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Pretest/Posttest Plus Prompts: Tools for Research and Evaluation

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We conducted a series of summer workshops on bioinformatics to increase educators' knowledge of this new field of inquiry with the assumption that their knowledge will, in turn, impact student achievement. The workshops incorporated experiential learning and self-reflection (Loucks-Horsley et al. 1998). Educators demonstrated significant increases in knowledge as revealed by pretest and posttest scores on the same test that was used during the field-testing of the module, *Bioinformatics and the Human Genome Project,* a component of the workshop. Qualitative analyses revealed that the workshop introduced methodologies (including guided inquiries, hands-on, problem-based and role-playing activities for teaching bioinformatics) that educators valued and planned to incorporate into their own classrooms. The only area in which teachers expected more than they received was in laboratory experiences. This exception may be explained by the fact that the nature of biological experimentation has now broadened to include computer-based or "in-silico" experiments (Bloom 2001). Biology educators, like research biologists, must learn the new language of biology and embrace a new tool for biological research.

Introduction

Technology now plays a vital role in every disciplinary field, especially in science. The process of updating information among various communication technologies is one of the challenges that globalization and techno-

logical revolution has imposed on the educational system (Kaechele 2006). Students strive to compete in the arena of global education, because computers and related peripherals influence the way students learn (Wang 1999). In recent years, to keep up with the advancements in education, expert courseware designers are finding ways to creatively apply learning research, use instructional design methods, and manage interdisciplinary curriculum (Rowley 2005). As promoted in the National Science Education Standards (NSES), students need to know how to use technology in order to access the information necessary to do science (NSES 1996). A study on science undergraduates' and graduates' understanding of scientific research processes concluded that students' did not have a clear understanding for the necessity of framework theories or scientific processes (Thoermer & Sodian 2002). Therefore, high school students should be provided with sufficient opportunity to practice scientific methods and more fully understand the nature of scientific processes.

Technology has become part of the process of instructional preparation (Okojie, Olinzock, & Okojie-Boulder 2006). If curriculum materials are properly blended with technology tools, learners can more easily understand concepts. One of the drawbacks of incorporating technology in curriculum development is the need for continuous updating; otherwise the curriculum loses its credibility. Thus, one-time reform is not applicable in science education, because it is not possible to accommodate the changes that are taking place every day in science. Curriculum supplements are developed in order to fill gaps caused by scientific advancements.

The NSES insist the goals and objectives of science education are flexible with respect to technology, in order to adapt to changes. The Standards further mention that it is the responsibility of the educational system to provide skilled professional teachers, sufficient classroom time, and a variety of learning materials, work space, and the community resources to the students in achieving high levels of performance (NSES 1996). Professional development sessions foster teachers understanding of real-life science and how to solve problems. In an annual meeting of the American Educational Research Association, Kennedy (1998) an educationist (who is involved in the professional development programs at the Wisconsin Center for Education Research) stated that "professional development programs that focus on subject matter are likely to have larger positive effects on student learning than are programs that focus on teaching behaviors" (p. 11). Teacher training workshops are necessary for biology teachers to know the use of technology, web-based resources and recent advancements in bioinformatics and how to incorporate them into their subjects. This workshop provided such an opportunity. Among other things, teachers practiced the computer-based

curriculum supplement *Bioinformatics and the Human Genome Project* (BSCS 2003). This supplement, a downloadable standalone instructional module, was developed by BSCS with funding from the U.S. Department of Energy, primarily for high school students and teachers. As is customary with BSCS (Grobman 1970), the module was field-tested in diverse schools across the United States with results showing positive impacts on both teachers and students. The lessons enable students to use the simulated Intranet website of a fictional biotechnology company in order to reinforce scientific principles that the lessons promote through guided-inquiry. BSCS identifies the following reasons to be the most compelling to develop the module.

1. To help students understand how and why computers are essential for analyzing the data produced by the Human Genome Project.
2. To introduce teachers and students to some of the most common bioinformatics methods; including searching for open reading frames, BLAST searches, and multiple sequence alignments.
3. To help students to appreciate the importance of sequence from model organisms to our understanding of the human genome.
4. To improve understanding of our genetic diversity, and
5. To raise some of the ethical issues associated with establishing and using genetic database.

LITERATURE REVIEW

Technology Integration in Biology

In the contemporary world, teaching biology and teaching with technology cannot be separated. Indeed, schools are urged to move from the generation of using technology to the generation of thinking with technology (Gershner & Snider 2001). The authors further recommend that innovations in many disciplines calls for appropriate professional development for teachers in order to better educate students with higher-order thinking skills. In his article 'The Interplay of Biology and Technology', Stanley Fields (2001), states that "biologists now operate in a time when technology is not merely appreciated but acclaimed". Technology claims its place in biology for all the recent advancements that are taking place in the medical, agricul-

tural and all other related fields (McGarry et al. 2006). Figure 1 shows an outline of the literature review.

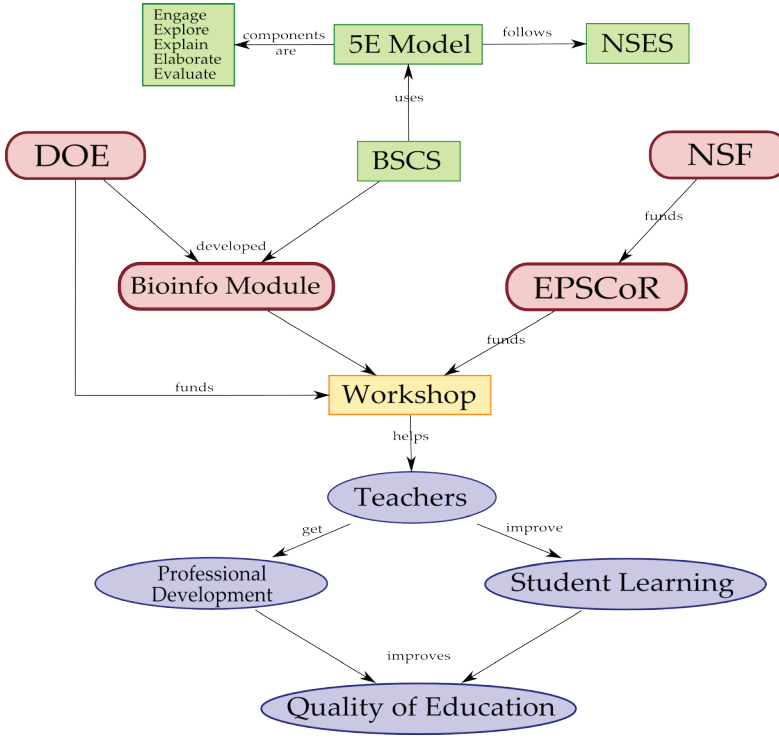

Figure 1. An outline of the literature review.

The NSES specifies the relation between science and technology as "the relationship between science and technology is so close that any presentation of science without developing an understanding of technology would portray an inaccurate picture of science"(NAS 1996; NSES 1996). Technology and biology are interrelated: technology provides the tools and biology provides the problems (Fields 2001).

Web-based instruction has become integral part of biology and it is necessary for every biology teacher to know how to use the appropriate technology for instruction. Web-based resources are effective in supporting student learning and web-based technologies are increasingly being used in schools to support teaching and learning (Napthine 2006). One of the primary assets of web-based instruction is its ability to adjust to individual learning preferences (Harris, Dwyer, & Leeming 2003). A study conducted

by Lee found that student evaluations of web-based political modules indicated that web learning adds value to the teaching and learning process and helps develop the necessary intellectual and personal transferable skills (Lee 2003). Engaging students in problem-solving activities will expose them to deeper insights into various conceptions of the natural world and help them develop insight into professional practice of scientists (Stewart & Rudolph 2001).

Bioinformatics is defined as a field of science in which biology, computer science, and information technology are merged to form a single discipline (BSCS 2001). Kalra (2005) concluded that the increase in and the enormity of information being produced from genetic field, with the convergence of genetics and computers, necessitated the emergence of bioinformatics as a trans-disciplinary field. An interdisciplinary curriculum requires a professional development program for teachers to stimulate creativity and to help them diversify the instructional strategies in their classrooms (Mamlok-Naaman, Hofstein, & Penick 2007). Web-based instruction provides an equal opportunity to support teaching and learning (Tate & Malancharuvil-Berkes 2006). If teaching ignores the role of computers in science and engineering, it would be a disservice to the students (Steinberg 2000). Without sufficient knowledge, students may not be able to use data to discover interrelationship and patterns hidden in the databases (Brusic & Zeleznikow 1999). Our knowledge about the structure of proteins and DNA has advanced to sequencing the genes and genomes within the past 50 years (Fogel & Corne 2003). Increasingly, students will be expected to know how to use the biological databases when they graduate from high school.

Bioinformatics, DOE and Human Genome Project -Module

The United States Department of Energy (DOE) and the National Institute of Health initiated the Human Genome Project (HGP) in 1990 (HGP 2008). Major goals specified by this project follow.

1. Identify all the genes in human DNA
2. Determine the chemical base pairs that make up human DNA
3. Store all the gene information in databases
4. Improve tools for analysis
5. Transfer related technologies to the private sector
6. Address the issues (ethical, legal and social) that may arise from the project

DOE-HGP maintains an official website which has all the details about the HGP (http://genomics.energy.gov/). This user-friendly site provides information about the HGP, related ethical, legal and social issues, Medicine and the New Genetics, Gene Gateway (guides and tutorials to help readers use the resources), Research Archive, Education resources for teachers and students, information about careers in genetics and the biosciences, web casts (online audio and video files about genetics and HGP), images on HGP, and HGP presentation materials. Education resources include HGP publications, teaching modules, teaching aids, videos, graphics animations, books, posters, presentations, workshops and trainings, and links to other genetic sites. One of the main advantages of using technology-based education lies in the ability of students to navigate through the web links on a topic and gather additional information to aid in understanding the topic (Zahorian et al. 2000).The *Bioinformatics and the Human Genome Project* (Bioinformatics-HGP) module is a part of the service provided by the DOE-HGP. The module was developed to help teachers and students to understand the importance of bioinformatics with respect to HGP. This module is a curriculum supplement and consists of learning materials for the students and teachers that could be used along with the existing biology textbooks. The module was field-tested in 26 high schools across the U.S with a total of 779 students. Analyzes of pretest and posttest scores revealed a significant increase in bioinformatics knowledge $t(25) = -14.779$, $p<0.001$ (two tailed) (BSCS 2005).

Gabric (2003) claims that integration of bioinformatics into the high school curriculum will improve biology teaching because high school biology students often use biotechnology techniques like DNA finger printing, gel electrophoresis and Polymerase Chain Reaction. The author concludes that "Bioinformatics turns students and teachers into researchers in their own classroom and inquirers into the teaching and learning process" (Garbic, 2003, p.5). In another article on using a modular approach to using computer technology for education and training, the author identified that a learning module with well-defined learning objectives, assessment measures, combination of multimedia tools and web-based delivery forms an excellent complement (Zahorian, Swart, Lakdawala, Leathrum, & Gonzalez 2000).

BSCS – 5E Instructional Model

Science education reform occurs in the classroom. Science teachers are expected to provide opportunities for students to explore science. The instructional design plays a central role in providing an opportunity for students to experience scientific methods and understand scientific concepts. The NSES specifies the content and methods that students should know and be able to apply at their respective grade levels (NSES, 1996). Since the mid-1990s, BSCS follows the goals and objectives of NSES as guidelines for preparing the curriculum in order to ensure students' highest achievement (Bybee 2004). BSCS encourages students to do and experience science rather than simply memorize facts, and has always promoted inquiry methods of teaching. The BSCS Executive Summary (2006) states that since the 1980s, a BSCS curriculum follows the 5E instructional model: Engage, Explore, Explain, Elaborate, and Evaluate (BSCS 5E 2002). As conceived by Johann Herbart who laid the foundation for 5E model in the early 20th century, the best pedagogy allows students to discover relationships among their experiences and the teacher gives direct instruction and explains ideas that the student would not discover by himself. Finally, the teacher provides opportunities for the student to demonstrate his/her understanding. In 1930s, John Dewey's instructional model recommended the following phases; sense a perplexing situation, clarify the problem, formulate the hypothesis, test the hypothesis, revise the tests and act on solutions. Such learning theories are the basis of 5E instructional model (Bybee et al. 2006a, 2006b). The following are the steps involved in 5E instructional model (Bybee et al. 2006a);

1. Engage: Instruction engages students with questions and creates curiosity. The teacher assesses students' prior knowledge about the content.
2. Explore: Students are encouraged to work and explore the ideas without any direct instruction. Students gather data to make predictions. Teacher provides time to work and gives them directions if necessary.
3. Explain: The teacher encourages the learners' to explain what they learned. The teacher introduces new terms, ideas and explanations.
4. Elaborate: The teacher encourages learners to apply the new knowledge to investigate further and helps students to practice the new knowledge.

5. Evaluate: The teacher observes students performance to assess their understanding. Students are expected to apply their new knowledge and skills as they perform.

Professional Development

As mentioned by (Supovitz & Turner 2000) high-quality professional development insists on inquiry-based teaching practices to further ensure high levels of student achievement. Teachers can improve their science knowledge and technology literacy through professional development. Workshops also provide an opportunity for teachers to develop an understanding of the methods of science and the ability to apply these methods in their teaching (Bybee & DeBoer 1994). Lever-Duffy & McDonald in their book *Teaching and Learning with Technology,* stressed the importance of in-service trainings for teachers for them to keep up with the advanced technology that are being using in education (Lever-Duffy & McDonald 2008). Computer-oriented skills are necessary for a teacher to understand and disseminate the knowledge that is acquired through professional development trainings ("Teacher Professional Development" 1996). The teacher who develops an understanding of scientific advancements extends his/her experience to their students. Professional development training offers an experience to the in-service teachers to share their knowledge with many subject experts and skilled professionals and eventually take the acquired knowledge to their classrooms. So, in-service trainings are necessary for science teachers to understand the current trends of science and to enrich their technology literacy.

The National Science Education Standards stresses the importance of professional development for science teachers and states that "Becoming an effective science teacher is a continuous process that stretches from preservice experiences in undergraduate years to the end of a professional career" (NSES, 1996). NSES suggests that a professional development for science teachers should provide learning experiences that includes scientific literature, media, and technological resources that expand their ability to access further knowledge (Trowbridge, Bybee, & Powell 2003). As discussed in an editorial, BSCS partnered with Northern Arizona University to conduct a professional development workshop that focused on an instructional module (ABT, 2008). This Mississippi-EPSCoR workshop also incorporated instruction using a BSCS module. A study on professional development for science teachers concluded that facilitators of professional devel-

opment should consider empowerment, communication and context aspects (Lavonen, Juuti, Aksela, & Meisalo 2006). The MS EPSCoR Bioinformatics workshop primarily includes both computer-lab and wet-lab experiences, as well as lectures from subject-area experts in bioinformatics, with the goal of empowering teachers to incorporate lab experiences related to bioinformatics into their classrooms.

Contents of the Bioinformatics and the HGP Module

Bioinformatics and the Human Genome Project, a module developed by BSCS in 2003, provides authentic web-based and print materials set within the context of a fictional biotechnology company to teach the principals of bioinformatics and explore related ethical issues. Cornford (1997) concludes that "modular courses do have strengths and will continue to be developed and implemented to satisfy specific training needs", and recommends features to be observed in constructing and designing modular courses (Cornford 1997 p.249). BSCS developed using a constructivist approach, also described in Cornford's article. Module contents are organized in such a way that the learners integrate theory with problem-solving skills, integrate content knowledge with the context of the workplace, and integrate both formative and summative assessment methods. The module includes teacher background material about the design of the module, bioinformatics, and the HGP, references, website resources, a glossary, and copy masters for students to complete as they progress through the lessons (BSCS 2003). Titles of the five lessons follow:

1. Engage: Assembling DNA sequences
2. Explore: Finding features in the genetic landscape
3. Explain: Mining the genome
4. Elaborate: Genetic variation and disease
5. Evaluate: An informed consent dilemma

One of the authors of this article contributed to the development of the module and has streamlined its presentation for college students and educators (see Appendix 1).

METHODS

With funding from MS NSF-EPSCoR project, Innovations in Computational Sciences, high school and college educators were invited to participate in a summer workshop. During the workshop, the first author guided educators through the "Bioinformatics and the HGP" module. Educators also heard lectures from and interacted with computational biologists and computer scientists, and conducted both computer and wet lab experiments. In total, three bioinformatics summer workshops (2006, 2007, and 2008) provided professional development to 71 secondary and postsecondary educators. We administered the same pretest and posttest questions to determine participants' knowledge that was used during the field-testing of the "Bioinformatics and HGP" module. The test consists of 28 questions with the options true, false and not sure (see Appendix 2). We sought to answer the following questions in this study:

1. Is there a significant increase in bioinformatics knowledge for the educators who attended the workshop?
2. Is there a significant difference between the pretest and posttest scores from the DOE-HGP field test data and the scores of the educators at the workshop?
3. What did educators hope to gain from this workshop?
4. How are their students going to benefit from these workshops?

To answer questions 1 and 2, we used quantitative statistical analyses, and to answer questions 3 and 4, we used qualitative methods of analyses.

Quantitative Analysis

In order to test our hypotheses in questions 1 and 2, we entered the pretest and posttest data into an Excel data file. The data was then analyzed using Excel and SPSS software 16.0 for Windows. The **paired-samples t-test** (Zimmerman 1997) was identified as the appropriate statistical test to determine if there was a significant change in scores before and after the workshop. Table 1 shows the statistical results for each year and averaged over the three years. In the 2006 workshop, the mean score of the pretest was 12.46 and posttest was 21.30, a statistically significant increase: $t(12) = -8.289$, $p < 0.001$ (two tailed). In 2007, the mean score of the pretest was

10.97 and posttest was 19.03, a statistically significant increase: t (28) = -7.991, p< 0.001 (two tailed). In 2008, the mean score of the pretest was 12.41 and posttest was 19.38, a statistically significant increase: t (28) = -9.326, p< 0.001(two tailed). In the three workshops, the mean score of the pretest was 11.83 and posttest was 19.59, a statistically significant increase: t (70) = -14.150, p<0.001 (two tailed). Figure 2 shows the average pretest and posttest score comparison of all three bioinformatics workshops. We can thus conclude that educators who attended the NSF-EPSCoR bioinformatics workshops experienced a significant increase in their knowledge of bioinformatics. We can feel confident that our program was designed to effectively deliver instruction in bioinformatics.

Table 1

Paired Samples Test of the 2006-2008 Bioinformatics Workshops

	Paired Differences							
	Mean Difference	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference		t	df	Sig. (2-tailed)
				Lower	Upper			
2006	8.85	3.84808	1.06726	-11.17152	-6.52078	-8.289	12	.000
2007	8.07	5.43751	1.00972	-10.13728	-6.00065	-7.991	28	.000
2008	6.96	4.02211	.74689	-8.49544	-5.43559	-9.326	28	.000
combined	7.76	4.62127	.54844	-8.85440	-6.66673	-14.150	70	.000

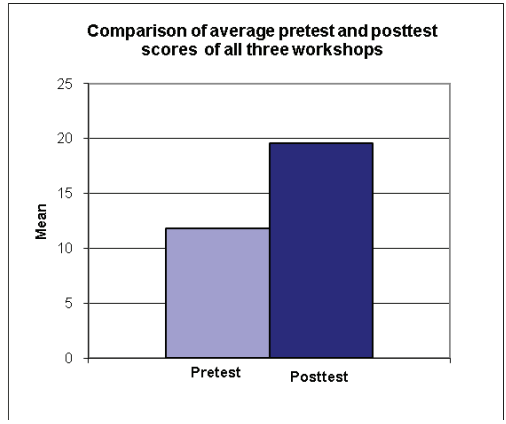

Figure 2. Comparison of the average pretest and posttest scores of the three bioinformatics workshops.

We compared the high school students pretest and posttest mean scores from the field-testing of the module to the teacher's workshop pretest and posttest mean scores. The BSCS report for the DOE-HGP indicates a significant increase between high school students pretest and posttest scores ($t(25) = -14.779$, $p<0.001$ (two tailed) and the bioinformatics workshop indicates that $t(70) = -14.150$, $p<0.001$ (two tailed). These results serve to both validate the test and to reassure us that our educators have greater content knowledge overall than high school students. Figure 3 compares the mean scores from the field test with the bioinformatics workshops.

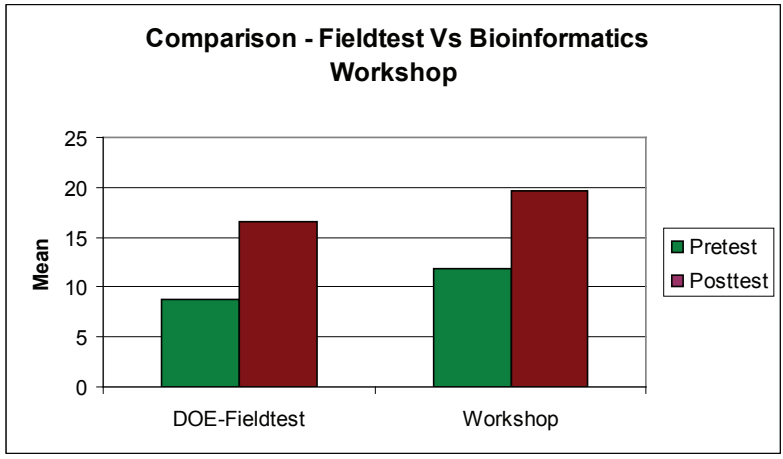

Figure 3. Comparison of the mean scores from the field test and those from the bioinformatics workshops.

Qualitative analysis

We set aside time at the end of the day to obtain feedback so that issues could be addressed, adjustments made, and impacts assessed. Participants responded anonymously to five prompts on a one-page reflection paper, with each prompt positioned within a large circle. Prompts included: I expected…, I got…, A thing of value…, I wish…, and Next I will or Next I need… In 2006, we collected daily reflections at the end of two of the three days; in 2007 at the end of each of the four days; and in 2008 at the end of three of the four days. We listed each participant's responses to each prompt in a Word document and coded all three workshops in the same manner. We also combined the categories that emerged for the entire workshop and represented them in pie charts.

The same four categories emerged from participant's responses to the first three prompts (I expected, I got, and a thing of value). Responses fell into the following categories: 1. lab experiences, 2. lectures, 3. resources received, and 4. bioinformatics knowledge. Responses that were categorized as laboratory experiences included both wet-lab and computer-lab activities. Sample responses for **"I expected…"** include: "computer hands-on workshop", and "to be familiarized with gel electrophoresis". Examples of responses categorized as lecture included: I expected…"a lot of dry information and that I would be bored", "boring presenters" and "listen to talks". Examples of responses categorized as resources included: "to receive materials to use in my classroom", "some useful websites and activities", and "good resources of videos and animations". Finally, responses categorized as bioinformatics knowledge included: "to learn about bioinformatics techniques", and "to learn about the HGP".

Responses to the prompt **"I got…"** provided more specific information, as seen in the following examples: I got…" to use computer programming to research a gene disorder", "to practice lab techniques and find resources on the internet", "to load and run gels", "excellent speakers", "terrific presentation on DNA sequencing", "great materials to use in my classrooms", "a ton of resources and websites", "a general idea about bioinformatics", "information about DNA testing", and "knowledge about the Dolan Learning Center".

We summed the responses for "I expected…" and "I got…" for all three years and converted the total into percentages. We then compared the responses for the two prompts as depicted in figure 4.

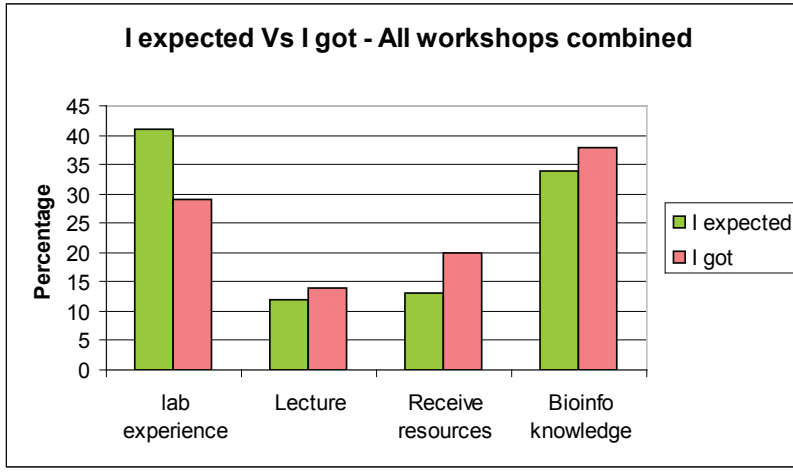

Figure 4. Comparison of summed responses for "I expected" and "I got" from the combined bioinformatics workshops.

Figure 4 reveals that 41% of the participants expected to experience laboratory activities and 29% indicated that they experienced laboratory activities, 12% of participants expected to hear lectures and 14% indicated that they did, 13% participants expected to receive resources and 20% indicated that they did, and 34% participants expected to learn about bioinformatics and 38% indicated that they did.

Four categories emerged from responses to the prompt **"I wish"**: 1. more time to do labs and use computers, 2. more computers to use, lab space, more drinks, etc., 3. more resources and information on ways to implement in teaching, and 4. to use the received resources in the future. Sample responses related to time include: I wish…" I had more time to spend on computational science", "we had spent more time in the biotech lab", "we could go through some of the activities little more slowly, but I understand we have a limited amount of time", and "some presenters would slow down a little". Sample responses related to using resources in the future include: I wish… "I had known about (the wet-lab instructor) and her resources when we had thousands of dollars to spend just a month ago', and "my students had more access to some of the technology used in this workshop". Figure 5 illustrates the percentages of the combined responses to the prompt 'I wish'.

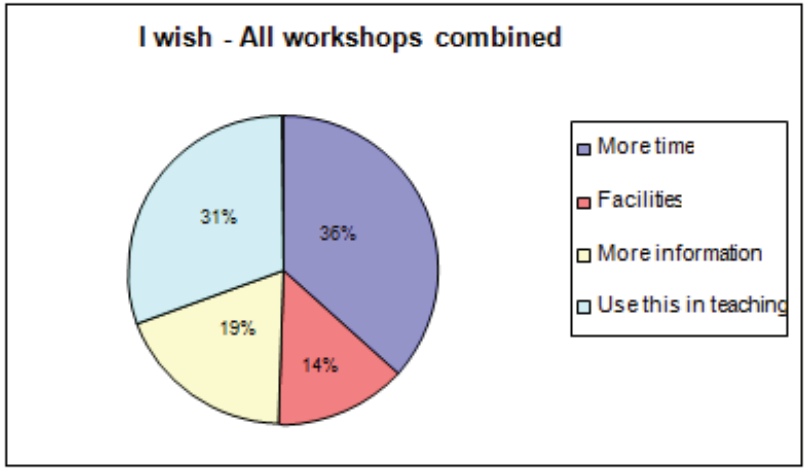

Figure 5. Percentages of the combined responses to the prompt "I wish"

Figure 5 reveals that 36% of the participants wanted more time to do labs and use the computers, 31% of the participants wished to use their newly acquired knowledge and resources in teaching, 19% of wished for more information about the ways to implement bioinformatics in their classrooms, and 14% wished for more facilities at their schools.

Sample responses to the prompt **"A thing of value"** include: "the opportunity to do gel electrophoresis, PCR, and DNA extraction", "the computer lab helped me to find resources and databases that I never even knew existed!", "background knowledge of genetics", "a great physiology modeling lecture", "free videos from Howard Hughes", "hands-on practice time with the bioinformatics module", and "knowledge of how closely computer programs and biology are linked". Figure 6 illustrates the percentages of the combined responses to the prompt "A thing of value".

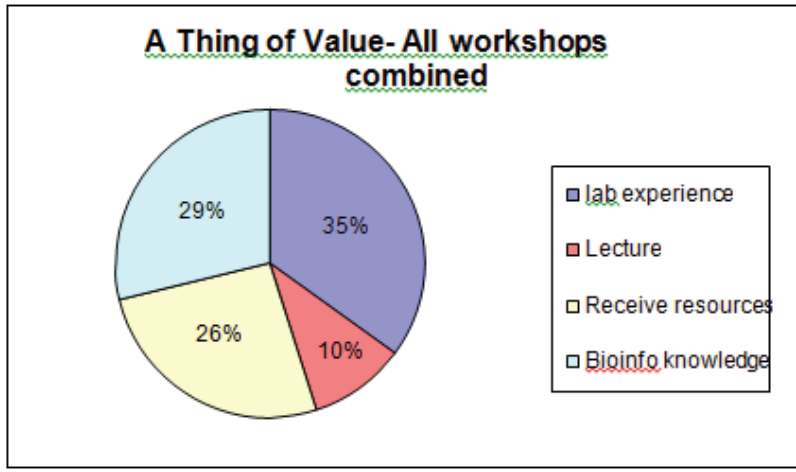

Figure 6. Percentages of the combined responses to the prompt "A thing of value"

Figure 6 shows that 35% of the participants valued the wet-lab experiences, 29% valued their knowledge of bioinformatics, 26% valued receiving new resources, and 10% valued the lectures.

Four categories emerged from participant's responses to the prompt "Next I will/Next I need…": 1. apply acquired knowledge to teaching, 2. attend more professional development trainings and encourage other educators to attend this workshop, 3. use received resources, and 4. learn more about bioinformatics. Sample responses include: Next I will…"structure this workshop for my classroom course", "decide what to use with my students from this workshop", "go home, study and reflect on all of this info and put it into perspective", and "to research these topics more on my own". Figure 7 illustrates the percentages of the combined responses to the prompt "Next I will".

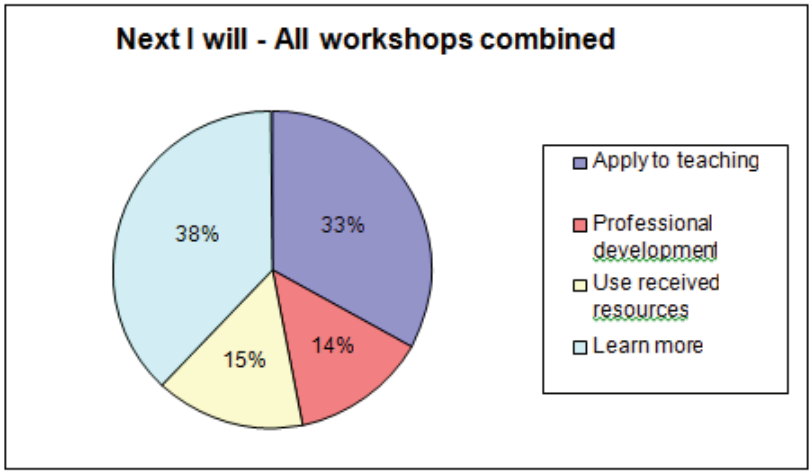

Figure 7. Percentages of the combined responses to the prompt "Next I will"

Figure 7 reveals that 38% of the participants intend to learn more about bioinformatics, 33% intend to apply their knowledge of bioinformatics to their teaching, 15% intend to use their new resources, and 14% intend to attend more professional development trainings and encourage other educators to attend this workshop.

Educators completed a traditional combined Likert-type and open-response instrument for workshop evaluation prior to departing. With 1 indicating low satisfaction and 5 high, the overall mean for the three years was 4.6. The open-response comments were generally positive, including these from 4 different participants: "Overall, an excellent workshop that definitely increased my knowledge of bioinformatics/molecular biology. Students will love it! I can use some of it. Information will help me to inform students of career choices."

CONCLUSIONS

We conducted a series of summer workshops on bioinformatics to increase educators' knowledge of this new field of inquiry with the assumption that their knowledge will, in turn, impact student achievement. Strong correlations exist between student achievement in science and mathematics and the teaching quality and level of knowledge of educators (NRC 2001). As supported by the literature on professional development, the workshops

incorporated experiential learning and self-reflection (Loucks-Horsley et al. 1998). In this article, we considered the first two levels of professional development as defined by Gusky (2000): participants' reactions and participants' learning. A study of the additional three levels - organization support and change, participants' use of new knowledge and skills, and student learning outcomes – extends beyond the scope of this article.

We can conclude that the workshop helped educators learn bioinformatics as indicated by quantitative analyses. Because the educators demonstrated significant increases in knowledge as revealed by the same test and using the same module as field-test students, we can also imply that the module, *Bioinformatics and the Human Genome Project,* is effective at communicating core knowledge. Our qualitative analyses revealed that the workshop introduced methodologies (including guided inquiries, hands-on, problem-based and role-playing activities for teaching bioinformatics) that educators valued and planned to incorporate into their own classrooms. Thus, the quantitative results of the study are both corroborated and enhanced by the qualitative results.

We conducted qualitative research in order to determine what educators hoped to gain from the workshops, what they thought they actually gained, and how they envisioned using their new knowledge and resources. If participants' expectations are incongruent with the goals of a professional development program, then they may be dissatisfied with the experience despite the quality of the program. In this regard, Krathwohl's affective domain taxonomy (1964) helps us frame the effectiveness of a professional development workshop by taking into account prior expectations. To review, Krathwohl posited that the minimum level of affect toward a learning environment is receiving, followed by responding, valuing, organization (assimilation), and finally, characterization. Receiving information during a professional development program can be assessed by superficially monitoring the activities of participants by asking, "Are participants paying attention?" Responding can be assessed by asking, "Are participants engaged in the discussions and activities?" The daily reflections, however, prompt participants to go further by making decisions about what experience(s) they valued the most and how they intend to organize new information to provide learning experiences for their students. In effect, the prompts facilitate the process of metacognition. Cognitive psychologists theorize that much of learning is a conscious process that incorporates metacognition (Brown et.al 1983). Metacognitive skills include determining what one truly understands and knowing how to achieve ones desired learning goals. White and Rederiksen (1998) collaborated with teachers to test the effects of metacognitive strategies in a middle school curriculum. In a controlled comparison, they found

that students' performance improved significantly on both physics and inquiry assessments for those that used the metacognitive process employed during the study.

Thus, the qualitative research instrument actually served a dual purpose: 1) to facilitate metacognition, and 2) to obtain formative assessment for immediate feedback regarding the conduct of the workshops so that adjustments could be made quickly. Analysis of the qualitative data revealed that, for the most part, the workshop exceeded teachers' expectations for the workshop, that they were eager to learn more about the topics presented, and eager to incorporate their knowledge into classroom instruction. Comparisons of responses to the prompts "I expected" and "I got" revealed that educators generally expected to hear boring lectures, but instead experienced a rich diversity of new and interesting activities. Some responses, however, indicated that too much information was presented in too little time. Considering the varied backgrounds and experiences of the educators - ranging from first-year teachers to master teachers to university professors - one would expect this.

The only area in which teachers expected more than they received was in laboratory experiences. This exception may be explained by the fact that the nature of biological experimentation has now broadened to include computer-based or "in-silico" experiments (Bloom 2001). During the workshops, educators spent an equal amount of time in a computer laboratory as they did in a traditional laboratory. "In-silico" experiments involve using multiple alignments, BLAST searches, and building phylogenetics trees on data obtained from computer databases. "Traditional" biotechnology experiments involve, among other things, restriction enzyme digests, electrophoresis, and DNA amplification. The laboratory research of biologists increasingly incorporates computer applications, thus exemplifying the quickly evolving nature of biology. Biology educators, like research biologists, must learn the new language of biology and embrace a new tool for biological research. We can conclude that these workshops were successful in helping biology educators keep pace with the new developments and emerging computer applications in biology.

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APPENDIX 1

Bioinformatics OncoX Project: Laboratory

Bioinformatics
and the Human Genome Project
Funded by the Department of Energy

- Produced by Biological Sciences Curriculum Study
- Mark Bloom, Project Director
- Sherry Herron, Senior Curriculum Developer

BSCS

Introduction

Sequence assembly begins by **cloning** DNA into bacterial cells. Enzymes that cut DNA sequences (**restriction enzymes**) and an enzyme that connects DNA sequences (**DNA ligase**) are used to insert the DNA to be sequenced into another DNA molecule called the **vector DNA**. Vector DNA contains sequences needed to replicate the molecule within the bacterial cells. Cloning the DNA into bacteria is fast, efficient, and provides an unlimited source of DNA for sequence analysis. Automated cycle sequencing of DNA usually involves using the chain termination method developed by Fredrick Sanger in the 1970s, coupled with the use of the heat-stable *Taq* DNA polymerase.

You will assume the role of an employee at a biotechnology company which is involved in developing new drugs. The company is engaged in **rational drug design**, so named because it derives from an objective understanding of the biochemical defect associated with the disease. This stands

in contrast to the traditional approach of screening millions of chemicals in the hope that one or more will help control the disease. Read the following memo from the Research Director and the Informed Consent Form.

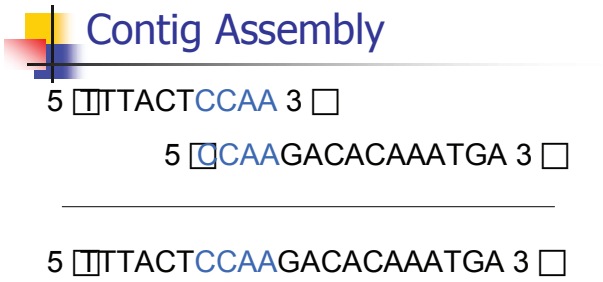
Memo

Our OncoX drug will be entering clinical trials soon. We must carefully design the trials to provide the maximum amount of data for the types of cancer that OncoX is most effective in treating. You will be sent raw sequence data for assembly and analysis. These sequences come from cancer patients and family members. Included is a control sequence from an individual without cancer. Please review the informed consent form. Each team will analyze the DNA sequence from a different individual. All teams will work with sequences from the same region of the genome. Work carefully! Mistakes can be costly.

Informed Consent Form

- You have been asked to participate in a study that will assess the effectiveness of a new drug in treating various types of cancer. Participation will require that you make a single blood donation. The study is being carried out by the Onconomics Corporation under the direction of Dr. Richard Welby.
- This study should not be confused with genetic testing. We are not obligated to provide you with information about your sample. The identity of your sample will be known only to designated staff and among its research collaborators. Your participation does not entitle you to financial compensation, and in no way compromises your medical treatment.

- Use the following guide to assemble the DNA fragments contained in your envelope into a long, continuous stretch of sequence. The process used individually sequenced fragments that have overlapping sequences at their ends. By aligning the overlaps, a long sequence can be put together. The assembled sequence is referred to as a *contig* because it is derived from a series of shorter sequences that were contiguous with each other on the chromosome.



- Now that you have simulated contig assembly, you will begin the job of extracting information from the raw data. Bioinformatics software can take a DNA sequence, transcribe it into its corresponding RNA sequence, and then translate the RNA sequence into an amino acid sequence. Since each DNA strand can be read in three different reading frames, the computer must perform six different translations for any given DNA sequence. You will transcribe and translate your DNA sequence on the following template using the single letter designations for the amino acids. **Remember that mRNA is translated in the 5' to 3' direction. Therefore, you will read this strand in reverse. Arrows are provided as a guide.**

- Programs also can be used to locate candidate genes. One of the first and most important indications that a sequence may be part of a gene is the presence of an **open reading frame (ORF**), a reading frame without stop codons. Stop codons are absent from reading frames that code for proteins – that is, until the end of the gene. For the purpose of this activity, an ORF refers to a reading frame that does not contain a single stop codon. **Highlight any ORFs.**

Bioinformatics OncoX Project: Laboratory Report

Directions: Compile your answers to the following questions in a typed report. Staple your completed Reading Frame Translations to your report.

1. Write down the sequence of each strand that you assembled. Number and leave a space after each 10th base.

5′ **3′**

3′ **5′**

---

2. The sequence from each of the 10 donors will be read aloud. (One of the 11 sequences is the control). Record any differences above or below your own sequence.
3. Some of the donors are homozygous and others are heterozygous. How do we know?
4. What does this mean in terms of the sequences themselves?
5. If all of these sequences come from the same region of the genome, why do some of them vary from one another?
6. How can you tell if a sequence variation occurs naturally in the population or comes from an error in sequencing?
7. How do mutations and arise in the genome?
8. Consider the informed consent form. Does it adequately protect the rights of the donors as well as the company? Why or why not?

Use the Onconomics Corporation Intranet Web site to review the OncoX Project DNA sequence data.

- Go to the company's Intranet Web site: *http://www.bscs.org/onco*
- Go to *Sequencing Department*

- Go to *Sequencing Protocols*
- Review the Cycle Sequencing Protocol and the sample electropherograms.

9. What are the key factors in cycle sequencing?
10. How does the electropherogram of a heterozygous individual differ from that of a homozygous individual?
11. How is a base that cannot be accurately identified on an electropherogram indicated?

Confirm your DNA sequence.

- Return to Sequencing Department
- Click on *OncoX* Project
- Compare your sequence with the electropherogram
- If your sequence is labeled as tentative, click on the *New Data* link to retrieve confirmed sequence data

Compare the OncoX set of DNA sequences (a CLUSTAL Analysis).

- Go to *Bioinformatics Department*
- Select the *OncoX Project* from the pull-down menu next to the *Multiple DNA Sequence Alignment* option

12. In table format, summarize the differences between the donor sequences and the control sequence. For example, Sequence 2 has an "A" at position 21 while the control sequence has a "C" at that position. If no differences exist, record "same as control sequence."

Compare the OncoX set of amino acid sequences (a CLUSTAL Analysis) for each open reading frame.

- Go to *Bioinformatics Department*
- Select the *OncoX Project Reading Frame 3* from the pull-down menu next to the *Multiple Amino Acid Sequence Alignment* option

13. In table format, summarize the differences between the donor amino acid sequences and the control sequence for reading frame 3.
14. Repeat the process for *Reading Frame 4* and summarize the differences.

Perform a BLASTN search to see if the control OncoX sequence comes from part of a gene and is therefore of potential interest to Onconomics Corporation.

- Go to *Bioinformatics Department*
- Select the *OncoX Project* from the pull-down menu next to *BLASTN*

15. Describe the sequences that perfectly match your input sequence.
16. In what other organisms are similar DNA sequences found?

Perform a BLASTP search to determine which of the two ORFs corresponds to the gene identified in the BLASTN search.

- Select *OncoX Reading Frame 3* from the pull-down menu next to *BLASTP*
- Return to *BLASTP*
- Select *OncoX Reading Frame 4* from the pull-down menu next to *BLASTP*

17. Which ORF corresponds to the gene(s) identified in the BLASTN search and why?

Use the company's Web site to access a public search engine to obtain information about ataxia telangiectasia.

- Go to *Bioinformatics Department*
- Type in *ataxia telangiectasia* into the *Public Search Engine*
- Click on *Submit*

18. What is the difference between a polymorphism and a mutation?
19. How many genes are associated with this disorder?
20. What chromosome is/are the gene(s) located on?
21. What mode of inheritance is demonstrated by this disease?
22. Does the gene product(s) have a known function, and if so, describe it.
23. What is the incidence of the disease in the United States?
24. What are the disease symptoms?
25. What is the prognosis for someone with the disease?
26. What is the prognosis for someone who is a carrier for the disease?
27. What treatment options are available?
28. Why are animal models being developed for this disease?
29. When did the A-T Children's Project begin and who started it?

30. Watch the video segments. When was the gene identified and where is research being conducted?
31. Where is the national research center for A-T located?
32. Name some of the celebrities who have worked for A-T fund-raising.

Use the company's Intranet Web site to access a private medical data base to perform a Mutation Analysis of the OncoX DNA Sequences for ataxia telangiectasia.

- Go to the *Bioinformatics Department*
- Type in *ataxia telangiectasia* into the *Private Medical Data Base*
- Click on *Submit*

OncoX sequence	Founder Mutation Present? Yes or No; If yes, which population?	Unaffected by A-T	Carrier for A-T	Affected by A-T
Sequence 1				
Sequence 2				
Sequence 3				
Sequence 4				
Sequence 5				
Sequence 6				
Sequence 7				
Sequence 8				
Sequence 9				
Sequence 10				
Sequence 11				

33. Recreate and complete the table in your report.
34. Can your analysis conclude that a person does or does not carry A-T?
35. Why does the company need to know if the donors have A-T or carry A-T?
36. Companies use bioinformatics analyses to guide decisions as to which areas of research to pursue. This company now finds itself in an ethical dilemma. Why is informed consent a potential problem for the OncoX samples?

APPENDIX 2

Bioinformatics and the Human Genome Project Module

Knowledge Survey

Instructions: Please complete this brief survey of knowledge on *Bioinformatics and the Human Genome Project* at the beginning of the workshop.

True False Not Sure

T F NS 1. Computers are required to analyze the vast quantity of DNA sequence data.
T F NS 2. The human genome is the same for every human.
T F NS 3. Scientists must obtain consent from individuals who supply samples for analysis.
T F NS 4. The genome of a human is completely unlike that of any other organism.
T F NS 5. DNA and RNA both contain nucleotides.
T F NS 6. Every mutation that occurs within a gene causes disease.
T F NS 7. Messenger RNA translation proceeds in the 3' to 5' direction.
T F NS 8. The base pairing of nucleotides (A with T; G with C) allows scientists to assemble DNA sequences from short sequences.
T F NS 9. The term polymorphism describes genetic variation between individuals.
T F NS 10. A sequence of 10 DNA bases codes for one amino acid.
T F NS 11. According to the central dogma, DNA is transcribed into RNA and RNA is translated into an amino acid.
T F NS 12. In order to look for a gene, scientists must analyze six reading frames for every section of DNA.
T F NS 13. An open reading frame contains both a start and a stop codon.
T F NS 14. A CLUSTAL analysis is used to translate DNA sequence to amino acid sequence.
T F NS 15. A BLAST search is used to compare a particular DNA se quence to all of the known DNA sequences in a data base.
T F NS 16. When you do a BLAST search, you find similar DNA sequences from different species.
T F NS 17. Computer programs have been designed for DNA sequence comparisons and searches only not for amino acid sequences.
T F NS 18. A BLAST search is commonly used to identify a particular individual in a population.

T F NS 19. A BLAST search may provide information about the.function of the protein for which the gene codes.
T F NS 20. Ataxia telangiectasia primarily affects the circulatory system of the body.
T F NS 21. Ataxia telangiectasia has a link to cancer.
T F NS 22. Bioinformatics has led to effective treatments for ataxia telan giectasia.
T F NS 23. Ataxia telangiectasia is inherited as a dominant allele.
T F NS 24. Individuals who give informed consent are automatically en titled to information about their sample as it becomes available.
T F NS 25. Bioinformatics is the process of obtaining informed consent for biological research.
T F NS 26. The data from the Human Genome Project are posted on the Internet for everyone to read.
T F NS 27. The growth of bioinformatics has revealed problems with obtaining informed consent.
T F NS 28. Most DNA polymorphisms are not associated with disease.

Thanks for completing the survey!