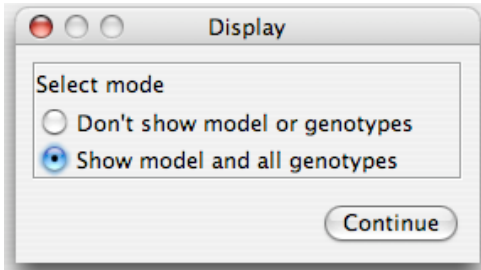


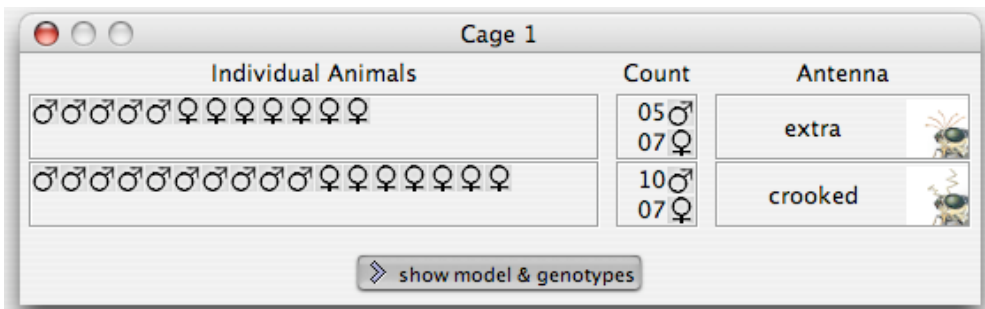
Orientation to the Virtual Genetics Lab (VGL 1.4.2)

After the pioneer work of the monk they call The Father of Genetics, Gregor Mendel, genetics lay dormant for many years unappreciated until rediscovered many years later and given wider notice by Punnett. The organism of choice shifted from garden peas to fruit flies. We will work with simulated ones in the application Virtual Genetics Lab.

You can approach VGL in two modes: examining the results of breeding fruit flies whose genetic model is known and crossing flies whose phenotype is known, but whose genetic model and genotype are not known but can become known by you and your team. Demonstrate your mastery of this task by showing how you know your answer is valid.

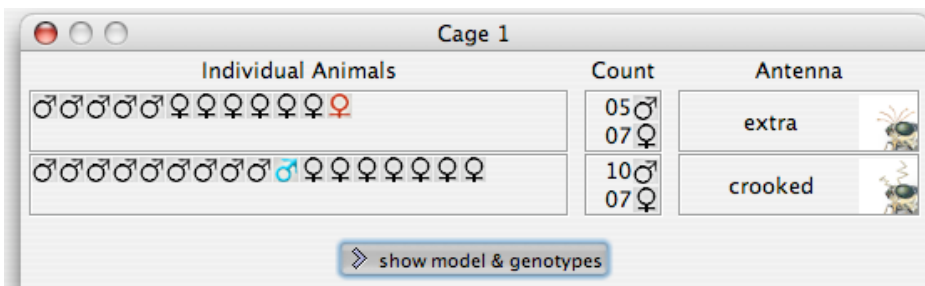


When you are in practice or tutorial mode you will be able to select the button for “Show model and all genotypes” but when you are in research or testing mode you’ll pick the “Don’t show...” option. Selecting “Show model...” just enables the feature but you don’t see it until you click **show model & genotypes** in Cage 1 so you can choose not to do so until you’ve come to your own conclusions. When it is clicked another window drops down with information about the genetic model. Also genotypes appear for each fly when you roll the cursor over its symbol. But let’s not peek yet.

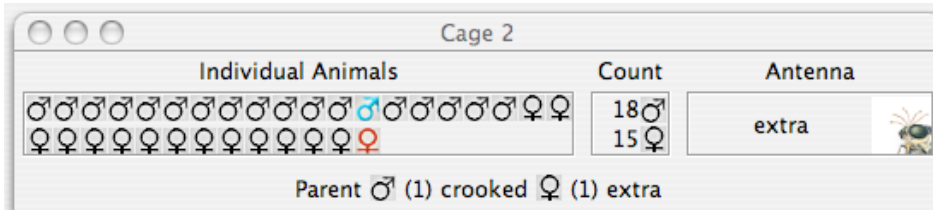


At the beginning of each problem you are given a Cage (1) of flies represented by the symbols for male (Mars’s spear) and female (Venus’s mirror). Each has its own genotype; your job is to discover it.

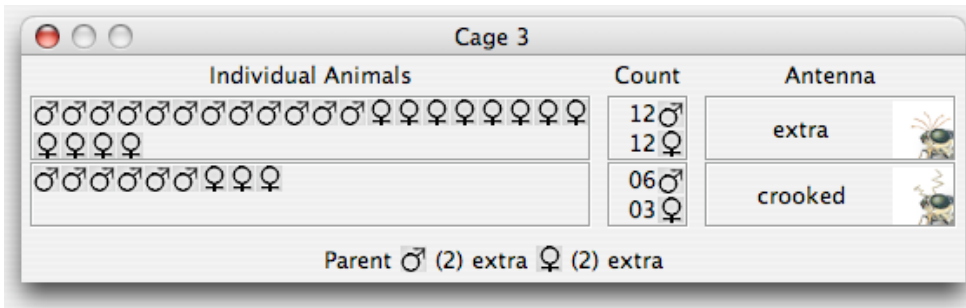
The menus for the program are relatively simple, as is the button bar. While working on your first practice problem try rolling the cursor over each button or even clicking it to see what it does. If you scramble everything up, just close that problem and start over. You can save problems you are working on but you don’t have to save everything. The button bar is a “tear off” menu. If you click on the grey diagonal striped end and drag it aside, you can position the button bar wherever is convenient.



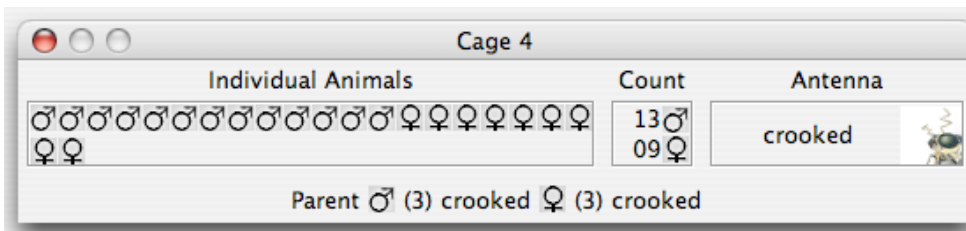
Here two flies have been selected for crossing: a male with “crooked” antennae and a female with “extra” antennae. Likely genotypes? VGL uses words, but we’ll use some abbreviated codes to save time and pencils.



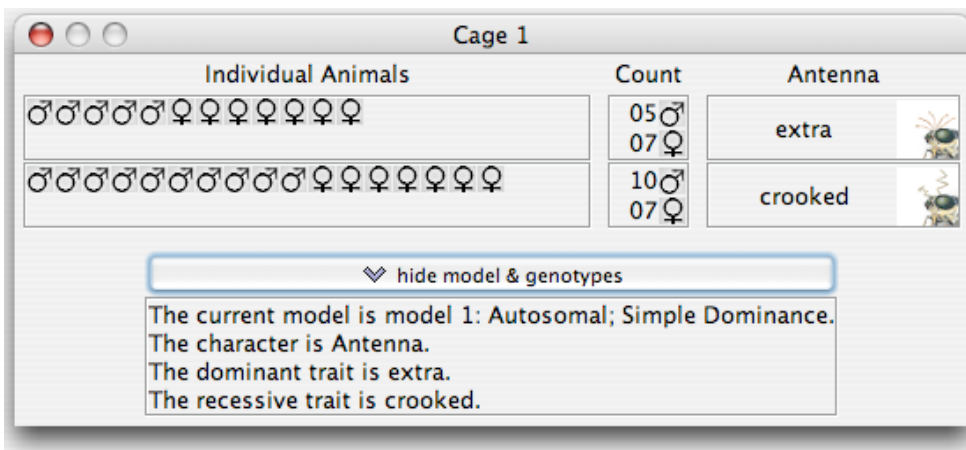
Cage 2 shows the results of the first cross and also the parents below. On the computer screen you could also see which flies have been selected for the next cross. Can you tell?



Here is the result of the second cross. When you are more experienced you will be able to see a cross like this and know which is the dominant trait. Can you tell now? Why that one?



Does this result support or confound the conclusion you made from Cage 3? Can you draw Punnett squares for these three crosses?



Here is Cage 1 after clicking the “show model & genotypes” button (the button now says “hide” so you can turn that feature on or off as suits your problem-solving style). Notice that the most common phenotype in Cage 1 is crooked antennae, the **recessive** trait!

If **A** symbolizes the dominant allele and **a** symbolizes the recessive allele, what would the phenotypes of the following flies look like, what genotypes would their offspring have and what would those offspring look like?

Parent Phenotypes	Parent Genotypes	Offspring Genotypes	Offspring Phenotypes
extra x extra	AA x AA		
	AA x Aa		
	aa x aa		
	Aa x Aa		
	AA x aa		
	Aa x aa		

What do you notice about the parents in the last two crosses as contrasted with the first four? What do you notice about the results produced in the same two groups of crosses? This analysis should lead to developing strategies for getting the most usable information out of the fewest number of crosses once you enter the research/testing mode.

Teamwork in the Virtual Genetics Lab (VGL 1.4.2)

Form a team of no more than three people. Teams will be reporting the results of their most challenging problem solutions. Points will be awarded based on 1) the difficulty level of problems, 2) the clarity and correctness of the solution presentation, and 3) number of crosses needed to find the solution (In real life each cross would involve time and money; intelligent crossing strategies save both).

You can use the File>Open Work command or the second icon on the button bar to see some problems that have been provided by the developers of VGL. Their names may provide a hint to the genetic model involved. One of them (Problem1.wrk) has a number of crosses already completed from which you can deduce the genetic model. When you have worked that out you should be able to assign the correct genotype to all the parents and most of the offspring in the crosses shown. Notice that no parents are shown for Cage 1; those flies are not siblings but just a random sample from a field population.

Use the File>New Problem command (first icon on the left) and locate the folder CSM VGL. It contains practice problems (01, 02, 04, 05, 07, 08) in which the genetic model is given (*e.g.* autosomal codominance or X-linked simple dominance) or advanced practice problems (03, 06, 09, 10) in which the model possibilities are more or less limited (*e.g.* autosomal, but could be simple dominance or codominance). They won't include any problems involving hierarchical or circular dominance. Once you have built some confidence based on success in solving problems your team will take on the Challenge level (11) in which any combination of simple dominance vs codominance and autosomal vs sex-linked may occur. Your team will present solutions to three Challenge problems, each with a different model involving two alleles (one of the first six listed below).

VGL offers 12 possible genetic models. A model with a single gene and two alleles may show Simple Dominance (the heterozygote has the same phenotype as the dominant homozygote) or Incomplete Dominance (the heterozygote has a different phenotype than either homozygote, possibly an intermediate). A model with a single gene and three alleles can show Hierarchical Dominance where A is dominant to all; A' is dominant to A''; A'' is recessive to all A > A' > A'' or possibly Circular Dominance where B is dominant to B'; B' is dominant to B'' (this one is theoretical). Whether or not it has two or three alleles the gene might be located on an autosome or on a sex chromosome so it is inherited differently in different sexes; in some species (like us) females are XX and males are XY (only the X chromosome carries anything but sex determination) but in other species (*e.g.* birds & butterflies) females are ZW and males are ZZ (only the Z chromosome carries anything but sex determination).

The 12 possible genetic models in VGL:

- Model 1: 2 alleles; Simple Dominance; Autosomal
- Model 2: 2 alleles; Incomplete Dominance; Autosomal
- Model 3: 2 alleles; Simple Dominance; XX/XY Sex linked
- Model 4: 2 alleles; Incomplete Dominance; XX/XY Sex linked
- Model 5: 2 alleles; Simple Dominance; ZZ/ZW Sex linked
- Model 6: 2 alleles; Incomplete Dominance; ZZ/ZW Sex linked
- Model 7: 3 alleles; Hierarchical Dominance; Autosomal
- Model 8: 3 alleles; Circular Dominance; Autosomal
- Model 9: 3 alleles; Hierarchical Dominance; XX/XY Sex linked
- Model 10: 3 alleles; Circular Dominance; XX/XY Sex linked
- Model 11: 3 alleles; Hierarchical Dominance; ZZ/ZW Sex linked
- Model 12: 3 alleles; Circular Dominance; ZZ/ZW Sex linked

In solving a problem you should state what genetic model is involved, how you know and draw a Punnett square for a cross that demonstrates the solution. This would include: for a case of simple dominance identifying the dominant and recessive; for a case of incomplete dominance identifying the heterozygous phenotype; for a sex-linked allele identifying whether on an X-chromosome or a Z-chromosome.