

## 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 Bioconductor R packages gdsfmt, SNPRelate, GWASTools, and GENESIS :

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install(c("GWASTools", "gdsfmt", "SNPRelate",
  "GENESIS"))
```

2. Now use GENESIS to perform a GWAS of the transferrin and height phenotypes using a linear mixed model. R scripts for this are provided on the course website.