Package 'mut'

May 2, 2017

Type Package

Title Pairwise Likelihood Ratios

Version 1.1

Date 2017-05-2

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Depends R (>= 3.2.0), Familias, paramlink, expm, IBDsim

Description Main function LR2 calculates likelihood ratio for non-inbred relationships accounting for mutation, silent alleles and theta correction. Egeland, Pinto and Amorim (2017) <DOI:10.1016/j.fsigen.2017.04.018>.

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

Date/Publication 2017-05-02 07:55:54 UTC

R topics documented:

`ibd1.parental` *Estimates for a pair of non-inbred individuals the probabilities of paternal origin when IBD is 1*

Description

Assume IBD is 1 for a pair of non-inbred individuals. The function estimates the probabilities of the four possible combinations of parental origin: (i) paternal-paternal, (ii) paternal-maternal, (iii) maternal-paternal and (iv) maternal-maternal.

Usage

```
ibd1.parental(x, id.pair, Nsim, cM = 10000, verbose = F, ...)
uniformMap(Mb = NULL, cM = NULL, M = NULL, cm.per.mb = 1,
        chromosome = 1)
```

Arguments

x	A pedigree in the form of a linkdat object.
id.pair	Integer vector of length 2 giving the pair of individuals.
Nsim	Integer. Number of simulations.
cM	NULL, or a non-negative number: The distance in centiMorgan between the two loci.
verbose	logical
...	Further arguments to be passed on to IBDsim.
Mb	Double
M	Double
cm.per.mb	Double
chromosome	integer

Details

This is a wrapper for IBDsim.

Value

alpha.sample	Each column gives the four alpha values.
alpha.hat	Estimates of alpha.

Author(s)

Magnus Dehli Vigeland and Thore Egeland

See Also

IBDsim.

Examples

```
library(IBDsim)
x = doubleFirstCousins()
ids = c(9,10)
ibd1.parental(x, ids, 10)$alpha.hat
x = swapSex(x,3)
ibd1.parental(x, ids, 10)$alpha.hat
```

lik2 *Pairwise likelihood with mutation*

Description

Detailed balance (DB) is assumed for the mutation model and the likelihood is calculated for a pair of non-inbred individuals.

Usage

```
lik2(g1, g2, n, p, M, kappa, alpha, theta, beta=0.5)
```

Arguments

g1	Genotype, two integers giving the alleles for individual 1.
g2	Genotype, two integers giving the alleles for individual 2.
n	Integer vector of length 4 giving the distance between paternal, paternal-maternal, maternal-paternal alleles and maternal.
p	Vector of real numbers. Allele frequency vector.
M	Matrix of real numbers. Mutation matrix.
kappa	Vector of real numbers describing relationship. IBD parameters for 0,1,2 IBD alleles.
alpha	Four probabilities, summing to 1, giving the probability, in case IBD=1, that the alleles are paternal, paternal-maternal, maternal-paternal, and maternal.
theta	Real in [0,1]. Kinship coefficient.
beta	Real in [0,1]. Probability of same parental origin when IBD=2.

Details

There are two non-inbred individuals A and B, with genotypes a/b and c/d, where the alleles may or may not differ. We calculate the likelihood assuming a relationship described by kappa.

Value

likelihood, real.

Author(s)

Thore Egeland <Thore.Egeland@nmbu.no>

References

Egeland, Pinto and Amorim, FSI:Genetics (2017), http://dx.doi.org/10.1016/j.fsigen.2017.04.018.

Examples

```
library(expm)
library(Familias)
# Example 1. Paternity case. Silent allele, mutation
p <- c(0.2, 0.75, 0.05); R <- 0.005
locus1 <- FamiliasLocus(frequencies=p, name="L1", allelenames=c("1","2",  "silent"),
femaleMutationRate = R, maleMutationRate =R,femaleMutationRange = 0.1,
maleMutationRange = 0.1,femaleMutationRate2 = 0, maleMutationRate2 = 0,
maleMutationModel="Proportional", femaleMutationModel="Proportional")
M <- locus1$maleMutationMatrix
theta <- 0.03
n <- c(0, 1, 1, 0); kappa.num <- c(0, 1, 0); kappa.den <- c(1, 0, 0);alpha <- c(0, 0.5, 0.5, 0)
t1 <- lik2(c(1,1), c(2,2), n, p, M, kappa.num, alpha, theta)
t2 <- lik2(c(1,3), c(2,2), n, p, M, kappa.num, alpha, theta)
t3 <- lik2(c(1,1), c(2,3), n, p, M, kappa.num, alpha, theta)
t4 <- lik2(c(1,3), c(2,3), n, p, M, kappa.num, alpha, theta)
u1 <- lik2(c(1,1), c(2,2), n, p, M, kappa.den, alpha, theta)
u2 <- lik2(c(1,3), c(2,2), n, p, M, kappa.den, alpha, theta)
u3 <- lik2(c(1,1), c(2,3), n, p, M, kappa.den, alpha, theta)
u4 <- lik2(c(1,3), c(2,3), n, p, M, kappa.den, alpha, theta)
num <- t1 + t2 + t3 + t4
den <- u1 + u2 + u3 + u4
LR1 <- num/den
# Below LR is checked using Familias
persons <- c("AF", "CH")
sex <- c("male", "male")
#Define the alternative pedigrees
ped1 <- FamiliasPedigree(id=persons, dadid=c(NA,"AF"),
momid=c(NA,NA), sex=c("male", "male"))
ped2 <- FamiliasPedigree(id=persons, dadid=c(NA,NA),
momid=c(NA,NA), sex=c("male", "male"))
pedigrees <- list(ped1,ped2)
datamatrix <- data.frame(locus1.1=c(1,2), locus1.2=c(1,2))
rownames(datamatrix) <- persons
result <- FamiliasPosterior(pedigrees, locus1, datamatrix, ref=2, kinship = theta)
LR2 <- result$LR[1]
stopifnot(abs(LR1 - LR2) <1e-15)
###
library(Familias)
test <- function(a, b, c, d, R, model="Proportional",
p=c(0.1,0.2,0.3,0.3,0.1), theta=0){
anames <- 1:length(p)
datamatrix <- cbind(c(NA,NA,a,c,NA,NA),c(NA,NA,b,d,NA,NA))
persons <- c("FA","MO", "B1", "B2","EM","EF")
rownames(datamatrix) <- persons
seks <- c("male", "female", "male", "male","male","female")
ped1 <- FamiliasPedigree(id=persons, dadid=c(NA, NA,"FA","FA",NA, NA),
        momid=c(NA, NA,NA,NA,NA, NA), sex = seks)
ped2 <- FamiliasPedigree(id=persons, dadid=c(NA, NA,"FA","FA",NA, NA),
        momid=c(NA, NA,"MO","MO",NA, NA), sex =seks)
ped3 <- FamiliasPedigree(id=persons, dadid=c(NA, NA,"B2",NA,NA, NA),
        momid=c(NA, NA,NA,NA,NA, NA), sex =seks)
```

```
ped4 <- FamiliasPedigree(id=persons, dadid=c(NA, NA,NA,NA,NA, NA),
        momid=c(NA, NA,NA,NA,NA, NA), sex =seks)
ped5 <- FamiliasPedigree(id=persons, dadid=c("B1", NA,NA,"FA",NA, NA),
        momid=c(NA, NA,NA,NA,NA, NA), sex =seks)
ped6 <- FamiliasPedigree(id=persons, dadid=c(NA, "B1",NA,"FA",NA, NA),
        momid=c("MO", NA,NA,NA,NA, NA), sex =seks)
ped7 <- FamiliasPedigree(id=persons, dadid=c("EM", "EM","FA",NA,NA, NA),
        momid=c("EF", "EF",NA,"MO",NA, NA), sex =seks)
ped8 <- FamiliasPedigree(id=persons, dadid=c("EM", "B1",NA,"FA",NA, NA),
        momid=c(NA, NA,NA,NA,"MO", NA), sex =seks)
ped9 <- FamiliasPedigree(id=persons, dadid=c(NA, NA,"FA","EM","FA", NA),
        momid=c(NA, NA,"MO",NA,"MO", NA), sex =seks)
ped10 <- FamiliasPedigree(id=persons, dadid=c(NA, NA,"FA","EM",NA, NA),
         momid=c("EF", NA,"MO","MO","EF", NA), sex =seks)
peds <- list(HS=ped1,FS=ped2, PO=ped3, UNR=ped4,GP=ped5, GR=ped6,
          CO=ped7,GGR=ped8,AVU=ped9,diff=ped10)
locus1 <- FamiliasLocus(frequencies=p, name="locus1",
          allelenames= anames, MutationRate=R, MutationModel=model)
res <- FamiliasPosterior(peds, locus1, datamatrix)
M <- locus1$maleMutationMatrix
g1 <- c(a,b); g2 <- c(c,d)
l1 <- lik2(g1, g2, n=c(1,0,0,0),p,M,
kappa=c(0.5,0.5,0), alpha=c(1,0,0,0), theta)
l2 <- lik2(g1, g2, n=c(1,1,1,1), p, M,
kappa=c(0.25,0.5,0.25), alpha=c(1,1,1,1)/4, theta)
l3 <- lik2(g1, g2, n=c(1,1, 0,0),p, M,
kappa=c(0,1,0.0), alpha=c(0.5, 0.5, 0, 0), theta)
l4 <- lik2(g1, g2, n=c(0,0,0,0), p, M,
kappa=c(1,0,0.0), alpha=c(1,1,1,1)/4, theta)
l5 <- lik2(g1, g2, n=c(1,1,0,0), p, M,
kappa=c(0.5, 0.5,0.0), alpha=c(0.5, 0.5, 0, 0), theta)
l6 <- lik2(g1, g2, n=c(2,2,0,0), p, M,
kappa=c(0.75, 0.25,0.0), alpha=c(0.5, 0.5, 0, 0), theta)
l7 <- lik2(g1, g2, n=c(0,4,0,0), p, M,
kappa=c(0.75, 0.25,0.0), alpha=c(0, 1, 0, 0), theta)
l8 <- lik2(g1, g2, n=c(3,3,0,0), p, M,
kappa=c(7/8, 1/8,0.0), alpha=c(0.5, 0.5, 0, 0), theta)
l9 <- lik2(g1, g2, n=c(3,3,0,0), p, M,
kappa=c(0.5, 0.5,0.0), alpha=c(0.5, 0.5, 0, 0), theta)
l10 <- lik2(g1, g2, n=c(4,0,0,0), p, M,
kappa=c(7, 8, 1)/16, alpha=c(1,0, 0, 0), theta)
fam <- res$likelihoods
exact <- c(l1,l2,l3,l4,l5,l6,l7,l8,l9,l10)
z <- abs(res$likelihoods-exact)
check <- all(z< 1e-10)
res <- cbind(fam,exact)
colnames(res) <- c("Familias","Exact")
rownames(res) <- c("HS","FS","PO", "UNR","GP","GGP","CO","GGGP", "UNC","HS+")
list(res, check=check)
}

data(NorwegianFrequencies)
d <- NorwegianFrequencies$D12S391
```

```
names(d) <- 1:length(d) #21=16, 22=17 etct
foo3 <- test(16,17,18,19,R=0.00,"Proportional", p=as.double(d))
foo3 <- foo3[[1]]
foo4 <- test(16,17,18,19,R=0.0021,"Proportional", p=as.double(d))
foo4 <- foo4[[1]]
foo5 <- test(16,17,18,19,R=0.0021,"Equal", p=as.double(d))
foo5 <- foo5[[1]]
foo6 <- test(18,19,16,17,R=0.0021,"Equal", p=as.double(d))
foo6 <- foo6[[1]]
foo <- cbind(foo3,foo4,foo5,foo6)
foo <- foo[,c(1,3,5,7)]
kappa <- c("(0.5,0.5,0)","(0.25,0.5,0.25)","(0,1,0)","1,0,0)",
           "(0.5,0.5,0)","(0.75,0.25,0)","(0.75,0.25,0)","(7/8,1/8,0)","(0.5,0.5,0)",
           "(7/16,8/16,1/16)")
Table1 <- data.frame(kappa,foo)
colnames(Table1) <- c("kappa","R=0","R=0.0021","R=0.0021(Eq)","Swapped")
Table1

# Example  First example of paper
foo1 <- test(1,1,2,2,R=0.005, model="Equal",p=c(0.1,0.9) )[[1]][3,1]
foo2 <- test(2,2,1,1,R=0.005, model="Equal",p=c(0.1,0.9) )[[1]][3,1]
foo1/foo2 #=9, i.e., no 1
foo1 <- test(1,1,2,2,R=0.005, model="Proportional",p=c(0.1,0.9) )[[1]][3,1]
foo2 <- test(2,2,1,1,R=0.005, model="Proportional",p=c(0.1,0.9) )[[1]][3,1]
foo1/foo2 # =1
#LR with general mutation matrix using Familias
library(Familias)
id <- c("I", "II")
I.II <- FamiliasPedigree(id, c(NA, "I"), c(NA, NA), c("male", "male"))
II.I <- FamiliasPedigree(id, c(NA, NA), c(NA, NA), c("male", "male"))
pedigrees <- list( I.II = I.II, II.I = II.I)
m12 <- 1/100; m21 <- 3/100
M <- rbind(c(1-m12,m12),c(m21,1-m21))
p1 <- m21/(m12+m21);p2 <- m12/(m12+m21); p <- c(p1,1-p1)
anames <- 1:length(p)
locus1 <-FamiliasLocus(frequencies = p,"locus1",
                       allelenames = anames,
          MutationModel="Custom", MutationMatrix=M)
locus2 <-FamiliasLocus(frequencies = p,"locus2",
                       allelenames = anames,
          MutationModel="Custom", MutationMatrix=M)
datamatrix <- data.frame(locus1.1=c(1,2), locus1.2=c(1,2), locus2.1=c(2,1),locus2.2=c(2,1))
rownames(datamatrix) <- c("I","II")
myloci <- list(locus1,locus2)
LRs <- FamiliasPosterior(pedigrees,myloci, datamatrix,ref=2)$LRperMarker[,1]
#Both above:
m12+m21
#Example 3 Stationarity not enough
library(Familias)
id <- c("I", "II")
I.II <- FamiliasPedigree(id, c(NA, "I"), c(NA, NA), c("male", "male"))
II.I <- FamiliasPedigree(id, c(NA, NA), c(NA, NA), c("male", "male"))
pedigrees <- list( I.II = I.II, II.I = II.I)
```

```
R <- 0.1
M <- rbind(c(1-2*R,3*R/2,R/2),c(R/2,1-R,R/2),c(R/2,R/2,1-R))
p <- c(3,7,5)/15
anames <- 1:length(p)
locus1 <-FamiliasLocus(frequencies = p,"locus1",
                       allelenames = anames,
          MutationModel="Custom", MutationMatrix=M)
locus2 <-FamiliasLocus(frequencies = p,"locus2",
                       allelenames = anames,
          MutationModel="Custom", MutationMatrix=M)
datamatrix <- data.frame(locus1.1=c(1,2), locus1.2=c(1,2), locus2.1=c(2,1),locus2.2=c(2,1))
rownames(datamatrix) <- c("I","II")
myloci <- list(locus1,locus2)
result1 <- FamiliasPosterior(pedigrees,myloci, datamatrix,ref=2)
result1$LRperMarker
result1$LRperMarker[1]-45*R/14
result1$LRperMarker[2]-35*R/14
for (i in 1:10000) p <- p
p

# Example 3
# Exact calculation with SNP-s for an example of the paper
example2 <- function(p=0.4,R=0.005){
k <- R/(2*p*(1-p))
m11 <- 1-k*(1-p)
m22 <- 1- k*p
HS <- 0.5*p^4+0.5*p^3*(m11^2+k^2*p*(1-p))
UNC <- 0.5*p^4+0.5*p^3*(m11^3+2*k^2*p*(1-p)*m11+k^2*(1-p)*p)
GGP <- 0.75*p^4+0.25*p^3*(m11^3+2*k^2*p*(1-p)*m11+k^2*(1-p)*p)
list(HS.GP=HS,UNC=UNC, GGP=GGP)
}
p <- 0.4; R <- 0.005
example2(p,R)
test(1,1,1,1,R=R,"Proportional", p=c(p,1-p))[[1]][c(1,5,9,6),1]

#Example 4
data(NorwegianFrequencies)
p<-as.double(NorwegianFrequencies$D12S391)
k <- 0.0021/sum(p*(1-p))

#Example 5
#Same mother, father brothers
rm(list=ls())
a <- 1;b <- 2; c <- 1;d <- 3
persons <- c("FA","MO", "B1", "B2","EM","EF","EM2")
seks <- c("male", "female", "male", "male","male","female","male")
R <- 0.0021; model <- "Proportional"; p <- c(0.1,0.2,0.3,0.3,0.1)
anames <- 1:length(p)
ped11 <- FamiliasPedigree(id=persons, dadid=c("EM2", NA,"FA","EM","EM2", NA,NA),
        momid=c("EF", NA,"MO","MO","EF", NA, NA), sex =seks)
datamatrix <- cbind(c(NA,NA,a,c,NA,NA,NA),c(NA,NA,b,d,NA,NA,NA))
rownames(datamatrix) <- persons
locus1 <- FamiliasLocus(frequencies=p, name="locus1",
```

```
             allelenames= anames, MutationRate=R, MutationModel=model)
res <- FamiliasPosterior(ped11, locus1, datamatrix)
M <- locus1$maleMutationMatrix
l11 <- lik2(c(a,b),c(c,d), n = c(4,0,0,2), p,M,
kappa=c(3/8,4/8,1/8), alpha=c(1/4,0,0,3/4), theta=0)
 c(res$likelihoodsPerSystem,l11)
```

LR2 *Pairwise LR with Mutation*

Description

Detailed balance (DB) is assumed for the mutation model and the LR is calculated for a pair of non-inbred individual as described in the paper Egeland, Pinto and Amorim, FSI: Genetics (2017).

Usage

```
LR2(g1, g2, n.num, n.den, p, M, kappa.num, kappa.den, alpha, theta, silent, beta)
```

Arguments

g1	Genotype, two integers giving the alleles for individual 1.
g2	Genotype, two integers giving the alleles for individual 2.
n.num	Integer vector of length 4 giving the distance in number of meioses between paternal, paternal-maternal, maternal-paternal alleles and maternal for numerator hypothesis.
n.den	Integer vector of length 4 giving the distance in number of meioses between paternal, paternal-maternal, maternal-paternal alleles and maternal for denominator hypothesis.
p	Vector of real numbers summing to 1. Allele frequency vector.
M	Matrix of real numbers in [0,1] with lines summing to 1. Mutation matrix.
kappa.num	Vector of real numbers in [0,1] summing to 1 describing relationship for numerator hypothesis. IBD parameters for 0,1,2 IBD alleles.
kappa.den	Vector of real numbers describing relationship for denominator hypothesis. IBD parameters for 0,1,2 IBD alleles.
alpha	Four probabilities, summing to 1, giving the probability, in case IBD=1, that the alleles are paternal-paternal, paternal-maternal, maternal-paternal, and maternal-maternal.
theta	Real in [0,1]. Kinship coefficient.
silent	Logical, see below.
beta	Real in [0,1]. Probability of same parental origin when IBD=2.

Details

There are two non-inbred individuals A and B, with genotypes a/b and c/d, where the alleles may or may not differ. We calculate the likelihood assuming a relationship described by kappa.num, the likelihood assuming kappa.den (typically unrelated) and the LR. If `silent=TRUE` the last allele frequency of p corresponds to the silent allele.

Value

numerator, denominator and LR=numerator/denominator.

Author(s)

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References

Egeland, Pinto and Amorim, FSI: Genetics (2017), http://dx.doi.org/10.1016/j.fsigen.2017.04.018.

Examples

```
library(expm)
library(Familias)
### The examples are from Egeland, Pinto and Amorim (2016)
### (referred to as the 'paper' below)
### Example 2.1.
### Consider a duo case and assume mutations are not possible.
p <- c(0.1,0.2,0.3,0.4)
M <- diag(c(1,1,1,1))
n.num <- c(2, 2, 2, 2)
n.den <- c(0, 0, 0, 0)
alpha <- c(1,1,1,1)/4
kappa.num <- c(0.25, 0.50, 0.25); kappa.den <- c(1,0,0); theta <- 0
# The next three LRs coincide with those found
# using exact formulae in the paper
LR2(c(1,2), c(3,4),  n.num, n.den, p, M, kappa.num,
  kappa.den, alpha, theta)$LR
LR2(c(1,2), c(1,3),  n.num, n.den, p, M, kappa.num,
  kappa.den, alpha, theta)$LR
LR2(c(1,2), c(1,2),  n.num, n.den, p, M, kappa.num,
  kappa.den, alpha, theta)$LR

### Example 2.2 Identifying parent-child with mutation
### "A father and a son are missing ..."
p <- 0.2; R <- 0.005; k <- R/(2*p*(1-p))
M <- rbind(c(1-k*(1-p),k*(1-p)),c(k*p,1-k*p))
n.num <- c(0, 1, 1, 0); kappa.num <- c(0, 1, 0)
n.den <- c(0, 0, 0, 0); kappa.den <- c(1, 0, 0)
alpha <- c(0, 0.5, 0.5, 0)
theta <- 0.0
# Below values coincide, this is no longer true if
# M is made unbalanced or theta>0
```

```
LR2(c(1,1), c(2,2),  n.num, n.den, c(p, 1-p), M,
    kappa.num, kappa.den, alpha, theta)$LR
LR2(c(2,2), c(1,1),  n.num, n.den, c(p, 1-p), M,
    kappa.num, kappa.den, alpha, theta)$LR

### Example 2.3
library(Familias)
persons <- c("Child", "Alleged father")
sex <- c("male", "male")
ped1 <- FamiliasPedigree(id=persons, dadid=c("Alleged father",NA),
  momid=c(NA,NA), sex=c("male", "male"))
ped2 <- FamiliasPedigree(id=persons, dadid=c(NA,NA), momid=c(NA,NA),
  sex=c("male", "male"))
pedigrees <- list(ped1,ped2)
R =.01; theta = 0.02
locus1 <- FamiliasLocus(frequencies=c(0.25,0.25,0.25,0.25),
  name="L1", allelenames=c("1","2","3","4"),
  MutationRate = R, MutationModel="Proportional")
loci <- list(locus1)
datamatrix <- data.frame(locus1.1=c("3","1"), locus1.2=c("4","2"))
datamatrix <- data.frame(locus1.1=c("1","3"), locus1.2=c("2","4")) #Swapped, same result
rownames(datamatrix) <- persons
result <- FamiliasPosterior(pedigrees, loci, datamatrix, ref=2, kinship=theta)
result$LR[1]
(1+2*theta)/(1-theta)*(4/3)*R

### Example 3.1 of paper, double first cousin example
p <- 0.2; q <- 1-p; R <- 0.005; k <- R/(2*p*(1-p))
k4 <- 1-(1-k)^4
m <- 1-k4*(1-p)
kappa0 <- 9/16; kappa1 <- 6/16; kappa2 <- 1/16
kappa0+kappa1*m/p+kappa2*m^2/p^2
# LR=3.759526 as confirmed by familias.name/DFC.SNP.fam
# Alternatively using library familias.name/mut.zip
alpha <- c(0,0.5,0.5, 0)
n.num <- c(0,4, 4, 0); n.den <- c(0,0,0,0)
kappaDFC <- c(kappa0, kappa1, kappa2)
LR2(c(1,1),c(1,1),n.num, n.den, M=M, p=c(p,1-p), kappa.num=kappaDFC,
    alpha=alpha, theta=0, beta=0)$LR
# Four alleles
p <- c(0.1,0.2,0.3,0.4)
locus1 <- FamiliasLocus(frequencies=p, name="locus1",
                  allelenames= 1:length(p), MutationRate=R, MutationModel="Proportional")
M <- locus1$maleMutationMatrix
LR2(c(1,1), c(1,1),n.num, n.den, M=M, p=p, kappa.num=kappaDFC,
    alpha=alpha, theta=0, beta=0)
# LR=10.15314 as confirmed by http://familias.name/DFC.4.fam (takes a few minutes)
# With ten alleles, all allele freq 0.1, and  "Equal" mutation model
p <- rep(0.1,10)
locus1 <- FamiliasLocus(frequencies=p, name="locus1",
                       allelenames= 1:length(p), MutationRate=R, MutationModel="Equal")
M <- locus1$maleMutationMatrix
LR2(c(1,1), c(1,1),n.num, n.den, M=M, p=p, kappa.num=kappaDFC,
```

```
    alpha=alpha, theta=0, beta=0)
# LR=10.24266 as confirmed by http://familias.name/DFC.10.fam (takes a few minutes)

### Example 3.2 of paper
library(paramlink)
library(Familias)
R <- 0.005; p <- c(0.01, 0.2, 0.3, 0.49)
g1 <- c(1,2); g2 <- c(1,3)
an <- 1:length(p)
nn1 <- nn2 <- 3; x <- doubleCousins(nn1, nn2)
v <- 3
kappa.num <- c((2^{2*v}-1)^2, 2*(2^{2*v}-1),1)/16^v
alpha <- c(0.5, 0, 0, 0.5)
locus1 <- FamiliasLocus(frequencies=p, name="locus1",
                        allelenames= an, MutationRate=R, MutationModel="Proportional")
M <- locus1$maleMutationMatrix
n1 <- nn1+nn2+2; n2 <- nn1+nn2+2
n.num <- c(n1, 0, 0, n2)
n.den <- c(0, 0, 0, 0)
kappa.den <- c(1,0,0)
myLR <- LR2(g1, g2, n.num, n.den, p, M, kappa.num, kappa.den, alpha, beta=0)
myLR$LR
#Exact
k <- R/(1-sum(p^2))
k10 <- 1-(1-k)^n2
kappa.num[1]+
  kappa.num[2]*(p[3]*(k10*p[1]+(1-k10*(1-p[1]))) +
                  (p[1]*2*k10*p[3]))/(4*p[1]*p[3])  +
  kappa.num[3]*2*((1-k10*(1-p[1]))*k10*p[3]+k10^2*p[1]*p[3])/(4*p[1]*p[3])

### Example 3.3 HS or GP versus avuncular
p <- c(0.1, 0.2, 0.3, 0.4); R <-0.005
locus1 <- FamiliasLocus(frequencies=p, name="L1", allelenames=1:4,
                    femaleMutationRate = R, maleMutationRate =R,femaleMutationRange = 0.1,
                    maleMutationRange = 0.1,femaleMutationRate2 = 0, maleMutationRate2 = 0,
                     maleMutationModel="Proportional",femaleMutationModel="Proportional")
M <- locus1$maleMutationMatrix
kappa.num <- kappa.den <-c(0.5,0.5,0)
alpha <- c(1,0,0,0)
n1 <- c(2,0,0,0)
n2 <- c(3,0,0,0)
a <- 1; b<-2; c<-3; d<-4
g1 <- c(a,b); g2 <- c(c,d)
LR.1 <- LR2(g1, g2,n.num=n1, n.den=n2, p=p, M, kappa.num,
            kappa.den, alpha, theta=0, beta=0)$LR
H <- 1-sum(p^2)
k <- R/H
k2 <- 1-(1-k)^2; k3 <- 1-(1-k)^3
# Case 1: a,b,c,d differ, no overlap in genotypes
LR.2 <- (1+k2)/(1+k3)
LR.1-LR.2#Equal
# Case 2 all a
g1 <- c(a,a); g2 <- c(a,a)
```

```
LR.1 <- LR2(g1, g2,n.num=n1, n.den=n2, p=p, M, kappa.num, kappa.den, alpha, theta=0)$LR
LR.2 <- (p[a]+1-k2*(1-p[a]))/(p[a]+1-k3*(1-p[a])) #all a
#Case 3 equal hetero
c <- 3; d <- 4
g1 <- c(c,d); g2 <- c(c,d)
LR.1 <- LR2(g1, g2,n.num=n1, n.den=n2, p=p, M, kappa.num, kappa.den, alpha, theta=0)$LR
num <- (4*p[c]*p[d]+p[d]*(1+k2*(2*p[c]-1))+p[c]*(1+k2*(2*p[d]-1)))
den <- (4*p[c]*p[d]+p[d]*(1+k3*(2*p[c]-1))+p[c]*(1+k3*(2*p[d]-1)))
LR.2 <- num/den
LR.1-LR.2

# Example QHFC Thompson p 22
p <- c(0.1, 0.9); R <- 0.005
kappa <-c(17,14,1)/32
alpha <- c(0.25,0.25,0.25,0.25)
n.num <- c(4,4,4,4); n.den <- c(0, 0, 0, 0)
locus1 <- FamiliasLocus(frequencies=p, name="locus1",
                  allelenames= 1:length(p), MutationRate=R, MutationModel="Proportional")
M <- locus1$maleMutationMatrix
LR2(c(1,2), c(1,1), n.num, n.den, M=M, p=p, kappa.num=kappa,
    alpha=alpha, theta=0, beta=0.5)
#=2.562366 See familias.name/QHFC.fam

# Example  Last line of Table 1 of old ms, to be balanced paper
data(NorwegianFrequencies)
d <- as.double(NorwegianFrequencies$D12S391)
names(d) <- 1:length(d) #21=16, 22=17 etct
n.num <- c(4,0,0,2); n.den <- c(0, 0, 0, 0)
alpha <- c(1/8,0,0, 7/8);kappa.num <- c(7/16,8/16,1/16)
line <-NULL
R <-0
locus1 <- FamiliasLocus(frequencies=d, name="locus1",
                  allelenames=1:length(d), MutationRate=R, MutationModel="Proportional")
M <- locus1$maleMutationMatrix
line <- c(line, LR2(c(16,17), c(18,19), n.num,  n.den,
                   d, M, kappa.num, alpha=alpha)$numerator)
R <-0.0021
locus1 <- FamiliasLocus(frequencies=d, name="locus1",
                  allelenames=1:length(d), MutationRate=R, MutationModel="Proportional")
M <- locus1$maleMutationMatrix
line <- c(line,LR2(c(16,17),c(18,19),n.num, n.den ,d,M,kappa.num, alpha=alpha)$numerator)
locus1 <- FamiliasLocus(frequencies=d, name="locus1",
                       allelenames=1:length(d), MutationRate=R, MutationModel="Equal")
M <- locus1$maleMutationMatrix
line <- c(line,LR2(c(16,17),c(18,19), n.num, n.den, d, M, kappa.num, alpha=alpha)$numerator)
line <- c(line,LR2(c(18,19),c(16,17), n.den, n.den, d, M, kappa.num, alpha=alpha)$numerator)
names(line) <- paste("col",1:4,sep="")
p <- d[c(16,17,18,19)]
(7/16)*4*prod(p)# First column

#Silent, mutation and kinship
p <- c(0.2, 0.75, 0.05); R <- 0.005
locus1 <- FamiliasLocus(frequencies=p, name="L1",
```

```
                        allelenames=c("1","2",  "silent"),
                    femaleMutationRate = R, maleMutationRate =R,femaleMutationRange = 0.1,
                    maleMutationRange = 0.1,femaleMutationRate2 = 0, maleMutationRate2 = 0,
                        maleMutationModel="Proportional",
                        femaleMutationModel="Proportional")
M <- locus1$maleMutationMatrix
persons <- c("AF", "CH")
sex <- c("male", "male")
H1 <- FamiliasPedigree(dadid=c(NA, "AF"), momid= c(NA,NA),
                       sex=sex, id=persons)
H2 <- FamiliasPedigree(dadid=c(NA, NA), momid= c(NA,NA),
                       sex=sex, id=persons)
dm <- rbind(c(1,1),
            c(2,2))
rownames(dm) <- persons
theta <- 0.03
alpha <- c(0.5, 0.5, 0, 0)
n.num <- c(1, 1, 0, 0)
n.den <- c(0, 0, 0, 0)
pedigrees <- list(H1, H2)
LRfam <- FamiliasPosterior(pedigrees, locus1, dm, ref=2,
                           kinship = theta)$LRperMarker[1]
LR <- LR2(c(1,1), c(2,2), n.num,n.den, p, M, c(0,1,0), c(1,0,0),
          alpha, theta, silent=TRUE)$LR #=0.1973758 as for Familias

# Example in Section 2.1.2. Duo with mutation and theta
R <- 0.01
theta <- 0.02
LR <- 4*(R/3)*(1+2*theta)/(1-theta) #Exact LR

g1 <- c(1,2); g2 <- c(3,4)
n.num <- c(1,0, 1,0); n.den <- c(0, 0, 0, 0)
p <- c(1, 1, 1, 1)/4
kappa.num <- c(0, 1, 0)
kappa.den <- c(1, 0, 0)
alpha <- c(0.5,0.0,0.5,0)
theta <- 0.02
silent <- 0
locus1 <- FamiliasLocus(frequencies=p, name="locus1",
                        allelenames= 1:4, MutationRate=R,
                        MutationModel="Proportional")
M <- locus1$maleMutationMatrix
LR2(g1, g2, n.num, n.den, p, M, kappa.num, kappa.den, alpha, theta, silent)
```

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