Big Science at Small Colleges: A Collaborative Model for Genomics Curriculum Development at Liberal Arts Colleges

A Project Sponsored by
The Teagle Foundation

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September 30, 2009

Table of Contents

APPENDICES

Abstract

”Big Science at Small Colleges” centered on a grassroots model for faculty development in genomics education at liberal arts colleges with research active faculty. Key features of this genomics curricular development project were: a) a pedagogical design framework based on the recommendations of a National Research Council report on successful laboratory learning experiences; b) financial and intellectual support for participating faculty members from a range of colleges to develop inquiry-based, integrated instructional units (I^{3}Us), using their choice of organism, and with a strong emphasis on integration of biology at multiple levels of organization from molecular/cellular through physiological and organismal to ecosystems, via approaches that included computational components and considerations of gene/genome evolution; and c) useful, data-rich assessment of each module and its implementation successes and barriers. The project also supported the construction of a dedicated infrastructure to disseminate the curricular modules, all associated documentation and links, and self-reported implementation and assessment outcomes, via a new website (http://serc.carleton.edu/genomics/index.html).

The specific objectives focused on faculty development to:

1) Support faculty learning about genomics.
2) Support faculty in developing curriculum and teaching materials informed by research in the learning sciences.
3) Prepare faculty to evaluate the efficacy of their genomics innovations.

The project implemented a three year-three workshop model that supported all three goals through a combination of learning from expertise within the participating group and from outside expertise on specific topics (specifically, to showcase existing teaching models in workshop I and to instruct on the use of specific bioinformatics and assessment tools at workshop II). Participants implemented their I^{3}Us and assessed their impact on student learning during the 2008-2009 academic year and reported on their results in workshop III. This model worked very effectively because it balanced opportunities to learn from leaders in the field with the need to customize this knowledge for application in specific learning environments with specific instructors and courses. Stipend recipients were able to integrate investigative genomics modules into courses addressing topics as diverse as mammalian behavior, nervous system function, and genetics. An unanticipated outcome of the project was a significant increase in participant understanding and use of assessment in their teaching and curriculum development.

We are now poised to create a core set of genomics assessment instruments, and a set of example implementations, that can support assessment of instructional units in the future. This project represents a new model for integrative teaching that leverages the resources of large research institutions to provide opportunities for small colleges to teach and assess inquiry-based science in fields (such as genomics) that are typically out of our reach because they are too resource-intensive.

I. Context and Motivation

The field of genomics informs some of the most pressing issues of our time, such as stem cell biology, transgenic agriculture, and cancer research. Rapid advances in genome sequencing and analysis offer unparalleled opportunity and challenge for biologists. A single sequencing run can now yield over 20 billion bases (the alphabet soup of genomes) which is seven times more base pairs than in the human genome. More data are being generated than can be analyzed and contextualized in traditional research models. Indeed, this explosion of data has spawned the rapid growth of the new discipline of bioinformatics, focused on development of the computational tools and approaches for managing and parsing biologically meaningful insights from the genomic data. It is essential for liberal arts colleges to train our students, both as scientists and as citizens, to understand the reasoning and strength of genomic evidence underlying high-impact public policy decisions and personal health choices. While liberal arts colleges historically prepare a disproportionate share of future PhDs in science (Cech 1999), it is difficult for small, undergraduate schools to develop hands-on genomic curricula for a number of reasons:

1. Genomics is inherently interdisciplinary, requiring training in biology, chemistry, computer science, and math. It is, therefore, typically taught in advanced courses not taken by humanities students.
2. Genomics is “big” science; its instrumentation and infrastructure require the resources of large research institutions.
3. Genomics is a rapidly evolving field; its tools and techniques can change dramatically over a few years, requiring continual training of faculty.

For educators, the availability of genomic data on the Internet can offer a way to engage undergraduates in authentic research and to democratize research which was previously possible only at research-intensive universities with vast instrumentation infrastructure. The other side of the coin, however, is the potential for widening gaps between the educational experiences of students at different types of institutions as genomics takes off at lightening pace, requiring students and faculty alike to think in new ways and at different scales. Our collaboration of small colleges coalesced around the need for faculty development and curriculum development in genomics.

Several models for integrating genomics in the curriculum have been developed concurrently. The Davidson College Genome Consortium for Active Teaching (GCAT) has enabled students from a range of institutions to investigate genome expression using microarrays that are analyzed on shared instrumentation (Check 2007). The Washington University Genomics Education Partnership (Lopatto et al. 2008) engages students across the country in contributing to the annotation of the *Drosophila* genome. The Howard Hughes Medical Institute (HHMI) Science Education Alliance (SEA) fully supports a year of collaborative introductory biology research at selected institutions where undergraduates isolate bacteriophages from local soils, prepare the phage DNA for sequencing at the Joint Genome Institute (JGI) and then analyze the genomes (http://www.hhmi.org/grants/sea/). The JGI’s Microbial Genome Annotation program supports institutions that “adopt” microbial genomes with an integrated analysis pipeline for annotation (http://www.jgi.doe.gov/education/genomeannotation.html). All these efforts, like ours, support faculty development through a combination of workshop offerings and web-based support. The distinguishing features of the Teagle "Big Science at Small Colleges" consortium include: 1) ongoing workshop support for the same cadre of faculty over the course of three summers, 2) focus on building faculty expertise in assessment, 3) faculty choice of organism with a strong emphasis on integration of biology at multiple levels of organization at the center of the curriculum, and 4) curriculum development using a grassroots/bottom up approach rather than a centralized dissemination model. Our initial model included genome sequencing at the Columbia Genome Sequencing Center. In the rapidly changing landscape of sequencing, this also evolved into a more distributed and flexible model with a number of different sequencing centers collaborating with the consortium.

The decision to incorporate multiple model and non-model organisms into our genomics education work is deeply rooted in a shared commitment to the value of fully integrated research and education as the ideal for student learning and faculty professional development. Our faculty's research programs are inextricably intertwined with our teaching, and we bring the excitement of new knowledge into our classrooms. We can capture the imaginations of our students by providing them with opportunities to formulate and investigate truly novel questions and to participate in authentic discovery. Students also gain hands-on experience in the research laboratory, where they are given substantial responsibility for the progress of the research and where they can shape its direction. Our students often present at professional meetings and they are frequent contributors to and co-authors on our scientific publications. Integrating authentic research experiences into the curriculum extends this powerful learning experience from a few students to a substantial number (Lopatto et al. 2008).

II. Goals

Improving genomics education at small schools to bring authentic research experiences to larger numbers of students was our overarching programmatic goal. Our specific objectives focused on faculty development to:

1) Support faculty learning about genomics.
2) Support faculty in developing curriculum and teaching materials informed by research in the learning sciences.
3) Prepare faculty to evaluate the efficacy of their genomics innovations.

III. Approach

Five core elements drove the design and implementation of our "Big Science at Small Colleges" initiative: 1) collaborative, community-based approach to professional development that is instructor driven, 2) adapting best practices in workshop design from the geoscience community, 3) building on vetted curriculum design principles, 4) providing support for learning, development and testing through a series of workshops, and 5) integrating assessment development with curriculum design. Each of these elements is described in greater detail below.

A. An Instructor-Driven Collaborative Approach

Our approach was to actively engage genomics educators and researchers in our curriculum development project. Retrospective analysis of the post-Sputnik science education reform concluded that the immense contributions of research scientists to science curriculum development could have been further strengthened by the active participation of teachers (Rudolph 2002). In our model we fully integrate the expertise of genomics researchers and educators. The diverse disciplinary background and scholarly interests of the faculty developers are leveraged and the instructor drives the design of the curriculum with the necessary support of a core group with expertise in genomics and education.

B. Building on the Geoscience Model

The geoscience education community has developed a proven workshop- and web-based dissemination model for undergraduate faculty and curriculum development efforts (Manduca, 2008; Macdonald et al, 2004; Manduca et al., 2006, McLaughlin, 2006). In this model, workshop participants are viewed as holding substantial teaching expertise of high interest to other participants. The workshop focuses on assisting participants in learning from one another while augmenting this knowledge base with needed expertise from beyond the participant community. Sharing is fostered in part by documenting teaching materials on a website. These resources are then discussed and enhanced during and following the workshop. This activity ensures that the participants transfer knowledge gained at the workshop into their own teaching and produce quality disseminable teaching resources that can be used immediately by other educators.

This model and the supporting web infrastructure at the Science Education Resource Center (serc.carleton.edu; Fox et al., 2005) were readily adapted to our initiative and provided an interactive site for workshop planning, capturing and sharing workshop elements with a broader audience, and supporting curriculum development that emphasized our goals and core elements (http://serc.carleton.edu/genomics). The interface for sharing curricula provided scaffolding for the faculty developers and ensured a flexible, but uniform feel to the collection. This approach offered efficiencies in time and cost, as well as the confidence in using a proven approach to faculty development.

C. Design Principles

Our project also built on the recommendations of the National Research Council 's (NRC) *America's Lab Report* (Singer et al. 2005). The report noted the prevalence and inadequacies of traditional lab experiences and documented the enhanced educational value of labs that require students to formulate questions, design their own investigations, and construct scientific arguments and explanations based on data they have gathered and analyzed. The evidence points to the effectiveness in achieving a range of learning goals of integrated instructional units which incorporate laboratory learning into the flow of instruction. The report provides vetted design principles for integrated instructional units: (1) they have clear pedagogical objectives; (2) they are integrated with lessons taught in the lecture; (3) they are designed to teach science content as well as process; and (4) they require student reflection and discussion. The study stressed the importance of the link between the classroom and the laboratory experience, and pointed out that undergraduate departments "rarely provide …laboratory experiences that follow the design principles [articulated above] derived from recent research" (p. 7).

All curriculum developers in our collaborative used the NRC design principles to build and assess inquiry-based integrated instructional units (I^3Us, Figure 1). To facilitate both faculty and curriculum development, participants worked from an online "Teaching Activity Page" developed by SERC. A sample form and directions for the activity page are available at http://serc.carleton.edu/genomics/I3U/submitting.html. The project is open ended and additional contributions to the site that conform to the design principles are welcome. Activities that were developed with Teagle funded workshop and assessment support will be identified as the resource grows. The activity page is an example of the effectiveness of building on the tested work of the geoscience community.

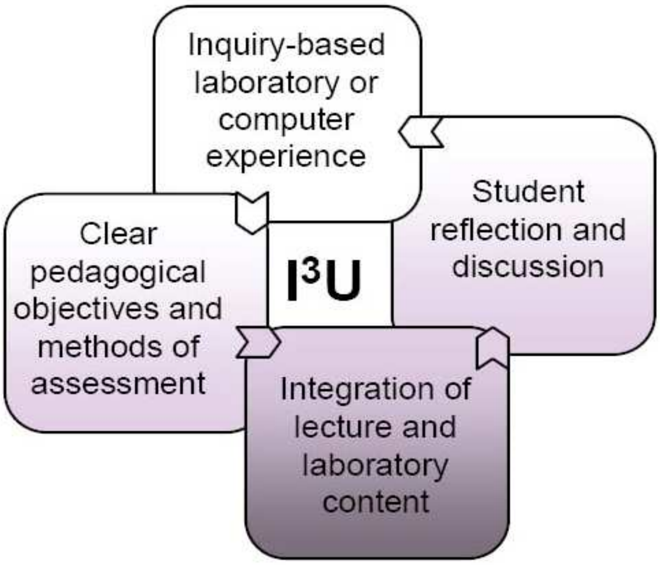


Figure 1. Curriculum development model for the development of I^{3}Us based on the design principles in America's Lab Report (Singer et al. 2005).

D. Integrating Research and Education

An overarching project goal was to support the integration of research and education in the curriculum project. Authentic research experiences for students are brought into the formal teaching lab, a sound pedagogical practice (Lopatto 2008). Faculty research at small colleges is more sustainable when there are synergies between the faculty member's teaching and research agenda and students from the formal lab can move into a research lab with relevant skills and motivation. While many aspects of our genomics education consortium are aligned with other national models, our emphasis on supporting faculty in integrating genomics into their existing research and curriculum required a flexible, grassroots approach in order to address a variety of organisms and curriculum structures.

In our model, faculty are supported in learning about the methods and principles of genomics and bioinformatics, as well as general principles of curriculum design. However, they select the specific biology content area in which they wish to focus their work. This model contrasts with the more centralized projects that introduce genomics around a specific organism or set of tools. While it poses challenges in assisting faculty with a wide range of data analysis tools, it has a number of positive features. First, our goal is to keep the biological questions at the center and to use genomics tools to address the questions. Using a faculty member's expertise enhances the quality and depth of questions that can be addressed. While some colleges develop specific courses in genomics, others are choosing to integrate genomics tools throughout the curriculum. Second, building on the expertise of a range of participants produces curricula relevant to many different courses in the undergraduate curriculum, including introductory biology. Third, the rapid-fire advances in genomics and requisite conceptual change required to ask questions at the scale of whole genomes can present a substantial barrier to mid-career faculty with well-established teaching and research programs. Working within the context of the faculty member's biological expertise emphasizes the value they bring to the curriculum development work and builds the confidence necessary to jump into a conceptually new area. The value of this strategy plays out not only in the classroom, but also in empowering faculty to integrate new genomics approaches into their research program. Anecdotally, a participant learned about a resource for modeling protein structure during one of our workshops and literally spent the evening adding an entirely new section to a research paper she was preparing.

E. A Workshop Series

A relatively unique feature of this initiative was the use of a series of workshops supporting introduction of genomics and pedagogic concepts, design and development, and implementation and assessment of curriculum materials over the course of three years. Many of the participants initially met at the Columbia University Genome Center when Lynn Caporale, then Associate Director of the Center, obtained Schering-Plough funding to establish a consortium of undergraduate faculty who would use either Illumina or 454 generated sequences of non-model organisms to integrate authentic research into introductory biology laboratories. Although Columbia was unable to move forward as the consortial sequencing center, the participants developed a coherence and mission that led to the Teagle Fresh Thinking award and three summers of workshops beyond the Columbia meetings. The initial plan was for two summer workshops, but the participants were so engaged that they lobbied the core group to find support for a third summer. This longitudinal design allowed a strong supportive community to form and share its expertise. The project leaders were able to learn about the strengths and needs of the group and adapt the workshop design to effectively support this specific set of individuals. Most importantly, a multi year approach was necessary given the scale of work. Mastering genomics concepts, data collection and analysis tools, designing effective assignments and developing skill in assessment required multiple sessions separated by time to reflect, research, and experiment pedagogically. This was clear from the outset and thus, an iterative, multi-workshop model was built into the project design from its inception.

F. Integrated Assessment

Assessment was a key feature of this project throughout, including both assessment of individual I^{3}Us and assessment of the overall faculty development effort. Ross Nehm, an assessment expert from The Ohio State University, worked with the core team and the participants throughout the funding period. Assessment workshops and consultations for participants were built into the model and the "Teaching Activities Form" prompted developers to include assessment. Faculty learned about assessment tools and the process of submitting assessment plans to Institutional Review Boards (IRBs). The integration of a unique web interface (www.serc.carleton.edu/genomics) that captured the workshops and activity development of faculty in real time provided a rich source for assessment as well. The unintended consequences of our assessment component on faculty development relative to both incorporating assessments and using research on learning are discussed later in this report.

IV. Implementation and Products

The Teagle working group held curricular development workshops during the summers of 2007, 2008, and 2009. As illustrated by the meeting program and resources on our website (http://serc.carleton.edu/genomics/index.html; Fig. 2), we brought together faculty with a breadth of experience and interests to learn from each other and specifically to develop curriculum within a common, pedagogically sound context. A pre-meeting survey was administered six months before the workshop so the planning committee could tailor the meeting to the needs and backgrounds of the participants (Appendix 1). An additional survey that included Likert-scale questions about participants' genomics teaching perspectives and experiences (Appendix 2) was administered at the beginning and end of each of the three workshops.

A. First Workshop

Twenty-nine participants in the summer 2007 workshop represented 14 colleges, including several invited speakers, learned about successful pedagogical and assessment strategies for teaching research-based genomics (e.g., http://serc.carleton.edu/files/genomics/workshop07/pedagogy_assessment.ppt; http://serc.carleton.edu/files/genomics/workshop07/ross.ppt), and established a framework for developing inquiry-based genomic curricula. The workshop concluded with a tour of the Columbia Genome Sequencing Center.

Teaching Big Science at Small Colleges: a Genomics Collaboration

The field of genomics informs some of the most pressing issues of our time: stem cell biology, transgenic agriculture, and cancer research. It is essential that liberal arts colleges educate our students to address genome-level questions. Barnard, Carleton, Vassar and Williams Colleges have been awarded a three-year grant from the Teagle Foundation to advance genomic curricula within liberal arts colleges.

- **Development of new genomics curriculum:** The first goal of this initiative is to advance genomics pedagogy through the development of inquiry-based integrated instructional units (I^{3}U). These instructional units can utilize a range of inquiry-based approaches, will allow instructors to integrate student learning from and within the modules into the flow of instruction, and otherwise follow the instructional design principles articulated in America's Lab Report (National Academy Press, 2005). We are calling on the faculty of schools within the Columbia Genome Consortium (CGC), first assembled by Lynn Caporale of the Columbia University Genome Center, to develop these modules.
- **Dissemination of curriculum:** The second goal of this project is to disseminate curricular models(on a dedicated website and in a teaching guide) about these curricular models to other colleges for their use and adaptation. Through the interactive website, we can exchange ideas and forge educational and research collaborations to elevate our ability to bring "big science" to our small schools.

Figure 2. Screenshot of the project homepage.

The full workshop program and a complete set of Powerpoint presentations from 2007 are available at http://serc.carleton.edu/genomics/workshop07/program.html. At the workshop, participants worked in small groups to design four new instructional modules. One of these, on microbial diversity in soil, now forms the basis for a multi-week course lab at Williams and has also been implemented at Vassar. A second, which integrates anatomical and genomics tools to study nervous system evolution, was expanded into a full I^{3}U by a team from Vassar and Whitman colleges and implemented at both colleges. Each of the four model I^{3}Us were designed within the framework we had established, using an online form provided by SERC on our project website to facilitate concrete definition of learning goals, appropriate course-level context, teaching plan, and assessment plan (Appendix 3). Pre- and post-workshop assessment surveys documented substantial gains in 10 of our 11 workshop goals (http://serc.carleton.edu/genomics/workshop07/goals.html), and open-ended responses indicated that the workshop was quite successful. Based on their experiences at the first workshop, four individuals and four teams of participants submitted proposals for summer stipends and supply money to develop I^{3}Us (see Appendix 4 for the request for proposals form).

B. Second Workshop

A second workshop, held at Williams in July 2008 (http://serc.carleton.edu/genomics/workshop08/index.html), provided training in web-based computational resources used in genomics and bioinformatics research and teaching, and served as a forum for the stipend recipients to help each other in their wet-lab and/or computational development efforts. To address gaps in participants' knowledge base, three experts in the tools/resources identified in our surveys as most desirable to our stipend recipients presented hands-on workshops on specific tools. Several core members of the Teagle project team also provided training within their areas of expertise. Sessions on assessment and submitting proposed assessments to IRBs were included. Gane Ka-Shu Wong, who holds an endowed chair in

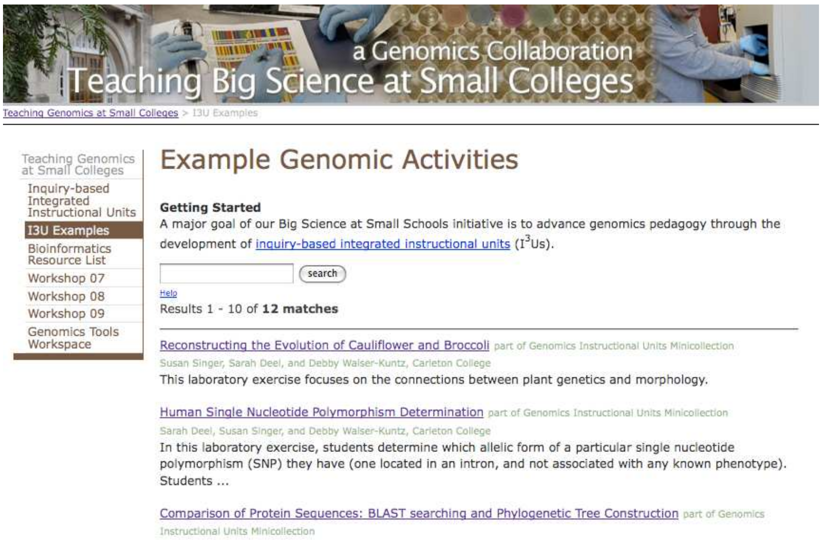
Biosystems Informatics at the University of Alberta and is associate director of the Beijing Genomics Institute (BGI), and his colleague Paul Lu, Professor of Computer Science at Alberta, joined us to explore ways that our small college projects could become a paradigm for the bioinformatics community for open-source development of genome-specific annotation tools.

C. Third Workshop

During the 2008-2009 academic year, the new instructional modules were implemented and assessed by their developers. Assessments were developed with assistance from assessment consultant Ross Nehm during the second workshop and throughout subsequent year. After implementation of the I^3U in the classroom, each faculty member filled out a reflections form (appendix 5) with their reflections on the effectiveness of the activity. Assessment results were discussed and additional plans for future assessment developed during the third workshop. The summer 2009 workshop (http://serc.carleton.edu/genomics/workshop09/index.html) provided a venue for developers to present their I^3Us, receive feedback and finalize the web-based presentations of their I^3Us. Each I^3U was presented formally to the group and discussed extensively. Each team also received feedback on the I^3U cover sheet and the effectiveness with which it presented the I^3U for use by other faculty. Time was provided for the teams to make changes to the I^3U and cover sheet during the workshop. The resulting products were reviewed a final time, final changes were made, and the activities were made public on the website. Final assessments of the overall project and time for reflection were built into the meeting schedule.

D. Website

One of the main products of this project is the “A Genomics Collaboration: Teaching Big Science at Small Colleges” website. This website includes a description of the I^3U framework we have established (http://serc.carleton.edu/genomics/i3u/index.html) and the final I^3Us (Fig. 3). The website also provides links to on-line assessment and pedagogical resources (http://serc.carleton.edu/genomics/workshop07/serclinks.html); all presentations from all three workshops as powerpoint slideshows; pre- and post-workshop content and logistical support including registration information, suggested readings provided by each workshop leader, and participants lists (also connected via a list-serve); and forms to upload documents or provide a link to a useful bioinformatics resource. Tools used to assess the overall project are included in the appendices of this report. Workshop participants and outside leaders reported high satisfaction with the level of organization provided by this website and its ease of use.



Example Genomic Activities

Getting Started
A major goal of our Big Science at Small Schools initiative is to advance genomics pedagogy through the development of inquiry-based integrated instructional units (I^3Us).

Results 1 - 10 of **12 matches**

Reconstructing the Evolution of Cauliflower and Broccoli part of Genomics Instructional Units Minicollection
Susan Singer, Sarah Deel, and Debby Walser-Kuntz, Carleton College
This laboratory exercise focuses on the connections between plant genetics and morphology.

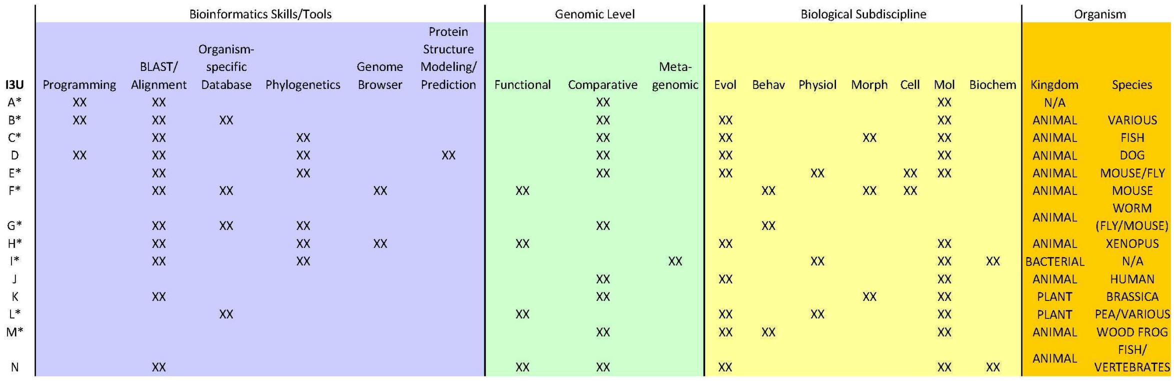
Human Single Nucleotide Polymorphism Determination part of Genomics Instructional Units Minicollection
Sarah Deel, Susan Singer, and Debby Walser-Kuntz, Carleton College
In this laboratory exercise, students determine which allelic form of a particular single nucleotide polymorphism (SNP) they have (one located in an intron, and not associated with any known phenotype). Students ...

Comparison of Protein Sequences: BLAST searching and Phylogenetic Tree Construction part of Genomics Instructional Units Minicollection

Figure 3. Screenshot of a page from the collection of I^3Us.

E. Inquiry-Based, Integrated, Instructional Units (I^3Us)

The curricular products resulting from this project were the collection of genomics I^3Us that are publicly accessible through the website. A description of the I^3Us that will be available on-line can be found in Table 1. The project website is supporting teaching of genomics beyond the workshop participants. In 2008, the website was visited by more than 7,500 users who saw on average 4.5 pages. The most heavily visited section of the site was the collection of I^3Us with over 5,500 visitors. We anticipate an increase in use as that collection has now increased from 4 to 12 examples. Just one anecdotal piece of evidence for the resource's value came from Trish More, a faculty member at the University of Exeter in the UK, who is adopting two of the I^3U modules in her courses and wrote, "The website and the activities were an absolute eye-opener in terms of what one could do with students in this area. For example, I was unaware of the Student Interface to the Biology Workbench. I will, of course, acknowledge both the authors of the activities and the Teaching Genomics at Small Colleges website. But I thought you might appreciate hearing that the project has reached 'across the pond'."



	Bioinformatics Skills/Tools						Genomic Level			Biological Subdiscipline							Organism	
I3U	Programming	BLAST/ Alignment	Organism-specific Database	Phylogenetics	Genome Browser	Protein Structure Modeling/ Prediction	Functional	Comparative	Meta-genomic	Evol	Behav	Physiol	Morph	Cell	Mol	Biochem	Kingdom	Species
A*	XX	XX						XX							XX		N/A	
B*	XX	XX	XX					XX		XX					XX		ANIMAL	VARIOUS
C*		XX		XX				XX		XX			XX		XX		ANIMAL	FISH
D	XX	XX		XX		XX		XX		XX					XX		ANIMAL	DOG
E*		XX		XX				XX		XX		XX		XX	XX		ANIMAL	MOUSE/FLY
F*		XX	XX		XX		XX				XX		XX	XX			ANIMAL	MOUSE
G*		XX	XX	XX				XX			XX						ANIMAL	WORM (FLY/MOUSE)
H*		XX		XX	XX		XX			XX					XX		ANIMAL	XENOPUS
I*		XX		XX					XX			XX			XX	XX	BACTERIAL	N/A
J								XX		XX					XX		ANIMAL	HUMAN
K		XX						XX					XX		XX		PLANT	BRASSICA
L*			XX				XX			XX		XX			XX		PLANT	PEA/VARIOUS
M*								XX		XX	XX				XX		ANIMAL	WOOD FROG
N		XX					XX	XX		XX					XX	XX	ANIMAL	FISH/ VERTEBRATES

A: Constructing and using a PAM-style scoring matrix (Eliot Bush, Harvey Mudd College)
B: Modeling Molecular Evolution (Marc Smith/JodiSchwarz, Vassar College)
C: Phylogenetic Analysis of Bony Fishes: Morphological and mtDNA Sequence Comparisons (Erica Crespi, Vassar College)
D: Comparison of a Highly Polymorphic Olfactory Receptor Gene Subfamily in Genetically Diverse Dog Breeds (Lois Banta/Norm Bell, Williams Colege)
E: Integrative Activities to Study the Evolution of Nervous System Function (Ginger Withers/Chris Wallace, Whitman College)
F: Behavior, Neuroanatomy, Genomics: What Can We Learn from Mouse Mutants? (Carol Ann Paul/Ginny Quinan, Wellesley College)
G: Expression of Gerontogenes in Neurons: A Comparative Genomic Approach to Studying the Role of the Nervous System in Lifespan/Aging (Kate Sussman, Vassar College)
H: Molecular Evolution of Gene Families (Cara Constance, Hiram College)
I: Metagenomic Analysis of Winogradsky Columns (David Esteban/Tebby Collins/Lois Banta, Vassar/Williams Colleges)
J: Human Single Nucleotide Polymorphism Determination (Sarah Deel/Susan Singer/Debby Walser-Kuntz, Carleton College)
K: Reconstructing the Evolution of Broccoli and Cauliflower (Susan Singer/Sarah Deel/ Debby Walser-Kuntz, Carleton College)
L: Exploring the Chamaecrista fasciculata Gene Space (Susan Singer, Carleton College)
M: Local Population Structure and Behavior of the Wood Frog Rana sylvatica (Derek Dean, Williams College)
N: Comparison of Cytochrome P450 Sequences, Biomarkers for Environmental Pollutant Exposure (Wade Powell, Kenyon College)
* Indicates I3U developed with funding provided by this project

Table 1. Pedagogical attributes (bioinformatic skills taught, genomic level of analysis, and scale of biological organization) of I3Us to be disseminated on project website

V. Lessons Learned for Faculty Development

The project design described above was successful in meeting each of our major goals:

1) Supporting faculty learning about genomics.
2) Supporting faculty in developing curriculum and teaching materials.
3) Preparing faculty to evaluate the efficacy of their genomics innovations.

Specifically, faculty members, including four participants with no previous background in genomics, were successful in learning about genomics generally, adapting this knowledge to support integration in existing courses, and designing and assessing new I^{3}Us.

Faculty self-evaluations of their I^{3}Us indicated that they perceived their I^{3}Us as effective or very effective in supporting students in meeting their learning goals. Six reported that nearly all students in their class had achieved the learning goals, two reported that between 50% and nearly all achieved their goals, and one reported that 50% had achieved the goals. These data suggest that participants received the support needed to enter fully into teaching genomics. Further, faculty self-report data indicated that the pedagogy employed in the I^{3}Us reflects the design principles and other best practices in teaching discussed in the workshops. In specific seven of nine scored their activities as encouraging student interest and attention to a high extent, including opportunities for students to reflect, discuss, and synthesize, and provided opportunities for students to confirm their understanding. All nine scored their activities as requiring students to integrate ideas and information from different sources. Finally, seven of eight participants indicated that they either already have used I^{3}U developed by others or will do so in the future. Thus in aggregate, the program design succeeded in supporting the entre of new faculty into teaching genomics, the development and testing of new materials, and the development of a product and culture that supports use of these materials by other faculty.

A. Key Elements in the Faculty Development Model Supporting Success

1. Development of a Learning Community or Community of Practice

A predominant theme in the end-of-workshop evaluations was the importance of the workshop in developing a network or community that supported learning and development of the I^{3}Us. Prior to participation in the first workshop, only one participant reported feeling part of a community of genomics educators from liberal arts colleges. Following this workshop 15 of 19 respondents agreed or strongly agreed with this statement. Eight of 19 respondents specifically mentioned the value of meeting and talking with colleagues in their description of the most valuable aspect of the workshop. Six respondents discussed the value of examples from others' teaching as the most valuable aspect of the workshop. In the second year, seven of nine respondents commented on the importance of the community and its communications in providing expertise, feedback and momentum. Several suggested strategies for ensuring that this support continue through the academic year. As discussed above, participants requested a third workshop for sharing results and receiving feedback on their work, affirming the value of these face-to-face encounters.

A central aspect of our model was sharing expertise within the group. End of workshop evaluations in all three years highlighted these examples as a successful and important part of the workshop programming. As described above, the group contained diverse expertise that supported incorporation of genomics in a wide variety of curricula with diverse foci. Different members of the group became known as experts in different areas and were called on to share this expertise during the academic year during small group or individual email communication. Communications between workshops took place primarily by personal email between pairs or small groups of participants. This mechanism was viewed as robust and efficient. Participants reported knowing who they wanted to contact and appeared comfortable making those contacts within the group. In some cases faculty visited between institutions. Acquiring specific information through consultation with these individual experts was mentioned in both 2008 and 2009 as a valuable aspect of workshop programming and essential to overcoming development challenges.

End of workshop evaluations consistently reported that learning about genomics concepts and data analysis, as well as assessment, were challenges to creating the I^{3}Us and that these were primary areas of learning during the workshops. Learning about activity design, scaffolding and other pedagogic techniques was also important. Thus the workshop programs appear to have been well designed to facilitate the exchange of critical expertise within the group.

Three of eight participants reported that a lack of confidence in working with genomics data and data analysis tools, or in teaching genomics was a primary challenge and attributed development of this confidence to the project. Participant comments in other years further showed that confidence was a barrier and that the program was effective in building this confidence. Our observations suggest that this confidence came in large part from descriptions of peers' programs, and discussions of each individual's I^{3}U plan. These discussions were a direct result of our collaborative learning model, and this finding is well aligned with other research on the impact of communities of practice.

2. External Expertise

A second critical feature of the professional development model was the inclusion of an assessment expert who provided one-on-one advice to participants throughout the development of the instructional unit. Details on the assessment components of our work are presented in a separate section later in this report. The focus on assessment, which is critical to our ability to evaluate the effectiveness of the instructional units, was initiated at the first workshop through a presentation by the assessment expert. In addition to a presentation at the second workshop, the assessment expert met with each development team to help them articulate their goals and define their assessment plan. During the subsequent year of development and testing, the assessment expert provided on-going advice and assistance by email. Participants' comments indicate that they went from not knowing much about assessment to valuing its role. Every project implemented an assessment that appropriately measured students success in learning from the instructional unit . Some groups were able to design and implement instruments that provided assessment data that could potentially be published in peer-reviewed journals. Participants discussed both the challenges of designing and implementing the assessments, and the value of the assessment expert during the final discussion of the project. They specifically endorsed development of a website sharing some of the instruments and lessons learned with others to ease this challenge.

3. Making Effective Use of the Website to Support Authoring, Sharing, Review and Dissemination

The I^{3}U pages developed for the website were an integral part of the professional development programming. The cover sheets (appendix 3) required participants to present their I^{3}U in a formalized and consistent way so that other faculty could learn from their experience. The participants reported in end of workshop conversations that the discipline of creating, reviewing and revising the I^{3}U pages for the website supported them in learning more about effective pedagogy. These products were then used to support presentation of the, the rational for design and the mechanics of implementation, and discussion of the strengths and weaknesses of the activity as implemented. This process was used in oral presentations at the first workshop to introduce a range of approaches to teaching genomics, and at the third workshop to review the completed I^{3}Us. Neither the leaders nor the participants anticipated in advance that they would learn so much about teaching. The opportunity to closely review the work of other faculty during the workshops was critical in supporting this learning.

4. A Protracted Workshop Series

As described above, the project was implemented as a series of workshops. Participants left the first workshop with an understanding of I^{3}U structure and an opportunity to apply for funding to support their work on development and testing. Seven of 13 participants who were not speakers left the workshop with specific plans to expand their teaching of genomics. Two of these participants planned to develop an I^{3}U. Four participants specifically indicated that they needed time to learn and to develop expertise before they could successfully create the module. This support was provided during the second workshop. End of workshop evaluations indicated that the workshop was successful in developing knowledge of and comfort with a suite of data analysis tools. In addition, participants commented on the importance of consultations, presentations, discussion and sharing in furthering their ability to design the I^{3}U. As described above, at this point, participants were relying on the project and their peers for support to motivate completion of the I^{3}U. Comments following the third workshop indicate the value of feedback after a trial run in the classroom in fostering pedagogic improvements and supporting design of improved assessments. End of project comments, however, indicate that assessment remained challenging to most participants. Five of nine participants self-evaluated their activities as only somewhat successful in engaging their students in data analysis and synthesis.

These data demonstrate that successful design of activities and associated assessments is challenging. Workshop participants appreciated the iterative approach to design and development with opportunities for feedback in subsequent summers. This approach provided needed time for participants to gain experience with genomics concepts, data analysis tools, and assessment strategies to successfully develop their I^3Us. It also allowed for iterative development including contemplation or trial of new genomics ideas during instruction following the first workshop; design of full activities after the second workshop; and enhancement of teaching materials published on the website during the third workshop. While in the end, there were still requests for more assistance and ideas for further refinements, participants left substantially empowered to move forward with their own learning and in touch with a community of supportive peers.

5. Supporting Faculty Learning about Genomics

At the first workshop held in 2007, most of the participants said that they did not have a clear sense of what defined genomics as an emerging field, and thus did not know how to incorporate genomics into their courses. After listening to speakers who have pioneered genomics education at research universities or other small colleges, it became clear that what distinguishes genomics from how genetics was taught in the pre-genomic era is that genomic research questions focus on examining the function, structure, and evolution of many genes within and among entire genomes. This increase in scale not only requires a significant change in mindset needed to generate research questions and approaches; it also requires the use of computational and bioinformatics tools to analyze the volume of data. Thus, the use of bioinformatics tools is inextricably linked to asking genomic-level questions.

Most of the participants did not have any training in bioinformatics, which was a primary reason for not already teaching a genomics module for their courses. It is very difficult for novice faculty to find and utilize tools and databases, because there is so little standardization among tools, which are dispersed over the web and are constantly undergoing changes. This moving target makes it difficult for novices to find, navigate, and explore tools, and requires constant surveillance of the tools as the course is being taught, to catch changes to websites, or versions of databases. Thus, the explicit goal of many of the faculty for joining the Teagle project was to gain experience and training in bioinformatics. Participants received hands-on training primarily during Workshop 2008, in which they spent three intensive days in several short workshops, becoming familiar with bioinformatic tools for finding sequences, predicting the structure of proteins, visualizing and comparing genomes, and constructing phylogenetic trees. Participants commented that “It was terrific actually using the tools during the workshop,” and when asked what the most useful aspect of the workshop was, the highest number of comments indicated that the hands-on training in the tools was highly valuable in gaining a comfort level and familiarity.

One of the biggest lessons learned through our project was the level and amount of training that faculty need to feel comfortable adopting bioinformatics approaches. It was clear that the 2008 workshop was just a first step, as the participants left the workshop feeling that they would benefit from additional training and support. While everyone left with ideas about which tools they might want to utilize for their I^3U, everyone needed significantly more time to explore the tools and develop self-sufficiency. They accomplished this primarily by maintaining communication with at least one of the presenters over the course of the year, to obtain more training and to get ideas. We also found that participants gravitated towards utilizing the tools that they had been exposed to during the workshops, rather than exploring new tools.

Although everyone started at a different level of bioinformatics proficiency, every participant made progress. The people who came in with no prior experience were able to identify tools that they would consider using for their I^{3}U, and the more experienced instructors discovered new tools or approaches that they could adapt for their courses.

B. Summary

In sum, the primary challenges faced by participants were both intellectual and emotional. Participants began the project acutely aware that teaching genomics is both important and challenging. Many lacked expertise needed to analyze sequence data or design wet labs and were overwhelmed by the array of possible tools, the need to understand which tools were useful in which scientific contexts, and the challenges of mastering their user interfaces. Some lacked confidence in beginning to understand this large field and its tools, others were concerned about teaching material with which they had little previous scientific experience. A majority had little experience with assessment and had difficulty designing assessments that would lead to rigorous demonstration of learning. Lastly, most were isolated from colleagues who shared their interest or had the needed expertise to support their initial learning in this area.

In the minds of participants the project was successful in meeting these challenges by providing access to expertise in genomics, genomics data analysis, pedagogy, and assessment, and to a supportive learning community that shared its classroom teaching experience and genomics expertise. Complementing programming that increased their general knowledge of genomics and strategies for genomics instruction, participants found consultation with individuals and discussions focused on their own specific activities of value and learned from discussion of others' activities. Lastly, they benefited extensively from on-line resources including the I^{3}U examples and on-line data analysis tools, as well as the structured form for describing their I^{3}U. Consistent with our findings regarding the value of several other project elements, they recommend further development of assessment resources specifically aimed at assessing genomics learning.

VI. Lessons Learned about Integrating Genomics into Undergraduate Curricula

Although we focused our pool of project participants on instructors at liberal arts colleges, we had a diverse representation of teaching and research expertise from which our collection of I^3Us were generated. In addition, there was a diverse representation of biology departmental curricula across institutions. The commonalities as well as the unique experiences of the participants have given us tremendous insight about how students learn genomics skills and concepts, and how instructors learn how to teach genomics. In the following sections, we summarize our findings in these areas.

A. Incorporating Genomics within a Single Biology Course

Most participants designed genomics I^3Us within the context of an existing biology course within their institution's curriculum (eight of ten I^3Us; the other two were incorporated into interdisciplinary Biology/Computer Science classes). Adding genomics within the context of courses such as microbiology, neurobiology or cell biology offered the opportunity for students to integrate across biological scales in their thinking. The I^3Us were a powerful mechanism through which students could think about how genetics and morphology, behavior, or community structure are related. Furthermore, this approach presents genomics not as a biological discipline unto itself, but rather, as an approach to asking questions within each of these fields of research. One of the costs to this integration is that it takes time away from teaching other content within each of these traditional disciplines. All participants acknowledged that incorporating a multi-week, inquiry-based genomics module into their course reduced the amount of time spent on doing more traditional laboratories that teach skills particular to each field. Not only does this reduce content, but we also found that spending time on the I^3Us sometimes conflicts with student expectations of what kind of instruction they would be receiving when taking these courses, therefore increasing student dissatisfaction. Overall, however, project participants thought that the interdisciplinary and integrative aspects of the genomics I^3Us were important models for preparing students to contribute to cutting-edge biological research. In addition, many students expressed appreciation for the interdisciplinary nature of the modules, as they realized that "this is the future of science."

All of the I^3Us designed within pre-existing, traditional biology courses were multi-week modules that successfully incorporated several modes of learning, including lectures, computer-based labs, and wet-labs. There was broad consensus that this approach was highly motivational and that students found these modules exciting and relevant. Students had a strong sense that they were "doing science" and gained a greater appreciation for the nature of scientific research. Some participants wished there had been more time to explore wet-lab genomics activities and indicated that more hands-on experience in wet-lab development during the workshops would have been helpful in their I^3U development. Indeed, we scheduled time for developing computer-based approaches and hands-on learning of computer software packages during the workshops, but we did not include wet-lab learning sessions for logistical and financial reasons.

B. Incorporating Genomics across Multiple Courses

Three of the participating institutions, Vassar College, Hiram College, and Williams College, have multiple instructors who incorporate genomics-related topics and I^{3}Us in multiple classes within the biology curriculum. There were definitely advantages experienced by the students and the instructors at these institutions, but also some challenges. One advantage is that learning is enhanced when there is iterative instruction, which gives students the opportunity to repeat skills and review concepts learned in prior courses, and add new skills, concepts and applications in subsequent courses. Generally, we found that, whether it is the instructor or the student, learning how to use bioinformatic tools and genomic-level ideas requires 1) multiple exposures and 2) incremental accumulation of skills from simple to more complex.

Vassar College incorporates genomics at all levels of the curriculum. A bioinformatics module to introduce students to basic bioinformatics tools to investigate genetic function (e.g., use of NCBI databases, BLAST searches) is included in the Introduction to Biological Investigation (100-level) course that all biology majors take. At the 200-level, in addition to a formal Genomics course, genomics I^{3}Us were designed as part of the Teagle initiative to be incorporated into the Microbiology, Introduction to Neurobiology, and Comparative Anatomy courses; each I^{3}U asked students to use the skills they had learned in Introductory Biology, then added new computer-based tools for more specific analyses depending the research questions of each course. At the advanced level, Vassar offers a Bioinformatics course which is open to students with either a Biology or a Computer Science background, and which focuses on collaborative learning and genomics research.

When assessment tools are coordinated among the instructors, student learning can be tracked as students proceed through the curriculum. For example, at Vassar, skills-based assessment questions were coordinated among the three instructors who designed I^{3}Us for their existing Biology courses. These faculty members found that although students came into the three 200-level I^{3}Us with introductory experience using bioinformatics tools (e.g., use of Genbank, Blast searching, sequence alignment), students did not feel confident in their use of them. After the I^{3}U experience, however, 84% (± 8.7 %) of students reported to be confident in their ability to use these tools. In addition, exposure to the use of bioinformatics tools may have affected the students' attitude about the importance of these tools in biological research, as 61% (± 7.0 %) of students said that the use of bioinformatics/genomic tools increased their interest in biological research and 78% (± 1.8 %) indicated that they would take another course that included genomics or bioinformatics. Finally, 87% (± 3.8%) of students agreed that the combination of computers and laboratory experiences increased their learning of the biological topic presented within the I^{3}U. Comments that genomics and bioinformatics skills learned either took away from their ability to learn more about the overarching topic of the course or was overrepresented in the courses within the curriculum were rare among the students surveyed.

Another advantage of offering multiple courses that incorporate genomics within a biology curriculum is that students learn more diverse genomics and bioinformatics skills. At Hiram College, there is a two-course molecular and cellular biology sequence that incorporates gene annotation of prokaryotic genomes in one course, and a genomics I^{3}U within a second course in eukaryotic cell biology. At Williams College, the introductory biology course teaches students how to use phylogenetic analysis tools, and students build on those skills in the upper-level, lab-intensive Bioinformatics, Genomics, and Proteomics (BiGP) capstone course as well as in the upper-level Evolution elective. Lois Banta, who teaches the BiGP course, noted that "the students have often had a better grasp of phylogenetic estimation than I did, at least in the early years of my course, and I learned from them!" Williams also has a genomic tutorial course at the sophomore level that pairs two students and one faculty member for meetings each week, and this experience often sparks student excitement about genomics, thereby motivating students to enroll and setting the stage for the content in the BiGP course.

While offering a variety of genomic-based courses and learning experiences ultimately expands the breadth of genomics and bioinformatics instruction given to the students, there are challenges. First, many students may not transfer knowledge gained about genomics and bioinformatics from one course or module to another. Also, the tendency to assume topics are covered in other courses may result in the omission of important areas of instruction within a module. When these knowledge deficiencies present themselves in the classroom, the planned module may become disorganized or impromptu inclusion of the instruction may cause time to run out before a conclusion could be reached. Finally, if the connections and distinctions between the genomics modules/learning experiences are not explicitly expressed to the students, they can feel "genomics overload," and feel that they are missing out on time spent learning important aspects of the course they are taking because they are doing yet another "genomics lab" or "Blast search." Therefore, communication among faculty is of the utmost importance when incorporating multiple levels and types of genomics instruction (e.g., lecture-based, wet lab, computer lab) within a department curriculum so that instruction is most efficient and complementary for the students. It is also important to have effective assessment tools that sometimes need to be coordinated among instructors to understand which skills and concepts are mastered as students track through the curriculum. Ultimately, the coordination of genomics curricula is time consuming and may come at a cost to other teaching and research responsibilities of the instructor.

C. Incorporating Computing and Bioinformatics in the Biology Curriculum

Computational approaches are such a critical part of doing genomics research that the terms "genomics" and "bioinformatics" are often used interchangeably. As one person put it, her hope in attending the first Teagle workshop 2007 was to "Try to expand the bioinformatics/genomic material in lab." However, bringing bioinformatics into the undergraduate classroom is a challenge for Biology faculty, as the vast majority of students in biology-focused courses have never taken a computer science class, and are often intimidated by computer science. All the participants were eager to learn and adopt bioinformatic approaches into their I^{3}U, and the final I^{3}Us all contained a significant bioinformatic component. There was agreement that stand-alone bioinformatics activities in a laboratory course are usually not well received by the students because they do not connect the activity to a biological question that they find compelling. We found that most of the participants designed their I^{3}U so that the computational component was integrated into a larger biological context, in which the bioinformatic analysis supported and informed a larger question that was investigated using both computational and traditional lab-based activities, such as measuring behavior, physiology, or anatomy. There was general consensus that the integration of bioinformatics into a larger, integrated, question significantly enhanced students' appreciation for the bioinformatic skills, and also their ability to connect the work they were doing at the computer to the biology that they were studying. However, several participants also found that the computational components were still less engaging than the biological components and that students often felt overwhelmed while learning to navigate and understand the bioinformatic tools that they were using. Most of the faculty also felt that they needed significantly more training in bioinformatics themselves to be able to help students at the level that they would like to, as reflected in the following comments: "Would have liked more hands-on exercises on how to use tools." "Would have helped to have more programming/math people here." "Would still like to see more explicit use of genome-scale data not just Blast, bioinformatics tools."

D. Incorporating Genomics across Disciplines

Genomics is a highly interdisciplinary field, and one approach to teaching Genomics is embodied in the I^{3}Us developed to fit into existing biology courses, in which students learn to use bioinformatic tools to address biological questions. Another approach is to create an interdisciplinary framework, especially between Biology and Computer Science. This was undertaken for two of the I^{3}Us developed for the Teagle Project. At Vassar, an I^{3}U was designed to fit into a Vassar team-taught cross-department course between Biology and Computer Science, in which students brought their own expertise in these disciplines. The collaborative research approach was highly appealing to these upper level students; the biology students left feeling empowered by their ability to design their own bioinformatic tools, and the computer science students felt empowered by discovering the rich set of biological questions that their training and background allowed them to address. While this approach was very successful, many institutions cannot support team-taught classes. Furthermore, several participants indicated that they had sought out potential teaching collaborators from other departments, but could not identify someone with the appropriate background or interests.

Another interdisciplinary approach is to train students in both biological and computational sciences simultaneously, thereby fostering the development of a new breed of computational biologists. At Harvey Mudd College, students in "Computational Approaches to the Genome" had acquired both a Biology and Computer Science background before entering the class. However, few faculty are able to support dual training of students, as few Biology faculty have any training in computer science themselves. One of the strengths of the Teagle workshops was providing targeted training to faculty who lack training in Computer Science so that they could gain a toe-hold into the bioinformatic tools that were most appropriate to their I^{3}U questions.

E. Incorporating Genomics across Institutions

Three of the project participants were neurobiologists (Vassar, Whitman, and Wellesley), and although they prepared I^{3}Us for very different courses, levels, and learning outcomes, the learning experience of these instructors was enhanced by their interaction at the Teagle Workshops themselves. However, interactions among these instructors between meetings was minimal, as they did not email or use the SERC listserv to communicate as they were planning and implementing their modules. The group coalesced at the final meeting, however, when I^{3}U implementation presentations were made, and they all indicated that they were interested in using or adapting each other's I^{3}U into their own teaching. This dissemination and transferability of modules between institutions was one of the major goals of this project, and the building of this community within the Teagle project may yield the most likely cross-institution usage of the resulting I^{3}Us. These instructors also plan to present their I^{3}Us as posters at the annual Neuroscience meeting, and plan to publish their I^{3}Us in a neuroscience-focused pedagogy journal.

F. Scaling in Genomics—A Conceptual Challenge

We found that most participants designed projects around similar themes: the evolution and function of a single gene or gene family in one or more species. In so doing, the participants made use of genome-scale databases, such as GenBank or organism-specific Genome databases, but restricted their activities to 1) searching through large genome databases to identify genes-of-interest, 2) constructing phylogenetic trees from alignments of multiple sequences, and 3) using bioinformatic tools to predict aspects of function or structure of individual genes. However, the nature of the questions asked were not at the scale of entire genomes or multiple genomes. Responses of the participants suggest that this was in part due to 1) comfort level with single gene approaches, given the research questions and the extent of training of the participants, 2) unfamiliarity with options for wet-lab approaches for whole genome questions, and 3) tendency to stick with the tools/approaches that were presented by the core group and the invited speakers. Because evolution can be applied in almost every biological context, scaling questions toward phylogenetics-level questions (inter-taxon comparisons of genes) became a component in some I^{3}Us. While this required the use of bioinformatic tools and databases, and asked students to think on a larger scale than a single organism, it did not reach the scale of comparative genomics. Because most of the faculty who developed I^{3}Us were themselves becoming trained in bioinformatic methods, it is likely that faculty used a single-gene approach first, as a stepping stone toward developing higher level questions. Thus, the training workshop (Summer 2008) focused on the use of bioinformatic tools and faculty successfully incorporated these tools into their I^{3}Us. A next step for these faculty could be a workshop on thinking and developing questions at the scale of entire genomes.

Although many faculty came into the project hoping to develop genome-scale wet lab activities, especially microarray analysis, this was not realized in many of the projects. In part this may be due to both 1) the cost and 2) the amount of time required to perform microarray experiments. Most of the participants were highly committed to asking their students to think across biological scales of organization (from molecule to evolution/ecology), with each week of the module consisting of a lab activity at one of the levels (behavior, physiology, cell, molecular). Given the amount of time devoted to all these different scales, participants may not have been willing to devote several weeks to a microarray experiment.

G. Summing Up: The I^{3}U as a Multidimensional Learning Experience

A unique aspect of the genomics pedagogy advocated within this project is that we sought to teach genomics within the format of inquiry-based, integrated instructional units. We initially incorporated this pedagogical model because we followed the design principles outlined in America's Lab Report (National Academy Press, 2005) to achieve our goals. An exciting, albeit unintended, outcome of teaching genomics within the I^{3}U framework was that instructors guided student thinking and learning along three axes of integration that can be described as 1) scale of biological organization, 2) genetic scale, and 3) evolutionary scale (see Table 1). As discussed earlier, asking genomic-level questions within the context of traditional biological disciplines forced students to think across multiple levels of biological organization: from genes to cells to physiology/neurobiology to organisms (e.g., morphology or behavior) to communities and ecosystems. In addition, within genomics, we are challenged to ask biological questions that scale from a single gene approach to multi-gene (e.g., gene family) to genome-wide approaches. Finally, most modules also had components that asked questions about the evolution of genes, which enabled instructors to exploit bioinformatics tools to incorporate a phylogenetic perspective to the modules. Therefore, modules challenged students to think about how genes evolved among organisms from multiple populations of a species, or among multiple families, classes, phyla or kingdoms.

For many, adapting bioinformatics tools into their modules was more easily accomplished by asking phylogenetic questions rather than adapting tools that could be used to explore genome-level questions of gene function or structure. Why this trend arose is not known; perhaps the participants were trained within a single gene approach and were not familiar with genomic-level questions they could address with bioinformatics tools at the level of the courses they were teaching. Alternatively, evolutionary questions may have been more easily integrated within the design of these particular I^{3}Us. Regardless of the reason, the ultimate result is that the I^{3}Us developed within this genomics initiative gave students the opportunity to integrate concepts of genetics and evolution within the context of multiple biological disciplines. At the same time, the use of bioinformatics tools and databases expanded the complexity of the analyses performed by students to a level that is on par with those currently used by graduate students and scientists at research universities.

VII. Preparing Faculty to Evaluate the Efficacy of their Genomics Teaching Innovations

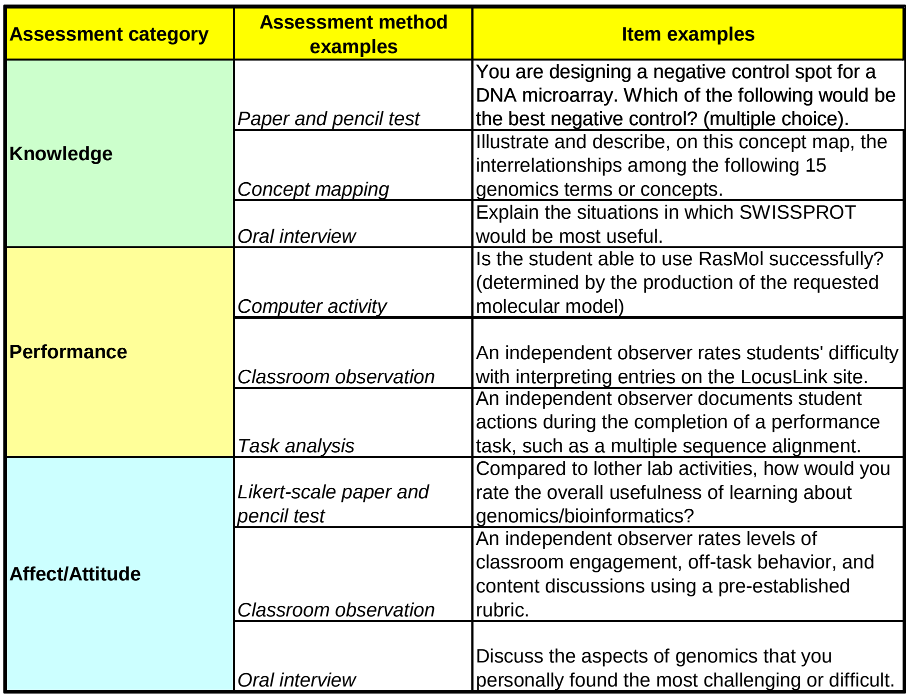
The overarching goal of our assessment work was to help prepare faculty to evaluate the efficacy of their genomics education innovations. The greatest challenge facing the Teagle genomics education consortium was that no robust assessment system—characterized by valid and reliable instruments evaluated by experts in education and psychometrics—existed to assess the efficacy of newly developed genomics and bioinformatics curricula. This situation is unsurprising given that genomics and bioinformatics are new and rapidly evolving scientific fields. Our project therefore required a novel solution to this assessment challenge.

In order to achieve our goal of improving genomics education in higher education, we needed to help faculty build assessment tools that they could then employ in order to assess the efficacy of their Teagle-funded genomics education innovations. Three activities were associated with building faculty expertise in science education assessment: (1) A professional development session for faculty participants that reviewed the basics of educational assessment and the types of tools that could be employed in assessment efforts; (2) Individualized consultations to help participants build their assessments; and (3) Individualized consultations with faculty to assist in the interpretation of assessment data derived from point (2) above. Each activity revealed important insights that may help others as they work to improve the quality of science teaching and learning in higher education.

A. Professional Development in Science Assessment

A professional development session was developed by consultant Nehm in order to provide Teagle faculty participants with an overview of educational assessment types and the diversity of assessment tools that could be employed in genomics education. The professional development session had two goals: expanding and diversifying faculty participants' perspectives on educational assessment and providing a "menu" of assessment options that could be matched to the disparate types of I^{3}Us being developed by the faculty. A basic outline of the assessment categories and methods that were emphasized in the session is illustrated in Table 2.

Table 2. The assessment framework provided to Teagle participants. Note that knowledge, performance (skills), and attitude categories were linked to particular assessment tools (such as paper and pencil tests, concept maps, and task analyses).



Assessment category	**Assessment method examples**	**Item examples**
Knowledge	*Paper and pencil test*	You are designing a negative control spot for a DNA microarray. Which of the following would be the best negative control? (multiple choice).
	Concept mapping	Illustrate and describe, on this concept map, the interrelationships among the following 15 genomics terms or concepts.
	Oral interview	Explain the situations in which SWISSPROT would be most useful.
Performance	*Computer activity*	Is the student able to use RasMol successfully? (determined by the production of the requested molecular model)
	Classroom observation	An independent observer rates students' difficulty with interpreting entries on the LocusLink site.
	Task analysis	An independent observer documents student actions during the completion of a performance task, such as a multiple sequence alignment.
Affect/Attitude	*Likert-scale paper and pencil test*	Compared to lother lab activities, how would you rate the overall usefulness of learning about genomics/bioinformatics?
	Classroom observation	An independent observer rates levels of classroom engagement, off-task behavior, and content discussions using a pre-established rubric.
	Oral interview	Discuss the aspects of genomics that you personally found the most challenging or difficult.

The SERC website was used as a resource for assessment tools as well as a repository of all professional development materials (http://serc.carleton.edu/NAGTWorkshops/assess/index.html). All of the faculty developing I^{3}Us were asked to use these resources, in combination with individualized assessment consultations, to include knowledge, performance (skill), and attitude measures as part of their "evaluation plans" and match appropriate assessment methods to these three categories. Thus, the professional development session was closely tied to the module development and evaluation task. All of the science faculty who were funded to develop I^{3}Us were provided with a minimum of one hour of individual professional development in assessment.

B. Evaluation of Faculty-Developed Genomics and Bioinformatics Assessments

Faculty-developed genomics assessments were evaluated using a mastery approach. This methodology was deemed appropriate given that other measures, such as gain scores (post-intervention vs. pre-intervention), would have been less meaningful because statistically significant gains on post-intervention measures would have been inevitable;

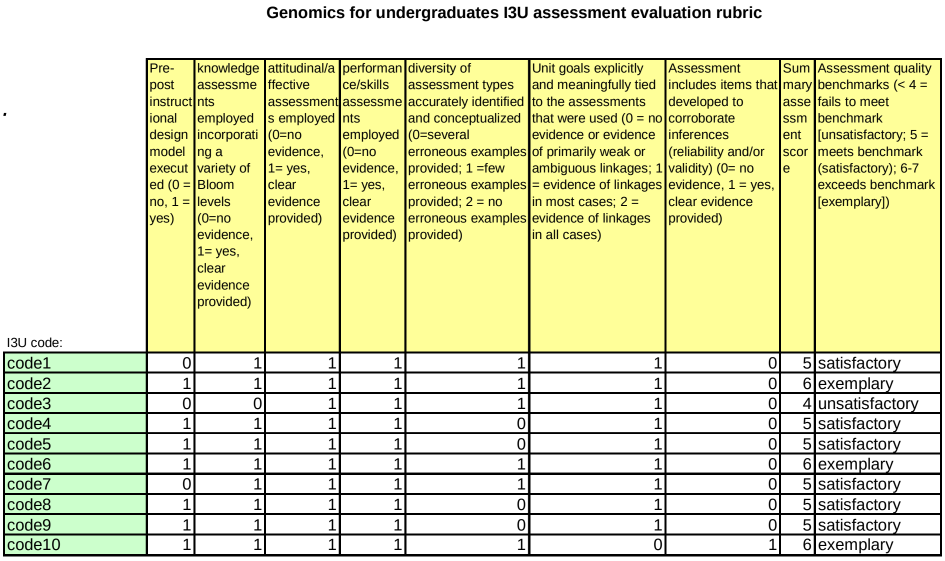
nearly all of the faculty began the “Big Science for Small Colleges” project with very little prior knowledge of assessment methods, tools, or concepts. For example, before the intervention few of the participating faculty had explicitly employed attitudinal and/or affective measures in their science courses, utilized pre-post test evaluation designs to measure instructional efficacy, or attempted to explicitly measure science performance task mastery. Thus, pre-post test designs to measure the impact of the Teagle-funded professional development work in genomics assessment would have guaranteed positive outcomes. In contrast, a ‘mastery’ evaluation approach permitted more meaningful, less biased, and more rigorous results because it allowed testing of whether faculty were able to achieve predetermined assessment quality benchmarks independent of prior knowledge.

We evaluated the I^{3}U genomics assessments relative to seven design features emphasized throughout the program: (1) Use of a pre-post test design; (2) incorporation of knowledge assessments at a variety of Bloom levels; (3) inclusion of attitudinal/affective measures about genomic science; (4) incorporation of performance or skill assessment measures; (5) accurate definition and conceptualization of knowledge, attitude, and performance variables; (6) explicit and meaningful connections between the learning goals and the assessment items; and (7) inclusion of items for use in corroborating assessment-derived inferences (e.g., reliability and validity). These seven assessment variables were reviewed for clarity and replicability, partitioned into categorical ordered states (e.g., 0 = unsuccessful task completion; 1 = successful task completion), and placed into a scoring rubric (Table 2). The rubric (containing these variables and states) was used to score the observable traits of the I^{3}U assessments (n = 10) delivered at the culmination of the Genomes for Undergraduates program. Incomplete and/or partially accurate evidence, while suggestive of mastery, was conservatively categorized as unsuccessful task achievement. Two sources of data were used to score faculty-generated genomics assessment tools: (1) I^{3}U postings on the SERC website and (2) an assessment attributes form (shown in Appendix 6).

In order to ensure consistent ratings and unbiased assessment scoring (using the rubric shown in Table 3), two trained raters (one involved in the professional development program and one not involved in the effort) independently scored the I^{3}Us. Composite scores (tabulated using the seven assessment mastery topics) were calculated for each of the ten I^{3}Us developed during this project and compared to the assessment mastery benchmarks (i.e., unsatisfactory [<4], satisfactory [5], exemplary [6-7], see Table 3).

Our analysis of the ten I^{3}Us produced composite scores ranging from four to seven; one genomics assessment failed to meet the satisfactory benchmark (composite score = 4), six assessments met the benchmark (score = 5), and three exceeded the mastery benchmark (score = 6). The lowest scores among all assessment features were located in category of “corroboratory inferences”; few faculty made explicit attempts to develop assessment items that could be used to corroborate response data and establish response reliability. The highest assessment scores occurred in the category of inclusion of attitudinal/affective measures. Considerable variability occurred in the category of assessment item recognition (e.g., performance vs. knowledge items; attitude vs. knowledge items). The majority of assessments included a pre-post test design and explicitly connected learning goals to assessment items. Overall, at the completion of the "Big Science for Small Colleges" program, the majority of faculty-produced genomics assessments were characterized as satisfactory or exemplary. Given the initial unfamiliarity of science assessment knowledge and abilities in faculty participants, this component of the program appears to have been successful. Nevertheless, further growth in overall assessment knowledge is possible and some aspects of assessment knowledge remain weak.

Table 3. Genomics for undergraduate I^{3}U assessment evaluation rubric



Genomics for undergraduates I3U assessment evaluation rubric

I3U code:	Pre-post instructional design model executed (0 = no, 1 = yes)	knowledge assessments employed incorporating a variety of Bloom levels (0=no evidence, 1= yes, clear evidence provided)	attitudinal/affective assessments employed (0=no evidence, 1= yes, clear evidence provided)	performance/skills assessments employed (0=no evidence, 1= yes, clear evidence provided)	diversity of assessment types accurately identified and conceptualized (0=several erroneous examples provided; 1 =few erroneous examples provided; 2 = no erroneous examples provided)	Unit goals explicitly and meaningfully tied to the assessments that were used (0 = no evidence or evidence of primarily weak or ambiguous linkages; 1 = evidence of linkages in most cases; 2 = evidence of linkages in all cases)	Assessment includes items that developed to corroborate inferences (reliability and/or validity) (0= no evidence, 1 = yes, clear evidence provided)	Summary assessment score	Assessment quality benchmarks (< 4 = fails to meet benchmark [unsatisfactory; 5 = meets benchmark (satisfactory); 6-7 exceeds benchmark [exemplary])
code1	0	1	1	1	1	1	0	5	satisfactory
code2	1	1	1	1	1	1	0	6	exemplary
code3	0	0	1	1	1	1	0	4	unsatisfactory
code4	1	1	1	1	0	1	0	5	satisfactory
code5	1	1	1	1	0	1	0	5	satisfactory
code6	1	1	1	1	1	1	0	6	exemplary
code7	0	1	1	1	1	1	0	5	satisfactory
code8	1	1	1	1	0	1	0	5	satisfactory
code9	1	1	1	1	0	1	0	5	satisfactory
code10	1	1	1	1	1	0	1	6	exemplary

C. Programmatic Assessment

Initially, no attempt was made to measure faculty participants' knowledge of assessment prior to the professional development session. In retrospect, this was a limitation of the programmatic assessment plan. Nevertheless, based on questions during the final session, and subsequent discussions and interactions with assessment consultant Nehm, it appeared that the science faculty who participated in the initial Teagle workshops had very limited educational assessment knowledge and skills. These knowledge limitations likely made it difficult for our programmatic assessment items (shown in Appendices 2 and 7) to accurately capture faculty *attitudes* toward assessment. Specifically, items attempting to capture faculty attitudes toward "assessment" were likely interpreted differently by each faculty member. Thus, faculty attitude measurement was likely conflated with individualized conceptualizations of what constituted “assessment”. As faculty learned more about assessment during the professional development activities and individualized consultation sessions (as our results from Table 3 suggest), it is likely that their conceptualizations of what “assessment” entailed changed. In other words, at the beginning of the workshop, faculty may have thought that they knew the basics of “assessment”, but as the Teagle project progressed, they may have started to realize that what they considered assessment was in fact quite different from what the field of science education considers to encompass “assessment”. These issues should be kept in mind when interpreting the overall qualitative and quantitative assessment data gathered in relation to faculty attitudes toward assessment.

D. Summary of Faculty Learning about Assessment

Most science faculty appeared to begin the Teagle initiative with very low levels of assessment knowledge. Given that one of the anticipated outcomes of the project was faculty self-evaluation of the efficacy of their genomics education modules (I^3Us), in retrospect this was an extremely ambitious but necessary goal. Many of the participating faculty displayed difficulty (a) developing clear assessment goals; (b) connecting learning outcomes to assessment items; (c) incorporating innovative assessment types (concept maps, Likert-scale items, etc.); (d) differentiating attitude and knowledge measures; (e) developing clear rubrics for scoring open-response items; (f) considering issues such as reliability and validity; and (g) statistically analyzing quantitative pre-post Likert-scale items. The long-term nature of the Teagle project fostered resolution of many, but not all, of these assessment challenges through the final discussion session and individualized consultations. One major finding was that greater allocation of time and resources to the assessment aspect may have been helpful. In addition, creation of an instrument to measure faculty knowledge of assessment would permit more rigorous evaluation of future faculty development efforts that include assessment development.

Overall, our Teagle-funded efforts produced three broad findings relative to assessment. We (1) documented a significant need for faculty professional development efforts in formulating science assessment tools; (2) demonstrated the efficacy of extended attention to the development of cutting-edge content assessment (i.e., in genomics); and (3) identified assessment topics that were particularly challenging for faculty.

VIII. Emerging Themes

A. Interdisciplinary Community Formed

In our initial model, the Columbia Genome Center was at the core of our community. What emerged instead was a core of committed faculty from a range of disciplines, who through interactions with each other, the broader group of participants, and the individual genomics communities they work with, are having a real effect on the integration of genomics research and education. Genomics is interdisciplinary by nature and the composition of our group reflects the diverse expertise requisite for success. Our community brings together expertise in:

- Assessment
- Professional faculty development, including two with expertise in directing faculty development centers
- Geoscience educators and researchers
- Web curriculum development and dissemination expertise (SERC)
- Education theory
- Phylogenetics
- Microbial and eukaryotic organisms
- Biological questions ranging from cell biology to neurobiology to plant biology to ecosystems
- Genome annotation experience with students at a national level
- Collaborating with other genomics education consortia
- Computation and computer science

B. Relevance to Other National Genomics Education Consortium

As noted in our introduction, our consortium grew in parallel with GCAT, the Genomics Education Partnership, SEA, and the Microbial Genome Annotation project. Each of these efforts increases the opportunities for genomics education to be integrated into undergraduate learning nationally. In addition to the range of curricular material our project disseminates through the SERC site, there are a number of lessons we can share with the larger community. Our grassroots approach with many different model and non-model systems used to address a broad range of biological questions supports the integration of research and learning, builds on faculty expertise, and makes it more likely that faculty will continue to integrate their genomics efforts into multiple courses and their own research. It is a particularly strong model for research-active faculty at small schools with substantial teaching loads. Other models bring faculty and students together around one or a few systems with a more coherent set of biological questions and approaches. These models build community in a different way than our community. Not all models have as strong an emphasis on the wet lab component of the curriculum. For schools with limited resources, the more stand alone bioinformatics-based approach has advantages.

C. Distributed Expertise

The “Big Science at Small Colleges” collaborative emphasizes distributed expertise and has leveraged a number of unanticipated collaborations. In addition we have created a network of external and participant advisors we can rely upon as questions arise in the future. The iterative workshops fostered the strong sense of community that is driving ongoing work. We built on the strengths of our existing situations, which were by no means uniform.

D. Fostering a Culture of Assessment

One of the most unexpected consequences of our work is the shift in participant understanding and use of assessment in their teaching and curriculum development. Collectively we moved from viewing assessment as grading and IRBs as daunting and foreign to actively doing research on learning. It is clear from our surveys and group discussions that it took the full three summers to get to this rather astonishing shift in perspective. Thus our integration of research and education for all participants actually has three strands: 1) genomics education, 2) genomics research, and 3) research on learning. To the best of our knowledge this is a truly unique feature of our genomics education consortium. While other groups are deeply committed to assessing their efforts, our group also empowered participants to ask and answer questions about the efficacy of teaching their students genomics.

E. Leveraging the Teagle Funding

Our pebble in the pond metaphor for our consortium has taken on new dimensions over the course of the funding period. Initially we viewed the core group at the center supporting the participants throughout the country who would then affect their own students. The actual "multiplier effect" has been far greater than our basic model. Participants connected with invited presenters at the workshop and the network expanded. For example, David Li, an undergraduate from Carleton College, is spending the summer of 2009 at the Beijing Genome Center after Gane Ka Shu Wong, Associate Director of the Beijing Genomics Institute, gave the plenary talk at the 2008 workshop and met David's advisor. Neurobiologists from Vassar, Wellesley, Whitman, and Hiram colleges began working collaboratively after meeting at the first workshop.

Lois Banta established collaboration with the microbial genome sequencing group at the Broad Institute of MIT and Harvard, a premier sequencing center and the largest contributor to the Human Genome Project. Together, the head of this group and Lois designed a novel research project in which the students in the Williams microbiology course investigated prokaryotic diversity in the sludge from three local ponds, each with two or three different sets of nutritional resources. The microbiology students isolated the bacterial DNA from 28 different samples taken from these microbial ecosystems and prepared it to be sequenced. The researchers at the Broad provided the students with 1500 sequences from each of these 28 samples, representing an enormously rich "metagenomic" dataset that is proving to be highly interesting and informative.

Metagenomics, a comprehensive genomic analysis of all the organisms in a particular ecological niche, represents a scale of inquiry virtually unimaginable just a few years ago. The Board of Life Sciences of the National Research Council recently issued a call for biology researchers and educators to begin to think about ways to bring metagenomics into an integrated research and education undergraduate curriculum "while it's still new." "By acting now to incorporate metagenomics into biology education and to utilize biology education to inform questions and future research paths for metagenomics, the life sciences community can begin to shift from the current situation, in which scientific advances take decades to reach the classroom, toward a system in which education and research are deliberately and strategically integrated with each other from the very beginning" (Jurkowski et al. 2007). The collaborative project with the Broad Institute is, to our knowledge, the first community-scale bacterial survey to be implemented at the level of an undergraduate course. The complete data-set generated in this project, along with material and resources enabling other faculty members to use the data in their own courses, will be made available through our Teagle-funded website once the Williams group has finished their analysis. Faculty members at other liberal arts colleges including David Esteban at Vassar have already extended this analysis to their own local ponds through one of the eight I^{3}U development stipends; as large-scale sequencing becomes ever cheaper, we can envision microbiology classes around the country sampling diverse geographical niches and sharing their massive datasets via the web. Recently Cofactor selected David Esteban's group as one of four recipients of free genome sequencing for their project. A second Cofactor sequencing award went to Jodi Schwarz at Vassar, another core member of our group. Thus the Teagle group received half of all the funding Cofactor offered in 2009.

Lois Banta's collaboration with the Broad led to additional, authentic research experiences for students. A student with substantial programming skills from high school wrote a PERL script to perform several steps in the data analysis process that the Broad researchers were doing by hand. Broad staff now use this tool in their research. This is an example of the task- oriented projects that Gane Ka Shu Wong proposed during the summer 2008 workshop, and it was highly successful in allowing the student to do something truly productive just in a 3.5 week winter study period. A Williams College student majoring in math and biology is currently developing the statistics tools to determine whether metagenomic populations are statistically significantly different from each other. These student-developed research tools will be used at Williams and at the Broad for their mammalian microbiota metagenomics. Williams students also generated samples for the Broad's mammalian microbiota project, applying a stratified ecosystems approach used in the pond sludge project to dog feces.

As a result of the Teagle funding, Jodi Schwarz (coral biologist at Vassar), Marc Smith (computer scientist at Vassar), Susan Singer (plant biologist at Carleton), and SERC initiated research on scaffolding genomics education with an online interface.
Their work is now supported by an NSF CCLI grant. Ross Nehm and Brian Morton received funding from the NSF CCLI program to develop assessment tools for genomics and bioinformatics education. With collaborators at UC Merced, Stanford, Oregon State University, as well as Marc Smith and two Vassar summer research students, Jodi Schwarz developed a public web resource for the sea anemone gene sequences (http://aiptasia.cs.vassar.edu/AiptasiaBase). Susan Singer also received an NSF grant to sequence the transcriptome of the non-model legume *Chamaecrista fasciculata*, partridge pea. That work has led to new collaborations with the National Center for Genome Resources, Cornell, and Iowa State. The *Chamaecrista* group launched their non-model system in a day long workshop at the International Conference on Legume Genomics and Genetics in Puerto Vallarta, Mexico in December 2008. It is the first genomics community to

focus on the integration of research and education from the start, and *Chamaecrista* will be featured on the cover of the journal Plant Physiology this fall.

F. Empowering Faculty

All participants and core group member gained new research ideas as a result of the Teagle activities. Regardless of career stage, faculty gained knowledge and confidence about pedagogical strategies and assessment. Faculty at all stages of in their career participated and co-mentoring occurred across the board. While junior faculty noted the value of mentoring from senior faculty, senior faculty also celebrated the mentoring they received from junior faculty. More senior faculty benefitted enormously from the genomics expertise that early career faculty generously shared. The collaborations that emerged involve a mix of junior and senior faculty.

Junior faculty learned much about teaching during a critical phase of their professional development. Opportunities to interact with others outside the constraint of departmental hierarchies were noted as a benefit. Early career faculty believe the initiative helped them develop a niche within their departments and encouraged the exchange of expertise with senior colleagues within their departments that led to more collegial and less hierarchical working relationships. The integration of research and education approach provided a springboard for new research and educational grants, a boost to scholarship at a critical career juncture.

IX. Overall Analysis of Our Approach and Final Conclusions

A. Analysis of Approach

Our grassroots model for faculty and curriculum development in genomics emphasizes synergies between research and education. Products include curricula adaptable to a range of teaching settings with a focus on many non-model and model systems, but equally important outcomes include faculty professional development. Faculty development emphasized genomics content and pedagogical approaches with benefits for early to mid-career faculty. The unanticipated consequence of building a culture of assessment and learning added a new dimension to the project. The number of collaborations and additional grants that began emerging early in the project are striking. The value of a dispersed model at all levels, from expertise to sources of sequencing, is evident in project outcomes. A number of factors contribute to our success: 1) building on faculty expertise and interests that keep the biology at the center, 2) utilizing vetted online tools and approaches from the geoscience community, 3) using vetted pedagogical design principles, 4) embedding assessment in all aspects of the project from inception, 5) moving a cohort of faculty through an iterative workshop series supported with strong web interfaces, and 6) project coordination by a core of individuals with diverse expertise and experience.

B. What Next?

The Teagle support has allowed us to establish proof of concept for a grassroots model for faculty development in genomics education at liberal arts colleges with research active faculty. Individual participants continue to more fully integrate genomics into their own research and teaching. Given the success of this project in developing reusable tested genomics teaching materials that can be broadly adopted, in supporting faculty in learning genomics concepts and gaining confidence in teaching in this area, and in developing faculty expertise in assessing the success of their genomics teaching in impacting student learning, we believe that this model is more broadly applicable and plan to extend our work in a number of directions if we can find appropriate funding. The “Big Science at Small Colleges” website is viewed as a dynamic site that we plan to continue growing. It is set up in a way that others can easily interact with our project and make contributions in a guided manner aligned with our philosophy and design principles. Extending this model beyond liberal arts colleges is a reasonable next step. David Baumler at the University of Wisconsin, Madison is already developing an I^3U to upload to the site. Colleagues at Cornell University and Iowa State became involved in the *Chameacrista* I^3U through a joint NSF grant with one of the core members.

Our group has experience and perspective to add to the national conversation about genomics education and we have been fortunate to be included in those emerging conversations. Lois Banta joined 13 other prominent faculty members, from research as well as teaching institutions, to help formulate the Howard Hughes Medical Institute’s Science Education Alliance, which recently launched a nation-wide, semester-long lab research experiment in genomics for first-year college students. Susan Singer represented the group at a meeting of leaders in genomics education, including Genomics Education Partnership, SEA, and the Microbial Genome Annotation project representatives, hosted by the iPlant Collaborative in St. Louis in June of 2009. The iPlant Collaborative is working on genomics pipeline tools that would be useful to a wide range of undergraduate genomics educators and their students. This is a promising effort to coordinately support the emerging field of genomics education with necessary and appropriate tools.

While we have been successful with a dispersed model for sequencing – Joint Genomes Institute, National Center for Genomics Research, the Broad Institute, and Cofactor are all providing sequence data for consortium members– there would be advantages to a clearer path to generating sequence data for interested faculty. There need not be a single sequencing center; indeed that may not be desirable. But a funding program that specifically targeted genomics educators interested in integrating non-model system genomics into authentic research experiences for undergraduates would be very helpful. As sequencing costs continue to drop, the potential for students to learn and simultaneously contribute new findings to the research community are enormous.

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Appendix 1:
Initial Survey

Please answer the following questions so we can make sure the workshop will meet your needs and expectations. Please email to genomicsworkshop@vassar.edu.

1) If you currently teach a genomics-based module/activity in a course or teach a full genomics course, please describe briefly. If you are not currently teaching genomics, do you anticipate teaching a genomics activity/course in the future (if so, describe briefly)?

2) How does/would your genomics teaching fit into your department's curriculum (Does your department currently incorporate genomics into existing curricula? If so, how has your department approached this: are there genomics modules/activities folded into existing courses, or is there an entire course devoted to genomics?)

3) If you currently teach genomics (either a single activity or an entire course), would you be interested in presenting a 10 minute overview/perspective on your current genomics teaching activity(ies)? If so, we will send you information about how to format your presentation.

4a) To assist in development of your genomics teaching activities, do you anticipate applying for a stipend and/or supplies funds to develop a genomics teaching 1^{3}U?

YES NO **NOT SURE YET**

5) If "YES" or "NOT SURE", describe generally your idea(s) for how stipend/supplies support for an I^{3}U would fit in with your genomics teaching activities.

6) What are the top three that you would like to learn/accomplish from the workshop:
- how to apply or design genomics wet-lab activities
- how to find, learn, and implement good bioinformatics resources and tools
- how to choose organisms that are amenable to investigate genomics-level questions, using currently available resources
- approaches for teaching eukaryote and prokaryote genomics
- How to apply models of inquiry-based learning to functional, structural or comparative genomics
- How to assess genomics teaching activities
- To establish educational collaborations with other small liberal arts colleges to explore genomics questions

Other areas/topics: What do we mean when we use the term "genomics?" What sorts of activities or questions are of interest for this initiative?

Appendix 2:
Post-workshop Survey – Likert scale questions

Teaching Big Science at Small Colleges Post-Workshop Participant information

To what extent do you agree or disagree with the following statements?

		Strongly **disagree**	Disagree	Not sure	Agree	Strongly **agree**
1	It is imperative that undergraduate education be revised to integrate genomics into the curriculum.	☐	☐	☐	☐	☐
2	I understand the principles, merits, and limitations of inquiry-based integrated instructional design.	☐	☐	☐	☐	☐
3	I know how to apply integrated inquiry-based approaches in the development of a genomics curriculum.	☐	☐	☐	☐	☐
4	I feel comfortable developing, using, and interpreting assessment strategies into a genomics curriculum.	☐	☐	☐	☐	☐
5	I found the requirement to include an assessment component in the I3U a burden.	☐	☐	☐	☐	☐
6	Inclusion of the assessment component of the I3U provided valuable information for me.	☐	☐	☐	☐	☐
7	I know of approaches for including wet lab activities in a genomics curriculum.	☐	☐	☐	☐	☐
8	I am aware of useful bioinformatics resources and tools that can be incorporated into genomics curricula, and feel confident in my ability to use them.	☐	☐	☐	☐	☐
9	I am aware of interdisciplinary opportunities for teaching genomics (within my institution or among different institutions).	☐	☐	☐	☐	☐
10	I know who to contact to establish collaborations with other colleges and universities to develop genomics curricula.	☐	☐	☐	☐	☐
11	I feel part of a community of genomics educators from liberal arts colleges.	☐	☐	☐	☐	☐
12	I know how to use the SERC website to assist in the development of a genomics curriculum.	☐	☐	☐	☐	☐
13	I am planning to use my I3U again in a future year.	☐	☐	☐	☐	☐
14	I know how to choose organisms that are amenable to investigate genomics-level questions because resources are available	☐	☐	☐	☐	☐

Appendix 3:
I^{3}U Submission Form from Project Website is Presented on the Following Pages

Teaching Genomics at Small Colleges > Inquiry-based Integrated Instructional Units > Submitting I^{3}U

Submit a Teaching Genomics I^{3}U

About Activity Sheets

The goal of the standardized format of the I^{3}U activity sheet is to concisely communicate to other faculty what the key elements of the activity are so that they can adapt the activity for their own environment; or perhaps use it as a source of inspiration and good ideas. An activity sheet will contain all the materials necessary to conduct the activity; student handouts, instructor notes, relevant web links, and bibliographic references.

Authors should be explicit about how I^{3}U design principles are integrated into the activity. These explanations can occur in different sections of this submission form:

- Learning outcomes (likely in "Goals" below)
- Sequence the flow of instruction ("Activity Description and Teaching Materials" or "Teaching Notes")
- Integrate content and process ("Teaching Notes")
- Student reflection and discussion ("Activity Description and Teaching Materials," "Teaching Notes," and/or "Assessment").

For more details on I^{3}Us, refer to Designing I^{3}Us.

Activity Title

The title should be evocative of the main point(s) of the activity. It needs to communicate the full context of the activity on its own as it will show up in places like search returns (e.g. Google) where people won't have any contextual clues. So it should convey the idea that this is a teaching activity, what the subject matter is and what the relevant pedagogical focus is. For example: *Solar Radiation: Sample Socratic Questions*

Title

Author

Name and institution of author(s) of the activity and any other appropriate attribution information. If the page is based on materials originally created elsewhere that should be noted with attribution given to the original authors and links provided to the original materials.

For example: *This page authored by Jon Smith, Big State University, based on an original activity by Jane Smith, Smallville College.*
Authorship and Attribution

Email

Email addresses of the activity author(s) separated by commas. These will not be displayed in the activity page but are used for internal tracking.

Email

Summary

This text should make it clear what the activity is. It should provide an overview of the things that students will do and the intended outcomes. The description should be concise and compelling: typically no more than 1-2 very brief paragraphs.

For Example
In this laboratory exercise, students determine which allelic form of a particular single nucleotide polymorphism (SNP) they have (one located in an intron, and not associated with any known phenotype). Students may be homozygous for the A/T pair or the G/C pair, or they may be heterozygous with A/T on one chromosome and G/C on the homologous chromosome. Students isolate their own DNA, perform polymerase chain reaction (PCR) to amplify a region surrounding this SNP, and use RFLP (restriction fragment length polymorphism) analysis to determine their genotype.

Summary

Related Image

A small (200 pixels wide or less) image 'of' the activity to provide visual interest and immediate context. This could be an image of the 'output' of the activity or a photo of people engaged in the activity (or something similar). Not required.

Browse...

Select Image Type

JPEG

Goals

What concepts and content should students learn from this activity? Are there higher-order thinking skills (e.g. critical thinking, data analysis, synthesis of ideas, model development) that are developed by this activity? Are there other skills (writing, oral presentation, techniques, equipment operation, etc.) that are developed by the activity.

Goals

Context for Use

This text should help faculty understand the types of teaching situations for which this activity is appropriate. Important types of context include educational level, class size, institution type, etc. Is it lab, lecture, or field exercise, or a longer project? How much time is needed for the activity. Is there special equipment that is necessary? Are there skills or concepts that students should have already mastered before encountering this activity? How is this activity situated in the course? How easy (or hard) would it be to adapt the activity for use in other settings?

Context

Activity Description and Teaching Materials

This section should include a narrative describing the mechanics of the activity and all the materials needed to implement the activity (or links and references to those materials).

- If the material is available on another site please provide the full url.
- If you have the materials in hand they can be uploaded using the fields below and they will be embedded in the final page so that they can be downloaded.
- If they are published print materials please provide a complete bibliographic reference.
- If the activity is fully documented at another site please provide the url along with a brief (one or two sentence) description of the other site.

For all materials include, in the box below, a brief description of each item covering what it is and what its role is in the activity.

If you upload files as part of your activity remember to consider their final use in deciding on appropriate formats. Materials that other faculty are likely to modify should be provided in easily editable formats (plain text, Word files), whereas materials that will be likely only used verbatim are most convenient in formats that are universally readable (PDF format is often a good choice).

Once this form has been submitted we can work with you to integrate the downloadable files into the text of this section.

Please be sure all materials you upload can be freely redistributed. For more information about copyright as it applies to materials you are sharing through this site please check our more detailed discussion (opens in a new window) of this issue.

Description including Teaching Materials

All uploaded files are public unless you are in a private workspace

Title: A descriptive, human readable title.

e.g. 'Student Handout for Sauerkraut Assignment'

Select the file: Make sure it has an appropriate suffix (e.g. .doc) or specify the type in the *Optional Fields* below

Browse...

Description: A very brief description of the file.

File Type:

Unknown Binary

The system will attempt to determine the correct file type based on the name of the file you've selected. Choosing the correct file type here will override that.

File Name:

e.g. 'student_handout'

This will be the name of the downloaded file. By default the system will generate this based on the title you specified and the type of file. If you specify a name here it will over-ride the automatically generated name. This is generally only useful when uploading file of a type not recognized by the system (not in the list of file types above). In that situation choose File Type: Unknown Binary and include the appropriate suffix in the file name here. e.g. myfile.m3z Avoid spaces or special characters in the file names.

Authorship/Reuse

Either:

☐ I am the author (copyright holder) of the contents of this file and people are allowed to reuse it for non-commercial purposes as long as they give me attribution as described by this creative commons license.

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Description: A very brief description of the file.

File Type:

Unknown Binary

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If you have more than 5 files include the first 5 here and then get in touch with the SERC office (serc@carleton.edu) after completing this form.

Teaching Notes

This section should include notes and tips for instructors who might use the activity. Information such as common areas of confusion, things that need reinforcement, safety guidelines and other practical tips, and pointers for making the best use of the activity are appropriate. Note that this section should complement, rather than repeat, the more general guidance about the teaching method provided in the methods module of which this activity is a part.

Teaching Notes and Tips

Assessment

This section should describe how the author determines whether or not students (either individually or collectively) are achieving the learning goals outlined for the activity. Other relevant assessment strategies may also be described in this section.

Assessment

Resources

This section should include references and links to online resources that discuss the specific activity or will support faculty and/or students using the activity. References related to the general teaching technique should not be included here, but should be recommended for inclusion in the associated module.

Web resources should include both the url and a brief description of the site (and why it is relevant). Print resource should include basic citation information as well as a brief description of the resource.

Resources

Short Description

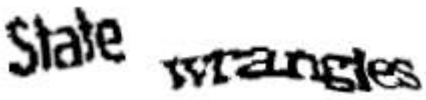
The short description should be a distillation of the summary above. This description will be displayed in search returns. The optimal length for this description is on the order of 1-2 sentences.

Short Description

If this activity uses/is based on a resource in a partner collection provide the url of that resource description here. For MERLOT activities provide the url of the MERLOT catalog page for the resource: http://www.merlot.org/merlot/viewMaterial.htm?id=90081 Only provide a single url.

Any other information you want to provide to SERC staff regarding this submission

*Please type the two distorted words into the box below. Separate them with a space. This helps us prevent spam. For more details or help click the question mark.



Type the two words:

Submit

Appendix 4:
Request for I^{3}U Proposals

Teagle Big Science for Small Colleges Request for Proposals

As we announced at the Teagle workshop in July, individuals or team of faculty members interested in developing I^{3}Us for inclusion on our project website are eligible to apply for stipends of up to $4000. Supply money needed for the development process will also be provided. I^{3}U development should occur during the summer of 2008, and stipend recipients are expected to attend the second workshop, to be held July 20-23, 2008, at Williams College in northwest Massachusetts. At this workshop, you will have the opportunity to share and get feedback on your I^{3}U in progress, and to work with Ross Nehm on developing assessment tools specific to your I^{3}U. If there is interest, training will be provided on common genomics/bioinformatics tools that you may want to use in your I^{3}U, and consultants will be available during the workshop to help you tailor these tools to your specific I^{3}U. Wet-lab and computer lab facilities will be available to us for the duration of the workshop. All expenses, including travel costs, will be paid by the Teagle grant. Recipients must be able to implement their I^{3}Us during the 2008-09 academic year, to upload the information about the I^{3}U (and associated online resources) in the format provided by the SERC website, and to collect and report assessment data by May, 2009. Stipend recipients will also contribute to writing the final White Paper, which is due to Teagle in August, 2009.

If you would like to apply for a stipend and/or supply funding, please submit a brief proposal by email to Lois Banta (lbanta@williams.edu) by January 25th. If this deadline poses a serious barrier to your participation (e.g., if you do not yet know what your teaching assignments will be for the coming academic year), please email Lois Banta expressing your intent to apply and provide a timeline for when you could finalize your plans and submit a proposal. Your proposal should include the following information:

1) Description of the I^{3}U: rough overview of the type of material (content and intellectual scope) the I^{3}U will include, pedagogical goal(s), length of time to be devoted to the I^{3}U, target audience.

2) Course for which the I^{3}U is planned: Is this an existing or a new course? What level is the course? Is it an elective, or required for the major? What is the typical or anticipated enrollment? In broad strokes, how does this course fit into your department's curriculum? Is the course team-taught or cross-listed among more than one department? If the course is team-taught, are other members of the team on board? Do you anticipate that your proposed I^{3}U could be adopted by other courses, at your institution or at others?

3) Faculty to be involved in the I^{3}U development process: Is this a team effort or an individual plan? Are you requesting stipends for one or more than one faculty member?

4) Supplies needed: What supplies will you need to develop your I^{3}U? What supplies will you need to implement your I^{3}U, and do you have departmental resources to cover the expenses associated with implementation? If you are requesting supply money from Teagle, please provide a budget and itemized list of supplies to be purchased.

5) Computational tools for which you would like more training: BLAST? Sequence alignments? Phylogenetics tools? Comparative genomics? Protein structure prediction?

Please feel free to copy and paste this list of questions and insert answers under each question in bullet format, if you wish. Proposals will be reviewed by a committee comprised of Lois Banta, Ross Nehm, and Lynn Caporale. Decisions will be made and stipend recipients notified by Feb. 15, 2008.

Appendix 5:
Reflections on I^{3}U Development Form

Introduction

You can use this form to gather your observations the way your I^{3}U works in your class

Title of teaching activity:

Why and How did you use the activity?

Educational level of students

- o Introductory
- o Upper division majors
- o Others:_______________

Size of class where activity was used:

- o 30 or fewer students
- o 31 to 80 students
- o 81 or more students

How did you use this activity in your teaching?
As: (check all that apply)

- ☐ illustrations in a lecture
- ☐ basis for discussion in class (following homework or not)
- ☐ think-pair-share with classroom response questions
- ☐ lab
- ☐ in-class activity
- ☐ problem set/homework assignment
- ☐ group project
- ☐ Other____

Did you use the activity as it was described? ___ yes ___ no
If no, how did you modify it for your class?

Why did you use this activity in your class? (check all that apply)

- ☐ To provide hands-on experience with scientific data
- ☐ To help students learn to analyze data
- ☐ To give students a better understanding of the application of data to geosciences processes
- ☐ To give students an opportunity to hone their basic map skills
- ☐ To help students make connections between geologic phenomena and data
- ☐ To give students an opportunity to integrate different techniques and observations
- ☐ To give students an opportunity to make and test hypotheses using data
- ☐ Other____

What did you **want** students to take away from this activity?

What **did** students take away from the activity?

Did students meet your learning goals?

What types of assessment did you use to evaluate your students?
(check all that apply)

☐ clicker questions
☐ test questions that incorporated concepts learned in the activity
☐ completed activity turned in
☐ class presentation or paper
☐ individual/group lab report
☐ used no assessments
☐ informal observations
☐ Other__________________________________

	None	A few	About half	Nearly all	Could not assess
What fraction of students achieved the learning goals for the activity?	1	2	3	4	na

How do you know that students met your goals?

- ☐ Performance on assessments
- ☐ Student engagement
- ☐ Individual feedback from students
- ☐ Gut feeling
- ☐ Other________________________

If only a small fraction of students succeeded, what challenges did most students encounter?

How effective was the activity in your classroom?

Education research identifies several aspects of activities that should enhance student learning. Indicate to what extent these aspects are true for using this activity:

	Not at all	A little	Somewhat	To a great extent	Not applicable in this teaching situation
Encouraged student interest and attention.	1	2	3	4	na
Included opportunities for students to reflect, discuss, and synthesize.	1	2	3	4	na
Engaged students in data analysis and synthesis	1	2	3	4	na
Helped students visualize data relationships, geologic processes, or their relationships.	1	2	3	4	na
Provided opportunities for students to confirm their understanding.	1	2	3	4	na
Required students to integrate ideas/information from different sources.	1	2	3	4	na

	Not at all effective	Some-what effective	Effective	Very effective	
Overall, how effective do you think the activity was in the classroom?	1	2	3	4	na

What's the most important aspect of this activity that made it work for you and your students?

What do faculty need to do to successfully use this activity?

Were you successful using the activity as it was described? ____ yes ____ no

What additional information would you have liked? (check all that apply)

- ☐ Tips for making the best use of the activity
- ☐ Recommended instructional strategies
- ☐ Suggestions for adapting the activity to different teaching contexts
- ☐ More complete description of the prerequisite knowledge needed
- ☐ Description of time needed to accomplish this activity
- ☐ Tips for circumventing technology challenges
- ☐ Other____

After using this activity, what else would you tell a colleague before they used it in their teaching?

Appendix 6:
Assessment Efficacy Survey

I^{3}U ASSESSMENT WORKSHEET (June 2009)

Name:__________
I^{3}U title:__________
Institution:__________

For a review of the original assessment information see:
http://serc.carleton.edu/dev/genomics/workshop08/program.html Tuesday July 22 2008

(1) Knowledge assessments (paste items/description here):

(2) Attitude and belief (and/or affective) assessments (paste items/description here):

(3) Performance assessments (paste items/description here):

Evaluation of I^{3}U assessments

Questions:

(1) Are the *three* assessment *types* represented in the assessment plan?

(2) Are the *unit goals* clearly and meaningfully tied to the assessments that were used? Are there gaps or redundancies?

(3) For each assessment *type*, were appropriate *methods* employed (e.g., assessment *type* = knowledge, *method* = concept mapping)?

(4) Is clear and appropriate guidance provided for the *scoring methods* (e.g., are *rubrics* provided for open-response data, interviews, concept maps)?

(5) Does the assessment plan consider issues such as reliability and/or validity? (e.g., corroborating data *interpretations*)

Appendix 7:
Final Workshop Survey: Open-Ended Questions (June 2009)

Final Post-Workshop Questionnaire

What challenges did you encounter in developing/implementing/assessing your I^3U?

In what ways did the workshops/consultants/project structure help you to overcome these challenges?

Which challenges were not adequately addressed by the project/workshop/consultants, and what additional assistance/support would have been useful?

Were there any I^3Us (other than your own) that you could envision yourself or your colleagues implementing, and if so, which ones?

The project coordinators noted that the listserv established by SERC was barely used by stipend recipients or others involved in the project. Do you have any feedback that would provide insights into its inactivity (i.e., did you find it user-unfriendly? Forgot it existed? Felt that any questions you might have posted were specific to your project? Had access to other resources and/or didn't encounter any question during your I^3U development/implementation/assessment process?)