ASSIGNMENT CHAPINGO – SSGBLUP AND SSGWAS

The data for this lab was simulated using QMSim (Sargolzaei & Schenkel, 2009). A single trait animal model was simulated assuming heritability of 0.40. All the genetic variance was explained by 500 QTL. Animals were genotyped for 45,000 SNP and the average LD was 0.18. The simulated additive genetic variance was 0.4 and the residual variance was 0.60. Phenotype was generated using the following model:

Phenotype = sex_effect + true_breeding_value + residual

Description of files:

data3.txt:
1: individual ID
2: generation
3: sex
4: phenotype
5: true breeding value (TBV)

ped3.txt:
1: individual ID
2: sire ID
3. dam ID

snp3.2k:
1: individual ID
2: SNP genotype

mrkmap.txt:
1: SNP ID
2: Chromosome
3: position
(Note: in this exercise, SNPs are sorted but this is not needed. The SNP ID has to match the order in the SNP file).

1. Given that SNP effects are calculated based on GEBV, run `blupf90+` to get the GEBV. Before that, check the options you will need to include in the parameter file, so `blupf90+` can provide all the files needed for the calculation of SNP effects and p-values. Assume that the quality control was already done (add OPTION no_quality_control).

2. Run `postGSf90` to compute p-values. Before that, check the options you will need to include in the parameter file. Check the output files and the content of each column. For additional information, check http://nce.ads.uga.edu/wiki/doku.php?id=readme.pregsf90. The the -log10(p-value) are in the file `chrsnp_pval`. The typical threshold for detection uses the Bonferroni correction, which is 0.05/number_of_SNP. Are there any significant ?