Probabilities of multilocus genotypes in SIB recombinant inbred lines

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1 Introduction

Set the working directory where the source functions file exists. You can download it from https://github.com/Kamel20/PMGISRIL.

```
# setwd("the directory")
# source("sibFun.R")
library(eply)
library(Matrix)
library(rlist)
library(rmarkdown)
```

2 Input

This code just needs to provide the locus number and the recombination rates values. For example for $L = 3$

```
L = 3
recRates = c(0.4, 0.2, 0.3)
```

3 The variables names

To gain time we found the variables contribute to the system before.

```
allvar = list.load("allVarTillL=10.rds")
SCHPE = list.load("allContrVarTillL=10.rds")
varNom = allvar[[L]]$symQs
nonSymQs = allvar[[L]]$nonsymQs
scEq = SCHPE[[L]]
```

Or you can use their function to create it again

```
allVar = systemVar(L)
```

```
##
##  Find the variables that are contributing to this system, please wait ...
## done.
```

So, the variable names are

```
varNom = allVar$symQs
```

and the nonsymmetric variable is

```
nonSymQs = allVar$nonsymQs
```

and all possible crossover are

```
scEq = allCrossOver(varNom = varNom)
```

```
##
##  Find the possible crossover for these variable, please wait ...
## done.
```

4 Find the system $AQ = B$

```
res = twoWayRILsib(L, varNom, nonSymQs, scEq)
```

```
##
##  # ====== 3  - Loci ====== #
##
##  Computing the inhomogeneous equation: done.
##
##  Computing the SCHP:  1 >>   2 >>   3 >>   4 >>   5 >>   6 >>   7 >>   8 >>   9 >>
##  done.
```

Hence, the matrix A is

```
A = res$A
A[1:3,1:2]
```

```
##      000                        001
## SQ  "4"                        "4"
## 000 "2*(0.5)*(1-r12)*(1-r23)-1" "0"
## 001 "2*(0.5)*(1-r12)*(r23)"     "-1"
```

and, the matrix B is

```
B = res$B
B[1:3]
```

```
## [1] 1 0 0
```

To solve this linear system you should evaluate this symbolic matrix

```
AA = evalMatrix(A = A, recRates = recRates)
```

```
## r12 = 0.4     r23 = 0.2     r34 = 0.3     r13 = 0.44     r24 = 0.38     r14 = 0.476
```

Hence,

```
sol = solve(AA, B)
names(sol) = varNom
sol
```

```
##          000        001        002        010        011        012
## 0.03413811 0.01322519 0.01308306 0.01125016 0.02666891 0.01045223
##          020        021        022        023
## 0.01164653 0.01027273 0.02641467 0.01048960
```

5 Verification

To verify that the sum of all Q's equal to 1

```
QsProbs = rbind(sol, table(nonSymQs))
sum(QsProbs[1,] * QsProbs[2,])
```

```
## [1] 1
```

For more detalis see (Jebreen, Petrizzelli and C.Martin, 2019).

Bibliography

Jebreen, Kamel, Marianyela Petrizzelli and Olivier C.Martin. 2019. "Probabilities of multilocus genotypes in SIB recombinant inbred lines." *Statistical Genetics and Methodology, a section of the journal Frontiers in Genetics.* p. Submitted.