

Proceedings of the Symposium on  
Life Science Education

North Carolina Biotechnology Center  
Hamner Conference Center, Congressional Room  
15 T.W. Alexander Drive  
Research Triangle Park, NC 27709-3547 USA

May 26th, 2009, 9am-5pm

Organizing Committee  
*Steffen Heber*, chair  
*Benjamin Wheeler*, co-chair  
*Zhao-Bang Zeng*, co-chair  
Department of Computer Science and  
Bioinformatics Research Center  
North Carolina State University

Welcome to the Symposium on Life Science Education! Our goal is to provide a forum to meet, discuss and exchange ideas on teaching and technology in Life Science Education. Please get to know your fellow participants and enjoy our speakers.  
 -- The Symposium Organizers

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## Symposium on Life Science Education

North Carolina Biotechnology Center,  
Hamner Conference Center, Congressional Room  
Tuesday, May 26th, 2009 9am - 5pm

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- 9:00 Welcome
- 9:05 Vincent J. Carey  
Teaching the analysis of genome-scale data using  
R and Bioconductor: Software, documents, and  
experiments
- 9:50 Steffen Heber and Leif Saul  
Bioinformatics in Motion: Animations for teaching  
Bioinformatics
- 10:20 Coffee Break
- 10:45 Bruce Nash  
CSHL: Tools to Teach Biology in the Genome Age
- 11:30 Lunch and Poster Session
- 2:00 Cheryl A. Kerfeld  
The Joint Genome Institute's Microbial Genome  
Annotation Program for Undergraduates
- 2:45 Coffee Break
- 3:00 A. Malcolm Campbell  
The Full Spectrum of Online Tools: From Synthetic  
Biology Research to Introductory Biology
- 3:45 Tom Miller and David Howard  
NCSU DELTA: Educational Technology in Dis-  
tance Education
- 4:15 Concluding Remarks
- 4:20 Social and Open Discussion

**SLSE PROGRAM**

**GRADUATE TEACHING ASSISTANTS’  
INSTRUCTIONAL FRAMING OF THE  
SOCIAL AND ETHICAL IMPLICATIONS OF  
GENETICALLY-MODIFIED CROPS**

***G.E. Gardner and M. G. Jones***  
**Dept. of Math, Science, & Technology Education**  
**North Carolina State University, Raleigh, NC**

Graduate teaching assistants (GTAs) are gaining an increasing responsibility for the delivery of science content to undergraduate biology students. Subsequently, understanding this group of science educators’ perspectives and practices in regards to science teaching and learning is important. This poster describes a research study that closely followed six GTAs who taught an introductory biology laboratory lesson on biotechnology (specifically genetically-modified crops) and its societal and ethical implications (SEI). Data sources included instructional observations and post-lesson semi-structured interviews. Qualitative analyses revealed that there was a disconnect between GTA perspectives about SEI and their teaching practice. While GTAs limited their instructional design and presentation to three frames (analytic, perspectives and biases, and individual reflection), the post-interviews revealed that their understanding of the importance of SEI to science instruction was much richer. Challenges for assisting GTAs in bridging the gap between perspectives and practices are discussed.

**EXPERTIZA: COLLABORATIVE LEARNING,  
PEER REVIEW, AND SOCIAL NETWORKING**

***E. F. Gehringer***  
**Dept. of Computer Science**  
**North Carolina State University, Raleigh, NC**

Expertiza is a collaborative-learning environment that can be used in any class. It helps extend collaborative active learning to out-of-classroom activities and distance education. As part of their homework in a class, students do projects that help update or improve the course. For example, they might research new developments related to a specific lecture in the course and write a hyperlinked summary. They might devise an active-learning exercise that could be used during a class session. Or they might make up questions that could be used on future home-

work or tests. All of these have been produced successively with Expertiza; we will summarize the results.

The Expertiza application supports individual or team submissions. For team projects, any team member can submit on behalf of the team. Submissions can be in the form of files, URLs, or wiki pages. Individual students can be assigned to review teams. Authors can give feedback to reviewers during the review period. There can be multiple rounds of review, allowing teams to update their submissions in accordance with the feedback that they have received from their reviewers. After the assignment is over, students fill out a questionnaire on their teammates contributions. All feedback in Expertiza is based on rubrics.

Currently, we are adding several social-networking features to Expertiza. Students will be able selectively to make their peer-review ratings visible to other class members and other Expertiza users. We hypothesize that by being able to share their achievements with the class, as well as attempt useful microtasks for extra credit, students will become more engaged with the class material and their fellow students. In addition, the course will be improved by the contributions that students will be motivated to create.

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## IBLEND: AN INTEGRATIVE BIOMATHEMATICAL LEARNING ENHANCEMENT NETWORK FOR DIVERSITY

***G.D. Goins<sup>1</sup>, T.C. Redd<sup>2</sup>, C.D. White<sup>1</sup>, V. Kelkar<sup>1</sup>, M. Chen<sup>2</sup>, and D.P. Clemence<sup>2</sup>***

**Dept. of Biology<sup>1</sup>**

**Dept. of Mathematics<sup>2</sup>**

**North Carolina A&T State University, Greensboro NC**

North Carolina Agricultural and Technical State University (NCATSU) is a historically minority-serving land-grant institution which has achieved high-research activity status. The University wishes to leverage this achievement by providing an institutional program that recruits and supports undergraduate biomathematical research and training experiences.

On an institutional level, the goal of our work is to significantly increase the number of biology and math majors at NCATSU who gain higher competitive knowledge-based research and training experiences. From 2006 to current, our NSF Undergraduate Biomath (UBM) Group program has been highly

... Poster abstracts continued from page 4

successful using research partnerships that provided NCATSU undergraduates with cutting-edge biomathematics research opportunities. The new iBLEND is a direct outgrowth of our current group UBM and is aimed at expanding the support to a much broader set of students.

The iBLEND is a student-centered long-term campus-wide experience specifically designed to keep more of our underserved undergraduates in the biomathematics pipeline. We will continue to implement this fertile open-loop model with knowledge sharing and faculty interaction to positively influence academic programs and integrative training for a broad and diverse range of students in biomathematics. The cross-cutting applied nature of systems biology will facilitate students from different disciplines to work together and gain a bigger view than single-investigator projects. Student teams will work on specific projects in order to gain experience with mathematical models of biological applications. This integrative model not only raises the bar for the incoming high-performing students, but seeks avenues that can amplify the overall supply of students who emerge from NCATSU on a competitive trajectory for biomathematical graduate study.

At the institutional level, we will leverage our past success into channels that disseminate biomathematics research activity to the thousands of underserved and underrepresented populations matriculating at NCATSU.

## ACTIVE LEARNING IN INTRODUCTORY BIOLOGY LECTURE COURSES USING SYNCHRONOUS VIRTUAL SPACES

*M. Ferzli*

**Dept. of Biology**

**North Carolina State University**

As the number of students continues to increase in the introductory biology majors courses, the lack of physical space and the large number of students (>240 students) in each lecture section become limiting factors for implementing active learning approaches in small collaborative groups. By using a synchronous virtual space (Elluminate Live(r)), students are given additional opportunities to engage with the course concepts in a setting that allows them to work actively and collaboratively

in small groups. Students sign up for a “problem session” in groups of no more than 24. When the students login, they enter a virtual classroom setting with a white board and the ability to text or voice chat with their peers or instructor. Students can ask questions, share documents and websites with each other and with the instructor. The instructor can invite them to write on the white board, to add to material already there or to present their own work. Students can enter “breakout rooms” where they can assemble into smaller groups and tackle specific problems or case studies. This environment also has the ability for quizzing and polling students. In these online groups, students work through case studies and problems which are then coupled to assessments done in class via personal response systems. In a pilot study of this approach, students who participated in the virtual problem sessions were more successful in learning the biology concepts in the course than those who opted out of the program. Student success was measured by survey responses as well as by examination scores in the course.

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## DEVELOPMENT OF AN ONLINE INTERDISCIPLINARY COURSE IN AGRICULTURAL BIOTECHNOLOGY

***C.V. Jordan<sup>1</sup>, C.E. Farin<sup>2</sup>, and E.B. Wilson<sup>3</sup>***

**Dept. of Plant Biology<sup>1</sup>**

**Dept. of Animal Science<sup>2</sup>**

**Dept. of Agricultural and Extension Education<sup>3</sup>**

**North Carolina State University, Raleigh NC**

A three-hour interdisciplinary online course entitled “Agricultural Biotechnology in Today’s Society” was developed to provide students with a foundation in basic environmental, animal, and plant biotechnology while integrating emerging and current trends and issues in each of these areas. Course modules included those on bioremediation, agricultural byproducts, biofuels, animal reproductive and genetic technologies, genetic selection, plant transformation and tissue culture, transgenic plant applications, and biotechnology regulation and ethics. Instruction was delivered using multimedia tools and utilization of learning management systems (Blackboard/Vista and Moodle) that allowed for mass delivery through a collaborative effort from three faculty members in the aforementioned disciplines.

Thirteen students completed a pilot offering of the course

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SLSE POSTER ABSTRACTS

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in summer 2008 and 22 students were enrolled in spring 2009. An optional synchronous on-campus lab was also developed and taught in spring 2009 to demonstrate lecture concepts. Two voluntary questionnaires were administered at the end of each offering using an online survey tool. The first questionnaire was a standard course evaluation on which students provided about the delivery of the integrated curriculum. The second questionnaire sought feedback regarding teaching methods used in each section to encourage the integration of science concepts and to improve the delivery of the science concepts in an agricultural context.

Efforts are currently underway to analyze survey data to assess the effectiveness of the integrated curriculum to teach science concepts, the attitudes of pre-service agricultural teachers and life science majors regarding the integration of science and agricultural concepts, and changes in student attitudes regarding agricultural biotechnology.

## CULTIVATING THE FUTURE OF BIOINFORMATICS THROUGH THE GOOGLE SUMMER OF CODE™ PROGRAM

*T. Vision and H. Lapp*

**National Evolutionary Synthesis Center, Durham NC  
UNC Chapel Hill, Chapel Hill NC**

Much of the most popular and important software in the life sciences is produced by highly interactive and geographically distributed communities of Free/Libre/Open Source Software (FLOSS) developers (e.g. Bioperl, R).

Unfortunately, there is little opportunity for life science students to receive training in the skills needed to contribute successfully to such projects. The National Evolutionary Synthesis Center has, since 2007, participated as a mentoring organization in the Google Summer of Code™. This program connects undergraduate and graduate students to a global community of mentors drawn from the ranks of senior FLOSS developers. Despite the demand for their skills, many of the mentors in this community often do not have the opportunity to teach these in traditional classroom settings.



Through summer internships with the community of mentors, students gain not only programming and remote collaboration skills, but also an increased awareness and understanding of the workings of collaborative open-source development. The range of problems to which students can make meaningful contributions is diverse, and the program is therefore open to students with varying interests, programming skills, and levels of expertise.

Through this program, NESCent is actively cultivating, and diversifying, the FLOSS development community and promoting the open, collaborative development of reusable, interoperable, standards-supporting bioinformatics tools.

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## COMPUTER SIMULATIONS INTEGRATING MOLECULAR BIOLOGY AND BIOINFORMATICS: CASE-BASED LEARNING IN INFECTIOUS DISEASES IN A PRE-COLLEGE RESIDENTIAL PROGRAM

*C.D. White*

**Department of Biology**

**North Carolina A&T State University, Greensboro NC**

The overarching goals of the Students Hot on the Sciences (S.H.O.T.S.) program in the Department of Biology at North Carolina Agricultural and Technical State University are to enhance science learning skills and increase the number of disadvantaged and minority high school students who are qualified and motivated to pursue science careers. Rising 11th and 12th grade underrepresented minority students throughout North Carolina participate in a multi-component year-round program, including a six week residential Summer Institute in Genome Science (SIGS).

SIGS is designed to engage students in hands-on, problem-based learning to improve reading comprehension and test taking skills and to increase student awareness of biomedical research. Therefore, we have successfully incorporated Case-It!, a web-based, case-based computer program, into the SIGS curriculum to integrate Molecular Biology and Bioinformatics concepts through 'real world' infectious disease case studies and wet-lab experiences.



In addition to our sponsors, we would especially like to thank Nagiza Samatova, Dahlia Nielson, Theresa-Maria Rhyne, Leif Saul, Melissa Seate, Ann Hunt, Bill Schy, Sue Carson, and Kathleen Kennedy for their invaluable assistance in organizing the Symposium.

Sponsors

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