Allozyme genotype data has been collected from a single population of rare middle earth Hobbits. The observed genotype frequencies are shown for one polymorphic locus that exhibited three alleles (F = fast, M = medium and S = slow for band migration rates in starch gels). Compute the observed genotype frequency and the expected genotype frequency under Hardy-Weinberg assumptions.

Genotypes	Observed #	Observed frequency	H-W expected frequency
FF	320	0.320	0.179 or 179
MM	120	0.120	0.0484 or 48
SS	235	0.235	0.127 or 127
FM	80	0.080	0.186 or 186
FS	125	0.125	0.302 or 302
MS	120	0.120	0.157 or 157
	total = 1000		

A. Estimate the fixation index (show all work such as estimates of allele frequencies and list H-W expected genotype frequencies in table above).

Let p = freq F allele, q = freq of M allele, r = freq S allele

By allele counting $p = \frac{2(320) + 80 + 125}{2000} = 0.423$

By genotype counting $q = \frac{120 + 0.5 * 80 + 0.5 * 120}{1000} = 0.22$

r = 1 – p – q = 0.357

H-W expected genotype frequencies:

FF: $(0.4225)^2 = 0.179$ MM: $(0.22)^2 = 0.0484$ SS: $(0.357)^2 = 0.127$

FM: 2(0.4225)(0.22) = 0.186 FS: 2(0.4225)(0.357) = 0.302 MS: 2(0.22)(0.357) = 0.157

He = 0.186 + 0.302 + 0.157 = 0.645 Ho = 0.080 + 0.125 + 0.120 = 0.325

F = (He – Ho)/He = (0.645 – 0.325)/0.645 = 0.496

total observed heterozygosity = 0.080 + 0.125 + 0.120 = 0.325

total observed homozygosity = 0.32 + 0.12 + 0.235 = 0.675

B. Is there random mating in this Hobbit population? What are *most likely* possible causes of the observed fixation index?

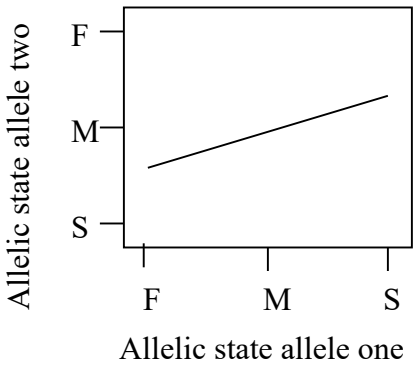
No, there is not random mating in this population since H-W genotype frequencies are not met. There is a deficit of heterozygotes. This deviation from H-W expected genotype frequencies can be explained by consanguineous mating (mating among relatives). For example, F = 0.5 is expected at equilibrium in a mating system of regular parent-offspring backcross mating.

C. Interpret the estimated fixation index (*F*) from the perspectives of (one or two sentences each):

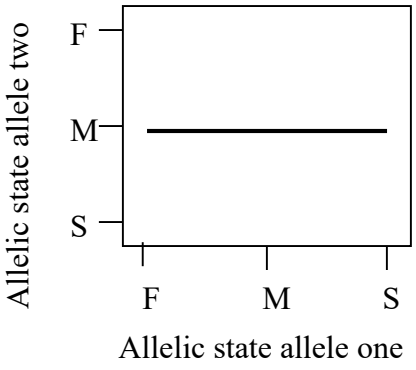
Excess or deficit of heterozygosity:
In this Hobbit population there is a 49.4% deficit of heterozygosity (or a 49.4% excess of homozygosity) compared to an ideal, randomly mating Hardy-Weinberg population with the same allele frequencies.

Probability of autozygosity:
In this Hobbit population there is a probability of 0.496 that the two alleles found in a genotype will be identical in state because they are identical by descent. Under random mating there is a zero chance (on average) of autozygosity. The Hobbits in this population are highly related (almost to the degree of full siblings, which would have an expected autozygosity of 0.5). The mating system of parent-progeny back-cross mating would also attain an autozygosity of 0.5 at equilibrium.

Correlation between the allelic states of uniting gametes:
In this Hobbit population there is a correlation of 0.496 among the states of the two alleles found in a diploid genotype. If a genotype contains one specific allele, say an F, there is a 50% chance that the other allele is also an F (rather than an M or S). Since the correlation is positive and not zero, genotypes tend to have alleles with the same states rather than independent allelic states (zero correlation) or dissimilar states (negative correlation).



Slope of correlation line = 0.50
for Hobbits



Slope of correlation line = 0.0
under Hardy-Weinberg

D. Using Hardy-Weinberg expected frequencies for each of the six genotypes, show that the fixation index serves to "adjust" the expected frequencies up or down in frequency to give the observed genotype frequencies. In other words, for each genotype use *only* 1) the H-W expected genotype frequency, and 2) the fixation index to obtain the observed genotype frequency.

F = 0.496 He/3 = 0.645/3 = 0.215

FF:
$p^2 + (He/3)F$
$(0.4225)^2 + (0.215)0.496 = 0.179 + 0.107 = 0.286$
or
$p^2 + Fpq + Fpr$
$(0.4225)^2 + (0.496)(0.4225)(0.22) + (0.496)(0.4225)(0.357) = 0.179 + 0.0461 + 0.0749 = 0.299$

MM:
$q^2 + (He/3)F$
$(0.22)^2 + (0.215)0.496 = 0.0484 + 0.107 = 0.1554$
or
$q^2 + Fpq + Fqr$
$(0.22)^2 + (0.496)(0.4225)(0.22) + (0.496)(0.22)(0.357) = 0.0484 + 0.0461 + 0.0389 = 0.1334$

SS:
$r^2 + (He/3)F$
$(0.355)^2 + (0.215)0.496 = 0.1260 + 0.107 = 0.2345$
or
$r^2 + Fpr + Fqr$
$(0.355)^2 + (0.496)(0.4225)(0.357) + (0.496)(0.22)(0.357) = 0.127 + 0.0749 + 0.0389 = 0.2408$

0.286 + 0.1554 + 0.2345 = 0.676 = observed total homozygosity to within rounding error
or
0.299 + 0.1334 + 0.2408 = 0.6741 = observed total homozygosity to within rounding error

FM:
2pq – F(2pq)
2(0.4225)(0.22) - (0.496)[2(0.4225)(0.22)]
= 0.186 – (0.496)(0.186) = 0.094

Or:
2pq – F(He/3)
2(0.4225)(0.22) - 0.496 (0.215)
= 0.186 – 0.107 = 0.081

FS:
2pr – F(2pr)
2(0.4225)(0.357) - (0.496)[2(0.4225)(0.357)]
= 0.302 – (0.496)(0.302) = 0.152

2pr – F(He/3)
2(0.4225)(0.357) - 0.496 (0.215)
= 0.302 – 0.107 = 0.195

MS:
2qr – F(2qr)
2(0.22)(0.357) - (0.496)[2(0.22)(0.357)]
= 0.157 – (0.496)(0.157) = 0.079

2qr – F(He/3)
2(0.22)(0.357) - 0.496 (0.215)
= 0.157 – 0.107 = 0.050

Note that on the left 0.094 + 0.152 + 0.079 = 0.325 = Ho to within rounding error.
Alternatively, 0.081 + 0.195 + 0.050 = 0.326 = Ho to within rounding error.

So the “adjustment” to H-W expected genotype frequencies exactly predicts the observed genotype frequencies when taken over all possible heterozygotes. Any difference between the adjusted predicted genotype frequency and the observed genotype frequency for any one heterozygote when using F is a consequence of the fact that F is an average over all heterozygotes.