Hardy Weinberg Equilibrium Worksheet
BIOL 01104 Fall 2019, Dr. Spielman

Scenario 1

Wing coloration in the scarlet tiger moth is governed by a single gene with two alleles, A and a, where each genotype has the given phenotype.

- Genotype **AA** individuals have white spots.
- Genotype **Aa** have intermediate-colored spots.
- Genotype **aa** have no spots at all.

This phenotype-genotype relationship provides an example of a *phenotypic incomplete dominance*, under *balancing* natural selection. Researchers studying a population of these moths found the following numbers of individuals for each phenotype (genotype): white-spotted (AA) = 1470, intermediate spots (Aa) = 140, and no spots (aa) = 10.

1. Calculate the values for p (frequency of allele "A") and q (frequency of allele "a") . Confirm you are correct by checking that $p+q=1$.

2. Calculate the ***expected NUMBER*** of individuals for each genotype using the formula $p^2 + 2pq + q^2$. (Hint: this formula will give you the expected frequencies of genotypes. You must multiply by the total number of individuals to get the expected number.)

3. Use the expected and observed **numbers** (not frequencies!) of individuals to calculate X^2 .

4. Determine your p-value from your X^2 calculation. Is there evidence that the population is evolving, or is it more likely under Hardy Weinberg Equilibrium?

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Scenario 2

You are studying an elusive population of blast-ended skrewts, who show heritable variation in their attack phenotypes - some preferentially shoot fire at and some preferentially sting their prey. You have further determined that this trait is controlled by a single gene, F/f (for fire!), such that:

- Genotype **FF and Ff** individuals shoot fire.
- Genotype **ff** individuals sting.

With a brave crew of research volunteers, you journey into the Forbidden Forest and take a small sample (very carefully!) from their tails to determine their genotypes. In the end, you found 250 skrewts with the following genotypes: 119 FF, 107 Ff, and 24 ff.

1. Calculate the values for p (frequency of allele "F") and q (frequency of allele "f") . Confirm you are correct by checking that $p+q=1$.

2. Calculate the expected NUMBER of individuals for each genotype using the formula $p^2 + 2pq + q^2$.

3. Use the expected and observed numbers of individuals to calculate X^2 .

4. Determine your p-value from your X^2 calculation. Is there evidence that the population is evolving, or is it more likely under Hardy Weinberg Equilibrium?