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:

1. Install the R package “GENESIS” from bioconductor on your laptop by first logging on to the internet. Then open an R session and enter the following command:

```
source("http://bioconductor.org/biocLite.R")
biocLite("GENESIS")
```

2. Now use GENESIS 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.