

Assignment 13

On GWAS; prepared by Ignacio Aguilar and Huiyu Wang

Copy files from /home/ignacio/labfri

Data:

Simulated data as in Wang et al., 2012

Simulation was done using QMSim.

Files

Data: phenotypes.txt

Maker: marker.geno.clean

Pedigree: pedigree

Map: chrmap

True QTL effect: QTL_Effect

Renumf90 parameter file: renum.par

Script for running examples: script.sh

phenotypes fields

1: mean effect

2: animal ID

3: phenotype

4: generation

pedigree fields

1: Animal ID

2: Sire ID

3: Dam ID

4: generation

marker file fields:

1: Animal ID

2: markers codes

QTL_Effect

1: qtl ID

2: Chromosome

3: position

4: True QTL effect

map fields

1: SNP ID

2: Chromosome

3: position

1. Check option from postGSf90 program from Wiki page
<http://nce.ads.uga.edu/wiki/doku.php?id=readme.pregsf90>

2. Run renumf90 program using 'renum.par' parameter file to renumber data, pedigree file and marker data.
3. From renf90.par create a new parameter file (par.b90) for running BLUPF90 with options to read weights from a file w1, and store Ginverse
4. From renf90.par create a new parameter file (postpar.b90) for running POSTGSF90 with options to read: Ginverse, map file and weights, and to get Manhattan plots
5. Run blupf90 using the parameter file created in 3 (par.b90)
6. Run postGSf90 using the parameter file created in 4 (postpar.b90)
7. Create a new weight file w2 using information (7th column) in snp_sol. Columns in snp_sol file are: trait number, effect number, SNP ID, Chromosome, position, SNP solutions, and weight
8. Make changes in parameter file to use the new weight file (w2) and run step 5 and 6
9. Try analyses using different type of weight (OPTION which_weight) and moving average for SNP solutions.
10. Look and run script file ren.sh using the command "bash ren.sh"
11. Look and run the script file s1.sh which will run scenario S1 as in Wang et al. 2012 paper
12. Look and run the file s2.sh which will run scenario S2 as in Wang et al. 2012 paper

OPTIONAL

Try with the maternal model from Thursday model to get SNP solutions for direct and maternal effect