

Assignment 5 - Single-step GWAS

Download and extract **postgs.zip** file from wiki.

The data for this lab was created using simulation for a single trait animal model. Simulation was done using QMSim (Sargolzaei, M. and F. S. Schenkel, 2009)

The simulated phenotype was generated using the following model:

$$\text{Phenotype} = \text{mean} + \text{true_ebv} + \text{residual}$$

Files are available in the folder postgs:

Description of files

pheno.txt:

- 1: mean
- 2: animal id
- 3: sire id
- 4: dam id
- 5: sex
- 6: generation
- 7: number of males progenies
- 8: number of females progenies
- 9: inbreeding
- 10: homozygosity
- 11: phenotype
- 12: simulated residual (e)
- 13: individual true breeding value for polygene
- 14: individual true breeding value for direct effect (qtl)
- 15: EBV from QMSim internal BLUP

pedigree.txt:

- 1: animal ID
- 2: sire ID
- 3: dam ID

mkr.txt:

- 1: animal ID
- 2: marker information

chrmap:

- 1: SNP ID
- 2: Chromosome
- 3: position

1. Go to <http://nce.ads.uga.edu/wiki/doku.php?id=readme.pregsf90> and check all options available for postGSf90
2. Run renumf90 program using 'renum.par' parameter file to renumber data, pedigree, and marker files
3. Run blupf90 and get solutions
4. Add an option to read a map file (*chrmap*) and run postGSf90. Check the output files.
5. Try analyses using option to get variance explained by windows of adjacent SNPs and add the option to generate Manhattan plots. Check the output files.
6. Prediction of DGV for young individuals. The postGSf90 creates a file *snp_pred* with information about the random effect (number of traits + correlated effects), the gene frequencies and the solutions of SNP effects.

Use program predf90 to predict DGV using a marker file for young individuals (*young_anim*)