VGL Challenges

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 that you have worked with before. Briefly, 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. 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 challenging problems generated by VGL. A solution is a genetic model that accounts for all your data. These are the most challenging VGL problems - there are 12 possible genetic models. All the problems in VGL at this level involve genetic models with one gene that has two or three alleles. Based on this, there are several features that can vary:

- The number of alleles; this can be either:
  - Two alleles (Models 1, 2, 3, 4, 5, and 6). Given this, there are two possible **Interactions between the alleles**:
    - Simple Dominance: (Models 1, 3, and 5) The heterozygote has the same phenotype as the dominant homozygote. That is, with two alleles A and a:
    - Incomplete Dominance: (Models 2, 4, and 6) The heterozygote has a different phenotype than either homozygote. In nature, this is usually intermediate; in VGL it need not be.
  - Three Alleles (Models 7, 8, 9, 10, 11, and 12). Given this, there are two possible **Interactions between alleles**:
    - Hierarchical Dominance: (Models 7, 9, and 11). A is dominant to all; A' is dominant to A'' and recessive to A; A'' is recessive to all (A > A' > A'').
    - Circular Dominance: (Models 8, 10, 12). B is dominant to B'; B' is dominant to B''; B'' is dominant to B.
- Whether the trait is sex-linked or not; this can be either:
  - Not sex-linked (Models 1, 2, 7, and 8) - the gene for the character is carried on an autosome so it is inherited identically in both sexes.
  - Sex-linked - the gene for the trait is located on a sex-chromosome so it is inherited differently in different sexes. **This can be either**:
    - XX/XY (Models 3, 4, 9, and 10) Females are XX; males are XY. Here, Y carries no genes except those needed to make the organism male.
    - ZZ/ZW (Models 5, 6, 11, and 12). Females are ZW; males are ZZ. Here, W carries no genes except those needed to make the organism female.

This leads to twelve possible genetic models.

<u>Model 1</u>: 2-alleles; Simple Dominance; Autosomal.
<u>Model 2</u>: 2-alleles; Incomplete Dominance; Autosomal.
<u>Model 3</u>: 2-alleles; Simple Dominance; XX/XY Sex-linked.
<u>Model 4</u>: 2-alleles; Incomplete Dominance; XX/XY Sex-linked.
<u>Model 5</u>: 2-alleles; Simple Dominance; ZZ/ZW Sex-linked.
<u>Model 6</u>: 2-alleles; Incomplete Dominance; ZZ/ZW Sex-linked.
<u>Model 7</u>: 3-alleles; Hierarchical Dominance; Autosomal
<u>Model 8</u>: 3-alleles; Circular Dominance; Autosomal
<u>Model 9</u>: 3-alleles; Hierarchical Dominance; XX/XY Sex-linked
<u>Model 10</u>: 3-alleles; Circular Dominance; XX/XY Sex-linked
<u>Model 11</u>: 3-alleles; Hierarchical Dominance; ZZ/ZW Sex-linked
<u>Model 12</u>: 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 work in groups of three people per computer. You may want to take turns using the computer. It is easy to fill the screen with cages of creatures and get totally confused so you should work slowly and deliberately and <u>keep careful notes about the experiments you do and the contents of each cage</u>. If you get very confused, you can quit the program and start fresh with a new problem.

       2) The program runs on all of the Macintosh computers in the lab. This is a lot like the jsVGL program you used in the Warm-ups; it is a little easier to use and has a few more featuers. You can also download the program and run it from your home computer; go to

          http://vgl.umb.edu

       3) To run the VGL program, click on the VGL icon in the Dock. 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) You should choose Level 10 problems found in the Problems/VGL/ folder 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 problem you demonstrate to your TA and the problem 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. You should enter your model into the **Model Builder** available from the **Utilities** menu; this is like the **Genetic Model** in jsVGL.

       7) Once you and your partners are convinced of your model, you will then present it to your TA for **<u>review</u>**. Your TA will then perform a cross with your creatures to test your model. You must do this until you have solved one sex-linked and one non-sex-linked problem.

       8) Finally, you must solve one more Level 10 problem for your Electronic Lab Report.
    We *strongly* advise you to work through this problem in lab, rather than at home. In lab, your TA can help you to make sure that you have worked it through completely. In addition, although you can run VGL on your home computer, there is no guarantee that this will work as well as it does in lab.
    <u>The problem you solve for your lab report must be more complex than a "two-allele, simple dominance, autosomal" problem.</u> That is, it must include at least one of the following: sex-linkage or incomplete dominance. Lab reports describing simper problems, or problems worked in practice mode, will receive no credit.

9) Once you have solved this problem to your satisfaction and entered your answer into the **Model Builder**, you should save your work for grading. It is very important that you do this correctly; if you submit a file in the wrong format, you will not get credit.
>   a) From the **File** menu, choose **Save Work for Grading**.
>   b) Name the file with the names of your group members and save it to the Desktop.
>   c) On the Desktop, you should see a file with a .gr2 ending.
>   d) E-mail the .gr2 file to your TA as an attachment. Be sure to include all the names of
>   your group members in the e-mail body.
>   e) **Do not quit VGLII yet!**

10) You will also need to save your work to a file that you can use for your lab report. VGLII can save files as web pages (.html files) that you can copy raw data from to use in your report. **Before you leave the lab, you should do the following:**
>   a) From the **File** menu, choose **Print Work to File…**
>   b) Name the file as you prefer and save it to the Desktop.
>   c) On the Desktop, you should see a file with a .html ending.
>   d) e-mail the file to yourself and all your group members (or put it on a USB stick).

Lab report:

It is very important that you follow all of the directions for preparing your lab report in order to receive full credit. Feel free to contact your TA in advance of the due date if you have any questions.

Overall notes
- Your lab report is due at the start of lab on the date listed in the syllabus. It will not be accepted late.
- Although you and your group members worked on the same problem, your lab report must be in your own words.
- Your lab report must be typed; handwritten lab reports will not be accepted.

Special notes for this lab
- (5 points) You must have e-mailed the .gr2 file to your TA.
- 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, we will grade this part 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, regular dominance, etc. By "relevant alternative models", we mean that, (for example) if you have shown that it must be 2 alleles, you only need to distinguish between incomplete and regular 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.