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Letter to the Editor

Vision and Change through the Genome Consortium for Active Teaching Using Next-Generation Sequencing (GCAT-SEEK)

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Dear Editor:

Following its initial description (Buonaccorsi *et al.*, 2011), the Genome Consortium for Active Teaching using Next-Generation Sequencing (GCAT-SEEK) has experienced growth in the opportunities it can sponsor for undergraduate educators. The network aims to use massively parallel sequencing data as a catalyst for improving undergraduate genomics education by offering students authentic research experiences that are associated with the research interests of network members. This is achieved by 1) sharing knowledge on experimental design, bioinformatics approaches, pedagogy, and assessment; 2) delivering faculty development workshops; 3) obtaining bulk discounts on runs, software, and supplies; 4) combining samples for pooled runs; 5) generating and disseminating data and pedagogic modules; and 6) providing access to necessary computational resources. Funding from the Howard Hughes Medical Institute undergraduate grant program and the National Science Founda-



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tion Research Coordination Networks for Undergraduate Biology Education program (NSF RCN/UBE) has aided our progress.

One of our key implementation strategies is the presentation of hands-on faculty/student workshops that include sequencing of participant research samples, the first of which occurred in June of 2013 at Juniata College. Workshops are free and open to network members through our listserv. They are meant for undergraduate educators and students who are novices with respect to next-generation sequencing and

bioinformatics approaches. Each workshop is a 4.5-d immersion experience that aims to assist in all key stages of scientific inquiry and teaching. The objectives of the workshop are for participants to improve in their ability to: 1) design experiments using next-generation sequencing technologies, 2) prepare nucleic acid samples and assess quality, 3) analyze their samples, 4) integrate modules that involve next-generation sequencing research into the classroom, and 5) set goals for student learning and assess progress toward achieving these goals. Workshops also include an introduction to the analysis of ethical, legal, and societal implications of genomics, an important aspect for students to consider as these new technologies create new challenges in society.

The first workshop included four concurrent breakout sessions covering RNAseq, metagenomics, eukaryotic genomics, and prokaryotic genomics subject areas. All protocols used at the 2013 workshop are now available on our website (<http://lycofs01.lycoming.edu/~gcat-seek/workshops.html>). Examples of how participant sequence data will be used in a classroom setting are also available (<http://lycofs01.lycoming.edu/~gcat-seek/curriculum.html>), with specific emphasis on identifying the Vision and Change (American Association for the Advancement of Science, 2009) core competencies addressed by each educational module. Twelve modules were developed by participants during the 2013 workshop, including three modules developed for introductory courses and nine for upper-level biology courses. The modules, as either an entire course or a small unit, are designed to demonstrate how high-throughput sequencing technologies can be used in a variety of different research projects to introduce undergraduates to authentic research experiences. The data generated from each project will be available, by request, for all network members on secured servers for educational purposes.

We aim to assess student learning related to the Vision and Change core concepts and core competencies through participation in GCAT-SEEK activities. Therefore, we developed a pilot GCAT-SEEK assessment instrument to assess skills and attitudes regarding next-generation sequencing techniques and data analysis. This instrument is available as a Google form via the GCAT-SEEK website but is still under development. The assessment instrument contains questions to assess both concepts and competencies, and it will be used to gauge improvements in these areas by both network members and impacted students over their participation period.

The next workshop will take place June 2–6, 2014, at Lycoming College, and applications will be distributed through the GCAT-SEEK listserv. Instructions for becoming

a member are available on the GCAT-SEEK Web page (www.gcat-seek.org). Beginning in 2015, five additional workshops will be presented over a 3-yr period, including two at Juniata College and one each at the minority-serving institutions: Hampton University, Morgan State University, and California State University, Los Angeles.

In addition to the workshops, the network has facilitated group sequencing runs to lower cost at the Pennsylvania State University GCAT-SEEK founding core facility. We have also negotiated reduced pricing for Illumina HiSeq, MiSeq, and Ion Torrent sequencing for network users with GCAT-SEEK-affiliated core facilities at Indiana University, Cincinnati Children's Hospital, and Ohio University. The latter also sponsored a competition for a free Ion Torrent run. Independent of the workshop, we are also in the process of facilitating several pooled sequencing runs using shared primers for metagenomic and RADseq analysis. The windows program NextGENe (www.softgenetics.com/NextGENe.html) has been purchased and is available to network members on a dedicated server (16 CPU; 64-gigabyte RAM). A computer cluster (144 CPU; 500-gigabyte RAM) running on Linux OS is also available for use by network members and will soon host a custom Galaxy instance for the network (<http://galaxyproject.org>).

Taken together, the presentation of the first GCAT-SEEK workshop, the available learning modules, the sequencing opportunities, and the launch of new computer resources mark a substantial growth for the GCAT-SEEK network. Moving forward, sequence data and additional pedagogical resources will be available to network members for use in a wide range of undergraduate educational settings. Future workshops and sequencing runs, combined with these resources, are likely to continue increasing the breadth of undergraduate impacts of the network. We encourage interested *CBE—Life Sciences Education* readers to join the network, apply to participate in one of the workshops, and make use of the opportunities and materials that our network can now offer.

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