

Genetic association studies - GWAS

EXERCISE: Researchers are interested in detecting new SNPs associated with BMI (body mass index). To do so, they performed a GWAS using DNA information about 425 individuals. Genotype information is available in plink format (files 'coronary.bed', 'coronary.bim', 'coronary.fam') while phenotypic information can be found in the file 'coronary.txt'.

- Read genotypes using `snpStats` library
- Verify that both data sets are in the same order (NOTE: 'id' variable in the file 'coronary.txt' must be used since it corresponds to the unique patient number)
- Perform some QC filtering of individuals
- Remove those SNPs that do not pass QC (HWE and low MAF)
- Assess association between BMI' and the SNPs (NOTE: remember that you are analyzing a **quantitative trait**)
- Calculate λ and create a Q-Q plot to assess population stratification
- Assess association between BMI' and the SNPs adjusting for population stratification (variables 'ev3' and 'ev4' in the file 'coronary.txt') (NOTE: remember that you are analyzing a **quantitative trait**). Are there differences with crude analysis?
- Create a Manhattan plot (use `qqman` library)