Fundulus heteroclitus (common name: mummichog) is a small fish that lives in bays and estuaries along the east coast of North America, from Newfoundland to Florida. It’s been extensively used in evolutionary studies.\(^1\)

Northern populations of F. heteroclitus are virtually completely homozygous for an allele of a liver enzyme called Ldh-B (lactate dehydrogenase B), an allele which is just called Ldh-B\(^a\). Southern populations are virtually completely homozygous for the other major allele of Ldh-B, referred to as Ldh-B\(^b\).

Ldh-B has an effect on the survival of fish embryos when exposed to temperature stress. In an experimental test of this survival, Fundulus heteroclitus eggs from different populations were incubated at 30°C, under heat stress. 57% of the eggs from a southern population hatched successfully at 30°C. Only 22% of the eggs from a northern population hatched. Interestingly enough, 87% of the eggs that were heterozygous at the Ldh-B locus successfully hatched.

a) Suppose you put 500 northern Fundulus fish and 500 southern fish in a large tank, allowed them to breed freely, and then incubated all the eggs at 30°C. Predict the frequencies of both alleles and genotypes after one generation.

For simplicity, I’ll call the two alleles A and B. Northern populations are virtually all AA, and Southern populations are virtually all BB.

500 AA fish and 500 BB fish means that the frequency of both alleles is 0.5. So let p = frequency(A) and q = frequency(B); p = q = 0.5.

You could use the raw survival percentages as fitness values and you’d end up with the right answer. But the math is easier, and the meaning is more intuitively right, if you divide them all by the highest. So

\[
\begin{align*}
    w_{AA} &= 0.22/0.87 = 0.25 \\
    w_{AB} &= 0.87/0.87 = 1.00 \\
    w_{BB} &= 0.57/0.87 = 0.66
\end{align*}
\]

Plug these numbers in to

\[
p^2w_{AA} + 2pqw_{AB} + q^2w_{BB} = w-\bar{b}:
\]

\[
(0.5)^2(0.25) + 2(0.5)(0.5)(1) + (0.5)^2(0.66) = w-\bar{b}
\]

\[
0.063 + 0.5 + 0.165 = 0.73
\]

Now the new genotype frequencies are given by dividing each term of the above equation by \( w_{\text{bar}} \). So:

new freq(AA) = \( p^2w_{\text{AA}}/w_{\text{bar}} = 0.063/0.73 = 0.086 \)
new freq(AB) = \( 2pqw_{\text{AB}}/w_{\text{bar}} = 0.5/0.73 = 0.685 \)
new freq(BB) = \( q^2w_{\text{BB}}/w_{\text{bar}} = 0.165/0.73 = 0.23 \)

Check: Do these three add up to 1? Yes, they do, allowing for round-off error.

Now you have to calculate the new allele frequencies. There are several ways you could do that, but here’s the long way:

new \( p = (86*2 + 685)/2000 = 0.428 \)
new \( q = (230*2 + 685)/2000 = 0.572 \)

**EITHER:**

b) Predict the frequencies of both alleles and genotypes after a second generation.

Start with

new \( p = (86*2 + 685)/2000 = 0.428 \)
new \( q = (230*2 + 685)/2000 = 0.572 \)

Use the fitness values from the previous problem, and calculate \( w_{\text{bar}} \):

\[
p^2w_{\text{AA}} + 2pqw_{\text{AB}} + q^2w_{\text{BB}} = w_{\text{bar}}:
\]

\[
(0.428)^2(0.25) + 2(0.428)(0.572)(1) + (0.572)^2(0.66) = w_{\text{bar}}
\]

\[
0.046 + 0.49 + 0.22 = 0.76
\]

Now the new genotype frequencies are given by dividing each term of the above equation by \( w_{\text{bar}} \). So:

new freq(AA) = \( p^2w_{\text{AA}}/w_{\text{bar}} = 0.046/0.76 = 0.06 \)
new freq(AB) = \( 2pqw_{\text{AB}}/w_{\text{bar}} = 0.49/0.76 = 0.64 \)
new freq(BB) = \( q^2w_{\text{BB}}/w_{\text{bar}} = 0.22/0.76 = 0.29 \)

Check: Do these add up to 1? Yes, they do, allowing for rounding off.

And now you have to calculate the new allele frequencies:
new p = (6*2 + 64)/200 = 0.38
new q = (29*2 + 64)/200 = 0.61

OR:

c) Suppose that, when you actually do this experiment, you discover that the actual heterozygote frequency is 0.55. Calculate F.

I graded this one very generously, as I later realized it wasn’t written as clearly as it might have been.

The right way to calculate F in this situation is one I think I mentioned in lecture but didn’t put on the handout: F = 1 - (H_o/H_e), where H_o is the observed frequency of heterozygotes and H_e is the expected frequency of heterozygotes. Here, H_o is 0.55, and H_e is the predicted heterozygote frequency. If it’s the second generation after the founding generation that we’re talking about, H_e = 0.68. H_o/H_e = 0.81, so F = 0.19.

You might have also remembered the formula that freq(AB) = 2pq - 2pqF. If you plug in the numbers there, you end up with a negative value for F. Technically, that’s not the right way to do it -- that formula works only if the only thing that’s pushing the population away from H-W Equilibrium is inbreeding. Here, we have selection going on as well, and that makes the math messier. I didn’t get into this in lecture. If you tried to work the problem in a way that made some sort of sense, even if you ended up with negative F, you got points.