Activities to Accompany the Genetics and Evolution App for iPad and iPhone

All of the following questions can be answered using the iPad version of the Genetics and Evolution App.

When using the iPhone version, there are a couple of things to be aware of:

-There is no Test Yourself Mode, only Simulate Mode. For questions 1 and 3 of the Cross Simulator module that uses the Test Yourself Mode, you can still try to use the app to guide you to the answer or try the questions out on your own without the app to give yourself some extra practice.

-There is no Pedigree Analyzer module. For all questions pertaining to this module, it would be excellent practice to use other online resources and/or your notes to work through the answers.

-All of the exercises for the Allele Freak module can be done, though there is no specific box that will tell you the number of generations it takes for the allele to be lost or fixed or that will give you exact allele frequencies. However, you will be able to notice the crucial trends that the questions ask about.

Use the Cross Simulator Module of the Genetics and Evolution App to answer the following questions.

1. Click the Test Yourself Mode button at the bottom of the screen, change the organism to clovers, and click the 2 traits button to answer this question.

You cross a purple female clover with a large stamen to a green male clover with a small stamen and get all purple offspring, in which half have large stamens and half have small stamens. (If you do not get the correct offspring phenotypes the first time you try this, choose other clovers in the box until you do.)

a. Based on this cross, can you conclude which of the two traits are dominant (purple vs. green and large stamen vs. small stamen)? If not, what cross would you set up next to find this out, and why? (Hint: You may want to answer part b first to help with this)
In this case, we know that purple has to be dominant since all of the offspring are purple when crossed to a green clover. Purple always trumped green, so green must be recessive. In this case, we know that both parents have to have been homozygous at the color locus in order for this to happen. We still don't know, however, whether large or small stamens are dominant.

Possible crosses:
We know that at least one parent has to be heterozygous and one parent has to be homozygous for the for the stamen trait in order to get the ½ large and ½ small stamen phenotypic ratios for the offspring. We just don't know which is heterozygous. It would be best to keep one parent the same, and just switch out the other until you find a cross that gives you valuable information. Here, I am just going to keep the female the same, and switch out the male each time for simplicity's sake.

Purple large stamen female to purple small stamen male: If you use the same female from the original cross in part a, all offspring should be purple. There are also a lot of options for purple small stamen males, so keep trying out different ones until you see that all of offspring have one stamen size. In this case, since the parents have different traits (large stamen and small stamen), if all of the kids eventually end up with all of one trait, we know it must be dominant. You should try multiple options of the purple small stamen male just to confirm this.

Purple large stamen female to green large stamen male: If you use the same female from the cross in part a, all offspring are purple, and all offspring have large stamens. However, since both parents have large stamens, we still can't really determine if this is due to dominance or not. The large stamen could be a recessive trait (in which both parents are homozygous bb), so we would have to do other crosses to figure this out.

Green large female to green small female: Since we know green is recessive, we should get all green offspring all the time no matter what. Again, just keep trying different choices of green/small stamen male until you find a cross that gives you all of one type of stamen

b. What are the possible genotypes of the parents for each trait? Use P and p for the color locus and L and l for the size locus. To check yourself, click the "Reveal/Hide All" button to show the genotypes.
purple/large stamen x green/small stamen

PPll	x	ppLl
PPLl	x	ppll

2. In butterflies, gene A controls spot color, in which "A" is dominant and produces black spots (as opposed to brown spots). Gene B controls spot number, in which "B" is dominant and produces lots of spots (as opposed to few spots). Genes A and B assort independently and are autosomal. Of the 80 offspring produced from a single cross, all of them have black spots, and only 20 of them have few spots. What are all the most likely combinations of genotypes of the parents? **Hint:** Use any organism you would like in the Simulate Mode, click on 2 traits, and click "Custom" under the change cross type button to look for genotype combinations that would give you the correct expected offspring phenotypic ratios.

AABb x AaBb OR AABb x AABb

3. Click the Test Yourself Mode button at the bottom of the screen, change the organism to snowman, and click on 1 trait to answer the following question.

In a snowmen, a single autosomal gene controls the presence of antennae, with no antennae being dominant to having antennae. In a single cross of parents of unknown genotype, all 20 of the offspring (10 males and 10 females) have no antennae.

A. What are ALL of the possible combinations of the parents?

TT x tt, TT x Tt, TT x TT

B. Using the phenotypes of the offspring, how would you be able to determine which of these combinations is correct based on crosses between offspring? Hint: Think about expected ratios of the offspring that would come from F1 crosses.

If the parents were TT x tt, all of the F1 offspring would be heterozygous, and we would see that ~1/4 of their offspring would have antennae for every single cross of F1s

If the parents were TT x Tt, half of the F1 offspring would be Tt and the other half would be TT. In some F1 crosses (TT x TT), we would see no antennae, but in some crosses if we paired up Tt x Tt, we would see some F2 progeny with antennae.

If the parents were TT x TT, all of the F2 offspring from every single cross would always have no antennae.

4. Click the Simulate Mode button, change the organism to peas, and click 2 traits to answer this question. For the change cross type button, choose "custom" to make your own crosses.

A. In peas, Gene A controls shape, in which round is dominant to wrinkled. Gene B controls color, in which yellow is dominant to green. These traits assort independently and are autosomal. What are all of the possible phenotypes of the offspring produced from the following cross: AaBB x aaBb?

Round yellow and wrinkled yellow

B. Are there any other potential parental genotypes that would yield the same possible offspring phenotypes? How about same offspring phenotypic ratios?

The only cross that produces just round yellow and wrinkled yellow offspring is AaBB x aaBB. It also has the same phenotypic ratio (½ round yellow, ½ wrinkled yellow).

5. Click the Simulate Mode, change the organism to clovers, click on 1 trait, and change the inheritance type to x-linked to answer the following question. Choose "custom" under the change cross type button to create your own genotype combinations.

A. Assume that color in clovers is inherited in an X-linked fashion, with purple being dominant over green. How many of the following combinations of parents and children are **IMPOSSIBLE**. Assume that females exhibiting the dominant trait can be either homozygous or heterozygous.

A. Purple mom, green dad, purple daughter, green daughter
B. Purple mom, green dad, green daughter, purple son, green son
C. Green mom, purple dad, purple daughter, purple son
D. Green mom, purple dad, green sons
E. Purple mom, purple dad, green daughter, purple son
F. Purple mom, purple dad, purple daughter, green son
G. Green mom, purple dad, green daughter, purple daughter, green son

B. For the choices that are not possible, state the individual(s) that make the statement NOT possible.

C: purple son, E: green daughter, G: green daughter

Use the Pedigree Analyzer Module of the Genetics and Evolution App to answer the following questions.

1. Fill in the blanks with the words dominant/recessive or x-linked/autosomal that best fits the descriptions.

If a trait is autosomal it will appear in males and females with equal frequency, but if it is x-linked, it will tend to appear in one sex more frequently than the other. If a trait is dominant, it will be present in every generation, but if a trait is recessive it has the potential to skip generations.

2. Select all of the following statement(s) that are **NOT TRUE** for autosomal dominant inheritance:

A. Both males and females can pass the trait on to their children
B. If both parents are unaffected, they can produce affected offspring
C. If a child is affected, at least one of their parents must also be affected
D. Two affected parents cannot produce unaffected children

3. Select all of the following statement(s) are **TRUE** for autosomal recessive inheritance:

A. Affected offspring can be born to two unaffected parents
B. The trait will always be present in every generation
C. The trait appears in both males and females with equal frequency
D. If both parents are affected, they can have children that are unaffected

4. Select all of the following statement(s) that are **TRUE** for X-linked dominant inheritance:

A. Both males and females can be affected
B. Affected sons do not have to have an affected mother
C. Affected daughters must have an affected mother
D. If the father is affected, all of his daughters will be affected
E. If both parents are affected, the all of their children will be affected
F. Often, more females than males are affected

5. Select all of the following statement(s) that are **NOT TRUE** for X-linked recessive inheritance:

A. Daughters can only get the trait if the father is affected
B. The trait can be passed from father to son
C. unaffected daughters of affected fathers are carriers
D. Affected sons cannot be born to unaffected mothers
E. If the mother is affected, all of her sons will be affected
F. Often, more males than females are affected

6. Select all of the following statement(s) that are **TRUE** for Y-linked inheritance:

A. The trait is only seen in males

B. affected fathers can produced both affected and unaffected sons

C. The trait does not skip generations if male sons are born to affected fathers

7. **A.** A single gene disease is inherited in an X-linked dominant fashion. How many of the following 9 combinations of parents and children are **POSSIBLE**.

A. affected mom, unaffected dad, unaffected sons, affected daughters
B. affected mom, affected dad, affected sons, affected daughter
C. unaffected mom, affected dad, unaffected daughter, unaffected son
D. affected mom, affected dad, unaffected son, affected son, affected daughters
E. affected mom, affected dad, affected sons, unaffected daughter
F. unaffected mom, affected dad, affected son, unaffected sons, affected daughter
G. unaffected mom, affected dad, unaffected son, affected daughters
H. affected mom, unaffected dad, affected son, unaffected son, unaffected daughter
I. unaffected mom, unaffected dad, affected son, unaffected daughters

B. For the choices that are not possible, state the individual(s) that make the statement NOT possible.

C: unaffected daughter, E: unaffected daughter, F: affected son, I: affected son

C. What if the disease was inherited in an <u>autosomal</u> dominant fashion? How would the phenotypes of the children for each combination of parents change? In each blank, write the phenotypes of all possible children that could be produced. For affected individuals, assume that they could be homozygous OR heterozygous for the disease allele.

Unaffected mom x Unaffected dad: (aa x aa)

Unaffected daughters, unaffected sons

Unaffected mom x Affected dad: (aa x AA OR aa x Aa)

Affected daughters, unaffected daughters, affected sons, unaffected sons

Affected mom x Affected dad: (AA x AA, Aa x AA, AA x Aa OR Aa x Aa)

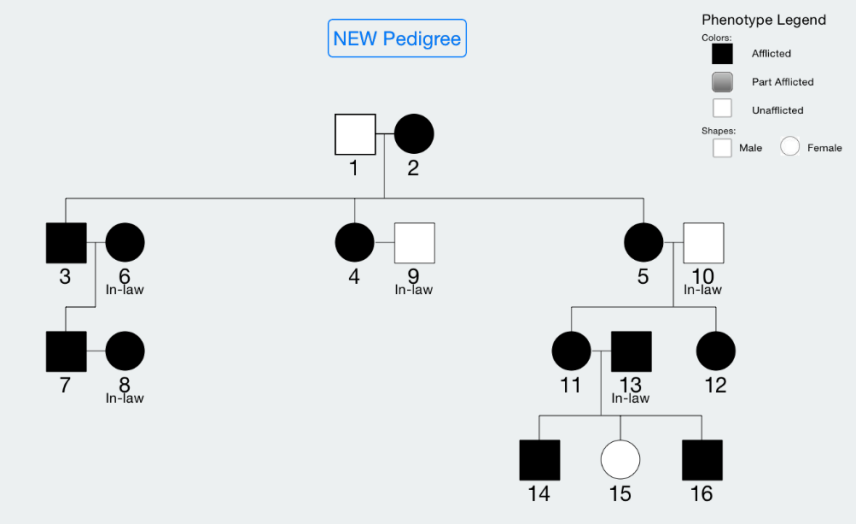
Affected daughters, unaffected daughters, affected sons, unaffected sons

Affected mom x Unaffected dad: (AA x aa OR Aa x aa)

Affected daughters, unaffected daughters, affected sons, unaffected sons

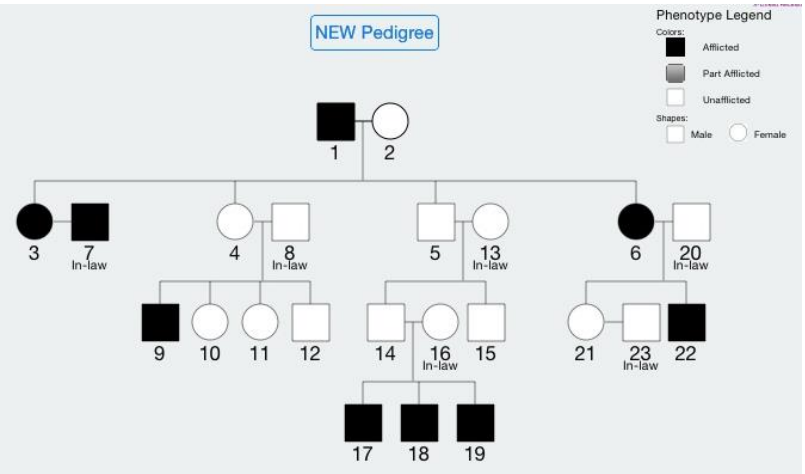
8. The pedigree below models autosomal dominant inheritance. Why can it NOT demonstrate X-linked dominant inheritance? Which individual(s) are inconsistent with X-linked inheritance?

Individual #15 would get the dominant X from dad and be affected



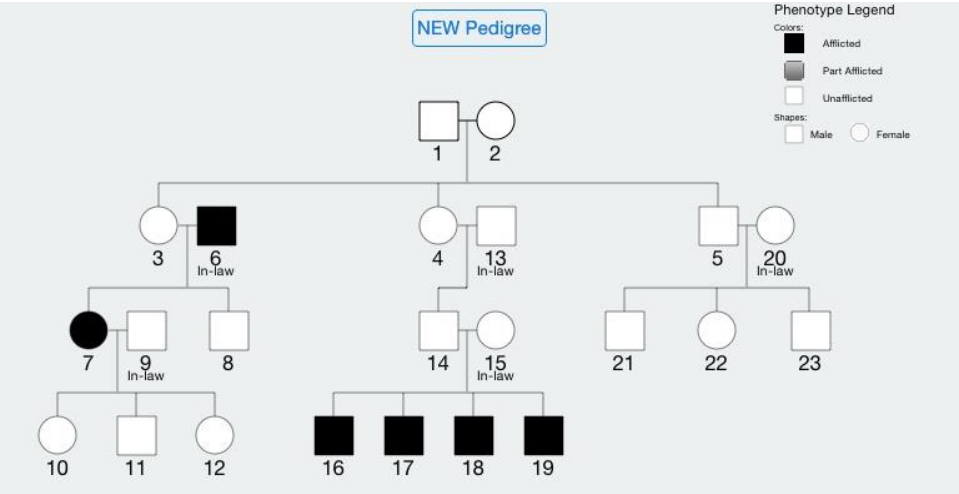
9. Explain why this pedigree represents recessive inheritance.

Affected individuals can be born to unaffected individuals, as seen in individuals 9, 17, 18, and 19



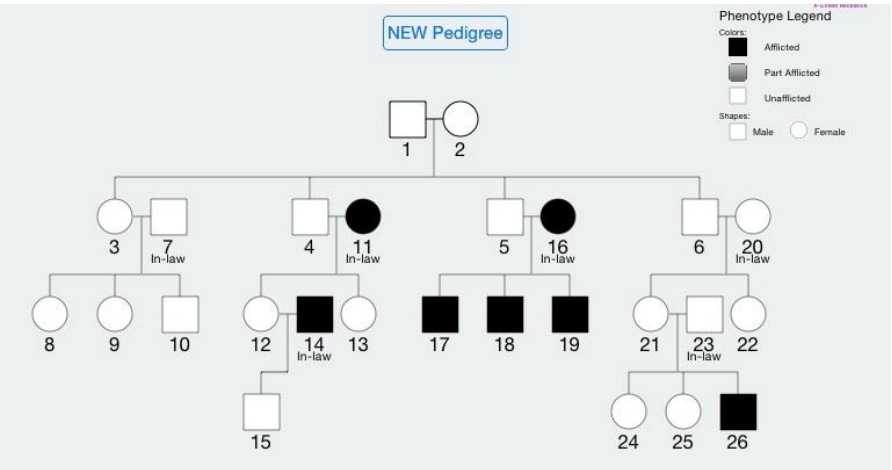
10. The pedigree below models autosomal recessive inheritance. Why does this NOT represent X-linked inheritance?

If it were x-linked, individual 7 would be X^aX^a, and her son (individual 11) would get only the X^a from her and be affected



11. Before solving this pedigree, what phenomena hints at the fact that this may be X-linked as opposed to autosomal?

The trait tends to affect males more than females, affected female 16 passes the trait to all of her sons, affected female 11 does not pass on the trait to any of her daughters (daughters are carriers), unaffected female passes the trait on to only her son (she is a carrier)



Rules for Determining Mode of Inheritance for Pedigrees:

True for autosomal dominant inheritance:
-both males and females can pass the trait on to their children
-if both parents are unaffected, they cannot produce affected offspring
-the trait appears in both males and females with equal frequency
-If a child is affected, at least one of their parents must also be affected
-two affected parents can produce unaffected children (both parents are heterozygous carriers)
-the trait does not generally skip generations

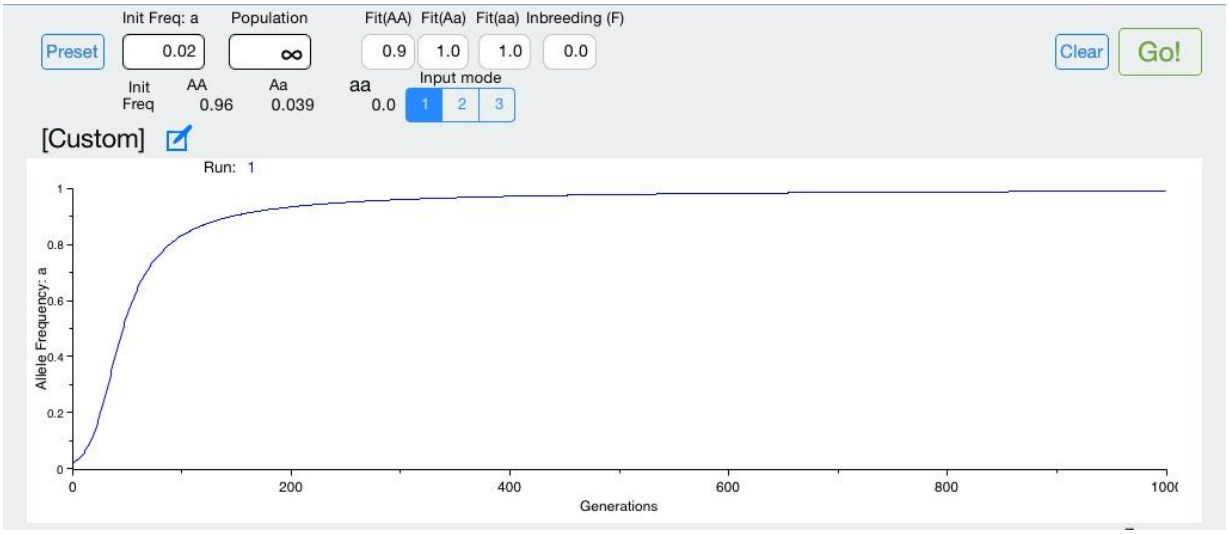
True for autosomal recessive inheritance:
-affected offspring can be born to two unaffected parents (both parents are carriers)
-the trait appears in both males and females with equal frequency
-if both parents are affected, all of their children will be affected
-the trait can skip generations

True for X-linked dominant inheritance:
-Both males and females can be affected
-affected sons have to have an affected mother
-affected daughters can have either an affected father or affected mother or both
-if the father is affected, all of his daughters will be affected
-if both parents are affected, the only potential unaffected children are males (this is if mom is a carrier)
-the trait does not generally skip generations
-often, more females than males are affected

True for X-linked recessive inheritance:
-the trait cannot be passed from father to son
-the trait can skip generations
-daughters can only get the trait if the father is affected
-the mother must be a carrier or affected to pass the trait on to daughters
-unaffected daughters of affected fathers are carriers (heterozygous for the trait)
-affected sons can be born to unaffected mothers (mother is a carrier)
-if the mother is affected, all of her sons will be affected
-often, more males than females are affected

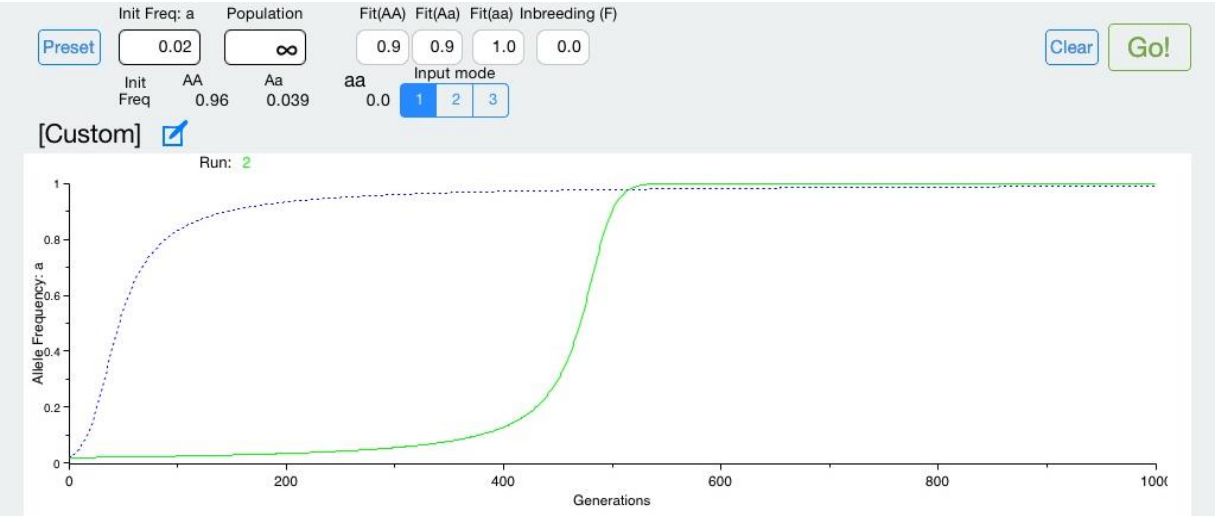
True for Y-linked inheritance:
-the trait is only seen in males
-affected fathers will produce all affected sons
-the trait does not skip generations if male sons are born to affected fathers

Use the Allele Freak module of the Genetics and Evolution App to answer the following questions.



1. A. The diagram above represents the spread of an advantageous dominant allele over the course of 1000 generations. Which is the dominant allele, A or a? How do you know?
   "a" because it has the highest fitness, and the heterozygote (Aa) and homozygote (aa) have the same fitness.
   B. Does this allele reach fixation during this time span? If so, when?
   No, at the end of 1000 generations, it is still hovering around a frequency of ~0.99

2. A. Do an additional simulation without clearing your line graph from question 1 that represents the spread of the "a" allele over time if the recessive allele is advantageous. Do this by changing the fitness of the heterozygote to 0.9 and leaving the fitness of the homozygote "AA" at 0.9.



B. Does the "a" allele reach fixation by the end of 1000 generations? If so, when?
Yes, generation 574

C. In which case does the "a" allele reach the highest frequency, when the recessive or dominant allele is advantageous? Why is this? Explain your answer in terms of how selection works on the different genotypes.
The allele reaches its highest frequency when the recessive allele is advantageous. When the dominant allele is advantageous, it is able to increase to high frequencies (extremely close to fixation) rapidly early on in the population since both the homozygous dominant individuals and heterozygotes would be positively selected for against homozygous recessive individuals. However, it takes a long time for the recessive alleles hiding in the heterozygotes to be removed from the populations once the homozygous dominant and heterozygous individuals become prominent in the population. When the recessive allele is advantageous, it takes a while to increase in the population since again, the allele is hiding in heterozygotes, but since those possessing the dominant allele (either one or two) are selected against, it is a lot easier for selection to kill off individuals manifesting the dominant trait, allowing the homozygous recessive individuals to go to fixation in a finite/quicker amount of time.

Now let's look at how these allele frequency dynamics change when using the same parameters, but in a FINITE population. Change the ∞ symbol to a population of 100.

3. Run the simulation that models the spread of the dominant advantageous allele. Use the same parameters as was done in question 1 with the new population size. Set the simulation to run 20 times.
   A. What happens to the "a" allele over 1000 generations. Is it lost, fixed, neither? Does the "a" allele exhibit the same pattern every time? Is there one pattern that it tends to exhibit more than others?
   It does not exhibit the same pattern every time. It tends to be fixed, or go near fixation more often than it is lost. But it tends to be lost in roughly about 6 or more of the 20 generations each time the simulation is repeated.
   B. If the "a" allele is fixed and/or is lost, on average, how many generations did it take for this to occur?
   Fixed: ~100-200 generations Lost: ~ 3-20 generations
   C. How do these line graphs look different from the graphs we saw in questions 1 and 2?
   The graphs are a lot more jagged and "zig-zaggy", with allele frequencies bouncing up and down a lot. It is not as smooth of a transition towards loss or fixation as seen in questions 1 and 2, and the allele frequency fluctuates quite a bit. (This is indicative of stronger influence of genetic drift here, as opposed to the stronger influence of selection in questions 1 and 2.)

4. Run the simulation that models the spread of the recessive advantageous allele. Use the same parameters as was done in question 2 with the new population size. Set the simulation to repeat 20 times.
   A. What happens to the "a" allele over 1000 generations. Is it lost, fixed, neither? Does the "a" allele exhibit the same pattern every time? Is there one pattern it tends to exhibit more than others?
      It does not exhibit the same pattern every time. It tends to be lost far more than it is fixed.
   B. If the "a" allele is fixed and/or lost, on average, how many generations did it take for this to occur?
      Lost: ~4-30 generations Fixed: ~90-150 generations

Further Practice: Repeat questions 3 and 4 and see if you get the same frequencies of loss and fixation of the "a" allele each time.

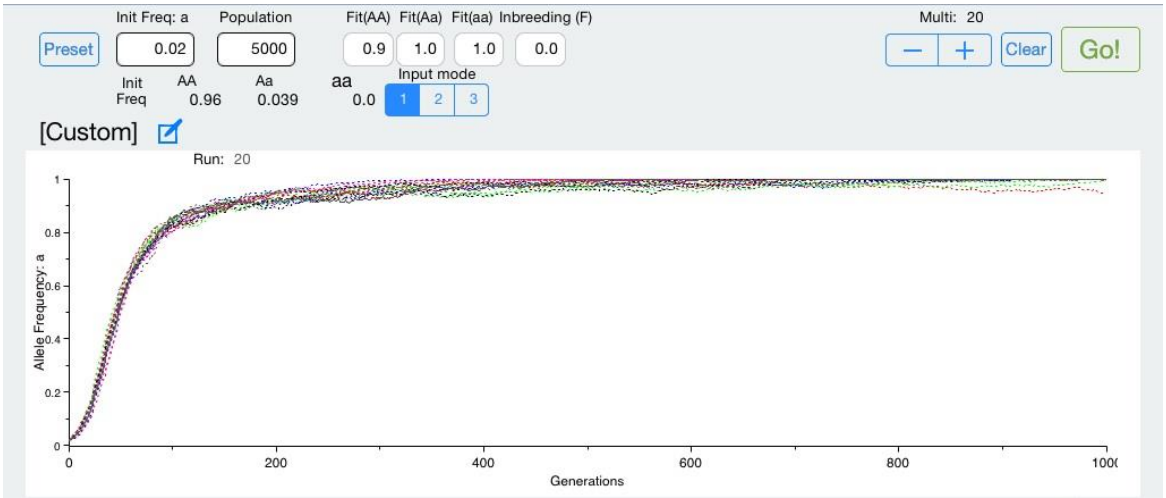
What have we learned so far? With selection acting alone or predominantly in populations (as seen in questions 1 and 2), it is better for alleles to be recessive in terms of spreading to high frequencies/fixation. When genetic drift acts alone or predominantly in populations (as seen in questions 3 and 4), it is better for alleles to be dominant to have a better chance of spreading to fixation.

5. Why is it that for both of the simulations in numbers 3 and 4, the "a" allele is not ALWAYS lost or fixed? Explain your answer in terms of the balance of natural selection and genetic drift in small population sizes.
   In small populations, genetic drift is far more prominent and stronger than selection. Genetic drift is a process of evolution in which allele frequencies change as a result of random sampling of alleles or chance events. Genetic drift does not discriminate between alleles that are better or more fit than others; it is a completely random process that happens independent of natural selection. Thus, this is why we see that either dominant advantageous or recessive advantageous alleles can be both lost or fixed depending on how these chance events take place. Just because they are advantageous doesn't mean that they will always reach high frequencies in populations!

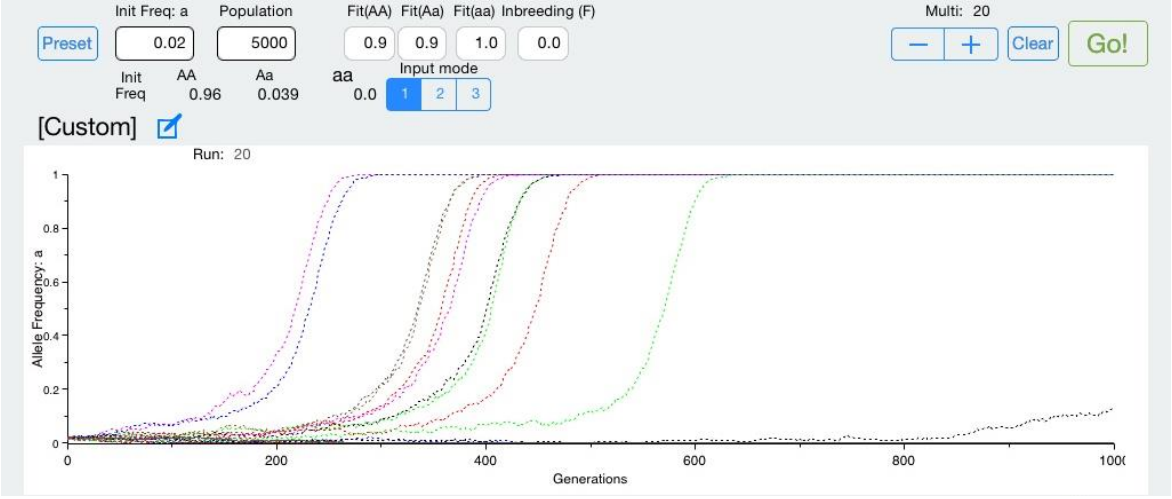
6. Repeat questions 3 and 4 with population sizes of 5,000 and 50,000. Once you get to 50,000, it will take a little longer for the app to run, but be patient! What do you notice about the frequency of the allele being fixed/lost and the appearance of the line graph as the population size gets larger and larger? Explain this in terms of the balance of natural selection and genetic drift in large populations.

In large populations, selection plays a much stronger role in influencing allele frequency outcomes than genetic drift. As populations get larger, drift plays less and less of a role and selection starts to play more of a role in determining the fate of allele frequencies in populations (as seen in the transition from a population of 5,000 to 50,000). In large populations, natural selection will tend to propagate alleles that are advantageous more efficiently than those that are not in a more predictable pattern. The influence of genetic drift in determining whether advantageous or detrimental alleles are fixed or lost is negligible in really large populations.

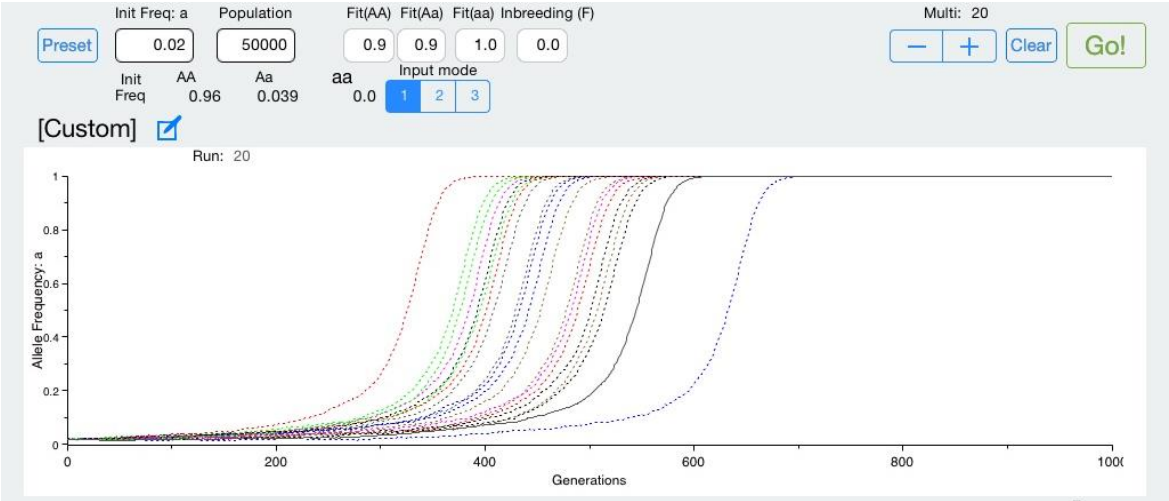
For the advantageous dominant model of a population of 5,000 repeated 20 times, most of the time the allele fixed, and if it didn't it had a frequency ranging from 0.95-0.99. Graph looks like the diagram in number 1.



For the advantageous recessive model of a population of 5,000 repeated 20 times, the allele tends to be lost as often as it is fixed, but lines are starting to look more and more like the diagram in number 2, though the time to fixation varies greatly in each.



For the advantageous recessive model of a population of 50,000 repeated 20 times, the allele fixed every time, and the graph looks exactly like the answer in number 2.



For the advantageous dominant allele model of a population of 50,000 repeated 20 times, the allele was so close to fixation (allele freq= 0.98-0.99) every time, and the graph looks exactly like the diagram in number 1.