

TUTORIAL 3 - Genome-Wide Association Analysis

This analysis will pull data from the `~/cbio2016/plink/clean` directory and will be direct the output to our `~/plinkout` directory. First, be sure to change directory into the `plinkout` directory.

```
student@courses:~$ cd plinkout
```

1) We can run a very quick genome-wide association analysis using PLINK. We need to be sure to load our phenotype file into PLINK as well - the one that includes our quantitative trait (BMI).

```
plink --bfile /student_data/cbio2016/plink/clean/bmi --pheno  
/student_data/cbio2016/plink/clean/bmi.phe --pheno-name BMI --assoc --out bmi
```

2) We can also run the analysis while controlling for (adjusting for) the information regarding genetic ancestry as estimated via MDS previously (covariates 2, 3 and 4 correspond to the first, second and third coordinate respectively).

```
plink --bfile /student_data/cbio2016/plink/clean/bmi --pheno  
/student_data/cbio2016/plink/clean/bmi.phe --pheno-name BMI --linear --covar  
bmi.mds --covar-number 2,3,4 --out bmi-corrected --hide-covar
```

3) Now, we can examine our results and graphically present them using R and the R package, “qqman”. For information on this package, please visit:

<http://www.gettinggeneticsdone.com/2014/05/qqman-r-package-for-qq-and-manhattan-plots-for-gwas-results.html>