

Package: malaria.em (via r-universe)

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Type Package

Title EM Estimation of Malaria Haplotype Probabilities from Multiply Infected Human Blood Samples

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Description Using EM algorithm to estimate malaria haplotype probabilities and the number of infections from multiply infected human blood samples. Estimated haplotype probabilities and their standard error are reported.

License GPL-2

LazyLoad yes

LazyData yes

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Repository <https://plasmogenepi.r-universe.dev>

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Contents

malaria.em 2

Index 4

malaria.em

EM Estimation of Malaria Haplotype Probabilities and Number of Infections from Multiply Infected Human Blood Samples

Description

Compute the maximum likelihood estimates for malaria haplotype probabilities and number of infections based on the malaria genotype data using Expectation-Maximization approach.

Usage

```
malaria.em(geno, sizes=c(2), locus.label=NA)
```

Arguments

geno	matrix of genotypes. Each column represents the alleles observed in each of the locus. The observed alleles in each locus are separated by a space, and the order of columns corresponds to the order of loci on a chromosome. If there are K loci, then $\text{ncol}(\text{geno}) = K$. Rows represent the genotypes for each subject.
sizes	An integer or a vector of possible number of parasite strains within individuals in observed data. For example, <code>sizes=c(1:6)</code> means the possible number of parasite strains is ranging from 1 to 6. If the length of sizes is greater than 1, the estimation will assume zero truncated Poisson distribution on the number of parasite strains.
locus.label	vector of labels for loci.

Details

This program is an extension of `haplo.em()` function in `haplo.stats` package, which computes the maximum likelihood estimates (MLEs) of haplotype probabilities in diploid population. Since in malaria setting, the number of the malaria parasite strains is unknown due to the possible multiple infections, we impose a probability distribution on this number. Parameter `sizes` determines the underlying probability distribution. Length of `sizes` more than one will lead to the estimation assuming a truncated Poisson distribution. In this case, the estimation of the Poisson rate and number of infections will be reported. Otherwise, if `sizes` is defined as an integer- `C` for example, the estimation will assume the number of strains is fixed at `C`. Although this assumption is not applicable for malaria setting, it is very useful for any genetic data, in which the number of chromosomes is same across all samples. By default, `sizes=2`, which reduces to `haplo.em()` and give the MLEs of the haplotype probabilities in diploid population.

Value

haplo.prob.tab	matrix of unique haplotypes, MLEs of estimated haplotype probabilities, and their standard errors.
haplotype	matrix of unique haplotypes. Each row represents a unique haplotype, and the number of columns is the number of loci.

haplo.prob	vector of MLEs of haplotype probabilities. The <i>i</i> th element of hap.prob corresponds to the <i>i</i> th row of haplotype.
haplo.prob.std	standard error of the estimated haplotype frequencies.
lambda	estimated Poisson parameter.
NumofInfection	estimated number of infections.
haplo.sets	List of all possible haplotype combinations and their posterior probability per subject. The first column named <i>ids</i> is a vector for row index of subjects after expanding to all possible haplotype combinations for each subject. If <i>ids=i</i> , then <i>i</i> is the <i>i</i> th row of <i>geno</i> . If the <i>i</i> th subject has <i>n</i> possible haplotype combinations that correspond to their marker genotype, then <i>i</i> is repeated <i>n</i> times. The value in the second column is the row numbers of the unique haplotypes in the returned haplotype matrix.
n.haplo.set	vector of maximum number of haplotype combinations per subject that are consistent with their marker data in the matrix <i>geno</i> . The length of <i>n.haplo.set</i> = <i>nrow(geno)</i> .
pred.haplo.set	Predicted haplotype combination that is consistent with their marker data for each subject. The values in <i>pred.haplo.set</i> are the row numbers of the unique haplotypes in the returned haplotype matrix.

Author(s)

Xiaohong Li

References

Li, X., Foulkes, A.S., Yucel, R. and Rich, S.M. (2007) An expectation maximization approach to estimate malaria haplotype frequencies in multiply infected children, *Statistical Applications in Genetics and Molecular Biology*, Vol. 6 : Iss. 1, Article 33.

Examples

```
data(geno)

sizes<-c(2)
ret1<-malaria.em(geno,sizes,locus.label=c("DQB","DRB") )

sizes<-c(1:3)
ret2<-malaria.em(geno,sizes,locus.label=c("DQB","DRB") )
```

Index

findCandidatesForAllGenotypes
(malaria.em), 2

findHaplotypeCandidateOneGenotype
(malaria.em), 2

funOfLambda (malaria.em), 2

genAllHaploSetList (malaria.em), 2

genAllHaploSetListForOneGenotype
(malaria.em), 2

geno (malaria.em), 2

getAllCoefficientQij.C (malaria.em), 2

getAllConfig.C (malaria.em), 2

getAllHaplotypes (malaria.em), 2

getAllQij.C (malaria.em), 2

getAllScore.C.em (malaria.em), 2

getAllWeight.C.em (malaria.em), 2

getCoefficientQij.C (malaria.em), 2

getDesignforAllGenotypes.additive.allhaplotype
(malaria.em), 2

getDesignforOneGenotype.additive
(malaria.em), 2

getHaplotypesWithLoci (malaria.em), 2

getLocitypeFromOneGenotype
(malaria.em), 2

getNextHaploSet (malaria.em), 2

getNextIndex (malaria.em), 2

getoneHaploSet.vector.C (malaria.em), 2

getOneHaplotype (malaria.em), 2

getoneL.C.em (malaria.em), 2

getOneNumset.C (malaria.em), 2

getOneQij.C (malaria.em), 2

getoneQij.vector.C (malaria.em), 2

getOneScore.C.em (malaria.em), 2

getOneScore.haplotype.em (malaria.em), 2

getoneWeight.C.em (malaria.em), 2

getStd.em (malaria.em), 2

getUniqueGenotype (malaria.em), 2

getUniqueGenotypeCount (malaria.em), 2

getVector.C (malaria.em), 2

Ginv (malaria.em), 2

haploSet2Genotype (malaria.em), 2

isLastSet (malaria.em), 2

logL (malaria.em), 2

malaria.em, 2

newton.glm (malaria.em), 2

num.unique.allele (malaria.em), 2

print.malaria.em (malaria.em), 2

sortGenotypes (malaria.em), 2

toGenotypes (malaria.em), 2