

Package 'rehh'

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Title Searching for Footprints of Selection using 'Extended Haplotype Homozygosity' Based Tests

Description Population genetic data such as 'Single Nucleotide Polymorphisms' (SNPs) is often used to identify genomic regions that have been under recent natural or artificial selection and might provide clues about the molecular mechanisms of adaptation. One approach, the concept of an 'Extended Haplotype Homozygosity' (EHH), introduced by (Sabeti 2002) <doi:10.1038/nature01140>, has given rise to several statistics designed for whole genome scans. The package provides functions to compute three of these, namely: 'iHS' (Voight 2006) <doi:10.1371/journal.pbio.0040072> for detecting positive or 'Darwinian' selection within a single population as well as 'Rsb' (Tang 2007) <doi:10.1371/journal.pbio.0050171> and 'XP-EHH' (Sabeti 2007) <doi:10.1038/nature06250>, targeted at differential selection between two populations. Various plotting functions are also included to facilitate visualization and interpretation of these statistics. Due to changes in the API, albeit mostly minor, this version is not compatible with versions 2.0.X.

Depends R (>= 2.10)

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URL <https://CRAN.R-project.org/package=rehh>,
<https://gitlab.com/oneoverx/rehh>

BugReports <https://gitlab.com/oneoverx/rehh/issues>

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rehh-package	<i>rehh: Searching for Footprints of Selection using 'Extended Haplotype Homozygosity' Based Tests</i>
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Description

Population genetic data such as 'Single Nucleotide Polymorphisms' (SNPs) is often used to identify genomic regions that have been under recent natural or artificial selection and might provide clues about the molecular mechanisms of adaptation. One approach, the concept of an 'Extended Haplotype Homozygosity' (EHH), introduced by (Sabeti 2002) <doi:10.1038/nature01140>, has given rise to several statistics designed for whole genome scans. The package provides functions to compute three of these, namely: 'iHS' (Voight 2006) <doi:10.1371/journal.pbio.0040072> for detecting positive or 'Darwinian' selection within a single population as well as 'Rsb' (Tang 2007) <doi:10.1371/journal.pbio.0050171> and 'XP-EHH' (Sabeti 2007) <doi:10.1038/nature06250>, targeted at differential selection between two populations. Various plotting functions are also included to facilitate visualization and interpretation of these statistics. Due to changes in the API, albeit mostly minor, this version is not compatible with versions 2.0.X.

Details

See `vignette("rehh", package = "rehh")` for an overview of the package and `vignette("examples", package = "rehh")` for a more detailed discussion of two small example data sets.

References

- Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.
- Gautier M. and Vitalis R. (2012). rehh: An R package to detect footprints of selection in genome-wide SNP data from haplotype structure. *Bioinformatics*, **28**(8), 1176-1177.
- Gautier M., Klassmann A., and Vitalis R. (2017). rehh 2.0: a reimplement of the R package rehh to detect positive selection from haplotype structure. *Molecular Ecology Resources*, **17**, 78-90.
- Sabeti, P.C. et al. (2002). Detecting recent positive selection in the human genome from haplotype structure. *Nature*, **419**, 832-837.
- Sabeti, P.C. et al. (2007). Genome-wide detection and characterization of positive selection in human populations. *Nature*, **449**, 913-918.
- Tang, K. and Thornton, K.R. and Stoneking, M. (2007). A New Approach for Using Genome Scans to Detect Recent Positive Selection in the Human Genome. *Plos Biology*, **7**, e171.
- Voight, B.F. and Kudravalli, S. and Wen, X. and Pritchard, J.K. (2006). A map of recent positive selection in the human genome. *Plos Biology*, **4**, e72.

See Also

Useful links:

- <https://CRAN.R-project.org/package=rehh>

- <https://gitlab.com/oneoverx/rehh>
- Report bugs at <https://gitlab.com/oneoverx/rehh/issues>

allelefurcation-class *An S4 class containing furcation trees for one allele of a focal marker*

Description

An S4 class containing the furcation trees for both sides of a focal marker for one allele.

Slots

allele the allele of the focal marker.
 description "ancestral", "derived", "major", "minor", etc.
 count the number of chromosomes with that allele.
 left furcation tree to the left of the marker.
 right furcation tree to the right of the marker.

See Also

[ftree](#), [furcation](#)

as.newick *Convert a furcation tree into Newick format*

Description

Convert a furcation tree into Newick format.

Usage

```
as.newick(furcation, allele = 0, side,
  hap.names = seq_len(furcation@nhap))
```

Arguments

furcation	an object of furcation-class .
allele	the allele to be considered (default 0).
side	side (either "left" or "right").
hap.names	names/labels of chromosomes in haplotype data file. Per default haplotypes are numbered by their order in the input file.

See Also

[ftree-class](#), [calc_furcation](#), [plot.furcation](#)

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#calculate furcation for the marker "F1205400"
#which displays a strong signal of selection
f <- calc_furcation(haplohh_cgu_bta12, mrk = "F1205400")
#get left tree of ancestral allele (coded as '0')
as.newick(f, 0, "left")
```

calc_candidate_regions

Determine candidate regions of selection

Description

Determine candidate regions of selection.

Usage

```
calc_candidate_regions(scan, threshold = NA, pval = FALSE,
  ignore_sign = FALSE, window_size = 1e+06, overlap = 0,
  right = TRUE, min_n_mrk = 1, min_n_extr_mrk = 1,
  min_perc_extr_mrk = 0, join_neighbors = TRUE)
```

Arguments

scan	a data frame containing scores (output of ihh2ihs , ines2rsb or ies2xpehh).
threshold	boundary score above which markers are defined as "extreme".
pval	logical. If TRUE use the (negative log-) p-value instead of the score.
ignore_sign	logical. If TRUE (default), take absolute values of score.
window_size	size of sliding windows. If set to 1, no windows are constructed and only the individual extremal markers are reported.
overlap	size of window overlap (default 0, i.e. no overlap).
right	logical, indicating if the windows should be closed on the right (and open on the left) or vice versa.
min_n_mrk	minimum number of markers per window.
min_n_extr_mrk	minimum number of markers with extreme value in a window.
min_perc_extr_mrk	minimum percentage of extremal markers among all markers.
join_neighbors	logical. If TRUE (default), merge neighboring windows with extreme values.

Details

There is no generally agreed method how to determine genomic regions which might have been under recent selection. Since selection tends to yield clusters of markers with outlier values, a common approach is to search for regions with an elevated number or fraction of outlier or extremal markers. This function allows to set three conditions a window must fulfill in order to classify as candidate region:

- `min_n_mrk` a minimum number of (any) markers.
- `min_n_extr_mrk` a minimum number of markers with outlier / extreme value.
- `min_perc_extr_mrk` a minimum percentage of extremal markers among all markers.

"Extreme" markers are defined by having a score above the specified threshold.

Value

A data frame with chromosomal regions, i.e. windows that fulfill the necessary conditions to qualify as candidate regions under selection. For each region the overall number of markers, their mean and maximum, the number of markers with extremal values, their percentage of all markers and their average are reported.

See Also

[calc_region_stats](#)

calc_ehh

EHH and iHH computation for a given focal marker

Description

Compute Extended Haplotype Homozygosity (EHH) and integrated EHH (iHH) for a given focal marker.

Usage

```
calc_ehh(haplohh, mrk, limhaplo = 2, limehh = 0.05,
         include_zero_values = FALSE, include_nhaplo = FALSE, phased = TRUE,
         polarized = TRUE, scalegap = NA, maxgap = NA,
         discard_integration_at_border = TRUE, lower_y_bound = limehh)
```

Arguments

`haplohh` an object of class `haplohh` (see [data2haplohh](#)).

`mrk` integer representing the number of the focal marker within the `haplohh` object or string representing its ID/name.

limhaplo	if there are less than limhaplo chromosomes that can be used for the calculation of EHH, the calculation is stopped. The option is intended for the case of missing data, which leads to the successive exclusion of haplotypes: the further away from the focal marker the less haplotypes contribute to EHH.
limehh	limit at which EHH stops to be evaluated
include_zero_values	logical. If FALSE, return values only for those positions where the calculation is actually performed, i.e. until stopped by reaching either limehh or limhaplo. If TRUE, report EHH values for all markers, the additional ones being zero.
include_nhaplo	logical. If TRUE, report the number of evaluated haplotypes at each marker (only informative, if missing data leads to a decrease of evaluated haplotypes).
phased	logical. If TRUE (default) chromosomes are expected to be phased. If FALSE, the haplotype data is assumed to consist of pairwise ordered chromosomes belonging to diploid individuals. EHH is then estimated over individuals which are homozygous at the focal marker.
polarized	logical. TRUE by default. If FALSE, use major and minor allele instead of ancestral and derived. If there are more than two alleles then the minor allele refers to the second-most frequent allele.
scalegap	scale or cap gaps larger than the specified size to the specified size (default=NA, i.e. no scaling).
maxgap	maximum allowed gap in bp between two markers. If exceeded, further calculation of EHH is stopped at the gap (default=NA, i.e. no limitation).
discard_integration_at_border	logical. If TRUE (default) and computation reaches first or last marker or a gap larger than maxgap, iHH is set to NA.
lower_y_bound	lower y boundary of the area to be integrated over (default: limehh). Can be set to zero for compatibility with the program hapbin.

Details

Values for allele-specific Extended Haplotype Homozygosity (EHH) are computed upstream and downstream of the focal marker for each of its alleles. These values are integrated with respect to their genomic positions to yield an 'integrated EHH' (iHH) value for each allele.

Value

The returned value is a list containing the following elements:

mrk.name The name/identifier of the focal marker.

freq A vector with the frequencies of the alleles of the focal marker.

ehh A data frame with EHH values for each allele of the focal marker.

ihh A vector with iHH (integrated EHH) values for each allele of the focal marker.

References

- Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.
- Sabeti, P.C. et al. (2002). Detecting recent positive selection in the human genome from haplotype structure. *Nature*, **419**, 832-837.
- Sabeti, P.C. et al. (2007). Genome-wide detection and characterization of positive selection in human populations. *Nature*, **449**, 913-918.
- Tang, K. and Thornton, K.R. and Stoneking, M. (2007). A New Approach for Using Genome Scans to Detect Recent Positive Selection in the Human Genome. *Plos Biology*, **7**, e171.
- Voight, B.F. and Kudravalli, S. and Wen, X. and Pritchard, J.K. (2006). A map of recent positive selection in the human genome. *Plos Biology*, **4**, e72.

See Also

[data2haplohh](#), [plot.ehh](#), [calc_ehhs](#), [scan_hh](#).

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#computing EHH statistics for the marker "F1205400"
#which displays a strong signal of selection
ehh <- calc_ehh(haplohh_cgu_bta12, mrk = "F1205400")
```

calc_ehhs

EHHS and iES computation for a given focal marker

Description

Compute site-specific Extended Haplotype Homozygosity (EHHS) and integrated EHHS (iES) for a given focal marker.

Usage

```
calc_ehhs(haplohh, mrk, limhaplo = 2, limehhs = 0.05,
  include_zero_values = FALSE, include_nhaplo = FALSE, phased = TRUE,
  scalegap = NA, maxgap = NA, discard_integration_at_border = TRUE,
  lower_y_bound = limehhs)
```

Arguments

haplohh an object of class haplohh (see [data2haplohh](#)).

mrk integer representing the number of the focal marker within the haplohh object or string representing its ID/name.

limhaplo	if there are less than limhaplo chromosomes that can be used for the calculation of EHH, the calculation is stopped. The option is intended for the case of missing data, which leads to the successive exclusion of haplotypes: the further away from the focal marker the less haplotypes contribute to EHH.
limehhs	limit at which EHHS stops to be evaluated.
include_zero_values	logical. If FALSE, return values only for those positions where the calculation is actually performed, i.e. until stopped by reaching either limehh or limhaplo. If TRUE, report EHH values for all markers, the additional ones being zero.
include_nhaplo	logical. If TRUE, report the number of evaluated haplotypes at each marker (only informative, if missing data leads to a decrease of evaluated haplotypes).
phased	logical. If TRUE (default) chromosomes are expected to be phased. If FALSE, the haplotype data is assumed to consist of pairwise ordered chromosomes belonging to diploid individuals. EHHS is then estimated over individuals which are homozygous at the focal marker.
scalegap	scale or cap gaps larger than the specified size to the specified size (default=NA, i.e. no scaling).
maxgap	maximum allowed gap in bp between two markers. If exceeded, further calculation of EHHS is stopped at the gap (default=NA, i.e no limitation).
discard_integration_at_border	logical. If TRUE (default) and computation reaches first or last marker or a gap larger than maxgap, iHH is set to NA.
lower_y_bound	lower y boundary of the area to be integrated over (default: limehhs). Can be set to zero for compatibility with the program hapbin.

Details

Values for site-specific Extended Haplotype Homozygosity (EHHS) are computed at each position upstream and downstream of the focal marker. These values are integrated with respect to their genomic position to yield an 'integrated EHHS' (IES) value.

Value

The returned value is a list containing the following elements:

mrk.name The name/identifier of the focal marker.

ehhs A table containing EHHS values as used by Sabeti et al. (2007), resp. the same values normalized to 1 at the focal marker (nEHHS) as used by Tang et al. (2007).

IES Integrated EHHS.

INES Integrated normalized EHHS.

References

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.

Sabeti, P.C. et al. (2002). Detecting recent positive selection in the human genome from haplotype structure. *Nature*, **419**, 832-837.

Sabeti, P.C. et al. (2007). Genome-wide detection and characterization of positive selection in human populations. *Nature*, **449**, 913-918.

Tang, K. and Thornton, K.R. and Stoneking, M. (2007). A New Approach for Using Genome Scans to Detect Recent Positive Selection in the Human Genome. *Plos Biology*, **7**, e171.

Voight, B.F. and Kudravalli, S. and Wen, X. and Pritchard, J.K. (2006). A map of recent positive selection in the human genome. *Plos Biology*, **4**, e72.

See Also

[data2haplohh](#), [plot.ehhs](#), [calc_ehh](#), [scan_hh](#).

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#computing EHHS statistics for the marker "F1205400"
#which displays a strong signal of selection
ehhs <- calc_ehhs(haplohh_cgu_bta12, mrk = "F1205400")
```

calc_furcation

calculate furcation trees around a focal marker

Description

Calculate furcation trees around a focal marker. A furcation tree captures in greater detail than EHH values the decrease of extended haplotype homozygosity at increasing distances from the selected focal marker.

Usage

```
calc_furcation(haplohh, mrk, allele = NA, limhaplo = 2,
  phased = TRUE, polarized = TRUE)
```

Arguments

haplohh	an object of class haplohh (see data2haplohh).
mrk	integer representing the number of the focal marker within the haplohh object or string representing its ID/name.
allele	a vector of alleles as coded internally, i.e. in case of polarized alleles, 0 represents the ancestral, 1 or higher the derived alleles. If NULL, all alleles of the focal marker are considered.

limhaplo	if there are less than limhaplo chromosomes that can be used for the calculation, it is stopped. This is useful in case of missing data, which lead to a successive exclusion of haplotypes: the further away from the focal marker the less haplotypes are evaluated.
phased	logical. If TRUE (default), chromosomes are expected to be phased. If FALSE, consecutive chromosomes are assumed to belong to diploid individuals and furcation trees are limited to within individuals which are homozygous at the focal marker.
polarized	logical. Affects only the order of furcations. If TRUE (default), the ancestral allele becomes the first furcation and derived alleles are sorted by their frequency. Otherwise all alleles are sorted by their frequency.

Details

A haplotype furcation tree visualizes the breakdown of LD at increasing distances from the focal marker. The root of each tree is an allele of the focal marker, which in turn is identified by a vertical dashed line. Moving either to the "left" or to the "right" of the focal marker, each further marker is an opportunity for a node; the tree either divides or does not, based on whether alleles at that marker distinguish between hitherto identical extended haplotypes. The thickness of the lines corresponds to the number of chromosomes sharing an extended haplotype.

Value

An object of class furcation, containing the furcation structure of the specified alleles at the focal marker.

References

Sabeti, P.C. and Reich, D.E. and Higgins, J.M. and Levine, H.Z.P and Richter, D.J. and Schaffner, S.F. and Gabriel, S.B. and Platko, J.V. and Patterson, N.J. and McDonald, G.J. and Ackerman, H.C. and Campbell, S.J. and Altshuler, D. and Cooper, R. and Kwiatkowski, D. and Ward, R. and Lander, E.S. (2002). Detecting recent positive selection in the human genome from haplotype structure. *Nature*, 419, 832-837.

See Also

[plot.furcation](#), [calc_haplen](#).

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#plotting a furcation diagram for both ancestral and derived allele
#from the marker "F1205400"
#which display a strong signal of selection
f <- calc_furcation(haplohh_cgu_bta12, mrk = "F1205400")
plot(f)
```

`calc_haplen`*Calculate length of haplotypes around a focal marker*

Description

Calculate for each chromosome the length of its extended haplotype homozygosity.

Usage

```
calc_haplen(furcation)
```

Arguments

`furcation` an object of class `furcation` calculated by `calc_furcation`.

Details

The length of an extended haplotype is defined as the region around a focal marker in which a particular chromosome shares a haplotype with (i.e. is homozygous to) at least one other chromosome. It is identical to the (horizontal) branch length from the root to the last furcation.

Value

The function returns a list containing four elements:

mrk.name name/identifier of the focal marker.

position position of the focal marker.

xlim positions of left- and rightmost markers covered by extended haplotypes.

haplen a data frame with the coordinates of extended haplotypes around the focal marker.

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#plotting haplotype lengths for both ancestral and derived allele
#of the marker "F1205400"
#which displays a strong signal of selection
f <- calc_furcation(haplohh_cgu_bta12, mrk = "F1205400")
h <- calc_haplen(f)
plot(h)
```

calc_region_stats *Calculate score statistics for given regions*

Description

Calculate score statistics (extremal values) for given regions. This function is intended for the comparison of different scores for the same chromosomal regions.

Usage

```
calc_region_stats(scan, regions, threshold = NA, pval = FALSE,
  ignore_sign = FALSE, right = TRUE)
```

Arguments

scan	a data frame containing scores (output of ihh2ihs , ines2rsb or ies2xpehh).
regions	a data frame with column names CHR, START and END, specifying chromosomal regions (e.g. as obtained by function calc_candidate_regions).
threshold	boundary score above which markers are defined as "extreme".
pval	logical. If TRUE use the (negative log-) p-value instead of the score.
ignore_sign	logical. If TRUE (default), take absolute values of score.
right	logical, indicating if the regions should be closed on the right (and open on the left) or vice versa.

Value

A data frame with chromosomal regions. For each region the overall number of markers, their mean and maximum, the number of markers with extremal values, their percentage of all markers and their average are reported.

See Also

[calc_candidate_regions](#)

data2haplohh *Convert data from input file to an object of class haplohh*

Description

Convert input data files to an object of [haplohh-class](#).

Usage

```
data2haplohh(hap_file, map_file = NA, min_perc_genotype.hap = NA,
  min_perc_genotype.mrk = 100, min_maf = NA, chr.name = NA,
  popsel = NA, recode.allele = FALSE, allele_coding = "12",
  haplotype.in.columns = FALSE, remove_multiple_markers = FALSE,
  polarize_vcf = TRUE, capitalize_AA = TRUE,
  position_scaling_factor = NA, verbose = TRUE)
```

Arguments

hap_file	file containing haplotype data (see details below).
map_file	file containing map information (see details below).
min_perc_genotype.hap	threshold on percentage of missing data for haplotypes (haplotypes with less than min_perc_genotype.hap percent of markers genotyped are discarded). Default is NA, hence no constraint.
min_perc_genotype.mrk	threshold on percentage of missing data for markers (markers genotyped on less than min_perc_genotype.mrk percent of haplotypes are discarded). By default, min_perc_genotype.mrk=100, hence only fully genotyped markers are retained. This value cannot be set to NA or zero.
min_maf	threshold on the Minor Allele Frequency. Markers having a MAF lower than or equal to minmaf are discarded. In case of multi-allelic markers the second-most frequent allele is referred to as minor allele. Setting this value to zero eliminates monomorphic sites. Default is NA, hence no constraint.
chr.name	name of the chromosome considered (relevant if data for several chromosomes is contained in the haplotype or map file).
popsel	code of the population considered (relevant for fastPHASE output which can contain haplotypes from various populations).
recode.allele	<i>*Deprecated*</i> . logical. FALSE by default. TRUE forces parameter allele_coding to "map", FALSE leaves it unchanged.
allele_coding	the allele coding provided by the user. Either "12" (default), "01", "map" or "none". The option is irrelevant for vcf files and ms output.
haplotype.in.columns	logical. If TRUE, phased input haplotypes are assumed to be in columns (as produced by the SHAPEIT2 program (O'Connell et al., 2014)).
remove_multiple_markers	logical. If FALSE (default), conversion stops, if multiple markers with the same chromosomal position are encountered. If TRUE, duplicated markers are removed (all but the first marker with identical positions).
polarize_vcf	logical. Only of relevance for vcf files. If TRUE (default), tries to polarize variants with help of the AA entry in the INFO field. Unpolarized alleles are discarded. If FALSE, allele coding of vcf file is used unchanged as internal coding.
capitalize_AA	logical. Only of relevance for vcf files with ancestral allele information. Low confidence ancestral alleles are usually coded by lower-case letters. If TRUE

	(default), these are changed to upper case before the alleles of the sample are matched for polarization.
position_scaling_factor	intended primarily for output of ms where positions lie in the interval [0,1]. These can be rescaled to sizes of typical markers in real data.
verbose	logical. If TRUE (default), report verbose progress.

Details

Five haplotype input formats are supported:

- a "standard format" with haplotypes in rows and markers in columns (with no header, but a haplotype ID/name in the first column).
- a "transposed format" similar to the one produced by the phasing program SHAPEIT2 (O'Connell et al., 2014) in which haplotypes are in columns and markers in rows (with neither header nor marker IDs nor haplotype IDs).
- output files from the fastPHASE program (Sheet and Stephens, 2006). If haplotypes from several different population were phased simultaneously (-u fastPHASE option was used), it is necessary to specify the population of interest by parameter popse1 (if this parameter is not or wrongly set, the error message will provide a list of the population numbers contained in the file).
- files in variant call format (vcf). No mapfile is needed in this case. If the file contains several chromosomes, it is necessary to choose one by parameter chr.name.
- output of the simulation program 'ms'. No mapfile is needed in this case. If the file contains several 'runs', a specific number has to be specified by the parameter chr.name.

The "transposed format" has to be explicitly set while the other formats are recognized automatically.

The map file contains marker information in three, or, if it is used for polarization (see below), five columns:

- marker name/id
- chromosome
- position (physical or genetic)
- ancestral allele encoding
- derived allele encoding

The markers must be in the same order as in the haplotype file. If several chromosomes are represented in the map file, it is necessary to choose that which corresponds to the haplotype file by parameter chr.name.

Haplotypes can be given either with alleles already coded as numbers (in two possible ways) or with the actual alleles (e.g. nucleotides) which can be translated into numbers either using the fourth and fifth column of the map file or by their alpha-numeric order. Correspondingly, the parameter allele_coding has to be set to either "12", "01", "map" or "none":

- "12": 0 represents missing values, 1 the ancestral allele and 2 (or higher integers) derived allele(s).

- "01": NA or '.' (a point) represent missing values, 0 the ancestral and 1 (or higher integers) derived allele(s).
- "map": for each marker, the fourth column of the map file defines the ancestral allele and the fifth column derived alleles. In case of multiple derived alleles, they must be separated by commas without space. Alleles in the haplotype file which do not appear in neither of the two columns of the map file are regarded as missing values (NA).
- "none": NA or '.' (a point) represent missing values, otherwise for each marker the allele that comes first in alpha-numeric order is coded by 0, the next by 1, etc. Evidently, this coding does not convey any information about allele status as ancestral or derived, hence the alleles cannot be regarded as polarized.

The information of allelic ancestry is exploited only in the frequency-bin-wise standardization of iHS (see [ihh2ihs](#)). However, although ancestry status does not figure in the formulas of the cross populations statistics Rsb and XP-EHH, their values do depend on the assigned status.

The arguments `min_perc_genos.hap`, `min_perc_genos.mrk` and `min_maf` are evaluated in this order.

Value

The returned value is an object of [haplohh-class](#).

References

Scheet P, Stephens M (2006) A fast and flexible statistical model for large-scale population genotype data: applications to inferring missing genotypes and haplotypic phase. *Am J Hum Genet*, **78**, 629-644.

O'Connell J, Gurdasani D, Delaneau O, et al (2014) A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genet*, **10**, e1004234.

Examples

```
#copy example files into the current working directory.
make.example.files()
#create object using a haplotype file in "standard format"
hap <- data2haplohh(hap_file = "bta12_cgu.hap",
                   map_file = "map.inp",
                   chr.name = 12,
                   allele_coding = "map")
#create object using fastPHASE output
hap <- data2haplohh(hap_file = "bta12_hapguess_switch.out",
                   map_file = "map.inp",
                   chr.name = 12,
                   popsel = 7,
                   allele_coding = "map")
#clean up demo files
remove.example.files()
```

distribplot *Plot distribution of standardized iHS, Rsb or XP-EHH values*

Description

Plot the observed distribution of standardized iHS, Rsb or XP-EHH values together with the standard Gaussian distribution.

Usage

```
distribplot(data, lty = 1, lwd = 1.5, col = c("blue", "red"),
  main = "Genome-wide distribution", xlab = "", qqplot = FALSE,
  pch = 20, ...)
```

Arguments

data	a vector of iHS, Rsb or XPEHH values.
lty	line type.
lwd	line width.
col	a vector describing the colors of the observed and Gaussian distribution, respectively.
main	an overall title for the plot.
xlab	a title for the x axis.
qqplot	logical. If TRUE a qq-plot is drawn instead of the distribution density curve.
pch	point character for qqplot (see points).
...	further arguments passed to plot.default .

Value

The function returns a plot.

See Also

[ihh2ihs](#), [ines2rsb](#), [ies2xpehh](#), [manhattanplot](#).

Examples

```
library(rehh.data)
#results from a genome scan (44,057 SNPs) see ?wgscan.cgu for details
data(wgscan.cgu)
#extract vector with iHS values from data frame
IHS <- ihh2ihs(wgscan.cgu)$ihs[["IHS"]]
distribplot(IHS, main = "iHS (CGU population)")
distribplot(IHS, main = "iHS (CGU population)", qqplot = TRUE)
```

extract_regions	<i>Extract regions from a scan</i>
-----------------	------------------------------------

Description

Extract regions from a scan data frame.

Usage

```
extract_regions(scan, regions, right = TRUE)
```

Arguments

scan	A data frame with chromosomal positions like obtained by scan_hh , ihh2ihs , ines2rsb or ies2xpehh .
regions	A data frame with genomic regions like the output of calc_candidate_regions .
right	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.

Value

A subset of data frame scan, retaining only positions belonging to the regions specified in data frame regions.

Examples

```
library(rehh.data)
data(wgscan.cgu)
regions <- data.frame(CHR = 12, START = 2.88e+7, END = 2.92e+7)
extract_regions(wgscan.cgu, regions)
```

freqbinplot	<i>Plot of unstandardized iHS within frequency bins</i>
-------------	---

Description

Plot of unstandardized iHS within frequency bins.

Usage

```
freqbinplot(x, spectrum = FALSE, main = NA,
  xlab = "Derived allele frequency", ylab = NA, xlim = c(0, 1),
  ylim = NULL, pch = 20, ...)
```

Arguments

x	data (output of function <code>ihh2ihs</code>)
spectrum	logical. If TRUE, plot frequency spectrum instead of iHS.
main	an overall title for the plot.
xlab	a title for the x axis.
ylab	a title for the y axis.
xlim	the x coordinate range of the plot.
ylim	the y coordinate range of the plot.
pch	plotting 'character' see <code>points</code> .
...	further arguments to be passed to <code>plot</code> resp. <code>points</code> .

Details

The plot shows the mean and the quantiles calculated by function `ihh2ihs` for the unstandardized iHS in each frequency bin. Note that the standardization of iHS is performed bin-wise in order to reduce the frequency-dependence of iHS values (expected under neutrality). An implicit assumption of this procedure is that each bin is dominated by neutral markers.

See Also

[ihh2ihs](#)

Examples

```
library(rehh.data)
data(wgscan.cgu)
#results from a genome scan (44,057 SNPs)
#see ?wgscan.eut and ?wgscan.cgu for details
wgscan.cgu.ihs <- ihh2ihs(wgscan.cgu)
freqbinplot(wgscan.cgu.ihs)
```

ftree-class	<i>An S4 class to represent a furcation tree on one side of one allele of a focal marker</i>
-------------	--

Description

An S4 class to represent a furcation tree on one side of one allele of a focal marker

Details

A furcation structure consists of two trees ("left" and "right") for each allele of a focal marker. If there are only bi-allelic markers and no missing values, the trees are bifurcating.

Missing values are treated similarly to an extra allele in so far as they cause a furcation. However, the resulting daughter node is marked accordingly and the chromosomes excluded from further calculations. If all chromosomes of a parent node have missing values, the "furcation" is degenerated and yields a single daughter node.

Note that a tree with n leaves can have at most $2n-1$ nodes.

In a furcation tree, the leaves do not necessarily represent single chromosomes, either due to multiple missing data or because the first/last marker was reached before all extended haplotypes were distinct.

Slots

`node_parent` a vector, representing the tree structure. Each node (number) is assigned its parent node (number).

`node_pos` a vector, assigning to each node (number) its position in the chromosome, i.e. at which marker position the furcation occurred.

`node_with_missing_data` a vector of type logical. Pseudo-furcations arise due to missing data at a marker. The daughter node (number) is marked accordingly.

`label_parent` a vector, that attaches an "extra leave", representing the haplotype number (defined by the order in the haplotype data file) to leaves of the tree. This is necessary because in general not all leaves of the original tree represent a single haplotype/chromosome.

<code>furcation-class</code>	<i>An S4 class representing the complete furcation pattern around a focal marker.</i>
------------------------------	---

Description

An S4 class representing the complete furcation pattern around a focal marker.

Slots

`.Data` a list containing for each allele an object of `allelefurcation-class`.

`mrk.name` the name/identifier of the focal marker.

`position` the chromosomal position of the focal marker.

`xlim` the range of marker positions.

`nhap` the number of haplotypes in the sample.

See Also

[calc_furcation](#)

Examples

```

# copy example files into working directory
make.example.files()
# read first example file
hh <- data2haplohh("example1.vcf")
# remove example files
remove.example.files()
# calculate furcation structure around marker "rs6"
f <- calc_furcation(hh, mrk = "rs6")
# extract left side tree of ancestral allele (which is coded by '0')
f[['0']]@left
# the tree consists of seven nodes, '1' being the root node
# nodes 2 and 3 have the root node as parent, etc.
# the first chromosome is attached as a label node to node 7, etc.
# For comparison, a plot of the complete furcation structure:
plot(f)

```

haplen-class

class for haplotype length

Description

class for haplotype length

haplohh-class

Class "haplohh"

Description

An object of this class contains the information needed for computation of EHH based statistics.

Usage

```

## S4 method for signature 'haplohh'
chr.name(x)

## S4 method for signature 'haplohh'
positions(x)

## S4 method for signature 'haplohh'
haplo(x)

## S4 method for signature 'haplohh'
nmrk(x)

## S4 method for signature 'haplohh'

```

```
mrk.names(x)

## S4 method for signature 'haplohh'
nhap(x)

## S4 method for signature 'haplohh'
hap.names(x)
```

Arguments

x an object of this class.

Details

This class is the basis for all calculations done by this package. Note that the matrix in slot `haplo` has to be of type `integer`, not `numeric`. Objects built by versions of `rehh` up to 2.0.4 coded this matrix as `numeric` and used a different coding scheme. They can be converted e.g. by `haplohh <- update_haplohh(old_haplohh)` in order to be used with the present version.

Slots

`chr.name` name of the chromosome/scaffold to which the markers belong.
`positions` vector of type `numeric` containing the marker positions within the chromosome.
`haplo` matrix of type `integer` containing haplotypes in rows and markers in columns.

See Also

[data2haplohh](#), [update_haplohh](#)

Examples

```
showClass("haplohh")
```

`haplohh_cgu_bta12` *Example of an haplohh object*

Description

The object contains haplotype data for 140 cattle individuals (280 haplotypes) belonging to the Creole breed from Guadeloupe (CGU) and 1424 markers (mapping to chromosome BTA12).

Usage

```
data(haplohh_cgu_bta12)
```

Format

An object of [haplohh-class](#).

References

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.

See Also

[data2haplohh](#)

ies2xpehh	<i>Compute XP-EHH</i>
-----------	-----------------------

Description

Compute XP-EHH (standardized ratio of iES of two populations).

Usage

```
ies2xpehh(scan_pop1, scan_pop2, popname1 = NA, popname2 = NA,
          standardize = TRUE, include_freq = FALSE, p.side = NA,
          p.adjust.method = "none", verbose = TRUE)
```

Arguments

scan_pop1	a data frame with markers in rows and columns with chromosome name, position of the marker, frequency of the ancestral allele and iES as obtained by scan_hh on the first population.
scan_pop2	a data frame with markers in rows and columns with chromosome name, position of the marker, frequency of the ancestral allele and iES as obtained by scan_hh on the second population.
popname1	short ID/name of the first population; to be added to an output column name.
popname2	short ID/name of the second population; to be added to an output column name.
standardize	logical. If TRUE (default), then standardize XP-EHH, else report unstandardized XP-EHH.
include_freq	logical. If TRUE include columns with allele frequencies into result.
p.side	side to which refers the p-value. Default NA, meaning two-sided. Can be set to "left" or "right".
p.adjust.method	method passed to function p.adjust to correct the p-value for multiple testing. Default "none".
verbose	logical. If TRUE (default), report number of markers of the two source data frames and result data frame.

Details

Log ratio of iES (population 1 over population 2) computed as described in Sabeti et al. (2007). Note that the two data frames are merged on the basis of chromosome and position. Marker names are kept, if they are identical and unique in both data frames.

Since the standardized XP-EHH values follow, if markers evolve predominantly neutrally, approximately a standard Gaussian distribution, it is practical to assign to the values a p-value relative to the null-hypothesis of neutral evolution. The parameter `p.side` determines if the p-value is assigned to both sides of the distribution or to one side of interest.

Value

The returned value is a data frame with markers in rows and columns for chromosome name, marker position, XP-EHH and, if standardized, p-value in a negative log10 scale. Optionally, allele frequencies are included.

References

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.

Sabeti, P.C. et al. (2007). Genome-wide detection and characterization of positive selection in human populations. *Nature*, **449**, 913-918.

See Also

[scan_hh](#), [distribplot](#), [manhattanplot](#)

Examples

```
library(rehh.data)
data(wgscan.cgu) ; data(wgscan.eut)
## results from a genome scan (44,057 SNPs)
##see ?wgscan.eut and ?wgscan.cgu for details
wgscan.xpehh <- ies2xpehh(wgscan.cgu, wgscan.eut, "CGU", "EUT")
```

ihh2ihs

Compute iHS

Description

Compute iHS (standardized ratio of iHH values of two alleles).

Usage

```
ihh2ihs(scan, freqbin = 0.025, min_maf = 0.05, min_nhaplo = NA,
        standardize = TRUE, include_freq = FALSE, right = FALSE,
        alpha = 0.05, p.side = NA, p.adjust.method = "none",
        verbose = TRUE)
```


Arguments

<code>scan</code>	a data frame with chromosome name, marker position, frequency of ancestral (resp. major) allele, frequency of derived (resp. minor) allele, and iHH for both alleles, as obtained from function <code>scan_hh</code> .
<code>freqbin</code>	size of the bins to standardize $\log(iHH_A/iHH_D)$. Markers are binned with respect to the derived allele frequency at the focal marker. The bins are built from <code>min_maf</code> to $1 - \text{min_maf}$ in steps of size <code>freqbin</code> . If set to 0, standardization is performed considering each observed frequency as a discrete frequency class (useful in case of a large number of markers and few different haplotypes). If set to an integer of 1 or greater, a corresponding number of equally sized bins are created.
<code>min_maf</code>	focal markers with a MAF (Minor Allele Frequency) lower than or equal to <code>min_maf</code> are discarded from the analysis (default 0.05).
<code>min_nhaplo</code>	focal markers with least one of the two compared alleles carried by fewer than <code>min_nhaplo</code> haplotypes, are discarded (default NA).
<code>standardize</code>	logical. If TRUE (default), then standardize iHS, else report unstandardized iHS.
<code>include_freq</code>	logical. If TRUE include columns with allele frequencies into result.
<code>right</code>	logical. If TRUE the bin intervals are closed on the right (and open on the left).
<code>alpha</code>	calculate quantiles $\alpha/2$ and $(1-\alpha/2)$ for unstandardized binned iHS.
<code>p.side</code>	side to which refers the p-value. Default NA, meaning two-sided. Can be set to "left" or "right".
<code>p.adjust.method</code>	method passed to function <code>p.adjust</code> to correct the p-value for multiple testing. Default "none".
<code>verbose</code>	logical. If TRUE (default), report number of markers of the source data frame and result data frame.

Details

Computes log ratio of iHH of two focal alleles as described in Voight et al. (2006). The standardization is performed within each bins separately because of the frequency-dependence of expected iHS values under neutrality. An implicit assumption of this approach is that each bin is dominated by neutral markers.

Since the standardized iHS values follow, if markers evolve predominantly neutrally, approximately a standard Gaussian distribution, it is practical to assign to the values a p-value relative to the null-hypothesis of neutral evolution. The parameter `p.side` determines if the p-value is assigned to both sides of the distribution or to one side of interest.

Value

The returned value is a list containing two elements

ihs a data frame with markers in rows and the columns for chromosome name, marker position, iHS and, if standardized, p-value in a negative log10 scale. Optionally, allele frequencies are included.

frequency.class a data frame with bins in rows and columns for the number of markers, mean uniHS, standard deviation uniHS, lower quantile uniHS, upper quantile uniHS.

References

- Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.
- Voight, B.F. and Kudravalli, S. and Wen, X. and Pritchard, J.K. (2006). A map of recent positive selection in the human genome. *Plos Biology*, **4**, e72.

See Also

[scan_hh](#), [distribplot](#), [freqbinplot](#), [manhattanplot](#)

Examples

```
library(rehh.data)
data(wgscan.cgu)
#results from a genome scan (44,057 SNPs)
#see ?wgscan.eut and ?wgscan.cgu for details
wgscan.cgu.ihs <- ihs2ihs(wgscan.cgu)
```

ines2rsb

Compute Rsb

Description

Compute Rsb (standardized ratio of inES of two populations).

Usage

```
ines2rsb(scan_pop1, scan_pop2, popname1 = NA, popname2 = NA,
         standardize = TRUE, include_freq = FALSE, p.side = NA,
         p.adjust.method = "none", verbose = TRUE)
```

Arguments

- | | |
|--------------|---|
| scan_pop1 | a data frame with markers in rows and columns with chromosome name, position of the marker, frequency of the ancestral allele and inES as obtained by scan_hh on the first population. |
| scan_pop2 | a data frame with markers in rows and columns with chromosome name, position of the marker, frequency of the ancestral allele and inES as obtained by scan_hh on the second population. |
| popname1 | short ID/name of the first population; to be added to an output column name. |
| popname2 | short ID/name of the second population; to be added to an output column name. |
| standardize | logical. If TRUE (default), then standardize Rsb, else report unstandardized Rsb. |
| include_freq | logical. If TRUE include columns with allele frequencies into result. |
| p.side | side to which refers the p-value. Default NA, meaning two-sided. Can be set to "left" or "right". |

p.adjust.method	method passed to function p.adjust to correct the p-value for multiple testing. Default "none".
verbose	logical. If TRUE (default), report number of markers of the two source data frames and result data frame.

Details

Log ratio of inES (population 1 over population 2) computed as described in Tang et al. (2007). Note that the two data frames are merged on the basis of chromosome and position. Marker names are kept, if they are identical and unique in both data frames.

Since the standardized Rsb values follow, if markers evolve predominantly neutrally, approximately a standard Gaussian distribution, it is practical to assign to the values a p-value relative to the null-hypothesis of neutral evolution. The parameter `p.side` determines if the p-value is assigned to both sides of the distribution or to one side of interest.

Value

The returned value is a data frame with markers in rows and columns for chromosome name, marker position, Rsb and, if standardized, p-value in a negative log10 scale. Optionally, allele frequencies are included.

References

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.

Tang, K. and Thornton, K.R. and Stoneking, M. (2007). A New Approach for Using Genome Scans to Detect Recent Positive Selection in the Human Genome. *Plos Biology*, **7**, e171.

See Also

[scan_hh](#), [distribplot](#), [manhattanplot](#)

Examples

```
library(rehh.data)
data(wgscan.cgu) ; data(wgscan.eut)
## results from a genome scan (44,057 SNPs)
##see ?wgscan.eut and ?wgscan.cgu for details
wgscan.rsb <- ines2rsb(wgscan.cgu, wgscan.eut, "CGU", "EUT")
```

make.example.files *Copy example input files into current working directory*

Description

This function copies the following example files to the current working directory:

- example1.hap "example 1" haplotype file in "standard format"
- example1.map "example 1" marker information file
- example1.vcf "example 1" as vcf file
- example2.hap "example 2" haplotype file in "standard format"
- example2.map "example 2" marker information file
- example2.vcf "example 2" as vcf file
- ms.out output from a small simulation by the program 'ms'
- bta12_cgu.hap an haplotype file in "standard format"
- bta12_cgu.thap an haplotype file in "transposed format"
- bta12_hapguess_switch.out an haplotype file in fastphase output format
- map.inp a marker information file for all bta_cgu markers

Example 1 was used in (Gautier 2017) to explain the various EHH derived statistics calculated by this package. Example 2 is an extension containing multi-allelic markers and missing values.

The bta12 files contain data for 280 haplotypes, originating from 140 individuals belonging to the Creole cattle breed from Guadeloupe, at 1.424 markers mapping to bovine chromosome 12 (BTA12) (Gautier 2011).

Usage

```
make.example.files()
```

References

Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.

Gautier, M., Klassmann, A. and Vitalis, R. (2017). rehh 2.0: a reimplement of the R package rehh to detect positive selection from haplotype structure. *Molecular Ecology Resources*, **17**, 78-90.

See Also

[data2haplohh](#), [remove.example.files](#)

manhattanplot *Manhattan plot of iHS, XP-EHH or Rsb over a genome.*

Description

Manhattanplot of iHS, XP-EHH or Rsb over a genome.

Usage

```
manhattanplot(data, pval = FALSE, threshold = c(-2, 2),
  chr.name = NA, cr = NULL, cr.col = "gray", cr.opacity = 0.5,
  cr.lab.cex = 0.6, cr.lab.offset = 0, cr.lab.pos = "top",
  main = NA, xlim = NULL, cex = 0.5, las = 1, pch = 20, ...)
```

Arguments

data	output of either ihh2ihs , ies2xpehh or ines2rsb .
pval	logical. If TRUE, the p-value is plotted, otherwise the score itself.
threshold	a horizontal line is added at the corresponding value(s), for instance to represent a significance threshold. A single value (upper or lower threshold) or two values (upper and lower) can be specified.
chr.name	if NA (default), all chromosomes are plotted, otherwise only those specified.
cr	highlight "candidate regions" specified by a data.frame with three columns: the first containing the chromosome, the other begin and end of the region as obtained by the function calc_candidate_regions .
cr.col	the color for highlighting
cr.opacity	a value between 0 (invisible) and 1 (opaque).
cr.lab.cex	text size of candidate region labels.
cr.lab.offset	offset of candidate region labels.
cr.lab.pos	if "top" (default) or "bottom", candidate regions are labeled by numbers; to turn off, use "none"
main	main title of the plot.
xlim	set x coordinate range of the plot. Ignored, if more than one chromosome is depicted.
cex	size of the points representing markers in the plot(s) (see par).
las	orientation of axis labels (see par).
pch	type of the points representing markers in the plot(s) (see points).
...	further arguments to be passed to plot.default .

Details

The color of chromosomes is taken from the "Graphics Palette", see [palette](#).

Value

The function returns a plot.

See Also

[ihh2ihs](#), [ies2xpehh](#), [ines2rsb](#), [calc_candidate_regions](#).

Examples

```
library(rehh.data)
data(wgscan.cgu)
## results from a genome scan (44,057 SNPs)
## see ?wgscan.eut and ?wgscan.cgu for details
wgscan.ihs <- ihh2ihs(wgscan.cgu)
manhattanplot(wgscan.ihs)
```

plot.ehh

Plot EHH around a focal marker

Description

Plot curve of EHH values around a focal marker.

Usage

```
## S3 method for class 'ehh'
plot(x, ylim = c(0, 1), type = "l",
     main = paste0("EHH around '", x$mrk.name, "'"), xlab = "Position",
     ylab = "Extended Haplotype Homozygosity", col = c("blue", "red",
     "violet", "orange"), mrk.col = "gray", bty = "n", lty = 1,
     legend = NA, legend.xy.coords = "automatic", ...)
```

Arguments

x	data (output of calc_ehh).
ylim	the y limits of the plot
type	plot type (see matplot).
main	title for the plot (default NA, i.e. none).
xlab	title for the x-axis.
ylab	title for the y-axis.
col	color for the ancestral and derived alleles (respectively) curves.
mrk.col	color of the vertical line at the focal marker position.
bty	box type around plot (see par).
lty	line type for the ancestral and derived allele EHH (respectively) curves.

legend legend text.
 legend.xy.coords if "automatic" (default) places legend either top left or top right; if "none", no legend is drawn; otherwise the argument is passed to [legend](#).
 ... further arguments to be passed to function [matplot](#).

See Also

[data2haplohh](#), [calc_ehh](#), [plot.ehhs](#), [scan_hh](#).

Examples

```

#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#computing EHH statistics for the marker "F1205400"
#which displays a strong signal of selection
ehh <- calc_ehh(haplohh_cgu_bta12, mrk = "F1205400")
plot(ehh)

```

plot.ehhs

Plot EHHS around a focal marker

Description

Plot curve of EHHS values around a focal marker.

Usage

```

## S3 method for class 'ehhs'
plot(x, nehhs = FALSE, ylim = c(0, 1), type = "l",
     main = paste0("EHHS around ", x$mrk.name, ""), xlab = "Position",
     ylab = "Extended Haplotype Homozygosity per Site", bty = "n",
     mrk.col = "gray", ...)

```

Arguments

x data (output of [calc_ehhs](#)).
 nehhs logical. If TRUE, plot normalized EHHS.
 ylim the y limits of the plot
 type plot type (see [matplot](#)).
 main title for the plot (default NA, i.e. none).
 xlab title for the x-axis.
 ylab title for the y-axis.
 bty box type around plot (see [par](#)).
 mrk.col color of the vertical line at the focal marker position.
 ... further arguments to be passed to function [plot](#).

See Also

[data2haplohh](#), [plot.ehh](#), [calc_ehhs](#), [scan_hh](#).

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#computing EHHS statistics for the marker "F1205400"
#which displays a strong signal of selection
ehhs <- calc_ehhs(haplohh_cgu_bta12, mrk = "F1205400")
plot(ehhs)
```

plot.furcation

Plots furcation trees around a focal marker

Description

Plots furcation trees around a focal marker

Usage

```
## S3 method for class 'furcation'
plot(x, allele = NA,
     main = paste0("Haplotype furcations around '", x@mrk.name, "'"),
     xlab = "Position", xlim = NULL, col = c("blue", "red", "violet",
     "orange"), mrk.col = "gray", lwd = 0.1, hap.names = NULL,
     bty = "n", cex.lab = 1, offset.lab = 0.5, legend = NA,
     legend.xy.coords = "automatic", ...)
```

Arguments

x	an object of class furcation (see calc_furcation).
allele	If NA (default), furcation trees for all alleles of the focal marker are plotted, otherwise for the specified alleles. Alleles must be specified by their internal coding, i.e. '0' for ancestral resp. major allele, etc.
main	title of the plot.
xlab	title of the x-axis.
xlim	x coordinate ranges. If NULL, maximal range of branch lengths are taken.
col	color for each allele (as coded internally).
mrk.col	color of the vertical line at the focal marker position.
lwd	controls the relative width of the diagram lines on the plot (default 0.1).
hap.names	a vector containing names of chromosomes.
bty	type of box around plots (see par).

cex.lab relative size of labels.
 offset.lab offset of labels.
 legend legend text.
 legend.xy.coords
 if "automatic" (default) places legend either top left or top right; if "none", no
 legend is drawn; otherwise argument is passed to [legend](#).
 ... other arguments to be passed to [plot.default](#).

See Also

[plot.haplen](#).

Examples

```

#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#plotting furcation diagram for both ancestral and derived allele
#from the marker "F1205400"
#which display a strong signal of selection
f <- calc_furcation(haplohh_cgu_bta12, mrk = "F1205400")
plot(f)
plot(f, xlim = c(2e+07,3.5e+07))
plot(f, xlim = c(2.7e+07,3.1e+07))
plot(f, xlim = c(2.7e+07,3.1e+07), hap.names = hap.names(haplohh_cgu_bta12), cex.lab=0.3)

```

plot.haplen

Plot the length of extended haplotypes around a focal marker

Description

Plot the length of extended haplotype around a focal marker.

Usage

```

## S3 method for class 'haplen'
plot(x, allele = NA, group_by_allele = TRUE,
     main = paste0("Haplotype length around '", x$mrk.name, "'"),
     xlab = "Position", xlim = NULL, col = c("blue", "red", "violet",
     "orange"), mrk.col = "gray", lwd = 1, hap.names = NULL,
     pos.lab = "left", offset.lab = 0.5, cex.lab = 1, bty = "n",
     legend = NA, legend.xy.coords = "automatic", ...)

```

Arguments

x	an object of class haplen generated by calc_haplen .
allele	if NA (default), haplotypes of all alleles are plotted, otherwise for the specified alleles. Alleles must be specified by their internal coding, i.e. '0' for ancestral resp. major allele, etc.
group_by_allele	logical. If TRUE (default), group chromosomes by their allele at the focal marker. Otherwise haplotypes are drawn by their order in the input file.
main	main title of the plot. By default, the name of the focal marker.
xlab	title of the x-axis.
xlim	x coordinate ranges. If NULL, maximal range of haplotype length are taken.
col	color for each allele (as coded internally).
mrk.col	color of the vertical line at the focal marker position.
lwd	line width.
hap.names	a vector containing the names of chromosomes.
pos.lab	position of haplotype labels. Either "left", "right" or "both".
offset.lab	offset of labels.
cex.lab	relative letter size of labels.
bty	type of box around plot (see par).
legend	legend text.
legend.xy.coords	if "automatic" (default) places legend either top left or top right; if "none", no legend is drawn; otherwise argument is passed to legend .
...	other parameters to be passed to plot.default .

See Also

[calc_haplen](#), [plot.furcation](#).

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#plotting length of extended haplotypes for both ancestral and derived allele
#of the marker "F1205400"
#which displays a strong signal of selection
f <- calc_furcation(haplohh_cgu_bta12, mrk = "F1205400")
h <- calc_haplen(f)
plot(h)
plot(h, hap.names = hap.names(haplohh_cgu_bta12), cex.lab = 0.3)
```

`remove.example.files` *Remove example files from current working directory.*

Description

Remove example files from current working directory.

Usage

```
remove.example.files()
```

Details

Removes the files created by `make.example.files()`. No error is thrown, if files do not exist.

See Also

[make.example.files](#)

`scan_hh` *Compute iHH, iES and inES over a whole chromosome*

Description

Compute integrated EHH (iHH), integrated EHHS (iES) and integrated normalized EHHS (inES) for all markers of a chromosome (or linkage group).

Usage

```
scan_hh(haplohh, limhaplo = 2, limehh = 0.05, limehhs = 0.05,
        phased = TRUE, polarized = TRUE, scalegap = NA, maxgap = NA,
        discard_integration_at_border = TRUE, lower_ehh_y_bound = limehh,
        lower_ehhs_y_bound = limehhs, threads = 1)
```

Arguments

<code>haplohh</code>	an object of class <code>haplohh</code> (see data2haplohh)
<code>limhaplo</code>	if there are less than <code>limhaplo</code> chromosomes that can be used for the calculation of EHH(S), the calculation is stopped. The option is intended for the case of missing data, which leads to the successive exclusion of haplotypes: the further away from the focal marker the less haplotypes contribute to EHH(S).
<code>limehh</code>	limit at which EHH stops to be evaluated.
<code>limehhs</code>	limit at which EHHS stops to be evaluated.

phased	logical. If TRUE (default) chromosomes are expected to be phased. If FALSE, the haplotype data is assumed to consist of pairwise ordered chromosomes belonging to diploid individuals. EHH(S) is then estimated over individuals which are homozygous at the focal marker.
polarized	logical. TRUE by default. If FALSE, use major and minor allele instead of ancestral and derived. If there are more than two alleles then the minor allele refers to the second-most frequent allele.
scalegap	scale or cap gaps larger than the specified size to the specified size (default=NA, i.e. no scaling).
maxgap	maximum allowed gap in bp between two markers. If exceeded, further calculation of EHH(S) is stopped at the gap (default=NA, i.e. no limitation).
discard_integration_at_border	logical. If TRUE (default) and computation reaches first or last marker or a gap larger than maxgap, iHH, iES and inES are set to NA.
lower_ehh_y_bound	lower y boundary of the area to be integrated over (default: limehh). Can be set to zero for compatibility with the program hapbin.
lower_ehhs_y_bound	lower y boundary of the area to be integrated (default: limehhs). Can be set to zero for compatibility with the program hapbin.
threads	number of threads to parallelize computation

Details

Integrated EHH (iHH), integrated EHHS (iES) and integrated normalized EHHS (inES) are computed for all markers of the chromosome (or linkage group). This function is several times faster as a procedure calling in turn `calc_ehh` and `calc_ehhs` for all markers. To perform a whole genome-scan this function needs to be called for each chromosome and results concatenated.

Value

The returned value is a dataframe with markers in rows and the following columns

1. chromosome name
2. position in the chromosome
3. sample frequency of the ancestral / major allele
4. sample frequency of the second-most frequent remaining allele
5. number of evaluated haplotypes at the focal marker for the ancestral / major allele
6. number of evaluated haplotypes at the focal marker for the second-most frequent remaining allele
7. iHH of the ancestral / major allele
8. iHH of the second-most frequent remaining allele
9. iES (used by Sabeti et al 2007)
10. inES (used by Tang et al 2007)

Note that while for phased data the number of evaluated haplotypes of an allele corresponds to its frequency in the sample, in case of unphased data the evaluation is restricted to haplotypes of homozygous individuals.

References

- Gautier, M. and Naves, M. (2011). Footprints of selection in the ancestral admixture of a New World Creole cattle breed. *Molecular Ecology*, **20**, 3128-3143.
- Sabeti, P.C. et al. (2002). Detecting recent positive selection in the human genome from haplotype structure. *Nature*, **419**, 832-837.
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- Tang, K. and Thornton, K.R. and Stoneking, M. (2007). A New Approach for Using Genome Scans to Detect Recent Positive Selection in the Human Genome. *Plos Biology*, **7**, e171.
- Voight, B.F. and Kudaravalli, S. and Wen, X. and Pritchard, J.K. (2006). A map of recent positive selection in the human genome. *Plos Biology*, **4**, e72.

See Also

[data2haplohh](#), [calc_ehh](#), [calc_ehhs](#) [ihh2ihs](#), [ines2rsb](#), [ies2xpehh](#)

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
scan <- scan_hh(haplohh_cgu_bta12)
```

subset.haplohh

Subsets object of haplohh-class

Description

Subsets the data of an object of class [haplohh-class](#), meeting certain conditions.

Usage

```
## S3 method for class 'haplohh'
subset(x, select.hap = NULL, select.mrk = NULL,
       min_perc_genom.hap = NA, min_perc_genom.mrk = 100, min_maf = NA,
       verbose = TRUE, ...)
```

Arguments

x	object of class haplohh-class to be subset.
select.hap	expression, indicating haplotypes to select.
select.mrk	expression, indicating markers to select.
min_percgeno.hap	threshold on percentage of missing data for haplotypes (haplotypes with less than min_percgeno.hap percent of markers genotyped are discarded). Default is NA, hence no constraint.
min_percgeno.mrk	threshold on percentage of missing data for markers (markers genotyped on less than min_percgeno.mrk percent of haplotypes are discarded). By default, min_percgeno.mrk=100, hence only fully genotyped markers are retained. This value cannot be set to NA or zero.
min_maf	threshold on the Minor Allele Frequency. Markers having a MAF lower than or equal to minmaf are discarded. In case of multi-allelic markers the second-most frequent allele is referred to as minor allele. Setting this value to zero eliminates monomorphic sites. Default is NA, hence no constraint.
verbose	logical. If TRUE (default), report verbose progress.
...	further arguments are ignored.

See Also

[haplohh-class](#), [data2haplohh](#)

Examples

```
#example haplohh object (280 haplotypes, 1424 SNPs)
#see ?haplohh_cgu_bta12 for details
data(haplohh_cgu_bta12)
#select subset of first 10 haplotypes and first 5 markers
subset(haplohh_cgu_bta12, select.hap = 1:10, select.mrk = 1:5)
```

update_haplohh

Update object of class haplohh

Description

Update object of class [haplohh-class](#) constructed by rehh versions up to version 2.0.4.

Usage

```
update_haplohh(haplohh)
```

Arguments

haplohh an object of an old version of [haplohh-class](#).

Details

This function is intended to update haplohh objects that have been built by rehh versions up to 2.0.4. These objects cannot be used in functions of the current version. The following changes have been made to the class definition: The internal representation of the haplotype matrix followed the encoding

- 0 missing value
- 1 ancestral allele
- 2 derived allele

and has been replaced by a vcf-like encoding:

- NA missing value
- 0 ancestral allele
- 1 derived allele.

Furthermore the slots nsnp, snp.name and nhap have been removed and slot position renamed to positions. An update of an old haplohh object is done as follows:

```
new_haplohh = update_haplohh(old_haplohh).
```

See Also

[haplohh-class](#), [data2haplohh](#).

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