Section 2 （tutorial 1 pdf）

Individual assignment

For the individual assignment, you need to work with the datafile “Income.RData” (from Canvas). This file contains personal income data from twins. Provide new evidence for the heritability of personal income (among females *and* among males; a separate model for each sex, similar as in this tutorial) using a classical twin study (input = raw data). No adjustment for assortative mating is needed (because we don’t know δm), but you may want to discuss in your report the influence of assortative mating on your results. In your report, describe the main intuition behind the classical twin study and discuss your findings. Use at least 1 scientifically formatted table to report the estimation results in this section.4 [+/- 500 words]

Section 3（tutorial 3 pdf）

Individual assignment

Download the files “Females.bed”, “Females.bim”, “Females.fam”, “Females\_income.pheno”, “Males.bed”, “Males.bim”, “Males.fam”, and “Males\_income.pheno” from Canvas. These files contain income data from 3,500 females and 3,500 males. The genetic files contain a representative genome-wide scans of SNPs (38,560 SNPs) for both samples.

Your goal is to provide new evidence for the heritability of personal income (among females *and* among males; a separate model for each sex) using GREML.2 In your report, describe the main intuition behind GREML and its main differences with the classical twin study. Discuss your findings and use at least 1 scientifically formatted table to report the estimation results in this section. [+/- 500 words]

Hints:

* The individuals in the sample are not closely related, but do make sure that cryptically related pairs of individuals (which may nevertheless be present) are excluded from the analysis (use the --grm-cutoff function with an appropriate threshold).
* For your report, it is not needed to perform a case-control GREML analysis. It is also not needed to perform a bivariate GREML analysis.

gcta64 --bfile Males --autosome --maf 0.01 --make-grm --out Males

gcta64 --bfile Males --autosome --maf 0.01 --make-grm-gz --out Males

gcta64 --grm Males --pheno Males \_height.pheno --reml --out Males\_height

gcta64 --grm Males --pheno Example\_height.pheno --reml --out Males\_height\_cutoff --grm-cutoff 0.025

gcta64 --grm Males --pheno Males\_height\_binary.pheno --reml – out Males\_height\_binary

gcta64 --grm Males --pheno Males\_height\_binary.pheno --reml -- out Males\_height\_binary\_cutoff\_liability\_scale --prevalence 0.1125 --grm-cutoff 0.025

gcta64 --grm Males --pheno Males\_height\_education\_bivariate.pheno --reml-bivar 1 2 --out Males\_height\_education\_bivariate --grm-cutoff 0.025

gcta64 --grm Males --pheno Males\_height\_education\_bivariate.pheno -- reml-bivar 1 2 --out Males\_height\_education\_bivariate2 --grm-cutoff 0.025 --reml-bivar-lrt-rg 0

gcta64 --grm Males --pheno Males\_height\_education\_bivariate.pheno -- reml-bivar 1 2 --out Males\_height\_education\_bivariate3 --grm-cutoff 0.025 --reml-bivar-lrt-rg 1

将上面所有’Males’替换成’Females’，会分别得出关于male和female的results，将结果按照示例表格制作成table

Section 4（tutorial 4 pdf）

Individual assignment2

* Use power calculations to assess under what statistical conditions (e.g., the expected *R2* of SNP) a GWAS on personal income is feasible. Use reasonable assumptions (e.g., based on earlier genetic associations reported in scientific papers) in your calculations, and use at least 1 scientifically formatted table to report the results.
* Run two times a GWAS on personal income, one for females and one for males, using the data from Tutorial 3. Use at least 2 scientifically formatted figures (QQ-plots and Manhattan plots) to report the results. Given your power calculations, discuss whether you are surprised by the GWAS results.