**Lab5 Single-Step GWAS**

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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 were generated using the following model:

*Phenotype = mean + true-ebv + residual*

Files are available in the folder:

/home/course/courseadmin/course/lab5

**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. Copy the full folder into your directory

**cp –rl /home/course/courseadmin/course/lab5 .**

Go to <http://nce.ads.uga.edu/wiki/doku.php?id=readme.pregsf90>

and check all options available for postGSf90

1. Run renumf90 program using ‘renum.par’ parameter file to renumber data, pedigree, and marker files
2. Run blupf90 and get solutions

1. Add an option to read a map file (*chrmap*) and run postGSf90. Check the output files.

1. 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.
2. 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 the program predf90 to predict DGV using a marker file for young individuals (*young\_anim*)