GCTA Heritability Estimation

Installation

We used GCTA version gcta-1.94.1-linux-kernel-3-x86_64.zip available for download from https://yanglab.westlake.edu.cn/software/gcta/#Download

Phenotype Processing

We created PLINK compatible pheno files using the script getting_pheno_data_in_PLINK.R

GRM Construction

We used the LD pruned genotype data for constructing the GRM using the command

gcta --bfile genotype --autosome-num 20 --autosome --thread-num 1 --make-grm-bin --out obesity_published_grm

An already constructed GRM can also be downloaded from https://library.ucsd.edu/dc/object/bb9156620z/_5_1.zip/download

File names:

- obesity_published_grm.grm.bin (binary file which contains the lower triangle elements of the GRM).
- obesity_published_grm.grm.N.bin (binary file which contains the number of SNPs used to calculate the GRM).
- obesity_published_grm.grm.id (no header line; columns are individual IDs).

GCTA Heritability Command

GCTA Heritability Estimation

gcta64 --reml --grm obesity_published_grm --pheno test.phen --out test

where --reml is the heritability command

--grm specifies the GRM to use

--pheno specifies the phenotype file name

--out specifies the output prefix