

## Exercise 5.1

### Genotype Assisted Selection using PopQTL

Familiarise yourself with the PopQTL module in GENUP. Maybe read the help file, and play with the graphing tool after making a run of the program.

The QTL effect selected on is the sum of the average effect of QTL alleles in the next generation, using knowledge of current QTL allele frequencies. You can use BLUP selection as well as index selection – the help file is out of date in this respect. For selection index, the selection criterion is, as in the help file:

$$(\text{Phenotype} - \text{QTLeffect}) * \text{IndexWt} + \text{QTLweight} * \text{EconWt} * \text{EBV\_QTL}$$

... summed over the 4 traits. QTLweight is discussed briefly in the help file. The criterion for BLUP is similar ...

$$\text{EBV}_{\text{polygenic}} + \text{QTLweight} * \text{EconWt} * \text{EBV\_QTL}$$

Try running the program with different modes of inheritance (recessive, additive, dominant, overdominant) and some very large QTL effects – maybe 2 phenotypic standard deviations. Do you get results that you might have expected?

Does a recessive starting at low frequency (say .01) ever get to high frequency despite no animals expressing the phenotypic effect in the foundation population? Why? (Note: this sort of run will not always work, as due to random chance!).

Does a fully dominant allele come to fixation? Why?

Try a run with additive inheritance, moderately strong QTL effect (to make the result more strong!) QTL genotypes known and weighting on QTL effect =1. Compare this with a run using 'QTL genotypes known' unchecked, such that no DNA testing is being carried out. Do the components of response make sense (polygenic response, 'P-Q', and QTL response, 'QTL')? Note also the differences between runs in QTL frequency. To get useful results, run the program for as many years as you need to get the favourable QTL allele to fixation in both runs.

**Genetic Evaluation with genetic markers**

Make a relationships matrix and a gametic relationships matrix for the following data, and calculate breeding values for polygenic and QTL effects. Total heritability is 40%, polygenic heritability = 30%. Vary the recombination rate between marker and QTL (0.10 vs 0.40)

animal	sire	dam	marker genotype	phenotype
1		?	M1M2	10
2	1	?	M1Mx	12
3	1	?	M2Mx	8

Use mixed model equations to solve this problem (answer in grm.m)

A further challenge. Suppose animals 2 and 3 have one more offspring each.

animal	sire	phenotype	marker genotype
4	2	-	M1My
5	3	-	M2My

Set up the mixed model equations and predict polygenic and QTL breeding value for these 2 new animals (answer in grm2.m).