A Genomics Education Alliance

VISION

The rapid pace of scientific advancement presents a continuing challenge to effective life science education. The genomics revolution brings with it a unique challenge for the biology educator, as skills from computer and data sciences have become core competencies to master. Integrating genomics into the undergraduate curriculum is a daunting proposition for the majority of life science faculty, most of whom completed formal training without the computational expertise needed to effectively engage in this field. Equally unique are the opportunities genomics holds to train students in computational approaches to biological questions, and to deliver curriculum in the form of course-based undergraduate research experiences (CUREs). CUREs not only develop students into evidence-based decision makers, but also address an urgent need to improve retention of a diverse student population in STEM. Our experience shows that genomics projects can engage large numbers of undergraduates, democratizing access to research experiences, science education, and preparation for the workforce. Our vision is to create a global, sustainable, community-driven Genomics Education Alliance (GEA). The mission of the GEA is to implement a framework in undergraduate education that brings together tools, curriculum, and expertise to support this transformative change. This whitepaper presents the arguments for creating this alliance of previously disparate efforts and outlines a call to action for all segments of the research and education community.

OPPORTUNITIES

Powered by rapid low-cost sequencing, genomics has transformed the life sciences and is relevant to biologists of every sub-discipline. Increased understanding of genomics will help develop solutions to challenges in human health, in feeding the world, and in maintaining the environment. To reach this understanding, biology education must prepare students to derive knowledge from genomic data. Fortunately, the study of genomics emerges from the principles of molecular biology already in the life science curriculum. Analyzing a genome prepares students to interact with "big data" and stimulates further interest in statistics, computer science, and related fields. Our experience, and that of many others, suggests genomics and bioinformatics curricula are accessible, and can prepare students for STEM careers via clear paths involving them as co-investigators in meaningful research. GEA can harness this potential in several ways:

CUREs Course-Based Undergraduate Research Experiences (CUREs) engage large numbers of undergraduates in doing meaningful science. Over the last decade, publications by the AAAS and

NSF[1] the President's Council of Advisors on Science and Technology[2], and the National Academy of Sciences[3] have all emphasized teaching using discovery-based research courses. CUREs and related inquiry-based interventions increase student retention in STEM[4] including improving the retention of minority students[3]. The success of genomics education in the context of CUREs is well-documented in the literature, with reports on outcomes from implementations involving thousands of students in a variety of contexts (from freshmen to seniors, at 2- and 4-year colleges, minority serving institutions, etc.) [5,6,7,8,9]. Existing educational models such as the Community College Undergraduate Research Initiative[10] and ComGen: The Community College Genomics Research Initiative[11] show how schools outside Research I contexts can participate via CUREs. Nearly 6.9 million students (46% of the nation's undergraduates) are enrolled annually in the nearly 1200 community colleges across the United States. Half of all baccalaureate degree recipients began their college careers at community colleges[12]. These schools have fewer financial resources. But genomics CUREs (which often have substantial bioinformatics components) require only modest budgets and infrastructure, and lab safety issues are few to non-existent. These attributes help genomics CUREs to scale to involve large numbers of undergraduates in common curriculum and research.

Open data, compute resources, and technology Students and educators working in genomics employ the same datasets, tools, and technologies used at the forefront of research. Over the past decade, DNA sequencing costs have decreased more than 50,000-fold[13]. DNA sequencing can literally be done in minutes on a device attached to a cell phone[14]. Data analysis (rather than data generation) is now the bottleneck in many cases. However, inexpensive commercial[15] and freely available NSF-funded cloud-compute resources[16,17] and easy-to-use interfaces for many tools[18] mean that any student with an internet connection can access research-grade software tools and computational resources.

Students and workforce First on NSF's 2016 list of six future big research ideas is "harnessing data for 21st century science and engineering."[19] Engaging every life science student would create a transformative workforce within genomics. "Massively parallel undergraduates" carefully analyzing data can accomplish research that could not be achieved otherwise[20,21]. While the number of students who could benefit is large, many of them are not exposed to the bioinformatics skills needed to engage in genomic analyses. A recent survey of U.S. faculty indicates that while 95% believe bioinformatics should be taught to undergraduates, less than half report integrating bioinformatics into their curriculum.[22,23] According to Science Careers, "(f)or

life scientists with expertise and an interest in bioinformatics, computer science, statistics, and related skill sets, the job outlook couldn't be rosier. Big pharma, biotech, and software companies are clamoring to hire professionals with experience in bioinformatics and the identification, compilation, analysis, and visualization of huge amounts of biological and health care information."[24]

CHALLENGES

The thousands of institutions grappling with genomics education have seemingly created as many solutions; unsurprisingly, there are many examples of duplicative efforts. Even the best innovations may only be locally available, or not disseminated at all. Existing projects in the genomics education space share curriculum materials within their respective groups and have significant overlap in goals and methods. The Genomics Education Alliance would provide a plausible solution to shared challenges and deliver a centralized effort that facilitates participation for all.

Faculty professional development and curriculum development are intertwined. For bioinformatics educators, there has been an explosion of new technologies and data types, and the bar for statistics and computational skills continues to rise. In the absence of formal training, educators may be reluctant to teach these subjects. Most biologists are still learning how to apply these tools to answer a biological research question, and navigating the vast array of resources available is an additional challenge for educators striving to generate productive experiences for their students. For most educators, finding time for self-teaching amid multiple work responsibilities is a significant issue at all career stages. Lack of opportunities for faculty to consider new ways to organize their courses and learning materials (for example, to switch to a CURE format) and work collaboratively across disciplinary fields remain a problem. Online meetings and workshops can scale but are typically limited in scope. Both online and in-person workshops require resources such as instructor time before, during and after a workshop, as well as resources for communications and computation.

Curriculum decisions Genome science (and bioinformatics generally) is deep and diverse. Faculty need to establish general standards for bioinformatics courses at different levels, striving in all cases to cultivate students' thinking skills to handle bioinformatics problems. Bioinformatics educators with biology backgrounds are generally not formally trained in computing, and often steer towards a tool-user approach, while bioinformatics experts originating from computer science push for more mathematical and statistical content, including various

levels of coding skills. Several groups[22,25] are converging on education core competencies, but the lack of clear standards indicates the need for continuing broad dialogue.

Maintaining tools and learning materials Maintaining curriculum in a fluid field is time consuming, and often lacks support. Web databases, user interfaces, software versions, and even best practices change at rapid rates in each of the various sub-disciplines of genomics. Since most tools are not built with the wider education community in mind, curricula depending on these software or web interfaces must be constantly updated. Like most scientific software, grant funding to maintain educational software is often not available beyond funding for initial development — but when one piece of the computing environment changes, software and associated curricula often become unusable. Constant change also makes this educational domain unattractive to commercial publishers who are more comfortable investing in relatively static textbooks.

Long-term funding Although genomics-focused CUREs are potentially low-cost, generation of sequence data, information storage and archiving, and data analysis infrastructure will have a significant impact on departmental budgets. Professional development and dissemination also involve significant investment – from faculty time and salary to the logistics of organizing a training workshop. Currently, there is no clear mechanism to sustain and disseminate even the most successful high-impact activities of grant-funded bioinformatics education projects once initial funding has concluded. Many granting agencies see their role as a catalyst for change, but limit their scope in a project's sustaining phase[26]. Federal funding mechanisms that support broad national dissemination, such as NSF TUES Central Resource Project awards, are no longer available. Hence successful strategies that have been developed for bringing genomics into the curriculum are only reaching a minority of the US 2- and 4-year colleges.

SOLUTIONS

To maximize these opportunities and overcome the challenges of integrating genomics into life science education more broadly, we propose the creation of the Genomics Education Alliance (GEA). The GEA will leverage established education consortia to build a network of networks that will provide standardized tools, protocols, and training to equip groups of faculty and students to engage in genomic-level inquiry. By unifying the people, tools, and platforms of genomics education initiatives, and computational and genome sequencing resources, with biology researchers and educators, the GEA aims to streamline adoption of best teaching practices. The alliance will build new educational opportunities

through faculty training and coordinate resource development and maintenance. Specifically, a GEA would:

Develop and maintain classroom-friendly computational infrastructure Existing high performance cyber-infrastructure provided by CyVerse[17] and Jetstream[16], as well as commercial cloud computing vendors (e.g., Amazon EC2, Microsoft Azure) can leverage the tools of open, reproducible science to create stable classroom computing environments. Virtualization, container technologies, and cloud computing provide a stable and scalable infrastructure for faculty and students to experiment with different bioinformatics tools and parameters[13]. Platforms such as Galaxy[18] can be used to develop tools and workflows for common bioinformatics tasks, such as constructing genome browsers, metagenomics analyses, or differential expression analyses with RNA-Seq. As an example, the G-OnRamp project (a collaboration between Galaxy and Genomics Education Partnership[5]) is building a workflow for generating a genome browser for newly sequenced organisms. These general tools and workflows can be shared with faculty and students so that they can be used in a classroom setting, facilitating collaborative research among large groups of students. Groups like GCAT-SEEK support Linux-based bioinformatics curricula for undergraduates that offers increased flexibility and power. A dedicated communal infrastructure will allow for a semester-long "freeze," followed by updates in between semesters to reflect changes to databases and tools. The technical staff at the GEA can provide support for core services to all alliance members, enabling them to focus on project-specific requirements.

Build faculty skills Faculty training based on GEA-developed 'roadmaps' could help faculty navigating the "forest" of available genomics tools and resources. Customized roadmaps tuned for novices and for more advanced users could cover basic computational tools and data management, all the way to working with high-performance computing. A common GEA roadmap could support both centrally coordinated and independently organized training workshops. Workshops can also prepare faculty to join on-going GEA-facilitated research projects (such as a large-scale annotation project) and/or teach faculty a defined set of skills that can be broadly applied to a wide array of genomics projects (Figure 1). A regional workshop model could seed local networks supporting follow-up training and 'help-desk' functions. In collaboration with organizations such as Software Carpentry and Data Carpentry, the GEA can operate on a model of shared, collaboratively developed curriculum. Train-the-trainer events could link community colleges and other small schools with larger universities having more

resources. Workshops would support computational and wet-lab approaches, including for example, affordable RNA-Seq library preparation[27].

Organize CUREs and distributed research projects The GEA would develop best practices for delivery of content and development of critical thinking skills. Rather than set up a separate clearinghouse for vetted curriculum materials, we plan to take advantage of existing resources for curation of curriculum, including CourseSource[28] and the NIBLSE[29] Resources on QUBES Hub[30]. We will solicit long-term projects from scientists in academia and industry to develop into CUREs, and disseminate

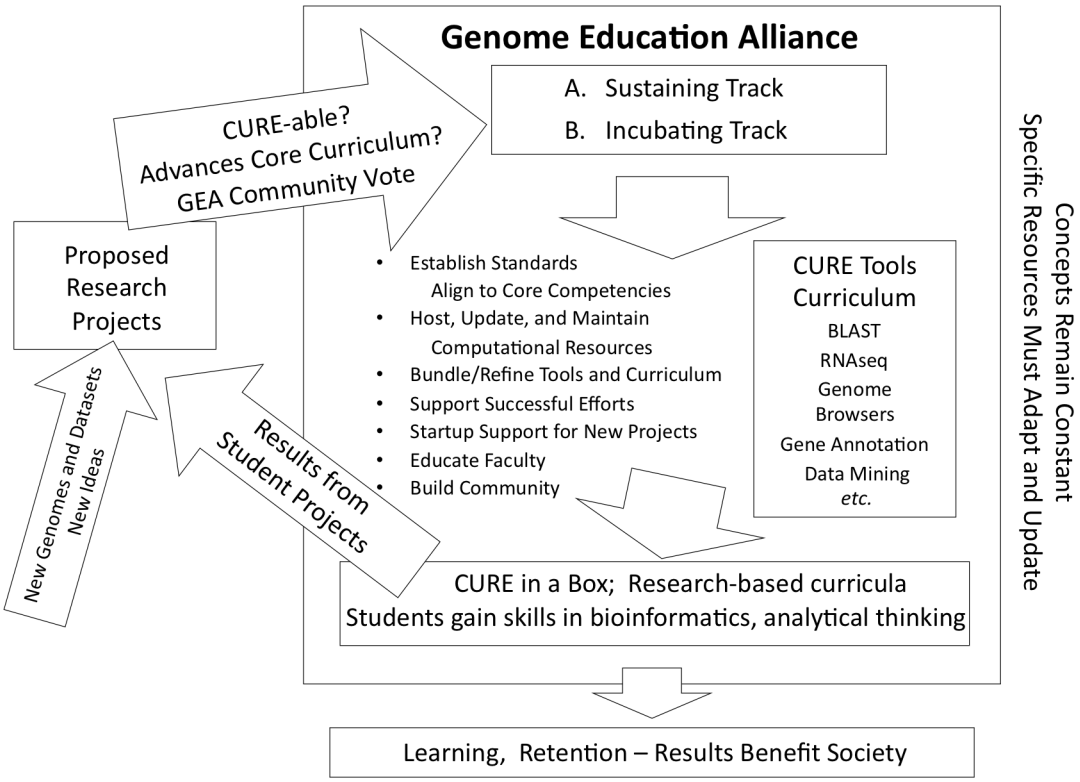


Figure 1: The cycle of the Genome Education Alliance (GEA) will serve to help nucleate, incubate, and sustain projects using bioinformatics and computational genomic tools in undergraduate education. Proposed research projects generated from new ideas or datasets will be evaluated by the GEA community for their potential to advance the core curriculum in bioinformatics education and/or to be transformed into a course-based undergraduate research experience (CURE). The basic concepts within genomics tend to remain constant, but the methods used to apply those concepts rapidly evolve with changes in technology and web-based interfaces. Thus, the GEA will facilitate the generation and maintenance of the CUREs by providing up-to-date curriculum and user-friendly, broadly applicable tools. In addition, the GEA structure will support professional development and build intercampus community among faculty through workshops on tools, curricula, assessment and joint publications. GEA products will include CURE curriculum that can be easily implemented in a classroom setting ("CURE-in-a-Box"), as well as more specific research-based curricula. Undergraduate students experiencing CUREs will produce useful scientific results that will be fed back into the originally proposed projects producing new scientific knowledge. Ultimately, the GEA will improve student learning and retention and benefit society by preparing graduates to be competitive in the modern biotech workforce, having both enhanced problem-solving experience and exposure to current genomics tools.

these projects through faculty workshops, enabling many undergraduates to engage in research as part of their coursework.

Create sustainable community and foster participation Faculty participation in ongoing projects increases expertise and builds a "community of practice"[29]. Subsequently, many faculty will want to pursue projects relevant to their particular research interests — developing these into new ideas and student research experiences. Community members can pool resources and lower costs on expensive procedures such as sequencing. (Price structure at genome core facilities often involves large initial setup fees followed by much lower per-library fees.) Microbial community profiling, for example, has a low read-per-sample requirement that allows pooling of many samples into a single sequencing run. The GEA can help continue existing collaborations, and can help others participate in this model.

Share and improve assessment An abundance of research has documented that students who participate in research experiences, including course-based undergraduate research experiences (CUREs), report a range of positive outcomes, including gains in their ability to think and work like scientists, increased enjoyment of and interest in science, and increased intentions to pursue careers or further education in science[8,31,32,33,34,35,36,37]. Much more research is needed to document the effectiveness of CUREs for diverse populations of students, to determine how to design and implement CUREs to achieve particular outcomes for students, and to understand fully the mechanisms by which CUREs promote student learning and development[3]. An alliance using common tools and approaches to engage students in diverse settings in research could contribute significantly to this effort.

CALL TO ACTION

The opportunities, challenges, and solutions we describe above are certainly not exhaustive; however, we believe they provide a basis for initiating a conversation around the idea of a Genomics Education Alliance. Creating an alliance will certainly not be easy, but the rewards of unifying disparate projects to avoid duplication of effort and make the whole more effective is, in our opinion, too compelling to ignore. Undoubtedly, there are many interested community members who could inform this effort, identifying existing solutions we haven't considered and most importantly, helping to define the most achievable organizational structure and scope.

We invite others interested in this challenge to join us. In the short term, we hope to collect comments and contributions in response to this paper. A medium-term goal to initiate our collaboration will be assembling invested community members to join us in submission of a "Research Coordination Network for Undergraduate Biology Education" proposal to the National Science Foundation to support establishment of the Alliance. Beyond that, we plan to seek core support for the coming five years, and to explore various mechanisms to provide long-term sustainability for this national (and potentially international) undergraduate research program.

If you are interested in undergraduate education and genomics, if you have a project that might benefit from many hands, or if you see an important future for the integration of bioinformatics into the biology curriculum, we call on you to comment, and to join the GEA.

CURRENT MEMBERS OF THE GENOMICS EDUCATION ALLIANCE:

Gita Bangera is the founding Dean of Undergraduate Research (and currently the Interim Vice President of Instruction) at Bellevue College. She is the Principle Investigator of ComGen: The Community College Genomics Research Initiative (ComGen), which aims to bring research into the classroom at two-year schools (http://www.bellevuecollege.edu/comgen/).

Vincent P. Buonaccorsi is Professor of Biology at Juniata College. He is the principle investigator of the Genome Consortium for Active Teaching using Next Generation Sequencing (GCAT-SEEK), which aims to facilitate massively parallel sequencing projects with undergraduates (http://gcat-seek.weebly.com/).

Douglas L. Chalker is Professor of Biology at Washington University in St. Louis. His research focuses on investigating mechanisms the guide programmed DNA rearrangements to probe how genomes are organized into the nucleus, thereby facilitating proper genetic regulation. He is a founding member of the Ciliate Genomics Consortium and has been engaging students in course-based functional genomics research since 2004. (https://pages.wustl.edu/chalker/people/doug-chalker).

Elizabeth Dinsdale is Associate Professor of Biology at San Diego State University. She has established next generation DNA sequencing courses for undergraduates at SDSU and teaches sequencing and bioinformatics to students and faculty internationally (https://dinsdalelab.sdsu.edu/).

Erin L. Dolan is the Georgia Athletic Association Professor of Innovative Science Education in the Department of Biochemistry & Molecular Biology at the University of Georgia. Her research focuses on scalable ways of involving undergraduates in science research and mentoring of undergraduate researchers in the life sciences. She is PI of CUREnet (http://curenet.cns.utexas.edu/), a network of people and programs, a network of people and programs integrating research experiences into undergraduate courses. (http://research.franklin.uga.edu/erindolan/)

Sarah C R Elgin is professor of Biology, Genetics, and Education at Washington University in St Louis, and an HHMI Professor. Her research is in Drosophila epigenetics and genomics. She is the founder and current Program Director of the Genomics Education Partnership (http://gep.wustl.edu).

Linnea Fletcher is Department Chair of Biotechnology at Austin Community College, Executive Director of the NSF funded ATE Center, AC2 Bio-Link Regional Center, and served as a program officer at NSF in DUE for two years. She working on meeting the bioinformatic/IT needs of the biotechnology workforce.

Arthur Hunt is a Professor in the Dept. of Plant and Soil Science at the University of Kentucky. His research focuses on mRNA processing and metabolism in plants. He is engaged in bringing accessible low-cost methods for RNA-Seq to the undergraduate laboratory and classroom.

Carolyn J. Lawrence-Dill is an Associate Professor of Genetics, Development and Cell Biology at Iowa State University. She is a maize (corn) researcher focused on creating novel genetics and genomics data access and analysis methods. She developed and teaches an undergraduate introduction to bioinformatics course that uses inquiry-based learning methods and regularly engages undergraduates in research efforts both in the classroom and in the lab. (https://dill-picl.org/).

Wilson Leung is Program Manager for the Genomics Education Partnership (GEP) web framework. He is responsible for developing and maintaining the software tools and genome browsers for the GEP sequence improvement and annotation projects. He also helps develop and update GEP curriculum materials, and provides technical and teaching support for GEP faculty and students.

Laura K. Reed is Associate Professor of Biology at the University of Alabama. She studies evolutionary genomics/metabolomics (http://flygxe.ua.edu) and is a long-time member of the Genome Education Partnership. She will be playing a leading role in the scientific vision of the GEP in the coming years.

Anne G. Rosenwald is Professor of Biology at Georgetown University. She is the principle investigator of the Genome Solver Project (http://genomesolver.org), which endeavors to teach basic skills in bioinformatics to faculty at 2- and 4-year institutions.

Sandesh Subramanya is a faculty member of the Departments of Biotechnology and Biology at Austin Community College in Austin, TX. He is spearheading efforts for introduction and implementation of genome sequencing projects at this community college to educate students for the bioinformatics/IT workplace.

Emily Wiley is Professor of Biology at Claremont McKenna, Pitzer, and Scripps Colleges. She helped create the Ciliate Genomics Consortium that engages undergraduates in gene structure/function research and a web database for publication of student discoveries (http://suprdb.org).

Jason Williams is Assistant Director, External Collaborations at Cold Spring Harbor Laboratory's DNA Learning Center (http://www.dnalc.org). As Education, Outreach, and Training Lead for the CyVerse life sciences cyberinfrastructure (http://www.cyverse.org), he provides training to researchers learning to use advanced computational tools and teaching faculty who want to bring bioinformatics into the classroom. He is also actively involved in Data and Software Carpentry (http://www.software-carpentry.org).

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