

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(epl)
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 details see (Jebreen, Petrizzelli, and C. Martin).

Bibliography

Jebreen, K., M. Petrizzelli, and Olivier. C. Martin. “Probabilities of Multilocus Genotypes in SIB Recombinant Inbred Lines.” Statistical Genetics and Methodology, a section of the journal Frontiers in Genetics. Submitted (05, 2019).