

# 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
##      [,1] [,2]
## [1,] 4.00  4
## [2,] -0.52  0
## [3,] 0.12 -1
```

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
```

This means,

```
## Q(0,0,0) = 0.03413811 , Q(0,0,1) = 0.01322519 , Q(0,0,2) = 0.01308306
## Q(0,1,0) = 0.01125016 , Q(0,1,1) = 0.02666891 , Q(0,1,2) = 0.01045223
## Q(0,2,0) = 0.01164653 , Q(0,2,1) = 0.01027273 , Q(0,2,2) = 0.02641467
## Q(0,2,3) = 0.0104896
```

## 5 Verification

Note 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 et al., 2019](#)).

## Bibliography

Jebreen, K., Petrizzelli, M., and Martin, O. C. (2019). Probabilities of multilocus genotypes in SIB recombinant inbred lines. (Submitted). *Statistical Genetics and Methodology, a section of the journal Frontiers in Genetics*.