Package 'HAPim'

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Description The package provides a set of functions whose aim is to propose 4 methods of QTL detection. HAPimLD is an interval-mapping method designed for unrelated individuals with no family information that makes use of linkage disequilibrium. HAPimLDL is an interval-mapping method for design of half-sib families. It combines linkage analysis and linkage disequilibrium. HaploMax is based on an analysis of variance with a dose haplotype effect. HaploMaxHS is based on an analysis of variance with a sire effect and a dose haplotype effect in half-sib family design. Fundings for the package development were provided to the LDLmapQTL project by the ANR GENANIMAL program and APIS-GENE.

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`HAPim-package` *HAPim*

Description

The package provides a set of functions whose aim is to propose 4 methods of QTL detection:

-HAPimLD is an interval-mapping method designed for unrelated individuals with no family information that makes use of linkage disequilibrium.

-HAPimLDL is an interval-mapping method for design of half-sib families. It combines linkage analysis and linkage disequilibrium.

-HaploMax is based on an analysis of variance with a dose haplotype effect.

-HaploMaxHS is based on an analysis of variance with a sire effect and a dose haplotype effect in half-sib family design.

Fundings for the package development were provided to the LDLmapQTL project by the ANR GENANIMAL program and APIS-GENE.

Details

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Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

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References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

`allele.marq` *alleles at markers*

Description

This function finds the alleles present at each marker. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
allele.marq(hap)
```

Arguments

`hap`	character matrix (n x p) of individual haplotypes.

Value

The returned value is a list of alleles for each marker.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

corresp *correspondance*

Description

The function can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
corresp(hap.o, res.structure)
```

Arguments

hap.o	numeric matrix (n x p).
res.structure	results provided by `structure.hap()` function, list of numeric objects.

Value

A list containing the following components:

corresp	numeric matrix (n x p).
assoc	numeric vector, associated haplotype

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

structure.hap

data.test *data.test*

Description

"data.test" is a list of 9 elements. We consider a 10 cM chromosomal region with 10 equally spaced biallelic markers and a design of 5 half-sib families, each sire having 10 sons. Data are prepared for a QTL detection in the middle of each marker intervalle.

Usage

```
data(data.test)
```

Format

A list containing the following components:

- map: vector (9) with numerical values
- hap.trans.mere: matrix (50 x 10) with character values
- hap.trans.pere: matrix (50 x 10) with character values
- hap.chrom1.pere: matrix (5 x 10) with character values
- hap.chrom2.pere: matrix (5 x 10) with character values
- perf: vector (50) with numerical values
- CD: vector (50) with numerical values
- PLA: matrix (50 x 9) with numerical values
- genea: matrix (50 x 2) with numerical values

Examples

```
data(data.test)

#distance between two consecutive markers on the chromosome
 map=data.test[[1]]
 map

#haplotype transmitted by dams
#son information (lines) are ordered following genea[,1]
 hap.trans.mere=data.test[[2]]
 hap.trans.mere

#haplotype transmitted by sires
#son information (lines) are ordered following genea[,1]
 hap.trans.pere=data.test[[3]]
 hap.trans.pere

#haplotype of the first chromosome for each sire
```

```
#sire information (lines) are ordered following unique(genea[,2])
 hap.chrom1.pere=data.test[[4]]
 hap.chrom1.pere

#haplotype of the second chromosome for each sire
#sire information (lines) are ordered following unique(genea[,2])
 hap.chrom2.pere=data.test[[5]]
 hap.chrom2.pere

#performances of sons
#son information are ordered following genea[,1]
 perf=data.test[[6]]
 perf

#CD of sons
#son information are ordered following genea[,1]
 CD=data.test[[7]]
 CD

#transmission probabilities of sons for each test position
#son information (lines) are ordered following genea[,1]
 PLA=data.test[[8]]
 PLA

#son index and  index of his father
 genea=data.test[[9]]
 genea
```

`depart.LD` *starting values for the optimization of HAPimLD method*

Description

the function calculates the starting values of the performance mean and the error variance for the optimization of HAPimLD method. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
depart.LD(perf, CD)
```

Arguments

`perf`	numeric vector of length=number of individuals which contains the performances of individuals.
`CD`	numeric vector of length=number of individuals which contains the CD of individuals.

Value

The value returned is a numeric vector of length=2 which contains estimates of the performance mean and the error variance.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

`depart.LDL` *starting values for the optimization of HAPimLDL method*

Description

The function calculates the starting value of the error variance and the starting value of the QTL effect for the optimization of HAPimLDL method. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
depart.LDL(moyenne.pere, perf, CD, PLA, desc.pere)
```

Arguments

`moyenne.pere`	results provided by `moyenne.pere()` function, mean of half-sib family performances.
`perf`	numeric vector of length=number of individuals which contains the performances of individuals.
`CD`	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=s/CD^2_i
`PLA`	numeric vector (number of individuals) which contains transmission probabilities at a single test position.
`desc.pere`	results provided by `descendant.pere()` function, numeric matrix (number of sires x 2) which gives for each sire, the first and last indexes of its progeny.

Value

The returned value is a numeric vector of length=2 which contains estimates of the error variance and the Q allele effect.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`moyenne.pere`, `descendant.pere`

---

descendant.pere *first and last indexes of each sire progeny*

Description

The function defines, for each sire, the first and last indexes of its progeny. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
descendant.pere(genea)
```

Arguments

genea	numeric matrix (number of individuals x 2) which contains the progeny index and its father index.

Details

Progeny data are prealably ordered by family

Value

The returned value is a numeric matrix (number of sires x 2) which gives for each sire, the first and last indexes of its progeny.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

distance.marqueurs *distance of markers*

Description

The function gives the distance of each marker to the first marker. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
distance.marqueurs(map)
```

Arguments

map	numeric vector of length=(number of markers-1) giving the distance between two consecutive markers on all the chromosome.

Value

the returned valueis a numeric vector of length=number of markers containing the positions of each marker from the beginning of the chromosome.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

distance.test *localisation of test positions*

Description

The function gives the distance of test positions from the first marker and sorts them out by marker interval. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
distance.test(position, dist.marq)
```

Arguments

position	numeric vector of test positions.
dist.marq	results provided by distance.marqueurs() function, numeric vector of length=number of markers which gives the distance of each marker from the bigining of the chromosome.

Value

the returned value is a list of n numeric vectors (n=number of markers-1). The jth vector contains the distance (from the first marker) of test positions belonging to the jth marker interval.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

distance.marqueurs

---

esp.freq.hap *expectation of extended haplotype frequencies*

Description

This function computes the expectation of (haplotype + Q allele) frequencies under a Wrigth-Fisher model. The function can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
esp.freq.hap(hap.assoc, piQ.t0, timeT, pi.hap, res.structure, poids.D)
```

Arguments

hap.assoc	numeric value, associated haplotype.
piQ.t0	frequency of Q allele at time t=0.
timeT	time of population evolution.
pi.hap	provided by pi.hap() function, list of numeric objects.
res.structure	provided by structure.hap() function, list of numeric objects.
poids.D	provided by poids.D() function, list of numeric objects.

Value

The value returned is a numeric vector containing for each observed haplotype, the frequencies of its extension with the Q allele.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`pi.hap`, `structure.hap`, `poids.D`

`freq.all` *allelic frequencies*

Description

The function calculates allelic frequencies by marker given a set of haplotypes. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
freq.all(hap)
```

Arguments

`hap`	numeric matrix (number of individuals x number of markers) which contains the haplotype of individuals.

Value

The returned value is a list of n elements (n=number of markers) which gives the allelic frequencies by marker, ranged in ascending order of allele index.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

`haldanem1` *recombination rate*

Description

The function calculates recombination rates using Haldane distance. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
haldanem1(distance)
```

Arguments

`distance`	vector of distances in Morgan.

Value

the returned value is a vector of recombination rates.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

Haldane, J.B.S. J. Genet. (1919), 8:299-309.

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

`hapim.LD.add` *HAPimLD method*

Description

HAPimLD is a method of QTL(Quantitative Trait Loci) detection developed by Boitard et al. (2006). It is an interval-mapping method designed for unrelated individuals with no family information. It is based on a maximum-likelihood calculation and makes use of linkage disequilibrium through a Wright-Fisher modelisation of the population evolution.

Usage

```
hapim.LD.add(hap.trans.pere, hap.trans.mere, perf, CD, map, position,

temps.depart, perfectLD, marq.hap.left)
```

Arguments

hap.trans.pere	character matrix (number of individuals x number of markers) which provides, for each individual, the haplotype transmitted by its father.
hap.trans.mere	character matrix (number of individuals x number of markers) which provides, for each individual, the haplotype transmitted by its mother.
perf	numeric vector of length=number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=error variance/CD^2_i
map	numeric vector of length=(number of markers-1) which contains the distance in Morgan between two consecutive markers on the chromosome.
position	numeric vector which contains the distance in Morgan of test positions from the beginning of the chromosome (first marker).
temps.depart	numeric value which provides a start value for the evolution time of the population.
perfectLD	need to be equal to TRUE: linkage disequilibrium is complete between mutated haplotype and Q allele at time 0.
marq.hap.left	(number of markers of the mutated haplotype)/2.

Details

Individual information have to be ranged in the same order in hap.trans.mere, hap.trans.pere, perf, CD.

All distances are assumed to be Haldame's distance in Morgan.

Value

The returned value is a data frame which contains 8 columns:

-Test positions

-Value of Likelihood Ratio Test (LRT)

-Mutated (i.e. associated to Q allele) haplotype

-Estimate of the error variance

-Estimate of the Q allele effect

-Estimate of the time of population evolution

-Estimate of the Q allele frequency at time t=0

-Estimate of the performance mean

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

Boitard et al. Linkage disequilibrium interval mapping of quantitative trait loci. BMC Genomics (2006) 7:54.

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

Examples

```
data(data.test)
map=data.test[[1]]
hap.trans.mere=data.test[[2]]
hap.trans.pere=data.test[[3]]
perf=data.test[[6]]
CD=data.test[[7]]


# In this example,marker positions are: 0, 0.010, 0.020, 0.030, 0.040, 0.050, 0.060,
# 0.070, 0.080, 0.090.
# We want to test the presence/absence of a QTL between 2 consecutive markers, so

position=c(0.005,0.015,0.025,0.035,0.045,0.055,0.065,0.075,0.085)

# we use a 2 markers-associated haplotype.
marq.hap.left=1

# We assume an evolution of 50 generations.
temps.depart=50
perfectLD=TRUE


hapim.LD.add=hapim.LD.add(hap.trans.pere,hap.trans.mere,perf,CD,map,position,

temps.depart,perfectLD,marq.hap.left)

hapim.LD.add
```

---

hapim.LDL.add *HAPimLDL method*

Description

HAPimLDL is a method of QTL (Quantitative Trait Loci) detection for a design of half-sib families. It is an interval-mapping method which uses family information and combines linkage analysis and linkage disequilibrium. It is based on a maximum-likelihood calculation and makes use of linkage disequilibrium through a Wright-Fisher modelisation of the population evolution.

Usage

```
hapim.LDL.add(hap.chrom1.pere, hap.chrom2.pere, hap.trans.mere, perf, CD,

genea, PLA, map, position, temps.depart, perfectLD, marq.hap.left)
```

Arguments

hap.chrom1.pere	character matrix (number of sires x number of markers) which gives the haplotype of the first chromosome for each sire.
hap.chrom2.pere	character matrix (number of sires x number of markers) which gives the haplotype of the second chromosome for each sire.
hap.trans.mere	numeric matrix (number of individuals x number of markers) which provides, for each individual, the haplotype transmitted by its mother.
perf	numeric vector of length=number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=error variance/CD^2_i
genea	numeric matrix (number of individuals x 2) which contains the progeny index and its father index.
PLA	numeric matrix (number of individuals x number of test positions) which contains transmission probabilities i.e probability that the progeny receives the first chromosome from its father at the test positions given marker information, see J.-M. Elsen, B. Mangin, B. Goffinet, D. Boichard, P. Le Roy. Alternative models for QTL detection in livestock. I. General introduction. Genet. Sel. Evol. 31 (1999) 213-224.
map	numeric vector of length=(number of markers-1) which contains the distance in Morgan between two consecutive markers on the chromosome.
position	numeric vector which contains the distance in Morgan of test positions from the beginning of the chromosome (first marker).
temps.depart	numeric value which provides a start value for the evolution time of the population.
perfectLD	need to be equal to TRUE: linkage disequilibrium is complete between mutated haplotype and Q allele at time 0.
marq.hap.left	(number of markers of the mutated haplotype)/2.

Details

Progeny information have to be ranged in the same order in genea, hap.trans.mere, perf, CD and PLA.

Columns of PLA have to correspond to test positions.

Sire information have to be ranged in the same order in unique(genea[,2]), hap.chrom1.pere and hap.chrom2.pere.

All distances are assumed to be Haldame's distance in Morgan.

Value

The returned value is a data frame which contains 8 columns:

-Test positions

-Value of Likelihood Ratio Test (LRT)

-Mutated (i.e. associated to Q allele) haplotype

-Estimate of the error variance

-Estimate of the Q allele effect

-Estimate of the time of population evolution

-Estimate of the Q allele frequency at time t=0

-Estimate of the performance mean

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

Examples

```
data(data.test)
map=data.test[[1]]
hap.trans.mere=data.test[[2]]
hap.chrom1.pere=data.test[[4]]
hap.chrom2.pere=data.test[[5]]
perf=data.test[[6]]
CD=data.test[[7]]
PLA=data.test[[8]]
genea=data.test[[9]]


# In this example, marker positions are : {0, 0.010, 0.020, 0.030, 0.040, 0.050, 0.060,
# 0.070, 0.080, 0.090 }.
# We want to test the presence/absence of a QTL between 2 consecutive markers, so
# transmission probabilities are given for the middle of each interval and

position=c(0.005,0.015,0.025,0.035,0.045,0.055,0.065,0.075,0.085)

# we use a 2 markers-associated haplotype.
marq.hap.left=1

# We assume an evolution of 50 generations.
temps.depart=50
perfectLD=TRUE
```

```
hapim.LDL.add=hapim.LDL.add(hap.chrom1.pere,hap.chrom2.pere,hap.trans.mere,perf,CD,genea,

PLA,map,position, temps.depart,perfectLD,marq.hap.left)

hapim.LDL.add
```

---

haplomax.add *HaploMax method in unrelated population*

Description

The function computes an analysis of variance with a dose haplotype effect.

Usage

```
haplomax.add(hap.trans.pere, hap.trans.mere, perf, CD, map, marq.hap)
```

Arguments

hap.trans.pere	character matrix (number of individuals x number of markers) which provides, for each individual, the haplotype transmitted by its father.
hap.trans.mere	character matrix (number of individuals x number of markers) which provides, for each individual, the haplotype transmitted by its mother.
perf	numeric vector of length=number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=error variance/CD^2_i
map	numeric vector of length=(number of markers-1) which contains the distance in Morgan between two consecutive markers on the chromosome.
marq.hap	number of markers of the mutated haplotype

Details

Individual information have to be ranged in the same order in hap.trans.mere, hap.trans.pere, perf, CD.

All distances are assumed to be Haldame's distance in Morgan.

Test positions are located on the middles of marq.hap marker sliding windows.

Value

The value returned is a data frame which contains 5 columns:

-Test positions

-Value of Fisher test

-Mutated (i.e. associated to Q allele) haplotype

-Estimate of the error variance

-Estimate of the Q allele effect

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

Examples

```
data(data.test)
map=data.test[[1]]
hap.trans.mere=data.test[[2]]
hap.trans.pere=data.test[[3]]
perf=data.test[[6]]
CD=data.test[[7]]

# In this example,marker positions are: {0, 0.010, 0.020, 0.030, 0.040, 0.050, 0.060,
# 0.070, 0.080, 0.090 }.
# we use a 2 markers-associated haplotype.
marq.hap=2

haplomax=haplomax.add(hap.trans.pere,hap.trans.mere,perf,CD,map, marq.hap)

haplomax
```

`haplomax.HS.add` *HaploMax method in half-sib family design*

Description

The function computes an analysis of variance with a sire effect and a dose haplotype effect.

Usage

```
haplomax.HS.add(hap.chrom1.pere, hap.chrom2.pere, hap.trans.pere,

hap.trans.mere, perf, CD, genea, map, marq.hap)
```

Arguments

hap.chrom1.pere	character matrix (number of sires x number of markers) which gives the haplotype of the first chromosome for each sire.
hap.chrom2.pere	character matrix (number of sires x number of markers) which gives the haplotype of the second chromosome for each sire.
hap.trans.pere	numeric matrix (number of individuals x number of markers) which provides, for each individual, the haplotype transmitted by its father.
hap.trans.mere	numeric matrix (number of individuals x number of markers) which provides, for each individual, the haplotype transmitted by its mother.
perf	numeric vector of length=number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=error variance/CD^2_i
genea	numeric matrix (number of individuals x 2) which contains the progeny index and its father index.
map	numeric vector of length=(number of markers-1) which contains the distance in Morgan between two consecutive markers on the chromosome.
marq.hap	number of markers of the mutated haplotype.

Details

Progeny information have to be ranged in the same order in genea, hap.trans.pere, hap.trans.mere, perf and CD.

Sire information have to be ranged in the same order in unique(genea[,2]), hap.chrom1.pere and hap.chrom2.pere.

All distances are assumed to be Haldame's distance in Morgan.

Test positions are located on the middles of marq.hap marker sliding windows.

Value

The returned value is a data frame which contains 5 columns:

-Test positions

-Value of Fisher test

-Mutated (i.e. associated to Q allele) haplotype

-Estimate of the error variance

-Estimate of the Q allele effect

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

Examples

```
data(data.test)
map=data.test[[1]]
hap.trans.mere=data.test[[2]]
hap.trans.pere=data.test[[3]]
hap.chrom1.pere=data.test[[4]]
hap.chrom2.pere=data.test[[5]]
perf=data.test[[6]]
CD=data.test[[7]]
genea=data.test[[9]]

# In this example, marker positions are : 0, 0.010, 0.020, 0.030, 0.040, 0.050, 0.060,
# 0.070, 0.080, 0.090.
# we use a 2 markers-associated haplotype

marq.hap=2

haplomax.HS=haplomax.HS.add(hap.chrom1.pere,hap.chrom2.pere,hap.trans.pere,hap.trans.mere,

perf,CD,genea,map,marq.hap)

haplomax.HS
```

---

moyenne.pere *average of performances per sire*

Description

The function computes the empirical performance mean per sire. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
moyenne.pere(perf, CD, desc.pere)
```

Arguments

perf	numeric vector of length=number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=error variance/CD^2_i
desc.pere	results provided by descendant.pere() function, numeric matrix (number of sires x 2) which gives for each sire, the first and last indexes of its progeny.

Value

The returned value is a vector of length=number of sires which contains the empirical performance mean per sire.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

descendant.pere

---

obj.haplomax.add *analysis of variance of the HaploMax method*

Description

The function computes the regression analysis with a dose haplotype effect. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
obj.haplomax.add(perf, CD, assoc, res.structure, pi.hap, cor.pere, cor.mere)
```

Arguments

perf	numeric vector of length=number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=s/CD^2_i
assoc	numeric value, associated haplotype.

res.structure	results provided by structure.hap() function, list of objects.
pi.hap	provided by pi.hap() function, list of numeric objects.
cor.pere	provided by corresp() function, list of numeric objects.
cor.mere	provided by corresp() function, list of numeric objects.

Value

The returned value is an object of aov class containing the dose haplotype regression.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

corresp, pi.hap, structure.hap,proba.DL

---

obj.haplomax.HS.add *Analysis of variance of the HaploMmax method in half-sib family design*

Description

The function computes the regression analysis with a dose haplotype effect and a sire effect in a design of half-sib families. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
obj.haplomax.HS.add(genea, perf, CD, assoc, res.structure, pi.hap, cor.pere,

cor.mere)
```

Arguments

genea	numeric matrix (number of individuals x 2) which contains individual index and corresponding sire index of each individual.
perf	numeric vector of length=number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=error variance/CD^2_i

assoc	numeric value, associated haplotype
res.structure	provided by structure.hap() function, list of objects.
pi.hap	provided by pi.hap() function, list of numeric objects.
cor.pere	provided by corresp() function, list of numeric objects.
cor.mere	provided by corresp() function, list of numeric objects.

Value

The returned value is an object of aov class containing the dose haplotype + sire effect regression.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

corresp, pi.hap, structure.hap

---

obj.LD.add *log-likelihood value of HAPimLD method under H1*

Description

The function calculates the log-likelihood value of HAPimLD method under alternative hypothesis H1. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
obj.LD.add(param,don)
```

Arguments

param	numeric vector of length=5 containing parameters to maximize: -error variance -Q allele effect -evolution time -frequency of Q allele at time t=0 -performances mean
don	list of 8 objects. Some objects are results provided by corresp(), pi.hap(), structure.hap(), poids.D() functions.

Value

The returned value is the log-likelihood value of HAPimLD method under hypothesis H1.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

depart.LD, corresp, pi.hap, structure.hap, poids.D

---

obj.LD.add.H0 *log-likelihood value of HAPimLD method under H0*

Description

The function calculates the log-likelihood value of HAPimLD method under hypothesis HO. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
obj.LD.add.H0(perf, CD)
```

Arguments

perf	numeric vector of length = number of individuals which contains the performances of individuals.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=s/CD^2_i

Value

The returned value is the log-likelihood value of HAPimLD method under hypothesis HO.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

`obj.LDL.add` *log-likelihood value of the HAPimLDL method under H1*

Description

The function gives the log-likelihood value of the HAPimLDL method under alternative hypothesis H1. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
obj.LDL.add(param,don)
```

Arguments

`param`	numeric vector of length=5 containing containing parameters to maximize: -error variance -Q allele effect -evolution time -Q allele frequency at time t=0 -performance mean
`don`	list of 12 objects. Some objects are results provided by `descendant.pere()`, `moyenne.pere()`, `corresp()`, `pi.hap()`, `structure.hap()`, `poids.D()` functions.

Value

The returned value is the log-likelihood value of the HAPimLDL method under alternative hypothesis H1.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`depart.LDL`, `descendant.pere`, `moyenne.pere`, `corresp`, `pi.hap`, `structure.hap`, `poids.D`

`obj.LDL.add.H0` *log-likelihood value of the HAPimLDL method under H0*

Description

The function calculates the log-likelihood value of the HAPimLDL method under hypothesis H0. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
obj.LDL.add.H0(moyenne.pere, perf, CD, desc.pere)
```

Arguments

`moyenne.pere`	results provided by `moyenne.pere()` function, mean of half-sib family performances.
`perf`	numeric vector of length=number of individuals which contains the performances of individuals.
`CD`	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=s/CD^2_i
`desc.pere`	results provided by `descendant.pere()` function, numeric matrix (number of sires x 2) which gives for each sire, the first and last indexes of its progeny.

Value

The returned value is the log-likelihood value of HAPimLDL method under hypothesis HO.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`moyenne.pere`, `descendant.pere`

pi.hap *haplotype frequencies*

Description

This function computes the frequencies of each haplotype. The function can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
pi.hap(freq.marq, res.structure)
```

Arguments

`freq.marq`	results provided by `freq.all()` function, list of numeric objects which contains the allele frequencies.
`res.structure`	results provided by `structure.hap()` function, list of objects.

Value

The returned value is a list of numeric vectors containing haplotypes freqencies estimated under marker independency.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`freq.all`, `structure.hap`

`pi.hap.NI` *haplotype frequencies*

Description

This function computes the observed frequencies of each haplotype. The function can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
pi.hap.NI(res.structure, cor.hap)
```

Arguments

`res.structure`	results provided by `structure.hap()` function, list of objects.
`cor.hap`	results provided by `corresp()` function, list of numeric objects.

Value

The returned value is a list of numeric vectors containing haplotypes freqencies estimated on haplotypes with non missing information.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`structure.hap`

poids.D *poids.D*

Description

This function calculates the probability of no recombinaison between loci for each Bennett's desequilibrium. The function can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
poids.D(dist.test, pos.QTL, res.structure)
```

Arguments

dist.test	results provided by distance.test() function, list of numeric objects.
pos.QTL	numeric value, interval of a test position
res.structure	results provided by structure.hap() function, list of objects.

Value

The returned value is a list of numeric objects.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

structure.hap, distance.test

proba.DL *conditional probabilities*

Description

The function calculates conditional probabilities of having Q allele given marker information due to linkage disequilibrium.

Usage

```
proba.DL(piQ.t0, esp.freq.hap, res.structure, pi.hap, res.corresp)
```

Arguments

piQ.t0	frequency of Q allele at time t=0.
esp.freq.hap	results provided by esp.freq.hap() function, numeric vector.
res.structure	results provided by structure.hap() function, list of numeric objects.
pi.hap	provided by pi.hap() function, list of numeric objects.
res.corresp	results provided by corresp() function, list of 2 numeric objects.

Value

The returned value is a numeric vector of length=number of individuals which contains conditional probabilities of having Q allele given marker information due to linkage disequilibrium.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

esp.freq.hap, structure.hap, pi.hap, corresp

`proba.DL.diplotype` *probabilities due to linkage disequilibrium*

Description

The function calculates probabilities due to linkage disequilibrium for a diplotype. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
proba.DL.diplotype(DL.chrom1, DL.chrom2)
```

Arguments

`DL.chrom1`	results provided by `proba.DL()` function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on the first chromosome given a genotype.
`DL.chrom2`	results provided by `proba.DL()` function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on the second chromosome given a genotype.

Value

The returned value is a numeric matrix (number of individuals x 4) containing probabilities due to linkage disequilibrium for a diplotype.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`proba.DL`

`recode.hap` *recoding of haplotypes*

Description

The function recodes haplotypes of individuals in consecutive numeric values. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
recode.hap(hap, all.marq)
```

Arguments

`hap`	character matrix (number of individuals x number of markers) which contains the haplotype of individuals.
`all.marq`	results provided by `allele.marq()` function, list of alleles (coded with character values) for each marker.

Value

the returned value is a numeric matrix (number of individuals x number of markers) which contains the recoded haplotype of individuals.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`allele.marq`

`retrouve.all` *haplotype reconstruction*

Description

The function finds alleles of the associated haplotype. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
retrouve.all(assoc, res.structure, all.marq)
```

Arguments

`assoc`	numeric value, associated haplotype.
`res.structure`	results provided by `structure.hap()` function, list of objects.
`all.marq`	results provided by `allele.marq()` function, list of alleles for each marker.

Value

The returned value is a character which corresponds to the concatenation of alleles of the associated haplotype.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`structure.hap`, `allele.marq`

structure.hap *Structure*

Description

The function can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
structure.hap(nbre.marq, nbre.all.marq)
```

Arguments

nbre.marq	number of markers.
nbre.all.marq	number of alleles per markers.

Value

The value returned is a list of objects.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

vrais.LD.add *log likelihood of HAPIimLD method under H1*

Description

The function calculates the value of log likelihood of HAPimLD method under alternative hypothesis H1. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
vrais.LD.add(mu, alpha.Q, s, CD, perf, DL.d)
```

Arguments

mu	parameter of the mean performances.
alpha.Q	parameter of QTL effect.
s	parameter of the error variance.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=s/CD^2_i
perf	numeric vector of length=number of individuals which contains the performances of individuals.
DL.d	results provided by proba.DL.diplotype() function, numeric matrix (number of individuals x 4) containing probabilities due to linkage disequilibrium for a diplotype.

Value

The returned value is the value of log likelihood of HAPimLD method under alternative hypothesis H1.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

proba.DL.diplotype

---

vrais.LDL.add *log likelihood of HAPimLDL method under H1*

Description

The function calculates the value of log likelihood of HAPimLDL method under alternative hypothesis H1. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
vrais.LDL.add(moyenne.pere, alpha.Q, s, CD, perf, PLA, DL.m,
DL.chrom1,

DL.chrom2, desc.pere, mean.gene)
```

Arguments

moyenne.pere	results provided by moyenne.pere() function, mean of half-sib family performances.
alpha.Q	parameter of QTL effect.
s	parameter of the error variance.
CD	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=s/CD^2_i
perf	numeric vector of length=number of individuals which contains the performances of individuals.
PLA	numeric vector (number of individuals) which contains transmission probabilities at a single test position.
DL.m	results provided by proba.DL() function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on dam.
DL.chrom1	results provided by proba.DL() function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on the first chromosome of sire.
DL.chrom2	results provided by proba.DL() function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on the second chromosome of sire.
desc.pere	results provided by descendant.pere() function, numeric matrix (number of sires x 2) which gives for each sire, the first and last indexes of its progeny.
mean.gene	parameter of the performance mean.

Value

The returned value is the value of log likelihood of HAPimLDL method under alternative hypothesis H1.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

moyenne.pere, descendant.pere, proba.DL

`vrais.LDL.add.pere` *intra-sire log likelihood of HAPimLDL method under H1.*

Description

The function calculates the value of intra-sire log likelihood of HAPimLDL method under alternative hypothesis H1. It can be viewed as an internal function. The user does not have to call it by himself.

Usage

```
vrais.LDL.add.pere(moyenne.pere, alpha.Q, s, CD, perf, PLA, LD.m, LD.chrom1,

LD.chrom2, mean.gene)
```

Arguments

`moyenne.pere`	results provided by `moyenne.pere()` function, mean of half-sib family performances.
`alpha.Q`	parameter of QTL effect.
`s`	parameter of the error variance.
`CD`	numeric vector of length=number of individuals which contains the CD of individuals. var(perf$_i$)=s/CD^2_i
`perf`	numeric vector of length=number of individuals which contains the performances of individuals.
`PLA`	numeric vector of length=number of individuals which contains transmission probabilities at a single test position
`LD.m`	results provided by `proba.DL()` function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on dam.
`LD.chrom1`	results provided by `proba.DL()` function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on the first chromosome of sire.
`LD.chrom2`	results provided by `proba.DL()` function, numeric vector of length=number of individuals which contains probabilities due to linkage disequilibrium on the second chromosome of sire.
`mean.gene`	parameter of performance mean.

Value

The returned value is the value of intra-sire log likelihood of HAPimLDL method under alternative hypothesis H1.

Author(s)

S. Dejean, N. Oumouhou, D. Estivals, B. Mangin

References

publication to be submitted: C. Cierco-Ayrolles, S. Dejean, A. Legarra, H. Gilbert, T. Druet, F. Ytournel, D. Estivals, N. Oumouhou and B. Mangin. Combining linkage analysis and linkage disequilibrium for QTL fine mapping in animal pedigrees.

See Also

`moyenne.pere`, `proba.DL`

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