages(
  IBD_list,
  dosage_matrix,
  parent1 = "P1",
  parent2 = "P2",
  rounding_error = 0.05,
  min_error_prior = 0.1,
  verbose = TRUE
)
```

Arguments

`IBD_list`	List of IBD probabilities
`dosage_matrix`	An integer matrix with markers in rows and individuals in columns. Note that probabilistic genotypes are not currently catered for here.
`parent1`	The identifier of parent 1, by default "P1"
`parent2`	The identifier of parent 2, by default "P2"
`rounding_error`	The maximum deviation from an integer value that an inputed value can have, by default 0.05. For example, an imputed score of 2.97 or 3.01 would both be rounded to a dosage of 3, while 2.87 would be deemed too far from an integer score, and would be made missing. If you find the output contains too many missing values, a possibility would be to increase the `rounding_error`. However this may also introduce more errors in the output!
`min_error_prior`	Suggestion for a suitably high error prior to be used in IBD calculations to ensure IBD smoothing is achieved. If IBD probabilities were estimated with a smaller error prior, the function aborts.
`verbose`	Should messages be written to standard output?

Examples

```
## Not run:
# Toy example only, as this will result in an Error: the original error prior was too low
data("IBD_4x","SNP_dosages.4x")
impute_dosages(IBD_list=IBD_4x,dosage_matrix=SNP_dosages.4x)

## End(Not run)
```

`maxL_IBD` *Wrapper function to run estimate_IBD function over multiple error priors*

Description

Function to run the `estimate_IBD` function over a range of possible error priors. The function returns a merged set of results that maximise the marginal likelihood per individual, i.e. allowing a per-individual error rate within the options provided in the errors argument.

Usage

```
maxL_IBD(errors = c(0.01, 0.05, 0.1, 0.2), ...)
```

Arguments

`errors`	Vector of offspring error priors to test (each between 0 and 1)
`...`	Arguments passed to `estimate_IBD`.

Value

A list containing the following components:

maxL_IBD A nested list as would have been returned by the estimate_IBD function, but composite across error priors to maximise the marginal likelihoods. Note that the $error values per linkage group are now the average error prior across the population per linkage group

MML A 3d array of the maximal marginal likelihoods, per error prior. Dimensions are individuals, linkage groups, error priors.

error_per_ind A matrix of the most likely genotyping error rates per individual (in rows) for each linkage group (in columns)

errors The error priors used (i.e. the input vector is returned for later reference.)

Examples

```
## Not run:
data("phased_maplist.4x","SNP_dosages.4x")
maxL_IBD(phased_maplist=phased_maplist.4x,genotypes=SNP_dosages.4x,
ploidy=4,errors=c(0.01,0.02,0.05,0.1))

## End(Not run)
```

`meiosis_report` *Generate a 'report' of predicted meiotic behaviour in an F1 population*

Description

Function to extract the chromosome pairing predictions as estimated by `estimate_IBD`. Apart from producing an overview of the pairing during parental meiosis (including counts of multivalents, per linkage group per parent), the function also applies a simple chi-squared test to look for evidence of non-random pairing behaviour from the bivalent counts (deviations from a polysomic model)

Usage

```
meiosis_report(IBD_list, visualise = FALSE, precision = 2)
```

Arguments

`IBD_list`	List of IBD probabilities as estimated by `estimate_IBD` using method 'hmm', or externally (e.g. using TetraOrigin)
`visualise`	Logical, by default `FALSE`. If `TRUE`, a plot of the pairing results is produced per LG. In order to flag extreme deviations from the expected numbers (associated with polysomic inheritance, considered the Null hypothesis), barplots are coloured according to the level of significance of the X2 test. Plots showing red bars indicate extreme deviations from a polysomic pattern.
`precision`	To how many decimal places should summed probabilities per bivalent pairing be rounded? By default 2.

Value

The function returns a nested list, with one element per linkage group in the same order as the input IBD list. Per linkage group, a list is returned containing the following components:

P1_multivalents The count of multivalents in parent 1 (only relevant if `bivalent_decoding = FALSE` during IBD calculation)

P2_multivalents Similarly, the count of multivalents in parent 2

P1_pairing The counts of each bivalent pairing predicted in parent 1, with an extra column Pr(X2) which gives the p-value of the X2 test of the off-diagonal terms in the matrix. In the case of a tetraploid, pairing A with B automatically implies C with D pairing, so the count table contains a lot of redundancy. The table should be read using both row and column names, so row A and column B corresponds to the count of individuals with A and B pairing (and hence C and D pairing). In a hexaploid, A-B pairing does not imply a particular pairing configuration in the remaining homologues. In this case, row A and column B is the count of individuals where A and B were predicted to have paired, summed over all three bivalent configurations with A and B paired (AB-CD-EF, AB-CE-DF, AB-CF,DE).

P2_pairing Same as P1_pairing, except using parent 2

ploidy The ploidy of parent 1

ploidy2 The ploidy of parent 2

Examples

```
data("IBD_4x")
mr.ls<-meiosis_report(IBD_list = IBD_4x)
```

`mr.ls` *Example output of meiosis report function*

Description

Example output of meiosis report function

Usage

```
mr.ls
```

Format

An object of class `list` of length 2.

`phased_maplist.4x` *Phased maplist for example tetraploid*

Description

Phased maplist for example tetraploid

Usage

```
phased_maplist.4x
```

Format

An object of class `list` of length 2.

`Phenotypes_4x` *Phenotypes for example tetraploid*

Description

Phenotypes for example tetraploid

Usage

```
Phenotypes_4x
```

Format

An object of class `data.frame` with 150 rows and 3 columns.

plotQTL *Plot the results of QTL scan.*

Description

Up to package v.0.0.9, there were three plotting functions for the output of QTLscan, namely plotQTL, plotLinearQTL and plotLinearQTL_list. Since release 0.1.0, the functionality of all three functions has been combined into a single general plotting function, named plotQTL. The plot layout is now specified by a new argument layout, allowing the user to plot results for single chromosomes separately, or together either adjacently or in a grid layout. Results from multiple analyses can be overlaid. Previously, it was possible to call the function plotQTL multiple times and overlay subsequent plots using the argument overlay = TRUE. This approach is no longer supported. Instead, if multiple results are to be overlaid, they can be provided as a list of QTLscan or singleMarkerRegression outputs. Note however that this is only possible using the default layout. If significance thresholds are present, the default behaviour is to rescale LOD values so that multiple plots can be combined with overlapping signficance thresholds. This rescaling behaviour can also be disabled (by setting rescale = FALSE). Note that not all arguments may be appropriate for all layouts.

Usage

```
plotQTL(
  LOD_data,
  layout = "l",
  inter_chm_gap = 5,
  ylimits = NULL,
  sig.unit = "LOD",
  plot_type = "lines",
  colour = c("black", "red", "dodgerblue", "sienna4"),
  add_xaxis = TRUE,
  add_rug = TRUE,
  add_thresh = TRUE,
  override_thresh = NULL,
  thresh.lty = 3,
  thresh.lwd = 2,
  thresh.col = "darkred",
  return_plotData = FALSE,
  show_thresh_CI = FALSE,
  use_LG_names = TRUE,
  axis_label.cex = 1,
  custom_LG_names = NULL,
  LGdiv.col = "gray42",
  ylab.at = 2.5,
  highlight_positions = NULL,
  mainTitle = FALSE,
  rescale = TRUE,
  ...
```

```
)

plotLinearQTL(
  LOD_data,
  layout = "l",
  inter_chm_gap = 5,
  ylimits = NULL,
  sig.unit = "LOD",
  plot_type = "lines",
  colour = c("black", "red", "dodgerblue", "sienna4"),
  add_xaxis = TRUE,
  add_rug = TRUE,
  add_thresh = TRUE,
  override_thresh = NULL,
  thresh.lty = 3,
  thresh.lwd = 2,
  thresh.col = "darkred",
  return_plotData = FALSE,
  show_thresh_CI = FALSE,
  use_LG_names = TRUE,
  axis_label.cex = 1,
  custom_LG_names = NULL,
  LGdiv.col = "gray42",
  ylab.at = 2.5,
  highlight_positions = NULL,
  mainTitle = FALSE,
  rescale = TRUE,
  ...
)

plotLinearQTL_list(
  LOD_data,
  layout = "l",
  inter_chm_gap = 5,
  ylimits = NULL,
  sig.unit = "LOD",
  plot_type = "lines",
  colour = c("black", "red", "dodgerblue", "sienna4"),
  add_xaxis = TRUE,
  add_rug = TRUE,
  add_thresh = TRUE,
  override_thresh = NULL,
  thresh.lty = 3,
  thresh.lwd = 2,
  thresh.col = "darkred",
  return_plotData = FALSE,
  show_thresh_CI = FALSE,
  use_LG_names = TRUE,
```

```
  axis_label.cex = 1,
  custom_LG_names = NULL,
  LGdiv.col = "gray42",
  ylab.at = 2.5,
  highlight_positions = NULL,
  mainTitle = FALSE,
  rescale = TRUE,
  ...
)
```

Arguments

LOD_data	Output of QTLscan function. If you wish to overlay multiple genome-wide QTLscan outputs, then first compile these into a single list and pass this to LOD_data, for example LOD_data = list(qtl_res1, qtl_res2). If this is passed as a named list and add_legend = TRUE, these names will be used in the legend as well.
layout	There are three possible plot layouts - single chromosome plots ("s"), genome-wide plots arranged adjacently in a linear fashion ("l") which is also the default, and genome-wide plots arranged in a grid ("g"), i.e. a grid of single chromosome plots. In the latter case, a suitable grid dimension will be determined based on the number of linkage groups detected in LOD_data. If you wish to overlay results from multiple multi-chromosome analyses, use the default layout.
inter_chm_gap	The gap size (in units of cM) between successive chromosomes when layout = "l". By default a gap of 5 cM is used. Normally the user should not need to change this.
ylimits	Use to specify ylimits of plot region, though by default NULL in which case a suitable plot region is automatically used.
sig.unit	Label to use on the y-axis for significance units, by default assumed to be LOD score.
plot_type	Plots can be either in line drawings ("lines", default) or scatter plot format ("points").
colour	Vector of colours to be used in the plotting. A default set of 4 colours is provided, the first of which is used when results from a single QTL scan are to be plotted.
add_xaxis	Should an x-axis be drawn? If multiple QTL analyses are performed on different traits, specifying this to be FALSE and using par(mar=c(0,4.1,4.1,2.1)) allows subsequent plots to be neatly stacked.
add_rug	Logical, by default TRUE - should original marker points be added to plot?
add_thresh	Logical, by default TRUE - should a significance threshold be added to plot?
override_thresh	By default NULL. Can be used to specify a (numeric) value for the significance threshold, overriding any stored in LOD_data. If you wish to override thresholds for multiple analyses (so, when LOD_data is a list of QTL outputs), can also provide a vector of numeric values here.
thresh.lty	Gives user control over the line type of the significance threshold to be drawn. Default threshold lty is 3.

thresh.lwd Gives user control over the line width of the significance threshold to be drawn. Default threshold lwd is 2.

thresh.col Gives user control over the line colour of the significance threshold to be drawn. Default threshold colour is dark red. If plotting multiple analyses with rescale = FALSE, it can be useful to provide the same colours to this argument as to colour, so that LOD profiles can be linked to their respective LOD thresholds.

return_plotData
Logical, by default FALSE. If TRUE, then the x and y coordinates of the plot data are returned when layout = "l", which can be useful for subsequent plot manipulations and overlays. For other layouts, no plot data is returned.

show_thresh_CI Logical, by default FALSE. Should confidence interval bounds around LOD threshold be shown if available? If LOD_data is a list from multiple analyses, this option is ignored to prevent plot becoming too cluttered.

use_LG_names Logical, by default TRUE. Should original character LG names (the names of list LOD_data) be used as axis labels? If FALSE, numbering is used instead.

axis_label.cex Argument to adjust the size of the axis labels. Can be useful if there are many linkage groups to plot

custom_LG_names
Option to specify a vector that contains custom linkage group names. By default NULL. See previous argument use_LG_names, which is the usual manner for controlling x-axis labels.

LGdiv.col Colour of dividing lines between linkage groups when layout = "l", by default grey.

ylab.at Distance from the y-axis to place label (by default at 2.5 points)

highlight_positions
Option to include a (list of) positions to highlight (e.g. peak QTL positions). Each list element should be a 2-column data.frame with columns giving the linkage group numbers (numeric) and the corresponding cM positions (numeric) to highlight. If LOD_data is the result of a single genome-wide scan, it is also possible to just directly provide the 2-column data.frame (again, with column 1 containing linkage group numbers and column 2 containing corresponding cM positions). If LOD_data has been provided as a list of multiple analyses, you may wish to highlight different positions from each analysis. Then highlight_positions should also be a list of the same length and in the same order as LOD_data. Each data.frame of positions will be coloured in the same colour as the LOD output. If no position is to be highlighted for some analyses, add the corresponding list element as NULL. For example, if you wish to highlight positions for analyses 1 and 3 in a 3-analysis overlay, then use something like highlight_positions = list(data.frame(lg = 1, cM = 50),NULL,data.frame(lg=c(2,3),cM=c(1
The default setting is NULL, meaning no positions are highlighted.

mainTitle Option to supply vector of plot titles if layout = "s" or layout = "g". Argument ignored if using the default layout. Single character vector also allowed and will be recycled. For no plot titles, leave as default, i.e. FALSE

rescale If results from multiple analyses are to be overlaid and different significance thresholds are detected, then by default plots will be rescaled so that threshold lines overlap. This behaviour can be disabled by setting rescale = FALSE.

... Arguments passed to plot, and lines or points as appropriate (see argument plot_type).

Value

The plot data, if return_plotData = TRUE. Otherwise NULL. Output is returned invisibly

Examples

```
## Not run:
data("qtl_LODs.4x")
plotQTL(LOD_data = qtl_LODs.4x,layout = "l")

## End(Not run)
```

---

plotRecLS *Plot the recombination landscape across the genome*

Description

Function which visualises the recombination landscape in two ways: per linkage group, and per individual. For the first analysis, a rudimentary spline is also fitted to estimate the recombination rate along a grid of positions defined by gap, which is also returned by the function.

Usage

```
plotRecLS(
  recombination_data,
  plot_per_LG = TRUE,
  plot_per_ind = TRUE,
  gap = 1,
  ...
)
```

Arguments

recombination_data
: Data on predicted recombination events, as returned by the function count_recombinations

plot_per_LG
: Logical argument, plot recombination events per linkage group? By default TRUE.

plot_per_ind
: Logical argument, plot recombination events per individual? By default TRUE.

gap
: The size (in cM) of the gap used to define the grid of positions to define the window in which to estimate recombination rate. By default 1 cM. Interpolated positions are taken to be the centre of an interval, so a 1 cM gap would result in predictions for positions 0.5 cM, 1.5 cM etc.

...
: Option to pass extra arguments to the plot function for the per_LG plots. This may lead to conflicts with arguments already declared internally (such as main for example).

Value

A list with two elements, per_LG and per_individual. The first of these is itself a list with the same length as recombination_data, giving the estimated recombination rates along the linkage group. This rate is simply estimated as the (weighted) count of recombination breakpoints divided by the population size.

Examples

```
data("Rec_Data_4x")
plotRecLS(Rec_Data_4x)
```

PVE *Function to determine the percentage variance explained (PVE) of a (maximal) QTL model, and explore sub-models.*

Description

This function builds a (maximal) QTL model from previously detected QTL peaks and outputs the percentage variance explained (PVE) of the full QTL model and all sub-models. It uses a similar approach to the fitting of genetic co-factors in the function QTLscan. The PVE is very similar to but not exactly equal to the adjusted R2 returned in QTLscan at each position (and note: in the former case, these R2 values are per-locus, while this function can estimate the PVE combined over multiple loci). The discrepancy has to do with how PVE is calculated using the formula 100(1 - RSS0/RSS1), where RSS0 and RSS1 are the residual sums of squares of the NULL and QTL models, respectively.

Usage

```
PVE(
  IBD_list,
  Phenotype.df,
  genotype.ID,
  trait.ID,
  block = NULL,
  QTL_df = NULL,
  prop_Pheno_rep = 0.5,
  log = NULL,
  verbose = FALSE
)
```

Arguments

IBD_list	List of IBD probabilities
Phenotype.df	A data.frame containing phenotypic values
genotype.ID	The colname of Phenotype.df that contains the offspring identifiers (F1 names)

trait.ID	The colname of Phenotype.df that contains the response variable to use in the model
block	The blocking factor to be used, if any (must be colname of Phenotype.df). By default NULL, in which case no blocking structure (for unreplicated experiments)
QTL_df	A 2-column data frame of previously-detected QTL; column 1 gives linkage group identifiers, column 2 specifies the cM position of the QTL. If not specified, an error results. It can be convenient to generate a compatible data.frame by first running the function check_cofactors to build a multi-QTL model.
prop_Pheno_rep	The minimum proportion of phenotypes represented across blocks. If less than this, the individual is removed from the analysis. If there is incomplete data, the missing phenotypes are imputed using the mean values across the recorded observations.
log	Character string specifying the log filename to which standard output should be written. If NULL log is send to stdout.
verbose	Should messages be written to standard output?

Value

A list with percentage variance explained of maximal QTL model and all sub-models

Examples

```
data("IBD_4x","Phenotypes_4x")
PVE(IBD_list = IBD_4x,
    Phenotype.df = Phenotypes_4x,
    genotype.ID = "geno",trait.ID = "pheno",
    block = "year",
    QTL_df = data.frame(LG=1,cM=12.3))
```

QTLscan *General QTL function that allows for co-factors, completely randomised block designs and the possibility to derive LOD thresholds using a permutation test*

Description

Function to run QTL analysis using IBD probabilties given (possibly replicated) phenotypes, assuming randomised experimental design

Usage

```
QTLscan(
  IBD_list,
  Phenotype.df,
  genotype.ID,
  trait.ID,
```

```
  block = NULL,
  cofactor_df = NULL,
  allelic_interaction = FALSE,
  folder = NULL,
  filename.short,
  prop_Pheno_rep = 0.5,
  perm_test = FALSE,
  N_perm.max = 1000,
  alpha = 0.05,
  gamma = 0.05,
  ncores = 1,
  log = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

IBD_list	List of IBD probabilities
Phenotype.df	A data.frame containing phenotypic values
genotype.ID	The colname of Phenotype.df that contains the offspring identifiers (F1 names)
trait.ID	The colname of Phenotype.df that contains the response variable to use in the model
block	The blocking factor to be used, if any (must be colname of Phenotype.df). By default NULL, in which case no blocking structure (for unreplicated experiments)
cofactor_df	A 3-column data frame of co-factor(s); column 1 gives the numeric linkage group identifier(s), column 2 specifies the cM position of the co-factor(s), column 3 specifies whether the QTL was fitted using "a" = additive effects or "f" = full allelic interactions (note that any other symbol for the full model will also be accepted, as long as it is not "a"). For backward compatibility with package versions <= 0.0.9, it is possible to just supply the first two columns, in which case an additive-effects model is assumed for each cofactor (so, a third column will be automatically filled with "a"). By default cofactor_df = NULL, in which case no co-factors are included in the analysis.
allelic_interaction	The QTL detection model can be for additive main effects only (by default allelic_interaction = FALSE). If TRUE, then the full model is used (i.e. all possible genotype combinations are included as predictors in the model). This runs the risk of overfitting, especially if double reduction was also allowed. Both types of analyses can ideally be performed and compared. Note that if IBD probabilities were estimated using the "heuristic" method rather than the HMM method (see estimate_IBD), then IBDs are actually haplotype probabilities rather than genotype probabilities, meaning that allelic interaction effects cannot be included in the model.
folder	If markers are to be used as co-factors, the path to the folder in which the imported IBD probabilities is contained can be provided here. By default this is NULL, if files are in working directory.

`filename.short` If TetraOrigin was used and co-factors are being included, the shortened stem of the filename of the `.csv` files containing the output of TetraOrigin, i.e. without the tail "_LinkageGroupX_Summary.csv" which is added by default to all output of TetraOrigin.

`prop_Pheno_rep` The minimum proportion of phenotypes represented across blocks. If less than this, the individual is removed from the analysis. If there is incomplete data, the missing phenotypes are imputed using the mean values across the recorded observations.

`perm_test` Logical, by default `FALSE`. If `TRUE`, a permutation test will be performed to determine a genome-wide significance threshold.

`N_perm.max` The maximum number of permutations to run if `perm_test` is `TRUE`; by default this is 1000.

`alpha` The P-value to be used in the selection of a threshold if `perm_test` is `TRUE`, by default 0.05 (i.e. the 0.95 quantile).

`gamma` The width of the confidence intervals used around the permutation test threshold using the approach of Nettleton & Doerge (2000), by default 0.05.

`ncores` Number of cores to use if parallel computing is required. Works both for Windows and UNIX (using `doParallel`). Use `parallel::detectCores()` to find out how many cores you have available.

`log` Character string specifying the log filename to which standard output should be written. If `NULL` log is send to stdout.

`verbose` Logical, by default `TRUE`. Should messages be printed during running?

`...` Arguments passed to `plot`

Value

A nested list; each list element (per linkage group) contains the following items:

QTL.res Single matrix of QTL results with columns chromosome, position, LOD, adj.r.squared and PVE (percentage variance explained).

Perm.res If `perm_test = FALSE`, this will be `NULL`. Otherwise, Perm.res contains a list of the results of the permutation test, with list items "quantile","threshold" and "scores". Quantile refers to which quantile of scores was used to determine the threshold. Note that scores are each of the maximal LOD scores across the entire genome scan per permutation, thus returning a genome-wide threshold rather than a chromosome-specific threshold. If the latter is preferred, restricting the `IBD_list` to a single chromosome and re-running the permutation test will provide the desired threshold.

Residuals If a blocking factor or co-factors are used, this is the (named) vector of residuals used as input for the QTL scan. Otherwise, this is the set of (raw) phenotypes used in the QTL scan.

Map Original map of genetic marker positions upon which the IBDs were based, most often used for adding rug of marker positions to QTL plots.

LG_names Names of the linkage groups

allelic_interaction Whether argument `allelic_interaction` was `TRUE` or `FALSE` in the QTL scan

Examples

```
data("IBD_4x","Phenotypes_4x")
qtl_LODs.4x <- QTLscan(IBD_list = IBD_4x,
                       Phenotype.df = Phenotypes_4x,
                       genotype.ID = "geno",
                       trait.ID = "pheno",
                       block = "year")
```

---

qtl_LODs.4x *QTL output for example tetraploid*

Description

QTL output for example tetraploid

Usage

```
qtl_LODs.4x
```

Format

An object of class `list` of length 6.

Rec_Data_4x *Recombination data for example tetraploid*

Description

Recombination data for example tetraploid

Usage

```
Rec_Data_4x
```

Format

An object of class `list` of length 2.

segList_2x *Expected segregation for all markers types of a diploid cross*

Description

Expected segregation for all markers types of a diploid cross

Usage

```
segList_2x
```

Format

An object of class `list` of length 8.

segList_3x *Expected segregation for all markers types of a triploid cross (4 x 2)*

Description

Expected segregation for all markers types of a triploid cross (4 x 2)

Usage

```
segList_3x
```

Format

An object of class `list` of length 27.

segList_3x_24 *Expected segregation for all markers types of a triploid cross (2 x 4)*

Description

Expected segregation for all markers types of a triploid cross (2 x 4)

Usage

```
segList_3x_24
```

Format

An object of class `list` of length 27.

segList_4x — *Expected segregation for all markers types of a tetraploid cross*

Description

Expected segregation for all markers types of a tetraploid cross

Usage

```
segList_4x
```

Format

An object of class `list` of length 224.

segList_6x — *Expected segregation for all markers types of a hexaploid cross*

Description

Expected segregation for all markers types of a hexaploid cross

Usage

```
segList_6x
```

Format

An object of class `list` of length 3735.

segMaker — *Create a list of possible QTL segregation types*

Description

Function to generate list of segregation types for the `exploreQTL` function

Usage

```
segMaker(ploidy, segtypes, modes = c("a", "d"))
```

Arguments

ploidy	The ploidy of the population. Currently assumed to be an even number for this function.
segtypes	List of QTL segregation types to consider, so e.g. c(1,0) would mean all possible simplex x nulliplex QTL (ie. 4 QTL, on each of homologues 1 - 4 of parent 1). Note that symmetrical QTL types that cannot be distinguished are not automatically removed and need to be manually identified. If this is an issue, use the inbuilt list for tetraploids provided with the package to search the full model space. Such an inbuilt list is currently only available for tetraploids, and is available from the exploreQTL function.
modes	Character vector of modes of QTL action to consider, with options "a" for "additive" and "d" for dominant QTL action.

---

singleMarkerRegression

Run a single marker regression using marker dosages

Description

Function to run a single marker regression using marker dosages

Usage

```
singleMarkerRegression(
  dosage_matrix,
  Phenotype.df,
  genotype.ID,
  trait.ID,
  maplist = NULL,
  perm_test = FALSE,
  N_perm = 1000,
  alpha = 0.05,
  ncores = 1,
  return_R2 = FALSE,
  log = NULL
)
```

Arguments

dosage_matrix	An integer matrix with markers in rows and individuals in columns. All markers in this matrix will be tested for association with the trait.
Phenotype.df	A data.frame containing phenotypic values
genotype.ID	The colname of Phenotype.df that contains the population identifiers (F1 names) (must be a colname of Phenotype.df)

trait.ID	The colname of Phenotype.df that contains the response variable to use in the model (must be a colname of Phenotype.df)
maplist	Option to include linkage map in the format returned by MDSMap_from_list from polymapR. If maplist is not specified (by default NULL) then no ordering of markers from dosage-matrix is performed. Note that all markers in dosage_matrix are tested; markers with dosages that were not on the maplist will be assigned unordered to linkage group 0 with dummy cM positions 1,2,3 etc.
perm_test	Logical, by default FALSE. If TRUE, a permutation test will be performed to determine a genome-wide significance threshold.
N_perm	Integer. The number of permutations to run if perm_test is TRUE; by default this is 1000.
alpha	Numeric. The P-value to be used in the selection of a threshold if perm_test is TRUE; by default 0.05 (i.e. the 0.95 quantile).
ncores	Number of cores to use if parallel processing required. Works both for Windows and UNIX (using doParallel). Use parallel::detectCores() to find out how many cores you have available.
return_R2	Should the (adjusted) R2 of the model fit also be determined?
log	Character string specifying the log filename to which standard output should be written. If NULL log is send to stdout.

Value

A list containing the following components:

QTL.res The -log(p) of the model fit per marker are returned as "LOD" scores, although "LOP" would have been a better description. If requested, R2 values are also returned in column "R2adj"

Perm.res The results of the permutation test if performed, otherwise NULL

Map The linkage map if provided, otherwise NULL

LG_names Names of the linkage groups, if a map was provided, otherwise NULL

Examples

```
data("SNP_dosages.4x","BLUEs.pheno")
Trait_1.smr <- singleMarkerRegression(dosage_matrix = SNP_dosages.4x,
Phenotype.df = BLUEs.pheno,genotype.ID = "Geno",trait.ID = "BLUE")
```

SNP_dosages.4x *SNP marker dosage data for example tetraploid*

Description

SNP marker dosage data for example tetraploid

Usage

```
SNP_dosages.4x
```

Format

An object of class matrix (inherits from array) with 186 rows and 52 columns.

---

spline_IBD *Fit splines to IBD probabilities*

Description

Fits splines to IBD probabilities at a grid of positions at user-defined spacing.

Usage

```
spline_IBD(IBD_list, gap, method = "cubic", ncores = 1, log = NULL)
```

Arguments

IBD_list	List of IBD probabilities
gap	The size (in centiMorgans) of the gap between splined positions
method	One of two options, either "linear" or "cubic". The default method (cubic) fits cubic splines, and although more accurate, becomes computationally expensive in higher-density data-sets, where the linear option may be preferable.
ncores	Number of cores to use, by default 1 only. Works both for Windows and UNIX (using doParallel). Use parallel::detectCores() to find out how many cores you have available. Note that with large datasets, using multiple cores will use large amounts of memory (RAM). Single-core or e.g. 2-core evaluations, although slower, is less memory-intensive.
log	Character string specifying the log filename to which standard output should be written. If NULL log is send to stdout.

Value

Returns a list of similar format as IBD_list, with a splined IBD_array in place of the original IBD_array

Examples

```
data("IBD_4x")
IBD_4x.spl <- spline_IBD(IBD_list = IBD_4x, gap = 1)
```

thinmap *Thin out map data*

Description

thinmap is a function for thinning out an integrated map, in order that IBD estimation runs more quickly. Especially useful for maps with very high marker densities for which the estimate_IBD function is to be used.

Usage

```
thinmap(
  maplist,
  dosage_matrix,
  bin_size = 1,
  bounds = NULL,
  remove_markers = NULL,
  plot_maps = TRUE,
  use_SN_phase = FALSE,
  parent1 = "P1",
  parent2 = "P2",
  log = NULL
)
```

Arguments

maplist	A list of maps. In the first column marker names and in the second their position.
dosage_matrix	An integer matrix with markers in rows and individuals in columns.
bin_size	Numeric. Size (in cM) of the bins to include. By default, a bin size of 1 cM is used. Larger bin_size results in fewer markers being left on the resulting map.
bounds	Numeric vector. If NULL (by default) then all positions are included, however if specified then output is limited to a specific region, which may be useful if fine-mapping a region of interest.
remove_markers	Optional vector of marker names to remove from the maps. Default is NULL.
plot_maps	Logical. Plot the marker positions of the selected markers using polymapR::plot_map.
use_SN_phase	Logical, by default FALSE. If TRUE, then 1x0 and 0x1 are binned per phase, to increase coverage of these marker types across parental homologues. If not, at most one of each are retained per bin.
parent1	Identifier of parent 1, by default assumed to be "P1"
parent2	Identifier of parent 2, by default assumed to be "P2"
log	Character string specifying the log filename to which standard output should be written. If NULL log is send to stdout.

Value

A maplist of the same structure as the input maplist, but with fewer markers based on the bin_size.

Examples

```
data("phased_maplist.4x","SNP_dosages.4x")
maplist_thin<-thinmap(maplist=phased_maplist.4x,dosage_matrix=SNP_dosages.4x)
```

---

visualiseGIC *Visualise Genotypic Information Coefficient*

Description

Function to visualise the GIC of a certain region

Usage

```
visualiseGIC(
  GIC_list,
  add_rug = TRUE,
  add_leg = FALSE,
  ylimits = NULL,
  gic.cex = 1,
  show_markers = TRUE,
  add.mainTitle = TRUE,
  plot.cols = NULL
)
```

Arguments

GIC_list	List of GIC data, the output of estimate_GIC
add_rug	Should original marker positions be added to the plot?
add_leg	Should a legend be added to the plot?
ylimits	Optional argument to control the plotting area, by default NULL
gic.cex	Option to increase the size of the GIC
show_markers	Should markers be shown?
add.mainTitle	Should a main title be added to the plot?
plot.cols	Optional argument to specify plot colours, otherwise suitable contrasting colours are chosen

Value

The phased map data for the specified region, recoded into 1's and 0's.

Examples

```
data("GIC_4x")
visualiseGIC(GIC_list = GIC_4x)
```

`visualiseHaplo` *Visualise haplotypes in certain individuals in a certain region*

Description

Function to visualise the haplotypes of a certain region in certain individuals

Usage

```
visualiseHaplo(
  IBD_list,
  display_by = c("phenotype", "name"),
  linkage_group = NULL,
  Phenotype.df = NULL,
  genotype.ID = NULL,
  trait.ID = NULL,
  pheno_range = NULL,
  cM_range = "all",
  highlight_region = NULL,
  select_offspring = NULL,
  recombinant_scan = NULL,
  allele_fish = NULL,
  presence_threshold = 0.95,
  xlabl = TRUE,
  ylabl = TRUE,
  mainTitle = NULL,
  multiplot = NULL,
  append = FALSE,
  colPal = c("white", "navyblue", "darkred"),
  hap.wd = 0.4,
  recombination_data = NULL,
  reset_par = TRUE,
  log = NULL
)
```

Arguments

`IBD_list`	List of IBD probabilities
`display_by`	Option to display a subset of the population's haplotypes either by `"phenotype"` or `"name"`. If `"phenotype"` is supplied, then `Phenotype.df`,`genotype.ID`,`trait.ID` and `pheno_range` must also be specified. if `"name"` is supplied, then `select_offspring` must be specified.

linkage_group Numeric identifier of the linkage group being examined, based on the order of IBD_list. Only a single linkage group is allowed. If IBD_list corresponds to a single linkage group, default value of NULL will suffice

Phenotype.df A data.frame containing phenotypic values, which can be used to select a subset of the population to visualise (with extreme phenotypes for example). By default NULL, in which case a subset of the population may be selected using the select_offspring argument.

genotype.ID The colname of Phenotype.df that contains the population identifiers (F1 names) (must be a colname of Phenotype.df)

trait.ID The colname of Phenotype.df that contains the response variable to use in the model (must be a colname of Phenotype.df)

pheno_range Vector of numeric bounds of the phenotypic scores to include (offspring selection).

cM_range Vector of numeric bounds of the genetic region to be explored. If none are specified, the default of "all" means all cM positions will be included.

highlight_region
Option to hightlight a particular genetic region on the plot; can be a single position or a vector of 2 positions. By default NULL.

select_offspring
Vector of offspring identifiers to visualise, must be supplied if display_by = "name". Specifying "all" will result in all offspring haplotypes being visualised.

recombinant_scan
Vector of homologue numbers between which to search for recombinant offspring in the visualised region and selected individuals. By default NULL, in which case no search is preformed.

allele_fish Vector of homologue numbers of interest, for which to search for offspring that carry these homologues (in the visualised region). By default NULL, in which case no search ("fishing") is performed.

presence_threshold
Numeric. The minimum probability used to declare presence of a homologue in an individual. This is only needed if a recombinant_scan is performed. By default a value of 0.95 is used. When searching for recombinants, this value is also used to denote the proportion of loci carrying the required number of homologues (i.e. by default 95 per cent of loci should have between 0.95 and 1.1 copies of the specified recombinant homologues).

xlabl Logical, by default TRUE. Should an x-axis label be used?

ylabl Logical, by default TRUE. Should a y-axis label be used?

mainTitle Option to override default plot titles with a (vector of) captions. By default NULL.

multiplot Vector of integers. By default NULL so haplotypes are plotted singly; otherwise a vector specifying the number of rows and columns in the plot layout.

append Option to allow user to append new plots to spaces generated by multiplot, otherwise these are filled with blank plots. By default FALSE. If TRUE, then a large enough multiplot grid should be generated to make this option meaningful.

colPal	Colour palette to use in the visualisation (best to provide 3 colours).
hap.wd	The width of the haplotype tracks to be plotted, generally recommended to be about 0.4 (default value)
recombination_data	List object as returned by the function count_recombinations. By default NULL, in which case no overlay of predicted recombination events is performed. However, it can be useful to visualise predicted recombination events, particularly as this might help inform the choice of argument plausible_pairing_prob of that function. See count_recombinations for more details.
reset_par	By default TRUE, reset par on exit.
log	Character string specifying the log filename to which standard output should be written. If NULL log is send to stdout.

Value

If recombinant_scan vector is supplied, a vector of recombinant offspring ID in the region of interest (otherwise NULL).

Examples

```
data("IBD_4x")
visualiseHaplo(IBD_list = IBD_4x,
               display_by = "name",
               linkage_group = 1,
               select_offspring = "all",
               multiplot = c(3,3))
```

---

visualisePairing *Visualise pairing of parental homologues*

Description

Function to visualise the pairing of parental homologues across the population using graph, with nodes to denote parental homologues and edges to denote deviations from expected proportions under a polysomic model of inheritance

Usage

```
visualisePairing(
  meiosis_report.ls,
  pos.col = "red",
  neg.col = "blue",
  parent,
  max.lwd = 20,
  datawidemax,
  add.label = TRUE,
  return.data = FALSE,
  ...
)
```

Arguments

meiosis_report.ls	List output of function meiosis_report
pos.col	Colour corresponding to excess of pairing associations predicted (positive deviations), by default red
neg.col	Colour corresponding to lack of pairing associations predicted (negative deviations), by default blue
parent	The parent, either "P1" (mother) or "P2 (father)
max.lwd	Maximum line width, by default 20
datawidemax	This argument is currently a work-around to allow multiple plots to have the same scale (line thicknesses consistent). No default is provided. To estimate this value, simply set argument return.data = TRUE, and record the maximum absolute value over columns 'count', which are the deviations from random expectations. This should be done over multiple function calls if e.g. comparing both P1 and P2 values. When a global maximum (absolute) deviation is known, re-run the function with this value for datawidemax. The line width specified by max.lwd will then be used for this, and all other line widths re-scaled accordingly.
add.label	Should a label be applied, giving the maximum deviation in the plot? By default TRUE
return.data	Should plot data be returned? By default FALSE
...	Optional arguments passed to plot.igraph

Value

If return.data = TRUE, the values for pairwise deviations from the expected numbers are returned, useful for determining the value datawidemax to provide consistent scaling across multiple plots

Examples

```
data("mr.ls")
visualisePairing(meiosis_report.ls = mr.ls,
                 parent = "P1",
                 datawidemax = 3)
```

---

visualiseQTLeffects *Visualise QTL homologue effects around a QTL position*

Description

Function to visualise the effect of parental homologues around a QTL peak across the population.

Usage

```
visualiseQTLeffects(
  IBD_list,
  Phenotype.df,
  genotype.ID,
  trait.ID,
  linkage_group,
  LOD_data,
  cM_range = NULL,
  col.pal = c("purple4", "white", "seagreen"),
  point.density = 50,
  zero.sum = FALSE,
  allelic_interaction = FALSE,
  exploreQTL_output = NULL,
  return_plotData = FALSE
)
```

Arguments

IBD_list	List of IBD probabilities
Phenotype.df	A data.frame containing phenotypic values
genotype.ID	The colname of Phenotype.df that contains the population identifiers (F1 names) (must be a colname of Phenotype.df)
trait.ID	The colname of Phenotype.df that contains the response variable to use in the model (must be a colname of Phenotype.df)
linkage_group	Numeric identifier of the linkage group being tested, based on the order of IBD_list. Only a single linkage group is allowed.
LOD_data	Output of QTLscan function
cM_range	If required, the plotting region can be restricted to a specified range of centiMorgan positions (provided as a vector of start and end positions).
col.pal	Vector of colours to use in the visualisations (it is best to provide two or three colours for simplicity). By default, effects will be coloured from purple to green through white.
point.density	Parameter to increase the smoothing of homologue effect tracks
zero.sum	How allele substitution effect should be defined. If FALSE (by default), the effect of each homologue is computed relative to the overall phenotypic mean, otherwise contrasts (against offspring without the inherited homologue) are used.
allelic_interaction	By default FALSE, in which case the additive effects of parental alleles are visualised. If TRUE, a plot of the mean effect of combinations of parental alleles is visualised instead. exploreQTL_output is required in this case.
exploreQTL_output	If allelic_interaction = TRUE, the output of the function exploreQTL must be provided.
return_plotData	Logical, by default FALSE. If TRUE, plot data is returned, otherwise NULL.

Value

The estimated effects of the homologues, used in the visualisation

Examples

```
data("IBD_4x","BLUEs.pheno","qtl_LODs.4x")
visualiseQTLeffects(IBD_list = IBD_4x,
                    Phenotype.df = BLUEs.pheno,
                    genotype.ID = "Geno",
                    trait.ID = "BLUE",
                    linkage_group = 2,
                    LOD_data = qtl_LODs.4x)
```

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