

**AN ONLINE BIOENGINEERING LEARNING MODULE:
PHYLOGENETIC RELATIONSHIPS**

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ABSTRACT

One of the greatest challenges in biology is understanding the diversity of life and the relationships between living organisms. Phylogeny is the evolutionary history of and relationships between organisms. Phylogenetic information can be inferred by quantifying genetic similarities and differences between organisms. Bioinformatic methods using computers, statistics and information technology are crucial to this challenge and therefore the field is one in which biology and engineering naturally intersect. An online learning module on phylogeny was designed and implemented in BIOL 295F - Introductory Quantitative Cellular Biology, a new undergraduate course for engineering students at Purdue University.

This paper will overview the design, implementation, and assessment of this online learning module. Student learning gains were assessed using pre-post test questions focused on concepts presented in the online learning module, as well as through module usage information. In addition, students' perceptions of the interactive online learning modules versus other modes of instruction and their actual use of the tool were assessed.

1. INTRODUCTION

Bioengineering includes the study of biological phenomena using the fundamental principles of engineering. Despite the rapid growth of bioengineering as a field of study for undergraduate students, the development of educational materials for bioengineering instructors has failed to keep pace. Until only a few years ago, the subject of bioengineering was predominantly limited to graduate level coursework and research labs. Only in recent years, due in part to the burgeoning of interdisciplinary research and the general increased growth of technology has bioengineering found its way into the undergraduate curriculum. Yet despite the expansion into undergraduate coursework, most instructors are limited to professional journal articles or complex tools aimed at those working in the field. Many of the textbooks covering bioengineering topics are outdated before they even arrive in bookstores, and are rarely targeted

towards teaching introductory material (Blanchard and Enderle, 1998). In a report on the progress of bioengineering as an independent field of study, Johnson (1997) explicitly states, “We have yet to develop texts and other teaching materials in biological engineering.” Moreover, because of the scale, complexity, and interdisciplinary nature of the study of most bioengineering phenomena, the development and implementation of hands-on experiments can be both costly and challenging at the early undergraduate level.

Though the growth of the internet has led to a general increase in web-based tools, those available to students for learning introductory cellular biology are still severely deficient in a number of areas. First, the majority of engineering students are classified as visual learners. In a validation study of the Felders-Soloman Index of Learning Style, Zywno (2003) summarized the results of 6 studies, finding that between 69% and 88% of engineering students are classified as learning material best when presented visually. Though most engineers are visual learners, the vast majority of instruction is still done using textual explanations and static images of complex phenomena, making it exceedingly difficult for students to develop a sound conceptual understanding.

The second problem that has plagued the available web-based tools is that they often lack the interactivity necessary to better engage students in the learning process. In the same validation study, Zywno (2003) found that between 55% and 69% of students were classified as active learners. “Active learners do not learn much in situations that require them to be passive (such as most lectures)” (Felder and Silverman, 1988). Many of the learning modules currently available do not require any response from the user, outside of the occasional “press here to continue” or multiple-choice question. These modules are often no better than traditional textbooks. This phenomenon of electronic versions of static textbooks is most likely due in part to the tremendous amount of time and effort required to develop course materials that take advantage of capabilities new technology has to offer (Renshaw, *et al.*, 2000). The time commitment needed to create an electronic textbook is much less than that required for more active forms of instruction and therefore a more common choice of educators looking to utilize technology in their classroom. The idea that students learn best when they are more involved in the learning process is not a new concept, but in the face of new technology, is often a forgotten concept.

An online learning module about phylogenetic relationships was specifically designed to resolve these two major problems, namely a lack of instruction that is both interactive and visually based. This paper discusses the design, implementation, and assessment of an online learning module aimed at introducing undergraduate engineering students to phylogeny and phylogenetic relationships. Student learning gains are assessed using a pre-post quiz focused on concepts presented in the learning module, as well as information obtained about their usage of the online learning module. In addition, students’ perceptions of the interactive learning module are assessed.

2. PHYLOGENETIC RELATIONSHIPS LEARNING MODULE

BIOL 295F, Quantitative Biology of the Living Cell, is a new 1-credit hour computer lab based course developed at Purdue University targeted at engineering students studying bioengineering or related fields. In Fall 2004, the course met once each week for 110 minutes in a computer lab. The objective of the course is to examine traditional cellular biology topics, but place them in an engineering context, identifying the fundamental engineering concepts that underlie many biological processes. This course is designed to be a co-requisite to BIOL 295E, Biology of the Living Cell, an existing 3-credit hour traditional introduction to cellular biology for engineering students.

The course developer, as part of the course creation process, envisioned seven topics, each with corresponding online learning modules. To allow for more rapid development and prototyping, Macromedia Flash MX 2004 was selected as the development environment of the modules and their associated architecture. To help with the data collection process, a PHP/MySQL database was connected to the Flash architecture. For the first iteration of the course, it was decided that three online learning modules would be developed. The remaining four modules are planned for later development based on the evaluation of the first three. Ion transport, phylogenetic relationships of organisms, and dynamic gene regulation were the topics selected for initial module development. These three topics were selected as they each require a fundamentally different type of interactivity; therefore, each topic provides a unique computer-based learning experience for the user. For example, the phylogenetic relationships topic allows for students to emulate one of the pioneering studies in organism classification. The gene regulation topic requires a simulation tool that allows students to interpret the results of changing specified input parameters to a system of differential equations; the emphasis being placed on cause and effect relationships between the input and output parameters. Though both provide an interactive component, they are fundamentally different in how they allow the user to interact with the module. This paper focuses exclusively on the development and implementation of the phylogenetic relationships module.

The phylogeny module covers four related concepts: steps of the Woese (Fox, *et al.*, 1997) experiment, performing the Woese experiment, calculating similarity coefficients (known as S-Values), and the creation of phylogenetic trees. Students are asked to complete four activities, each corresponding to one of the four concepts. Each activity has a number of tasks associated with it. Within each task, participants are presented with a number of interactive situations.

While repetition has long been viewed as advantageous for student learning, one of the significant problems is the memorization effect, where students become better at the specific problem they are repeating but fail to learn the underlying concepts. By utilizing computer-based instruction, more randomization can be built into the system, allowing for a unique problem to be generated with each attempt. This approach was used in the development on the online learning module. Whenever possible, randomization was employed to change the problem. Incorporation of randomization allowed for more repetition while virtually eliminating the “memorize-and-regurgitate” response.

When students begin using the module, they are presented with a “Background” slide showing them the objects they will be interacting with for the remainder of the module. The objects include images of a cell, unsequenced 16S rRNA strands, and sequenced rRNA. This slide enables students to become familiar with the objects before having to interact with them.

The first activity, Steps in the Woese Experiment, consists of one task in which participants are presented with the five basic steps in random order. To complete the activity, students must drag the steps from the random order on the left and drop them in to the correct order on the right (Figure 1). When all 5 steps have been placed, participants are given feedback about their ordering. If a student has not correctly ordered the steps, the student must repeat the activity until the correct ordering is achieved. Each attempt starts with the five steps in a different order, forcing students to learn the order of the steps, not the order of the boxes.

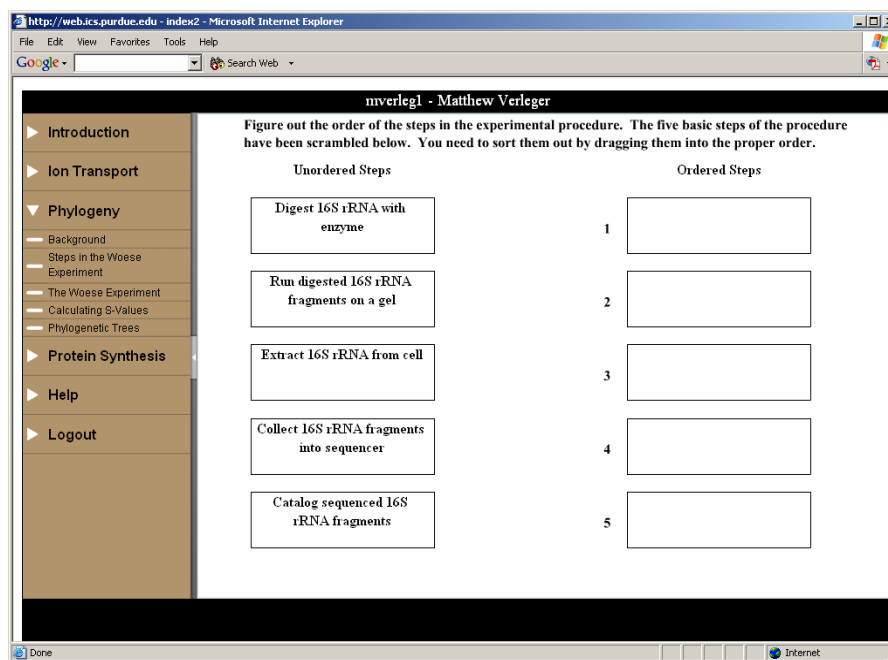


Figure 1: Steps in the Woese experiment activity.

The second activity builds upon the first activity by having students perform a simulation of the five steps in the Woese experiment, resulting in the calculation of an S-Value, a measure of genetic similarity. Students begin with the basic equipment needed to perform the experiment; a cell containing the rRNA of an arbitrary species, an enzyme, a beaker, an electrophoresis gel, and a sequencer. Students begin by dragging both the enzyme and the rRNA from the cell into the beaker. When both items are located in the beaker, the students will see the rRNA strands dissolve into smaller pieces. They must then drag the beaker to the electrophoresis gel, where they will again be presented with an animation of the separation process. Finally, they must drag five pieces of gelled rRNA to the sequencer, revealing five sequenced rRNA fragments (Figure 2). Once the participants have been guided through the process for one species, they must repeat the process for a second species. When they have sequenced five fragments for a second species, they begin the cataloging process. Cataloging sequenced rRNA involves examining each sequenced rRNA fragment and identifying those species in which the fragment appears (Figure

3). When the participants have cataloged their ten fragments, an animation shows that the process is repeated for all of the rRNA fragments for all of the species in question. Finally, students are presented with the calculation of the S-Value.

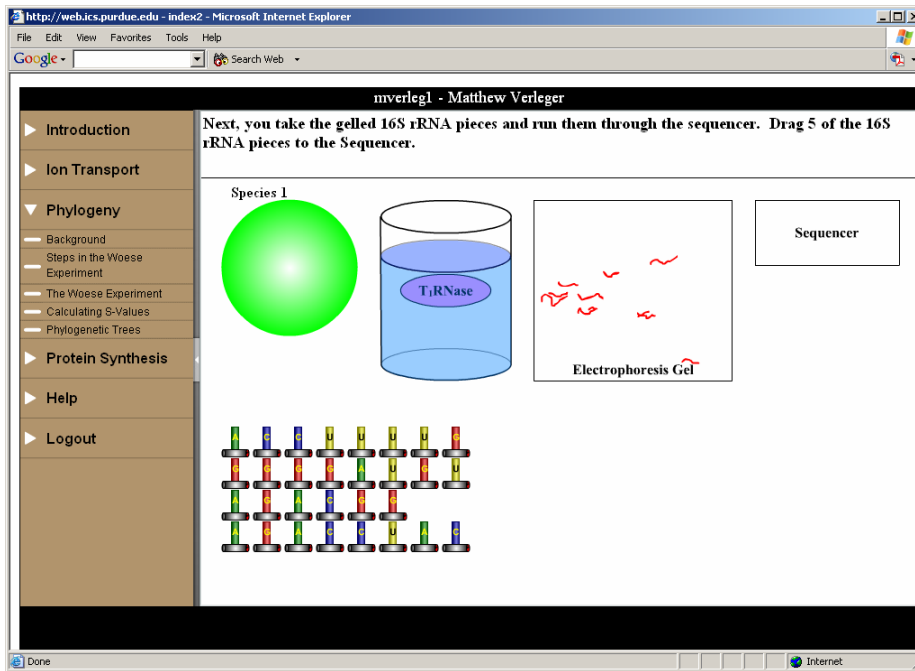


Figure 2: The Woese experiment – sequencing.

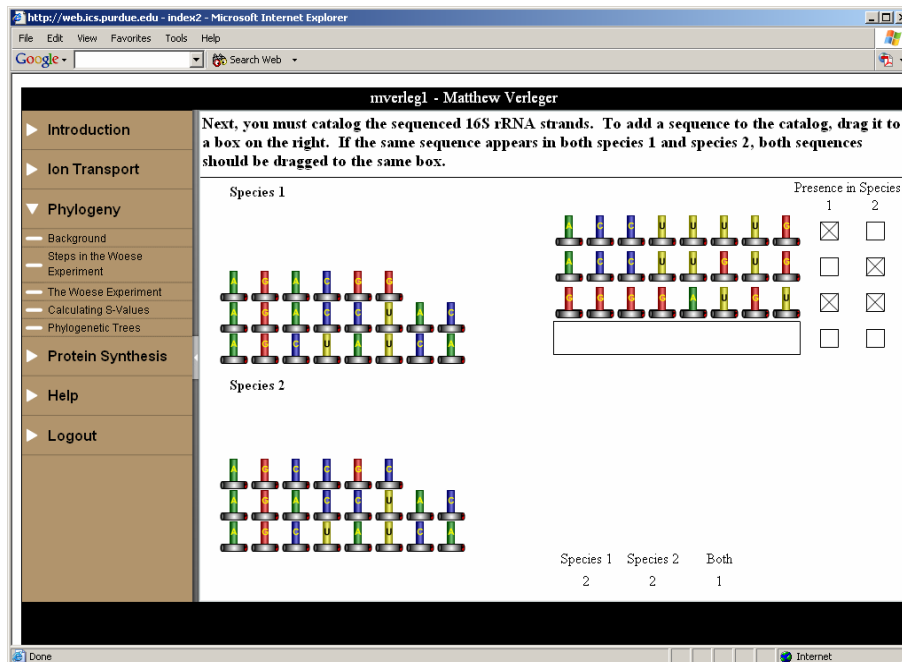


Figure 3: The Woese experiment – cataloging rRNA fragments.

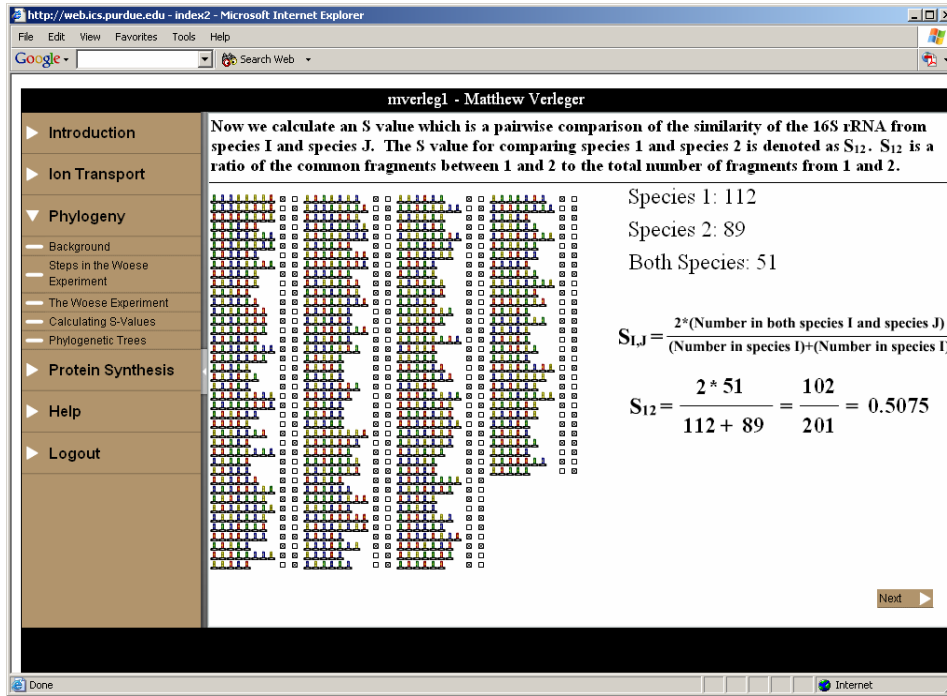


Figure 4: The Woese experiment – calculating the S-Value.

The third activity asks students to calculate the genetic similarity between pairs of species. Students are presented with a 10x10 table listing the number of common sequences between 10 species. They are also presented with a list of the total number of sequences cataloged for each of those 10 species. Students are asked to calculate the S-Value for four pairs of species (Figure 5). When they have finished their calculations, they are given feedback about their calculated values. If the participant does not correctly calculate the four requested S-Values, they must repeat the activity, calculating four different S-Values.

The fourth and final activity requires students construct a phylogenetic tree. A phylogenetic tree is a visual representation of the genetic similarities between species; in this case the same 10 species used in the third activity. To complete this activity, the participants must correctly drag the 10 species from a randomized list to their correct location within the tree (Figure 5). What made this task different from many of the previous tasks was that the next button would only appear when they correctly placed all 10 species. Due to the structure of the problem, there was no discernable way to provide feedback to the students without directly giving them the answer. To determine the location within the tree, the students had to examine a table of the S-values between all 10 species. A higher coefficient between two species implies that those two species are more closely related and should therefore appear closer to one another on the tree.

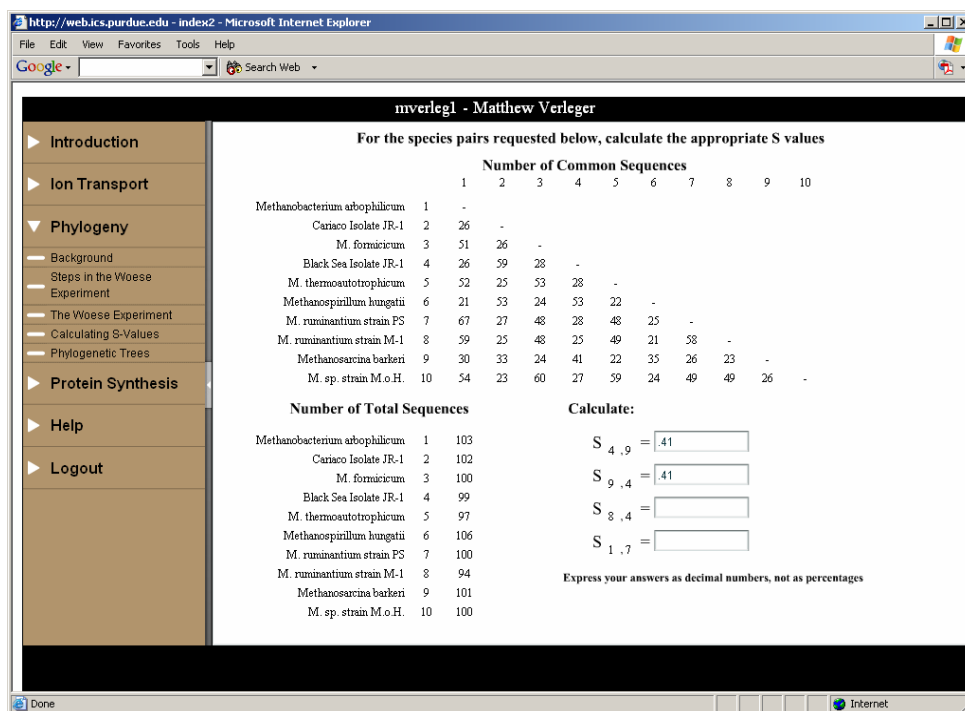


Figure 5: Placing species in a phylogenetic tree.

3. IMPLEMENTATION

Though the course is required for agricultural and biological engineering students, BIOL 295F was made available to any student concurrently enrolled in BIOL 295E, providing a cross-section of students from a variety of engineering disciplines. In total, 15 students registered for the course from six different engineering fields of study. Six students were pursuing degrees in Agricultural and Biological Engineering; making it the most well represented engineering discipline. Five students were classified as second year students, eight as third year, and two as fourth year.

As the second of three online learning modules, the phylogeny lesson began during the 12th week of the semester with an instructor led discussion. The discussion provided the background material necessary to begin using the online learning module. It also provided a brief introduction to the topics found in the module so as to give students a starting point. In addition to the discussion, students were also expected to have read a portion of their BIOL 295E textbook relating to phylogeny and the classification of organisms. The modules were not designed to be complete stand-alone learning modules independent of other instruction, but more as an extension to a more traditional instructional package. In addition to using the online learning module designed for this course, students were also guided in the use of another online bioinformatics tool used by professionals. Building on the knowledge that the students had from using the phylogeny online learning module, this portion of the lab helped students see how biologists use the same principles for large data sets of multiple species. Over the course of three

weeks, students took a pre-quiz, worked through the online module, took a post-quiz and completed an attitudinal survey. A full timeline can be seen in Table 1.

Table 1: Timeline of phylogeny lesson

Week	Activity
12	Lecture
13	Pre-Quiz Module work
14	Post-Quiz Attitudinal Survey

The pre-quiz and post-quiz were paper-based multiple-choice and short answer quizzes. A question relating directly to the phylogenetic module usage appeared on both the pre and post quizzes. This question asked students to list the five steps of the Woese experiment. In addition, a question appearing only on the post test asked students to calculate an S-value for a given pair of species.

After students had completed the lesson, they were given an attitudinal survey to assess their perceptions of the online learning module. The survey was broken into three sections. The first section consisted of questions asking how students felt the module related to the course and learning the course material. The second section asked students to compare the online learning module to other forms of instruction, including traditional lectures and live demonstrations. Finally, students were asked to rate the usability of the learning module. Questions in each section were rated using a 5-point Likert scale. Open-ended questions followed the first two sections asking students to explain their responses.

As participants work through the problems in the learning module, they must complete certain tasks. Their responses to those tasks are stored to a database for later review by the course instructor. For example, all incorrect orderings of the five steps to the Woese Experiment are stored to the database. At the same time, a number of time-based measurements are collected, including how long a student spends on any particular problem. Some of this information can be seen in Section VI.

4. DATA ANALYSIS

Due to the relatively small class size ($N = 15$), no statistical analysis was performed beyond simple counts. It should be mentioned that 2 students failed to take the pre-quiz, and a third student failed to take the post-quiz and attitudinal survey. Their numbers have been excluded where appropriate.

5. PRE-POST QUIZ RESULTS & DISCUSSION

The Woese experiment consists of five basic steps and was one of the pioneering experiments in the study of phylogenetic similarities. One of the reasons for the strong emphasis on the Woese

experiment is because many of the ideas behind Woese’s method are relevant to today’s most modern classification techniques.

Table 2 shows which steps in the Woese experiment the students were able to correctly identify on the pre and post quizzes. The correct steps are:

1. **Extract** that 16S rRNA from the cell
2. **Digest** the 16S rRNA with the enzyme
3. Run the rRNA on an electrophoresis **gel**
4. **Sequence** the rRNA fragments
5. **Catalog** the sequenced rRNA

Eleven of the 12 students who took both the pre and post quizzes performed as well or better at identifying the steps. Student 7, the only student who performed worse on the post-quiz than their pre-quiz, made no attempt to answer the question on the post-quiz. Despite having been assigned a passage in their textbook describing the Woese experiment and an instructor led discussion of that passage occurred as part of the lecture, pre-quiz performance was low. In addition to showing marked improvement in their knowledge of the steps, students also showed improved knowledge of the appropriate terminology. Many of the pre-quiz responses used non-technical terms to describe the experimental procedure. For example, one student stated that during the extraction stage, Woese “took the 16S rRNA”. That same student described the same step on the post-quiz by stating that “the 16S rRNA is taken from a particular source prokaryote.” Many of the respondents showed a similar increase in their usage of appropriate vocabulary. The drastic increase in post-quiz scores, combined with the usage information described in Section IV, would indicate that most students knew very little of the steps in the Woese experiment before using the module, but were quickly able to learn both the steps and the terminology associated with the experiment.

Table 2: Pre-Post quiz results – steps of the Woese experiment.

Student		10	1	2	8	9	6	11	5	3	12	4	7
Pre-Quiz	Extract			Y	Y	Y	Y		Y	Y	Y	Y	Y
	Digest					Y				Y	Y		
	Gel			Y						Y	Y	Y	
	Sequence				Y				Y	Y			
	Catalog							Y	Y	Y	Y		
	Total Correct	0	0	2	2	2	1	1	3	5	4	2	1
Post-Quiz	Extract	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	
	Digest	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y		
	Gel	Y	Y	Y	Y	Y	Y	Y	Y	Y			
	Sequence	Y		Y	Y	Y			Y	Y	Y	Y	
	Catalog	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y		
	Total Correct	5	4	5	5	5	4	4	5	5	4	2	0
Improvement	5	4	3	3	3	3	3	2	0	0	0	-1	

Though no pre-quiz question was given, a post-test question was given asking students to calculate the S-value between two species. Of the 14 students who answered the post-quiz question, 13 correctly calculated the appropriate S-Value.

6. MODULE USAGE RESULTS & DISCUSSION

During each of the four activities, select usage data is collected about the participant's actions. During the first activity, each attempt at correctly ordering the steps in the Woese experiment is logged. Most students, 9 of the 15, were able to correctly order the steps on the first attempt, indicating that once they were given short descriptions of the steps, they did indeed know the correct answer, but were unable to generate the steps on their own. Three of the 15 were able to complete the task on their second try, with the remaining three students requiring three or more attempts to achieve the correct sequence. Of particular interest is that six students utilized the tool after they had already obtained a correct answer; four of them using it shortly before the post-quiz. This indicates that some students recognized that the tool could be used as a study aide.

The second activity had students working through an emulation of the Woese experiment. The objective behind the activity was to help students visualize the textual descriptions of the Woese experiment. Because the activity was a reproduction of a scientific experiment, the opportunities to provide highly interactive experiences in which users can reveal their thinking were less than those available in other activities. One student did work through the activity on two separate occasions, once on the day of the post-quiz, again supporting the claim that students did recognize the usefulness of the module as a study aide.

The third activity, calculation of S-Values, proved to be quite simple for most of the students, with all participants obtaining a correct answer by their second attempt, and most getting it correct on the first try. Though they were able to obtain correct answers by their second attempt, a number of students fell victim to a programming error, causing them to repeat the problem multiple times.

The fourth activity did prove challenging to students. Time spent building the phylogenetic tree ranged from 17 - 44 minutes, with an average of 29 minutes and a standard deviation of 9 minutes. All students except one were able to build a correct tree. Based on the wide range of times, it seems that some students had difficulty with portions of the construction, but the eventual success rate would indicate that most students were able to develop a correct tree configuration. With over 3.6 million possible tree layouts, a trial-and-error approach to solving the problem is too impractical to be successful.

7. ATTITUDINAL SURVEY RESULTS & DISCUSSION

Attitudinal Survey – Relation to Course Material. Table 3 contains the responses for the two questions on the attitudinal survey about how the online learning module relates to the course material. In general, participants felt the module was well related to the course material, ranking

it positively in both its benefit towards learning and its relation to the course objectives. Of the 10 students who chose to comment on the learning benefits of the tool, 8 participants specifically mentioned that the online module helped them better visualize the concepts. One student noted that the tool helped them to “understand the material a great deal better by visualizing.”

Table 3: Attitudinal survey - relation to course material.

Item	Strongly Disagree	Disagree	Neutral	Agree	Strongly Agree
This tool was of benefit to me when learning the concepts taught in this module	0	0	0	10	4
This tool was appropriate for meeting the learning objectives for this module	0	0	0	10	4

Attitudinal Survey – Comparison to Other Forms of Instruction. Table 4 contains responses for the three questions on the attitudinal survey asking students to compare the tool to more traditional forms of instruction. As with the relation to course material, the response towards the module was favorable when compared to other forms of instruction. Overwhelmingly, students preferred the online module to traditional textbook reading, with 11 of the 14 respondents stating that the module was significantly better. All respondents found the online module to be as much or more preferable than a traditional lecture. As one student stated, “I would not have retained as much from a lecture, especially on this topic which is quite detailed.” While the response was still positive, a few students still preferred traditional laboratory experiments, though multiple students noted that for some topics, live demonstrations and labs simply are not feasible. One student pointed out, “If it would be possible to have live demonstrations, then it would be preferable.”

Table 4: Attitudinal Survey – Comparison to Other Forms of Instruction.

Item	Significantly Worse	Somewhat Worse	About the Same	Somewhat Better	Significantly Better
If given the choice between the Phylogeny tool and... ^a					
Independent Reading such as textbooks and journal articles	0	0	1	2	11
Traditional Lectures	0	0	3	4	7
Live Demonstrations or Lab Experiments	1	1	5	6	1

^a i.e. “If given the choice between the Phylogeny tool and Traditional Lectures, I would find using the Phylogeny tool to be:”

Attitudinal Survey - Module Usage. Table 5 contains responses for the five questions on the attitudinal survey that asked students about their perceptions of using the module. Positive responses were recorded here as well, with most students finding the tool both easy to use and worth the time spent. One student disagreed that the tool was easy to use, however based on their comments this is most likely because an error was discovered which caused some students to needlessly repeat the third activity multiple times. This error was quickly corrected and students were allowed to move on.

Table 5: Attitudinal survey – module usage.

Item	Strongly Disagree	Disagree	Neutral	Agree	Strongly Agree
Complimented the course materials	0	0	1	7	6
Was relatively easy to use	0	1	1	5	7
Was worth the time spent using it	0	0	1	7	6
There was sufficient support provided to effectively use the tool	0	0	0	10	4
I learned more in class as a result of using the tool outside of class	0	0	4	3	7

8. CONCLUSION & NEXT STEPS

An interactive online quantitative cellular biology learning module for the phylogenetic relationships between organisms was developed for an undergraduate engineering course at Purdue University. Analysis of student performance on the pre-post quiz reveals that the module successfully helped students to learn the steps performed in the Woese experiment, a pioneering study in phylogenetic research. More testing is needed to determine if the other components of the online learning module are as successful. Based on the attitudinal survey, the students clearly enjoyed using the module more than other forms of instruction.

Though overall the results are favorable, the module does fall short of the intended design goals, insofar as it does not achieve the level of interactivity and higher-order thinking originally desired. The second activity, though crucial to helping students better visualize the Woese experiment, allows for very little insight into student's understanding. Additionally, the fourth activity does not lend itself to automated feedback, making it difficult for students to attempt the problem without using some amount of trial-and-error.

In addition to more pre-post testing, students' use of the tool should be more thoroughly analyzed. This includes a more detailed analysis of the time based data as well as student responses to the in-module activities. Detailed timing data was collected during a number of the activities. For example, during the tree construction activity, each time the user selected an object on the screen, a timestamp and description of the object with which they were interacting were recorded. A more thorough analysis of this data can be used to estimate the amount of

trial-and-error student undertook. Following this analysis, changes should be made to the tool to further improve the student understanding of the conceptual information.

Though there are still areas for improvement, the initial results of module use warrant further development and usage of both the phylogenetic relationships module as well as other similar modules.

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