

Weekly logs of Master thesis

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1 Week 1

Date: 2023/2/8

1.1 Software Download

REGENIE: Stacked block ridge regression method for Mixed Linear Model.

Advantages:

1. Fast and Memory friendly.
2. Can process both quantitative and binary traits.
3. When Case-control unbalanced, h^2_{SNP} will get too high due to the too low MAC(minor allele count).
REGENIE can fix this.

Plink

Bolt-LMM

GEMMA

SAIGE problems occur

1.2 QC

Filter out SNPs with genotype missingness > 10%, samples with > 10% missingness, MAF < 5%, minor allele count(MAC) < 100.

Cmd:

```
./software/plink --bfile data --geno 0.1 --mind 0.1 --maf 0.05 --mac 100 \
--make-bed --out data_qc
```

Output: data_qc

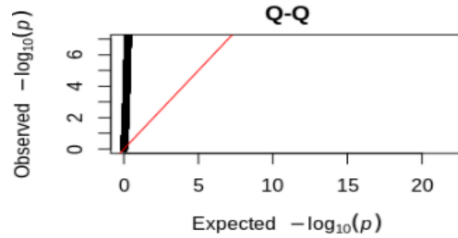
1.3 Plink

Worst result ever.

Cmd:

```
./software/plink --bfile data_qc --linear --pheno height.pheno --allow-no-sex \
--out data_plink_height
```

Q-Q plot: Figure 1



(a) Manhattan plot of REGENIE on height

Figure 1: **QQ plot of plink**

1.4 REGENIE for association study

I took height as the phenotype.

Step 1:

Input files: data_qc(3 files), covar1.covars, height1.pheno. Since REGENIE required labels in each column, I modified covar.covars and height.pheno with labels.

Cmd:

```
regenie \
--step 1 \
--bed data_qc \
--covarFile covar1.covars \
--phenoFile height1.pheno \
--bsize 100 \
--out data_regenie_out
```

Output: A predicting matrix W for h_{SNP}^2 , in file: data_regenie_out_pred.list

Step 2: Association test and LRT

Cmd:

```
regenie \
--step 2 \
--bgen data_qc.bgen \
```

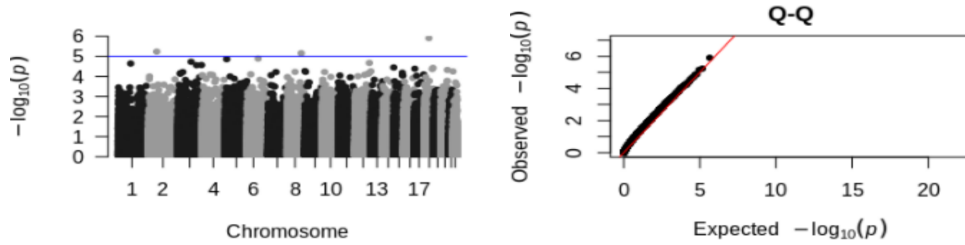
```

—covarFile covar1.covars \
—phenoFile height1.pheno \
—bsize 200 \
—qt \
—firth —approx \
—pThresh 0.01 \
—pred data_regenie_out_pred.list \
—out data_regenie_out_firth

```

Output: data_regenie_out_firth_Phenotype.regenie

The result can be seen in Figure 2



(a) Manhattan plot of REGENIE on height

(b) QQ plot of REGENIE on height

Figure 2: **GWAS results from REGENIE on height**(a)Manhattan plot. (b)QQ plot.

Benchmark:

See in Table 1

Method	Step	CPU time	Elapsed time(s)	Memory usage(GB)
REGENIE(null)	1		1492.8	10
REGENIE-Firth	2		4992.47	0.289

Table 1: **Computational performance of REGENIE-Firth**

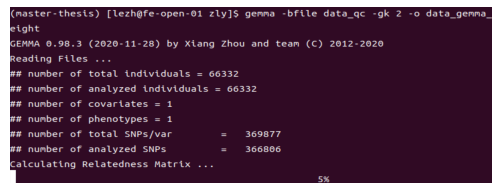
Refer to: [Mbatchou et al. \(2021\)](#)

1.5 GEMMA

1. Before using GEMMA, the 6th column of .fam should be replaced by real phenotypes.
2. Calculate Kinship Matrix

```
gemma -bfile data_qc -gk 2 -o data_gemma_height
```

While it stuck here for hours, as in Figure 3



```
(master-thesis) [lezh@fe-open-01 zly]$. gemma -bfile data_qc -gk 2 -o data_gemma_h
eight
GEMMA 0.98.3 (2020-11-28) by Xiang Zhou and team (C) 2012-2020
Reading Files ...
## number of total individuals = 66332
## number of analyzed individuals = 66332
## number of covariates = 1
## number of phenotypes = 1
## number of total SNPs/var      = 369877
## number of analyzed SNPs      = 366806
Calculating Relatedness Matrix ...
5%
```

(a) Problem with GEMMA

Figure 3: **Problem with GEMMA**

1.6 fastGWA

1. After download, see: **gcta** in ./software folder
2. GCTA-GRM: calculating the genetic relationship matrix (GRM) from all the autosomal SNPs:

```
./software/gcta --bfile data_qc --chr 1 --maf 0.01 --make-grm \
--out data_qc_chr1 --thread-num 10
./software/gcta --bfile data_qc --chr 2 --maf 0.01 --make-grm \
--out data_qc_chr2 --thread-num 10
...
./software/gcta --bfile data_qc --chr 22 --maf 0.01 --make-grm \
--out data_qc_chr22 --thread-num 10
```

Output: .grm.bin, .grm.N.bin, .grm.id

3. To generate a sparse GRM from SNP data:

```
./software/gcta --bfile data_qc --autosome --maf 0.01 --make-grm \
--out data_qc_gcta --thread-num 10
./software/gcta --grm data_qc_gcta --make-bK-sparse 0.05 \
--out sp_grm_gcta
```

4. Association study

I didn't use PCs

```
./software/gcta --bfile data_qc --grm-sparse sp_grm_gcta \
--fastGWA-mlm --pheno height.pheno --qcovar covar.covars \
--thread-num 10 --out data_fastgwa_height
```

Problem comes from step 4, Figure 4:

```
Reading the sparse GRM file from [sp_grm_gcta]...
After matching all the files, 66151 individuals to be included in the analysis.
Estimating the genetic variance (Vg) by fastGWA-REML (grid search)...
```

(a) Problem with GEMMA

Figure 4: **Problem with fastGWA**

It is stuck here also for hours, is it normal? I'll open the computer for the night and see.

Still stuck there in the morning...

1.7 Bolt-lmm

```
./software/BOLT-LMM.v2.4/bolt --bfile=data_qc --phenoFile=height1.pheno --phenoCol=I
--covarFile=covar1.covars --qCovarCol --lmmForceNonInf --statsFile=data_bolt_height
```

The problem occurs at Figure 5.

```
Reading bed file #1: data_qc.bed
Expecting 6117025826 (+3) bytes for 66151 indivs, 369877 snps
ERROR: Wrong file size or reading error for bed file: data_qc.bed
```

(a) Problem

Figure 5: **Problem with Bolt-LMM**

1.8 Question

1. What should I do with CV and LOOCV? What for?
2. How can I detect the Type I errors? By prediction?
3. When I tried SAIGE, I found it need me to use Rscript, how to do?

```
Rscript createSparseGRM.R \
--plinkFile=${LD_pruned_PLINK_file} \
--nThreads=72 \
--outputPrefix=${OUTNAME} \
--numRandomMarkerforSparseKin=5000 \
--relatednessCutoff=0.05
```

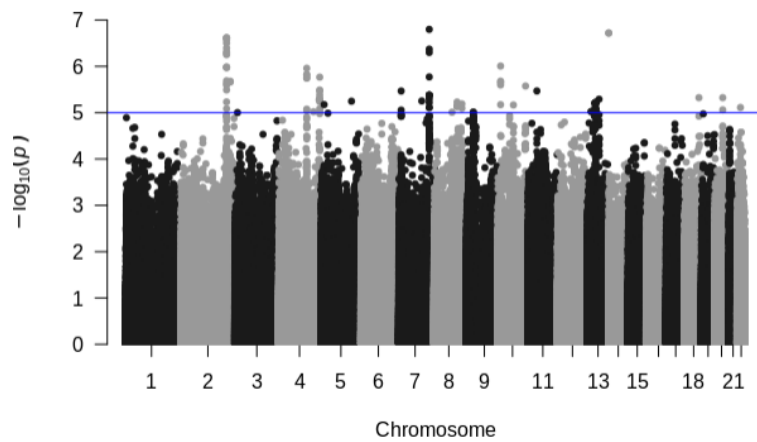
2 Week 2

2.20 - 2.26

Since there are a lot problems occuring with UKBB data, I use 1000g as a demo. If it can work, I'll run on UKBB.

See in [commands_Week2.md](#)

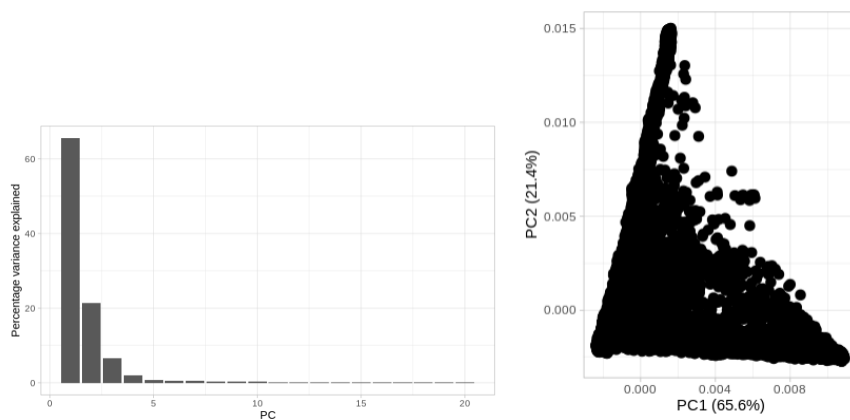
2.1 fastGWA, 1000g



(a) Manhattan plot of fastGWA on 1000g, qt

Figure 6: **fastGWA** on 1000g

2.2 PCA



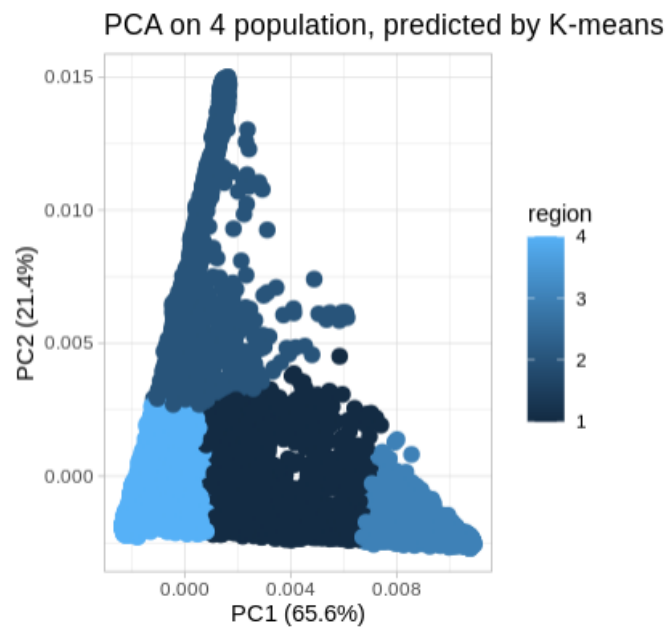
(a) PCs explained

(b) PCA

Figure 7: **GWAS** results from **REGENIE** on height

2.3 PCA for population prediction, K-means

$$y < - > PC1 + PC2$$

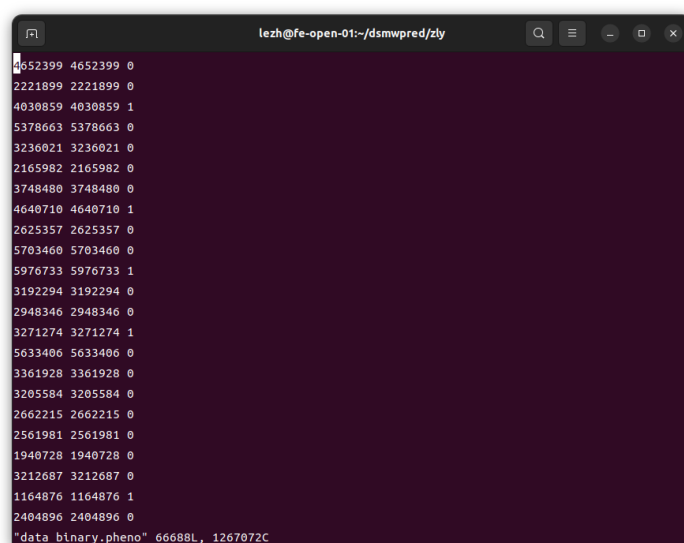


(a) 4 populations

Figure 8: **K-means clustering on PCA**

Problem: I cannot evaluate the result.

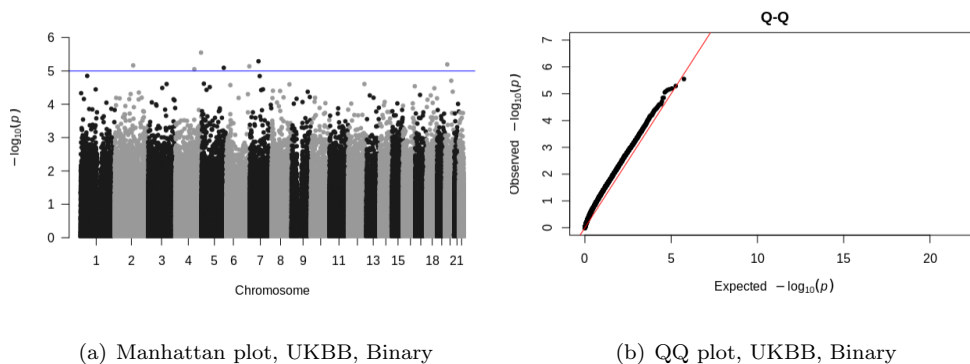
2.4 Simulate Binary Phenotype with LDAK



(a) ukbb, simulation

Figure 9: Binary Phenotypes UKBB simulation

2.5 Regenie for UKBB, binary

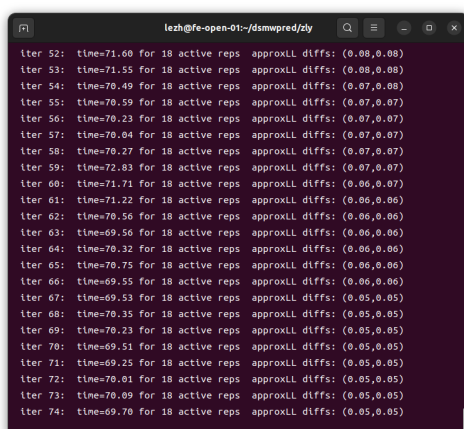


(a) Manhattan plot, UKBB, Binary

(b) QQ plot, UKBB, Binary

Figure 10: Regenie results of UKBB on binary traits

2.6 Bolt-LMM, 1000g, awaiting



```
lezh@fe-open-01:~/dsmwpred/ply
lter 52: time=71.60 for 18 active reps approxLL dffs: (0.08,0.08)
lter 53: time=71.55 for 18 active reps approxLL dffs: (0.08,0.08)
lter 54: time=70.49 for 18 active reps approxLL dffs: (0.07,0.08)
lter 55: time=70.59 for 18 active reps approxLL dffs: (0.07,0.07)
lter 56: time=70.23 for 18 active reps approxLL dffs: (0.07,0.07)
lter 57: time=70.04 for 18 active reps approxLL dffs: (0.07,0.07)
lter 58: time=70.27 for 18 active reps approxLL dffs: (0.07,0.07)
lter 59: time=72.83 for 18 active reps approxLL dffs: (0.07,0.07)
lter 60: time=71.71 for 18 active reps approxLL dffs: (0.06,0.07)
lter 61: time=71.22 for 18 active reps approxLL dffs: (0.06,0.06)
lter 62: time=70.56 for 18 active reps approxLL dffs: (0.06,0.06)
lter 63: time=69.56 for 18 active reps approxLL dffs: (0.06,0.06)
lter 64: time=70.32 for 18 active reps approxLL dffs: (0.06,0.06)
lter 65: time=70.75 for 18 active reps approxLL dffs: (0.06,0.06)
lter 66: time=69.55 for 18 active reps approxLL dffs: (0.06,0.06)
lter 67: time=69.53 for 18 active reps approxLL dffs: (0.05,0.05)
lter 68: time=70.35 for 18 active reps approxLL dffs: (0.05,0.05)
lter 69: time=70.23 for 18 active reps approxLL dffs: (0.05,0.05)
lter 70: time=69.51 for 18 active reps approxLL dffs: (0.05,0.05)
lter 71: time=69.25 for 18 active reps approxLL dffs: (0.05,0.05)
lter 72: time=70.01 for 18 active reps approxLL dffs: (0.05,0.05)
lter 73: time=70.09 for 18 active reps approxLL dffs: (0.05,0.05)
lter 74: time=69.70 for 18 active reps approxLL dffs: (0.05,0.05)
```

(a) CV processing

Figure 11: **Bolt result awaiting**

The code has run for 24 hours, not consistent with the brilliant result from the paper, [Loh et al. \(2015\)](#).

2.7 Ancestry Inference

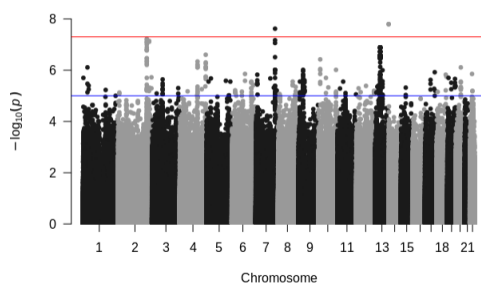
1. as shown in the section [2.3](#) [PCA for population prediction, K-means].
2. Using software: ADMIXTURE and fastSTRUCTURE for clustering.

Update: 2023/2/23

SNP Number: 6M

Time elapsed: 97449.4 sec

2.8 Bolt-LMM, 1000g, result



(a) Bolt result manhattan

```
lezh@fe-open-01:~/dsmwpred/zy
Converged at iter 271: approxLL diffs each have been < LLtol=0.01
Time breakdown: dgemm = 44.9%, memory/overhead = 55.1%
Filtering to SNPs with chisq stats, LD Scores, and MAF > 0.01
# of SNPs passing filters before outlier removal: 6864241/6864249
Masking windows around outlier snps (chisq > 20.0)
# of SNPs remaining after outlier window removal: 6584726/6864241
Intercept of LD Score regression for ref stats: 1.220 (0.007)
Estimated attenuation: 2.744 (0.268)
Intercept of LD Score regression for cur stats: 0.959 (0.007)
Calibration factor (ref/cur) to multiply by: 1.272 (0.003)

Time for computing Bayesian mixed model assoc stats = 19334.5 sec

Calibration stats: mean and lambdaGC (over SNPs used in GRM)
(note that both should be >1 because of polygenicity)
Mean BOLT_LMM_INF: 1.0903 (6864241 good SNPs) lambdaGC: 1.08206
Mean BOLT_LMM: 1.09685 (6864241 good SNPs) lambdaGC: 1.08604

=== Streaming genotypes to compute and write assoc stats at all SNPs ===

Time for streaming genotypes and writing output = 269.781 sec

Total elapsed time for analysis = 97449.4 sec
[lezh@fe-open-01 zy]$
```

(b) Bolt time elapsed

Figure 12: Bolt result and performance

References

- Loh, P.-R., Tucker, G., Bulik-Sullivan, B. K., Vilhjálmsson, B. J., Finucane, H. K., Salem, R. M., ... Price, A. L. (2015, 3). Efficient bayesian mixed-model analysis increases association power in large cohorts. *Nature Genetics*, *47*, 284-290. DOI: 10.1038/ng.3190
- Mbatchou, J., Barnard, L., Backman, J., Marcketta, A., Kosmicki, J. A., Ziyatdinov, A., ... Marchini, J. (2021, 7). Computationally efficient whole-genome regression for quantitative and binary traits. *Nature Genetics*, *53*, 1097-1103. DOI: 10.1038/s41588-021-00870-7