**Genomic prediction of autotetraploids; influence of relationship matrices, allele dosage, and continuous genotyping calls in phenotype prediction**

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# Pedigree-based relationship matrices

### **Model A2**

It is a diploid pedigree-based relationship computed as presented in Mrode (2014) as described by Henderson (1976). The algorithm computes the matrix with elements considering the proportion of parental gametes that are identity by descent. Thus, for every individual with parents (mom) and (dad):

If and of are unknown, they are assumed unrelated, and

; for every from 1 to

If only is known, is assumed nonrelated, and

; for every from 1 to

If and are known, then:

; for every from 1 to

### **Model A4**

It is an autotetraploid pedigree-based relationship matrix computed as presented in Kerr et al. (2012). The algorithm first computes the matrix with elements considering the proportion of parental gametes that are identity by descent. As we do not have evidence of double-reduction phenomenon in blueberries, we did not consider it proportion in the matrices, i.e., in the original Kerr et al. (2012). Thus, for every individual with parents (mom) and (dad):

If and of are unknown, they are assumed unrelated, and

; for every from 1 to

If only is known, is assumed nonrelated, and

; for every from 1 to

If and are known, then:

; for every from 1 to

Finally, the matrix is given by **.**

# Marker-base matrices

They are marker-base relationship matrices derived from VanRaden (2008) and Aguilar et al. (2011). It is noteworthy Model G4 is also used in Ashraf et al. 2016).

### **Model G2**

The marker matrix with markers and genotypes has values corresponding to gene content of the second allele where the elements are set to -1, 0, and 1, for the homozygote, heterozygote, and other homozygote, respectively. A centered matrix , where , is built. Then, the relationship matrix is given by:

Being is a scale factor equal and .

### **Model G4**

The marker matrix has values corresponding to gene content of the second allele (0, 1, 2, 3, and 4). is the mean-centered . Then, the relationship matrix is given by:

Being is a scale factor equal where and is the variance of the vector (centered marker vector).

### Model Gr

The marker matrix has values corresponding to the genotypic ratio , where is the allele count of the alternative allele and is the allele count of reference allele. No dosage calling was performed in this moded. is the mean-centered . Then, the relationship matrix is given by:

Being is a scale factor equal where and is the variance of the vector (centered marker vector).

# Pseudo-r code to generate the matrices

**----------------------------------------------------------------------**

## Installing and loading AGHmatrix package ##

install.packages("AGHmatrix"); library(AGHmatrix)

## Loading the data

pedigree <- read.table("pedigree.csv")

markers\_diploid <- read.table("SNPs\_diploid.csv")

markers\_tetraploid <- read.table("SNPs\_tetraploid.csv")

markers\_ratio <- read.table("SNPs\_ratio.csv")

## Building A2 matrix

A2 <- Amatrix(ped, ploidy=2)

## Building A4 matrix

A4 <- Amatrix(ped, ploidy=4)

## Building G2 matrix

G2 <- Gmatrix(markers\_diploid, ploidy=2)

## Building G4 matrix

G4 <- Gmatrix(markers\_tetraploid, ploidy=4)

## Building Gr matrix

Gr <- Gmatrix(markers\_ratio, ratio=TRUE)

**----------------------------------------------------------------------**

# References

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