Applied Statistical Methods – Excercise 1

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Problem 1: Breeding Values

During the lecture the computation of the breeding values for a given genotype was shown for a completely additive locus which means the genotypic value d of the heterozygous genotypes is 0. In this exercise, we want to compute the general solution for the breeding values of all three genotypes under a monogenic model. We are given a single locus G with two alleles G_1 and G_2 which are closely linked to a QTL for a trait of interest. We assume that the population is in Hardy-Weinberg equilibrium at the given locus G. The allele frequencies are

Allele	Frequency
G_1	p
G_2	q

Allele G_1 is the one with a positive effect on the trait of interest. The genotypic values are given in the following table.

Genotype	Value
G_1G_1	a
G_1G_2	d
G_2G_2	$-a$

Your Task

- Compute the breeding values for all three genotypes G_1G_1, G_1G_2 and G_2G_2.
- Verify the results presented in the lecture by setting $d = 0$ in the breeding values you computed before.

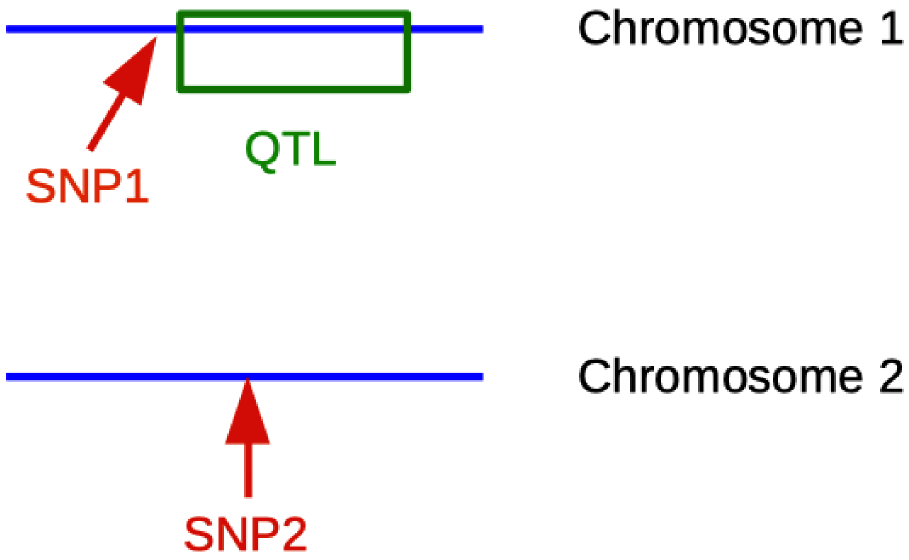

Figure 1: Linkage Between an SNP and a QTL and an independent SNP on a different Chromosome

Problem 2: Linkage Between SNP and QTL

In a population of breeding animals, we are given a trait of interest which is determined by a QTL Q on chromosome 1. QTL Q is modeled as a bi-allelic QTL with alleles Q_1 and Q_2. Furthermore we have genotyped our population for two SNPs R and S with two alleles each. One of the SNPs is on chromosome 1 and is closely linked to Q. The other SNP is on chromosome 2 and is unlinked. Figure 1 shows the situation in a diagram.

Based on the following small dataset, determine which of the two SNPs R and/or S is linked to QTL Q.

From the above table it might be difficult to decide which SNP is linked to the QTL. Plotting the data may help. Showing the observations as a function of the genotypes leads to Figure 2.

Your Tasks

- Determine which of the two SNPs R or S is closely linked to the QTL
- Estimate a value for a obtained based on the data
- Try to fit a linear model through the genotypes that SNP which is linked to the QTL using the `lm()` function. The genotype data is available from

`https://charlotte-ngs.github.io/GELASMSS2019/ex/w02/asm_w02_ex01_p02_genodatafile.csv`

Table 3: Dataset showing linkage between SNP and QTL

SNP R	SNP S	Observation
R_1R_1	S_1S_2	-0.23
R_2R_2	S_1S_2	-2.54
R_1R_2	S_2S_2	-24.27
R_1R_2	S_1S_2	0.17
R_1R_2	S_2S_2	-19.42
R_2R_2	S_2S_2	-24.08
R_1R_1	S_1S_2	5.62
R_1R_2	S_1S_2	-0.14
R_1R_1	S_1S_2	1.30
R_1R_2	S_1S_1	25.96
R_2R_2	S_2S_2	-23.71
R_1R_2	S_1S_1	22.99

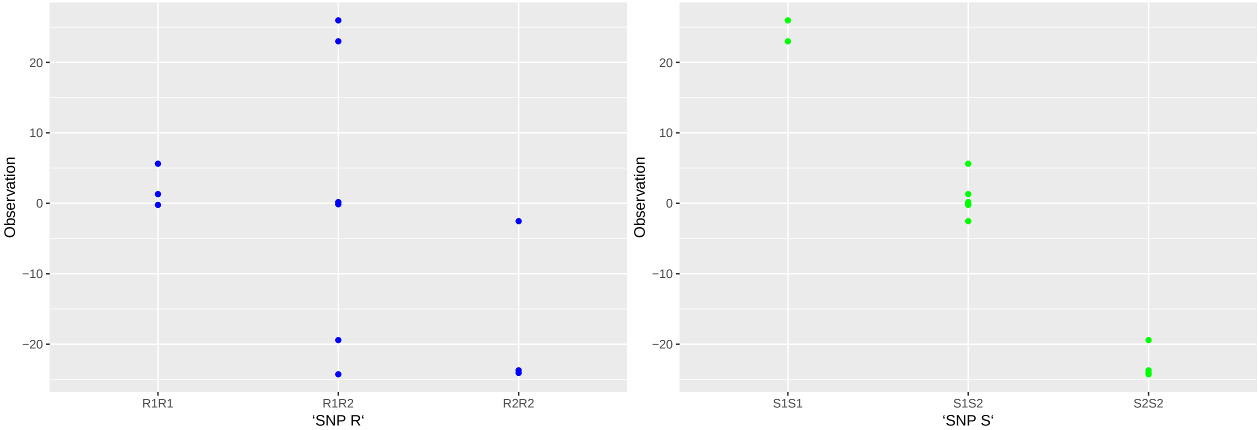

Figure 2: Observations Grouped by SNP Genotypes