IBI* SERIES WINNER

Keeping an Eye on Biology

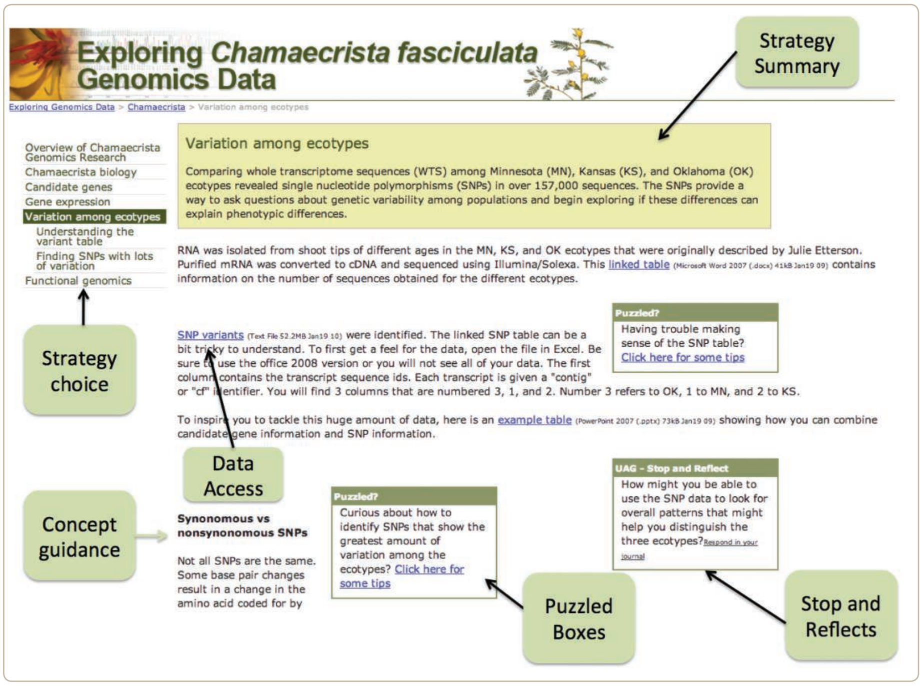
Genomics Explorers, an IBI prize–winning module, engages students with bioinformatics and molecular research.

Susan R. Singer,[1]*§ Jodi A. Schwarz,[2] Cathryn A. Manduca,[3] Sean P. Fox,[3] Ellen R. Iverson,[3] Benjamin J. Taylor,[4]† Steven B. Cannon,[5] Gregory D. May,[6]‡ Sonja L. Maki,[1] Andrew D. Farmer,[6] Jeffrey J. Doyle[7]

Genomic data sets offer opportunities for students to generate original findings without expensive laboratory equipment, extending the benefits of undergraduate research to the classroom (*1*–*4*). Yet, working with data sets online can frustrate biology students who may miss connections to fascinating biological questions. Integrating organismal and molecular biology with bioinformatics can enhance student learning. We have developed a program in genomics, adapted for a plant (*Chamaecrista fasciculata*) and an animal (*Aiptasia pallida*), designed to support student learning with a Web-based guide (http://serc.carleton.edu/exploring_genomics/index.html) (see the first chart).

Curriculum development began with a collaborative effort, "Teaching Big Science at Small Colleges," to develop, assess, and share inquiry-based, integrated instructional units (I^{3}Us) in genomics (http://serc.carleton.edu/genomics/index.html) (*5*). All I^{3}Us are aligned with the evidence-based design principles described in *America's Lab Report* (*6*). Incorporating our own genomics research on nonmodel organisms resulted in our learning module, Genomics Explorers (*7*). Students ask questions on several levels of biological organization, from genes to genomes to organisms to evolution and environment (see the second chart).

Students initially worked with whole-transcriptome data from individuals with schizophrenia, shared by our collaborators at the National Center for Genome Resources. Despite the human interest factor, students were quickly lost in a sea of nucleotides without a biological context and were frustrated trying to use the available bioinformatics tools. Classroom observers noted that, rather than asking questions at the level of whole transcriptomes, students defaulted to a strategy of hunting for a single, often poorly chosen, gene. Conceptual understanding is particularly challenging for undergraduates dealing with very small or very large scales (*8*). We realized it was essential to guide student learning of both the biology and the bioinformatics.



***Chamaecrista* Genomics Explorer supports problem solving.** The Explorer guides students to choose as a starting point: a literature-based entry to the biology of *Chamaecrista*, a candidate gene approach, or variation among three known ecotypes (a SNP-based approach). Links to tools and data are available centrally and as students need them. We include concept guidance, "Puzzled?" boxes that link to hints where our study shows that students frequently get stuck, and "Stop and Reflect" boxes that encourage both reflection and higher-order cognitive thinking. Reflecting on a lab learning experience has been shown to enhance student understanding of the nature of science (*6*).

We shifted to our own research organisms and developed a module introducing students to questions about interactions between organisms and their environments. We illustrate our approach with *Chamaecrista*. Students explore both the living organism and large data sets that are less abstract than DNA sequences. They use a photoperiod calculator to compare the flowering time of *Chamaecrista* from different latitudes (data available in the Explorer) with flowering time for perennial lilacs (*Syringa*) in a public phenology data set. After contrasting flowering time and latitude for the two plants, students generate explanations. In the second activity, students encounter whole-transcriptome data sets from *Chamaecrista* and are asked to formulate questions that can be addressed by comparing transcriptomes from different *Chamaecrista* ecotypes and organs at different stages of development.

To support students in developing and answering questions with transcriptomes, we organized our Web site around genomics problem-solving strategies. Our goal is to have students concurrently use science practices and biological concepts, a more effective approach than separating them (*9*). The site provides local data access and links to tools. For example, *Chamaecrista* transcriptome and genome sequence data are searchable on the *Chamaecrista* Genomics Explorer with a local BLAST search. Although the integrated approach supported students as they explored

[1]Department of Biology, Carleton College, Northfield, MN 55057, USA. [2]Department of Biology, Vassar College, Poughkeepsie, NY 12604, USA. [3]Science Education Resource Center, Carleton College, Northfield MN 55057, USA. [4]Department of Entomology, University of Wisconsin, Madison WI 53706, USA. [5]U.S. Department of Agriculture Agricultural Research Service, Iowa State University, Ames, IA 50010, USA. [6]National Center for Genome Resources, Santa Fe, NM 87505, USA. [7]Department of Plant Biology, Cornell University, Ithaca, NY 14853, USA.

*IBI, *Science* Prize for Inquiry-Based Instruction; www.sciencemag.org/site/feature/data/prizes/inquiry/.
†Present address: Anoka Technical College, Anoka, MN 55303, USA. ‡Present address: Dupont Pioneer, Johnston, IA 50131, USA. §Author for correspondence. E-mail: ssinger@carleton.edu (SRS).

Published by AAAS

the different strategies (fig. S1), the lack of a central resource for data and tools was frustrating. In response, we added tool and data pages in the main selection menu.

Interacting with the Web site in one or two laboratory sessions allows students to revise their questions and explore multiple strategies. At the end of each session, students (either individually or in teams) briefly present their findings and next question to the entire lab, which encourages collaboration. We added visualization tools to support students in making comparisons among data sets, including mapping the transcriptome onto the soybean (*Glycine max*) genome.

In a third activity, students shift to a molecular lab experience, conducting expression analyses by isolating RNA and performing semiquantitative or quantitative polymerase chain reaction (PCR). Students have found nonsynonymous, single-nucleotide polymorphisms (SNPs) among ecotypes and then used restriction digests of their PCR products to determine whether the SNP was valid or an artifact of sequencing. Some chose to sequence their PCR products, providing additional information and validation for their work. If cost is a barrier, students can design functional genomics experiments without actually conducting them.

Groups present their experimental plans to the class for critique, and collaboration among groups is encouraged. Often, a whole class experiment emerges addressing a more comprehensive question. For example, several groups can collectively investigate the relative effects of different temperatures and photoperiods on the developmental expression of one or more genes of interest in two different ecotypes. The process is designed so students own their questions.

Students make their thinking visible with short presentations on their experimental questions and findings, lab notebook records, a final presentation and paper, and a model for the effects of genes and environment on flowering time (fig. S2). Each group produces a paper focused on their research question that includes an investigation seeking patterns at the level of the transcriptomes, not simply individual genes. Peer and instructor feedback is provided each week, and the final paper must address the points raised.

Genomic Explorers enables students to identify a research strategy and to use bioinformatics tools for investigation, without relying on the instructor for assistance. Off-loading the basic instruction to the Web site creates space for the in-depth conversations among students and the instructor on the nature of research and biology that typically arise during a traditional undergraduate research experience.

Week 1: *Chamaecrista* whole-plant analysis and phenology

Strategy: Biology

↓

Week 2-3: *Chamaecrista* transcriptome analysis

Strategies:
- Biology
- Gene expression
- Candidate gene
- Variants

↓

Week 4: RNA isolation and primer design

Strategy: Functional genomics

↓

Week 5: RNA quantification, PCR

Strategy: Functional genomics

↓

Week 6: Gel electrophoresis, imaging, qualitative expression analysis

Strategy: Functional genomics

↓

Week 7: Opportunity to repeat experiments

Strategies:
- Biology
- Variants
- Candidate gene
- Functional genomics
- Gene expression

↓

Week 8: Data analysis

Strategies:
- Biology
- Variants
- Candidate gene
- Functional genomics
- Gene expression

↓

Week 9: Group presentations and feedback

↓

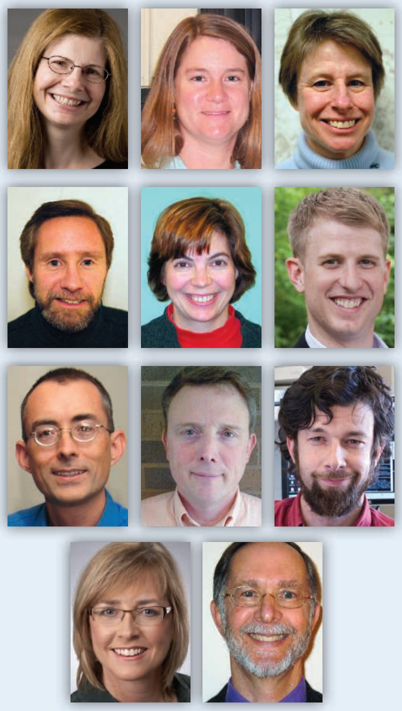
Week 10: Final paper due, incorporating feedback

Flow of *Chamaecrista* instructional modules.

PHOTO CREDIT: SEAN FOX; AUTHOR PHOTOS: SARA RUBINSTEIN, JERRY CALVIN, SEAN FOX, SEAN FOX, SEAN FOX, BENJAMIN TAYLOR, DAN KUESTER, GREGORY MAY, ANDREW FARMER, KATHY BERARD, JANE DOYLE, SONJA MAKI

About the authors

Shown left to right and top to bottom: Susan Singer, Jodi Schwarz, Cathy Manduca, Sean Fox, Ellen Iverson, Benjamin Taylor, Steven Cannon, Greg May, Andrew Farmer, Sonja Maki, and Jeff Doyle.



References and Notes

1. D. Lopatto, *Science in Solution: The Impact of Undergraduate Research on Student Learning* (Research Corporation for Science Advancement, Tucson, AZ, 2009).
2. S. Laursen, A.-B. Hunter, E. Seymour, H. Thiry, G. Melton, *Undergraduate Research in the Sciences* (Jossey-Bass, San Francisco, CA, 2010).
3. American Association for the Advancement of Science (AAAS), *Vision and Change in Undergraduate Biology Education: A Call to Action* (AAAS, Washington, DC, 2011).
4. C. A. Wei, T. Woodin, *CBE Life Sci. Educ.* **10**, 123 (2011).
5. L. M. Banta *et al.*, *CBE Life Sci. Educ.* **11**, 203 (2012).
6. S. R. Singer, M. L. Hilton, H. A. Schweingruber, Eds., *America's Lab Report: Investigations in High School Science* (National Academies Press, Washington, DC, 2005).
7. S. R. Singer *et al.*, *Plant Physiol.* **151**, 1041 (2009).
8. S. R. Singer, N. R. Nielsen, H. A. Schweingruber, Eds., *Discipline-Based Education Research: Understanding and Improving Learning in Undergraduate Science and Engineering Education* (National Academies Press, Washington, DC, 2012).
9. National Research Council, *A Framework for K–12 Science Education: Practices, Crosscutting Concepts, and Core Ideas* (National Academies Press, Washington, DC, 2011).

10. Our work was supported by NSF DEB 0746571 and DUE 0837375 to S.R.S. S.R.S. and J.A.S. thank the Carleton and Vassar students who participated in our study. S.R.S. and J.A.S. developed the curriculum and participated in the biology and education research analyses. S.P.F. created the Web site infrastructure and aided in classroom observation and research analysis, along with C.A.M., E.R.I., and B.J.T. S.R.S., S.B.C., G.D.M., S.L.M., A.D.F., and J.J.D. contributed to the *Chamaecrista* research, including sequencing and assembling the *Chamaecrista* transcriptome. Institutional review Board approval 08-09 006 (Carleton and Vassar Colleges).

Supplementary Materials
www.sciencemag.org/cgi/content/full/339/6118/408/DC1

10.1126/science.1229848