Exercise 3.21

Models for QTL analysis

We continue with the case as in Exercise 2.2. We have now 8 half sib progeny from the sire with the following data:

Paternal marker haplotype	phenotype
M1M2	9.7
M1M2	10.3
M1m2	10.2
M1m2	9.5
m1M2	9.8
m1M2	9.2
m1m2	9.3
m1m2	8.8

- Estimate relevant effects (which?) for a QTL that is positioned at 10 cM from marker locus 1 and 30 cM from Marker locus 2.

- Test whether there is a significant QTL effect at this location.

Now use the excel spreadsheet QTLDET.XLS.
The spreadsheet allows you to enter data in the blue cells about position of marker and QTL, and to give QTL parameters.

- Verify the answers you obtained from exercise 2.2 concerning maker haplotype probabilities, and Q-probabilities conditional on marker haplotypes.

The spreadsheet also allows you to simulate data for a half sib group.

- Simulate data for 200 progeny, using the parameters as given in Exercise 2.2 and 1.3. Use a variance of 1.

- What can you conclude concerning the QTL effect from your simulation? What evidence/criteria have you used to draw such conclusions.

- Now simulate 10 such data sets. Determine the average value for the relevant QTL parameters, and their standard deviation.

- Try to work out what would be a reasonable (minimal) progeny group size to detect this QTL

- You can also work out the minimal progeny group size needed to detect a QTL of 0.5 and 2, respectively.

- Does the size of the marker bracket have a large effect on the minimal progeny group size?