Module 2: Linkage Disequilibrium in R

Fundamentals of Genomic Prediction and Data-Drive Crop Breeding

(August 4-8, 2025)

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August 3, 2025

Contents

Install and load the packages

- Here in this section we will install and load the required packages

```
>   rm(list=ls()) # remove the previous history
> # Install
>   #install.packages("BGLR")
>   #install.packages("genetics")
> # Installing snpStats package from Bioconuctor
>   #if (!requireNamespace("BiocManager", quietly = TRUE))
>     #install.packages("BiocManager")
> #BiocManager::install("snpStats")
> # Load the packages
>   library(BGLR)
>   library(genetics)
>   library(pheatmap)
>   #library(LDheatmap)
```

Load the Data

Here we will use R package genetics to measure LD. We will use **mice marker data** given with the package and subset only first 20 markers to estimate LD. The data sets are also available in the folder.

```
> # Read the mice marker data
>   #mice.X<-read.csv(file="mice.X.csv", header = TRUE)
> # Load the mice data
>   data(mice)
> # Subset the mice data, first 20 markers
>   mice.20<- mice.X[, 1:20] # use the first 10 markers
> # Visualize first 5 rows and columns
>   mice.20[1:5, 1:5] # Data is coded 0, 1 and 2
           rs3683945_G rs3707673_G rs6269442_G rs6336442_G rs13475700_A
A048005080           1           1           1           1            0
A048006063           1           1           2           1            1
A048006555           2           0           2           2            0
A048007096           1           1           1           1            1
A048010273           2           0           2           2            0
```

Estimate LD

First we will convert the allele counts into genotypes or haplotypes using ***makeGenotypes*** function of genetics package. Then we will measure LD using function ***LD***. Function ***LD*** return you list of 8 outputs including D and r^2 values.

```
> # Make genotypes
>   mice.20.G<- makeGenotypes(mice.20, convert=c(colnames(mice.20)), method=as.genotype.allele.count)
> # Visualize first 5 rows and columns
>   mice.20.G[1:5, 1:5] # Data is coded 0, 1 and 2
```

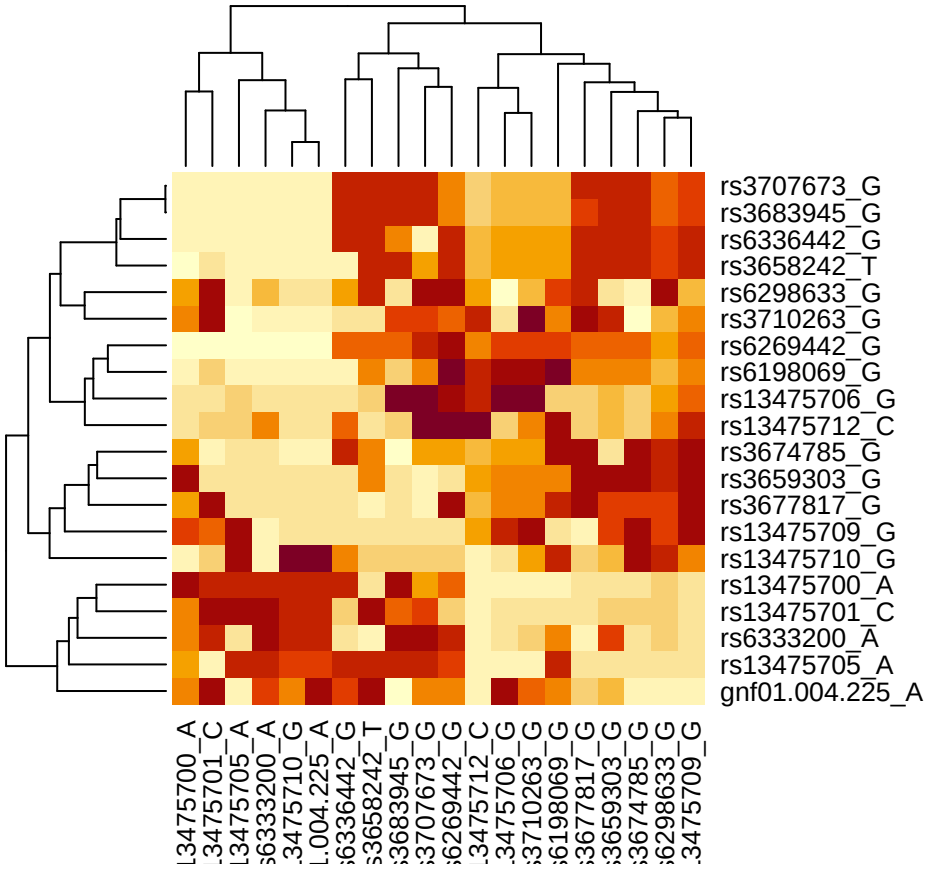
	rs3683945_G	rs3707673_G	rs6269442_G	rs6336442_G	rs13475700_A
A048005080	A/B	B/A	A/B	A/B	B/B
A048006063	A/B	B/A	A/A	A/B	B/A
A048006555	A/A	B/B	A/A	A/A	B/B
A048007096	A/B	B/A	A/B	A/B	B/A
A048010273	A/A	B/B	A/A	A/A	B/B

```
> # Now calculate the LD
>   LD.20<- LD(mice.20.G) # This will return the list
>   names (LD.20)
[1] "call"    "D"       "D'"      "r"       "R^2"     "n"       "X^2"
[8] "P-value"
> # Extract r2 ( Hill and Robertson (1968)
>   r2<-LD.20$`R^2`
> # Copy upper part of matrix to lower for visualizations
>   lowerTriangle(r2) <- upperTriangle(r2)
> # Convert Diagonal to 1
>   diag(r2)<-1
```

Heat map to Visualize the lD

- Here we will visualize the r^2 matrix as heatmap.

```
> ld.map<-heatmap(r2)
```




```
> ld.map
$rowInd
 [1] 19 12 15  7  5 18 16 11  9 10 20 13  8  3 14 17  6  4  1  2

$colInd
 [1]  5  7 12 15 18 19  4  6  1  2  3 20 13 14  8 11  9 10 17 16

$Rowv
NULL

$Colv
NULL
```

Additional Read and Literature

- Genome-wide association studies
- Next-generation genetics in plants
- Association study designs for complex diseases
- Linkage Disequilibrium and the Search for Complex Disease Genes
- Linkage disequilibrium: what history has to tell us
- Methods for linkage disequilibrium mapping in crops
- Structure of linkage disequilibrium in plants

For any suggestions or comments, please feel to reach at waseem.hussain@irri.org; m.anumalla@irri.org