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A Course-Based Research Experience: How Benefits Change with Increased Investment in Instructional Time

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Article

A Course-Based Research Experience: How Benefits Change with Increased Investment in Instructional Time

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There is widespread agreement that science, technology, engineering, and mathematics programs should provide undergraduates with research experience. Practical issues and limited resources, however, make this a challenge. We have developed a bioinformatics project that provides a course-based research experience for students at a diverse group of schools and offers the opportunity to tailor this experience to local curriculum and institution-specific student needs. We assessed both attitude and knowledge gains, looking for insights into how students respond given this wide range of curricular and institutional variables. While different approaches all appear to result in learning gains, we find that a significant investment of course time is required to enable students to show gains commensurate to a summer research experience. An alumni survey revealed that time spent on a research project is also a significant factor in the value former students assign to the experience one or more years later. We conclude: 1) implementation of a bioinformatics project within the biology curriculum provides a mechanism for successfully engaging large numbers of students in undergraduate research; 2) benefits to students are achievable at a wide variety of academic institutions; and 3) successful implementation of course-based research experiences requires significant investment of instructional time for students to gain full benefit.

INTRODUCTION

A growing body of literature has established the benefits of research experiences for undergraduate students in the sciences (Seymour *et al.*, 2004; Lopatto, 2006, 2009; Laursen *et al.*, 2010). Indeed, integration of research experiences into the academic-year curriculum, along with the use of other active-learning strategies, is a central theme in calls for undergraduate biology education reform. (See *BIO2010: Transforming Undergraduate Education for Future Research Biologists* [National Research Council (NRC), 2003] and *Vision and Change in Undergraduate Biology Education: A Call to Action* [American Association for the Advancement of Science, 2011].) Such experiences can be particularly beneficial for first-generation students, underrepresented minorities, and at-risk students, significantly improving retention rates in the sciences for these groups (Nagda *et al.*, 1998; Hathaway *et al.*, 2002; Lopatto, 2006, 2007; Locks and Gregerman, 2008; Goins *et al.*, 2009). Perhaps as a consequence, the second recommendation in the recent President's Council of Advisors on Science and Technology (PCAST) report, *Engage to Excel* (2012, pp. 16, 25, and 38), is to "advocate and provide support for replacing standard laboratory courses with discovery-based research courses." Utilizing results from a diverse group of institutions, the growth in the Genomics Education Partnership (GEP) provides us with the opportunity to examine key features of undergraduate instruction that can contribute to student gains from a research experience embedded in an academic-year class (Shaffer *et al.*, 2010). Importantly, we find that these results are independent of institution characteristics. Rather, the key variable is the length of time spent on the project.

Genomics studies as a focus for undergraduate research provide many opportunities, and are especially useful for teaching institutions limited by minimal research infrastructure and budgetary support. First, there is a huge amount of raw genomics data, most archived and publicly available (National Center for Biotechnology Information [NCBI], www.ncbi.nlm.nih.gov). Most of this sequence data has been analyzed only by individual prediction programs at the time

of posting, providing ample opportunities for undergraduates to improve this analysis and carry out their own investigations mining information from genomes. "Turning data into knowledge" (Brenner, 2002) is in fact the major bottleneck in genomics today, and a large-scale undergraduate project in sequence improvement and analysis results in new understandings and improved data sets that can benefit the research community as a whole (Boomer *et al.*, 2002; Elwess and Latourelle, 2004; Drew and Triplett, 2008). Further, with DNA sequencing continuously becoming less expensive, we can anticipate many more institutions initiating genome-sequencing or RNA-sequencing projects in the not-too-distant future, allowing students to explore local ecosystems and characterize genomes of local organisms (e.g., see Oleksyk *et al.*, 2012). In addition, the "tools of the trade" in genomics and bioinformatics are generally publicly available (e.g., at the NCBI) and lend themselves well to peer instruction. Today's students are often very adept at using computers, and students who are familiar with the computer-based tools of bioinformatics from previous experience prove to be effective coaches for newcomers, serving as peer instructors or teaching assistants (TAs). Peers can promote the development of a dynamic undergraduate research community in which students can serve as scientific mentors, with attendant benefits (Harrison *et al.*, 2010; Dunbar *et al.*, 2012). A faculty member with the requisite background in the fundamentals of genetics, molecular biology, and/or evolutionary biology can coach students to think critically about their observations and to question, probe, and analyze the data to address relevant scientific questions. Together, faculty and peer instructors can create the foundation for a lively genomics research team that is actively contributing to the scientific body of knowledge. Success in this project can provide students with the increased confidence that is a hallmark of research experiences for undergraduates. In the National Survey of Student Engagement (Bennett *et al.*, 2007), students deem research experience to be a high-impact practice.

To this end, several national programs have been established during the past few years that take advantage of genomics to engage undergraduates in research (Hanauer *et al.*, 2006; Hatfull *et al.*, 2006; Campbell *et al.*, 2007; Hingamp *et al.*, 2008; Shaffer *et al.*, 2010; Ditty *et al.*, 2010; Banta *et al.*, 2012; Singer *et al.*, 2013), in keeping with the recommendations of PCAST (2012), *Vision and Change* (AAAS, 2011), and *BIO2010* (NRC, 2003). Despite these reported successes and positive reports from long-range studies (Bauer and Bennett, 2003; Brodl, 2005), we have encountered some skepticism as to whether basing curriculum on a research project is an approach that is an efficient use of time and/or is broadly applicable to a diverse population of students, or whether it is best reserved for high-achieving students working in the summer, the current tradition.

The GEP provides an opportunity to evaluate the efficacy of a research project specifically in genomics in both attaining student learning objectives and achieving informed student attitudes regarding research experiences, drawing from a diverse pool of students. The GEP is designed to engage undergraduates in a joint research project in genomics while introducing them to bioinformatics tools and resources with the goal of increasing their understanding of eukaryotic genes and genomes, as well as immersing them in the practice of science. This project, initiated in 2006, now has ~100 affiliated schools and has engaged more than 1000 students at ~60 different colleges and universities during the past year alone. Training materials to familiarize students with bioinformatics tools and relevant strategies have been developed at Washington University and at GEP member schools, with collaborative assessment and revision. Undergraduate students participating in the program can improve the quality of genomic sequence and annotate genes and other features, elucidating meaning from DNA sequence. Research questions in genomics are addressed using the results of these efforts, leading to student presentations both locally and nationally, and ultimately research publications. Since 2006, students involved in the program have worked with the Genome Institute at Washington University in St. Louis (WUSTL) to improve more than 7 million bases of draft genomic sequence from several species of *Drosophila*. Using a suite of bioinformatics tools selected and/or developed in collaboration between the Department of Biology and Department of Computer Science and Engineering at Washington University (often with additional input generated on their campus), students have produced hundreds of gene models using evidence-based manual annotation. Improved sequences are submitted to GenBank (2013) and used in studies exploring genome evolution (e.g., see Leung *et al.*, 2010; other manuscripts are currently in preparation).

Since our initial assessment of students enrolled in 2008–2009 (Shaffer *et al.*, 2010), the GEP has doubled in size and attracted a diverse group of schools in terms of size, educational mission, and public versus private support. Faculty members have collaboratively developed a variety of ways to use the GEP approach in their teaching, including short (~10 h) modules in a genetics course, longer modules within molecular biology laboratory courses, stand-alone genomics lab courses, and independent research studies. This diversity of schools and approaches has allowed us to look for critical variables for student success, measured both in terms of responses to an online SURE-style survey (SURE is the Sur-

vey of Undergraduate Research Experiences [Lopatto, 2004, 2007]), which we will refer to as the “learning survey,” as well as an online knowledge-based quiz. In addition, to determine long-term impacts on students’ subsequent actions and careers, we have surveyed occupations and attitudes of students one or more years after the completion of a GEP-affiliated course. We find that institutional characteristics have little correlation with student success, indicating that diverse students in diverse settings benefit from curriculum-based research experiences of this type. We see a similar impact on student attitudes from the GEP course compared with a traditional independent summer research experience as measured by the learning survey, but find that the impact correlates with the amount of time the instructor was able to devote to the project. The impact of time spent is seen not only with students at the end of their GEP course experience, but also in their reports on their experiences in subsequent years. The data make a strong argument for allotting more instructional time to research-based work in the undergraduate curriculum.

MATERIALS AND METHODS

The Student Research Project

The GEP is a collaborative effort between the Department of Biology, the Department of Computer Science and Engineering, and the Genome Institute, all located at WUSTL, and a growing number of colleges and universities. (See http://gеп.wustl.edu/community/current_members for a list of currently affiliated schools, and Figure 6 later in this article for characteristics of the schools participating in this assessment.) The project is organized around a central database housed and maintained by WUSTL on a pair of SUSE Enterprise Linux servers that host a variety of services utilized by the GEP community, including curriculum modules, access to research projects and bioinformatics tools, and assessment and communications tools (see <http://gеп.wustl.edu> and Shaffer *et al.*, 2010).

Our current research efforts focus on exploring the evolution of the small fourth chromosome (dot chromosome or Muller F element) using some of the 20 species of *Drosophila* for which genome sequence is currently available (Clark *et al.*, 2007; Baylor College of Medicine, 2012). This chromosome, previously studied primarily in *Drosophila melanogaster*, is unusual in that, while the chromosome as a whole exhibits heterochromatic properties (intense DAPI [4',6-diamidino-2-phenylindole]) staining, late replication, no meiotic recombination, high repeat density, and high levels of chromatin marks associated with gene silencing, including HP1a and H3K9me3, the distal 1.2 Mb exhibit euchromatic properties such as replication during polyteny and a normal gene density (Riddle *et al.*, 2009, 2012). Leung *et al.* (2010) presented results from a comparison of the *D. virilis* and *D. melanogaster* dot chromosomes carried out by Washington University undergraduates in a pilot project for the current GEP initiative. Over the past several years, GEP undergraduates have analyzed this chromosomal region from *D. erecta*, *D. mojavensis*, and *D. grimshawi*, and a comparable euchromatic region from *D. erecta* and *D. mojavensis*, covering 40 million years of evolution in reference to *D. melanogaster*.

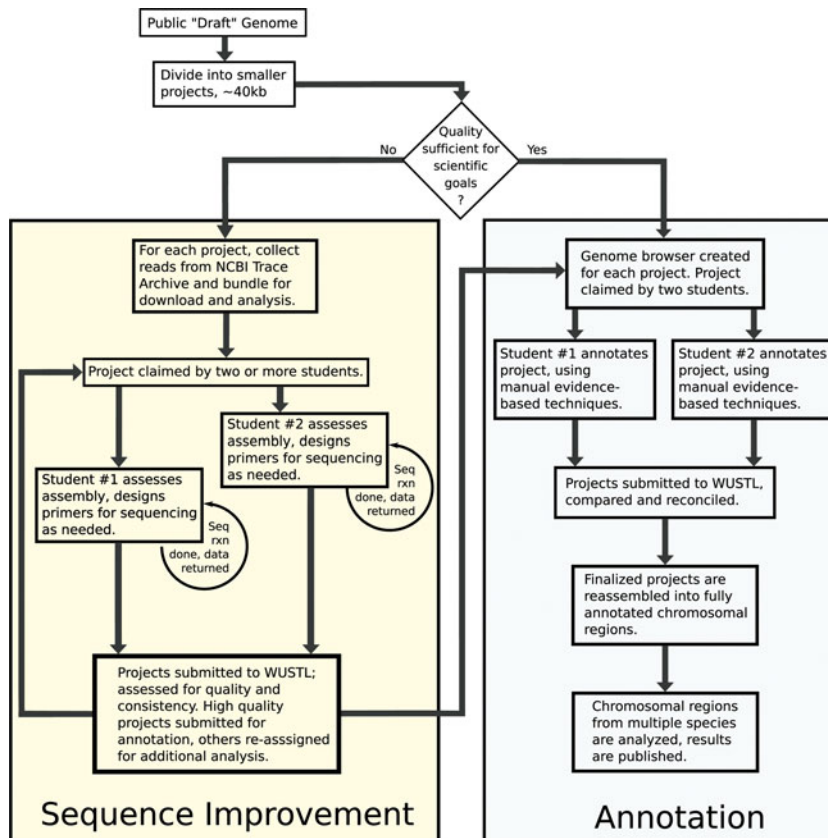


Figure 1. The GEP sequence improvement and annotation workflow. All projects are completed at least twice independently, and the results are reconciled before final assembly and analysis. While the quality of the genome sequence assembly available is sufficient to proceed directly to annotation for some species, in other cases it is necessary to improve the genome assembly ("finishing") by generating additional sequencing data and manually resolving misassemblies.

GEP students are challenged to verify the sequence assembly of an ~40-kb region of a *Drosophila* genome, and/or to annotate the region, identifying elements of interest and creating defensible gene models while working either individually or in teams (Figure 1). Projects are claimed and results submitted through the GEP website (Genomics Education Partnership, 2013a) using a standard, detailed reporting form along with appropriate sequence files. Each ~40-kb project is completed at least twice independently, and any discrepancies are resolved by experienced students working at WUSTL. GEP students and staff are able to draw on the expertise of the Genome Institute and the Department of Computer Science and Engineering for resolution of difficult issues. Reconciled projects are used in a reassembly of the chromosome region for characterization of the domain as a whole, and comparative analysis among species to chart evolutionary changes.

Most GEP students have been involved in annotation, with ~20% working on finishing as well; consequently, we will focus on the annotation experience in this paper. In the annotation research project, a predicted gene model (generated by an ab initio gene-finding algorithm such as GenScan, GeneID, etc.) serves as the starting hypothesis. While the overarching scientific question is predetermined by the group project (in this case, the properties and evolution of the *Drosophila* dot chromosome), we find that, with a little guidance, the student can be challenged to traverse the whole of the scientific research process, as shown in Table 1.

Faculty Implementation Strategies

GEP faculty members have utilized the GEP project in a variety of types of courses, including a first course in genetics, a molecular biology course, a lab in bioinformatics, independent study, and many courses that fall in between these descriptors. To capture the rich experience of the partnership, faculty responses to the two questions "How do you use GEP materials in your curriculum?" and "What advice would you offer to instructors interested in adapting this approach to fit the needs of their students?" are given in the Supplemental Material. One of the advantages of a consortium is the ability to share training materials and other curriculum items, which are posted on the GEP website. Current members have attended a 3- to 5-d workshop at Washington University to gain familiarity with the material. Much of the information provided at these workshops is readily accessible online, and we invite all educators to use the curriculum resources posted on the GEP website, under a Creative Commons license. (For an example of a ready-to-use script, see "An Introduction to NCBI BLAST" at http://gep.wustl.edu/curriculum/course_materials_WU/annotation/tutorials_and_walkthroughs.) While most GEP members participate in the broad research effort, claiming projects from the dot chromosome or comparison domain under study, an annotation problem can also be used simply to teach about eukaryotic genes and genomes. An example of a 3-wk lab module that introduces students to the structure of eukaryotic genes is posted at http://gep.wustl.edu/curriculum/course_materials_GEP_partners/able_workshop (Emerson *et al.*,

Table 1. Traversing the scientific process through student investigations within the GEP

The general process	The GEP process
1. Define the question	What genes or other features are present in this segment of a <i>Drosophila</i> species genome? What is the most likely gene structure? How has this region evolved?
2. Gather background information	<i>D. melanogaster</i> has been very well annotated; its evolutionary relationship with species under study allows for comparative analysis.
3. Experimental design	Students must decide which computational tools to use directly (e.g., BLAST to look for evidence of homology) and learn to seek other evidence from results displayed in a genome browser (e.g., ab initio gene predictors to look for computational evidence for the presence of a gene).
4. Collect experimental observations	Students generate BLAST results and collect other results (e.g., RNA-seq data) from a genome browser for their region of the genome.
5. Analyze collected data	Students create a gene model and test it using the collected observations; what gene model is best supported by the evidence?
6. Disseminate results	Students write papers and/or prepare talks or posters on their results, describing their results and defending their conclusions; pooled results are submitted to GenBank and linked to FlyBase.

2013), while a quick start for a longer investigation is posted at <http://gep.wustl.edu/curriculum/quickstart>.

Assessment Instruments

Learning Surveys. For the purpose of comparing the GEP experience with a summer research experience, we constructed a student survey that combines verbatim the 20 items previously used by a published survey (SURE survey [Lopatto, 2004, 2007]) with new items specific to the use of GEP materials. The SURE survey is a postexperience survey that asks students to respond to a list of 20 different knowledge or attitudinal benefits with respect to their research experience. Students are asked to rate their gains from 1 (none or very small gain) to 5 (very large gain). Using the SURE questions allows comparison of GEP student gains with those reported by students spending a summer working in a research laboratory. To compare attitudes of GEP alumni (students who completed a course with GEP materials one or more years prior) with those of students who had just completed the GEP curriculum, we prepared an alumni survey that contained questions identical to a portion of the GEP survey, as well as demographic questions about the alumni themselves. (All survey items are provided in the Supplemental Material.)

Knowledge Quizzes. We assessed knowledge gains of GEP students involved in annotation using a quiz composed of 20 multiple-choice questions. Quiz questions, written by the GEP faculty, were designed to test both conceptual knowledge about genes and genomes and specific skills related to the annotation process. The quiz questions assess a range of skills, from mastery of basic terminology and concepts to more complex cognitive skills, including data analysis and evaluation. [See Supplemental Table S1 for a tally of quiz questions as they relate to the revised Bloom's taxonomy (Anderson *et al.*, 2001).] Two versions of the quiz have been created to avoid the effect of repeated testing. This quiz is distinct from that used in a prior publication (Shaffer *et al.*, 2010) in both the attention to Bloom's taxonomy in question design and in the pre/postcourse administration protocol. The online quizzes are available by request.

Data Collection and Analysis. Both the learning survey and the knowledge quizzes were accessed by the students

through the GEP website. Confidentiality was maintained by applying a cryptographic hash function to an identifier provided by the student. Participation was entirely voluntary, and students were able to opt out of the entire process or any single question. Approval to conduct assessment for scholarly purposes was obtained from the local Institutional Review Board (IRB) at each participating institution. For a comparison group for the quiz, we recruited students at participating schools who had completed the prerequisites to the GEP-affiliated course but were not engaged in the GEP research-based curriculum.

During the academic years 2010–2011 and 2011–2012, of ~2000 students eligible to participate, 751 postcourse learning surveys were collected; 1026 students took the precourse knowledge quizzes, and 748 took the postcourse knowledge quizzes. Students from 57 schools contributed to this data set. Data loss due to students' missing the pretest, the posttest, or using faulty or no identification yielded a matched data set of 394 sets of quizzes. To avoid the possibility that any improvement from pre- to postcourse scores was due to student exposure to the precourse quiz, we used two similar quizzes covering the same material but using different questions, as noted above. Students taking the precourse quiz were randomly assigned to one version and then given the other version when they returned for the postcourse quiz. Comparison of these data with the posttest-only data revealed no significant differences based on either the experience of the pretest or the version of the quizzes that the students encountered (unpublished data). Student affiliation with a participating partner school is maintained, allowing cross-correlation with institutional characteristics (as reported by U.S. News & World Report Staff [2011] and verified by the GEP faculty) and with course characteristics reported by the GEP faculty members.

For the alumni survey, GEP faculty members obtained IRB approval at their institutions and disseminated a link to the online survey to all of their GEP alumni. Of 1645 students eligible, 473 students (29%) from 41 institutions participated. As above, participation was entirely voluntary, and students were able to opt out of the entire process or any single question. The survey requested identification of the student's GEP school, type of GEP course, and other course details; asked about career status/plans and the value of the GEP experience; and invited recommendations and comments.

Except for items that collected demographic or categorical data or that provided text boxes asking for comments in which participants were allowed to enter any arbitrary input, all items across all surveys asked participants to indicate their feelings/responses on a 1–5 scale (e.g., see section on *Learning Surveys*). We treated these responses as numerical data. Unless otherwise stated, all averages reported are means, and errors are reported as ± 2 SEM; significance was determined at $p < 0.05$. To compare classroom-based GEP responses with those reported by summer (SURE) research students, we used an independent-groups t test. To test for correlation between the institutional characteristics and student learning outcomes (both learning survey responses and knowledge gains shown on quizzes), we applied multiple linear regression using IBM SPSS Statistics Version 20. This package was also used for all subsequent analysis. To look for any difference between groups of students with respect to both knowledge and learning gains, we used one-factor analysis of variance (between groups). The quartiles used in the analysis of outcomes relative to time spent in class on GEP material were defined by rank ordering all classes by time spent (as reported by GEP faculty members) and separating them into four groups with equal numbers of participating schools.

For the numerical analyses of comments, we classified each sentence as “positive” if the sentence contained a conventionally positive emotion (“liked,” “loved,” “appreciated,” “enjoyed,” etc.) and as “negative” if the sentence contained a conventionally negative emotion (“disliked,” “confused,” etc.). Other groupings were built on the key words indicated, including similar phrases, variants, and synonyms thereof; for example, “independence,” “independent,” “independently,” were grouped together along with synonyms such as “freedom” or “on my own.”

To describe quiz questions with respect to categories in Bloom’s revised taxonomy, 10 GEP faculty members evaluated each question independently. The results indicated that many of the questions required the use of more than one skill category. Therefore, we created four intervals of overlapping adjacent categories (shown in Table S1) and calculated the modal score for each question with respect to those four categories. In most cases, there was agreement on this binning (10 out of 10 responses falling into these two categories), but responses were quite wide-ranging in a few cases, with only six of 10 responses falling in these two categories.

RESULTS

Gene Annotation Requires Students to “Think Like a Scientist”

The GEP facilitates the process by which a student confronts the challenges of annotating a 40- to 60-kb stretch of *Drosophila* DNA. To generate a defensible annotation, students must analyze and evaluate multiple available lines of evidence to generate gene models within their claimed sequence. The GEP project is set up using the genome browser software developed by the Genome Bioinformatics group at the University of California–Santa Cruz (Kent *et al.*, 2002). The browser is hosted at WUSTL and populated with in-house-generated evidence tracks for each stu-

dent project (GEP, 2013b). By selecting appropriate tracks, the student can see the results of a BLASTX search against *D. melanogaster* (identifying conserved protein-coding regions), the predictions obtained with several different ab initio and evidence-based gene finders, the results from RepeatMasker, any RNA-seq data available, TopHat analysis of the RNA-sequencing data (suggesting exon/intron splice sites), predicted splice site donors/acceptors, various conservation tracks, and so on (Figure 2). Inevitably, some of the lines of evidence supporting the presence of a gene will be contradictory, particularly for the details of exon/intron structure. The student must decide which collection of evidence should be given most weight in deriving his or her final gene model and be prepared to defend that conclusion.

The execution of a GEP research project is designed to require a student to traverse all six categories of cognitive skills found in Bloom’s taxonomy (Bloom and Krathwohl, 1956; Anderson *et al.*, 2001; Table 2). Students start with practice annotation problems (posted on the GEP website at http://gеп.wustl.edu/curriculum/course_materials_WU/annotation/annotation_exercises) and are guided by a general GEP protocol. Research outcomes will include the expected and the unexpected—all “rules” are broken at least some of the time! Among the latter, students have identified new genes not present in *D. melanogaster*, instances of stop-codon read-through, changes in exon number, shifts in splice sites, use of noncanonical splice sites, insertions of additional amino acids, and the loss and gain of isoforms. Another annotation challenge can be found with pseudogenes, which are rare in *Drosophila* but do occur. Changes in gene order and orientation within the element are observed, and ~10% of all genes have moved from one chromosome to another during 40 million years of evolution (for examples, see Leung *et al.*, 2010). Thus, while students are guided by their knowledge of the well-annotated *D. melanogaster* genome, each new species presents numerous challenges and reveals a new perspective on genome structure. At the end of their analysis, students submit a standard report to the GEP. In addition, most faculty members (96%) require students to communicate their findings to their colleagues, mentors, and/or the broader community as part of the overall process. As reported by GEP faculty, a variety of mechanisms have been implemented, including oral (83%), written (94%), and poster (40%) formats.

Project results are compared and reconciled by undergraduates working at WUSTL during the summer. We find complete congruence in 50–65% of submitted gene models, varying with the level of difficulty as judged by the degree of sequence divergence from our reference species, *D. melanogaster*. (Work on a given species usually stretches over more than one semester; as a consequence, some recorded discrepancies occur simply because the *D. melanogaster* annotation has changed between the first and second round of GEP student annotation.) Common errors, most of them readily rectified by experienced students, include missing an annotation for a gene present in that project, missing a possible isoform, or choosing a nonoptimal intron/exon splice site. Generally, students make poor choices when they rely exclusively on one source of data (BLAST alignments, gene predictors, or other), rather than assessing all of the data available to identify genes, isoforms, and splice sites.

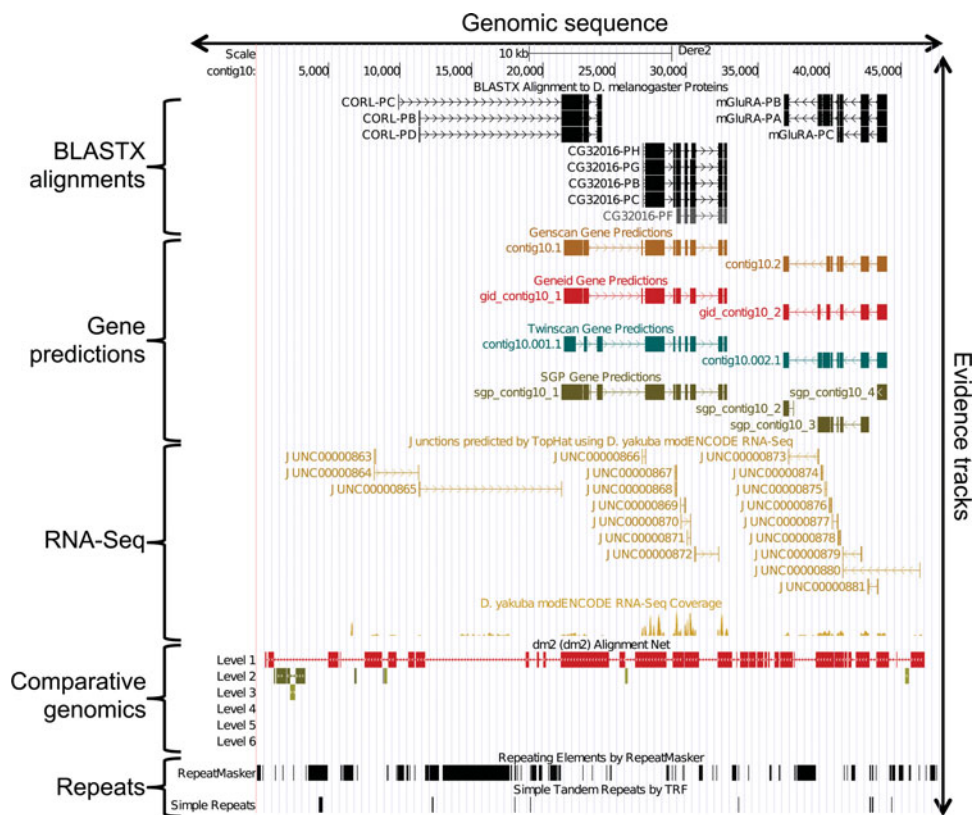


Figure 2. The GEP UCSC Genome Browser. Students are challenged to analyze and evaluate the available evidence assembled on the genome browser to create optimal gene models and explore other genomic features. A sample of the available tracks is shown here. Often the available evidence is contradictory; e.g., see the discrepancy between some of the gene predictions and the organization of genes suggested by homology with *D. melanogaster* (BLASTX alignments).

Collectively, GEP students in collaboration with the Genome Institute at WUSTL have examined and improved the quality of more than 7 million base pairs of sequence from these species and have generated more than 1000 gene models, providing a detailed picture of the differing characteristics of the genes present on the fourth chromosome and the pattern of evolution of this domain. We are currently preparing a manuscript describing student-generated results from this study that will have ~500 student and ~50 faculty coauthors and will acknowledge contributions from many classes.

Participation in GEP Projects Promotes Knowledge Gains

GEP projects are designed to easily integrate student research into laboratory curriculum suitable for use during the academic year while remaining fundamentally grounded in research. Success toward this goal is measured by student gains in both cognitive and affective domains. The desired outcome is that GEP students are learning the concepts and skills being taught, becoming engaged and confident in their skills, and perceiving their work as a valuable research contribution.

Table 2. GEP students completing a research experience utilize a range of cognitive skills from Bloom’s taxonomy^a

Taxonomic skill	Utilization by GEP students
Remembering	Correctly use and define terms
Understanding	Explain steps required for gene annotation
Applying	Use BLAST to identify sequences similar to the sequence of interest Use FlyBase, UCSC Genome Browser, Gene Record Finder to retrieve information about a gene
Analyzing	Diagram possible gene structure
Evaluating	Identify features (CDS, exons, repeats) in a genomic DNA sequence Evaluate alternative gene models
Creating	Select most likely gene model and support choice using multiple lines of evidence Assemble a well-documented annotation for a region of the genome under study

^aBloom and Krathwohl, 1956; Anderson *et al.*, 2001.

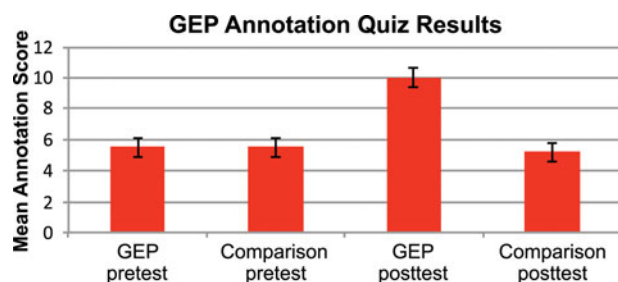


Figure 3. GEP students show gains in their understanding of genes and genomes. The bars depict the mean scores on a 20-point quiz on genes and genomes attained by GEP students who participated in annotation and by a comparison group over 2010–2011 and 2011–2012. The GEP pretest data include 1026 observations; the GEP posttest data include 748 observations. The increase in scores was evaluated in two ways: first, with an independent-groups t test ($t = 26.1$, $df = 1836$, $p < 0.05$), and second, with a paired t test for matched data ($t = 21.9$, $df = 393$, $p < 0.05$). The comparison pretest data include 133 observations, while the comparison posttest represents 87 results from non-GEP students. The error bars represent two SEM. Cronbach's alpha statistic averaged 0.84 for these quizzes in 2011–2012.

We assessed knowledge gains concerning genes and genomes using the quizzes described above. Comparing the performance of all GEP students on a pre- and postquiz, we find that the average score increased by 4.4 points (out of 20) at the end of the course (Figure 3). This increase was not seen in the comparison students who had not been exposed to the material through a research-based curriculum. We note that students were provided no external incentive to make an effort to perform well on this quiz, suggesting that the gains shown reflect secure knowledge. Those students who participated in sequence improvement (finishing) showed similar gains on a finishing quiz (Supplemental Figure S1). These results are consistent with the previously reported knowledge gains for a smaller group of students measured using an earlier version of the quizzes (Shaffer *et al.*, 2010).

To investigate these gains in detail, we categorized quiz questions based on the cognitive skills tested using Bloom's taxonomy and found that questions correctly answered by GEP students on the postquiz spanned all skill categories. To look specifically for gains in higher-order cognitive skills, we compared results for quiz questions that tested lower-level skills (Bloom's levels 1–2; see Table S1) with results for the other quiz questions, which were designed to test higher-level skills. Comparing the performance of all GEP students on the pre- and postquiz, we find that the average score for lower-level quiz questions increased from 4.20–5.75 points, while the average score for higher-level quiz questions increased from 1.56–4.4 points (total $n = 382$ for this matched set). These data suggest that students' engagement in the annotation project provided practice and subsequent learning gains across a wide range of cognitive skills (see Table 2), and point to gains in higher-order skills. Although the absolute scores on the current quiz were lower than those previously reported (Shaffer *et al.*, 2010), the degree of change is similar. We attribute the shift in absolute scores to the relative difficulty of the current versions of the quiz. Nearly half of the questions on the new quizzes used here test higher-order cognitive skills, while the earlier version focused on lower-level skills.

Students Engaged in GEP Show Learning Gains Similar to Students in an Independent Summer Research Project

We assessed student attitudes and perceptions of their GEP-related experience using a modified SURE learning survey (Lopatto *et al.*, 2008). For comparison, we used data collected from students who were involved in a traditional summer undergraduate research experience in research laboratories. In a section identical to the SURE survey, we asked students to report their learning gains on 20 items. The average responses from the classroom-based GEP students show greater gains than those reported by summer (SURE) students on 19 of 20 items, although for many of the items, the difference was not statistically significant (Figure 4). The results from this larger and more diverse pool of students confirm our prior finding that the GEP research project is as effective as a summer research experience by this measure (Shaffer *et al.*, 2010), but the larger data set allows a more detailed analysis as well.

The survey comparison reveals several noteworthy differences between the GEP and the SURE experiences. The two single items with the largest difference involved statements wherein students indicated how much they felt they gained in understanding science. For both the statement "Understanding how knowledge is constructed in this field" and the more general "Understanding science," GEP student responses averaged above 3.85, while the averages of the SURE student responses were below 3.53. (For both of these categories the SE for the averages of the SURE and GEP responses is < 0.04 .) We suggest that it is the process of grappling with contradictory evidence and the need to generate a defensible resolution in a rather short period of time (during one semester) that elicits these gains. While desirable, this sort of challenge does not always occur during the summer research experience. Similar differences were also seen for "Understanding that scientific assertions require supporting evidence" and "Ability to analyze data and other information." Another noteworthy item is "Learning laboratory techniques," for which the SURE responses averaged significantly above those of the GEP students (3.82 vs. 3.46). It is clear that not all students view their acquisition of new computer-based skills as "learning laboratory techniques," presumably because they associate laboratory techniques with traditional bench or field experimentation.

Because they are designed to be group projects centered on genomics, the GEP courses provide the opportunity for students to gain additional skills not reflected in the SURE design. Indeed, GEP students also reported significant and reproducible gains in learning computer skills, skill in reasoning from data, self-confidence in discussing science with peers and mentors, skill in scientific writing, and learning to work as part of a team (average ~ 3.8 on a scale of 1–5, as above). Despite the reported gains in learning, students reported smaller gains in their willingness to take additional courses in math and computer science. The results were consistent year to year (Figure 5).

As part of the GEP-specific attitudinal survey, students were asked to assess how much they gained from the various teaching materials and course activities. As reported previously (Shaffer *et al.*, 2010), students gave the highest ratings to working on their own projects, in agreement with previous findings stressing the importance of student "ownership" (Hanauer *et al.*, 2006). Student comments were

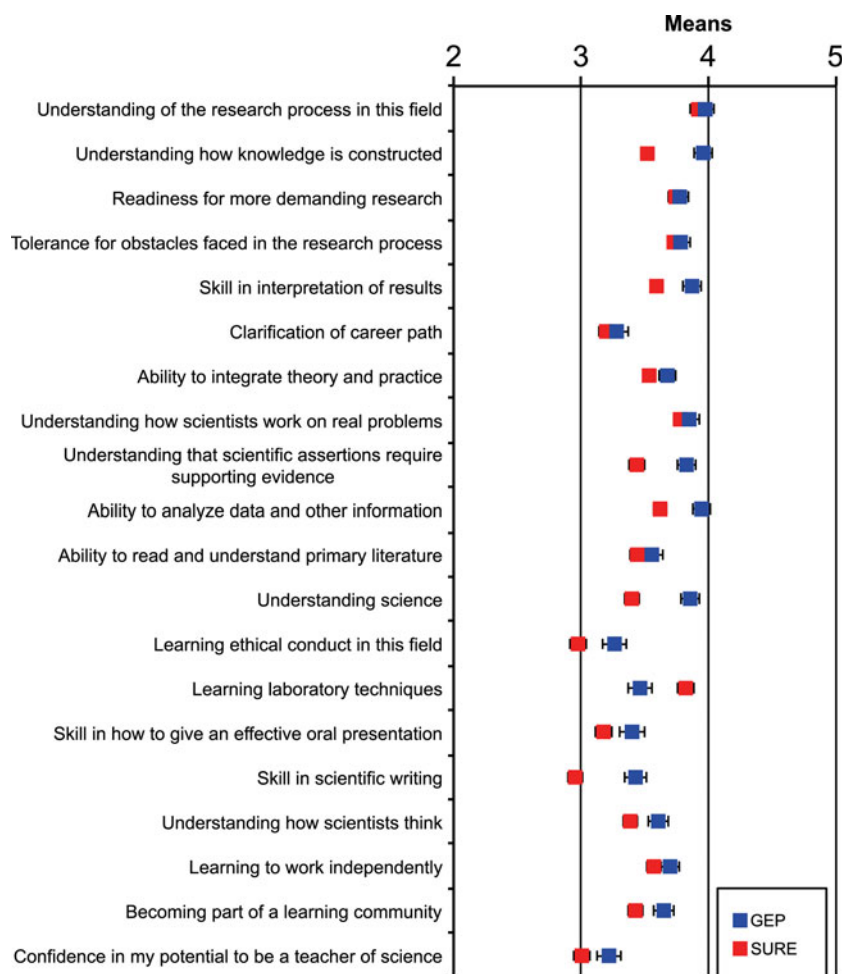


Figure 4. Self-reported student learning gains using the SURE survey. Blue squares indicate the mean for GEP students, while red squares indicate the mean for SURE summer research students, 2009. Error bars represent two SEs below and above the means. The SE for the averages of the GEP and SURE responses was <0.04 . Data shown combine results from surveys given in academic years 2010–11 and 2011–12; the data include between 652 and 751 responses on each of the 20 items from GEP students. The comparison group is the 2009 SURE survey of 1653 students who had just completed a summer in the lab. The large number of students allows for smaller error estimates than in our previous study (Lopatto *et al.*, 2008).

invited at the end of the survey; these comments also stressed the importance of being responsible for their own projects, while participating as a team member.

Students at Diverse Institutions Show Similar Gains in Project Outcomes Assessment

Having a large data set from diverse institutions allows us to correlate various aspects of the GEP experience with desirable outcomes. The GEP is made up of a very diverse group

of schools (see current members at GEP website), allowing us to look for possible moderators influencing student performance. Institutional parameters examined included public or private status, size (total enrollment), degree types granted in biology, selectivity of admission, and other publicly available data. We collected additional data on the character of the student body, including the percentage of the student body that is residential versus commuter, minority, first generation to college, or nontraditional (more than 25 yr old). Thus, we selected 10 characteristics of interest and

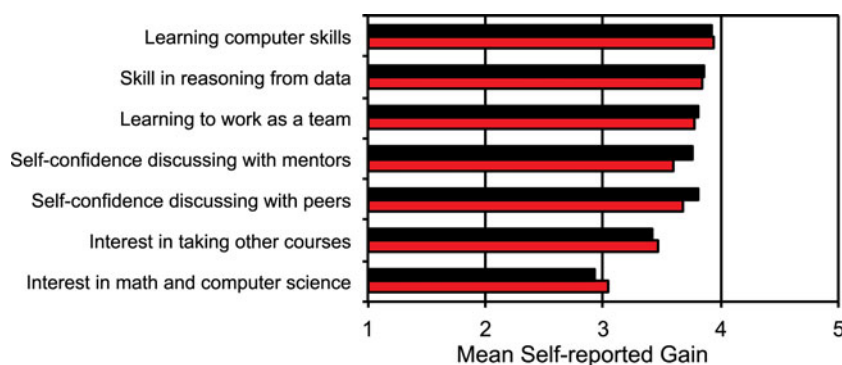


Figure 5. Additional gains from a GEP experience not queried in the SURE survey. Student self-reported gains, assessed on a scale of 1 (no gain) to 5 (very large gain). GEP 2011 (337–344 cases): black; GEP 2012 (391–394 cases): red.

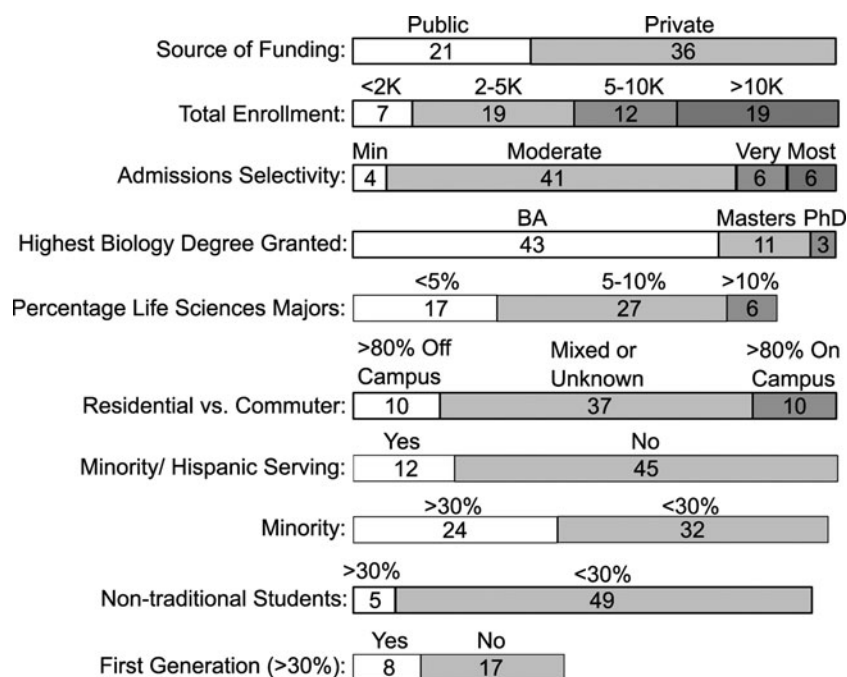


Figure 6. Diversity of GEP institutions with students participating in the above assessment during 2010–2011 and 2011–2012. For the purposes of this survey, nontraditional students are defined as those over age 25. Total number of schools represented is 57. Some schools do not collect some of the above data, resulting in some incomplete data sets. Data from U.S. News & World Report Staff (2011) or supplied by the institution.

binned the schools into various categories based on these data (Figure 6).

We then tested these categorical data to see whether the characteristics correlated with student outcomes as measured above. Using multiple linear regression to test for correlation, we found that neither student improvement on the annotation quizzes nor positive responses on the GEP SURE-matched learning survey correlated significantly with most characteristics of the home institution. Correlations were not found to be statistically significant for public versus private school, student body size, the presence or absence of advanced degree programs in biology, or service to any particular type of student (e.g., first generation, nontraditional, commuter, and/or minority). All institutional characteristics (shown in Figure 6) taken together accounted for only ~6% of the total variance within the annotation quizzes and self-reported SURE learning benefits (averaged over 20 benefits). Looking at student subpopulations, we find that students across all ethnic groups benefited; there is no statistically significant difference in pre/postquiz gains and no difference in GEP SURE learning benefits among ethnic groups. While we understand that these measures may not have captured all the ways in which institutional differences can affect student outcomes, we have found from individual experiences that the GEP offers a pedagogical approach that has been successful in many settings. To expand on this theme, we as faculty have compiled our personal experiences in response to the question “What has been the impact on your students?” These responses are provided in the Supplemental Material (Text S2). We are encouraged to believe that students from diverse institutions and backgrounds can greatly benefit from a research-oriented laboratory experience in genomics such as the one outlined here.

Time Devoted to the Project Is a Critical Factor in Gaining a Research Experience.

As noted above, we have utilized GEP project materials in a variety of types of courses. See the table of faculty members on the GEP website (http://gep.wustl.edu/wiki/index.php/Table_of_Faculty) for a listing of syllabi, indicating the participating school and type of course. We used the table of faculty reports to gain insights into how the GEP curriculum was being implemented. When the GEP research project is a central focus of the course, 48 faculty members report that they organize the class such that students do the majority of the work in class and typically (40 of 48) devote a total of 25–45 instructional hours to the project (lecture, discussion, demonstration, lab work). Some faculty members (six) use a course design in which students are expected to do a substantial fraction of their analysis outside class time; for these courses, 10–25 h of class time is devoted to the project. An independent study course may focus on the GEP project all semester or be combined with another topic. In contrast to these, a 3-wk lab module designed primarily to introduce students to the structure of eukaryotic genes may require as little as 10 h (see example posted at [http://gep.wustl.edu/curriculum/course_materials_GEP_partners/able_workshop;Emerson et al., 2013](http://gep.wustl.edu/curriculum/course_materials_GEP_partners/able_workshop;Emerson_et_al.,_2013)). While the latter utilization of GEP material serves its immediate purposes of teaching the structure of eukaryotic genes and exposing students to bioinformatics tools and databases, it raises questions as to whether the students can gain what can be classified as “research experience” in such a short time interval. To address this question, we compared student gains as assessed through the postcourse survey with the amount of time spent using GEP materials. Faculty members reported participation levels that ranged from 3 to 64 h per term. From these data, we created four quartiles (Q1–Q4) of

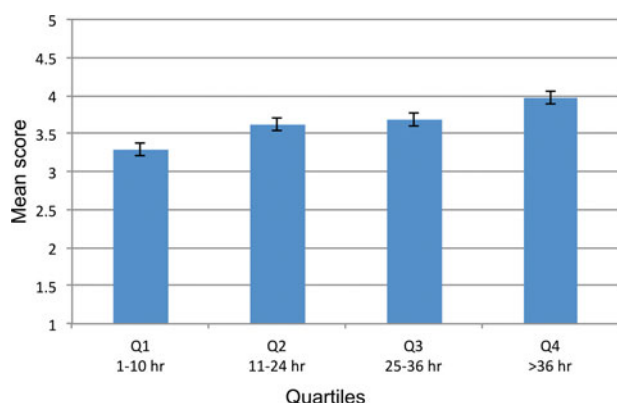


Figure 7. The 20 learning gains (SURE) reported by GEP students were averaged and plotted against the four quartiles of annotation project hours. There was a significant difference in average learning gains across quartile groups ($F = 11.9$, $df = 3, 374$, $p < 0.05$). Pairwise contrasts indicate a significant difference between Q2 and Q4, but not between Q3 and Q4. The number of class hours utilized by each quartile group are shown above. The number of student respondents in each quartile is: Q1: 58; Q2: 139; Q3: 65; Q4: 116. (Respondents tallied here are only those who answered all 20 questions on the SURE survey.) Error bars represent two SEM.

instruction time. A bar graph showing the relationship between annotation instruction time and student learning outcomes (SURE-type survey) is shown in Figure 7. The results show a strong relationship, with higher learning gains (the average of all 20 SURE questions) resulting from more time devoted to the project.

These results argue that it is necessary to invest significant course time (combined lecture, discussion, lab work time, etc.) for students to gain a research experience, as defined by the questions in the SURE survey, when a genome annotation project is used. Faculty observations suggest that a time investment is needed to gain familiarity with using the bioinformatics tools before students can begin to ask their own questions, feel comfortable in interrogating the data, and gain confidence in their own analytical abilities. Nonetheless, the instructional time needed is quite short compared with a summer in the lab, in which multiple weeks of preparation and work are necessary to provide mentorship for a relatively small number of students. The average time spent by Q2 faculty was 20.4 h, while that spent by Q4 faculty was 45.5 h.

To investigate in detail the influence of time spent on student learning gains, we mapped the average gain for students in each quartile onto the individual potential learning gains from the student surveys. The results on comparing the average gains of the Q1 and Q4 students, as seen in Figure 8, reemphasize the advantage of devoting extended class time to the development of a successful project. The seven additional learning benefits that GEP students evaluated show similar differences (Figure 9). Note that reporting the data in this way allows a tally of all responses to a given item, resulting in a significantly larger pool of respondents. The results support our prior conclusion, specifically, that a significant commitment of class time (>36 h) is required to obtain the full benefits of a research experience.

Alumni Attitudes Also Show Increased Value with More Time Invested

To determine the effect of this curriculum-based research experience on student career trajectories, we obtained demographic and attitudinal data on students who had formerly taken a GEP course or served as a TA in a GEP course. Data were collected during the summer and fall of 2012 by an online survey that included demographic and attitudinal questions. The earliest cohort surveyed took GEP classes in 2005, the last cohort in Fall 2011. We had 473 valid responses (29% of the students contacted); however, because all questions were voluntary, the total number of responses to any one question rarely totaled 473. The students reported that they came from 41 different institutions. The diversity of institutions represented is similar to that found in the student survey (Figure 6; see data in Figure S2). Of the respondents, 200 described themselves as male, 268 as female; the pool was 59% Caucasian, 20% Asian, 17% underrepresented minorities (African American, African, Hispanic), and 5% mixed plus other. All others declined to respond.

To investigate the current occupations of the alumni respondents, we gave them a series of 16 career categories and allowed students to select one or more as appropriate. Figure 10 shows the total number of alumni that selected each category. The three largest areas of occupation (pooling some categories) reported by the alumni were being a postsecondary student in science (pursuing an MA, PhD, or other professional degree: 30%), medical school student (pursuing an MD or MD/PhD: 22%), and employment in science (19%). Only 9% indicated they were no longer in science (pooled PhD nonscience, other professional nonscience, and employed nonscience). These results are very encouraging; however, as in any survey of this type, the findings may be impacted by response bias; that is, those students continuing in science may have been more inclined to respond to the request to participate in the survey.

To examine the attitudes these alumni had toward science in general and their experience with the GEP in particular, we asked them to complete a survey much the same as our original postcourse learning survey. Alumni were asked to reflect on and evaluate their experiences and learning gains, given that some time had passed since they had taken the GEP course. Figure 11 shows the average response to these questions, with 1 being “strongly disagree” and 5 being “strongly agree,” that their GEP experience fulfilled each particular goal. In addition to the overall average for these topics, we also cross-correlated the results with the extent of the GEP experience to which each student was exposed. Students were asked to pick one of four responses as describing the type of GEP course that they took. These were: 1) a course devoted primarily to the GEP project, 2) a course spending half or more of the time on the GEP project, 3) a course that spent a quarter of the time on the GEP project, and 4) a course in which just one to three labs were devoted to the GEP project. Figure 11 shows the average responses for each of these groups (numerical data in Table S2). In general, there was a clear and consistent increase in attitudinal gains as students spent more course time working on their GEP project. The average of all items for each group was 1) 4.02, 2) 3.62, 3) 3.30, and 4) 3.03.

Items common to both the alumni and current student surveys allow us to directly compare responses from current

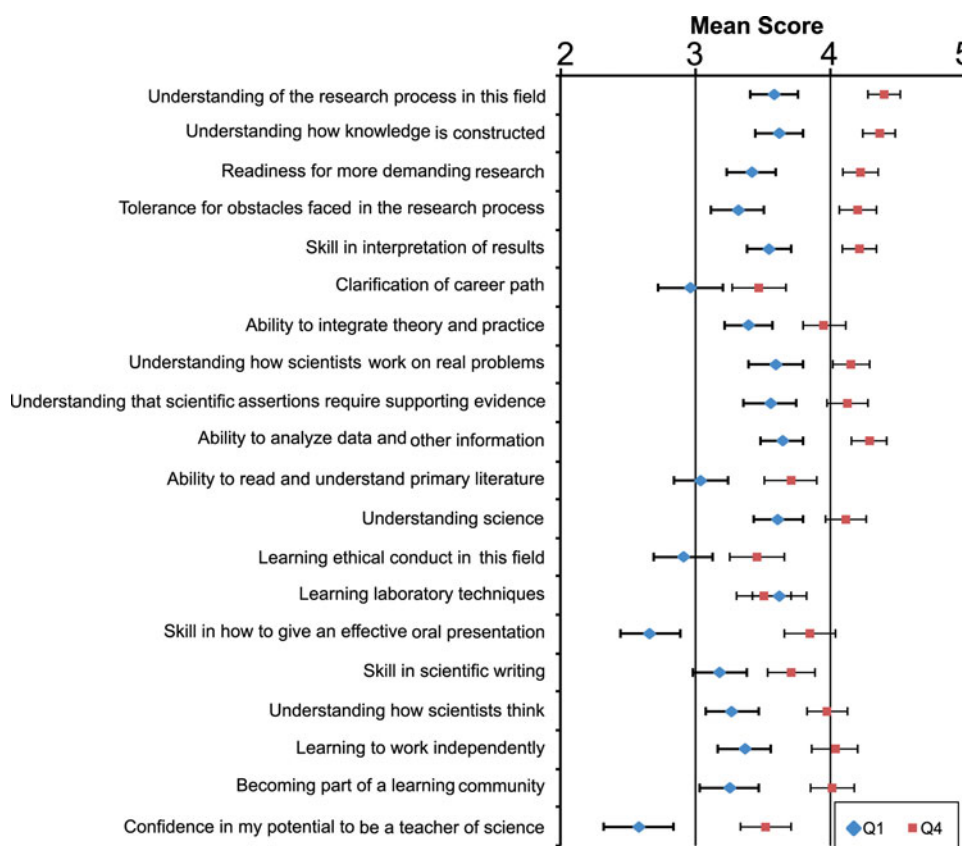


Figure 8. Comparison of student responses on the 20 learning gain items (mean and SEM) from the SURE survey. The data are classified by instructor reports of the number of hours devoted to the annotation project. These were divided into four quartiles as shown in Figure 7; the responses from the Q1 (1–10 h) and Q4 (>36 h) students are shown here. The Q1 group includes 86–112 observations; the Q4 group includes 149–175 observations. (Respondents tallied here were those who answered the specific question on the SURE survey.) Error bars represent 2 SEM.

2012–2013 GEP students with those of the alumni. Figure 12 shows these comparison data. In most cases, the alumni had a very positive response to their GEP experience, showing an average response to each item that was ~0.25–0.4 units higher than the average from the current GEP 2012 cohort. One item, “Genomics is awesome,” showed a difference larger than the typical range, with a difference of 0.63. These results suggest that the students value the experience more as they find that what they learned in their annotation project has applicability to their further pursuits.

Again, one might be concerned about response bias. In particular, we asked whether the students who had spent more time working on the GEP research project were disproportionately represented in the pool of students who responded to the alumni survey. We found that 30% of the alumni respondents fell into the group having a brief GEP experience (one to three lab sessions, the equivalent of Q1 above), while 26% of the current students fall into Q1 (<10 h work with GEP). Thus, the two pools are roughly similar in distribution across the course types through which the GEP project is offered.

Alumni students were also invited to comment on their GEP experience. In particular, students were invited to respond to the question “Please comment on your GEP experience: What was good about it, and what changes would have made it better?” Most of the student comments were fa-

vorable (~90%). The most common comments from alumni stated that they enjoyed the course, they enjoyed the independence, they appreciated having a real research project, they learned a lot, and the experience made them feel like researchers. Other comments emphasized that the experience was relevant to their future plans, was interesting, and inspired teamwork. Several students commented on their initial confusion and subsequent development of understanding. (See Table 3 for a numerical analysis of the 320 comments, as well as sample comments for each category.) The results of this survey support the conclusion that we can provide a robust learning experience in genomics through a research project. They further reinforce the notion that an in-depth research experience with a considerable time investment produces the most tangible and long-term gains.

DISCUSSION

The importance of providing research experiences for science, technology, engineering, and mathematics undergraduates is well documented (see references cited in the *Introduction*). However, providing such experiences has been challenging due to the substantial resource and personnel requirements for individual mentored research. Classroom-based undergraduate research experiences can provide an alternative,

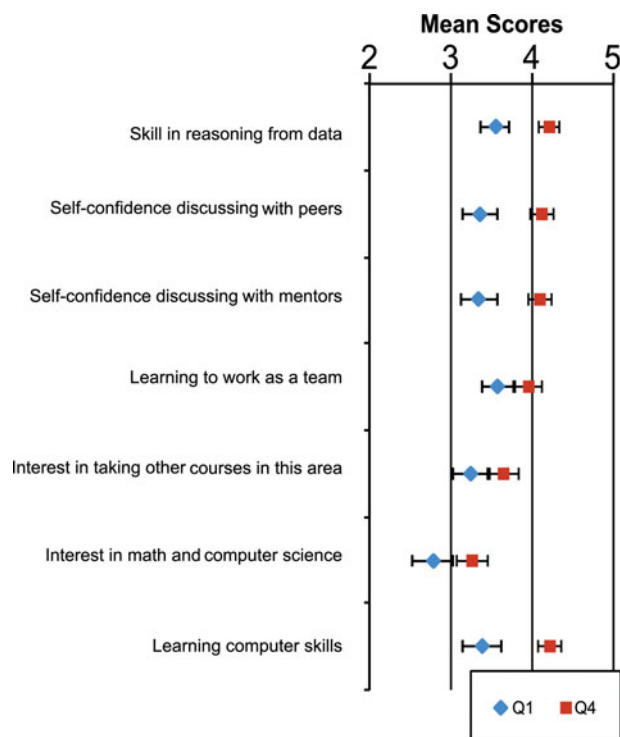


Figure 9. Comparison of student responses on seven additional learning benefit items categorized by the reported number of hours of instruction and lab work on the annotation project (Q1: 1–10 h; Q4: > 36 h). The Q1 group includes 105–107 observations; the Q4 group includes 172–174 observations. (Respondents tallied here were those who answered the specific question.) The error bars represent two SEM.

but despite this, many outstanding pilot projects (see *Introduction*) have not been widely adopted, perhaps because of concerns about the different needs and cultures of institutions of various sizes, missions, and budget, or of students with diverse levels of preparation. The expansion of the GEP to ~100 affiliated schools in the past 3 yr has allowed for the collection and analysis of student outcomes to determine whether specific factors contribute to the knowledge gains (quizzes)

and self-reported learning gains in understanding research (survey) observed among GEP students. Institutional characteristics such as public or private funding, student body size, the presence or absence of advanced degree programs in biology, or the prevalence of particular subgroups of students such as first-generation college students or minority students had no significant effect on the overall knowledge and learning survey scores. Interestingly, responses by both current students and GEP alumni indicate that gains are enhanced by increased time invested in the research project in the classroom.

These findings demonstrate the utility of a broad-based, centrally organized genomics research project in providing successful classroom research experiences for undergraduates across diverse institutions. They further suggest that it is worthwhile to devote a significant amount of class time to achieve the full benefits of a research experience for a large number of students. The outcomes of student participation in such a program compare favorably with extracurricular undergraduate research experiences in terms of positive influence on students over time. This outcome may in part be the result of features of the project structure that mirror both the scientific process and utilization of the cognitive skills outlined in Bloom's taxonomy; student responses indicate strong gains, particularly in learning about the nature of science and the research process, along with attainment of competence and confidence in research skills, particularly in analyzing conflicting data and achieving a defensible resolution.

The data demonstrate a significant correlation between the amount of time devoted in a course to GEP materials and the perception of the experience by undergraduates as actual research, a result seen among both current students and GEP alumni. Importantly, students who were exposed to as little as 10 total semester hours of GEP work showed significant learning gains, as did students exposed to an average of 45.5 instructional hours (Q4) in a semester. However, the distinction between smaller and larger faculty investments of class time in the research project is revealed when assessing student confidence data; a significant investment of classroom time in the project is necessary to provide an experience that attains the full benefits of a research experience. This time-dependent variation in our learning versus confidence outcomes reflects

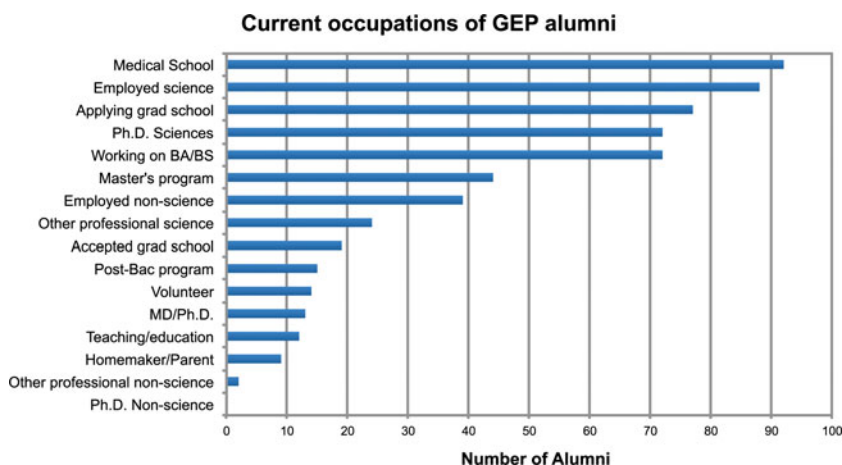


Figure 10. The current occupations of GEP alumni as self-reported on the alumni survey.

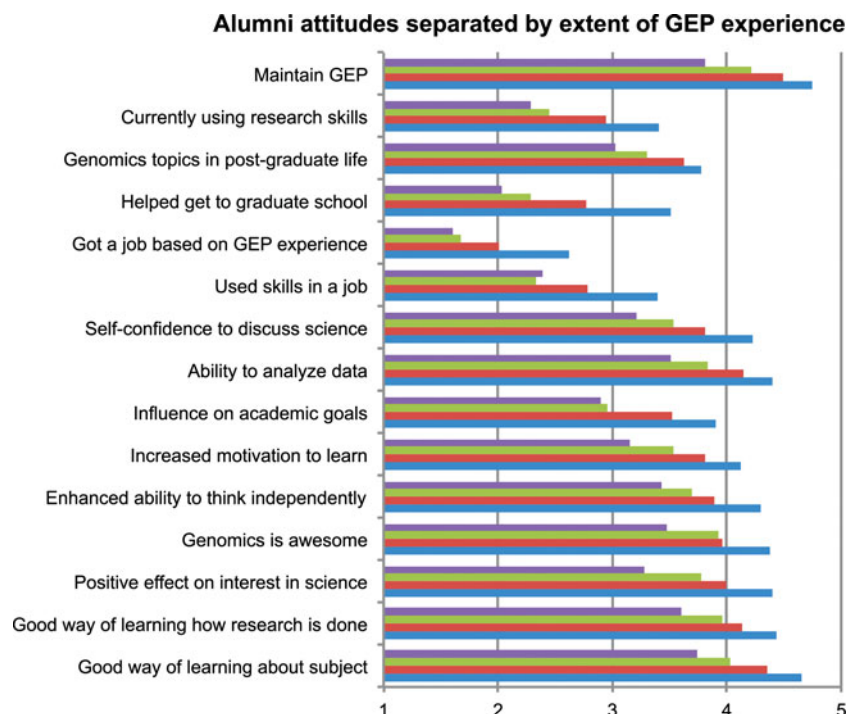


Figure 11. Alumni student attitudes separated by extent of GEP experience. Purple: “Took up just 1–3 labs”; green: “Course spent quarter”; red: “Course spent half or more”; blue: “Course devoted primarily to the GEP project.” Scale is 1–5, with 1 being “strongly disagree” and 5 being “strongly agree.” See Table S2 for numerical values.

the classic question of “content versus experience” that is at the heart of many pedagogical debates in science education: Is the student educational experience compromised by sacrificing emphasis on content for a more inquiry-based and experiential learning? We would argue, based on our above findings, that the use of a research project as a significant component of a biology course has significantly bolstered student confidence and competence, as evidenced by GEP alumni student comments and by them continuing their careers in the sciences. An increase in the science-literate workforce is one of the most tangible goals as we respond to calls for increased undergraduate research opportunities.

A notable outcome of implementation of the GEP curriculum as compared with a SURE experience is the same or larger reported student learning gains in understanding the practice of science. The differences in scores between GEP and SURE students may be influenced by the fact that students in a research-based classroom environment are in a large community of peer learners. Undergraduate students involved in a summer research experience at a university are often working with a postdoc or graduate student and few direct

peers. The parallel research experiences provided as part of a research-based course allow for peers to assist and support one another in deeper and more meaningful ways than they might otherwise have the opportunity to do. The simultaneous act of mentoring and being mentored contributes to the opportunities that students have to gain practice and confidence in their abilities as scientists. Additionally, not all undergraduate students involved in a SURE program have a substantial stake in the research project. Indeed, student comments on their GEP experiences often stress the importance of being responsible for their own projects, while participating as a team member. Finally, more than 90% of the implementations of the GEP curriculum required students to report their results in some manner to a broader scientific community, either to their class, to others at their institution, or to those assembled for regional or national scientific meetings. This opportunity for students to participate in the scientific community, as scientists do, contributes much toward shifting students from their accustomed roles as observers of the scientific process to active and competent participants in the scientific process.

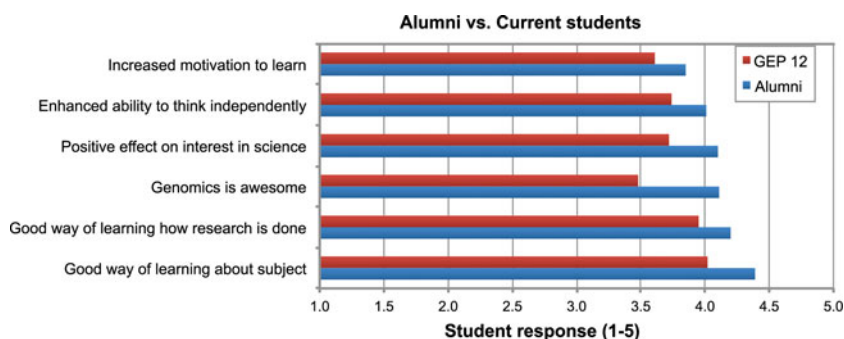


Figure 12. Comparison of alumni and current student responses to six attitudinal survey questions. Scale is 1–5, with 1 being “strongly disagree” and 5 being “strongly agree.”

Table 3. Frequency analysis of alumni responses to the question “Please comment on your GEP experience: What was good about it, and what changes would have made it better?”

Comment	Frequency	Examples ^a
Enjoyment (literally saying “I enjoyed the course” or a thought much like it).	42	<p>I enjoyed getting to experience the ownership of a portion of a project (my fosmid) while still being able to have the opportunity to work in a group setting and learn with my peers.</p> <p>I enjoyed participating in the GEP program because it allowed myself and a partner to really take a hands on approach to genomic education. The project was ours, had our name on it and we really felt like we contributed to the science. The process was long and at times difficult but overall, I enjoyed being part of it.</p> <p>I really enjoyed the feeling of participating in a meaning [<i>sic</i>] research project. In addition, I think it encouraged active participation in the class and encouraged partners to work diligently together to achieve a common goal.</p>
Research-like (comments about how either the topic or the work made the student feel like a researcher as opposed to a passive student).	10	<p>Working on near-independent projects in the small-group setting really set the course apart from other college experiences; it is certainly the closest a course ever came to emulating an actual research project.</p> <p>I liked that we were doing real, primary research, working directly with original sequence data.</p> <p>It was nice to actually be doing science “first-hand.”</p>
Important or significant (similar to faculty comments that it was useful to be engaged in significant research).	6	<p>I liked that what I did actually counted!</p> <p>It was very rewarding to take a class in which your work truly has an impact on the scientific community in comparison to most other classes where the learning is essentially to achieve personal means of learning the information and performing well on the examinations.</p>
Confusion to clarity (comments that the early part of the course was confusing or frustrating but then learning led to clarity and understanding).	6	<p>I thought it was great to contribute to something practical and useful.</p> <p>From what I recall, it was initially confusing as I got familiar with the websites and software required to analyze fosmid. Once I got going, though, it was like solving a puzzle, and I was satisfied with my work when the project was over. I can’t think of anything in particular I would like to change.</p> <p>Frustration can easily occur when looking for a your fosmid. However, struggling through this research is also the best part because it is the best way to learn and understand your research.</p> <p>Constantly it was a trial and error for figuring out which key to use or tab, but once I knew how to use it, it was very easy but for the first couple of times it was confusing.</p>
Relevant (was relevant to science or to grad school or career).	8	<p>I think genomics is becoming a more relevant field and every student with an interest in bioinformatics, cell/molecular biology, or genetics should be exposed to the GEP course.</p> <p>I really enjoyed learning how to use all of the online bioinformatics resources. They have been extremely useful in my graduate studies. I think a stronger emphasis on annotation should be made due to the advances in sequencing technology [that] will probably make finishing obsolete in the future.</p> <p>The GEP experience was very helpful in introducing me to the field of bioinformatics and its associated tools. I consistently make use of the skills I gained while taking the course now, during the completion of my PhD program. It also helped to improve communicating scientific data, as I presented my results during the class and will also be a coauthor in an upcoming scientific article.</p>
Realistic (the research was on a “real” or “authentic” problem as opposed to a scripted lab).	16	<p>I liked that we were doing real, primary research, working directly with original sequence data.</p> <p>Gave a chance to get students involved in real-world work in the field of molecular biology and bioinformatics. Interesting and a great way to problem solve.</p> <p>Having a hand in generating real primary research as an undergraduate gave me so much more independence in my view of science. I did feel like I owned my project and was contributing to the greater field of knowledge.</p>

(Continued).

Table 3. Continued

Comment	Frequency	Examples ^a
Independence (working and thinking independently).	22	It really involved a lot of independent thought and problem solving ability. I enjoyed the challenge and I enjoyed the fact that I was contributing to the knowledge base. I truly enjoyed working independently on our GEP project. It was the only course I had in my undergraduate career that had novel research findings and did not require work with a partner. It was somewhat difficult to keep a "notebook" during the course, though I believe that this is a reflection of how parts of research are becoming more computational and are not as conducive to a traditional daily log of research. Working independently (separate from the professor) on a project where the answers were not previously known was an invaluable lesson about the scientific process.
Learned a lot.	14	I learned more about genomics in this class than I did in any other class I took in school. I really did learn an immense amount of information while taking the course. Before taking this course, I had no idea how to annotate genes of any specimen and had never heard of websites such as pubmed, NCBI, flybase, etc. This GEP course really exposed me to a whole new topic within what we had learned in high school. I really enjoyed being able to understand the complex, yet stimulating GEP information in this course. I learned a lot about genomics, bioinformatics tools and about research. I think that it was a great experience.
Interesting.	5	The experience that I received increased my interest in bioinformatics. It was interesting to learn how to use the interactive tools and fun to discover new genes. It made me feel as if I was a part of something important. At first, I was somewhat confused as to what it was that we (my partner and I) had to do, but with time it became more and more interesting and fun.
Teamwork is important.	4	Teamwork was good and the feeling of contributing to science. Working as a team with my partner was fun. I learned a lot about sequencing.
Negative (comments about time and clarity of instruction).	36	Great experience of working together as a team and the results were perfect. We should have spent more time doing the project. It was frustrating to spend all that time learning how to complete the project and then only doing one fosmid. I feel there needed to be more time spent introducing and really explaining the subject matter. I felt thrown into it and it only tangentially related to my course material. The entire process should have been explained more. I was not sure what I was doing.

^aVerbatim sample quotes are shown for each category.

Clearly, we have not yet fully explored questions of scale. Those GEP-affiliated courses that strive for a full research experience are typically laboratory courses that enroll between five and 32 students, or independent study/research courses that enroll two to five students working together. Some GEP faculty members have used the project to provide an introduction to bioinformatics and gene annotation within a midlevel course in genetics enrolling 100–200 students. The instances to date devote only ~10 h to the GEP project, so presumably have a lower impact, as documented above. Anecdotal observations suggest that one trained individual for every six to seven novices is required to avoid the inevitable frustrations that come with learning any new computational system, and implementation on a large scale therefore requires a cadre of instructors. While the participation of one or more senior scientists who can provide perspective and context for the research itself is an important part of the cohort of mentors, much of the mentoring required is procedural and is often best supplied by peer instructors (undergraduate TAs) who can easily communicate the ins and outs of computational infrastructure. How large a class could

grow and still show significant student gains is unknown. Given appropriate staffing, and a willingness to devote class/lab time to the effort, it should be possible to expand the research experience to hundreds of students. How best to organize a large cohort to preserve the sense of a learning community and ensure that all students gain a sense of increased efficacy in doing science, has not yet been explored.

What sorts of projects are well suited for a research-based laboratory course that can be implemented at a range of different institutional types? Ideally, one would like to see a range of projects of this type available, to provide a good match with the different research interests of faculty members. Our thoughts have been shaped by discussions with other faculty members who are experimenting with this style of teaching, particularly with HHMI professors Utpal Banerjee (see Chen *et al.*, 2005; Call *et al.*, 2007; Evans *et al.*, 2009), Graham Hatfull (see Hanauer *et al.*, 2006; Jacob-Sera *et al.*, 2012), and Scott Strobel (see Bascom-Slack *et al.*, 2012). The following concepts, highlighted by the work of Hatfull *et al.* (2006, see Table 3 therein), fit many undergraduate programs but apply to bioinformatics particularly well.

The most important characteristic to consider in designing a research-based course is the development of a *parallel project*, one that allows the instructor to teach the students a common set of research tools and approaches while providing individual projects for the students. Ideally, the findings of the group as a whole provide added value to the individual results (e.g., the data will be more meaningful when brought together). For instance, given a starting DNA sequence assembly, a region of interest can be readily divided up among a class into smaller, overlapping projects, and the results subsequently used to reassemble the whole. The combined work of GEP students has allowed us to improve and provide careful annotation of megabase regions of selected eukaryotic genomes, something that could not be efficiently accomplished in any other way. Next, *technical simplicity* must be considered to maintain safety, provide compatibility with scheduling constraints, and ensure a high probability of success. A genomics research project has low start-up costs, requiring only computers with Internet access. There are no safety issues, and access to the project can be provided 24/7. There are no scheduling demands as such—no overnight incubations, no generation times to wait for, and so on. Many experiments, being electronic, can be repeated quickly in real time, so failure does not result in any significant costs or time penalties, and there is a high probability that one will learn something of value in the process. Third, a genomics research project can be *designed at many levels*, depending on the level of the students. For example, college freshmen generally do very well in annotating a prokaryotic genome or the genome of a phage (Hatfull *et al.*, 2006; Caruso *et al.*, 2009; Harrison *et al.*, 2011) while upperclassmen are ready to annotate and analyze a eukaryotic genome with its additional complexities, including multi-exon genes (Leung *et al.*, 2010; Shaffer *et al.*, 2010). Once students are engaged in the project, they find that there are always more questions to ask. Students taking computer science as well as biology can generate their own programs to address questions of interest. A research course can also be *designed to teach students skills* in accessing various databases and using bioinformatics tools appropriately, with homework or quizzes to test those skills. We find that it is important to utilize various checkpoints (e.g., requiring a report on the first attempt to annotate a gene) to provide feedback to students and develop their confidence. Also, if one *introduces students to the basic tools of the trade* (e.g., EMBOSS, 2013; NCBI, 2013; UCSC Genome Browser, 2013; etc.), the skills they develop can of course be applied subsequently to analysis of other genes and genomes. Importantly, all research has as its goal *publishable original findings*, and this aspect gives students an added sense of responsibility, knowing that other scientists will build on their work; the prospect of a coauthorship provides a tangible reward for their efforts. Even if time does not permit commitment to the research goal, introducing students to the research tools and challenging them to analyze raw data are of value. Finally, the effort involved in *completing one's own project*, while part of a group receiving similar training and struggling with similar challenges, appears to generate student ownership of the projects and creates a dynamic partnership overall.

Similar projects to the *Drosophila* number described here could be constructed around any number of model organisms to provide an accurate annotation of genomic regions of special interest and/or to address specific questions concerning the

organization and evolution of genes and genomes (for additional examples, see Kerfeld and Simons, 2007; Ditty *et al.*, 2010; Goff *et al.*, 2011; Banta *et al.*, 2012; Singer *et al.*, 2013). A consortium clearly has cost/benefit advantages, and we believe that more national projects of this type should be supported by agencies interested in improving undergraduate science education in the United States in partnership with those interested in the daunting task of improving the utility of large data sets such as genomic sequences. Both the need for and the value of bona fide research experiences for undergraduates are well established, and the success of the GEP experience confirms that such experiences can be provided for students economically in terms of both time and money. The continued success of such efforts generally encourages us to believe that such in-class research will become an increasingly common part of the undergraduate science experience.

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Supplemental Material

CBE—Life Sciences Education

Shaffer et al.

Supplemental Tables

	Quiz A	Quiz B
Remembering or Understanding	11	11
Understanding or Applying	2	2
Applying or Analyzing	5	6
Analyzing or Evaluating	2	1

Table S1. Categorization of quiz questions. The number of questions assigned to different categories of the revised Bloom's taxonomy by consensus of 10 GEP faculty evaluations. Concepts covered include initiation of transcription, start codons, initiation of translation, reading frames, splicing, split codons, translation, stop codons, alternative splicing, BLAST nomenclature, sequence alignment, BLAST e-values, gene homology, ESTs, gene models, gene prediction, phylogenetics, and pseudogenes.

My GEP affiliated laboratory course in genomics ...	ALL	full course	½ or more of course	about ¼ of course	just 1-3 labs
Good way of learning about subject	4.39	4.65	4.35	4.03	3.74
Good way of learning how research is done	4.20	4.43	4.13	3.96	3.60
Positive effect on interest in science	4.10	4.40	4.00	3.78	3.28
Genomics is awesome	4.11	4.37	3.96	3.93	3.48
Enhanced ability to think independently	4.01	4.29	3.89	3.70	3.43
Increased motivation to learn	3.85	4.12	3.81	3.53	3.15
Influence on academic goals	3.56	3.90	3.52	2.95	2.90
Ability to analyze data	4.16	4.40	4.15	3.83	3.51
Self-confidence to discuss science	3.90	4.22	3.81	3.53	3.21
Used skills in a job	2.95	3.39	2.78	2.33	2.39
Got a job based on GEP experience	2.17	2.62	2.01	1.67	1.60
Helped get to graduate school	2.96	3.51	2.77	2.28	2.03
Genomics topics in post-graduate life	3.58	3.77	3.62	3.30	3.03
Currently using research skills	3.04	3.41	2.94	2.45	2.29
Maintain GEP	4.51	4.75	4.49	4.21	3.81

Table S2: Results of the alumni survey. Numerical data for Figure 11.

Supplemental Figures

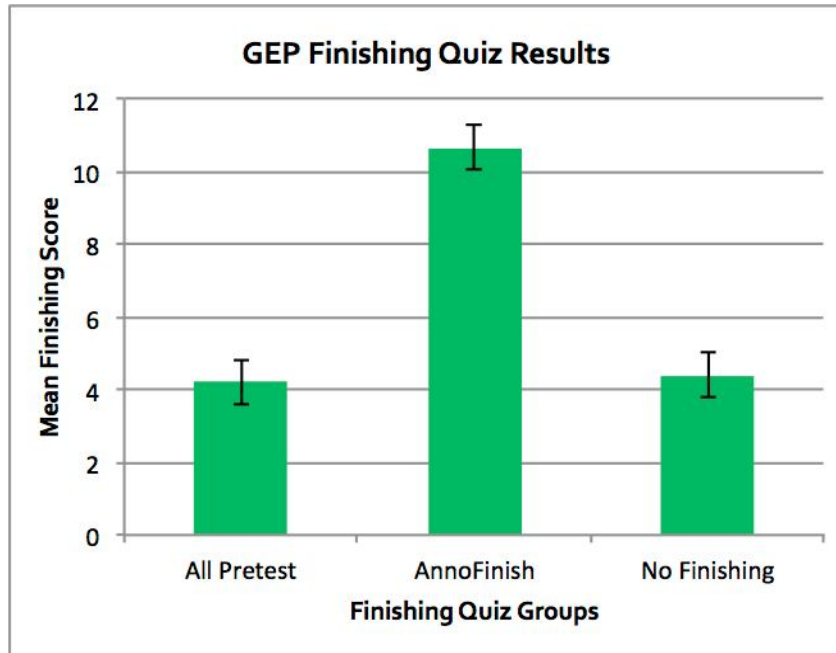


Figure S1. The bars depict the mean scores on an 18-point quiz on finishing by GEP students. The pretest data include 1026 observations; the “AnnoFinish” group had instruction in finishing ($n = 87$); the “No Finishing” group did not ($n = 661$). The increase in scores was evaluated with a between-groups statistic for complete available scores ($F = 170.5$; $df = 1, 417$; $p < .05$). Error bars depict 2 SEM.

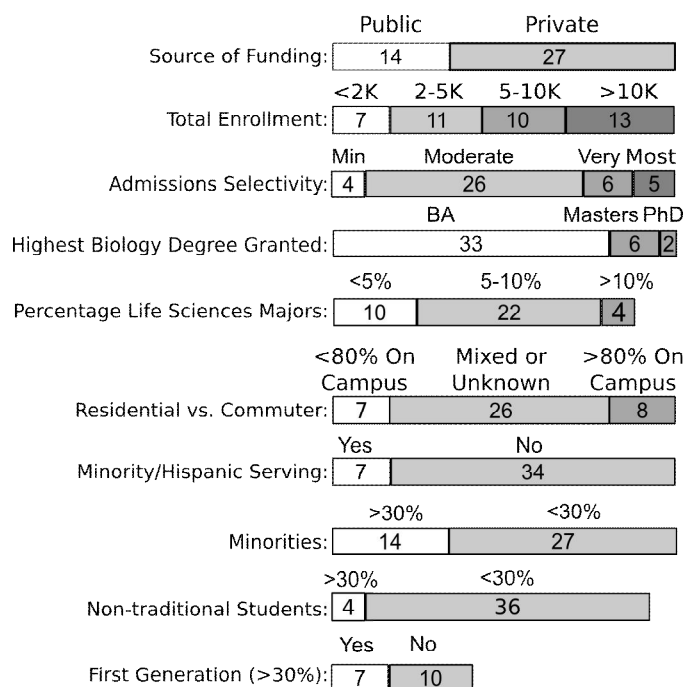


Figure S2. Diversity of GEP participating institutions for the alumni survey. For the purposes of this survey, “Non-tradition Students” are defined as those over age 25. Total number of schools represented = 41. Some schools did not collect some of the data points, resulting in some data sets with fewer than 41 entries.

Supplemental Text

Supplemental Text S1. Responses to the question: How do you use GEP materials in your curriculum? What advice would you offer to instructors interested in adapting this approach to fit the needs of their students?

Consuelo Alvarez, Longwood University:

I have used the GEP finishing and annotation materials to teach an undergraduate class spring semester (three offerings since 2008). In three other semesters, students have used the GEP annotation project to do independent studies.

The advice I can offer to instructors interested in adapting this approach is that it is worth all the challenges that one will go through, for requesting your institution to set-up computers, and the adjustment that the students go through, because now they are free to make their own decisions on their projects. In two instances, students have considered applying for annotation jobs because they like this approach to learning and research work.

Cheryl Bailey, University of Nebraska-Lincoln:

I used GEP annotation materials to teach a new undergraduate bioinformatics class. The advice I have is to warn students that they will likely feel frustrated at first, but then it will come together and they will be excited! I think that warning them about the frustration does lessen it, and it helps them to push through that initial period of learning. Also, the homework practice assignments from the GEP help the students learn those first steps.

Daron Barnard, Worcester State University:

I have use GEP materials in three ways: as modules in a genetics course as part of the lab, as the basis of the lab of an upper level molecular biology course, and as independent study projects for students. I found that as a module in the genetics course it was important to keep in mind that it was a first introduction to bioinformatics for most students. Some students could move right through the basic material, while others struggled. The lab for the molecular biology course was an ideal setting for the annotation project. The difficulties that I encountered revolved around keeping the students working on the project out of lab. When they only work on the annotation during a 3-hour lab once a week, they spend the first hour establishing where they were at the end of the last lab. To counter this I would suggest assignments that would move them forward over the course of the week, and a good system of documentation (see the Annotation Progress Tracker in the Curriculum pages - GEP Partners for suggestions). At the end of the course I had the students do an RNA isolation and RT-PCR to verify their models. I found that the independent study worked well as it was a flexible project that students could work on at any time. I have had several students work on a project at the same time, and at other times it has been a single student. Having more than one student work on annotation at the same time (whether the same fosmid or not) was helpful for the support they provided each other, but not necessary.

Chris Bazinet, St. John's College (New York):

Current enrolment: 12. How we're currently using it: We are transitioning from a course in which the students performed "canned" web-based exercises to one in which the GEP genome annotation project constitutes the concrete substance that our lecture/discussion sessions and laboratory sessions are all addressed to. This semester, about $\frac{3}{4}$ of our laboratory activities are working on the annotation project, with the rest devoted to building a computer, learning web tools most likely to be of help in their molecular biology projects in research labs, and an introduction to Linux and free Unix-based bioinformatics tools.

Why we think it's better: Most biology students' general impression of bioinformatics is pretty vague- and somewhat intimidating given its statistical and computational underpinnings. Having a true research project to work on and potentially make a real contribution to genomics overcomes some of these hesitations, and allows them to address the basics of bioinformatics with grounding in a project. We are concentrating on the annotation project as a way of engaging them in a deeper understanding of the problems, concepts and tools of bioinformatics. I find that my students are much more engaged with bioinformatics now that they are participating in a true genomics research project. Applying bioinformatics principles and methods to an actual piece of genome seems to be transforming them from passive spectators to active participants, providing them with a substantial exercise forcing them to integrate the concepts and tools of bioinformatics. For those who have not participated in a laboratory research project, it is a critical introduction to the true open-ended nature of real scientific problems, challenging them to think more independently. They now extend the laboratory hours to work on their projects – way cool!

Dale Beach, Longwood University:

I use the GEP materials essentially to compliment my own understanding and background, as well as provide materials for student projects. The GEP program provides data, analytical tools, and training support for the finishing and annotation projects. The resources and structure of GEP coordinate and develop the "ranked" project system that allows me to introduce topics with "green" projects, and subsequently push advanced students in to the "red." I would not necessarily have the time to create these projects without the program, even a single model project that would be redundantly reviewed by all of my students. The specialized analytical requirements for this program are supported by curricular materials that provide "workshop" style hands on training for the instructor (at WU), and training "walk-throughs" for the students to demonstrate finishing and annotation strategies before they begin working with the research projects.

James E.J. Bedard, University of the Fraser Valley, Canada:

Previously, I have used GEP materials for the laboratory component of a 4-credit hour 400-level course (Molecular Biology II). The materials were used for an entire semester for student gene annotation projects. The class met 4 times per week, for three 50 minute periods devoted to lecture and one weekly 3 hour lab devoted to GEP materials and annotation projects. I have also used the materials for a student independent study course. Currently I am using the materials for student projects in a 3-credit hour upper level course (Genomics). The students

are doing group projects on gene annotation, which will be done in parallel to lecture material each week for an entire semester. The class meets one time per week for a 3 hour block. The time is split between lecture and project work. Each student has their own computer, but they work in pairs on their projects.

For instructors considering using the GEP materials, I would offer the following advice:

it is important to introduce students to certain concepts and tools before having them work on the annotation projects, such as BLAST, and to have them do some practice with the tools; if possible, the project work should be done in blocks of time that are adequate (at least 2 hour blocks would be ideal); have students work in pairs for projects, which will promote collaboration, and ease the burden for the instructor (fewer student projects to oversee at one time); due to the large number of questions from students during project work in the classroom setting, it is very beneficial to have a teaching assistant if possible.

April Bednarski, Lindenwood University:

I use GEP materials to teach the laboratory component of a biochemistry course covering metabolism and genomics. The laboratory for this course meets for one 2 1/2 hour session per week and is all computer-based. I start with 4 weeks of introduction to bioinformatics tools using Bio 3055 curriculum from the GEP website. At the end of those weeks, students are familiar with NCBI Gene, OMIM, and KEGG databases, BLAST, and analyzing multiple sequence alignments. Then I spend 2 weeks introducing students to annotation materials at the GEP site using primarily the Simple Annotation Problem. Finally, students claim annotation projects and work in groups of two to complete their projects. They present their results in an oral presentation the last week of lab. I have found that students seem a little intimidated by the lab at first, but as they begin to understand and become familiar with the tools and techniques, their confidence grows and they enjoy the process and being part of the consortium. I found it helps to split the projects up between two students to have enough time for them to complete the annotation.

Satish Bhalla, Johnson C. Smith University:

I have used GEP teaching material in three 3-credit courses: 1. Genomics – The course is built around genome annotation in *Drosophila* sp. 2. Intro to Bioinformatics – This course includes topics on Annotation and BLAST (tutorial and exercises). 3. Senior Investigative Paper – An independent study course where a student picks a topic (annotation) and writes an investigative report on it. At the completion of their investigations, three students presented their findings as posters/talks in conferences. All these approaches have worked out for our undergraduate students and I highly recommend that other instructors try it.

John Braverman, Saint Joseph's University:

The primary course in which I use the GEP material is in Bioinformatics, an upper-level undergraduate course for Biology majors. The class covers many topics in the field, including PAM matrices, BLAST, and phylogenetics. I use annotation as a means to help students better understand genomics. It is a central project for students. They each receive one contig. But to arrive at the point of being able to annotate on their own, I first walk them through two guided

annotations, one very simple and the second more complicated. At the end of the semester, they give presentations on their annotations.

My advice is: (1) Teachers ought to keep in mind how much about annotation is new to students. It takes them a lot of time and practice to learn the process. Even after many iterations, they easily forget the steps. Of course, annotation also takes a lot of training because of the decision-making, choices and judgments required. (2) Grading annotation material is not easy. It takes a long time. Each time I teach the material, I introduce more mechanisms to get them to annotate better and format the Annotation Report more properly. Be prepared for that, and guide the students to produce properly-formatted results, even if they are inaccurate.

Martin Burg, Grand Valley State University:

I have used GEP material in several ways. Primarily, I have used GEP materials in developing a course that is entitled 'Drosophila Genomics', which is designed for juniors (and seniors) that desire to get additional coursework in genetics and also gain some experience in participating in a research project. I have colleagues at GVSU using GEP materials both in a general Genetics Laboratory experience and a Junior-level Bioinformatics course, so some students have some understanding of annotation before they come into the class (as well as understanding the proper use of BLAST and other analysis tools). I have students participate both in sequence finishing and later sequence annotation, spending 7 hours of class time each week (two 3-hour lab periods and one 1-hour lecture period) for a 3 credit-hour class. I do introduce major concepts in lectures, using many materials from the GEP (and a few of my own), then have students go through tutorials and then complete assignments to demonstrate their abilities to perform DNA sequence finishing and annotation (through the GEP Website Management System). Students are paired up, sharing a computer throughout the course and are responsible for completing an entire project for finishing and for annotation (with the assistance of the other student-'peer assisted' learning). I made the class work primarily by leveraging the abilities and knowledge of others available through the GEP to avoid some significant roadblocks and enhance success of the students (and ultimately myself). I have two undergraduate TAs that assist in taking care of many functional issues, providing them further learning as well as assisting students taking the course who encounter these concepts and tools for the first time. I also have several students each year interested in independent study; for this we may extend analysis of the annotation projects done in class or claim new ones to complete. Typically TAs for the next course will take part in an independent study prior to the course.

Some advice: First, don't think you have to do it all yourself- the GEP group and curriculum it supports has been a great source of support, without which, I would not be able to conduct this particular experience for students. Second, get the support of your administrators to conduct this type of a course, by selling the fact that students are getting an excellent experience at a lower cost than traditional mentoring programs (which we also have). Last, get involved if you are sitting on the fence- students change, and their attitudes towards careers in science change drastically when they experience this type of course- bring research into the classroom!

Vidya Chandrasekaran, Saint Mary's College of California:

I have used GEP annotation materials as the lab portion of an existing Genetics course and as an independent study project for student research. As part of Genetics Lab: The lab sections are around 16 students. Students work in pairs and spend 6 - 7 weeks of 4 hour laboratory sessions on annotation. Since my students had minimal knowledge of Genomics and Bioinformatics, I typically start with a basic framework of the genome and genome sequencing technology. Having the students visit a sequencing facility and/or view the sequencing video has been a useful tool for me to get them excited about the project. Then, we go over BLAST and basic bioinformatics sites needed for annotation before starting the project.

Some advice: Implementing GEP-based curriculum has been fun and a learning experience for me. Ensure that you provide adequate background information to allow the students to get started. I typically assign the same contig to two students and ask them to do the annotation independently and then crosscheck. This allows me to do an internal check for consistency before submission to GEP. Even if the students appear to be in over their heads at the beginning, don't give up. The GEP approach is especially useful if you are in a small college (like mine) with limited research resources. Implementing annotation projects has allowed me to provide a flavor of research to many students. I have found that stressing that their lab results could be published and be used by *Drosophila* geneticists increased their ownership of the project. By the end, students gain an appreciation for the organization of the genome. Even the ones who were overwhelmed at the start become comfortable with using the bioinformatics tools. They realize simple things, like a gene can be transcribed from either strand of DNA but not simultaneously from both strands, exons don't end all the time with all bases of a codon, etc. They see the importance of splicing, gain a better understanding of alternative splicing and are amazed by how conserved sequences are for some genes across species.

Hui-Min Chung, University of West Florida:

Independent study and a genetic engineering course have offered students annotation projects as the main materials of the courses; the class size was 2-8 students. Additionally, the course materials posted on the GEP site were used as part of a genetics course as bioinformatics supplementary material. It is easier to implement GEP materials in the courses that focus on annotation, as the goal is very straight-forward and clear, i.e.: to achieve gene models. In this regard, a good map of course progress designed with baby steps is very beneficial, for example a homework assignment before students claim their fosmid, and scheduled peer instruction/review sections. Adopting GEP materials as a supplement for a course that has several projects might require the instructor to revise the posted GEP materials, carefully blending them into one's own teaching materials/projects. For example, if the posted GEP material uses 8 websites to explain/demonstrate the bioinformatic application, make sure you need all 8, or would 4-5 be enough to cover your learning objectives. Often less is more; the devil is in the details for students to learn to appreciate the topic. Also, it can be beneficial to use the bioinformatics tools or materials at spaced intervals, giving students time over short intervals to digest and to retain the knowledge.

Kari Clase, Purdue University:

Currently I use the GEP materials for independent research projects for students during the spring semester. The students that have participated thus far are upper level undergraduate students from engineering and science majors that have completed the HHMI SEA phage annotation project and want additional experience with current research in bioinformatics, exploring a eukaryotic genome.

In my experience, I have found that it is more difficult to engage students in the bioinformatics lab research activities when compared to the wet lab research activities. I have been trying to implement this approach for the past two years and I made some adjustments this semester based upon my experience last year. Initially I tried to have each student select a project that they could work on independently, and scheduled regular research meeting times to discuss progress. The students struggled to complete the project and understand the context of their findings. This semester, the students are working collaboratively in a small group on a single project and this seems to be more effective in helping them make progress. It can also be helpful to have IT support, as each year the students have to overcome the learning curve of working with the software to accomplish the goals of their research project. I think that collaborations with other faculty beyond one's department can be helpful for successful implementation of interdisciplinary projects like this one. I am currently working with another faculty member to help with a more sustainable implementation of the project within the classroom, beyond an independent research experience.

Randall J. DeJong, Calvin College:

GEP annotation materials were used as part of the laboratory portion of an upper level Genetics course. A lecture prior to the first annotation lab introduced the project, and the students completed the practice exercises in the first lab. Students spent six weeks of 3hr laboratory sessions on annotation projects, working mostly in pairs. The labs had 16 students each and it was difficult for one instructor to answer their questions as needed – a trained or experienced student would have been very helpful. Instructors should also be ready to give some students some sustained attention, both in the case of struggling students and students who have selected more difficult genomic regions. Six weeks (18 hrs.) was not quite enough time for some students to complete their annotation.

Justin R. DiAngelo, Hofstra University:

I have used GEP materials in both an independent study course and a stand-alone Genomics course. The GEP annotation research project is the major focus of both types of implementation. After giving background lectures on the Research Question, Genome Sequencing and BLAST (relying heavily on the PowerPoint files provided by the GEP), I have my students complete a practice annotation problem and then they jump right into their annotation research project. As time allows, I introduce my students to other types of large-scale approaches such as proteomics and metabolomics. My students get really frustrated with the annotation process at first, but once they get the hang of it and really make the connections between what a gene looks like in theory (what they learn out of a textbook) and what it looks like in terms of the DNA sequence, they really get a deep understanding of gene structure, and even have some fun designing gene models! The GEP project and the materials provided by

the GEP do an excellent job helping students learn both gene structure and genome-wide techniques.

Chunguang (Charles) Du, Montclair State University:

I have been using the GEP teaching materials for my BIOL 497 Genomics course since 2007. This very unique experience helped me secure a grant from NSF in 2009. Currently my Genomics students learn the annotation background and bioinformatics skills from GEP teaching materials and interrogate the DNA sequences generated from my NSF project. My students find that working through the annotation homework exercises prior to tackling their own independent research projects is very helpful for them. The students who register for my course are mainly juniors and seniors along with some master's students. I would not recommend that freshmen take this course, since they have not yet taken Cell & Molecular Biology and Genetics.

David Dunbar, Cabrini College:

I teach a one semester three-credit course called Bioinformatics. This course is focused on the annotation part of the GEP pipeline. I find upper-level students doing annotation projects as a stand-alone course is completely doable within the time frame of a semester. However, we are sometimes pressed for time at the end of the semester for students to successfully submit their claimed annotation projects back to Washington University in St. Louis. For the semester-long course, each student claims his/her own annotation project, but students work in teams of two and assist each other with their assigned annotation projects. Each time I have taught the course, several students get really excited about the annotation project and proceed with additional annotation/finishing projects as independent projects.

The GEP program has been transformative both for me and for my students. The course has allowed me to consider and apply different pedagogical approaches to teaching Genetics and Molecular Biology. By having students actively engage in eukaryotic gene annotation projects, it allows me to realize what students have mastered in lower-level entry Core Biology courses, such as my Cell & Molecular Biology course. For instance, the first time I taught the GEP-based course, I realized that our upper-level students did not have a firm command of splicing, translational reading frames, etc.

My overall advice is that if you would like to teach GEP materials as a stand-alone course, it should be at least a three credit-hour course for just the annotation work alone, if one desires to give students their own annotation projects. If finishing projects are included, the course should be offered as either more than three credit-hours, or as another stand-alone finishing course separate from the annotation work.

Todd Eckdahl, Missouri Western State University:

The Genomics Education Partnership is all about lowering barriers for faculty to meet the needs of undergraduate students at a variety of types of institutions with diverse needs. Student needs vary widely because of difference in background, course preparation, and experience with genetics and genomics, but they must be met if students are to learn genomics successfully. GEP meets the varied needs of students by providing a tremendous amount of flexibility for implementation of genomics education and research. Materials have been developed for use by faculty members with varying levels of expertise, by students with various backgrounds, and in

courses that have different time constraints. I would advise faculty members to pick and choose GEP resources in a way that enables them to tailor the GEP genomics research experience to the particulars of their students, their course and curriculum, and their own interests and expertise.

Heather Eisler, University of the Cumberland:

I use GEP materials to introduce my students to genomic research both as part of a larger Biotechnology course for upperclassmen and individually through independent study. So far, I have only worked with annotation. For the course, we do this as a portion of the lab. I approach this both from the genomics/genetics side and from the speciation side. From the genomics/genetics side we focus on looking at the nuts and bolts of what makes up a gene and what tools do we use to study them. For the speciation side we look at how the genes have changed since the two *Drosophila* species shared a common ancestor. I find the speciation approach helps address the students' concerns that things don't align perfectly. Some of the students are a bit frustrated with the idea that there isn't a known correct answer. After a couple of times working with their project, and certainly after their first gene, they seem to settle into it. Everyone has their own project, but I encourage them to help each other out. We once had a gene with 20+ exons, and it took several students to help to finish it. (In general plus strand genes are easier than minus strand genes.) I also try to set up the experience as a research lab. The students are encouraged to bring their own music players, so they can rock out while working on their project. Unlike a research lab, I bring in chocolate, which so far seems to have been greatly appreciated. Students become very proficient after the initial shock, and they become very attached to their project. I tell them from the start that their work will be published, and they get very excited about this and take a great deal of care with their work. Each student has to present at the local level about their project – what they found, what they went through, and their favorite gene. I encourage other students from my other classes and other faculty to come to see these presentations. I also encourage my independent students to present at local conferences.

Sarah C. R. Elgin, Washington University in St. Louis:

We use GEP materials in an upper-level lab course, "Research Explorations in Genomics." The course is taught jointly with Prof Elaine Mardis (Genome Institute, WUMS), Wilson Leung, and Dr. Chris Shaffer. The course meets 8 hours per week for combined lecture, demonstration, discussion and lab work time; with this much time available each student can complete both a finishing project and an annotation project, with time available for some guest lectures on other on-going research in genomics, to provide a broader perspective, and some other explorations of genomic tools. We find that two hours is the minimal time for a work period to be effective, so we meet 1:30 - 5 pm two afternoons per week, with a break in mid-session. Students do several GEP exercises to learn the tools, but their major effort goes into the project itself, with both a major paper laying out their work and an oral presentation prepared for both the finishing project and the annotation project.

Peer instruction is an important part of the course. Once students have mastered the basic software, they are adept at helping each other. Each year I recruit TA's from members of the prior class. Always make sure you have juniors in the class! In addition, we maintain an open

and collaborative atmosphere during lab sessions. Students appreciate being part of a research team, and the process as a whole appears to help them gain confidence in themselves as scientists.

Julia A. Emerson, Amherst College:

One of the appealing characteristics of the GEP curriculum is its versatility and adaptability. At Amherst College, gene annotation has been integrated into the existing laboratory curriculum of the semester-long course, Biology 191 (Molecules, Genes and Cells). Biology 191 is one of two required introductory courses for the biology major, and the roster is predominately made up of first-semester sophomores, due to a chemistry pre-requisite. Class enrollment is 90-120 students each year, lab enrollment is 20-24 students per section, and students receive assistance in each of the weekly 3-hour labs from one faculty instructor and two undergraduate teaching assistants. The total amount of in-class time devoted to gene annotation in the past four years has ranged from 12 hours (one hour of discussion and 11 hours of lab over one quarter of the semester) to a single 3-hour laboratory period. In the lengthier iterations, the goals of the annotation labs are equally balanced between (1) involving large numbers of introductory biology students in a nationwide, collaborative research project; and (2) having students gain a richer understanding of eukaryotic gene structure and RNA processing than from lectures and problem sets alone. In the one-week lab, we de-emphasize the research objective of this work to focus on introducing students to bioinformatics tools while reinforcing concepts of eukaryotic gene structure, mRNA splicing and translation reading frames. Students in each lab section work as a group to annotate the same gene and create a gene model during a single lab section (see the 2012 files linked to the Emerson GEP Wiki page).

Amy Frary, Mount Holyoke College:

I have taught gene annotation using GEP materials as part of an upper-division undergraduate course in Molecular Evolution. Students spent the first three weeks of lab working in small groups, becoming familiar with BLAST and tackling an annotation project of their own. They then moved on to another project that required them to analyze a sequence of interest, retrieve putative homologs from GenBank, create sequence alignments, and construct phylogenetic trees. Thus, the time spent on annotation was rather constrained. I think that the quality of the student annotation projects would have benefitted from some preparatory practice exercises and additional lab time devoted to annotation. Nevertheless, I was pleased with the results of integrating the GEP projects into the course: the students were invested in an authentic research experience, they learned to work cooperatively, and they gained an excellent understanding of eukaryotic gene structure. Semester-long GEP projects would be terrific in a bioinformatics or genomics course.

Don Frohlich, University of St. Thomas (Texas):

I used the GEP approach for three years in a one-credit special topics course, "Annotations," required of Bioinformatics majors. One unexpected benefit of the course was that students applied tools learned there to a group independent research project, outside of class, called the Operon Architecture Data Base (OADB). The project involved the design of a database and search tools to assess and compare rearrangements in bacterial operons. Results were

presented at a conference at Baylor College of Medicine (BCM) [Institutional Research and Academic Career Development Award (IRACDA)] and two of the students are now pursuing graduate degrees in Bioinformatics. (Resulting presentations: S. Ghaziyani, L. Simon, L. Turrubiarres, D. Frohlich, J. Starner, M. Larios-Sanz. 2010. Operon architecture data base. IRACDA: BCM, Houston. L. Turrubiarres, S. Ghaziyani, L. Simon, D. Frohlich, M. Larios-Sanz, J. Starner. 2010. OADB: The entity relationship. IRACDA: BCM, Houston. L. Simon, S. Ghaziyani, L. Turrubiarres, D. Frohlich, M. Larios-Sanz and J. Starner. 2010. OADB: Data mining. IRACDA: BCM, Houston.)

For future faculty I would echo the sentiment that the course not be taken on as an overload. I also note that the approach can be difficult to structure during regular class hours. Students were frustrated at first but got comfortable after a few sessions and were noticeably comfortable when beginning work on the OADB project. We are only now instituting labs for Genetics and Molecular Biology (advanced) and I would like to see GEP projects included.

Anya Goodman, California Polytechnic State University – San Luis Obispo:

I teach a junior/senior level elective "Bioinformatics Applications." We do GEP annotation projects in the laboratory to apply topics discussed in lecture (tools for analyzing DNA and protein sequence, next generation sequencing technologies, genomics). The annotation projects are motivating in themselves: students get to be the detectives hunting down the genes. These projects give meaning to lecture: we apply what we learn in lecture to something useful. Students appreciate the opportunity to practice their reasoning skills, make decisions based on the evidence they collect, and defend their decisions to their peers. During training, we go over examples, but when students are annotating their own projects, they often encounter the unexpected, and they enjoy presenting to the class how they tackled a challenge. For doing annotation research in a class of 24 students, it is important to organize students into teams and to provide collaboration tools: we use a wiki with team pages to share data, distribute the workload, troubleshoot, and keep track of progress.

Yuying Gosser, Engineering, The City College of New York, CUNY:

The gene annotation research project provides a focus for our course "Bioinformatics and Biomolecular Systems" (Sci280), which is a computer lab based, research-oriented course with an emphasis on genomics and protein structure and function. Beginning from central dogma, followed by introduction of protein structure and modeling, and finally a focus on gene annotation, all students were required to complete a project on protein structure-function analysis and homology modeling, and a gene annotation project. Since Fall 2009, this course has been offered to more than 100 students; about 30% are from Biomedical and Chemical Engineering, and more than 100 annotation projects have been completed with ca. 80% passing rate. (By the end of 2012, 85 annotation projects had been submitted to the GEP database at WUSTL.)

The students successfully engaged in responsive research. From identifying the exon coordinates to constructing a gene model, locating the conserved regions in the evolutionary path, and from organizing the data table to writing a complete research report, they became familiar with genomics vocabulary, the major databases -NCBI, PDB, Flybase, and EBI, and the basic tools of comparative genomics – BLAST and CLUSTALW, as well as the major literature

database - Pubmed. The students also learned to think like a scientist and recognized the “uncertainty” in research, i.e. that a unique definitive answer may not exist. The Central Dogma of molecular biology provides a framework for students to understand the genome and biological systems. Research-oriented projects, like gene annotation and protein structure-function analysis, train students to use the primary bioinformatics database and online tools, setting the stage for them to learn by themselves and further explore the world of Biology.

Shubha Govind, Biology, The City College of New York, CUNY:

In Spring of 2010, I used GEP annotation methods for 10 weeks of a 14-week semester. Students contributed to the annotation of several genes in the *D. mojavensis* dot chromosome closely following the method described in this paper.

There was an unexpected twist at the end of the same semester however, when my laboratory obtained raw Sanger sequence reads of roughly 1000 cDNA clones for an ongoing transcriptome analysis. These cDNA sequences are derived from an organism whose genome is not yet sequenced. I took advantage of the students’ ability to quickly navigate between various web sites/search engines, which is part of the “GEP drill”. Students successfully provided tables of homologous proteins, with descriptions of protein domains, etc. This activity was not planned initially, but the timing was just right. Thus, students not only benefitted from the GEP experience itself, but could utilize their skills more generally to contribute to an unrelated project. In addition, as we use *Drosophila* as a model organism in my lab, we routinely use GEP materials in Independent Study and Honors research projects.

GEP is flexible in format with simple to more challenging activities. With experience, instructors can gauge the appropriate level and format of instruction. I would encourage introduction and integration of these methods at early stages in the curriculum. Students who enter labs for wet-lab research are trained to approach research projects more systematically: they realize that they must follow a protocol, must repeat the protocol correctly, must review results periodically, and that they will fail before they succeed. They must therefore persist. GEP is a cost-effective method of introducing them to these valuable lessons. In addition, they become familiar with model organism databases and can access and grasp the significant amounts of genetic information available in these databases.

Adam Haberman, Oberlin College:

I used GEP materials as a semester-long lab course taught in conjunction with a Genomics lecture. In the first half of the semester, we work on sequence improvement, while lecture covers sequencing methodology and comparative genomics before moving to other, less connected topics. In the second half of the semester, we work on annotation. By this point, students have studied the mechanics of BLAST searches and now apply this knowledge in their research. Lecture material at this time includes discussion of transcriptomes, which is immediately relevant to understanding the RNA-Seq data in the research projects. GEP projects strongly reinforce these topics from the lecture. One area I want to improve is my preparation of the students for their sequence improvement projects. Many students are intimidated by these projects, which seem open-ended and arcane to them. Students report feeling lost or overwhelmed, as these projects do not have a concrete blueprint they can follow as other lab projects they encounter do. This aspect of the project is ultimately good for students, in my

opinion, but I would advise instructors to spend significant time developing student understanding of the project and the software before giving them their individual data to work on.

Amy T. Hark, Muhlenberg College:

Thus far, I have primarily used GEP materials with research/independent study students. Students typically spend the first four weeks of a fifteen-week semester doing background reading and practice exercises with BLAST and annotation (the latter are GEP curricular materials, which work very well). This prepares students for working on their own fosmids/contigs. Several of my students have continued their work into a second semester, tackling tougher annotation projects and/or extending their work with Clustal analysis, investigation of biological function of genes within their contig, etc. Other students move on to wet-lab projects in my research group. Overall I have found the GEP curriculum an excellent way to introduce students to the research process, typically after they have had some coursework in basic molecular biology.

Charles Hauser, St Edward's University:

The GEP has been a very rewarding experience for me and my students alike. To see the transformation of students, who have taken molecular biology, as they work thru annotation and finishing problems using real datasets and discover for themselves the reality of the material covered in classes, illustrates the effectiveness of the approach. For students, the opportunity to work in a collaborative environment on a research project is transformative: they up their game, and it provides a glimpse of what life after a BS degree will entail. Anyone interested in this approach should talk with GEP faculty who are at a similar institution to learn how best to implement genomics in their own courses, or to find out what aspects of our approach work and what problems we've encountered.

Arlene J. Hoogewerf, Calvin College:

I used GEP materials as part of the laboratory portion of an upper level Genetics course. The background and scientific questions associated with the *Drosophila* project were introduced using a PowerPoint lecture, followed by assignment of practice exercises with BLAST and annotation. For the seven weeks following the practice exercises, each student was assigned his/her own fosmid to annotate, prepare the GEP report, and prepare a report that included background information, methods, results, and discussion, including repeat, synteny, and CLUSTAL analyses. Students presented their reports to the class. Some advice for others who wish to implement GEP materials into the curriculum include having more than one instructor or TA available when students begin their annotation, as most students individually require at least an hour of one-on-one undivided assistance as they begin their projects. Another suggestion is to have students present their annotation work-in-progress to each other after a few weeks so that students can learn from the challenges that others have overcome.

Laura L. M. Hoopes, Pomona College:

I have used GEP materials in *Drosophila* Genomics, where I based most of the laboratory on both finishing and annotation through GEP, and as a lab project in Genetic Regulation in

Eukaryotes, where I had each student annotate ("own") his or her own fosmid and work on its annotation, albeit in laboratory with lots of student-student, student-faculty, and student-TA interactions. One of the great things about this series of laboratories is that the student is producing new knowledge and takes pride in the project. I always encourage working together, although each one has a fosmid of his/her own, because through working together, they reinforce what they know and share techniques; they may also discover that some of the same genes (or parts of them) can be on the other student's fosmid (as projects are designed to overlap), and then they can work together for a time to make sense of that discovery. Students enjoy this work and tend to use much more out-of-class time than I actually require of them. No one wants to present a report to peers with "I don't know" as the bottom line. So they get very creative and work hard...what every professor wants from the students! It does seem like an independent project to them, which is probably why its benefits are so similar to those of summer research. Another pleasing aspect is that it's not always the A students who excel at the task. A lot of hard work and networking can more than compensate for lack of theoretical background. But then the A student can contribute things, like why certain settings are best when calling for sequences, etc. It builds on each person's strengths.

Carina E. Howell, Lock Haven University of Pennsylvania:

I use the GEP materials for my Bioinformatics and Genomics course, BIOL323, and also for Independent Study projects, BIOL499. I implemented the GEP materials in the Bioinformatics and Genomics course first. This is a junior or senior level course, for 3 credit hours, that is taught in a computer lab, with a class time of three hours per week (two 75 minute sessions). I first introduced students to a number of concepts that would be critical for them to understand where to start with the annotations projects, and had them perform computer lab-based assignments on these topics. The topics for assignments included an introduction to nucleotide and protein databases, BLAST, and multiple sequence alignments. Next, students completed some practice annotations using GEP curricular materials. Then students worked in pairs to annotate a contig containing multiple genes. Weekly stepwise assignments were completed by the students, which helped them break down the overall annotation into smaller steps (i.e. the first assignment was to annotate three exon boundaries, the next was to fully annotate one isoform of a gene, the next was to annotate more isoforms, etc.). Once students completed their annotations, they submitted the GEP Annotation Report as their final assignment. Finally, students completed an additional assignment that investigated one of the genes they annotated in more detail. This report included information about protein function of their gene in other species; they found additional homologs of the gene from a variety of organisms, and constructed a multiple sequence alignment and phylogenetic tree of homologs. They summarized their findings in the final report. I found that students were overwhelmed at first with the annotation project, as it seemed daunting to them, as did the idea that they were responsible for doing novel research. But as they got more comfortable with the process, I found that they were excited and very proud of the work they were doing. In a survey at the end of the semester, students commented that this research project taught them: how to work independently and with others, responsibility, computer skills, patience, confidence to conduct and report research findings, proficiency with online genomics tools, problem-solving skills, time management skills, critical thinking skills, spatial reasoning skills, and the ability to dissect

scientific data and critically think about it. More than one student also reported that they enjoyed the chance to fail in science (for example, when they got an exon boundary wrong), and then have to work hard to figure out what was wrong. They expressed that the "cookbook" experiments often completed in traditional labs do not give them a chance to fail and to problem solve. I thought this was a significant insight on their part. Some advice: I would recommend for implementation to make sure that you have ample in-class time to help students. My classes were only 75 minutes long, which is not sufficient. I am changing the class time to be three hours per session. Making smaller assignments along the way to give students an opportunity to get feedback is important. Having teaching assistants to help guide students would be very helpful also.

Diana Johnson, George Washington University:

I have used the GEP annotation materials for 7 weeks in a 14 week Genetics Lab course. Before we do annotation, we have sequenced different alleles, normal and mutant, of the sepia gene and had students look for changes in gene sequences and predict the effect of the changes on protein structure. Despite getting down to the sequence level this way, my students still have problems grasping what annotation is all about. One of their main issues is making the connections between the big picture, i.e. a gene diagram, and how the sequence is annotated. One of the benefits of the annotation project for them is that they correct some of their misconceptions about eukaryotic gene structure. Another benefit is to have a project in which they must succeed to proceed. Realizing that in real research, the professor doesn't provide the data if the experiment didn't work is invaluable.

I have made a great deal of use of the GEP materials for this project (with attribution) and I have designed a few PowerPoint illustrations, using them as a guide while the students and I simultaneously all annotated one gene together as an introduction to the process. I give individual students projects. Initially I gave them whole contigs, but that was too difficult for some students. Now I give them individual genes. As they finish one, I have them do another. For students that are doing very well, I have them run Genscan predictions. I also use these students as unofficial TAs to aid other students. Finally, for the past several years I have tried to choose neighboring contigs/fosmids, and then we made a map of our gene order and orientation and compare it to the *D. melanogaster* map. This year I do not have this, so we will probably make some simple gene trees and do the order and orientation for one or two fosmids. One thing I noticed is that the seating arrangement is important. The first times I taught this, I used a computer classroom with typical desks arranged in rows. Then I taught it in the laboratory room that has tables around which 5-6 students sit. The latter has proved very helpful for getting students to communicate with each other and has increased student success with annotation.

I cannot emphasize enough the help of the GEP staff, computer tools, and other materials. The workshops have been invaluable also. Even though I annotated genes before I began this process, GEP gave me a better framework for doing this. In addition, using computer tools and understanding what they do and do not do is very good for the students. Further, my participation in the process was helpful in getting an NSF grant.

Christopher J. Jones, Moravian College:

My primary use of GEP materials is in an upper-level elective course entitled “Genomics,” which is a hybrid lab/lecture fusion run in a computer lab. It has a very hands-on/applied focus, but supplemented with discussion of textbook chapters and primary literature articles. I spend the first half of the semester (7 weeks) on finishing and the second half on annotation. I make extensive use of the tutorials, lecture materials (e.g. PowerPoint presentations), and homework packages developed by GEP members to guide my students’ development in using the necessary tools and thinking about genomics questions. I have also used smaller modules, such as annotating a single gene, as part of the laboratory portion of my Genetics survey course.

The GEP has been a fantastic resource for both me and my students; without its support there would have been no way for me to become fluent enough in the concepts and approaches of genomics to be able to offer this experience to my students. Anyone interested in this approach should talk with GEP faculty who are at a similar institution to learn how best to implement genomics in their own courses, or to find out what aspects of our approach work and what problems we’ve encountered.

Lisa Kadlec, Wilkes University:

I have used GEP materials as one module in the laboratory component of my upper level Genetics elective. During the lab period prior to starting our annotation work I give a PowerPoint presentation on “Ab Initio Gene Finding and Basics of BLAST.” The students do an introduction to BLAST exercise as homework, and in the next period there is a PowerPoint covering an example of genome annotation and a hands-on annotation exercise. This is followed by several weeks when the students are working (with partners) on an annotation project (a portion of a fosmid from the current GEP project listing).

I have found participation in GEP to be rewarding for both me and my students. I am much more knowledgeable in the area of genomics/genome annotation than before I joined the group, and my students are exposed to an area of biology and biological research that they would probably not otherwise see, at least not in such a hands-on way.

I would advise instructors considering the GEP approach to contact the GEP organizers and also current GEP faculty - we are a diverse group and use the materials in a wide variety of ways, and so they are likely to find faculty members who are already using the materials in a way that might be helpful to them as a model. The new faculty workshops are also top notch and really give you the tools to get started bringing the material to your students.

Marian Kaehler, Luther College:

I have used the GEP materials in an independent study, and for three years as a 2-lab unit adapted for a large genetics course (80-100 students, 4-5 lab sections). The independent study student had first enrolled in the student workshop, and it was a significant enrichment experience for him. Working with 2-3 students on annotation of a fosmid can work very well. The difficulty with integration of GEP into a Genetics course is primarily providing sufficient background in genomics – especially the role of rearrangements – to provide perspective. Most of my Genetics students benefitted from the annotation exercise in two ways: 1) familiarity with

bioinformatics tools and sites, and the annotation process itself; and 2) appreciation for key fine structure characteristics of individual genes (stop codon frequency at gene ends and incorrect reading frames, degeneracy, consensus splice sites, etc.) Few students, however, have the ability to step back from the nucleotide level of annotation to consider genomic level evolution. I find this to be the greatest pedagogical challenge: to integrate comparative genomic perspective into the process of annotating a few genes in a fosmid. Introductory lectures must incorporate an explanation of gene search tools and computerized annotation, chromosomal as well as point mutations, and the significance of synteny. Without this intentional focus, which I still have not mastered for the class, students will see leaves and trees, but forget to think about the forest!

S. Catherine Silver Key, North Carolina Central University:

I have used the GEP materials in 3 courses since 2009: 1) as a ½ semester long module in a didactic, lab-intensive Techniques course; 2) as a 1/3rd semester-long module within a didactic lab/lecture Genetics course; and 3) in a non-didactic Introduction to Research course. Although the lab-intensive Techniques course was dropped from our curriculum, it showed the greatest potential for implementation of a research module within a standing course. I have had the most success with students taking the non-didactic Introduction to Research course, as it allows students the time to immerse themselves in the research experience and succeed in annotating entire contigs! Typically, Introduction to Research students who do not have prior research experience will wash dishes, make solutions and observe more experienced students setting up experiments. However, by using GEP materials, the Introduction to Research students can participate in a meaningful research experience resulting in poster presentations, co-authorship on a research paper, and a line on their resume useful for applications to research internships and professional schools. In the didactic Genetics course, I use GEP materials for 5 weeks of the 15-week semester in weekly 2-hour lab sessions, plus I replace at least one week of lecture time (two 75 min time slots) with hands-on annotation activities (total 12 hours). This is a more challenging format for research success. While NCCU Genetics students, working in groups of four, have not completely annotated an entire contig, they do succeed in annotating multiple isoforms and are always ecstatic when they see the 'green' icons in Gene Model Checker indicating that their proposed gene model is possible! Despite the reduced time-frame, which decreases the likelihood that they will have achieved a true research experience, anecdotal evidence (student-instructor communications) suggests that students have often gained skills in bioinformatics research useful to cutting-edge science. Students often mention to me that they are grateful for the experience AFTER they have left the course, and found that they are using these skills in their research internships; skills they would have lacked in the absence of the GEP experience. Thus, while students show much frustration during the genomics experience, I would recommend that future GEP instructors emphasize two things: 1) the value of learning these research skills for the future workplace, and 2) the significance of the annotation project itself. The second area of emphasis is necessary as students can be taught to realize that differences found during the laborious analysis of nucleotide and amino acid sequences, and chromosomal rearrangements, provide evidence of how species have evolved (their differences), but also that any conservations (similarities) in gene sequence, for example, underscores the importance of the resulting protein's function in the living organism. Since

humans and flies share 50% of their genetic information, we can selfishly apply what we learn from flies to ourselves. I would also advise a new GEP instructor who aims to have the full research experience for their students to have a limited class size (12 students maximum), experienced TAs, and modify the GEP directed exercises to train their specific students on how to navigate the professional websites.

Adam Kleinschmit, Adams State University:

I have used GEP materials for the lab component of an upper division undergraduate Molecular Biology course. Additionally, I am currently using GEP materials in a more informal setting, with students looking for independent research-based projects. In order to use the GEP materials effectively, I would suggest allowing for a minimum of 4 hours (broken up into multiple sessions) of student exercise work / acclimation to the computational resources, in order for the students to come away with a good understanding of their utility. After watching students tackle this initial hurdle, I have been extremely impressed by the level of higher order thinking skills demonstrated by students while teasing apart their own independent projects (annotation problems). I would highly recommend using GEP materials as a viable alternative to more traditional resource-intensive wet bench independent research projects. Additionally, it integrates many core genomics/bioinformatics principles, which makes GEP projects a great first-hand student experience for instructors looking to design a lab component for a genomics course.

Nighat P. Kokan, Cardinal Stritch University:

I have used GEP materials and genome sequence annotation research projects in several configurations since spring of 2009. It has been implemented mainly in the lab component of an upper level genetics course (BL308). I have also used it as directed study, and in an independent research course (BL402); in addition, I have used GEP "extensions beyond annotation" in a bioinformatics course (BL302). The project can be challenging for the first few times of implementation for the student and well as the instructors. With large classes, it is helpful to have a TA and/or have cooperative learning between the students, students helping each other out. The learning process can be frustrating for the students, but very rewarding for most.

Olga Ruiz Kopp, Utah Valley University:

I have used GEP materials in annotation in a genomics course and also as independent group research projects for students. The advice I have for instructors is to try to keep your best students as TAs, and to involve students in group projects. When a student finds an easy way to do something, encourage them to share that with the rest of the students. Use the resources of the GEP and the staff of GEP; they are great at helping.

Gary Kuleck, University of Detroit Mercy and Loyola Marymount University:

I have been a GEP member since 2007 and used GEP materials in an upper division Bioinformatics laboratory (BIOL 499), as exercises in a lower division Genetics course (BIOL 202) and as independent research projects for undergraduates. The activities have ranged from complete annotation and finishing, both for individual students and as team research projects, to annotation exercises. The student's participation in a research project, coupled with the

integration of bioinformatics principles, has made the GEP materials and research projects the most effective tools that I have used in teaching bioinformatics. Some of my students have gone on to graduate careers in bioinformatics; most have finished with a much deeper understanding of gene structure and function. I would advise GEP 'beginners' to gear what they are attempting to do to the level of the students. It can be frustrating for students encountering bioinformatics for the first time, but having pairs of students work together will alleviate some of the frustration.

Judith Leatherman, University of Northern Colorado:

I use GEP materials in a four-week module in the laboratory portion of my sophomore-level Genetics course, using the curriculum outline developed by Julia Emerson (GEP member). Briefly, the first two weeks are spent working through a BLAST tutorial and a sample annotation problem. Then each group of 2-3 students is assigned one gene (or one isoform of one gene) to annotate. This is a rather short exposure to gene annotation, but I think it is effective in helping students learn about eukaryotic gene structure. Students tend to get quite frustrated at first, but once they figure things out, it seems very rewarding to them. When their gene model finally "passes" the checker, they are so pleased! I have also started using undergraduate TAs, recruited from the previous semester, to help with each lab section during the project. So far, I have had plenty of students volunteer to TA--more than I need.

Jane Lopilato, Simmons College:

We've implemented the GEP materials as follows: 1. In my fall Genetics course, we've used the sandbox contigs for practice. Jeanette Hauke, a student with extensive experience in annotation, made a presentation introducing both of my lab sections to annotation this past 2012 fall. 2. This semester in Molecular Biology, we've claimed a dot chromosome contig, and, with Jeanette's help, are working on it right now.

Advice to others: 1. It really helps to have the assistance of a TA when teaching annotation. Jeanette made a presentation to the entire class and then spent 90 minutes with each of the lab sections where the students followed along on their computers. 2. One of the students in my Mol Bio lab section had already done annotation with Dr. Jennifer Canfield in the Chemistry Dept., so she is acting informally as a TA. She helped the students with a BLAST search yesterday. 3. Jeanette did a group of annotation projects for her independent research project and really benefited. (At Simmons, all of our seniors are required to do independent learning through research or an internship.) I would love to have another independent study student. We introduced GEP and annotation at our juniors meeting last week to promote this.

Christy MacKinnon, University of the Incarnate Word:

I primarily use project management support, annotation resources, data repository, curriculum resources, WU IRB approval document, and Faculty Resources. I frequently use the GEP Forum for my own questions and to read others' questions. The responses are fast and extremely helpful. I couldn't manage annotation problems without the GEP Forum!

Juan Carlos Martínez-Cruzado, University of Puerto Rico at Mayagüez:

The GEP materials are an excellent resource for teaching annotation. In addition, the genome of most *Drosophila* species is complex enough to be challenging for starting students (who are the vast majority), but manageable enough so that more often than not students will find in a 50 kb segment a complete and conserved gene that is simple to annotate. When students fully annotate their first gene, they gain confidence and pick up very quickly from then on. GEP resources such as the UCSC Genome Browser and the Gene Model Checker are extremely valuable for the instructor. I have used GEP resources both in a class setting and in individual projects, and have found the class setting more effective because students learn a lot from each other. I have two important points of advice for any instructors who will be adapting this educational approach. First, to themselves fully annotate a couple of projects (fosmids) beforehand. This will allow them to understand how easily and in which cases a student can become confused. Quick and effective intervention will bar frustration among students. Second, just after the introductory lectures and before assigning the projects, have the students take a quiz in which they will annotate a simple gene. The quiz will obligate them to study, and the annotation of a single gene right before receiving the assignment will lift up confidence and enthusiasm when it is needed the most.

Gerard P. McNeil, York College, CUNY:

I have been a participating member in GEP since 2007 and have implemented the materials in several ways, including as part of a lab course, as the focus of an entire course, as a summer research workshop for high school and undergraduate students, and both as a group and as an individual independent study project. I have incorporated research-based annotation projects into a cell biology lab class as a complement to wet lab experiments. I run a yearly bioinformatics class that is based entirely on GEP materials where we have the student complete both finishing and annotation projects (~ 7 weeks each), individually or in pairs. I have also offered a group independent study class where the number of students can remain small. This is an effective approach to start out, especially if you lack teaching assistants. Students can be required to complete both a finishing and an annotation project, or just an annotation project. Another approach using the independent student forum that I have used successfully is having all students working in my research lab complete an annotation project, in addition to their wet lab projects. For instructors starting out trying to implement these materials, I would suggest working with a small group of juniors and/or seniors who have taken an upper-level genetics class. This will allow the instructor to get through the problems that arise in the beginning and to enable them to give the students the attention they require using this research-based approach. Also, since finishing is harder to learn and is dependent on specific software, starting with just annotation first would be advisable.

Stephanie Mel, University of California - San Diego:

I joined the GEP in 2009, and then offered a stand-alone course at UC San Diego in 2010. UCSD is a large public research university with more than 20,000 undergraduate students. I had 20 undergraduate biology majors enrolled in the GEP course. We met twice a week for 10 weeks, 2 hours each meeting. I required a grade of at least a B in the Molecular Biology lecture course as a prerequisite for joining the course. The general outline of the course was as follows: 1. Intro to BLAST 2. Intro to DNA Sequencing 3. Intro to Finishing/Consed (we did not do

Finishing in the course) 4. Basics of Annotation 5. Claim, work on, submit annotation projects 6. Present projects, course evaluation. Preparatory background information included short lectures and practice exercises. My students submitted a total of 21 projects after 10 weeks (some students more than one project). Student grades were based on one homework, 2 quizzes, an oral presentation and a written report.

The material is challenging and there is a steep learning curve, so it is important to choose students who have the appropriate background and who are motivated to work independently when teaching a stand-alone course such as this. Because I had only one TA (and myself) for 20 students doing annotation projects, it was difficult at first to get help to everyone who needed it. Fortunately, stronger students were able to help weaker students so this turned out to be a great peer-learning/teaching experience. We also had students work on the first annotation project as pairs. Getting the IRB for the course (to participate in the GEP student assessment) was much more time consuming than I expected, and I had difficulty finding the appropriate control group for the GEP assessment, both things to consider when designing a course. But it is well worth it!

Hemlata Mistry, Widener University:

In my sophomore-level Genetics class, I incorporate GEP materials in three laboratory sessions to cover two core concepts: gene structure, and evolution of genes and genomes. Specifically, I adapt GEP materials on annotation of DNA sequences to help students determine the structure of genes of interest (exon-intron boundaries, untranslated regions, coding sequences etc.). I adapt GEP materials on BLAST searches using the same genes of interest to help students identify homology at DNA and protein levels across different taxonomic groups. Many of my Genetics students move onto GEP annotation projects in their junior and senior years with my colleague Alexis Nagengast, therefore I design my laboratory class to prepare them for their upcoming research experience.

Alexis Nagengast, Widener University:

I first used GEP materials in a stand-alone Genomics course, but now do a 7-8 week annotation project in the first half of my Biochemistry II lab followed by a microarray project for the remainder of the semester. The first two lab periods are devoted to a practice annotation exercise using the ATP synthase gene from *Drosophila erecta* that I adapted from the GEP website. I also do a few quick PowerPoint lectures adapted from the GEP website to provide background during the first 3 weeks. For the annotation project, I have picked *D. erecta* fosmids with 10-14 genes on each and have 5-6 students work on each fosmid. They can decide if they want to work in pairs or individually but each student typically turns in a GEP report with at least 2 genes annotated. Students who are quick learners or enjoy annotation have the option of annotating additional genes on their fosmid and also can help other students who may be struggling with their annotation. Some students find annotation very tedious and don't fully understand the process until they get a "pass" on the Gene Model Checker. All students seem to get a great sense of satisfaction and pride in passing their annotation through Gene Model Checker.

In the beginning, we quickly find that the gene predictions are not accurate and students need to re-adjust their original gene "claims." This leads to a great discussion on manually curated or

computer-predicted gene models on various databases that the students keep in mind for the rest of the semester. Students also seem to better understand gene structure, reading frames and alternative splicing after annotating a gene. At the end of the project, students must complete a GEP report and do a 10-15 minute oral report on one of their annotated genes that includes information on its conservation throughout the Drosophilids and up to mammals (sequence, synteny, etc.), any expression information or putative gene function listed on FlyBase, and any known protein structure function information. Students become very familiar with BLAST and FlyBase and use these skills to identify gene function and pathways in their subsequent microarray experiment.

I have found the GEP materials easy to adapt and incorporate into my lab to cover the material I am most interested in pedagogically. My class is offered every other year so I don't have the option of TAs. I get around this by staggering the time that students start lab so I can work with them in smaller groups when they are first starting to annotate. This allows me to reach more students in the beginning when they all have questions and need more attention. Additionally, my colleague Hemlata Mistry introduces gene annotation in a lab in her sophomore level Genetics course that many of my students took the year before. She designed her lab project with the GEP annotation project in mind and her students perform BLAST searches and use FlyBase. Those students are noticeably more prepared to jump right in to my annotation project when they take Biochem II the next year.

Paul Overvoorde, Macalester College:

During the past five years I have used GEP materials in a number of ways. The annotation project was used as the organizing theme for a 1st year course in Bioinformatics and Genomics. My upper-level Advanced Genetics course includes a module on genome annotation. Finally, students have used GEP-related materials as the basis for an independent research project. Each of these adaptations, and in fact the ideas for how to make them work, were made possible through conversations at the workshops held each year at Washington University. I would strongly encourage faculty who are considering implementing materials or who are curious to discuss ways that resources might be adapted or modified to meet a specific need on your campus to attend one of these workshops.

Don Paetkau, Saint Mary's College (Indiana):

I have used the GEP materials four different ways. 1) I used the "Investigating a Mutation in HIV-1" (from BioQuest) and "Bioinformatics Tools Tutorial Project - KRas" from the "Introducing Students to DNA Sequencing and Genomic Analysis" section as individual labs in both a Biotechnology and a Molecular Cell Biology course prior to attending the Workshop. 2) After attending the Workshop, I started teaching Annotation projects as half of my Biotechnology course (both lab and lecture during that portion of the course) during the fall semester. 3) Three students worked together setting up Finishing projects and completed several Annotation projects as their independent junior/senior research projects. This project included literature preparation during the junior spring and Annotation during the senior fall. The literature preparation was greatly facilitated by the Literature list supplied by the GEP. We had computer issues with the Finishing set up (as some of the software used is written for Macs) and so they focused on Annotation. 4) Changes in scheduling and excellent help with the computer issues

provided the opportunity to teach the Finishing and Annotation projects as a single lab/lecture course in the spring semester of the last two years. I spend half of the course on Finishing and half on Annotation. I will often lecture for a portion of the Tuesday 75-minute lecture period, using modified lectures from the GEP site, especially at the beginning of the course. We use the first ~45 minutes of the Tuesday 3 hour lab section to discuss papers or readings. These readings often come from the "Literature" section of the GEP curriculum site but may also include recently published genomics papers (Gorilla genome paper, for example). This year we included Rebecca Skloot's book, "The Immortal Life of Henrietta Lacks", as a reading. (Rebecca and Henrietta's son were both campus speakers this semester.) Grading is based on homework (one finishing and two annotation problem sets), weekly reading/progress reports, oral and written project reports and submission of the project to the GEP. Students work in pairs on two finishing projects and as individuals for the annotation projects. This year I added five 15-minute tests to encourage the one or two students that coasted a bit last year to stop this practice. There is a lot of frustration at the beginning of the course, but I was recently told by a current medical student that this was an excellent course to prepare her for medical school, so something must be working.

The advice I would provide to new instructors is to use the materials where you are able (as a single lab, for example), because they are excellent products that engage students, especially when they are paired with primary research readings. Having said this, if it is at all possible, teach the whole course. The level of frustration is much higher, but you also have the time for that frustration to blossom into appreciation and a real sense of accomplishment. This course is very different from many courses our students take. Some love it, and others find the need to learn on their own and the frustration of research intimidating. But, as I recently said to a teary eyed student, this is how the next stage of life will work. If you can't get the help when you need it and find ways to understand what you need to do, you will be fired from your next job. This course is a way to start working on those skills. Use the quotes from the AMA that every medical student should have a genomics course, the testimonials of GEP instructors, or anything else that you can to convince your administration that bringing this type of curriculum to your campus makes you cutting edge and innovative. Depending on how you set up the course, it can be an excellent preparation for both the MCAT (or other standardized tests), medical school, graduate school or a technical career in science right out of undergrad. Finally, let the frustration of students wash over you; provide help in excess; find a enthusiastic peer instructors; and use the GEP forum to ask even the simplest questions, as response time from your colleagues, including the brilliant and always patient Wilson, is incredibly fast and helpful.

Susan Parrish, McDaniel College:

Since 2009, I have used GEP annotation materials as the basis for the second half of a Bio 3312 Genomics Laboratory course and as the focus of several independent study research projects. For the laboratory course, during the first half of the semester I introduce students to genomics tools such as BLAST and ClustalW, which the students use to answer "weblems", problems that require application of bioinformatics algorithms and databases. The students are each then assigned a human disease-associated gene sequence; they have to use these tools to assimilate the data for a case study paper.

When we begin the annotation portion of the laboratory, I walk them through a sample annotation, which the students find helpful. I then have students complete projects in pairs to encourage teamwork. Students who finish early are either assigned another project or perform more advanced analysis of the genes in their contig/fosmid. At the end of project, students write up their work in the format of a journal article and present their work during the final exam period of the course. For independent study students, I introduce them to the annotation project in a condensed format and then allow them to work independently.

Celeste Peterson, Suffolk University:

I use GEP materials in the laboratory portion of an upper level Molecular Genetics course. The course has a wet lab component where students do a genetic screen, and the GEP annotation component. I expose students to the GEP material gradually throughout the course. I introduce basic concepts in early lectures, we review materials during downtimes in the experiments, get students started on their own fosmids, and finally devote the last third of the class to annotations only. The website is a fantastic help in this process and has been a great resource for adding materials to the lectures, creating a more integrated class.

One of my own motivations going into this was the novel research aspect, and the students truly appreciate that they were doing something real. What I had not anticipated, however, was how extremely excited they were about working in a larger consortium: just knowing that other schools are involved, and in fact depend upon their work, really made them work harder and more enthusiastically.

My main advice is to take advantage of the tremendously helpful TA program – having somebody trained on the GEP work with me in the class really made all the difference. I highly recommend this material for Genetics or Molecular Genetics courses.

Mary Preuss, Webster University:

My students were able to use the GEP materials and resources to do independent research projects. Having annotation projects coded at different levels of difficulty allowed my students to develop the basic skills first, then apply these skills to more challenging projects as they progressed. If my students had had more time to continue the research, they would have tested some of their gene predictions in the laboratory by designing PCR primers, amplifying the gene of interest by RT-PCR, and sequencing the product.

Laura K. Reed, University of Alabama - Tuscaloosa:

I teach a course titled "Integrated Genomics," which is a lab-intensive advanced undergraduate biology majors' course. I use the annotation of a fosmid to complement the wet lab portion of the course and give the student some exposure to the computational techniques used in genomics research. Since many molecular methods require waiting (e.g. while the PCR machine runs), I find that having the GEP activities to keep the students engaged during that time enriches their lab experience. In the space I use for this lab, the students can work on their personal laptops at a central table near but not at the molecular benches. Having the students working physically adjacent to each other on their individual projects leads to a good deal of peer-to-peer teaching..

Catherine Reinke, Linfield College.

In the context of a one-semester Molecular Cell Biology course at Linfield College, junior and senior biology and biochemistry majors engage in a 4-week, 12-hour genome annotation laboratory module, utilizing the GEP materials and curriculum as described by Emerson et al., 2013. Student work is preceded by an introduction to experimental questions regarding genome evolution, and a discussion of the utility of annotated *Drosophila* genomes to address these questions. Students annotate a unique region of the *D. biarmipes* dot chromosome, following an introduction to BLAST, the UCSC genome browser, and basic approaches to genome annotation. Following completion of their gene models, students present their results to the group. This work is paired with a 4-week, 12-hour molecular genetics laboratory module, in which students generate a *Saccharomyces cerevisiae* genomic library and analyze representative library clones using enzyme digests, DNA sequencing, and in silico analysis of the annotated *Saccharomyces* genome. In the course of these two projects, students first generate relevant annotation data for a genome, and subsequently pursue a project that requires them to utilize an annotated genome. To enrich student experience, instructors should consider framing student projects to help students discover that the process of scientific inquiry requires research for the generation and for the use of experimental tools, and that the work of investigators is thus highly interrelated and interdependent. Student understanding of gene structure, genome organization, and the practice of science is greatly enhanced through research that results in student contributions to an annotated genome.

Dennis Revie, California Lutheran University:

I have used both finishing and annotation for my Molecular Biology class. Each of these topics gives the students different views of research. For the finishing, they have to examine the data, and determine how to improve it. Since the desired experiment (generating additional sequence data from the fosmid template) works only part of the time, they then repeat it again and again. It makes them aware of the iterative process of lab work (i.e., how to beat your head against a wall). For the annotation, students have to make sense of a large amount of imperfect data. They have to propose a gene model that makes the most sense, despite having some data suggesting a different model. They must argue for why their model is the best choice. This lets them better understand that science isn't a cut-and-dried process, but requires sorting through contradictory data to find the most likely solution. The two parts are therefore both useful and complementary. Both parts have worked well for the lab in Molecular Biology. Recently, I have used them in a stand-alone class. This allows for more time spent on both parts and better understanding on the part of the students. The learning curve for finishing and annotation is steep, but the students learn a lot about the process of science.

Srebrenka Robic, Agnes Scott College:

I teach gene annotation as a part of my Bioinformatics (BIO 260) course. I started by incorporating GEP annotation into a special project with four undergraduate research students. I recommend this approach to instructors interested in adopting GEP materials into teaching. Starting with just a few students allowed me to develop a sense for how long it takes for students to learn the material, and helped me better design my syllabus and specific assignments. I like to have my students work in pairs, with more experienced students serving as informal mentors.

Jennifer A. Roecklein-Canfield, Simmons College:

I have used the GEP curriculum as part of two separate majors biochemistry courses here at Simmons. I introduce molecular evolution and BLAST analysis in CHEM345 Biochemistry. This course is a 7hr per week lecture and lab course for Biochemistry majors. We use the BLAST tutorials and assignments from the GEP curriculum first, and then implement BLAST as part of a laboratory assignment on protein expression and isolation. The students can then take an elective course, CHEM347 Advanced Topics in Biochemistry, which is a research-integrated laboratory class that meets for 8 hours per week for a 14 week semester. We introduce bioinformatics utilizing topics from advanced molecular evolution, genomics, and proteomics. The first half of the course is spent on implementing the GEP annotation curriculum, and then each student group selects a contig and completes the annotation and submission to GEP. The remaining half of the course is spent on designing and implementing projects involving analysis of data from the Human Microbiome Project. Recent projects (2010 and 2011) used lateral gene transfer as a core theme. Students examined genes in the Ras GTPase family and Insertion Sequences (IS) in gut microbes such as *Bifidobacterium longum*. The students use techniques learned during the implementation of the GEP curriculum to analyze their genes/gene families, while also performing wet lab experiments to answer biological questions about the Human Microbiome.

Using the GEP tools and interacting with other GEP faculty has led to a collaboration with Anne Rosenwald (Georgetown University) to develop bioinformatics curriculum centered around the Human Microbiome project, and has led us to start an online faculty resource website (<http://genomesolver.org>) to help other faculty interested in this project.

Anne G. Rosenwald, Georgetown University:

Using GEP tools in my Cell Biology class encouraged me to branch out and develop additional Bioinformatics courses and tools. I am now involved in teaching a Microbial Genomics course, based on the rich data available through the Human Microbiome Project. We've also branched out to help other faculty learn the tools to examine these data. Visit <http://www.genomesolver.org> to learn more!

Faculty seeking to use these kinds of exercises in their classes should be prepared to say "I don't know" to their students as the occasion demands - a potentially scary confession. However, by modeling how to get beyond the not knowing, to knowing by struggling to figure it out, faculty demonstrate to their students what it means to be a practicing scientist.

Michael R. Rubin, University of Puerto Rico at Cayey:

GEP materials have been used in three ways at UPR-Cayey. These materials have been used in a research-focused Bioinformatics course where students annotate genomic regions in fosmids of various species of *Drosophila*. The genomic annotation was extended to examine in detail the included regulatory regions as well as the encoded genes, and the structures and functions of their products. Evolutionary processes were also examined using bioinformatics tools to compare genome features and organization in different *Drosophila* species. In this way, students developed skills using major tools for bioinformatics research while creating new knowledge. Students were also introduced to the process of science including the preparation

and defense of a research proposal, hypothesis driven experimentation, keeping careful laboratory records, and preparing a research manuscript followed by an oral presentation of their scientific projects and results. GEP materials are also being used as a platform for independent student research projects. Small groups of students collaborate, with the help of experienced teaching assistants (who excelled in previous GEP based courses), to improve fosmid sequences and annotate genomic regions with extensions to examine evolutionary processes, regulatory regions, gene structure, and the structure and function of encoded proteins. As before, students use the scientific process and major bioinformatics tools to create new knowledge. These results are communicated in research manuscripts and oral presentations. Finally, GEP materials have been used as a curricular enhancement integrated into a lesson plan for a Genetics course to provide research experiences related to evolution, gene regulation, gene structure, and splicing. Students were introduced to bioinformatics tools used for genomic annotation, working in pairs to annotate a small region of a *Drosophila* fosmid and producing a final report using a standard format. This use of GEP materials can be extended to illustrate many important concepts in an introductory Genetics course.

I encourage other educators to use the excellent genomics platform available as part of the Genomics Education Partnership as a springboard to provide original research experiences for their students as courses or parts of courses both in the classroom and in the laboratory. There are many ways to extend GEP related student research experiences as mentioned to understand the roles of numerous features comprising genomic regions. These endeavors provide students with a deep understanding of genome organization, function, and evolution as well as their importance in modern biology.

Kenneth Saville, Albion College:

I have been a member of the GEP collaboration since 2007. I have used GEP materials in a variety of settings. I first conducted a stand-alone course, with 10-12 students focused primarily on sequence finishing (or sequence improvement). I have also used the materials as part of a lab component of a traditional genetics course, typically with two lab sections of 16-18 students each. In the larger course we do only annotation projects. In this larger class format, students exhibit a range of interest in and patience for the annotation process. Typically pairs of students annotate one gene over the last 4-6 weeks of the course. Recently we have changed our curriculum, requiring a lecture-only genetics course as the third course in our introductory sequence. We now offer a stand alone, advanced genetics lab as an elective. I am teaching this lab for the first time this semester and am using the GEP materials exclusively. There are nine students in the class and we meet once a week for three hours. Our plan this semester is to have each pair of students (or in one case an individual student) complete the annotation of an entire fosmid. We have selected fosmids of moderate difficulty, each with 4 to 6 genes and up to several isoforms per gene. Because all of the students have recently had our genetics lecture course, they are all at a similar level of preparation. However, there is still wide variation in levels of interest and ability. We spent the first two weeks with general introductory materials, and then completed a practice annotation using a gene from the 'sandbox' portion of the GEP. This practice included all steps in the process from initial examination of a fosmid, a step-by-step walkthrough of one isoform, independent annotation of a second isoform of that gene,

verification with gene model checker, and completion of the final report. A write-up describing this approach will be added to the GEP website.

The best advice I can give others is that this is an excellent approach to teach about gene structure, genomics and evolution. But, more than this, it teaches the students about problem solving, persistence, and working through frustration. I often explicitly ask students to reflect on the frustration they experience early in the process and to remember this when, in a few weeks, they find the basic annotation process to be easy to the point of being boring. I have them reflect on the process of going from 'confusion to clarity', a process we call learning. A challenge to keep in mind is that individual students progress at very different rates. If possible, gauge the ability of the student during the practice annotation and assign projects of varying levels of difficulty accordingly. One final suggestion is to not hesitate to contact a GEP faculty member at a similar school to ask for specific guidance.

Stephanie Schroeder, Webster University:

I used GEP projects as a unit in an upper level Gene Expression course. The course met for 2 days a week, 90 minutes each. I had a GEP-trained TA and a class of 14 students. We worked on four "easy" fosmids, with each student being responsible for a part. The tutorials were extremely helpful. Although there were frustrations and challenges in the fosmids we had chosen, the students found it to be a very useful experience. They also liked being part of a larger project. Two of the students performed annotation analysis as part of their senior research project with Dr. Mary Preuss.

What I learned is that I should have devoted more time in the course to this unit - the students needed more time to learn the background of splicing and gene organization than I had anticipated. About the time the unit was over, they were becoming more comfortable and it would have been good to continue with further annotation to support their learning. It has also been extremely helpful to have a colleague at my institution who is also using GEP projects, as we are able to learn from each other's experiences.

Karim Sharif, LaGuardia Community College:

I implemented GEP projects for students who were interested in performing independent research projects and also for those wishing to complete their research internship requirements. GEP materials were an indispensable resource, as the students had not taken any upper level course in genetics or genomics. It was challenging to start them on a gene annotation project because they lacked the necessary background knowledge in eukaryotic gene structure and comparative genomics. After one-on-one teaching in the basic concepts, I used GEP materials for them to read to understand basics of BLAST and its use in gene annotation as well as the tutorials for the GEP UCSC mirror browser. Students found the tutorial videos to be extremely helpful. I would then ask them to complete the "Simple Annotation Problem;" upon successful completion of this assignment, students were asked to attempt annotating a fosmid from the demo sandbox. Students felt more confident after completing the demo exercise and progressed well from then on in the gene annotation projects.

I find it very helpful to let students work in my office or the sitting area outside the office, as this affords them the ability to ask me any questions about something that may need further explanation. Once they have successfully attempted a demo exercise, they are pretty much able

to work independently at their own schedule; however, the GEP materials remain a very helpful reference for problem solving for projects at the higher difficulty levels. One of my students presented a poster in a regional science fair and won a 3rd place, competing against undergraduate students from senior colleges as well as the graduate students from various colleges and universities of the region.

Mary Shaw, New Mexico Highlands University:

My main use of GEP annotation materials has been as independent research projects with students. NMHU has a research project requirement for students seeking a BS in biology. Annotation of a fosmid works well for this research requirement. However, most students want to work in a wet lab, so I have been considering what a reasonable wet laboratory component would be.

Gary Skuse, Rochester Institute of Technology:

Each year I offer a dedicated, advanced course entitled Advanced Applied Genomics. We promote it as a more advanced version of a course in Genomics that our Biotechnology & Bioinformatics students take. In the advanced course students spend two 3-hour laboratory sessions each week working on the sequences we obtain from Washington University. They prepare several intermediate written reports and one final comprehensive report detailing their work on the finishing and annotation projects. At the end of the term they give an oral presentation of their work for their peers. In addition, each week we spend one additional hour formally discussing various aspects of their projects and when necessary during the laboratory times we will have impromptu "chalk talks" during which any student who is facing a difficult challenge can discuss it with the class in order to get their input and advice. Throughout the course the atmosphere is one of research and collaboration.

I advise anyone who would like to create a similar course to make it clear from the outset that the course is unique in that it involves research, much like the work a student might undertake with an individual faculty member. Once their expectations are aligned with this notion, it is useful to reinforce it frequently throughout the term by enabling them to ask each other questions and generally collaborate. Despite the frustration that is an inescapable part of doing research, and the substantial time commitment my course requires, the vast majority of the students who have taken it comment that the course was a valuable and enjoyable experience. Several have gotten jobs doing similar work after graduation. Not only do those students see a clear benefit from taking the course, but they provide inspiration for those current students who are in the midst of their own projects. Once the course is taught one or more times, there will be similar opportunities for anyone teaching a similar course elsewhere to use former students as models for current students.

Christopher D. Smith, San Francisco State University:

I have used the GEP materials in my introductory Bioinformatics & Genome Annotation course for several years. My course is split between Junior and Senior undergraduates (1 sophomore) and MS-seeking students. Most students entering this course have no background in genome science, annotation, or the resources available for bioinformatics research. I use the GEP materials as an introduction to many topics and then dive deeper with the students, having them

install software on the command line, execute analyses on the command line, and annotate gene models using the Apollo Genome Annotation Curation Tool. The tours of the Washington University sequencing center are always popular with students and a good introduction to the various sequencing technologies. I use this to launch into more in-depth examination of each sequencing platform (e.g. 454, Illumina, SOLID, Sanger) using YouTube videos and background on the chemistry. My students take the course in the fall so they focus on annotation only and not sequence finishing. We use the GEP chimp chunks exercise as a launching point to introduce pseudogenes and then follow up with some review articles and end with Ka/Ks analysis to discern the selection type on gene models that the students annotate in comparison to other Drosophilids. We also get into some detail on the various gene predictors, BLAST analyses, and repeat masking in the GEP chunks. I then have students learn how to install these programs and perform their own analyses on the command line and merge their results into the GEP chunks to improve the data coverage. We use the Korf & Yandell O'Reilly BLAST book to do an in depth unit on sequence alignment scoring and the various parameters. We also read a paper on SNAP and do work on simple HMMs, and train an HMM for the species we are working on. A few students from this class have continued on in my lab to use their annotation skills on other insect genomes (wasps, ants, bees, flies) and have been co-authors on publications for their work. I also use the GEP report format as a starting point for the students to give 5-10 minute oral presentations in addition to their written reports at the end of the semester.

My implementation of the GEP model is a bit more focused on command-line processing and understanding the algorithms behind the data than other courses may be. I lose approximately 25% of my enrollment in the 1st month, but students who stay generally are very positive about what they have learned. My implementation is particularly labor intensive to set up. Having a dedicated computer lab where each student is fixed on a machine is essential since it minimizes wasted time picking up where they left off. Getting admin access for my students to install software was also problematic, but ultimately gave them the power to direct and understand their own work in a way that pre-installed software does not. The use of the command line is not the most popular aspect of the course, but I see it as an introduction to how work is actually done in a research setting, and although students struggle with this, they've indicated that it gives them a tangible feel for what it is like to execute this kind of work. I heavily use electronic quizzes using the Moodle platform, which helps simplify the testing and grading for me. I test them on readings, basic science content, and command line to execute tasks. These quizzes are usually timed and allow a few chances with feedback when they get things wrong. I then use the quality of their final project, their oral report, and written report to figure out their grade. Students almost universally need to attend extra computer lab hours beyond the course (two times 2 hours a week) to complete their annotations. The teaching assistant is absolutely essential since it is impossible to answer in-depth annotation questions for more than half a dozen students per class session (typical enrollment is 12-20). Keeping class size small (2-3 fewer than the number of working computers) is essential. Having a TA keep the computer lab open for 2-3 hours extra a week is also essential.

Mary A. Smith, North Carolina A & T State University:

I use the GEP materials in a course titled 'Introduction to Genomics and Bioinformatics.' The course includes predominantly undergraduate biology majors, a few MS degree-seeking students, and occasionally students with a mathematics or computer science background. Most of the students in the class have little knowledge of the vast amount of biological information in biological databases that can be retrieved and used to foster biological research. The course introduces students to a variety of computational techniques and tools to expand and integrate the knowledge gained from previous courses in biochemistry, genetics and molecular biology. We use the GEP resources, lectures and exercises to teach students how to use bioinformatics and genomics tools to answer biological questions. We focus on the annotation project to give the students an in-class collaborative research experience and practical experience in genomics and bioinformatics.

My advice to others interested in adopting the annotation project is to expect students to be initially intimidated and to feel lost, because they are being exposed for the first time to numerous online computational tools and to concepts that they have never seen before. Over time, as they begin to solve small pieces of the project, they gain confidence and begin to help each other. Having a teaching assistant in the class is very helpful, in addition to the quality of resources on the GEP website. In the end, the students are able to write a paper that allows them to synthesize their work, and that is when it becomes apparent that they have achieved some of the important outcomes for the course.

Sheryl T. Smith, Arcadia University:

I incorporate GEP materials into a 300-level interdisciplinary course in Bioinformatics that I co-teach with Carlos Ortiz from the Department of Computer Science/Mathematics. The main focus of this course is on genomics. While concepts in gene structure and function are introduced to varying degrees in our foundation courses in General Biology and Genetics, as well as in other courses in the Biology major, I have found that the hands-on approach to gene annotation afforded by using GEP materials allows students to gain a significantly deeper understanding of these concepts. Importantly, by engaging in research projects, distributed and managed by the GEP, students also gain insight into genome organization and evolution. Many students have expressed that they were highly motivated by actively participating in current research that addresses important questions in genome evolution.

The students enrolled in our Bioinformatics course are from diverse educational backgrounds. Although most are undergraduate students with a background in Biology, we have an increasing number of students with a Computer Science/Math background enrolled in the course. Recently we have included graduate students from our Forensic Science program, most of whom have a background in Biology or Chemistry. Our course makes extensive use of GEP materials and support in order to carry out annotation, but also includes a module on sequence manipulation and programming using Perl.

We have taught Bioinformatics for the past three years, with ten students enrolled in our first class in 2010. By 2012 the class enrollment had grown to twenty-four students. Since annotation is a highly interactive process that often requires one-on-one instruction, the instructor/TA to student ratio should be taken into account when considering class size. Ideally, we have found that we need at least one instructor/TA for every five students. We recruit

undergraduate and graduate students, who have taken the course to act as in-class tutors/teaching assistants/graduate assistants the following year.

Eric Spana, Duke University:

The materials I use most are the walk-through/guides to individual sections (finishing, annotation). These give students a feel for what steps are involved, and allow them to walk through the steps at their own pace. For me, the biggest use of GEP materials has been as a guide for making similar materials for my genetics course. Advice: be flexible and allow for more time for discussion than you expect.

Mary Spratt, William Woods University:

My main use of annotation research with students has been in an upper division required course in Cell & Molecular Biology. Since I felt compelled to also incorporate traditional topics & lab experiences for this course, time was limited, with mainly short "teachable moments" being incorporated into lecture time, and about half of the labs devoted for all 3 hours to genomics work. The first two times we incorporated this material, we did both annotation and finishing. In addition to not having enough time, problems with technology, including difficulties using PCs for a then-Mac based finishing system, led to a lot of frustration. This last year I used only annotation with students because of limited time. The initial weeks in each case were devoted to learning about the tools and databases, so the research part was somewhat squeezed for time. Most of our students come to this course with no prior research experience, and many are initially frustrated at not being told the "right answer". A student who had already completed the course elected to do Annotation in an Independent Study, which was an excellent experience and probably helped in her being hired full time by a biotech firm. Ideally, I would like to see Annotation (and/or Finishing) become a stand-alone course with more time available, at least until other faculty begin incorporating introductory genomics ideas and independent research into their courses. With new faculty joining us now, this is likely to become a reality.

Aparna Sreenivasan, California State University - Monterey Bay:

I incorporated the GEP curriculum, particularly the annotation projects, into my BIO 361 - Eukaryotic Molecular Biology course. We have used GEP curriculum for two years. In my class, I introduce genomics, the Drosophila genomes, and the main research questions in with classroom discussions, reading and journal clubs, and lecture. We have a 4 hour session twice per week, which allows us to incorporate versions of the simple annotation problem, and basic annotation work. I then assign students (in groups of 2 and 3) to a specific annotation project through the GEP interface. The students work on these in class and out of class. If a group finishes their annotation in a shorter time than the other groups, they take on a more difficult annotation project. The students are required to write a project report, and submit the GEP project report. They all give a group presentation about this project. This portion of the course is very well received, and my evaluations from students are outstanding. In addition, since introducing the genomics curriculum, a number of my students (many of whom are first generation and /or minority as we are an HSI), have expressed an interest in pursuing genomics for their graduate study or careers. This year I have helped three students obtain REUs that are in the genomics realm - all of these students took my BIO 361 course. I also use the genomics

curriculum for senior capstone (thesis) projects. I had one student successfully complete an annotation project and develop a poster presentation for the capstone festival. Suggestions and comments for faculty interested in incorporating genomics into their classroom/laboratory: a. I am in the process of purchasing 20 computers that will be devoted to genomics in my classroom. I think having a bank of computers - and I like MACs for this process better than PCs - is helpful for the instructor. b. I am working hard to gain more buy-in from our faculty, who are traditionally more ecology-based and for some reason don't always understand the value of genomics. c. We are working on a genomics track in our major, which will help our underrepresented students gain necessary skill-sets for jobs and / or graduate school that will set them apart from other Biology students.

Joyce Stamm, University of Evansville:

I use GEP materials in a stand-alone Genomics course that covers both finishing and annotation. The GEP lectures, lab exercises and tutorials have been absolutely invaluable for introducing the research problem and training students in the techniques they need. My students have been very enthusiastic about the course, and are excellent recruiters each time I teach it (every other year). My advice to new instructors - don't be afraid to learn along with the students. Each of the three times I have taught this course, new issues have arisen which I've had to work out with my students. The scientific/technical support at Wash U is outstanding, and it has been really fun to figure out how to tackle each new problem.

Paul Szauter, University of New Mexico:

I teach BIOL 419/519 Bioinformatics Research, a one-semester course focused on annotation. We use the GEP materials for annotation as the basis for a semester project. I supplement the GEP materials with a course website with additional content. The course website is also a repository for student work as it develops. Student response has been very enthusiastic; some of my students have never had a research experience, and are thrilled to take ownership of an annotation project that no other researcher has examined in detail. My advice to instructors using the GEP materials is to ease students into the annotation workflow with practice annotation projects that the class can complete together, and to get students to submit work on a regular basis as they progress. Students struggle to learn three things simultaneously: the various web-based tools that they need for annotation, the vocabulary of genomics, and the broad concepts behind the research question. Getting regular reports from students allows me to see how they are progressing.

Jeffrey S. Thompson, Denison University:

I teach an upper-level course in Genomics, which has been offered since 2008. The course has a laboratory component, and I have made use of GEP annotation projects in this course every year it has been offered. The fact that these projects are "real research" serves as a powerful motivator to encourage student engagement. It does require a notable time commitment in the course; even a "simple" annotation may require 3-4 weeks of work (3+ hours per week), and some flexibility must be built into the schedule to accommodate unexpected challenges and issues that arise. While I suspect that these projects may be a bit too challenging for

introductory level students, those who have had some prior experience in molecular biology/genetics will likely be in a strong position to benefit from these opportunities.

Matthew Wawersik, College of William & Mary:

I have taught GEP materials in the context of a 1 credit (3 hours per week for 15 weeks) Genomics and Functional Proteomics lab course. This course is not linked to a lecture, so there is a mixture of lab exercises and mini-lectures. During the first few weeks of the class we focus on the process of sequencing a genome, while the rest of the class time focuses on genome annotation, as well as uses of *Drosophila* for examining gene function that would not be possible if a full genome were not completed. I allocate 8 weeks to genome annotation projects where each student is asked to complete 1-2 gene features on a contig that has been assigned to a group of students. In addition to the annotation process, class time is spent on mini-lectures on the basics of BLAST, a sample annotation project, discussions of synteny and repeat elements, a demonstration of Clustal analysis, and oral presentations by each student of their annotation project. Exercises on fly rearing and genetics are interspersed as well so that students can undertake genetics projects. In this context, I have found that it is difficult for students to complete their annotation project (unless it is a straight-forward one) with less than 7 weeks allocated. However, I expect that things would go much faster if a lecture course were linked to this lab. I have also found that early guidance in the form of annotation walk-throughs and a high faculty/TA to student ratio helps things proceed more efficiently, as students often get stalled on simple things related to program set-up (e.g. not being able to find the “align two sequence” box in BLAST, or not enabling specific “tracks” in the UCSC Genome Browser). These road blocks can be extremely frustrating to students at first, but once they move past them they can move forward independently, and quickly see the value of the annotation process both in the context of practical skills and as a research project.

Michael Wolyniak, Hampden-Sydney College:

I have used GEP materials to give students who have shown an interest in genomics and bioinformatics the opportunity to perform independent research. The students involved in these projects work closely together to solve the problems that arise in the annotation process, which provides a wonderful peer learning environment. As new students are brought into the project, senior students take a key role in training them in how the GEP system works and, more generally, how to decipher the various gene prediction models presented in the data. The key piece of advice I can offer to new faculty is to not get scared. The GEP materials are overwhelming at first - in fact, they still are from time to time, since there is so much information provided with each project! However, the challenge of engaging with an on-going research project and guiding students through the experience is well worth it, especially when students demonstrate high levels of acquired genomics knowledge in future projects and classes and become inspired to pursue research as a career option as a direct result of GEP participation.

James Youngblom, California State University - Stanislaus:

I have used the GEP materials in my senior level genetics class every spring semester since 2007. I usually have 20-26 students. I recruit one or two students from the previous year to serve as my lab TAs. We discuss contemporary genetic biotechnology in lecture on Mondays

and Wednesdays and then use computers for a bioinformatics lab every Friday for 15 weeks. The first four labs are exercises to prepare the students for *Drosophila* gene annotation (introductions to BLAST, Genome Browser, etc.). Next pairs of students work together and have 8 weeks to successfully complete annotation of all the genes and all of the isoforms in their fosmid. The last 3 weeks of lab periods are devoted to a follow-up molecular phylogeny project. For other instructors interested in a similar approach to genomic teaching, I would advise that you learn as much as you can about any DNA analysis program you are going to introduce in class. This is a never-ending process, but my class gets better every year, not because my students are better but because I am better prepared to teach them. I work hard to limit my directions to the students at the beginning of any lab. I try to introduce the basics and then let the students get to work.

Leming Zhou, University of Pittsburgh:

I have used the GEP materials in three different courses: the first one is a 3-credit stand-alone course (Genomics and Personalized Care); the second is an 8-hour (4 sessions, two lectures and two labs) course module; and the third is a 4-hour (2 sessions, one lecture and one lab) course module. In the stand-alone course, I have specific lectures about sequence alignment, BLAST searches, genome browsers, and gene finding methods and practices. Thereafter, students felt comfortable about working on gene annotation projects, including the most challenging ones. All of the students (junior, senior, and graduate students) in the course finished their annotation projects successfully. One junior student who took this course worked with me subsequently on research projects. He published two journal articles with me by the time of his college graduation. In the 8-hour course module, five 3-hour lectures related to gene annotation were squeezed into two 2-hour lectures, one lab session to demonstrate annotation techniques, and one lab session for guided practice. Students (mainly junior students) could work individually or in a small group to finish gene annotation projects. However, they could only work on simpler projects (*D. erecta*). In the 4-hour course module, I could only provide one overview lecture and one demonstration lab session. Students (junior students only) in this class could only get some ideas about genomics and gene annotation. They did not have sufficient time to grasp the technique of gene annotation. Therefore, according to my teaching experience, we need at least 8 hours to successfully introduce gene annotation techniques to students who do not have extensive knowledge in biology. A stand-alone 3-credit course is even better.

Supplemental Text S2. Responses to the question: What has been the impact on your students?

Consuelo Alvarez, Longwood University:

At the end of the semester, the students loved this type of open-minded research work, even though at the beginning, students would fight to be told what to do.

Cheryl Bailey, University of Nebraska-Lincoln:

The impact on my students was that they were able to participate in a national research project and thereby participate in the community of science. They had a teaching assistant and a faculty member teaching the course who were trained by professionals to use tools that they otherwise would not have known how to use. The students had access to raw data in a format with support that allowed them to identify and annotate this new DNA sequence.

The impact on my students was to make judgments. Some were making judgments for the first time in their college experience; many were not participating in individual research experiences. Plus they learned about evolutionary principles by using sequence and genome comparisons during class. They also learned about gene models, and this helped them in the courses they were taking.

Students rated this experience very highly. The experience culminated in a poster presentation and many had not made a poster or presented science to peers and faculty before. Students used this experience as a research experience on their applications to graduate school, professional schools and jobs in industry, and talked about this experience on their interviews.

This was a high impact experience for these students.

Daron Barnard, Worcester State University:

This has allowed students at WSU, who might not have otherwise had a chance to participate in research, to do so. Students found it challenging, but took ownership of the projects and really felt like they had something to contribute to the research community. It has also allowed further engagement with the scientific community, by providing students the opportunity to present at local and regional meetings.

Christopher Bazinet, St. John's College (New York):

For the most part, students found it interesting, even exciting, to be learning by doing. Some students did not adjust well to independently (or semi-independently) thinking through new/original problems. They seemed to need the comfort of there being an absolute answer or result that they could anticipate and use for comparison. But the majority appear to have enjoyed the annotation experience, and I am convinced it broadened their biological perspective considerably.

Dale Beach, Longwood University:

Generally the students found this course to be a huge wake-up call. First, this was their first exposure to research. They found that working without knowing the answers to be novel and challenging. Often students worried more about making a mistake and ruining the research than about exploring multiple, possible solutions to find the "best fit." Students wanted to solve the puzzle, get the answer, and be done without the extra work of checking and validating their own work. Many in the class found the time commitment required to actually complete and verify their work difficult to handle. Second, the students simply had not been exposed to the idea of whole genome sequencing and annotation. Although methods were discussed in their Genetics course, the application had completely eluded them. Students discussed how much they disliked the course, and were confused by the work, until the last few weeks when everything "seemed to fit together." In the end, some students realized that they did not like the research paradigm, but most of the class felt that they had acquired a better idea of how to work in research and a deeper understanding of genomic sciences.

James E.J. Bedard, University of the Fraser Valley, Canada:

The impact on my students has been significant. Former students have loved the opportunity (and challenge) to work on actual research projects during the regular academic year. It has provided them with the required undergraduate research experiences for applying to professional programs. In 2012, two students were accepted into graduate school, one in medical school, and another in dentistry. All four spoke very passionately about their GEP experiences in their applications and interviews. Before graduation, two of these students had presented their gene annotation project data at an international conference and the majority of attendees assumed they were graduate students, based on the level and quality of their work. One conference attendee (a CEO of a biotech company) was even trying to recruit them for positions after they graduated. Overall the GEP has had a very positive impact on my students.

April Bednarski, Lindenwood University:

I felt the results were most visible when the students presented their gene annotation reports in front of each other. The students were animated and proud to show what they figured out, plus their methods. They seemed interested in each other's work and how different the projects could be, as well as the various challenges that they encountered. I think the students gained a sense of pride in their work and dedication to their project that only comes with an original research project like this. They also learned a great deal about eukaryotic gene structure and using bioinformatics tools for research.

Satish Bhalla, Johnson C. Smith University:

I have used the GEP material in the Introductory Bioinformatics class. The students enjoy hands-on and enjoy the research aspect of the assignments. There is a spirit of competition in completing the assignments. There has been a definite improvement in the student performance.

John Braverman, Saint Joseph's University:

Sometimes one hears that undergraduates are very tech-savvy. However, in my Bioinformatics class, I find that the students really grow in their ability to use computers. They

really had not been trained to take full advantage of the incredible technology available, especially with respect to Internet and communication. Perhaps one of the most important areas of learning is saving and backing up data files. No matter what biology these students learn, they are now a lot closer to surviving in a highly computerized world. With respect to science, a major area of impact is the imaginative appreciation of the genome. Prior to the annotation experience, my students had a very vague sense of the organization and structure of genes in a eukaryotic genome. Many of them stated outright they improved in this area.

Martin Burg, Grand Valley State University:

The impact on students has been significant. We have a very large undergraduate major program and only a few positions to provide students with a research experience at all (1300 majors, 25 faculty). Some students who have gone on to careers in medicine and other health care professions have specifically benefitted from the approach taken in the GEP course that I teach. One student confided in me and others that, although she had two years experience in an organic chemistry research lab and had co-authored two papers, interviewers at medical schools were asking more questions about her experiences in finishing and annotating than about her organic chemistry research experience. Students complete the semester with a feel for what research really involves, by completing projects, going through review presenting their results orally, and writing a paper based on their projects; I have had several go on to Ph.D. programs as well as master's level programs. The course, which is still temporary, generated a lot of interest among students this year, having a wait list of 40 (taking in 14 students due to space constraints). There is certainly interest in this type of approach (conducting a real research project in a classroom environment) and demand for it is here at GVSU. In general, students complete an entire semester course feeling as if they really have accomplished something on their own, using their own approach to solving the problems encountered.

In addition to the semester-long course that I have been able to teach, I also have several independent research students who use what they have learned in the class and have continued their work. They then continue on by serving as TAs the following year-and many of them are now in either Ph.D. programs or medical school.

Vidya Chandrasekaran, Saint Mary's College of California:

The implementation of annotation projects has allowed students to gain some research experience. A number of students have told me that this has been useful in their quest for internships and entry into medical schools. I have had students come to me semesters later to tell me that they had used the bioinformatics tools in other courses and were excited that they could do something better than other students in the class and finish their labs earlier. One of my students applied to a Masters in Bioinformatics program because of how much she loved her annotation project.

Hui-Min Chung, University of West Florida:

There are overall two major impacts on the students who did annotation projects: 1) the research component no doubt benefits their abilities in reasoning (making educated guesses, trial and error) and communication, and 2) students are much more aware of the power of computational biology, which gets them seriously thinking about working in the bioinformatics

field in the future.

Kari Clase, Purdue University:

Students have initially struggled with the technology since the programs used for analysis are different from what they have encountered before in their classes. The project has stretched them to troubleshoot. Once they begin to work on the project in more depth, they have found that it helps them apply the concepts they are learning in their other courses, such as the distinction between eukaryotic and prokaryotic organisms.

Randall J. DeJong, Calvin College:

Students remarked that this experience solidified or even changed for them their concept of what a gene is, as opposed to having it described in a textbook. Some also appreciated the complexity and variation that genes from even one organism can exhibit. Students appreciated the opportunity to participate in a larger genomics project.

Justin R. DiAngelo, Hofstra University:

Incorporating a genomics research project through the GEP into our curriculum has had two major impacts on my students. The first is pedagogical: annotating *Drosophila* genes has solidified my students' knowledge of gene structure. Even though they have learned about the structure of eukaryotic genes in two courses before my Genomics course, annotating genes seems to be the approach that causes this concept to "stick." The other major impact is in increasing my students' confidence in themselves as scientists. By being responsible for a small chunk of a larger research project, they were able to design an approach to solve a specific scientific/experimental problem, develop their critical thinking skills, and learn how to troubleshoot/deal with technical problems. This type of experience is impossible to replicate in a standard lecture or laboratory course.

Chunguang (Charles) Du, Montclair State University:

The first few cohorts of students have moved on to their careers. Some are working in the pharmaceutical industry and others are in graduate school. They really appreciated the bioinformatics skills that they learned from Genomics class, which is the only course at my school which provides access to genomics annotation research.

David Dunbar, Cabrini College:

The impact on Cabrini students has been huge! Several students have indicated that they have acquired prestigious internships or jobs after graduation as a direct result of their experience using the bioinformatics tools that are part of the GEP program. The program has also allowed undergraduates to consider careers that have more of an emphasis on bioinformatics. Without the GEP course, students at our institution would not be getting robust instruction in cutting-edge bioinformatics.

Todd Eckdahl, Missouri Western State University:

Former students have commented that they appreciated getting the chance to become familiar with genome annotation because it helped them in graduate school. They explained

that they had experience that their peers in the same program did not have. Others mentioned that the GEP experience helped them to get a job in the life science industry. They were able to explain how they had used computer analysis to conduct genome annotation, and this was viewed as a demonstration of their ability to learn and adapt to new research methods.

Heather Eisler, University of the Cumberlands:

The students are much more confident when they finish annotating. At first the students are a bit frustrated that there isn't a preset right answer, but the sense of accomplishment they take away rivals any wet lab research I have ever done with students. I have some students get so excited that they eagerly dive into another contig and sign up for additional semesters.

All Independent Study students present at local conferences. They take a very strong sense of ownership of their work, and they refine their understanding, as they have to be able to explain it to others. Frequently the audience includes students and faculty from a variety of different disciplines, so this is great practice for medical school and graduate school interviews.

Sarah C. R. Elgin, Washington University in St. Louis:

The impact of this research project for students has been very positive. The work is challenging, but they are eager to gain expertise using bioinformatics tools, and pleased that their efforts contribute to our on-going research, rather than being disposed of at the end of the semester. (A common sentiment seems to be "Thank goodness someone is treating me like a grown-up for once!") Students clearly gain confidence in their problem-solving skills, and improve their ability to present and defend their work. The course consistently rates very high in student assessments, with comments such as the following: "...a rare opportunity to get hands-on experience in Real Biology while becoming self-sufficient enough to do your own work - I loved it;" "...I was able to learn a lot about genetics through the class...;" "...one of the most productive and fulfilling courses I have taken...;" "...I wish there were more like it...;" "The hands-on approach on real research allowed me to get a very intimate understanding of the material...Further, this also made me very passionate about giving my best effort to the projects."

Julie Emerson, Amherst College:

From 2009-2011, each student used parts of three or four laboratory periods to receive training and then perform annotation of a randomly selected gene. Our students liked being part of a national research collaborative with students from across the country, and were challenged by projects that did not have "known" answers. Students also felt that the activity was highly integrative. One sample quote from a 2010 student evaluation is as follows: "The genome sequencing for the last part of lab was very interesting, as it was an application of some of the things we had learned earlier in the semester about transcription and translation, while also adding to our biology skill set... it was very interesting and instructive in terms of genetics and evolution."

In 2012, all students learned the basics of gene annotation by annotating the same, pre-selected gene during a single laboratory period. Although students missed out on the excitement of working on their "own" uncharted genes in this one-week lab, we believe that they

nonetheless gained a richer understanding of eukaryotic gene structure and how to use on-line genomics databases, which will serve them well in their upper-level biology course work, future research experiences and post-graduate studies in the biological or biomedical sciences.

A cautionary note for doing gene annotation in introductory biology courses, regardless of the length of time devoted to this activity: in-depth instructor/TA training and a high (TA+faculty):student ratio is essential, as many novice biology students are easily frustrated if they are unable to obtain adequate help while learning how to use the databases and search engines.

Amy Frary, Mount Holyoke College:

Students are eager for what they see as "marketable skills," and this research experience provides them with just that. It also gives them a good sense of the hard work, frustrations and joys involved in grappling with a scientific problem, so that they are better prepared for graduate school.

Donald Frohlich, University of St. Thomas (Texas):

GEP participation has shown students that are not particularly wet-lab oriented that they too can participate in research and make significant contributions. Students have also been particularly impressed with the fact that they can construct hypotheses and test them on the spot, so-to-speak. Not having a 'canned' answer known only by the instructor also raises their level of self-esteem and confidence. I cannot over emphasize the teaching value of collaboration. Our students tend to love the field of molecular biology, and GEP projects allow them direct and immediate access as participants and not just as observers.

Anya Goodman, California Polytechnic State University – San Luis Obispo:

My students love being treated as professionals in the GEP course: they have a goal and the tools they need, they manage the project within the team (divide up the tasks, decide when and how much work to put in, give each other help and feedback). By completing the GEP annotation projects, students get to practice their research and communication skills, learn to overcome difficulties and become more confident in their abilities to learn.

Yuying Gosser, Engineering, The City College of New York, CUNY:

GEP provides an opportunity for students to engage in responsive research in genomics. The major impacts on the students:

- a) Deepens their understanding of the central dogma of molecular biology and biological systems, increases their knowledge of bioinformatics databases (such as NCBI, PDB, FlyBase, and Genome Browsers), and helps them to master basic tools for comparative genomics (BLAST, ClustalW), as well as a literature database (Pubmed);
- b) Broadens their view of biology and genomics; for engineering students, this adds another dimension to their research interests and career considerations;
- c) By the time they complete their "open-ended" gene annotation projects, students recognized the "uncertainty" in scientific research and began "thinking like a scientist."

Shubha Govind, Biology, The City College of New York, CUNY:

The greatest impact is on building students' confidence in their ability to learn and contribute to knowledge. In addition, the students apply the bioinformatics tools they learn in GEP in their lab-based research projects, and in some cases, in finding positions in the job market.

Adam Haberman, Oberlin College:

I find that students begin feeling unprepared to approach these projects, and end up with a sense of accomplishment. Many of my students tell me they want to continue to work on genome-scale projects. I have found that projects must be significantly challenging in order for the students to feel like they are really learning anything from their efforts.

Amy T. Hark, Muhlenberg College:

In open-ended reflective essays, students typically report increased understanding of molecular genetics (including how genes evolve, how splicing works, etc.) as well as improved ability to generate and collect necessary information using bioinformatics tools, make arguments supported by available evidence, and solve problems.

Charles Hauser, St. Edward's University:

Students' initial frustration with the open-ended nature of finishing and annotation projects transitions to confidence as they learn to apply the principles covered in previous courses and reinforced in the GEP materials. Students learn to work collaboratively, build critical thinking skills, understand the challenges of carrying out scientific research and take pride in their ability to contribute to the larger project.

Arlene J. Hoogewerf, Calvin College:

The biggest impact on students comes from their ability to be part of a bigger, significant research project that advances scientific knowledge even though they are undergraduate students at a liberal arts institution and have only a semester to work at the project.

Laura L. M. Hoopes, Pomona College:

Student enthusiasm and interest abound when they own a project like this. My students, even if they struggle to discuss papers in class, dive into knowing all about "their" fosmid and would never dream of presenting an oral report to the class that didn't include a full understanding of that fosmid. I love the sense of collaboration I see during class sessions in the computer lab.

Carina E. Howell, Lock Haven University of Pennsylvania:

I implement the GEP project into my junior and senior level elective class in Bioinformatics and Genomics. Comments from students on an evaluation of the project included: "It teaches about the actual research process, especially the challenges of no one else knowing the answer", "It taught me to work independently and forced me to learn what I was doing instead of memorizing", "I had to use time management because this project wasn't something that could be done in a couple hours the night before it was due", "It gave me hands on experience in the techniques described in lecture which I think is very important", and "The annotation project was, by far, the most useful project I have done in my collegiate career. Unlike most other projects, the answers were unknown, and that allowed for the feel of real scientific research". I

believe that these comments reflect the general consensus on the impact that the GEP project had on my students. They enjoyed actually being involved in a novel research experience and very much appreciated that they got hands-on experience. The project evaluations were consistently positive from all students involved in the project.

Diana Johnson, George Washington University:

Most students have become very interested and excited as they progress through their annotations. They are initially nervous about doing work that has no known answer. Further, some students take this course to satisfy a requirement. They often are used to just getting by on each assignment, so that the thought of keeping working on something is novel to them. The students gain a much better understanding of eukaryotic gene structure. They also see first hand the concept of conserved protein-coding sequences versus variable intron sequences. By the end of the project I find that almost all students are converted to enthusiasts for doing this work and having the experience of research.

Christopher J. Jones, Moravian College:

I've had students at a variety of levels and with a variety of interests over the years. Some have told me that they've subsequently used some of the skills learned in their Genomics course, while others don't see it as being terribly relevant to what they're currently doing. The great majority report increased self-confidence regarding research after taking the course, and appreciate the opportunity to contribute to an open-ended scientific project (even though the lack of known "correct" answers is initially frustrating for them). Student course evaluations have been uniformly very positive.

Lisa Kadlec, Wilkes University:

I do genome annotation as one part of the lab portion of my genetics course. Although students learn a bit about genomics in earlier courses, my genetics students find annotation challenging and it definitely increases their understanding of and appreciation for genomics. By the end of the annotation part of the lab, the students have increased confidence in their knowledge and skills in the areas of genomics and bioinformatics. All of our biology majors are required to do a senior research project, and many of the students start working in a research group before their senior year, but for those who haven't started research yet, the GEP annotation gives them important experience in terms of working on a project that is at least in part their own and which doesn't have a known answer.

Marian Kaehler, Luther College:

Because I only use a two-week annotation exercise, adapted from the GEP research project, Luther students are not experiencing research directly. However, all students gain exposure to key genomic principles and tools, with the development of an appreciation for the importance of gene annotation at both gene and genomic levels. In addition, by annotating even a couple of genes, the better students also recognize evolutionary pressures, having seen stop codons in the non-reading frames, multiple stop codons at gene termini, splice site consensus sequences, etc.

S. Catherine Silver Key, North Carolina Central University:

The 5-week experience students gain through the GEP project in the Genetics course provides them a taste of how research is conducted. Most students have never performed a BLAST search before the GEP experience. They find it tedious, but often after the course has ended I will hear from students about how their GEP experience had provided them with a leg up in other classes or in their research internships!

Adam Kleinschmit, Adams State University:

Students have a new sense of motivation to excel and see projects through, knowing that their efforts will be utilized by other scientists in the field. GEP-based research has also allowed a number of my students the flexibility to take on an independent research project, in which they were able to make significant progress within a semester's time. This has been especially valuable for pre-med students.

Nighat P. Kokan, Cardinal Stritch University:

I have implemented annotation in different configurations in many of my courses. The students have had the opportunity to do novel research and get excited about owning their part of the project. Students have indicated in class surveys that they like knowing that their contributions will benefit the greater scientific community and that they are not doing another cookbook lab. Many students have been able to present their work in poster format at local or national meetings. Some students have told me that the GEP experience has helped them get internship positions and work on projects that built on the skills they gained from their genomic annotation project.

Olga Ruiz Kopp, Utah Valley University:

Students love the opportunity to participate in a project that produces results that the community at large can use. Students working in groups become very engaged in the troubleshooting process and learn important critical thinking skills. Students also love the opportunity to add this experience to their resume.

Gary Kuleck, University of Detroit Mercy and Loyola Marymount University:

The impact of the GEP approach to student engagement cannot be understated in my experience. Since the learning curve is steep initially, I have paired students to work on projects and even had full class participation to complete the projects. Most students respond very positively once they begin to grasp enough bioinformatics to make substantial progress. The students who have had a GEP experience seem to have a much more grounded understanding of bioinformatics and some are very enthused. Some of my students have gone on to graduate school with aspirations for a career that will involve some level of bioinformatics. I don't think that this would have happened without the GEP experience.

Judith Leatherman, University of Northern Colorado:

I use GEP annotation as a short four-week module in Genetics. This is our students' first exposure to BLAST and working with primary DNA sequences. It can be very frustrating at first, but students seem to gain a strong feeling of accomplishment when they figure things out. In

the longer term, I think students gain a better understanding of how we make sense out of all the genomic data currently being generated, and develop a much more concrete understanding of eukaryotic gene structure.

Jane Lopilato, Simmons College:

GEP introduces our students to genomics. For many, it is their first introduction to a research project and, certainly, for all of us, to a “nation-wide research project.” Students list their annotation experience on their resumes now.

From their experiences with GEP, students gain a much better understanding and appreciation of eukaryotic genes. Their starting point is a model of a prokaryotic gene, showing the DNA sequence with the encoded amino acids indicated. Then, to tackle the DNA sequence of a eukaryotic gene, something that isn’t just a drawing with blocks of exons and introns, as in their textbooks, opens their minds to the complexity of actually finding genes on a chromosome. Yes, the students get frustrated but they quickly learn to use the basic tools of annotation.

Christy MacKinnon, University of the Incarnate Word:

The impact of the GEP research projects on my students has been significant. Students work in groups of 4-5 to annotate an isoform of an assigned contig/fosmid, and they quickly become peer tutors without prompting or instructions on my part. It has been amazing to observe the transformation of students from reluctant learners to enthusiastic participants! As part of their final project report, students prepare a group poster in a format for presentation at a scientific meeting. For most groups, the final product exceeds the requirements of the grading rubric. Student performance on exams shows most students can readily interpret a BLAST report, analyze a Genome Browser screen shot, and justify the coordinates for a given exon.

Juan Carlos Martínez-Cruzado, University of Puerto Rico at Mayagüez:

The impact of the GEP experience on students can vary considerably. Most find it challenging at the beginning and fun at the end. Even though it may be more challenging than the Introductory Genetics course, the dropout rate is approximately half, probably because Annotation is far more successful as students interact and learn from each other, as is typical of a research project. It is a very special course experience for most of them. Some students become really enthusiastic and apply the following semester for a Special Problems course in which they can have their own individual project annotating the Puerto Rican parrot (PRP) genome.

Gerard P. McNeil, York College, CUNY:

This course has had a tremendous impact on many of the students. They come in thinking they know everything about what a gene is and its structure, and then find out how little they really know. This humbles them and makes them think more critically about what they think they understand. They also gain an appreciation for how real research is done and the role that interaction with others plays. They struggle with the idea that the instructor doesn’t know the answer to the question and that they must think and not just follow a protocol with a known result. At the end, they begin to learn how to think critically and appreciate their

accomplishments. Many that have gone on to medical or graduate school have told me how important the course was in preparing them for how to approach scientific questions and gain understanding from the literature. In addition, some have told me that it was a great addition to their experiences in the wet lab. The opportunity to gain some knowledge of genomics and bioinformatics has also been appreciated by the students, with some going into the field as a result.

Stephanie Mel, University of California - San Diego:

Coming from an institution where students routinely take classes with several hundred students, the opportunity for students to take a small, highly interactive research-based course was priceless. The course had a tremendous impact on students because of the hands-on nature of the material and the fact that each student group was working on a unique problem. They loved that it was "real" and were very engaged as a result of this. As one student said, "this is a class that other classes should be modeled after. It takes what students have learned in other classes and really applies it to a research question." Students learned how to work independently, but also how to collaborate with a partner, and they learned how to approach questions that did not have the pre-packaged answers that are typical for lab courses. Students gained confidence that they could tackle an unknown problem. They also learned a great deal about gene structure and bioinformatics. This course helped develop critical thinking skills, but also got students excited about science and research in a way that most other courses do not.

Hemlata Mistry, Widener University:

I work closely with Alexis Nagengast. By using the GEP style of applying lecture concepts directly to a research question, I have found that our students are better able to connect eukaryotic gene structure with gene expression and function. Further, I find that our students are better able to think critically, trouble-shoot experiments and draw on knowledge from different courses to help them answer their research questions. Those students who have gone on to medical or graduate school have reported using their genomics skills in their post-graduate courses and research.

Alexis Nagengast, Widener University:

Students who have taken my GEP-affiliated course seem to become more involved in other research projects in our Science Division, and bring to that project what they learned in annotating. They seem to become more independent thinkers, and are more comfortable with trouble-shooting. Additionally, students have reported using their genomics skills in other classes and in graduate school.

Paul Overvoorde, Macalester College:

The use of GEP materials prompted students to consider genome organization more deeply. The pattern finding and sequence comparisons made during gene annotation provided concrete examples of the abstract ideas of RNA processing and alternative splicing. Furthermore, students developed the habits of mind that enabled them to become efficient and confident when examining a new sequence of DNA, regardless of its origin. The ability to query databases and interpret alignments allowed them to use distinct lines of evidence to support

claims about the coding and repetitive sequences found in such a sequence. Through this process students engaged an unstructured problem, thought critically about web-based resources, and generated a set of claims that required interpretation of multiple lines of evidence.

Don Paetkau, Saint Mary's College (Indiana).

Students gain increased confidence compared to what they achieve in a lecture-based course. They have increased confidence in their abilities to do research, with computer-based research, with genomics research, with the field of genomics and why it is important to have a population that understands it, with reading primary literature, with the presentation of research, and with problem solving (which is what research really is).

Susan Parrish, McDaniel College:

The students gain a much better understanding of gene structure and genome organization, and how to use bioinformatics databases and algorithms. They also take pride in their work and are enthusiastic about making a real contribution to science.

Celeste Peterson, Suffolk University:

By the end of the project, the students felt more confident in what they were doing and liked knowing that their work was going to be incorporated into a larger project. Some students decided that they really enjoyed the bioinformatics side of research and discussed with me how they could use genomics in different post-graduate options such as graduate school or careers in genetic counseling.

Mary Preuss, Webster University:

The impact of the GEP on my independent research students has been huge. It provides resources for my students to get experience in bioinformatics, which is not currently taught at our university. It provided the tools for students to develop specific skills in sequence analysis. But I believe the greatest advantage was that it gave our students the ability to be part of and contribute to a larger research project.

Laura K. Reed, University of Alabama – Tuscaloosa:

My students have generally really appreciated the bioinformatics experience. Many of them feel it gives them a better sense of what types of jobs might be available to them in the field of computational biology. I had one student who had a lot of potential but was distracted from his studies; because of his experience in GEP he rededicated himself to his academics and is now attending a graduate program in biology.

Catherine Reinke, Linfield College:

Linfield students who have participated in the GEP have gained a robust research experience that they frequently discuss when applying for employment and to graduate school; this experience helps them to demonstrate a sophisticated understanding of the nature of scientific research. From the students' perspectives, they report an improved sense of the number and scope of unanswered scientific questions, and a better understanding of the work that scientists

do. Students begin to consider themselves to be scientists as they pursue a novel research question, develop a defined skill set, and learn to use the tools commonly employed in bioinformatics analyses. In addition, students point to their laboratory work as instrumental in solidifying concepts of genomes and gene expression introduced in the course.

Dennis Revie, California Lutheran University:

The impact I see is interesting, because some students really don't like the whole research process, while others really enjoy it. The ones that like it see that they are discovering something new, while the ones that dislike the process seem to dislike the uncertainty and the failures that occur.

Srebrenka Robic, Agnes Scott College:

The biggest impact I noticed among my students was the sense of ownership and confidence gained by tackling genomics research projects. It is incredibly satisfying to see undergraduate women transition from being overwhelmed by the tools and software to using them confidently and teaching their fellow students.

Jennifer A. Roecklein-Canfield, Simmons College:

As our curriculum is entirely research integrated, the greatest impact on our students was the observation that not all research is done at the lab bench. The students were particularly interested in the ability to engage in real research projects using computer technology. The recognition of novel ways to perform data analysis was critical.

Anne G. Rosenwald, Georgetown University:

The GEP projects give students a chance to experience authentic research in a course, rather than performing a laboratory exercise where the outcome is known in advance. Students who have gone on to medical school or graduate school have reported that having experience in bioinformatics has been extremely helpful, since this is becoming a standard part of both medical and biology/biochemistry curriculum at the graduate level.

Michael R. Rubin, University of Puerto Rico at Cayey:

The impact on students at UPR-Cayey has been extremely positive. Students quickly learn basic bioinformatics skills and become proficient in sequence improvement and especially genome annotation. They welcome opportunities to participate in original research. They realize that they are contributing new knowledge as part of a national project in which many of their peers from other institutions are also involved. In addition, students actively learn about the process of science, as well as developing their understanding of sophisticated biological concepts about genome organization, gene structure and regulation, protein structure and function, and the implications of comparative genomics for understanding evolution. Students develop abilities in effective teamwork, analytical reasoning and problem solving, and scientific communication. Student participants also gain considerable satisfaction upon completion and submission of their genomic annotation projects.

Kenneth Saville, Albion College:

I have involved students in the GEP project in a variety of settings, from a 2-3 week module in the lab component of a genetics course to a full semester intensive lab experience. In all settings, the students begin with a high level of discomfort and frustration with the project; the approach is relatively foreign to them, even though they have had some previous experience with tools such as BLAST. In the vast majority of cases students work through this frustration and reach that 'aha' moment when things start to make sense. In my opinion, one of the biggest impacts is this grappling with a difficult problem and seeing it through. The most significant impact on students is in the more intensive lab courses. These students are able to get an idea of the bigger research question and get experience with several aspects of the research process: tackling a larger scale research problem, writing full reports, submitting their analyses to the GEP core, and presenting their research at our campus-wide research symposium. I believe this presentation gives them a sense of doing 'real' research, along with those students who are presenting more traditional independent study and thesis projects. Several students have gone on to do genetics research in graduate school. While I don't have any survey data, I have heard informally from a few that they were surprised at how much bioinformatics was involved in their graduate research, and that they felt somewhat better prepared having been through this course.

Stephanie Schroeder, Webster University:

The impact on the students of having the hands-on experience with genomics research, and feeling part of a larger project, was huge. It also had a great impact on me as an instructor, to learn along with the students as we tackled issues with annotation.

Karim Sharif, LaGuardia Community College:

Research work on the genomic analysis of *Drosophila erecta* resulted in presentation of a poster by two of my students, Jason Macias and Dionesha Duarte, in the Annual Biomedical Research Conference for Minority Students (ABRCMS) held in St. Louis, MO in 2011, and a second poster by Jason Macias in ABRCMS 2012, held in San Jose, CA. This research has afforded these students the opportunity to be trained in scientific methods of inquiry and in the art of scientific presentation. Jason presented a poster in the Alliances for Graduate Education and the Professoriate (AGEP) conference in 2012, and won a 3rd place prize competing against students from senior colleges as well as the graduate students from CUNY and other universities from the region. The research work was also presented by Jason at the Annual CSTEP Conference held on April 13-15, 2012 at the Sagamore, Lake George, NY.

My students who performed GEP research were able to transfer successfully to senior colleges and universities such as SUNY at Stony Brook, Hunter College of CUNY, York College of CUNY, and Ohio State University. Some students become very enthusiastic about the GEP research experience; Jason, even after graduating from LaGuardia and transferring to Hunter College, continues to come back to do GEP research with us, and Karvyn and Tenzin have plans to do the same.

Mary Shaw, New Mexico Highlands University:

Several students have received significant benefit from their work on GEP projects. One went on to receive a PhD in *Drosophila*-based research, and others have used the knowledge and

skills in PhD programs or jobs. One of the students, Daniel Delgado, presented several posters at national and local meetings such as the New Mexico Bioinformatics Symposium. The impact on many of the students was more subtle, as they learned to work on an open-ended project where no one knew the "right" answer.

Gary Skuse, Rochester Institute of Technology:

Experiences in our Advanced Applied Genomics course, which is based on the GEP curriculum, has impacted our students in two ways. First, while taking the course it is clear that they become invested in their respective projects to the point that they contact me outside of class to share ideas and ask questions. While this may happen in other courses, students clearly demonstrate ownership of their "unique" project within the course. They truly view their work in this course as research, not simply as a set of exercises designed to teach them something. Second, many of our students have either gone on to continue their bioinformatics education at the doctoral level, or have obtained jobs in which they directly use the tools and techniques they learn in this course.

Christopher D. Smith, San Francisco State University:

The implementation of the GEP curricula at my university has had varied impact for my students. Two students in my class before affiliating with the GEP later became GEP-trained TAs. One went on to increase the genomic component of his project and subsequently pursued a PhD in bioinformatics. He also trained my next cohort, which had a very talented student who became my TA for several years and ultimately joined my lab to co-author several papers on genome projects. He also is in a prominent bioinformatics PhD program now. A third undergraduate student from his class similarly contributed to a publication. The activities of the students in the lab closely mirrored the course curricula, including annotating genes in insect systems to provide a well-researched, high level of annotation that ultimately can support functional studies. The background in genome technologies, different types of genes, concepts about algorithms, and other course topics became relevant parts for roughly 1/2 of the students. Since a high proportion of the students in the class were already affiliated with labs, many of them took their new skills to other projects. This fostered some internal collaborations in the department.

Some of the students clearly struggled but persisted, and none failed (although the drop rate was about 30%). The internal university evaluations were very positive and comments from students typically indicated that they learned something new and felt more conversant in and proficient with bioinformatics and genomic research. Scalability was an issue for the course, and it was challenging to think of simple ways to scale the experience. I think student impact might have been greater if the publication mechanism was faster. Although not easy for GEP to control, timelier co-authorship on publications is typically more beneficial to students - within 2-3 years, when they apply for fellowships or graduate programs. Overall I think the GEP program had very high impact for several of my students (and myself). My best research students, hands down, came from those that I mentored in my GEP-based class. Many went on to PhD or other secondary programs.

Mary A. Smith, North Carolina A & T State University:

At our institution, the GEP annotation project is incorporated into an introductory bioinformatics and genomics course. This is the first introduction of most of the students in the course to bioinformatics and genomics, and more importantly, to *in silico* experimentation. The annotation project requires students not only to apply concepts learned in molecular biology, genetics, and biochemistry, but also to integrate their knowledge and learn science the way it is practiced by life scientists. Students are challenged to solve a portion of a larger cutting-edge research problem that is being investigated by a broad scientific community. Through this experience students gain a deeper understanding of the importance of quantitative and computational tools and techniques for solving biological problems. They also learn the importance of using a variety of techniques and corroborative evidence to justify an answer to a research question. Initially the students work outside of their comfort zone, as a result of having little experience in applying computational tools to solve a problem where even the instructor does not know answer. Consequently, the project fosters collaboration and peer teaching/learning. Some students grasp the new concepts and techniques at a much faster pace than others and are able to teach their peers. Over time, the students find that they do not rely solely on the instructor for answers; the environment changes to a more student-centered one as students seek help and/or provide assistance to their peers voluntarily. In the process, students develop a true appreciation for collaborative research and how the scientific process works.

Sheryl T. Smith, Arcadia University:

The impact on the students in our Bioinformatics course has been significant. Using GEP annotation materials, our students have gained a deeper understanding of gene structure and genome evolution (concepts briefly introduced in other courses). Many of our students who have gone on to graduate programs that require Bioinformatics as part of the curriculum have reported how helpful it was to have acquired foundational skills in genomics through the use of GEP materials. Two of our students have changed their career tracks based on participation in the course. One student is now in a graduate program with a focus on Biostatistics. Another of our students will be applying for doctoral programs in Bioinformatics. As the need for trained professionals in the area of bioinformatics continues to grow, I believe that courses that utilize GEP materials will be extremely helpful in recruiting students to this important field.

Eric Spana, Duke University:

Student impact has been two-fold. First there are the glowing reviews of how much better they understand the genomics material, and what fun they had in a lab class where they were actually discovering, rather than performing repetitions of previous semesters. Second, I've used the GEP format of having a solid research question, engendering student engagement and ownership, and moved it into my genetics & developmental biology course. I could not have made this course as good as it now is without what I learned in GEP.

Mary Spratt, William Woods University:

Some students have benefited greatly professionally from my GEP-affiliated course, as they have moved on to graduate programs and careers. Others may stay "stuck" in the initial frustration that they felt during the course in not being told or able to memorize the "right"

answer. It is not always the best academic student in more traditional classes that does best in research; there have been some wonderful surprises with students really getting "turned on" for the first time to the excitement of new discovery. Less academically secure students seem to adjust more slowly to this experience. I love the fact that this type of research can enable all students at even the most financially challenged institutions to experience real research.

Aparna Sreenivasan – California State University - Monterey Bay:

My students benefitted in a number of exciting ways. First, their evaluations of the course state that this is one of their most valuable hands-on learning experiences. Next, I now have students interested in pursuing careers in genomics and genetics, because these students love computers and didn't initially realize that computer-based genomics is "real research!" This year alone I had more than three students apply for genomics-related REU experiences, wanting to gain a greater understanding of the field and more experience so that they could apply for graduate programs and/or jobs in this area of research. The GEP allows me to bring hands-on research inexpensively to more students; indeed, if I made this an entire course, I wouldn't need to cap it at a level as small as a traditional wet lab course, and could reach even more students. One of my students, after taking the GEP portion and training as a TA for my class, spearheaded a Python course for BIO majors by contacting the Computer science faculty and explaining some of the "needs" of BIO students that are interested in genomics. This generated a huge discussion in our faculty and allowed me to push for more genomics curricula.

Finally this type of course benefits all of the students, as every one of them comes away with valuable knowledge about how research is conducted, how to analyze genomes, and this junction between computer science, biology, and genetics.

Joyce Stamm, University of Evansville:

Beyond providing an excellent way for students to learn the basics of eukaryotic gene structure, the course also allows students to understand that science is not simply a collection of facts, but a process of discovery. They become very invested in the fact that they are contributing to a larger body of knowledge, and they are extremely engaged in their projects. One of my former students is currently working in a genomics company; he believes that he got the job at least in part because of his experience with the course.

Paul Szauter, University of New Mexico:

Most of my students have only had lecture courses before this, and over half had never engaged in research. The major impact that I observe is that, for many, this was their first exposure to the unknown. At first, many students wanted absolute rules that they could apply to solve their research problem, as if it were an exercise in a lecture class. Students gradually learned that each project was different, and while the initial approach could be easily sketched out, many projects require unique solutions that involve a fair amount of trial and error. Several students presented their work as posters at a local research symposium. As the day of the presentations drew near, one student told me that he had tried to look up papers on stop codon read-through in Ten-m (the subject of his poster), but the only mention that he could find of it was in the supplemental materials to a paper that I had given him. I explained to him that this was a research project, and it was very unlikely that there were any other papers on this

problem. This course was able to provide this student with his first direct experience that our scientific knowledge is incomplete, and will never be complete. Other students, when submitting their projects, have asked how they will know if they were right. I have explained that their gene model is a hypothesis, and while it will have to compete with other models when it is evaluated, there is no way of knowing whether it is correct in an absolute sense. I wish that students could learn these things earlier in their study of science (most of my students are seniors or higher), and I will try to get students to take this course earlier in the years to come.

Jeffrey S. Thompson, Denison University:

My students benefit tremendously from their engagement in GEP projects. Knowing that they are involved in a large scale, collaborative effort provides a huge incentive to encourage them to invest the time and energy required to complete these projects. They come out of the experience with a notably broadened perspective on how research can be done, and their understanding of the fundamentals of molecular biology is dramatically enhanced.

Matthew Wawersik, College of William & Mary:

The impact of this course has been multifaceted and depends very much on the level of student experience. For students with less laboratory experience, a major impact is generating excitement for the research process; it's a pleasure to watch students take ownership of a project and push it forward because they want to be the first to see the outcome of analyzing an unknown problem. For students who have already had the opportunity to work in research labs, a major benefit is learning the power of genomic databases that have application to other research projects. Regardless of the student experience level, however, the process of gene annotation helps all students gain a tangible understanding of gene structure and regulation.

Michael Wolyniak, Hampden-Sydney College:

The students that have been involved with GEP have shown a level of excitement and passion for research in biology that I have not seen amongst other students. By becoming involved in an authentic research experience, these students have developed a strong interest in furthering their involvement in research and in pursuing careers in which research is a central component.

James Youngblom, California State University – Stanislaus:

My students are much better geneticists after completing the GEP exercises. In particular, my students are supplementing the classic examples presented in genetics textbooks with messier, real examples. At the start of the term very few can describe a typical eukaryotic gene in detail; few can explain alternative splicing; none can describe an appropriate use of a BLAST search. It takes hands-on examples for them to figure these things out. Finding for themselves non-coding exons or seeing for themselves how differently spliced transcripts can produce the same peptide or discovering for themselves introns with atypical splice donors is not the same as reading about them in a book. After the GEP gene annotation experience, my students understand what it means to work in bioinformatics. They now comprehend the need for 'bioinformaticists.' They appreciate the power of the union between the molecular genetics and modern computing.

Leming Zhou, University of Pittsburgh:

My students were typically quite frustrated at the very beginning (because of a lot of new concepts and techniques), and very excited when they succeeded in completing their annotation projects. They all reported that this research experience made them more active learners and that they had gained some ideas about how research is done. One student even changed his major from a professional major to biology after he took the genomics course.



Genomics Education Partnership Classroom Undergraduate Research Experiences: Pre-course Survey

Welcome to the GEP-CURE survey site. This project is a collaborative effort involving the faculty and students from many undergraduate institutions participating in the GEP. Together we are learning more about the success of our science courses in empowering student learning. To accomplish this task we have developed a pre-course post-course research design to measure the learning gains and other outcomes of courses that include our shared genomics project. This research is funded by the Howard Hughes Medical Institute. It has been approved by the institutional review board at Washington University.

If you are beginning a course and the instructor has asked you to participate in this education research, please fill out the pre-course survey questions by clicking the link below. Because of the complexity of tracking the data from many courses in many institutions, we ask you to identify your college and course. The computer will also generate for you a personal identification code. To create this code we will ask you to enter your name as it appears on your drivers license. Your name will then be converted into an encrypted number and sent with your responses. The encryption is being done in such a way that it is not possible to convert from the number back to your name to ensure anonymity. The reason for the code is to enable us to match your pre-course information with a post-course evaluation that we will ask you to complete at the end of the term. This alignment of your pre-course responses with your post-course responses permits a sensitive measure of change. Your individual data will not be revealed to your course instructor. The lead analyst for the project, Prof. David Lopatto of Grinnell College, will keep all individual data confidential. Only aggregate pre-course-post-course data will be reported back to your institution and to the GEP as a whole. Your data cannot be used by instructors to determine your grade in the course.

As with any research, you are not compelled to participate. You may elect not to answer individual questions. A "not applicable" or "N.A." option is available for the questions as an alternative; use this if the question is irrelevant or if you choose not to answer. If you change your mind about completing the survey, just leave the site. It is assumed that the submission of a completed survey is your consent for participation. If you have any questions or comments regarding the survey, please send an email to Prof. Lopatto (lopatto@grinnell.edu). Thanks!

After you complete the post-survey, we offer you an opportunity to be entered into a raffle for a \$50 gift certificate from Amazon.com, as a "thank you" for your participation. Ten email addresses will be selected at random in June, after the academic year is over. If you wish to be entered in the raffle, we will need your email to contact you if you win. Please be assured that the file containing these emails will be completely separate from the file of survey responses; this list of names will not be used for any other purpose.

[Proceed to the survey](#)



Part I: Some general information about you and your situation.

Please type in your personal identification (your name as it appears on your drivers license or student ID), identify your school, and type in your pertinent course name and number. Your personal identification will be used to generate a code number that will be used only to match pre-course information to post-course information. Only the code number will be sent to the GEP servers.

Personal identification code: (Your name as it appears on your driver's license)

College or University:

What is your anticipated year of graduation?

☐ 2013 ☐ 2014 ☐ 2015 ☐ 2016 ☐ Not Applicable

Your gender: ☐ Male ☐ Female

Your Ethnicity:

- ☐ Caucasian
- ☐ Asian
- ☐ Afro-American
- ☐ Hispanic or Latino
- ☐ Native American
- ☐ Mixed
- ☐ Other
- ☐ NA

Course dept and number:

Have you declared a major or concentration yet?

- ☐ Yes
- ☐ No

If you have declared a major or concentration, please write it here (include double majors, concentrations, etc.)

If you have not yet declared a major or concentration, please indicate if you considering a major/concentration in the

sciences.

- ☐ Definitely yes
☐ It is likely
☐ I'm not sure
☐ It is unlikely
☐ Definitely no
☐ Prefer not to answer

Here is a list of common reasons for taking a course. Please read each one and indicate if the reason was important to your decision to take this course.

Reasons:	Not Important	Moderately Important	Very Important	Not Applicable
To fill a distribution requirement	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
To fill a requirement for my major	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I need it for graduate or professional school	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I need it for my desired employment after college.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Interest in the subject matter	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
To learn wet lab techniques	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
To learn about science and the research process	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
To get research experience	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
It fit in my schedule	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The course has a good reputation	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The Instructor has a good reputation	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
To learn in-silico/computer based experimental techniques	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Please look over this inventory of elements that might be included in a course. For each element, give an estimate of your current level of ability before the course begins. Please use this scale: mark a "1" if you have no experience or you feel inexperienced, mark a "2" if you have some experience, or mark a "3" if you have much experience or feel you have mastered this element. Your current level of ability may be a result of courses in high school or college, or it may be a result of other experiences such as jobs or special programs.

If students are expected to do the following course element...I have...

Element:	1 - no experience or feel inexperienced	2 - some experience	3 - much experience or mastered this element	Not Applicable
a scripted lab or project in which the students know the expected outcome	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
lab or project in which only the instructor knows the outcome	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
lab or project where no one knows the outcome	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
at least one project that is assigned and structured by the				

instructor	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
a project in which students have some input into the research process and/or what is being studied	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
a project entirely of the student's own design	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
work individually	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
work as a whole class	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
work in small groups	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
become responsible for a part of the project	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
read primary scientific literature	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
write a research proposal	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
collect data	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
analyze data	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
present results orally	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
present results in written papers or reports	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
present posters	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
critique the work of other students	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
listen to lectures	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
read a textbook	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
work on problem sets	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
take tests in class	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
discuss reading materials in class	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
maintain a lab notebook	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Use computer-based experimental techniques	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Which of the following experiences of research have you already had before taking this course?

- Did Independent or small-group research with a science faculty member.
☐ Yes ☐ No
- Was employed in a science faculty member's lab.
☐ Yes ☐ No
- Did a research project in another science class.
☐ Yes ☐ No
- Did an independent science research project while in high school.
☐ Yes ☐ No
- Did a research project in a non-science class.
☐ Yes ☐ No
- Did independent research with a faculty member outside of the sciences.
☐ Yes ☐ No

If you have had some other type of research experience, not listed here, please describe it.

Part II: Your opinions about yourself and about science.

It has become common to say that no student is an empty bucket, waiting for a teacher to pour in knowledge. Research on learning acknowledges that students approach a course with well-formed opinions of themselves and of the subject matter. In this section we present questions about science and questions about you. These will help us put your learning in context.

For each item below please rate your agreement with the item. (response choices: strongly agree, agree, neutral, disagree, strongly disagree, n.a.)

Opinions:	Strongly agree	Agree	Neutral	Disagree	Strongly disagree	Not Applicable
Even if I forget the facts, I'll still be able to use the thinking skills I learn in science.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
You can rely on scientific results to be true and correct.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The process of writing in science is helpful for understanding scientific ideas.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
When scientific results conflict with my personal experience, I follow my experience in making choices.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Students who do not major/concentrate in science should not have to take science courses.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I wish science instructors would just tell us what we need to know so we can learn it.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Creativity does not play a role in science.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Science is not connected to non-science fields such as history, literature, economics, or art.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
When experts disagree on a science question, it's because they don't know all the facts yet.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I get personal satisfaction when I solve a scientific problem by figuring it out myself.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Since nothing in science is known for certain, all theories are equally valid.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Science is essentially an accumulation of facts, rules, and formulas.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I can do well in science courses.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Real scientists don't follow the scientific method in a straight line.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
There is too much emphasis in science classes on figuring things out for yourself.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Only scientific experts are qualified to make judgments on scientific issues.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Scientists know what the results of their experiments will be before they start.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Explaining science ideas to others has helped me understand the ideas better.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The main job of the instructor is to structure the work so that we can learn it ourselves.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Scientists play with statistics to support their own ideas.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Lab experiments are used to confirm information studied in science class.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
If an experiment shows that something doesn't work, the experiment was a failure.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Below are ten descriptive statements. The number scale between them is used to indicate how well a statement or a pair of statements describes you. For example, on the first pair, a "6" would indicate you are very action oriented, while a "4" would indicate you were more action-oriented than reflective, but somewhat reflective. For each pair of statements, choose a number that indicates how well the statement describes you. Do not worry that some pairs are not opposites.

I would describe myself as reflective.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I would describe myself as action oriented	<input type="radio"/> Not Applicable
I prefer subjects with precise answers.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I prefer subjects with multiple interpretations.	<input type="radio"/> Not Applicable
I value patience.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I value getting things done.	<input type="radio"/> Not Applicable
I like things to be varied and colorful.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I like things to be exact and precise.	<input type="radio"/> Not Applicable
I would describe myself as a doer.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I would describe myself as an observer.	<input type="radio"/> Not Applicable
I take a creative and imaginative approach to solving problems.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I take a precise and calculated approach to solving problems.	<input type="radio"/> Not Applicable
I would describe myself as evaluative and logical	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I would describe myself as receptive and accepting.	<input type="radio"/> Not Applicable
I like to watch what is going on	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I like to see the results of my actions	<input type="radio"/> Not Applicable
I strive for versatility.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I strive for accuracy.	<input type="radio"/> Not Applicable
I am reserved.	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5 <input type="radio"/> 6	I am prepared.	<input type="radio"/> Not Applicable

Submit

Clear form



Genomics Education Partnership Classroom Undergraduate Research Experiences:

Pre-course Quiz

Welcome to the GEP pre-course quiz site. This project is a collaborative effort involving the faculty and students from many undergraduate institutions participating in the GEP. Together we are learning more about the success of our science courses in empowering student learning. To accomplish this task we have developed a pre-course/post-course research design to measure the learning gains and other outcomes of courses that include our shared genomics project. This research is funded by the Howard Hughes Medical Institute. It has been approved by the institutional review board at Washington University.

If you are beginning a course and the instructor has asked you to participate in this education research, either as a GEP student or a "control" student please complete the pre-course quiz questions by clicking the link below. Because of the complexity of tracking the data from many courses in many institutions, we ask you to identify your college and course. The computer will also generate for you a personal identification code. To create this code we will ask you to enter your name as it appears on your driver's license. Your name will then be converted into an encrypted number and sent with your responses. The encryption is being done in such a way that it is not possible to convert from the number back to your name to ensure anonymity. The reason for the code is to enable us to match your pre-course quiz evaluation with a post-course evaluation that we will ask you to complete at the end of the term. This alignment of your pre-course responses with your post-course responses permits a sensitive measure of change. Your individual data will not be revealed to your course instructor. The lead analyst for the project, Prof. David Lopatto of Grinnell College, will keep all individual data confidential. Only aggregate pre-course/post-course data will be reported back to your institution and to the GEP as a whole. Your data cannot be used by instructors to determine your grade in the course.

As with any research, you are not compelled to participate. You may elect not to answer individual questions. A "not applicable" or "N.A." option is available for the questions as an alternative; use this if the question is irrelevant or if you choose not to answer. If you change your mind about completing the quiz, just leave the site. It is assumed that the submission of a completed quiz is your consent for participation. If you have any questions or comments regarding the survey, please send an email to Prof. Lopatto (lopatto@grinnell.edu). Thanks!

After you complete this pre-course quiz, we offer you an opportunity to be entered into a raffle for a \$50 gift certificate from Amazon.com, as a "thank you" for your participation. Five email addresses will be selected at random in June after the academic year is over. If you wish to be entered in the raffle, we will need your email address to contact you if you win. Please be assured that the file containing this information will be completely separate from the file of quiz responses; this list of names will not be used for any other purpose.

Next



Genomics Education Partnership Pre-course Quiz on Genomics Sequencing and Annotation

Some general information about you.

Please type in your personal identification (your name as it appears on your drivers license or student ID), identify your school, and type in your pertinent course name and number. Your personal identification will be used to generate a code number that will be used only to match pre-course information to post-course information. Only the code number will be sent to the GEP servers.

Personal identification code: (Your name as it appears on your driver's license)

College or University:

What is your anticipated year of graduation?

☐ 2013 ☐ 2014 ☐ 2015 ☐ 2016 ☐ Not Applicable

Your gender: ☐ Male ☐ Female

Your Ethnicity:

- ☐ Caucasian
☐ Asian
☐ Afro-American
☐ Hispanic or Latino
☐ Native American
☐ Mixed
☐ Other
☐ NA

Course dept and number:

Does this course involve you in a genomics research problem (with the Genomics Education Partnership, GEP) improving sequence and/or annotating genes in Drosophila?

- ☐ Yes
☐ No

Have you declared a major or concentration yet?

- ☐ Yes
☐ No

If you have declared a major or concentration, please write it here (include double majors, concentrations, etc.)

If you have not yet declared a major or concentration, please indicate if you considering a major/concentration in the sciences.

- ☐ Definitely yes
- ☐ It is likely
- ☐ I'm not sure
- ☐ It is unlikely
- ☐ Definitely no
- ☐ Prefer not to answer

Proceed to Quiz



Genomics Education Partnership Post-course Quiz on Genomics Sequencing and Annotation

Some general information about you.

Please type in your personal identification (your name as it appears on your drivers license or student ID), identify your school, and type in your pertinent course name and number. Your personal identification will be used to generate a code number that will be used only to match pre-course information to post-course information. Only the code number will be sent to the GEP servers.

Personal identification code: (Your name as it appears on your driver's license)

College or University:

What is your anticipated year of graduation?

☐ 2013 ☐ 2014 ☐ 2015 ☐ 2016 ☐ Not Applicable

Your gender: ☐ Male ☐ Female

Your Ethnicity:

- ☐ Caucasian
☐ Asian
☐ Afro-American
☐ Hispanic or Latino
☐ Native American
☐ Mixed
☐ Other
☐ NA

Course dept and number:

Does this course involve you in a genomics research problem (with the Genomics Education Partnership, GEP) improving sequence and/or annotating genes in Drosophila?

- ☐ Yes
☐ No

Have you declared a major or concentration yet?

- ☐ Yes
☐ No

If you have declared a major or concentration, please write it here (include double majors, concentrations, etc.)

If you have not yet declared a major or concentration, please indicate if you considering a major/concentration in the sciences.

- ☐ Definitely yes
- ☐ It is likely
- ☐ I'm not sure
- ☐ It is unlikely
- ☐ Definitely no
- ☐ Prefer not to answer

Proceed to Quiz



Genomics Education Partnership Classroom Undergraduate Research Experiences: Post-course Survey

Welcome (or welcome back) to the GEP-CURE survey site. This project is a collaborative effort involving faculty and students from several colleges and universities participating in the GEP. Together we are learning more about how our science courses can empower student learning. To accomplish this task we have developed a pre-course post-course research design to measure learning gains and other outcomes of taking a research-oriented science laboratory course including genomics. This study is funded by the Howard Hughes Medical Institute. It has been approved by the institutional review board at Washington University in St. Louis.

If you are taking a course in which the instructor has asked you to participate in this study, you probably filled out a pre-course survey at the beginning of the term. Because of the complexity of tracking the data from many courses in many institutions, we asked you to identify yourself by giving your name (as it appears on your drivers license), to identify your college, and to identify your course. The computer used your name to generate an encrypted number sent with your responses. The encryption is done in such a way that it is not possible to convert from the number back to your name, to ensure anonymity. Now the reason for this identification becomes clear: we will match your pre-course information with your post-course evaluation using your personal identification number. This alignment of your pre-course responses with your post-course responses permits a sensitive measure of change. Your individual responses will not be revealed to your course instructor. The lead analyst for the project, Prof. David Lopatto of Grinnell College, will keep your data confidential. Only aggregate pre-course - post-course data will be reported back to your institution and to the GEP administration. Your answers cannot affect your grade in the course.

As with any educational study, you are not compelled to participate. You may elect to not answer individual questions. A "not applicable" or "no answer" NA option is available for all questions as an alternative if the question is irrelevant or you choose not to answer. If you change your mind about completing the survey, just leave the site. It is assumed that the submission of a completed survey is your consent for participation. If you have any questions or comments regarding the survey, please send an email to Prof. Lopatto (lopatto@grinnell.edu). Thanks!

In a final box, we offer you an opportunity to be entered into a raffle for a \$50 gift certificate from Amazon.com, as a "thank you" for your participation. Five email addresses will be selected at random in June, at the end of the academic year. If you wish to be entered in the raffle, we will need your email address to contact you if you win. Please be assured that the file containing these email addresses will be completely separate from the file of survey responses; this list of email addresses will not be used for any other purpose.

[Proceed to the survey](#)



I: Some general information about you.

Please type in your personal identification (your name as it appears on your drivers license or student ID), identify your school, and type in your pertinent course name and number. Your personal identification will be used to generate a code number that will be used only to match pre-course information to post-course information. Only the code number will be sent to the GEP servers.

Personal identification code: (Your name as it appears on your driver's license)

College or University:

What is your anticipated year of graduation?

☐ 2013 ☐ 2014 ☐ 2015 ☐ 2016 ☐ Not Applicable

Your gender: ☐ Male ☐ Female

Your Ethnicity:

- ☐ Caucasian
☐ Asian
☐ Afro-American
☐ Hispanic or Latino
☐ Native American
☐ Mixed
☐ Other
☐ NA

Course dept and number:

Have you declared a major or concentration yet?

- ☐ Yes
☐ No

If you have declared a major or concentration, please write it here (include double majors, concentrations, etc.)

If you have not yet declared a major, once again indicate if you are considering a major/concentration in the sciences.

- ☐ Definitely yes
☐ It is likely
☐ I'm not sure
☐ It is unlikely
☐ Definitely no
☐ Prefer not to answer

II. Course Elements

Please rate how much you gained from each element you experienced in this course. The scale measuring your gain is from 1 (no or very

small gain) to 5 (very large gain). Some elements may not have happened at all. If the item is not relevant or you prefer not to answer, please choose the "not applicable" option.

Elements:	1 (no or very small gain)	2	3	4	5 (very large gain)	Not Applicable
a scripted lab or project in which students know the expected outcome	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
a lab or project in which only the instructor knows the outcome.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
a lab or project where no one knows the outcome.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
at least one project that is assigned and structured by the instructor.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
a project in which students have some input into the research process and/or what is being studied.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
a project entirely of the student's own design.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
working individually.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
working as a whole class.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
working in small groups.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
becoming responsible for a part of the project.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
reading primary scientific literature.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
writing a research proposal.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
collecting data.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
analyzing data.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
presenting results orally.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
presenting results in written papers or reports.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
presenting posters.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
critiquing the work of other students.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
listening to lectures.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
reading a textbook.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
working on problem sets.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
taking tests in class.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
discussing reading materials in class.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
maintaining a lab notebook.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
computer based experimental techniques	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

III. Benefits

Benefits. Below are some possible gains you may have made as a result of taking this course. The scale measuring your gain is from 1 (no or very small gain) to 5 (very large gain). Select the number that reflects your experience in this course. If the item is not relevant or you prefer not to answer, please choose the "not applicable" option.

Benefits:	1=no gain or very small	2=small gain	3=moderate gain	4=large gain	5=very large gain	6=Not Applicable
	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

	gain					
Understanding of the research process in this field	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Understanding how knowledge is constructed in this field	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Readiness for more demanding research	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Tolerance for obstacles faced in the research process	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Skill in interpretation of results	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Clarification of my career path	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Ability to integrate theory and practice	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Understanding how scientists work on real problems	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Understanding that scientific assertions require supporting evidence	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Ability to analyze data and other information	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Ability to read and understand primary literature	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Understanding science	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Learning ethical conduct in this field	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Learning laboratory skills	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Learning computer skills	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Skill in how to give an effective oral presentation	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Skill in reasoning from data	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Self-confidence in discussing science with peers	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Self-confidence in discussing science with mentors/instructors	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Skill in scientific writing	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Understanding how scientists think	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Learning to work independently	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Learning to work as part of a team	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Becoming part of a learning community	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Interest in taking other courses in this area	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Interest in taking additional courses in math and computer science	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Confidence in my potential to be a teacher of science	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

IV. Learning Experiences

Below is a list of specific teaching tools or activities that may have been part of your course. Please rate each component, indicating to what degree this component contributed to your learning experience in the course (1 = very little learning; 5 = very beneficial to learning). If that component was not used in your course, check not applicable. If you did not do a finishing project, **skip to part B**.

A. Finishing a DNA sequence	1 (Very little learning)	2	3	4	5 (very beneficial to learning)	Not Applicable
Finishing DNA sequence data	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Descriptive material about Consed (Guide, Introduction)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Finishing lab practice as a group	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
My own efforts to finish my fosmid	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Preparation of my written report on finishing	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Preparation of my oral report on finishing	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Defending my conclusions

☐☐☐☐☐☐

B. Annotating a DNA sequence	1 (Very little learning)	2	3	4	5 (very beneficial to learning)	Not Applicable
Annotating my gene / fosmid	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Using BLAST for Detecting and interpreting homology	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Using EST databases	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Identifying genes and pseudogenes	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Annotating the assigned fosmid/contig/gene	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Using Clustal software	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Analyzing repeats	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Preparation of my written report on Drosophila annotation	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Preparation of my oral report or poster on Drosophila annotation	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Defending my conclusions	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

V. Overall Evaluation

For each item below please rate your own agreement with the item. (5-point scale: 'strongly agree, agree, neutral, disagree, strongly disagree).

Overall Evaluation:	Strongly agree	agree	neutral	disagree	strongly disagree	Not Applicable
This course was a good way of learning about the subject matter.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
This course was a good way of learning about the process of scientific research.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
This course had a positive effect on my interest in science.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I was able to ask questions in this class and get helpful responses.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I would take another research-oriented lab course if given the opportunity	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I expect to use these tools/techniques in future research	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Genomics is awesome! I love the power of data bases!	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Taking this course helped me to become a more active learner.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Taking this course has helped me learn to think independently.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Taking this course has increased my motivation to learn.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I would recommend this course to a friend	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Knowing that my results will be part of a public database used by other students and scientists motivated me to do a careful and through job.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Analyzing data is challenging; it doesn't matter to me whether I am working on my own project or analyzing a paper generated by other scientists.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Having an opportunity to be a co-author on a scientific paper is important to me.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I loved the fact that this project was for real! I've done enough cookbook labs in my life, I'm ready to move on to the real thing.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

VI. Impact on Future Plans

How were your plans for future education impacted by participating in a course including genomics? (*Choose one*)

- ☐ I had a plan for post-BA education in the life sciences, and this has not changed.
- ☐ I had a plan for post-BA education in the life sciences, and this plan has been confirmed.

- ☐ My plan for post-BA education will now include a greater emphasis on genomics.
☐ I had a plan for post-BA education in the life sciences, and I have now decided to drop this because of this course
☐ I had a plan for post-BA education in the life sciences, and I have now decided to drop this for other reasons.
☐ I did not have a plan for post-BA education in the life sciences, and I have now decided to develop such a plan.
☐ I do not have a plan for post-BA education in the life sciences.

VII. Your opinions about science

In the pretest you responded to questions about science. Below the questions are posed again. Your answers will help us decide between two hypotheses, that such opinions are constant over time or that opinions change as a result of experience.

For each item below please rate your agreement with the item. (response choices: strongly agree, agree, neutral, disagree, strongly disagree, n.a.)

Your opinions about science:	Strongly agree	agree	neutral	disagree	strongly disagree	Not Applicable
Even if I forget the facts, I'll still be able to use the thinking skills I learn in science.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
You can rely on scientific results to be true and correct.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The process of writing in science is helpful for understanding scientific ideas.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
When scientific results conflict with my personal experience, I follow my experience in making choices.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Students who do not major/concentrate in science should not have to take science courses.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I wish science instructors would just tell us what we need to know so we can learn it.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Creativity does not play a role in science.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Science is not connected to non-science fields such as history, literature, economics, or art.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
When experts disagree on a science question, it's because they don't know all the facts yet.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I get personal satisfaction when I solve a scientific problem by figuring it out myself.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Since nothing in science is known for certain, all theories are equally valid.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Science is essentially an accumulation of facts, rules, and formulas.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I can do well in science courses.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Real scientists don't follow the scientific method in a straight line.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
There is too much emphasis in science classes on figuring things out for yourself.	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Only scientific experts are qualified to make judgments on scientific issues.	<input type="radio"/>					
Scientists know what the results of their experiments will be before they start.						
Explaining science ideas to others has helped me understand the ideas better.						
The main job of the instructor is to structure the work so that we can learn it ourselves.						
Scientists play with statistics to support their own ideas.						
Lab experiments are used to confirm information studied in science class.						
If an experiment shows that something doesn't work, the experiment was a failure.						

Please comment on the effort made to integrate research and teaching in genomics in this course. What were the strengths and weaknesses? What was of special value to you? Should this effort be continued?



Submit Clear form

This survey is hosted by the Department of Biology at Washington University in St. Louis.



Genomics Education Partnership Classroom Undergraduate Research Experiences: Student Alumni Survey

Welcome to the GEP-CURE survey site. This project is a collaborative effort involving the faculty and students from many undergraduate institutions who are participating in the GEP project to finish and annotate the dot chromosomes of *Drosophila*. Together we are learning more about the success of our science courses in empowering student learning and subsequent careers in the sciences. To accomplish this task we have developed this survey of former GEP students, to ask you what you are doing now, and to ask you to reflect on your GEP experience, and how it influenced your subsequent studies. This research is funded by the Howard Hughes Medical Institute. It has been approved by the Institutional Review Board at Washington University.

The survey can be accessed by clicking the link below. Because of the complexity of tracking the data from many courses in many institutions, we ask you to identify your college/university and course. Your name is not collected and your individual data cannot be revealed to your course instructor. The lead analyst for the project, Prof. David Lopatto of Grinnell College, will keep all individual data confidential. Only aggregate data will be reported back to your institution and to the GEP as a whole. Your data cannot be accessed by your instructor in any way for any purpose.

As with any research, you are not compelled to participate. You may elect not to answer individual questions. A "not applicable" or "N.A." option is available for the questions as an alternative; use this if the question is irrelevant or if you choose not to answer. If you change your mind about completing the survey, just leave the site. It is assumed that the submission of a completed survey is your consent for participation. If you have any questions or comments regarding the survey, please send an email to Prof. Lopatto (lopatto@grinnell.edu). Thanks!

After you complete the post-survey, we offer you an opportunity to be entered into a raffle for a \$100 gift certificate from Amazon.com, as a "thank you" for your participation. Five email addresses will be selected at random in October, after the survey is closed. If you wish to be entered in the raffle, we will need your email to contact you if you win. Please be assured that the file containing these emails will be completely separate from the file of survey responses; this list of names will not be used for any other purpose.

[Proceed to Survey](#)



GEP Student Alumni Survey Spring 2012

1. What year did you participate in GEP Genomics Project?

- ☐ 2005
☐ 2006
☐ 2007
☐ 2008
☐ 2009
☐ 2010
☐ 2011
☐ 2012

2. Which school were you attending?

Please select your school

3. Who was your professor or instructor who taught you the GEP materials?

Please select professor's name

4. Do you still have personal contact with your GEP instructor?

- ☐ Yes ☐ No ☐ NA

If you are still in touch with your GEP instructor, briefly describe the interaction.

5. Do you still have personal contact with your GEP teaching assistant(s)??

- ☐ Yes ☐ No ☐ NA

6. Do you still have personal contact with some of your GEP classmates?

- ☐ Yes ☐ No ☐ NA

7. Have you completed your first baccalaureate (BA/BS) degree?

- ☐ Yes ☐ No ☐ NA

If so, what year?

Please select grad year

8. What is your current occupation? (*check all that apply*)

- ☐ Still working on my BA/BS degree
☐ Post-Bac program
☐ Master's program
☐ Ph.D. program in the sciences (including math and computer science)
☐ Ph.D. program in a non-science field

- ☐ Medical school
- ☐ MD/Ph.D program
- ☐ Other professional school in a science field
- ☐ Other professional school in a non-science field
- ☐ Employed in a non-science field
- ☐ Employed in a science-related field
- ☐ Teaching/education (including Teach for America)
- ☐ Homemaker and/or parent
- ☐ Volunteering (including Peace Corp, national or local projects)
- ☐ Accepted and planning to attend graduate/medical school
- ☐ Thinking about applying to graduate/medical school
- ☐ N/A
- ☐ Other

If other, please describe.

9. Have you been awarded any scholarships, fellowships, or grants for your post-BA/BS education?

- ☐ Yes ☐ No ☐ NA

If yes, please describe:

10. Have you completed a second degree since receiving your first BA/BS?

- ☐ Yes ☐ No ☐ NA

If yes, please check below all earned degrees:

- ☐ 2nd BA/BS
- ☐ MA/MS
- ☐ MBA
- ☐ PhD
- ☐ Law
- ☐ MD
- ☐ OD
- ☐ DDS
- ☐ DVM
- ☐ Teaching credential
- ☐ Other
- ☐ N/A

11. Are you currently active in any professional activities (attending meetings, writing papers, etc.)?

- ☐ Yes ☐ No ☐ NA

If yes, please describe:

12. Your gender:

☐ male ☐ female ☐ NA

13. Your ethnicity:

Please select your ethnicity ▾

14. Your age range:

☐ 18-21
☐ 22-25
☐ 26-30
☐ 31-40
☐ 40-50
☐ NA

15. Your GEP experience: did you participate in

☐ a course devoted primarily to the GEP project
☐ a course that spent half or more of the time on the GEP project
☐ a course that spent a quarter of the time on the GEP project
☐ a course in which the GEP project took up just a 1-3 lab sessions (less than 15 hrs instructional time)
☐ independent study/research
☐ N/A, prefer not to answer

16. Did your class

☐ use GEP materials to learn about bioinformatics
☐ participate in the research annotation problem
☐ participate in sequence improvement
☐ participate in both sequence improvement and annotation
☐ N/A, prefer not to answer

17. Did you serve as a Teaching Assistant (TA) for a GEP course?

☐ Yes, I received GEP training at Washington University in St. Louis
☐ Yes, I served as a TA after taking the GEP-affiliated course at my home institution
☐ No, I did not serve as a TA
☐ N/A, prefer not to answer

18. If you served as a TA, please reflect on the experience and/or gains made by the students you were working with (Agree/disagree, scale 1 to 5, with 5 being the most gains and 1 being the least) Did your students:

<input type="radio"/> agree <input type="radio"/> disagree	Recognize that there is not a fixed answer	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	Find the experience frustrating	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	Learn to be resourceful	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	Learn how to brain-storm with colleagues	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	Learn to tackle the problem again if their first efforts were inconclusive	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	Learn to keep a lab "notebook"	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	Realize that students can make a contribution	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	Gain "ownership" of their project	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5

19. If you served as a TA, please comment on your experience:

20. Now that you have had time to reflect, evaluate your current opinions about the GEP course:

Strongly agree(5) Agree(4) are Neutral (3) Disagree (2) Strongly disagree (1) or N/A

This course was a good way of learning about the subject matter	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
The course was a good way of learning how scientific research is done	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
The course had a positive effect on my interest in science	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
Genomics is awesome!	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
Taking this course enhanced my ability to think independently	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
Taking this course increased my motivation to learn	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
Taking this course influenced my academic goals	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
The GEP experience improved my ability to analyze data	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
The GEP experience improved my self-confidence in discussing scientific information	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
I have or had a job where I used skills learned doing my GEP project	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
I got a job based on my GEP project experience	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
My GEP experience helped me get into medical/graduate school	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
I have been exposed to genomics topics in my post-graduate experience	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
I am currently using research skills that I learned during my GEP experience	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
The GEP should be maintained, so that future students can benefit from it	<input type="radio"/> N/A <input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5

21. Did you complete a sequence improvement (finishing) and/or annotation project, contributing to the GEP research project?

- ☐ Yes, I completed one or more fosmids (40 kb) myself
- ☐ Yes, I completed one or more fosmids working with a partner
- ☐ Yes, I worked with a large group to complete a fosmid
- ☐ No, I was unable to complete my assigned project
- ☐ No, my class only used practice projects, so we did not submit any research
- ☐ No, my class only used practice projects, so we did not submit any research results back to the GEP

22. Please comment on your GEP experience: what was good about it, and what changes would have made it better.

23. Please comment about the GEP impact overall: Did you enjoy learning by participating in research? Should this course be sustained?



24. Recommendations (Agree/disagree scale 1-5 with 5 being the greatest enthusiasm and 1 being the least)

<input type="radio"/> agree <input type="radio"/> disagree	I would encourage students at my school to take this course	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	I would encourage (appropriate) students to serve as a TA for the course	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	I would encourage my institution to continue to support this course	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5
<input type="radio"/> agree <input type="radio"/> disagree	I would encourage other biology faculty to incorporate research into their courses	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3 <input type="radio"/> 4 <input type="radio"/> 5