

# Package ‘hsphase’

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**Type** Package

**Title** Phasing, Pedigree Reconstruction, Sire Imputation and  
Recombination Events Identification of Half-sib Families Using  
SNP Data

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**Author** Mohammad Ferdosi <mferdosi@myune.edu.au>, Cedric Gondro <gondroce@msu.edu>

**Maintainer** Mohammad Ferdosi <mferdosi@myune.edu.au>

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**Description** Identification of recombination events, haplotype reconstruction, sire imputation and pedigree reconstruction using half-sib family SNP data.

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hsphase-package	<i>Phasing, Pedigree Reconstruction, Sire Imputation and Recombination Events Identification for Half-sib Families</i>
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## Description

Identification of recombination events, haplotype reconstruction and sire imputation using half-sib family SNP data.

## Details

Package: hsphase  
 Type: Package  
 Version: 2.0.1  
 Date: 2014-6-17  
 License: GPL 3

### Main Functions:

[bmh](#): Block partitioning  
[ssp](#): Sire inference  
[ai](#): Phasing  
[imageplot](#): Image plot of the block structure  
[rpoh](#): Reconstruct pedigree based on opposing homozygote

### Auxiliary Functions

[hss](#): Half-sib family splitter  
[cs](#): Chromosome splitter

`para`: Parallel data analysis

*Note*: These functions can be used to analyse large datasets.

### Author(s)

Mohammad H. Ferdosi <mferdosi@une.edu.au>, Cedric Gondro <cgondro2@une.edu.au> Maintainer: Mohammad H. Ferdosi <mferdosi@myune.edu.au>

### References

Ferdosi, M. H., Kinghorn, B. P., van der Werf, J. H., & Gondro, C (2013). Effect of genotype and pedigree error on detection of recombination events, sire imputation and haplotype inference using the hspbase algorithm. In Proc. Assoc. Advmt. Anim. Breed. Genet (Vol. 20, pp. 546-549). AAABG; Napier, New Zealand.

Ferdosi, M. H., Kinghorn, B. P., van der Werf, J. H., & Gondro, C. (2014). Detection of recombination events, haplotype reconstruction and imputation of sires using half-sib SNP genotypes. Genetics, selection, evolution: GSE, 46(1), 11.

Ferdosi, M. H., Kinghorn, B. P., van der Werf, J. H., Lee, S. H., & Gondro, C. (2014). hspbase: an R package for pedigree reconstruction, detection of recombination events, phasing and imputation of half-sib family groups. BMC Bioinformatics, 15(1), 172.

Ferdosi, M. H., & Boerner, V. (2014). A fast method for evaluating opposing homozygosity in large SNP data sets. Livestock Science.

### Examples

```
genotype <- matrix(c(
  0,0,0,0,1,2,2,2,0,0,2,0,0,0,
  2,2,2,2,1,0,0,0,2,2,2,2,2,2,
  2,2,2,2,1,2,2,2,0,0,2,2,2,2,
  2,2,2,2,0,0,0,0,2,2,2,2,2,2,
  0,0,0,0,0,2,2,2,2,2,2,0,0,0), ncol = 14, byrow = TRUE)
ssp(bmh(genotype), genotype)
aio(genotype)
imageplot(bmh(genotype), title = "ImagePlot example")
rplot(genotype, c(1:14))
```

### Description

Phasing of a half-sib family group.

**Usage**

```
aio(genotypeMatrix, bmh_forwardVectorSize = 30, bmh_excludeFP = TRUE,
    bmh_nsap = 3, output = "phase")
```

**Arguments**

genotypeMatrix	matrix half-sib genotypes (one half-sib per row, with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 respectively for AA, AB and BB. Use 9 for missing data)
bmh_forwardVectorSize	integer number of heterozygous sites used to validate recombination events or check for genotyping errors
bmh_excludeFP	logical excludes SNPs that may cause heterozygous sites in the sire due to genotyping errors or map errors
bmh_nsap	integer number of SNP per block to validate recombinations
output	character if equal to the phase the 'aio' will only return the phasing results

**Details**

This function calls the [bmh](#), [ssp](#) and [phf](#) functions.

**Value**

Returns a list of matrices. The first element (phasedHalfSibs) is a matrix with two rows (phased haplotypes) per individual (first paternal and second maternal). Data in format 0 (A), 1 (B) and 9 (unphased or missing). The second (sireHaplotype) and third (blockStructure) elements are the same as the output of [ssp](#) and [bmh](#).

**Note**

Only this function needs to be called to phase a half-sib family. The genotype's matrix must contain individuals from only one half-sib family and one ordered chromosome.

**See Also**

[bmh](#), [ssp](#) and [phf](#)

**Examples**

```
genotype <- matrix(c(      # Define a Half-sib Genotype Matrix
  2,1,0,                  # Individual 1
  2,0,0,                  # Individual 2
  0,0,2,                  # Individual 3
), byrow = TRUE, ncol = 3) # There are 3 individuals with three SNPs

aio(genotype)             # The genotypes must include only one half-sib family and one chromosome
```

---

**bmh** *Block Partitioning*

---

**Description**

Identifies the block structure (chromosome segments) in the half-sib family that each individual inherited from its sire.

**Usage**

```
bmh(GenotypeMatrix, forwardVectorSize = 30, excludeFP = TRUE, nsap = 3)
```

**Arguments**

**GenotypeMatrix** matrix half-sib genotypes (one half-sib per row, with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 respectively for AA, AB and BB. Use 9 for missing data)

**forwardVectorSize** integer number of heterozygous sites used to validate recombination events or check for genotyping errors (50k -> 30, 700k -> 120)

**excludeFP** logical excludes SNPs that may cause heterozygous sites in the sire due to genotyping errors or map errors

**nsap** integer number of SNP per block to validate recombinations (50k -> 3, 700k -> 10)

**Value**

Returns a matrix of the blocking structure that contains 1s, 2s and 0s. 1s and 2s are the two sire strands. The choice of strand is arbitrary for each chromosome and not consistent across chromosomes. 0s indicate regions of unknown origin.

**Note**

The genotype's matrix must contain individuals from only one half-sib family and one ordered chromosome.

**See Also**

[ssp](#), [phf](#), [aio](#) and [imageplot](#)

**Examples**

```
genotype <- matrix(c(
  0,2,1,1,1,
  2,0,1,2,2,
  2,2,1,0,2,
  2,2,1,1,1,
```

```
0,0,2,1,0), ncol = 5, byrow = TRUE)
(result <- bmh(genotype))
```

---

co *Crossover Detection*

---

### Description

Detect all possible crossover events.

### Usage

```
co(genotypeMatrix)
```

### Arguments

`genotypeMatrix` matrix half-sib genotypes (one half-sib per row, with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 for respectively AA, AB and BB. Use 9 for missing data)

### Value

Returns a matrix with the number of crossover events for each site.

### Examples

```
genotype <- matrix(c(      # Define a Half-sib Genotype Matrix
  2,1,0,                  # Individual 1
  2,0,2,                  # Individual 2
  0,0,2,                  # Individual 3
), byrow = TRUE, ncol = 3) # There are 3 individuals with three SNPs

co(genotype)
```

---

cs *Chromosome Splitter*

---

### Description

This function splits the genotypes list generated by [hss](#) into the different chromosomes based on a map file and orders SNP based on chromosomal position.

### Usage

```
cs(halfsib, mapPath, separator = " ")
```

**Arguments**

halfsib	list list with matrices of half-sib genotypes, one family per list item
mapPath	character path to the map file (column 1 -> SNP names, column 2 -> chromosome name and column 3 -> SNP position in base pairs) or, alternatively, the name of a dataframe with the mapping information (in the same format)
separator	character separator character used in the the map file

**Details**

The map file should include only the chromosomes that will be analyzed. For example, the Y and X chromosomes should be excluded (and others optionally). Names of each element in the list can be used for further categorization. The header must be "Name Chr Position".

**Value**

Returns a list of matrices, the number of elements in this list is the number of half-sib families multiplied by the number of chromosomes.

**Examples**

```
# Please run demo(hsphase)
```

---

genotypes	<i>Example of Genotype Data Set</i>
-----------	-------------------------------------

---

**Description**

An example of genotype matrix for hsphase.

**Usage**

```
data(genotypes)
```

**Format**

a genotype matrix with the following columns and rows:

- Columns: SNPs
- Rows: Animals

---

## hbp *Haplotype Blocks of Phased Data*

---

**Description**

Creates a blocking structure matrix of the half-sib family based on phased data of the sire and half-sib family.

**Usage**

```
hbp(PhasedGenotypeMatrix, PhasedSireGenotype, strand = "auto")
```

**Arguments**

PhasedGenotypeMatrix	matrix haplotypes for a half-sib family (two rows per individual)
PhasedSireGenotype	matrix haplotypes of sire
strand	character method for identification of paternal strand (1 and 2 for strand one and two of the offsprings)

**Value**

Returns a matrix where 3 or 4 stands for the SNP originating in, respectively, strands 1 and 2. 0 indicates that the source strand for the SNP is unknown.

**Note**

The input matrices must only contain individuals from one half-sib family and one ordered chromosome. The `strand` option should be set to "auto" (default value).

**See Also**

[aio](#), [ssp](#)

**Examples**

```
sire <- matrix(c(
  0,0,0,0,0,1,      # Haplotype one of the sire
  0,1,1,1,1,0      # Haplotype two of the sire
), byrow = TRUE, ncol = 6)

haplotypeHalfsib <- matrix(c(
  1,0,1,1,1,1,      # Individual one, haplotype one
  0,1,0,0,0,0,      # Individual one, haplotype two
  0,1,1,0,1,1,      # Individual two, haplotype one
  1,0,0,1,0,0,      # Individual two, haplotype two
), byrow = TRUE, ncol = 6) # 0s and 1s are allele a and b
```



```
hhp(haplotypeHalfsib, sire)
```

---

hh *Heatmap of Half-sibs*

---

## Description

The hh function creates a heatmap of the half-sib families using the matrix of opposing homozygotes.

## Usage

```
hh(oh, inferredPedigree, realPedigree, pedOnly = TRUE)
```

## Arguments

oh                   matrix Opposing homozygotes matrix (output of ohg)  
inferredPedigree    matrix inferred pedigree (output of rpoh)  
realPedigree        matrix original pedigree  
pedOnly             logical Consider only individuals that are exist in the real pedigree

## Value

Returns the heatmap of the matrix of opposing homozygotes with sidebars colour coded by sires from the inferred and original pedigree.

## Author(s)

The fuction uses the colour generated by *getcol* function in the *made4* package (Aedin Culhane).

## See Also

[ohg](#) and [rpoh](#)

## Examples

```
c1h1 <- .simulateHalfsib(numInd = 62, numSNP = 5000)  
c1h2 <- .simulateHalfsib(numInd = 38, numSNP = 5000)  
Genotype <- rbind(c1h1, c1h2)  
oh <- ohg(Genotype) # creating the Opposing Homozygote matrix  
hh(oh)
```

---

hss *Half-sib Family Splitter*

---

**Description**

Splits the dataset into half-sib family groups based on a pedigree.

**Usage**

```
hss(pedigree, genotype, check = TRUE)
```

**Arguments**

pedigree	matrix the pedigree matrix should contain at least two columns, the first column with the half-sib IDs and the second column with the sires IDs
genotype	matrix genotype matrix with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 respectively for AA, AB and BB. Use 9 for missing data
check	logical check the genotype file for the possible errors

**Details**

Only half-sib groups that have more than 3 individuals will be returned.

**Value**

Returns a list of numeric matrices, each matrix is a half-sib family.

**Note**

Pedigree must have at least two columns with sample ids (Column 1) and sire ids (Column 2).

**Examples**

```
# Please run demo(hsphase)
```

---

`imageplot`*Image Plot of Blocking Structure*

---

### Description

Create an imageplot of the blocking structure.

### Usage

```
imageplot(x, title, rv = FALSE, ...)
```

### Arguments

<code>x</code>	matrix blocking structure (output of <code>bmh</code> or <code>hbp</code> functions)
<code>title</code>	character title of imageplot
<code>rv</code>	logical reverse the colour
<code>...</code>	

### Details

White indicates regions of unknown origin, red and blue correspond to the two sire strands.

### Author(s)

This is a modified version of a function written by Chris Seidel.  
[http://www.phaget4.org/R/image\\_matrix.html](http://www.phaget4.org/R/image_matrix.html)

### See Also

[bmh](#) and [aio](#)

### Examples

```
genotype <- matrix(c(
  0,2,1,1,1,
  2,0,1,2,2,
  2,2,1,0,2,
  2,2,1,1,1,
  0,0,2,1,0), ncol = 5, byrow = TRUE) # each row contains the SNP of individuals
imageplot(bmh(genotype))
```

---

impute	<i>Impute of Low Density SNP Marker to High Density (Paternal Strand)</i>
--------	---

---

### Description

Impute the paternal strand from low density to high density utilising high density sire haplotype.

### Usage

```
impute(halfsib_genotype_ld, sire_hd, bmh_forwardVectorSize = 30,  
       bmh_excludeFP = TRUE, bmh_nsap = 3)
```

### Arguments

halfsib_genotype_ld	matrix half-sib genotypes with low density marker (one half-sib per row, with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 respectively for AA, AB and BB. Use 9 for missing data)
sire_hd	matrix haplotype of sire (this parameter can be sequence data or any phased sire - the matrix should have rownames which are the sample IDs and colnames which are the SNP names)
bmh_forwardVectorSize	integer number of heterozygous sites used to validate recombination events or check for genotyping errors
bmh_excludeFP	logical exclude SNPs that may cause heterozygous sites in the sire due to genotyping errors or map errors
bmh_nsap	integer number of SNPs per block

### Value

Return an imputed half-sib matrix.

### See Also

[bmh](#), [ssp](#) and [phf](#)

---

map	<i>Example of Map File</i>
-----	----------------------------

---

**Description**

An example of map for hspbase.

**Usage**

```
data(map)
```

**Format**

a data frame with the following columns:

- Name: SNP name
- Chr: chromosome
- Position: SNP position in base pairs

---

ohd	<i>Opposing Homozygote Detection</i>
-----	--------------------------------------

---

**Description**

Counts the number of opposing homozygotes for each animal that caused a heterozygous site in the sire.

**Usage**

```
ohd(genotypeMatrix, unique_check = FALSE, SNPs = 6000)
```

**Arguments**

genotypeMatrix	matrix half-sib genotypes (one half-sib per row, with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 respectively for AA, AB and BB. Use 9 for missing data)
unique_check	logical check if samples uniquely originate an opposing homozygote at a locus
SNPs	integer number of SNP to use

**Value**

Returns a vector with the number of heterozygous sites that each sample caused.

**Note**

This function can be used to identify pedigree errors; i.e., the outliers.

**Author(s)**

This method is suggested by Bruce Tier <btier@une.edu.au> to identify pedigree errors.

**Examples**

```
genotype <- matrix(c(
  2,1,0,
  2,0,0,
  0,0,2
), byrow = TRUE, ncol = 3)

ohd(genotype)
```

---

ohg

*Matrix of Opposing Homozygotes*

---

**Description**

Creates a matrix of opposing homozygotes from the genotype matrix.

**Usage**

```
ohg(genotypeMatrix)
```

**Arguments**

genotypeMatrix matrix genotype (Data should be numeric. Use 0, 1 and 2 respectively for AA, AB and BB. Use 9 for missing data)

**Value**

Returns a square matrix (sample X sample) with the pairwise counts of opposing homozygotes.

**Note**

This function can be slow with a large data set. The fast version of this function will be available after publish of the related manuscript.

**Author(s)**

Ferdosi, M. H., & Boerner, V. (2014). A fast method for evaluating opposing homozygosity in large SNP data sets. *Livestock Science*.

**See Also**

[rpoh](#)

**Examples**

```
genotype <- matrix(c(
  2,1,0,
  2,0,0,
  0,0,2
), byrow = TRUE, ncol = 3)

ohg(genotype)
```

ohplot

*Opposing Homozygotes Plot***Description**

Plot the sorted vectorized matrix of Opposing Homozygotes.

**Usage**

```
ohplot(oh, genotype, pedigree, check = FALSE)
```

**Arguments**

oh	integer Opposing homozygotes matrix (Output of <a href="#">ohg</a> )
genotype	matrix genotype of one chromosome (data should be numeric. Use 0, 1 and 2 for respectively AA, AB and BB. Use 9 for missing data)
pedigree	matrix the pedigree matrix should contain at least two columns, the first column with the half-sib IDs and the second column with the sires IDs. This argument is optional.
check	logical check the genotype file for the possible errors

**Details**

The cut off line shows the edge of most different groups.

**See Also**

[ohg](#) and [rpoh](#)

**Examples**

```
set.seed(100)
chr <- list()
sire <- list()
set.seed(1)
chr <- list()
for(i in 1:5)
{
chr[[i]] <- .simulateHalfsib(numInd = 20, numSNP = 5000, recbound = 1:10)
```

```

sire[[i]] <- ssp(bmh(chr[[i]]), chr[[i]])
sire[[i]] <- sire[[i]][1,] + sire[[i]][2,]
sire[[i]][sire[[i]] == 18] <- 9
}

Genotype <- do.call(rbind, chr)
rownames(Genotype) <- 6:(nrow(Genotype) + 5)
sire <- do.call(rbind, sire)
rownames(sire) <- 1:5
Genotype <- rbind(sire, Genotype)
oh <- ohg(Genotype) # creating the Opposing Homozygote matrix
pedigree <- as.matrix(data.frame(c(1:5, 6:(nrow(Genotype))),
rep = c(rep(0,5), rep(1:5, rep(20,5))))))
ohplot(oh, Genotype, pedigree, check = TRUE)

```

---

para

*Parallel Analysis of Data*


---

## Description

This function uses the list of matrices (the output of `cs`) and runs one of the options, on each element of the list, in parallel.

## Usage

```
para(halfsibs, cpus = 1, option = "bmh", type = "SOCK", bmh_forwardVectorSize = 30,
    bmh_excludeFP = TRUE, bmh_nsap = 3, pmMethod = "constant")
```

## Arguments

<code>halfsibs</code>	list list of matrices of half-sibs (can be generated with <code>hss</code> and <code>cs</code> functions)
<code>cpus</code>	numeric number of CPUs (thread)
<code>option</code>	character type of analysis
<code>type</code>	character type of cluster for parallel analysis
<code>bmh_forwardVectorSize</code>	integer number of heterozygous sites used to validate recombination events or check for genotyping errors
<code>bmh_excludeFP</code>	logical exclude SNPs that may cause heterozygous sites in the sire due to genotyping errors or map errors
<code>bmh_nsap</code>	integer number of SNPs per block
<code>pmMethod</code>	character method for creating the recombination matrix

## Details

Type of analysis can be `bmh`, `ssp`, `aio`, `pm`, or `rec` (refer to `pm`, `rplot` and vignette for more information about `rec`).



**Value**

Returns a list of matrices with the results (formats specific to the option selected).

**Examples**

```
# Please run demo(hsphase)
```

---

pedigree	<i>Example Pedigree</i>
----------	-------------------------

---

**Description**

An example pedigree for hsphase.

**Usage**

```
data(pedigree)
```

**Format**

a data frame with the following columns:

- First Column: half-sibs
- Second Column: sires

---

pedigreeNaming	<i>Fix Pedigree Errors</i>
----------------	----------------------------

---

**Description**

Tries to link the inferred pedigree from [rpoh](#) with the sire IDs in the original pedigree and fix pedigree errors.

**Usage**

```
pedigreeNaming(inferredPedigree, realPedigree)
```

**Arguments**

```
inferredPedigree      matrix inferred pedigree (output of rpoh )
realPedigree           matrix original pedigree
```

**Details**

This function calls the [bmh](#) and [recombinations](#) functions to count the number of recombinations in each half-sib group.

**Value**

Returns the inferred pedigree with the best fit to the sire names used in the original pedigree file.

**See Also**

[rpoh](#) and [ohg](#)

**Examples**

```
# Please run demo(hsphase)
```

---

phf *Half-Sib Family Phasing*

---

**Description**

Phases the half-sib family by using the blocking structure and imputed sire matrices.

**Usage**

```
phf(GenotypeMatrix, blockMatrix, sirePhasedMatrix)
```

**Arguments**

`GenotypeMatrix` matrix half-sib genotypes (one half-sib per row, with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 respectively for AA, AB and BB. Use 9 for missing data)

`blockMatrix` matrix blocking structure (output of [bmh](#))

`sirePhasedMatrix`  
matrix imputed sire (output of [ssp](#))

**Value**

Returns a matrix that contains the phased parental haplotypes of the half-sibs. It uses 1, 0 and 9 for A, B and missing.

**Note**

The genotype matrix must only contain individuals from one half-sib family and one ordered chromosome. This function is used by the [aio](#) function for complete phasing of a half-sib group.

**See Also**[aio](#)**Examples**

```
genotype <- matrix(c(
  2,1,0,
  2,0,0,
  0,0,2), byrow = TRUE, ncol = 3)
block <- bmh(genotype)
phf(genotype, block, ssp(block, genotype))
```

pm

*Probability Matrix***Description**

Creates a recombination matrix based on the blocking structure.

**Usage**

```
pm(blockMatrix, method = "constant")
```

**Arguments**

blockMatrix	matrix blocking structure (Output of <a href="#">bmh</a> )
method	character method for creating the recombination matrix

**Details**

This function finds the recombination between two consecutive sites, and marks the recombination site with a 1; if there are unknown sites between two blocks it will also mark these sites with a 1 (constant method) or 1 divided by number of unknown site (relative method).

**Examples**

```
genotype <- matrix(c(
  0,2,0,1,0,
  2,0,1,2,2,
  2,2,1,0,2,
  2,2,1,1,1,
  0,0,2,1,0), ncol = 5, byrow = TRUE) # each row contains the SNP of individuals

(result <- bmh(genotype))
pm(result)
```

---

pogc

*Parent Offspring Group Constructor*

---

### Description

Assign offsprings to the parents.

### Usage

```
pogc(oh, genotypeError)
```

### Arguments

oh                    integer opposing homozygotes matrix (Output of [ohg](#))  
 genotypeError    integer number of genotypeing error allowed in the oh matrix

### Value

Return a data frame with two columns. The first column is the animal ID and the second column is the parent ID.

### See Also

[ohg](#), [hss](#) and [rpoh](#)

### Examples

```
set.seed(100)
chr <- list()
sire <- list()
set.seed(1)
chr <- list()
for(i in 1:5)
{
  chr[[i]] <- .simulateHalfsib(numInd = 20, numSNP = 5000, rebound = 1:10)
  sire[[i]] <- ssp(bmh(chr[[i]]), chr[[i]])
  sire[[i]] <- sire[[i]][1,] + sire[[i]][2,]
  sire[[i]][sire[[i]] == 18] <- 9
}

Genotype <- do.call(rbind, chr)
rownames(Genotype) <- 6:(nrow(Genotype) + 5)
sire <- do.call(rbind, sire)
rownames(sire) <- 1:5
Genotype <- rbind(sire, Genotype)
oh <- ohg(Genotype) # creating the Opposing Homozygote matrix
pogc(oh, 5)
```

---

readGenotype	<i>Read and Check the Genotype File</i>
--------------	---

---

**Description**

This function reads and checks genotype files.

**Usage**

```
readGenotype(genotypePath, separatorGenotype = " ", check = TRUE)
```

**Arguments**

genotypePath	character genotype path (animals (rows) and SNP (columns), SNP should be coded as 0, 1 and 2 for respectively AA, AB and BB. Use 9 for missing data. please refer to vignette for more information)
separatorGenotype	character separator character for genotype
check	logical check the genotype file for possible errors

**Value**

Returns the genotype matrix.

**Note**

Please refer to vignette for more information.

**Examples**

```
# A comprehensive demo and example dataset is available from  
# http://www-personal.une.edu.au/~cgondro2/hsphase.html
```

---

recombinations	<i>Recombination Number</i>
----------------	-----------------------------

---

**Description**

Counts the number of recombinations for each individual.

**Usage**

```
recombinations(blockMatrix)
```

**Arguments**

blockMatrix	matrix block structure (Output of <a href="#">bmh</a> )
-------------	---

**Value**

Returns a vector of recombinations. The number of elements in this vector is equal to the number of individuals, i.e. each element holds the number of recombinations identified for each sample.

**See Also**

[bmh](#)

**Examples**

```
genotype <- matrix(c(
  2,1,0,0,
  2,0,2,2,
  0,0,2,2,
  0,2,0,0
), byrow = TRUE, ncol = 4)

recombinations(bmh(genotype))
```

---

rplot

*Recombination Plot*

---

**Description**

This function creates a plot which shows the sum of all recombination events across a half-sib family.

**Usage**

```
rplot(x, distance, start = 1, end = ncol(x), maximum = 100,
      overwrite = FALSE, method = "constant")
```

**Arguments**

x	matrix of half-sib genotypes (one half-sib per row, with SNP ordered by mapping position in the columns. Data should be numeric. Use 0, 1 and 2 for respectively AA, AB and BB. Use 9 for missing data).
distance	integer of physical distances between markers
start	integer first marker selected for the plot
end	integer last marker selected for the plot
maximum	integer maximum number of recombinations to show (higher recombination rates will be omitted from the plot)
overwrite	logical draw a diagram over the current diagram (default FALSE)
method	character please refer to the <a href="#">pm</a> document

**Examples**

```
genotype <- matrix(c(
  0,2,0,1,0,
  2,0,1,2,2,
  2,2,1,0,2,
  2,2,1,1,1,
  0,0,2,1,0), ncol = 5, byrow = TRUE) # each row contains the SNP of individuals

rplot(genotype, c(1,2,3,4,8))
```

rpoh

*Reconstruct Pedigree Based on Matrix of Opposing Homozygotes***Description**

Reconstructs a half-sib pedigree based on a matrix of opposing homozygotes.

**Usage**

```
rpoh(genotypeMatrix, oh, forwardVectorSize = 30, excludeFP = TRUE, nsap = 3,
maxRec = 15, intercept = 26.3415, coefficient = 77.3171, snpnooh, method, maxsnpnooh)
```

**Arguments**

genotypeMatrix	matrix genotype of one chromosome (data should be numeric. Use 0, 1 and 2 for respectively AA, AB and BB. Use 9 for missing data)
oh	integer Opposing homozygotes matrix (Output of <a href="#">ohg</a> )
forwardVectorSize	integer number of heterozygous sites used to validate recombination events or check for genotyping errors
excludeFP	logical excludes SNPs that may cause heterozygous sites in the sire due to genotyping errors or map errors
nsap	integer number of SNP per block to validate recombinations
maxRec	integer maximum number of expected recombinations per individual
intercept	integer intercept of fitted model
coefficient	integer coefficient of fitted model
snpnooh	integer number of SNPs used to create <i>oh</i> matrix (this number must be divided by 1000)
method	character pedigree reconstruction method
maxsnpnooh	numeric the maximum number of allowing opposing homozygote in a half-sib family

**Details**

Four methods *simple*, *recombinations*, *calus* and *manual* can be utilized to reconstruct the pedigree.

The following examples show the arguments require for each method.

```
pedigree1 <- rpoh(oh = oh, snpnooh = 732, method = "simple")
pedigree2 <- rpoh(genotypeMatrix = genotypeChr1, oh = ohg(genotype), maxRec = 10, method =
"recombinations")
pedigree3 <- rpoh(genotypeMatrix = genotype, oh = oh, method = "calus")
pedigree4 <- rpoh(oh = oh, maxsnpnooh = 31662, method = "manual")
```

**Value**

Returns a data frame with two columns, the first column is animals' ID and the second column is sire identifiers (randomly generated).

**Note**

Method can be *recombinations*, *simple*, *calus* or *manual*. Please refer to vignette for more information.

The sire genotype should be removed before using this function utilizing [pogc](#) function.

**See Also**

[bmh](#) and [recombinations](#)

**Examples**

```
# Please run demo(hsphase)
```

---

 ssp

*Sire Imputation and Phasing*


---

**Description**

Infer (impute) and phase sire's genotype based on the block structure matrix (recombination blocks) and homozygous sites of the half-sib genotype matrix.

**Usage**

```
ssp(blockMatrix, genotypeMatrix)
```

**Arguments**

**blockMatrix** matrix block structure (Output of [bmh](#))  
**genotypeMatrix** matrix half-sibs genotype (each row includes the SNP of individuals, 0, 1 and 2 for respectively AA, AB and BB. Use 9 for missing data)



**Value**

Returns a matrix (Imputed Sire) with two rows one for each haplotype of the sire (columns are SNP in the order of the genotype matrix). Alleles are coded as 0 (A) and 1 (B). Alleles that could not be imputed are coded as 9.

**See Also**

[phf](#), [aio](#) and [imageplot](#)

**Examples**

```
genotype <- matrix(c(
  0,2,1,1,1,
  2,0,1,2,2,
  2,2,1,0,2,
  2,2,1,1,1,
  0,0,2,1,0), ncol = 5, byrow = TRUE) # each row contains the SNP of individuals

(result <- ssp(bmh(genotype), genotype))
```

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