Internet Instruments (Videos, Animations, Simulations, and Assignments) That Can Be Used to Prepare Students for Laboratory, Test Understanding, or Extend the Laboratory Experience

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Introduction

In the Fall of 2008, an on-line laboratory component was added to the distance version of Introductory Biology at North Carolina State University (NCSU) that treats cell and developmental biology so that students could earn full credit for the course without attending campus laboratory sessions. The laboratory was extremely well received by students. Since much of the success of the distance lab rested on the instruments developed for on-line delivery such as videos, animations, simulations, we wanted to share the more instructor-modifiable animations and simulations with the ABLE audience. All programs are copyrighted by NCSU, but can be modified and used as needed, as long as NCSU's contribution to your final product is acknowledged. Please email us and let us know how you are using the programs so we know how to modify the programs in the future to make them more useful resources for instructors. We will graciously acknowledge, and thank you, for any feedback received.

Instructor's Notes

The major emphasis in the course is on cell structure and function. The programs come in three flavors: A. use or not as presented. B. Instructor can modify some parameters. C. Instructor can modify most parameters. Please work with these programs at **http://www.ncsu.edu/project/interactivebiology/** and send us any feedbacks if you encounter any problems. **All programs can be downloaded from that site.** Most downloads also contain instructions for modifying programs to suit your teaching objectives and style.

A List of Available Animations and Simulations

1. Fill-in respiration diagram (**A**). This is an example of a preparatory quiz that students take prior to tackling the "lab". Students felt the interactive diagram helped them prepare for exams as well as review the concepts prior to attempting the distance laboratory exercises. It should be helpful for preparing students for any laboratory on respiration. The problem is that it needs to be used as is. This is a common problem with web-downloaded animations, and to some extent, simulations. They are either exactly what you need or you live with terminology and more importantly, foci that may not completely reflect your own style and objectives. We include this simulation to emphasis our teaching style, which tends to downplay rote memorization.   Even in this "quiz" students who submit answers only receive an indication of how many of their answers are correct.   With 11 questions and ten possible answers per

question, students quickly determine that reviewing the material before subsequent attempts is probably less time-consuming and certainly less frustrating than trying to guess the right answers.

2. Plotter (A): This is a resource that essentially graphs points. The advantage of this web resource is that the plotter can be embedded on a page on your website. So you do not have to leave your website and open an application such as Excel to graph data you might wish to discuss in lecture). Plotter is actually a very powerful utility for graphing in which students can change axes titles or add a line or regression to a plot of points. Instructions for using the plotter are included in the downloadable plotter folder.

3. Pedigree (B): This simulation generates multiple-generation pedigrees to portray the inheritance of a genetic disease. Students must determine whether the trait is inherited as a recessive or dominant allele and whether the locus responsible is autosomal or sex linked. The simulation generates as many pedigrees as required to resolve the basis for inheritance. Students may submit their "hypothesis" regarding a particular trait at any time. If their hypothesis is rejected, students are prompted to examine more pedigrees. There is a "teaching" version that an instructor could use in the laboratory or in lecture. The instructor can specify a particular pattern of inheritance (of the four available, dominant or recessive autosomal, or dominant or recessive sex-linked) and the program will only draw pedigrees that fit this mode of inheritance. This version should prove useful to instructors who are trying to tutor students in how to examine pedigrees. We assume most instructors will use the desired simulations as is, but downloadable instructions are available that explain how to change some parameters of the code for the simulation such as frequency of different modes of inheritance. Default is 25% for each mode, recessive autosomal, dominant autosomal, recessive sex-linked and dominant sex-linked.
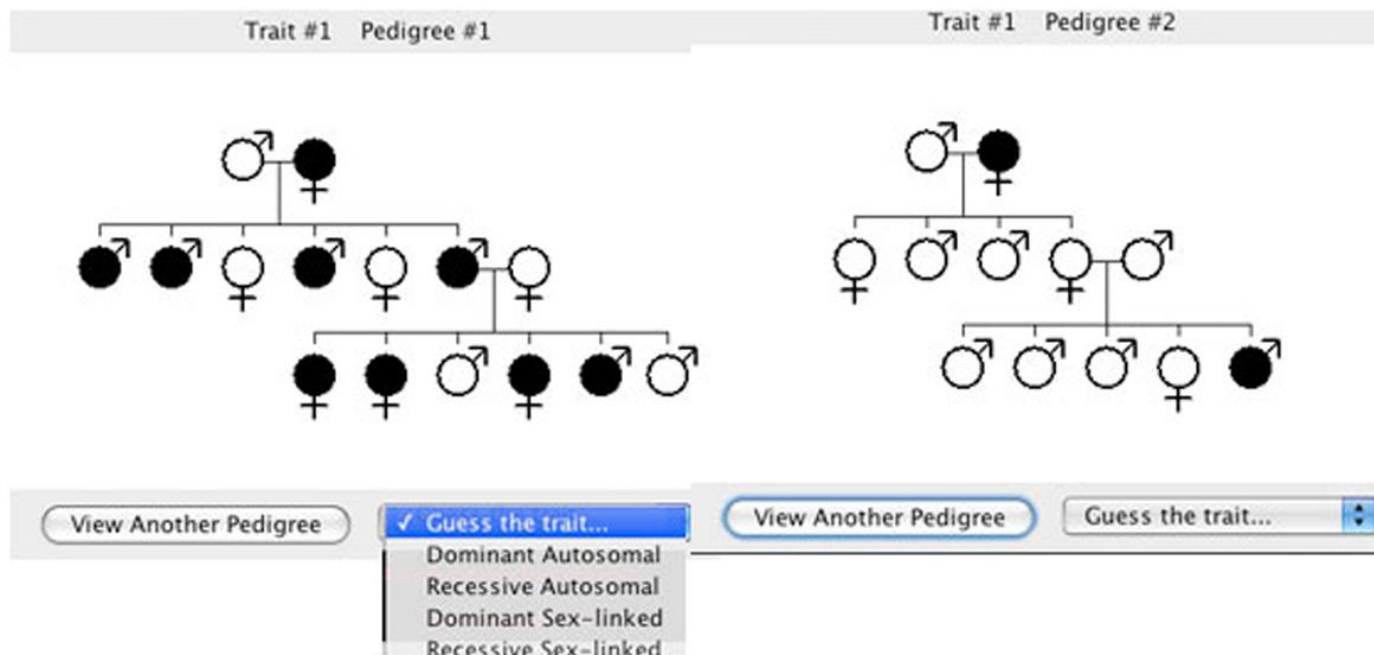

Figure 1. Pedigree simulation: Students determine mode of inheritance and can generate a number of pedigrees for each trait.

4. DNA "fingerprinting" (B): DNA banding patterns are generated for a group of organisms whose relationships are unknown (since the mating system may vary). Students need to extend and apply what they have learned about biotechnology to be able to work with the data provided. The RFLP banding patterns (how often, for example, two unrelated individuals will share bands) are based on data for humans. To keep any biases out of the analyses you could present the data as based on imaginary creatures (we call them Innorts in one course) whose social groupings resemble those of some modern day lemurs. Species vary in social group constitution. Males may or may not forage with a number of females who may have mated with one or several males that season. The young in any band of individuals then may or may not be related to the accompanying male. In some species, social group composition may change with season or some other ecological agent. Students must rely then on the DNA evidence simulated and cannot assume any degree of relatedness exists between young, males and females found together. This program is one that allows some instructor modification. Instructors can modify the number of young, for example. The social setting is modifiable using a text or html editor. Unfortunately instructors cannot modify the number of banding patterns produced. We have included four versions of the simulation. In the first two, students simply determine which individual is unrelated to the others. In the third and fourth simulations, they determine paternity. Instructors can simply copy the html page in the folder that contains the simulations and delete the simulations they do not want.
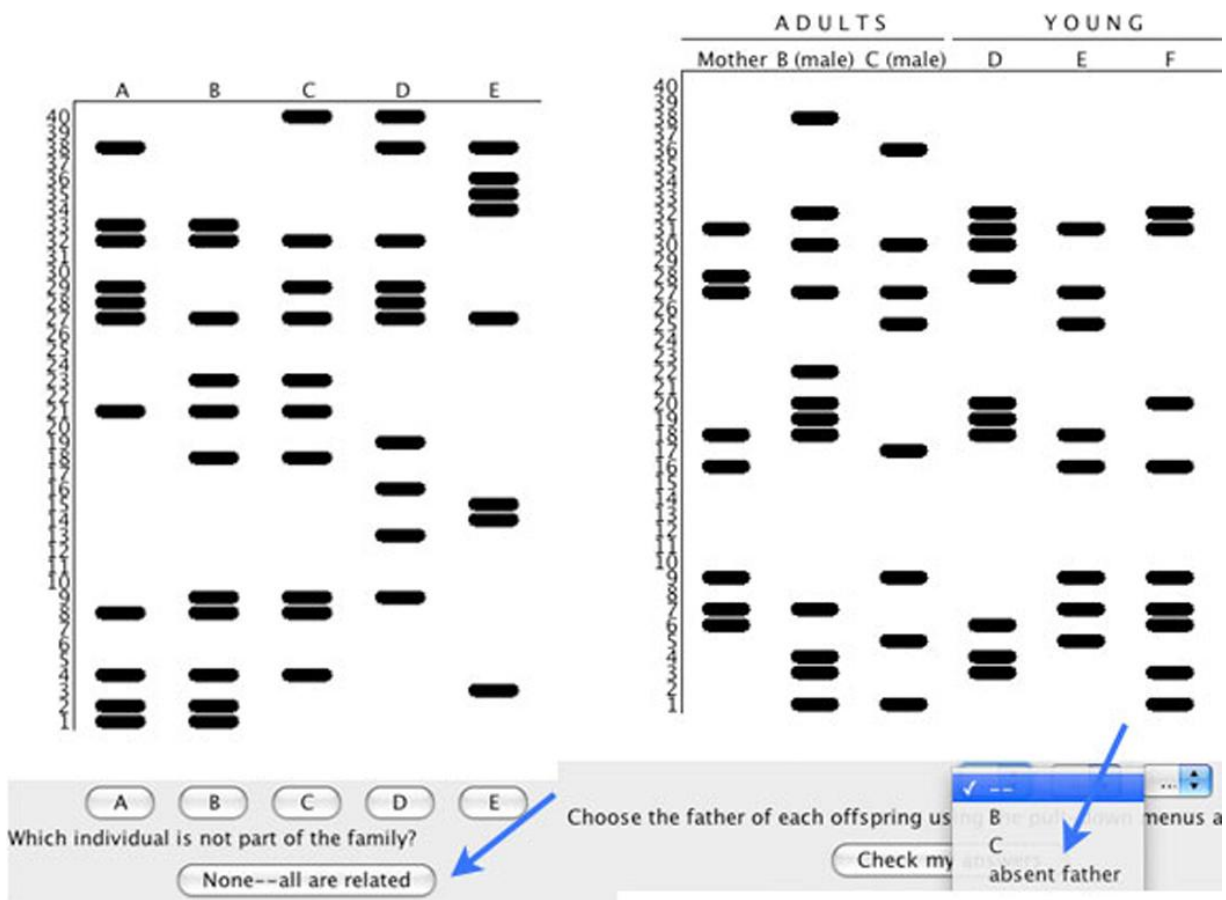

Figure 2. DNA fingerprinting simulations: Instructors can specify whether an unrelatedindividual is present in first simulation or if a father can be absent in the second.

5. Spectrophotometer (C): This is the simulation we use in the laboratory examining photosynthesis and the laboratory examining enzyme function for our distance students. Students enter an X value (such as different pH or temperatures) and the spectrophotometer generates a Y value (% absorption or transmission) for every X. Multiple Xs as well as multiple Ys will be accepted. It is completely editable using a text or html editor.
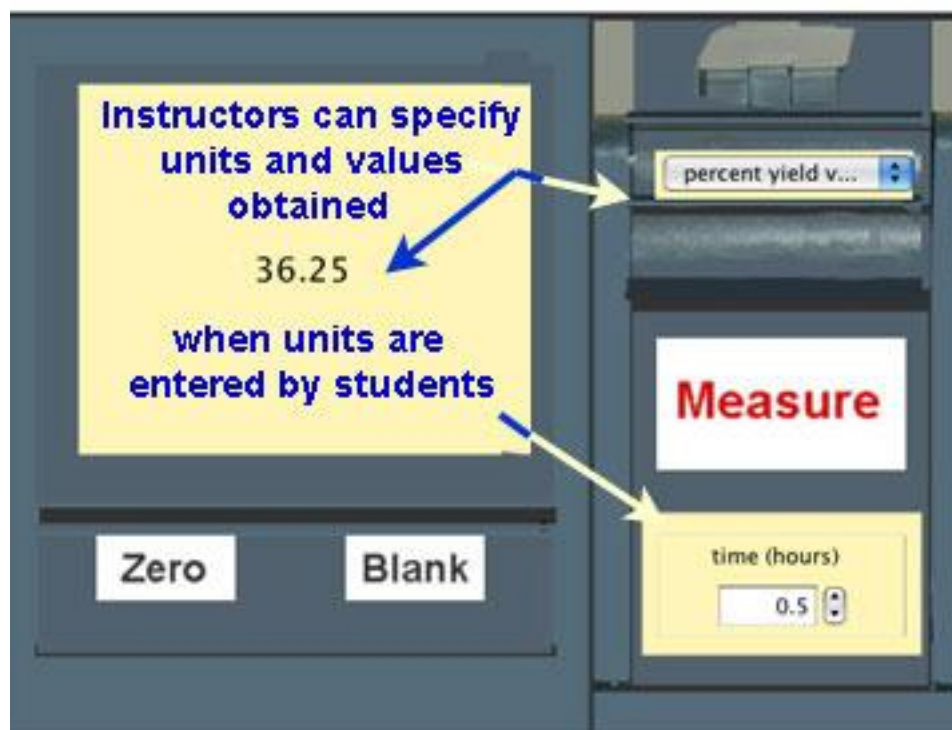

Figure 3. Spectrophotometer: Instructors can program the units entered by students and the values obtained for units.

6. Gel animation (C): We developed these animations to emphasize the concept that proteins are products of genes that are turned on or off in different tissues, and at different times in development. Students in the wet lab separated proteins by electrophoresis, comparing the banding patterns produced by denatured proteins extracted from green and white corn seedlings, different parts of the same plant (such as flowers and leaves) and different stages of the life cycle of the fruit fly *Drosophila virilis*. Since students had already investigated the Mendelian ratios produced when different corn plants are crossed, this exercise served to review these concepts as well as introduce upcoming laboratories which treat development in animals and plants. More importantly, this exercise distinguishes between differences in phenotype resulting from differential gene inheritance, and those differences among tissues and stages in the life cycle of multicellular organisms that result from differential gene activity in genetically identical cells. The animations are available in two flavors. One folder, the sample folder, contains un-editable animations that simply mimic the results students obtained when we did this lab as a campus wet lab. The custom folder contains an animation that is completely customizable and so can be used to simulate DNA or protein separation. Instructors can determine the number of bands, number of lanes, and even band intensity and color (so it can be used to simulate chromatograms in some cases). It is completely editable using a text or html editor. The last folder, corn_diff_versions, provides an example of how the custom animation can be modified.
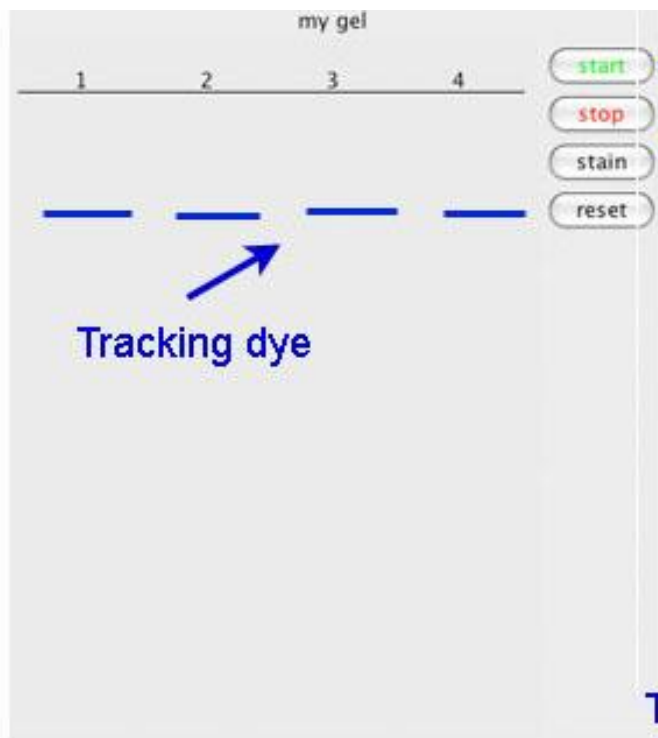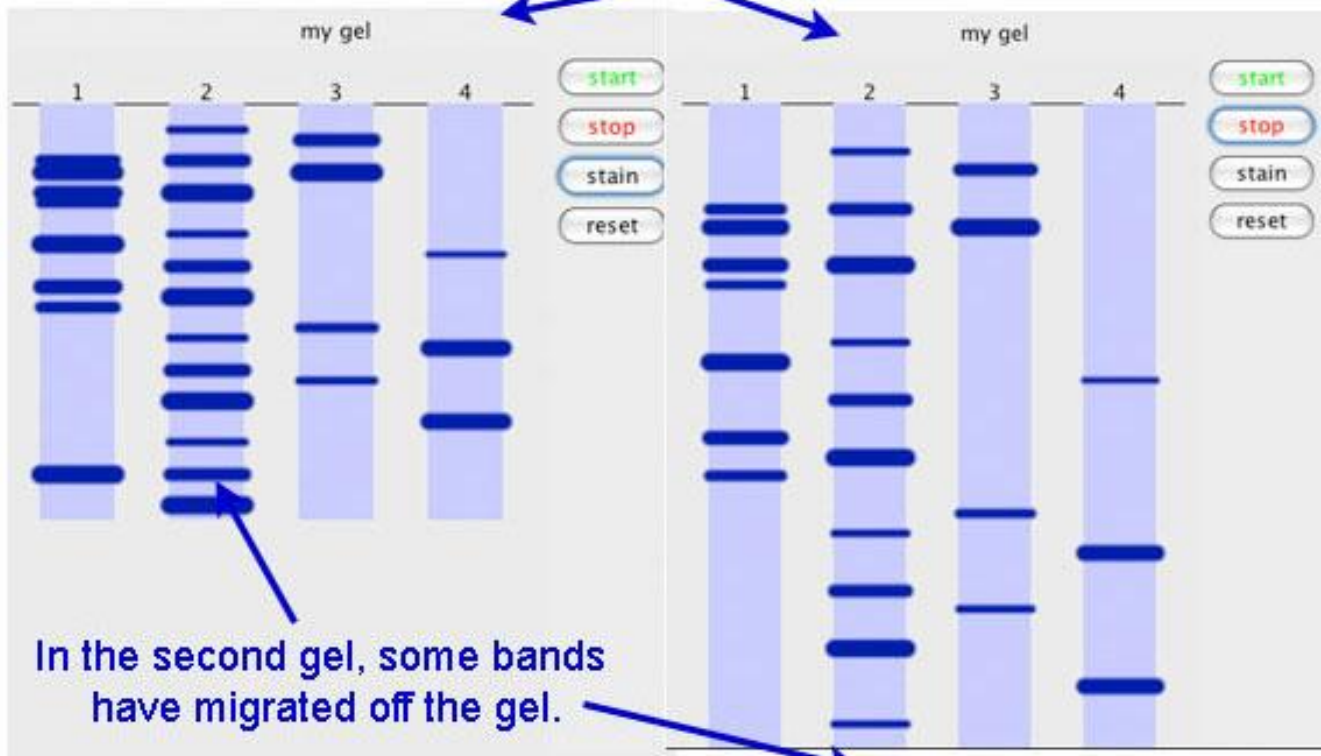
Figure 4. Custom gel simulation: Instructors can produce gels that students must start, stop and stain before bands are visible. Instructors can also produce the banding pattern viewed by students.

These last two programs provide some of the same quizzing options provided by a number of different teaching resources (such as Hot Potatoes). They are Java-based and so will easily generate web-friendly quizzes that can become part of your website.

7. Sorter (C) This program allows instructors to build interactive quizzes that ask student to sequence items. It is completely editable in terms of images or text sorted, size of background field and whether the items are displayed horizontally or vertically. The downside is that since Microsoft has decided that Word will no longer read .xml files, you will need another text or html editor to edit these files. The simple text editor that came with my Mac worked fine.
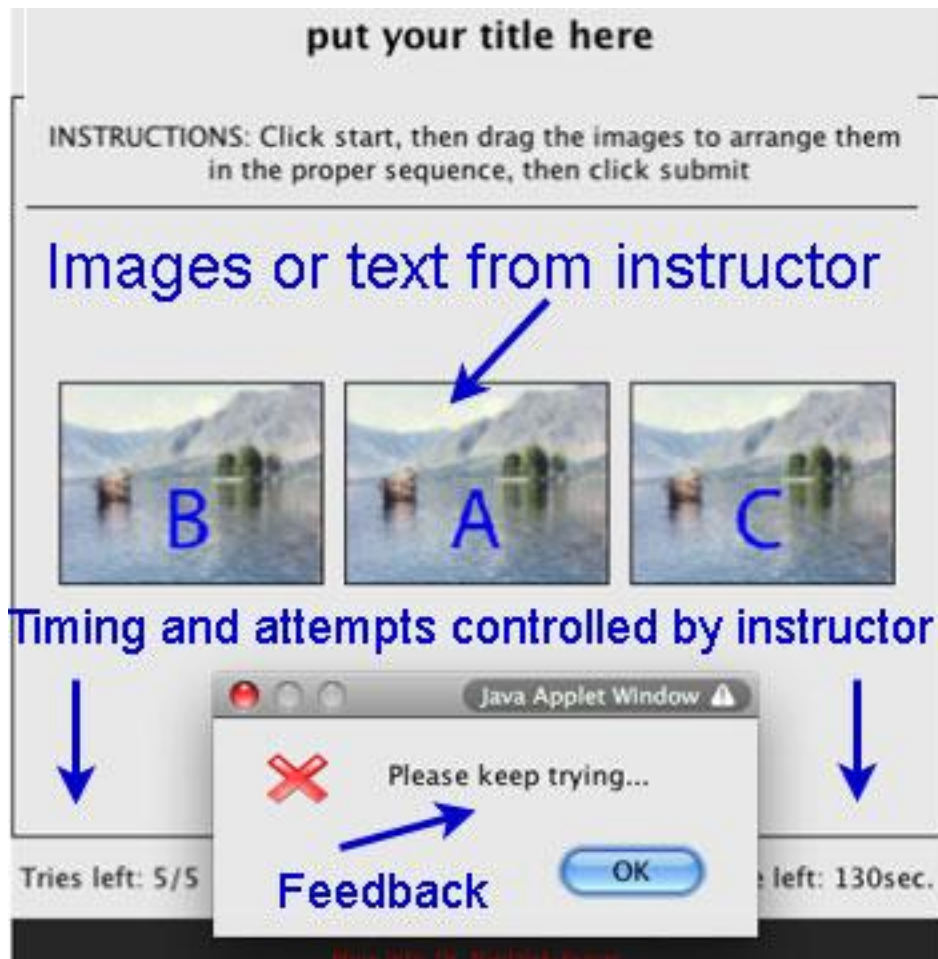
Figure 5. Sequence simulation: Instructors supply images or text to be sequenced. Instructors can also specify time to sequence and the number of attempts by students.

8. Matching (C) This program allows instructor to build matching programs. It is completely editable in terms of questions asked, answers and prompts provided. It has the same downside as the Sorter. Since Microsoft has decided that Word will no longer read .xml files, you will need another text or html editor to edit these files, although you can still use Microsoft Word to edit all the html files. The text editor that come with any Mac or PC should prove suitable. Of course, in any dedicated html editor

such as Adobe Dreamweaver you may edit both types of files. We provide three examples on our web site for you to examine so you can see the different types of feedback to students that are available.

Figure 6. Matching simulation: Instructor supplies text, diagrams or pictures to be matched. Various different types of feedback are available. Instructor can control if feedback is provided during the matching attempt or only after student has submitted answers. The instructor can also control the time students have to match, or number of attempts available to students.

More Explanation on How Simulations Are Put Together
All simulations and animations can be found in folders that contain four types of files.

1 and 2. htm (html) and jar extension files: For all programs, there are htm or html files that you link to that your browser will use to display the simulation or animation. This page (or pages) must be in the same folder as the .jar (for a few simulations .class) files that contain the code that creates the simulation or animation desired. The name of these files cannot be changed, as the html file will not be able to find the code, and so, load the program on to the page. The html page is then simply a web page that acts as a holder or display page for the simulations whose code actually resides in the .jar (in some cases .class) files. Anyone who knows Java is welcome to change the code in these .jar files, at their own risk, to personalize the code for their own use. However NCSU copyright requires that somewhere you acknowledge you have based some part of the new code from code obtained from NCSU.

3. .xml files are also found for some of the more flexible problems that allow extensive editing of text or data to be loaded by the code. See the specific instructions that accompany each program for tailoring these files to your needs, but do not change the names of these files. They too must be found in the same folder as the htm file and .jar files for a particular simulation or animation.

4. Data files are other files, such as jpegs, etc. you may want to use in some of our more editable programs that generate sequence or matching quizzes. These **must** also be found in the folder containing the .htm (html), .jar and .xml files for a particular simulation. For those of you new to these programs, I would keep the same names provided initially for these files as you try out the programs. Simply replace our example figures with some of yours, using the names provided, in a copy of a folder containing the simulation of interest. Once you are familiar with these programs you will know where in the .html source code or .xml source code for that simulation you can change the name of a figure or other type of file needed for your quiz.

Editing Files or Changing the Source Code
All files are edited the same way. If you have an html editor go to Source View. If you do not have an editor, you can open the .htm(html) page in any text editor. Just open it in an application such as Word and again select the Source html view. Make any changes desired using instructions provided for each program. When you have completed your changes, if you are using an html editor, simply save them. If you are using a text editor choose to save the file as a .txt file. Once it is saved change the extension back to .htm and open in a browser. Xml files are modified the same way except you must use a text editor other than Microsoft Word. Do not change the name of an .xml file. Html pages will call upon .jar files (do not change anything about a jar file, including its name) which will then call upon .xml files. Since the .jar file is locked, it will not find the .xml file if you change its name.

The programmer's instructions for changing these parameters can be found on the source page as well. These instructions if present are found under Parameter explanations on the html page. They can be seen if the page is displayed in Source View even in the browser and will appear a different color than the source code, usually grey. Any parameters that can be changed will usually appear in some bold color, such as blue or green, in this view. Unfortunately you lose this color coding when you open your .htm pages in a text editor.

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Example: Using our custom gel program you can create various type of gels including those that students must stop the migration (or protein bands move off the gel) and stain before viewing. You can

also program as many lanes and however many bands (1-40) with various thicknesses in each lane you desire.   On the html page under Source View you see the following code.
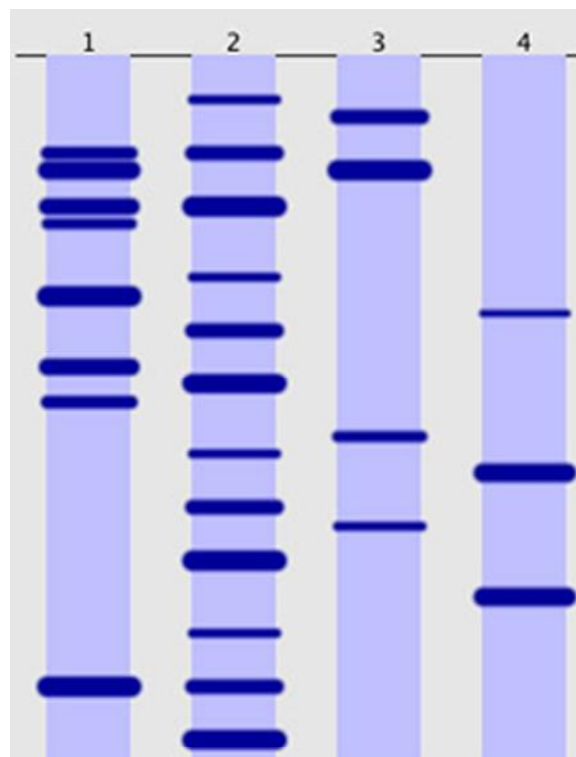
Source code

```
<param name="lane1"
value="0,0,0,0,0,5,8,0,7,4,0,0,0,9,0,0,0,7,0,5,0,0,0,0,0,0,0,0,0,0,0,0,0,0,9,0,0,0,0" />
<param name="lane2"
value="0,0,3,0,0,6,0,0,9,0,0,0,3,0,0,6,0,0,9,0,0,0,3,0,0,6,0,0,9,0,0,0,3,0,0,6,0,0,9,0" />
<param name="lane3"
value="0,0,0,6,0,0,9,0,0,0,0,0,0,0,0,0,0,0,0,0,0,4,0,0,0,0,3,0,0,0,0,0,0,0,0,0,0,0,0,0">
<param name="lane4"
value="0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,0,0,0,0,0,0,0,0,8,0,0,0,0,0,0,8,0,0,0,0,0,0,0,0,0">
<!-- add as many lanes as desired, copy a lane, change its name to 5, 6, etc. and place bands (as
numbers) were desired -->
```

The numbers in the source code above produced the banding pattern in Figure 7.   Each lane you add to the gel is a 40 position array where placing a five as in lane one above, results in a band of thickness five in the sixth position of 40 possible positions.

Figure 7. Shows a custom gel with bands as specified in the parameters for lanes 1-4 in the example source code array.

For some of the applications in which extensive changes can be made to the appearance of the simulation, additional instructions are found on a Microsoft or pdf file in the same folder as the

simulation or animation of interest. For most of these, I have illustrated the changes that can be made and how the simulation or animation looks after those changes are made.

Simulations and animations will be available for testing on h**ttp://www.ncsu.edu/project/interactivebiology/. You may also download zip packages of programs and instructions from this site**

In the future, movies and other multi-media used in this course will be available on **http://www.explorethelor.org/** (the North Carolina Learning Object Repository web site). You may sign in as a guest to view or download materials from this site. Please use the search terms: biomovies and simulations. Additionally, the on-line laboratory exercises, including videos and simulations, can be viewed at **http://www.ncsu.edu/project/bio183de.** If you use any of our resources, we would appreciate feedback and any suggestions for improvement. Please email Marianne Niedzlek-Feaver, for questions regarding simulations and Betty Black for questions regarding course exercises including videos produced for these exercises.

Acknowledgments

About the Authors

Marianne Niedzlek-Feaver received her Ph.D. from the University of Michigan. As an evolutionary ecologist, she is interested in identifying factors that shape the mating systems of grasshoppers and katydids. She currently teaches Evolution, Invertebrate Zoology and Introductory Biology courses. She has received various grants to improve the laboratory experience, and is a member of the NCSU Academy of Outstanding Teachers.

Betty L Black received her Ph.D. from Washington University (St. Louis). She teaches a course in Developmental Anatomy plus distance education courses in Introductory Biology, Histology, and Animal Diversity. She has received two University awards for "Innovative Excellence in Teaching and Learning with Technology" and has 12 publications on teaching technology topics.