**Analysis plan (simplified)**

09/02/2022

Step 1: QC and SNP set

We recommend using HapMap3 SNPs and filter those with a MAF>1% in your sample.

Use a single genotype file (PLINK format) that contains all autosomal chromosomes (1 to 22).

Step 2: Create GRM and DRM

a) Download “makeDRM” from github

[prompt]$

b) Calculate the GRM and DRM simultaneously from a single genotype file

[prompt]$ **makeDRM** --bfile AA\_all\_chroms --out myGRMfolder/AA

This will produce three type of files:

* \*.gpd.grm.log
* \*.grm.bin and \*.grm.id (standard GRM)
* \*.gpd.grm.bin and \*.gpd.grm.id (the DRM)

Step 3: Analyse trait with GCTA (recommended to include Principal Components as fixed effects)

1. Create “mgrm” file with prefix corresponding to within- and between-chromosomes GRMs

[prompt]$ cat mgrm.analyse-data.txt

myGRMfolder/AA

myGRMfolder/AA.gpd

1. Single GRM analysis

[prompt]$ **gcta64** –grm myGRMfolder/AA \

--pheno myPhenotype-file.txt --mpheno 1 –reml \

--qcovar myQuantitativeCovariates.txt \

--reml-no-constrain --out myResultsFolder/AA.singleGRM

1. Two-GRM analysis

[prompt]$ **gcta64** –mgrm mgrm.analyse-data.txt \

--pheno myPhenotype-file.txt --mpheno 1 –reml \

--qcovar myQuantitativeCovariates.txt \

--reml-no-constrain--out myResultsFolder/AA.twoGRM

Step 4: Share results:

* All log files from Step 2
* All \*.hsq files from Step 3

Traits: height, BMI, education, blood pressure, etc.

**\*\*\* If you have an issue with the DRM program...**

1) Download the eigen library

[prompt]$ wget https://gitlab.com/libeigen/eigen/-/archive/3.4.0/eigen-3.4.0.tar.gz

2) Replace "./eigen-3.4.0/" in the Makefile with the path pointing to where you’ve downloaded the library (e.g., “~/Eigen/eigen-3.4.0/”)

3) Recompile the program on your local cluster/server.

[prompt]$ make clean

[prompt]$ make

If still does not work then, please contact me (l.yengo@imb.uq.edu.au)