

INVESTIGATION 2

MATHEMATICAL MODELING: HARDY-WEINBERG *

Record your thoughts, assumptions, and strategies on modeling as you work through the lab.

Building a Simple Mathematical Model

Think about a recessive Mendelian trait such as cystic fibrosis.

1. Why do recessive alleles like cystic fibrosis stay in the human population?
2. Why don't they gradually disappear?
3. Polydactyly is a dominant trait, but it is not a *common* trait in most human populations. Why not?
4. Gametes for the next generation are selected totally at random. What does that mean?
5. Assumptions of model on page S29.

a. _____

b. _____

c. _____

d. _____

e. _____

f. _____

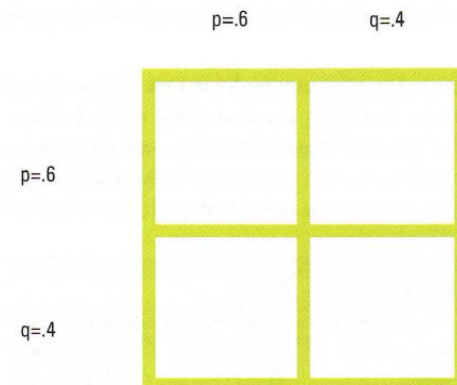
6. Page S31;
 - a. After hitting return, what do you find in the cell?
 - b. If you are on a PC, try hitting the F9 key several times to force recalculation. On a Mac, enter cmd + or cmd =. What happens to the value in the cell?

7. Page S32; Try recalculating 10-20 times.
 - a. Are your results consistent with what you expect?
 - b. Do both cells (E5 and F5) change to A or B in the ratios you'd expect from your p value?
 - c. Try changing your p value to 0.8 or 0.9. Does the spreadsheet still work as expected?
8. Page S36; Describe your thinking and procedure for checking the spreadsheet.

Testing Your Mathematical Model

1. What would happen if there were no randomness to this selection?
2. What kind of pattern of genotypes would you expect in the next generation?

Creating a Formula that Predicts the Genotypes of the Next Generation



1. In the absence of random events (an infinitely large population), are the allele frequencies of the original population expected to change from generation to generation?
2. How does this compare to a population that has random gamete selection but is small?
3. What happens to allele frequencies in such a population? Is it predictable?
4. What factors can cause allele frequencies to change in a population? (Hint: There are many.)
5. How could you model these factors using your spreadsheet?

