1) Consider selection for a trait with (total) heritability 0.2 and phenotypic standard deviation equal to 50. For this trait, an additive biallelic QTL has been identified with effect \( a = 20 \) and frequency of the favourable allele equal to 0.2. The following sources of information are available for selection:
- own QTL genotype
- own phenotype
- QTL genotype of the individual’s sire
- Phenotype of the individual’s sire

Assume the top 20% individuals are selected. Derive the optimal selection criterion and predict accuracy of selection on the index and the genetic superiority of the selected individuals using the following two approaches:

a) Selection index with uncorrected phenotypes (own and sire) and QTL genotypes (own and sire).

b) Selection index with phenotypes corrected for QTL genotype (see notes), along with QTL genotypes.

For approaches a) and b), you can use the Selection Index Program with the total genetic value as the trait in the breeding goal (or, alternatively, by including polygenic BV and QTL BV as two separate traits with economic values equal to 1, such that the breeding goal is: polygenic BV + QTL BV, which is equal to the total genetic value) and by including phenotype (corrected or uncorrected) and QTL genotype as records (own and sire) in the index. Using the correct heritabilities and phenotypic and genetic correlations between the two “traits”, SIP can then be used to derive the optimal indexes.

Note: If you entered everything correctly, a) and b) should lead to the same accuracy and response.

c) Explain why the index from b) has a zero weight on QTL genotype of the sire. Also, try to explain the magnitude of the weight that is placed on QTL genotype of the sire in index a).

d) Now, predict response to selection (both in genetic value and in frequency of the QTL) using the mixture distribution approach, using multitrcn.xls (the spreadsheet you used for homework #2). For this approach, you will need to derive the standard deviation of the polygenic EBV. This can be derived using SIP by including the polygenic BV as trait in the breeding goal and deriving an index using own and sire phenotype. Compare responses predicted using this approach to those from a) and b).

e) Implement selection using the indexes from a) and b) into the spreadsheet MAS_simulation.xls (see AnS652X class folder), evaluate achieved accuracy and response to selection (in both genetic value and QTL frequency), compare those to results from a), b), and c), and explain any differences or similarities. Replicate, as in previous homework.

f) Now implement 2-stage selection on the QTL in the spreadsheet by first selecting individuals based on QTL genotype and then, among those, individuals with the highest polygenic EBV. Compare responses from this selection to those obtained under e) and discuss any differences/similarities. E-mail a copy of the spreadsheet that you used for this to me at jdekkers@iastate.edu.