

Problem Set 2

Due 3/12/2025

Use workflowr to set up the appropriate folders structures to make is easier to grade your work (1 pt).

1. Read in the file "Pedigree.csv" and write an R function to calculate the additive relationships (first calculate the coefficients of coancestry and then multiply by 2 to get the additive relationships) (5 pts)
2. Read in the file "SNP_data.csv" and write an R function to calculate the genomic relationship matrix. (5 pts)
3. Plot the off diagonals of the pedigree relationship matrix (x-axis) and the genomic relationship matrix (y-axis). Identify at least 1 difference and provide an explanation (2 pts)
4. Plot the diagonals of the pedigree relationship matrix (x-axis) and the genomic relationship matrix (y-axis). Identify at least 1 difference and provide an explanation (2 pts)

Some resources to help

Plotting off diagonals:

```
offDiag <- function(relMat){  
  return(c(relMat[upper.tri(relMat)]))  
}  
plot(offDiag(aMat),offDiag(snpRelMatAll))
```

Plotting diagonals:

```
plot(diag(aMat),diag(snpRelMatAll))
```

Solutions for the pedigree and genomic relationship matrices (for you to check the output of your code):

"Pedigree_Rel.csv" – pedigree relationship matrix

"Genomic_Rel.csv" – genomic relationship matrix