

# Probabilities of multilocus genotypes in SIB recombinant inbred lines

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## 1 Introduction

Set the working directory to the emplacement of the source file “PMG\_SIB\_RILs\_OM.R” and load it to the working environment. You can download the “PMG\_SIB\_RILs\_OM.R” file from <https://github.com/Kamel20/PMGISRIL>,

```
setwd("the directory")
source("PMG_SIB_RILs_OM.R")
```

Then load the required packages:

```
library(epl)
library(rlist)
library(rmarkdown)
```

## 2 Input

This code just needs to input the locus number  $L_{loci}$  and the recombination rates for successive intervals which is a vector of length  $L_{loci} - 1$ . For example, for  $L_{loci} = 3$

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

## 3 The variables names (all Qs and all non-equivalent Qs)

To gain time we found the list of inheritance indexes (all Qs) that contribute in the system (till  $L_{loci} = 10$

```
allQs = list.load("allVarTillL=10.rds")
allvpForallup = list.load("allContrVarTillL=10.rds")

nonEquivalentQs = allQs[[L]]$symQs
allQsMappedToNonEquivalent = allQs[[L]]$nonsymQs
allvpForallup = allvpForallup[[L]]
```

or you can get all indices to work with using their functions using to const

```
allQs = systemVar(L_loci)
```

```
##
```

```
## Find the inheritance indexes that are contributing to this system, please wait ...
```

Note that, the non-equivalents Qs are

```
nonEquivalentQs = allQs$symQs
```

and the distinct Qs are

```
allQsMappedToNonEquivalent = allQs$indicesAllQs
```

Note that the first equation of the linear system is given by the fact that  $\sum(Qs) = 1$

```
multiplicityQs = table(allQsMappedToNonEquivalent)
```

This means that

```
## 4Q(000)+4Q(001)+8Q(002)+4Q(010)+4Q(011)+8Q(012)+8Q(020)+8Q(021)+8Q(022)+8Q(023)=1
```

Now, Constructs the list of all  $v'$  given the  $u'$  to be used to construct the self-consistent equations.

```
allvpForallup = allvprimeForEachuprime(nonEquivalentQs)
```

```
## 10% 20% 30% 40% 50% 60% 70% 80% 90% 100%
```

## 4 Find the system $AQ = B$

The analytic expressions of the system of linear equations to be solved are

```
analyticEquations = twoWayRILsib(L_loci, nonEquivalentQs, allQsMappedToNonEquivalent, allvpForallup
```

```
##
## # ===== 3 - Loci ===== #
##
## 1. The First equation in the system is:
## 4Q(000)+4Q(001)+8Q(002)+4Q(010)+4Q(011)+8Q(012)+8Q(020)+8Q(021)+8Q(022)+8Q(023)=1
##
## 2. Computing the self-consistent equations: ...
## 1 of 9
2 of 9
3 of 9
4 of 9
5 of 9
6 of 9
7 of 9
8 of 9
9 of 9
## done
```

Hence, the matrix of equations is

```
Amatrix = analyticEquations$A
Amatrix[1:3,1:2]
```

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

and, the coefficient matrix is

```
Bvector = analyticEquations$B
Bvector[1:3]
```

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

By substitute the numerical values of the recombination rates

```
numericAmatrix = evalMatrix(A = Amatrix, recRates = recRates)

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

For example,

```
numericAmatrix[1:3,1:2]

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

Hence, the solution for the  $N_Q(L)$  unknown (non-equivalent)  $Q$ s is

```
solution = solve(numericAmatrix, Bvector)
names(solution) = nonEquivalentQs
solution

##      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 Convert $Q_s$ to RIL multilocus genotype probabilities

To Convert  $Q_s$  (RIL IBD probabilities) to RIL multilocus genotype probabilities by computing the  $2^L$  probabilities of multilocus SIB RIL genotypes

```
allProbabilitiesOfRilGenotypes= QsToGenotypeProbabilities(L_loci, solution)

## 10% 20% 30% 40% 50% 60% 70% 80% 90% 100%

allProbabilitiesOfRilGenotypes

## [1] 0.17056473 0.09414115 0.08767703 0.14761709 0.14761709 0.08767703
## [7] 0.09414115 0.17056473
```

Note the that the sum of these probabilities should be one

```
sumAllProbabilities = sum(allProbabilitiesOfRilGenotypes)
sumAllProbabilities

## [1] 1
```

For more detalis see (Jebreen et al., 2019).

## Bibliography

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