Exercise 3.2

Models for multiple QTL

Data is analysed from an experiment where we have hypothesised two QTL, each with two alleles (A and for the first locus and B and b for the second locus, respectively.

We have estimated the means for 16 QTL genotypes using phenotypic and marker genotype data from a QTL experiment. The QTL genotypes are inferred based on hypothetical QTL positions that were derived from the marker haplotypes.

- Investigate for the following data the genetic model.

- Estimate additive and dominance effects at each QTL.

- Test whether effects are significant

- Test whether there is epistasis between the QTLs

Genotype	Mean	Number observed
AABB	13.08	25
AABb	9.79	21
AabB	9.83	16
Aabb	8.72	23
AaBB	14.18	28
AaBb	9.62	32
AabB	10.15	17
Aabb	10.58	31
aABB	12.16	27
aABb	10.23	28
aAbB	9.79	19
aAbb	7.65	17
aaBB	7.97	34
aaBb	5.62	18
aabB	7.65	24
aabb	6.89	27