Session 6: GWAS in Samples with Structure

GWAS for in R using Linear Mixed Model

(Note: This exercise is computationally intensive and can take your computer several hours to complete!)

Before you begin:

- Install the R package "GenAbel" and "SNPRelate" on your laptop by first loggin on to the internet. Then open an R session and enter the following command:

  ```
  install.packages("GenABEL")
  ```

1. Use PLINK and Transferrin.bed, Transferrin.bed, and Transferrin.fam files, create a transposed pedigree file (tped). The following command can be used:

   ```
   plink  --bfile Transferrin  --maf 0.05 --geno 0.01 --
   hwe 0.001   --recode --transpose  --out
   Transposed_Transferrin  --noweb
   ```

2. Now use R package GenAbel to perform a GWAS of the transferrin and height phenotypes using a linear mixed model. An R script for this is provided on the course website.