## **Assignment 12**

On single step; prepared by Ignacio Aguilar and Daniela Lino

Copy files from /home/ignacio/labthr

## Data:

16 mat

Simulated data for a Maternal Model Simulation was done using QMSim.

Data filename: newdat.txt

The phenotypes were calculated as pheno=mean+qtl1+mat+e(i)

The newdata.txt has the following columns:

```
# animal id
1 animal
2 sire
             # sire id
3 dam
             # dam id
4 G1
             # generation
5 sexo
             # sex
6 mean
             # mu
7 nmp1
             # number of males progenies
8 nfp1
             # number of females progenies
9 F1
             # inbreeding
10 qtl1
             # true by direct
11 qtl2
             # true by mater
12 pheno
             \# mean(0.5) + qtl(d)i + qtl(m)m + e(i)
13 febv1
             # ebv from gmsim direct
14 febv2
             # ebv from qmsim maternal
15 e(i)
             # residual simulated outside gmsim
```

# qtl(m)m

- 1. From raw data modify renumf90 parameter file (renlab.par) according to the data file and model (use the same model as the simulated one).
- 2. Run renumf90 program to renumber data, pedigree file and marker data.
- 3. Check the renf90.par, renf90.dat and renaddxx.ped. From the renaddxx.ped file, identify genotyped animals, and check with wiki (<a href="http://nce.ads.uga.edu/wiki/doku.php?id=readme.renumf90">http://nce.ads.uga.edu/wiki/doku.php?id=readme.renumf90</a>) the content of each column.
- 4. Estimate variance components considering and ignoring marker information.
- 5. Run preGSf90 and save Hinv matrix

- 6. Run blupf90 using two different types of random effects: additive effect with genomic information or user\_file, and check that solutions are the same.
- 7. Remove the phenotypic information from the 5th generation and obtain solutions from a model with marker information and with no marker information. Compute and compare correlations with true breeding values for direct and maternal effects. Hint: have renumf90 output column containing "generations" and delete records from renf90.dat phenotypes for the 5<sup>th</sup> generation.

If generation column is number 7, this can be done with Linux tool awk: awk '\$7!=5' renf90.dat > renf90.dat.pred

8. Take a look of the Makefile and try run programs using for example:

make ren
make blup