

Virtual Genetics Lab (VGL) 5

This is it!

Objective

To use your knowledge of genetics to design and interpret crosses to figure out the inheritance of very complex characters (these can include: sex-linkage, and incomplete dominance). This should bring together all parts of the genetics portion of the course. You will also be asked to write up a lab report in the approximate format of a scientific paper; this will help you to understand hypothesis testing and the process of science.

Description

VGL is a computer simulation of genetics. The computer randomly picks a character with two traits. It then randomly chooses which form of the character will be dominant and which will be recessive. That way, each time you start the program, you get a different problem (also, every group will get a different problem). Finally, it creates a population of creatures with random genotypes called the Field Population.

As in a real lab, the creatures are kept in cages; Cage 1 contains the Field Population. You can select any two creatures (one must be male and the other female) and cross them; the computer automatically puts their progeny in a new cage.

The task:

To solve two different problems generated by VGL. A solution is a genetic model that accounts for all your data.

There are twelve possible genetic models.

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

Your task is to find the genetic model that best fits your data.

You should know that, since VGL selects traits randomly, the particular traits do not necessarily indicate the dominance relationships. That is, although you might expect otherwise, having no antennae may be dominant to having antennae. Similarly, having 4 legs may not be the heterozygote of 2-legs and 6-legs.

Starting up VGL:

1) You will alone. It is easy to fill the screen with cages of creatures and get totally confused so you should work slowly and deliberately and keep careful notes about the experiments you do and the contents of each cage. If you get very confused, you can quit the program and start fresh with a new problem.

2) You can also download the program and run it from your home computer; go to <http://intro.bio.umb.edu/VGL/index.htm>

You may have to install Java. The program should guide you.

You need to get or install the student.key file in the same folder. You will need to save your file for grading.

3) To run the VGL program, click on the VGL. It looks like a small fly-like insect.

4) If you want to read the VGL manual, click on the Help button at the top of the VGL window.

5) Open the VGL problem folder. You should choose Level 10 problems for this lab session. For practice, you can choose Level 9, which will allow you to see the underlying genetic model and the genotype of each fly (to see the genotypes, just leave the cursor over a creature's symbol and a window will pop up that shows its genotype). The problems you solve for your lab report must be Level 10.

6) The objective is to make a genetic model to explain the inheritance of the traits you are studying. There is no way to find the "right answer"; you decide whether you're convinced or not. A complete model would look like:

"The shape of the thorax is controlled by one gene with two alleles:

T - tetraltera (dominant)

t - grooveless (recessive)"

or: "In this creature, XX are female; XY are male. The color of the eyes is controlled by one gene, located on the X-chromosome with 2 alleles:

X^B - black (dominant)

X^b - blue (recessive)

Y - no contribution to phenotype”

7) Once you are convinced of your model, you will write it up.

8) You must solve two Level 10 problems for your Lab Report.

The problem you solve for your lab report should be more complex than a “two-allele, simple dominance, autosomal” problem. That is, it must include at least one of the following: sex-linkage, three-alleles, or incomplete dominance. Lab reports describing simpler problems, or problems worked in practice mode, will receive significantly less credit.

9) Once you have solved this problem to your satisfaction, you **should** save this problem. This is for several reasons:

- So that you can go back and look at all of your data after you leave lab.
- So that you can do more crosses in your problem after you’ve left lab.
- So that I can check to be sure that you analyzed your data correctly if there are any questions

Procedure

a) From the “File” menu, choose “Save As” and find your USB (or save to the desktop and email to yourself...

b) Enter a descriptive (but not too long) name for your problem file.

10) Once you have solved the problems to your satisfaction you **MUST** save the grading file and email it to me. By now you know how to do this. If you are correct this will get you the extra credit. For even more credit-write a lab report....

Lab report:

It is very important that you follow **all** of the directions for preparing your lab report in order to receive full credit.

Overall notes

- Your lab report must be typed; handwritten lab reports will not be accepted without severe penalty-you are using a computer for the lab, use it write the report!

Special notes for this lab

- The lab report **must be in the format described below** including titles for each section (Abstract, etc.). Lab reports that are not in this format will receive an automatic deduction of 10 points.

Parts of the Lab Report

This will be structured like a scientific paper to introduce you to this important format as well as the aspects of the nature of science that it illustrates.

The most important thing to keep in mind is that a scientific paper is not the story of what you did. It is a logical argument in a prescribed format designed to convince your reader that your conclusions are correct. The most crucial issue is making a clear and logical argument that is supported by data. This means that, in most cases, you will not present your data in the order that you got it; you should present it in a way that makes the clearest case for your interpretation.

These are the remaining parts of the lab report. *Descriptions in italics indicate their role in the argument you are developing.*

- (5 points) **Abstract** A 1-3 sentence description of the genetic model that explains the inheritance of your trait. *This introduces your reader to the model you are going to be arguing for.*
- (5 points) **Introduction** A short paragraph that explains the research question being addressed (the inheritance of your trait) and why the methodology being used (crossing individual organisms and looking at the offspring) is believed to be able to answer that question. *This introduces the background behind your studies and why they are worth reading about.*
- (5 points) **Materials and Methods** A short paragraph that explains what you did. **Do not** give the details of **all** the crosses you did. All you need here is a few sentence summary of: how many crosses you did; roughly how many of those were necessary to figure out the model; and any strategies you used in choosing what to cross (just describe these in general **do not** talk about each and every cross in detail). *This tells the reader the details of the techniques you used.*
- (25 points) **Results and Discussion** *This is the most important part of the paper. It is where you make the argument for your interpretation of the data.* Start by introducing the genetic model you have found and defining appropriate symbols (5 points). Then go point-by-point to show the evidence for your model. This is not a narrative or a history, it is a logical argument supported by data. Do not present all your crosses in the order you did them; present them in the order that makes the clearest argument for the model you described in the Abstract.

It is probably best to break this down into parts. For each part of your model, give the evidence for that part. For example, if you want to argue that red eyes are XX/XY sex-linked dominant, you would have separate arguments to show that it is (1) XX/XY sex-linked and (2) dominant.

In addition to the 5 points for defining the symbols, this part will be graded using the following rubric:

- *All parts of model are supported* (0 - 8 points). All parts of the model you presented are specifically supported by one or more pieces of data. Less than full credit will be given for answers that do not support all parts of your model. That is, if you say it is “ZZ/ZW sex-linked incomplete dominant”, you have to show data that it is ZZ/ZW, sex-linked, and incomplete dominant.
- *Data rule out all possible alternative models* (0 - 6 points). You present data that specifically exclude all relevant alternative models. Less than full credit if other interpretations are possible. That is, if you choose the above model, you would have to show that it cannot be autosomal, XX/XY sex-linked, circular dominance, etc. By “relevant alternative models”, we mean that, (for example) if you have shown that it must be 3 alleles, you only need to distinguish between incomplete, circular, and hierarchical dominance.
- *Only relevant data are presented* (0 - 6 points). All pieces of data presented are part of an explicit argument that supports the selected model or rules out other models. Less than full credit for data presented that are not part of your argument.