Annotated Bioinformatics Education Bibliography

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Altman, R. B. (1998). "A curriculum for bioinformatics: the time is ripe." Bioinformatics 14(7): 549-550.

Bloom, M. (2001). "Biology in silico: the bioinformatics revolution." The American Biology Teacher 63(6): 397-403.

Boomer, S. M., D. P. Lodge, et al. (2002). Bacterial diversity studies using the 16S rRNA gene provide a powerful research-based curriculum for molecular biology laboratory, Microbelibrary.org.

We have developed a ten-week curriculum for molecular biology that uses 16S ribosomal RNA genes to characterize and compare novel bacteria from hot spring communities in Yellowstone National Park. The 16S rRNA approach bypasses selective culture-based methods. Our molecular biology course offered the opportunity for students to learn broadly applicable methods while contributing to a long-term research project. Specifically, students isolated and characterized clones that contained novel 16S rRNA inserts using restriction enzyme, DNA sequencing, and computer-based phylogenetic methods. In both classes, students retrieved novel bacterial 16S rRNA genes, several of which were most similar to Green Nonsulfur bacterial isolates. During class, we evaluated student performance and mastery of skills and concepts using quizzes, formal lab notebooks, and a broad project assignment. For this report, we also assessed student performance alongside data quality and discussed the significance, our goal being to improve both research and teaching methods.

Boyle, J. A. (2002). "Using the human genome: a case study in education." Biochemistry and Molecular Biology Education 30: 368-371.

The working drafts of the human genome, announced in February 2001, have clearly provided a breakthrough in biochemistry and molecular biology research. The scientific data also provide an opportunity to vary a typical approach to teaching. Advanced graduate students at our university can elect to take a course in molecular genetics. The human genome drafts and the initial publications generated by the drafts were used as the framework for a variation of this course in the fall of 2001. Instead of a traditional, linear lecture-driven course, this approach provided a more methods-driven focus to the topics considered. It also required the introduction of some recent historical facts to put the material into proper context. The bulk of the topics normally taught remained unchanged; however, their order of appearance was greatly modified. Nevertheless, the material remained coherent because of the constant tie-in with the genome data. Evaluation of student performance was challenging because of the variety of material presented. Web-based assignments proved useful as mechanisms to probe the level of student understanding as well as providing another means of imparting information.

Brass, A. (2000). "Bioinformatics education- a UK perspective." Bioinformatics 16(2): 77-78.

Campbell, A. M. (2000). Rocket science or basic science? A consortium of teachers makes genomic methods accessible. 2000 Education Committee Workshop, American Society for Cell Biology.

The new field of functional genomics is transforming many areas of biology but the undergraduate curriculum has not been able to incorporate this transformation. Undergraduates need to understand this new field where gene expression levels of every gene in a genome is studied simultaneously. Unfortunately, functional genomic methods are expensive and unfamiliar to faculty who spend most of their time teaching. In December1999, the Genome Consortium for Active Teaching (GCAT) was created to facilitate the introduction of genomic methods into the undergraduate curriculum in a cost-effective manner. GCAT is a non-profit, educational consortium comprised of faculty who teach undergraduate <www.bio.davidson.edu/GCAT>. GCAT will use collective purchasing power, core facilities, and an

accumulation of experience to enable students at any institution to conduct experiments with genomic tools. There are two primary conditions for participation in GCAT: 1) members will use the DNA microarrays to conduct experiments with undergraduate students only and 2) all data and interpretations will be public domain and available via the internet. In September of 2000, the first cohort of GCAT members (23 faculty from the US and Canada) obtained 135 yeast DNA microarrays (provided by Dr. Pat Brown; Stanford University) which consist of every open reading frame from the budding yeast S. cerevisiae. Genesphere has developed a new method for producing probes and produced smaller kit sizes at a reduced price for GCAT members. Several microarray manufacturers agreed to read the GCAT microarrays for the first year. The inaugural experiments were conducted during the fall semester of 2000 and results will be presented. During the breakout session, participants will discuss future participation in GCAT and long-term plans. The discussion can be continued at the poster session.

Campbell, A. M. (2002). "Meeting report: genomics in the undergraduate curriculum-rocket science or basic science?" The American Society for Cell Biology 1(Fall): 70-72.

Canning, D. R. and J. R. Cox (2001). "Teaching the structural nature of biological molecules: molecular visualization in the classroom and in the hands of students." Chemistry Education: Research and Practice in Europe 2(2): 109-122.

The use of molecular visualization software has made a tremendous impact in the biochemistry and cell biology classroom. Instructors no longer have to rely on static images in textbooks to teach the structural nature of biological molecules. The emergence of many different molecular graphics programs and technology-based classrooms has enhanced the ability of instructors to teach structural concepts such as noncovalent interactions and levels of organization in proteins. Many web-based tutorials are also available for instructors to use during lecture or for students to explore outside of the classroom. Students can also obtain hands-on experience with the graphics programs to explore the structural aspects of macromolecular systems. This report shows that students involved in visualization projects become skilled at identifying various structural motifs they have discussed in class or are discovering for the first time. This student-centered approach enhances the ability of students to comprehend structural concepts and to realize the importance of weak interactions in the structure of large molecules.

Clendening, B. (2002). "An advanced molecular techniques laboratory course using drosophila melanogaster." Bioscene 28(1): 1-19.

This advanced molecular biology laboratory course uses a project approach to learning and incorporates an independent research component. The students use enhancer trap techniques in Drosophila melanogaster to work on two related projects. For one project, a set of experiments has been worked out in advance to take the students from a behavior mutant (flightless), to a cloned and sequenced gene (gene for muscle myosin heavy chain protein), and an analysis of the gene. These experiments expose the students to a wide range of the common molecular techniques and demonstrate the logical progression of a research program. Techniques covered include: isolation of genomic and plasmid DNA, isolation of RNA, acrylamide and agarose gel electrophoresis, recombinant DNA techniques, characterization of mutants by Southern and Northern analysis, screening of a cDNA library, PCR, DNA sequencing and database analysis and protein isolation. The second project is an independent research project that starts with mutants of unknown genetic identity. The students use the techniques that they have learned during the first project to clone and sequence the gene and to begin to study the protein.

Cotter, D. (1999). "About the Biology Workbench." BIOQUEST Notes 9(3): 8-10.

Counsell, D. (2002). "A review of bioinformatics education in the UK." Briefings in Bioinformatics 3(4): 432-446.

If the completion of the first draft of the human genome represents the coming of age of bioinformatics, then the emergence of bioinformatics as a university degree subject represents its

establishment. In this article I discuss bioinformatics as a subject for formal study, rather than as a subject for research, and review a selection of the taught, mainly graduate, courses currently available in the United Kingdom.
Throughout, I try to draw parallels between the current integration of bioinformatics into biomedical research and teaching, and that of molecular biology, two decades ago. Others have made this analogy between these two relatively young disciplines [Pearson01]. Although I reference research sources, I make no pretence of objectivity. This article contains my views, and those of a number of current bioinformatics course organizers whose comments on the subject I solicited in advance specifically for this article. They kindly responded by telling me how they planned their curricula, and by drawing my attention to the special strengths of their programmes. I also invited comment from present and former students of several bioinformatics degree programmes. Except where individuals are directly quoted, any opinions expressed herein should be considered mine. Unlike the sister piece, this article is less about funding policy—which, in the UK, has lately (if belatedly) been more generous towards bioinformatics teaching. It is, however, about practice and content; the requirements of the bioinformatics research communities, the corresponding emphases of bioinformatics courses, and the general market for holders of bioinformatics degrees. Individual courses are cited throughout as examples, but the final section contains a full annotated listing with links. Based on my own experience of practising and teaching bioinformatics I describe kinds of abilities I believe will be most useful to bioinformaticians in the near future and suggest ways we might prepare students of bioinformatics for a fall in demand for those abilities.

Cox, J. R. (2000). “Teaching noncovalent interactions in the biochemistry curriculum through molecular visualization: the search for p interactions.” Journal of Chemical Education 77: 1424-1428.

Daron, H. and J. Aull (1986). “Microcomputer simulation of steady-state enzyme kinetics for educational purposes.” Bioinformatics 2(3): 207-209.

A BASIC program to assist the instruction of steady-state enzyme kinetics has been developed for the IBM PC microcomputer. Its purpose is to simulate laboratory experiments in order to minimize the time required to obtain kinetic data from which students deduce kinetic mechanisms and determine kinetic constants of enzyme-catalyzed reactions. The program randomly selects a kinetic scheme from various sequential, ping pong, and iso reaction sequences as well as values for the kinetic constants. The scheme and kinetic constants are unknown to the student at this time; the only thing he or she knows is the stoichiometry of the catalyzed reaction which can have two or three substrates and products. The student is prompted to enter values for concentrations of substrates and products; several different concentrations for each substrate and product can be entered in a single experiment. The program then calculates, displays and prints (if desired) the corresponding initial steady-state velocities. The student can perform as many experiments as desired until enough information is obtained to determine the kinetic mechanism and to calculate values for the kinetic constants.

Denison, S. H., P. Meylan, et al. (2000). mtDNA Haplotype Determination by Students in Genetics Laboratory Course Elucidates Sea Turtle Ecological Geography. 2000 Education Committee Workshop, American Society for Cell Biology.

Dyer, B. D. and M. D. LeBlanc (2002). “Meeting report: incorporating genomics research into undergraduate curricula.” The American Society for Cell Biology 1(Winter): 101-104.

In the first of two National Science Foundation (NSF)–funded workshops, 30 professors of biology and computer science from 18 institutions met at Wheaton College in Norton, Massachusetts, on June 6–7, 2002, to share ideas on how to incorporate genomics research into undergraduate curricula. The participants included nine pairs or trios of biologists and computer scientists, anticipating or already implementing collaborations. In a before-and-after format, the two workshops are intended to encourage experimentation in the classroom (June 2002) followed by reflection on and evaluation of ideas (June 2003).

Feig, A. L. and E. Jabri (2002). “Incorporation of Bioinformatics exercises into undergraduate biochemistry curriculum.” Biochemistry and Molecular Biology Education 30: 224-231.

The field of bioinformatics is developing faster than most biochemistry textbooks can adapt. Supplementing the undergraduate biochemistry curriculum with data-mining exercises is an ideal way to expose the students to the common databases and tools that take advantage of this vast repository of biochemical information. An integrated collection of exercises based on pet proteins has been assembled. The exercises described are applicable to either a lecture or laboratory format and require only basic desktop computers, an Internet connection, a current web browser, and the free Chime plug-in module. In an open-ended, inquiry-based format, the assignments ask students to explore concepts such as the relative information content of the different biopolymers, the relationship between primary sequence and tertiary structure, and how sequence conservation can be used to find an enzyme active site.

Galewsky, S. (2000). “Sequencing cDNAs: an introduction to DNA sequence analysis in the undergraduate molecular genetics course.” Bioscene 26(4): 1-3.

DNA sequence analysis is a cornerstone of modern molecular genetics, yet it is difficult to provide students in the teaching lab with an experience that is meaningful and cost effective. At Millikin University in the upper division Molecular Genetics course, a series of lab exercises that culminates with a cDNA sequence that students can use for homology searches and open reading frame analysis has been implemented. The exercises begin with students picking a single colony from a Drosophila melanogaster embryo cDNA library. They purify the plasmid then analyze the insert through restriction digests and gel electrophoresis. In this semester’s example, three cDNAs were then randomly picked from the group and sent out for sequencing. The students had an ownership and interest in the sequence data because they represent an unknown gene and were selected by them.

Gerrard, J. H. and A. D. Sparrow (2002). “Turning biochemistry insideout: a new approach to teaching metabolism inthe post-genomic era.” Biochemistry and Molecular Biology Education 30(5): 293-295.

This article describes a new approach to teaching metabolic pathways, designed to engage students with the material, and its complexities. Based on a novel way of presenting metabolic pathways, in which the focus is placed on proteins rather than metabolites [1], simple tutorial-based exercises and mini-projects are described, bringing metabolism to life, yet requiring very few resources.

Gross, L. J. (2000). “Education for a biocomplex future.” Science 288(5467): 807.

Honts, J. E. (??). Evolving strategies for the incorporation of bioinformatics within the undergraduate cell biology curriculum: 1-34.

Rapid advances in genomic sequencing and structural biology have resulted in the rapid increase in biological data available from Internet-accessible databases. In order to help students effectively use this vast repository of information, I have introduced undergraduate biology students at Drake University to bioinformatics software and databases in three different courses, beginning with the introductory course in cell biology. The exercises and projects that I have used in these courses to help students develop literacy in bioinformatics are described, along with an account of how these activities have evolved with improvements in student access to computing resources. In one of these courses, an introduction to bioinformatics, students developed their own simple sequence analysis tool used in Perl programming language. The value of this experience is described from the point of view of the instructor as well as the students. An assessment is made of the degree to which I have achieved my goal of encouraging students to develop a working knowledge of bioinformatics concepts and methods. Finally some conclusions are drawn from these experiences that may be helpful to others wishing to introduce bioinformatics within the undergraduate biology curriculum.

Honts, J. E. (2000). Introducing bioinformatics within the undergraduate cell biology curriculum. 2000 Education Committee Workshop, American Society for Cell Biology.

The recent completion of a first draft of the human genomic DNA sequence heralds a new era, not only in the conduct of biological and biomedical research, but also in undergraduate education in biology. Students have ready access via the Internet to genomic resources shared by researchers around the world. The challenge for cell biology faculty is to find ways to introduce undergraduates to the bioinformatic concepts, tools, and databases that underlie genomics, proteomics, and structural biology. The basic concepts of bioinformatics have been introduced within the introductory cell biology course in the context of a progressive series of papers that review the cell biology of Ras and its role in cancer. Students work in teams to identify and decode the protein-encoding portions of the human genomic H-Ras gene. Subsequently the students use the molecular graphics program RasMol to visualize and understand the effects of specific oncogenic mutations on the three-dimensional structure of Ras and interacting proteins such as Ras-GAP. Finally students see how a detailed understanding of the structure and function of the Ras protein can be used to design anti-cancer therapeutics, such as the farnesyltransferase inhibitors that mimic the Ras C-terminal CAAX sequence. Throughout this discussion section, students see concrete examples of how DNA sequence determines the amino acid sequence of a protein, which in turn determines the protein's structure, function, and interactions. A similar approach is taken in the second semester molecular biology course, with the focus being on the well- studied tumor suppressor protein p53. In addition a more intensive course for senior undergraduates is available to those students who wish to deepen their understanding of these concepts.

Jakobsson, E. BIOQUEST Notes.

Jungck, J. R. (1997). “Ten equations that changed biology: mathematics in problem-solving biology curricula.” Bioscene 23(1): 1-26.

Mathematics has played exceptionally important roles throughout the history of biology. Too frequently, these roles have been unappreciated in biology curricula because textbook authors assume that biology students have an inadequate mathematical preparation. This practice: (1) deskills many biology students, (2) is inconsistent with our requirements, (3) misrepresents contemporary biological research and, hence, (4) under prepares students to read many articles or to contribute to many areas of biology. However, the recent calculus reform movement has empowered thousands of American undergraduate biologists to become proficient in the use of mathematical software packages that could be used to investigate the behavior of many famous mathematical models in biology. But where can they look? There are numerous recent texts in mathematical biology, research journals, web sites, and some advanced biological texts which are replete with numerous models. However, there is a need to identify a succinct list of achievements that represent the power of mathematics in biology. Hence, ten equations and a brief description of their historical importance are presented here in order to draw students' and faculty's attention to a variety of mathematical models that have been intrinsic to many of the significant discoveries in biology in the twentieth century.

Jungck, J. R., S. Donovan, et al. (2000). Evolution as a basis of bioinformatics education. 2000 Education Committee Workshop, American Society for Cell Biology.

With the extraordinary number of opportunities available to scientists with expertise in bioinformatics, numerous institutions are beginning to develop courses and curricula at both the undergraduate and graduate level. In response to this challenge, the BioQUEST Curriculum Consortium (BioQUEST = Quality Undergraduate Educational Tools and Simulations in Biology), a fourteen year old national curricular reform initiative, in collaboration with EOTPACI (Education, Outreach and Training – Partnership for Advanced Computing Infrastructure), is developing problem solving approaches to bioinformatics that stress the foundational importance of evolutionary biology. While many definitions for bioinformatics exist, Ming-Ying Leung and J. Aaron Cassill (NSF DUE EMD Award - #9981104) have defined bioinformatics as the “study [that] integrates mathematical and computational techniques with biological knowledge to extract, organize, and interpret information from a wealth of genetic sequence data obtained from various genome projects.” This foregrounding of mathematics and computer science in

bioinformatics education has meant either that students major in these two disciplineswith a minimal exposure to biology or that students in biology take almost all of their cognate coursework in these two areas. Unfortunately, both types of extant programs have to date ignored any deep education in evolutionary biology. BioQUEST has a long history of trying to help undergraduates learn long term strategies of research by working on open-ended problems with powerful professional tools with a consistent learner-centered pedagogical philosophy: problem posing, problem solving, and persuading peers. In this case, we (http://www.bioquest.org/bioinformatics) have combined the use of a powerful bioinformatics package, Biology Workbench, (http://biology.ncsa.uiuc.edu) (http://workbench.sdsc.edu) developed at the supercomputer centers at the University of Illinois and the University of California San Diego, with typologies of evolutionary problem solving that we have developed to differentiate between spatial, temporal, and genealogical hypotheses or between evolutionary, genetic, and developmental biological levels of analysis. With bioinformatics, evolutionary biologists have the potential to inform students on how it is a powerful heuristic for interpreting DNA, RNA, and protein sequence homology based upon both orthologous and paralologus relationships.

Kaspar, R. L. (2002). "Integrating internet assignments into a biochemistry/molecular biology laboratory course." Biochemistry and Molecular Biology Education 30(1): 36-39.

A main challenge in educating undergraduate students is to introduce them to the Internet and to teach them how to effectively use it in research. To this end, an Internet assignment was developed that introduces students to websites related to biomedical research at the beginning of a biochemistry/molecular biology laboratory course. The basic sites introduced cover many subjects, include searching for specific DNA sequences, restriction enzyme mapping, RNA folding, analyzing three-dimensional protein images, and literature searches. These newly learned Internet skills are incorporated into other aspects of the laboratory course. In the example illustrated here, students sequence DNA inserts from randomly chosen bacterial colonies prepared from a human cDNA plasmid library. The obtained DNA sequence is used to search on-line data bases introduced in the initial Internet assignment to determine whether the cDNAs have already been identified. The sequencing "wet-lab" module, coupled with the Internet assignment, gives students experience in four areas. 1) purifying plasmid DNA, 2) performing restriction endonuclease digests on the plasmid DNA, 3) sequencing double-stranded DNA, and 4) comparison of obtained sequence data to known DNA sequences in the human genome data base in a way that simulates a research experience.

Kim, T. D. (2002). "Using sequence analysis software to teach molecular biology basics." Biochemistry and Molecular Biology Education 30: 211-212.

Mooney, E. and A. M. Campbell (1999). "A project-based biotechnology laboratory course using isocitrate dehydrogenase." Bioscene 25(2): 1-9.

We have utilized the yeast genome to let students discover how electronic databases are combined with laboratory procedures to clone a new gene. A semester-long laboratory course has been developed which models current research trends that utilize genomic data, and is similar to a rotation project for first year graduate students. Students are provided with amino acid sequences of the model enzyme isocitrate dehydrogenase (IDH) from species other than yeast and use the yeast database to electronically clone the yeast homolog. At the bench, they design PCR primers, amplify the gene from genomic DNA, clone the product, express yeast IDH in Escherichia coli (E. coli), and perform a western blot using an epitope tag. From this common beginning, students can perform a range of experiments such as running a native gel and staining for IDH activity, or performing a Southern blot on a range of species' DNA with the yeast IDH as a probe. This semester-long series of experiments provides students with a laboratory experience that has the feel of original research where results from one lab are needed for the next step in the process.

Morse, P. (2003). "Preparing biologists for the 21st century." Bioscience 53(1): 9.

Nelson, K. E., I. T. Paulson, et al. (2001). “Microbial genome sequencing: a window into evolution and physiology.”.

Surprises, such as the extent of lateral gene transfers, could be overlooked if microbial genome sequencers opt not to complete their analyses. Who would have thought 20 years ago that we would be publishing completed microbial genomes at the current rate? Who would have thought that we would have this approach to analyzing microbes, and that it would reveal so quickly how little we really know about them?

Nichols, A., E. Coonrod, et al. (2002). Incorporating bioinformatics into the biology classroom through DNA sequence analysis.

The area of bioinformatics is rapidly evolving due to daily discoveries in the area of molecular biology and computer technology. It is important that students are introduced to this new field. This activity will give the students an opportunity to investigate how bioinformatics can be used to make direct comparisons of DNA sequences. The students will gather a variety of DNA sequences for a gene; analyze by comparing the GC content, codon usage, melting temperatures, and through phylogenetic analysis.

Palladino, M. A. (2002). “Learning about the human genome project via the web: internet resources for biology students.” The American Biology Teacher 64(2): 110-116.

Parslow, G. (2002). “Commentary: molecular visualization tools are good teaching aids when used appropriately.” Biochemistry and Molecular Biology Education 30(2): 128-129.

Pearson, W. R. (2001). “Training for bioinformatics and computational biology.” Bioinformatics 17(9): 761-762.

Peterson, R. R. and J. R. Cox (2001). “Integrating computational chemistry into a project-oriented biochemistry laboratory experience: a new twist on lysozyme experiment.” Journal of Chemical Education 78(11): 1551-1555.

Ping, L. Y., J.-O. Höög, et al. (2002). “International online education: the S-Star trial bioinformatics course.” CAL-laborate 8.

Six universities from five continents collaborated to provide the S-Star Trial Bioinformatics Online course (http://www.s-star.org/). The course is a global experiment in Bioinformatics Distance Education. The S* Life Science Informatics Alliance is the result of cooperation between Karolinska Institutet Sweden, the National University of Singapore, Stanford University USA, Uppsala University Sweden, The University of Sydney Australia, and the University of Western Cape South Africa. The S-Star group will be joined by the University of California San Diego, through the San Diego Supercomputer Center.

Porter, S. and T. Smith (2000). “Bioinformatics in the community college.” Journal of Industrial Microbiology & Biotechnology 24: 314-318.

Biotechnology is becoming an information-based field. In his article we describe some resources available to instructors, shown how these resources are used in the biotechnology training program, and provide examples of activities used by non-science majors to increase their understanding of biology. We discuss some of the challenges we have encountered using these tools in the classroom.

Puterbaugh, M. and J. G. Burleigh (2000). Investigating evolutionary questions using online molecular databases: 1-26.

Puterbaugh, M. N. and J. G. Burleigh (2001). “Investigating evolutionary questions using online molecular databases.” The American Biology Teacher 63(6): 422-431.

Richardson, D. C. and J. S. Richardson (2002). “Teaching Molecular 3-D literacy.” Biochemistry and Molecular Biology Education 30(1): 21-26.

Saier, M. H. (2003). “Answering fundamental questions in biology with bioinformatics.” ASM News 69(4): 175-181.

Sears, D. W. (2002). “Using inquiry-based exercises and interactive visuals to teach protein structure/function relationships.” Biochemistry and Molecular Biology Education 30: 208.

Singer, F., J. B. Hagen, et al. (2001). “The comparative method, hypothesis testing & phylogenetic analysis: an introductory laboratory.” The American Biology Teacher 63(7): 518-523.

Smith, T. M. and D. S. Emmeluth (2002). “Introducing bioinformatics into the biology classroom: exploring the national center for biotechnology information.” Bioinformatics for the biology curriculum 64(2): 93-99.

Sutton, F. Discription of her course.

Tillotson, J. K. (2002). “Strategies for introducing computer technologies into a biology laboratory program.” Biochemistry and Molecular Biology Education 30(4): 232-234.

Computers have been installed in the General Biology laboratory at Purchase College and incorporated into the laboratory curriculum for all biology majors at the introductory level. The goal is to ensure that all students become familiar with general computer applications in the biological sciences and are comfortable enough to use them regularly. Thus, students will be prepared for later courses involving use of computer applications in bioinformatics or other technologically advanced subjects.

Vega, Q. (2000). Molecular research in a teaching laboratory analysis of RET co-receptor function. 2000 Education Committee Workshop, American Society for Cell Biology.

Although it is important for molecular biology students to learn the basic techniques of molecular biology, it is equally important for these students to understand the concepts behind the experiments and to understand how these individual experiments are connected. In this project, students were required to use specific molecular biology techniques in order to answer a question about cell function. Specifically, these students were presented with the background of RET, a receptor tyrosine kinase activated through a ligand/co-receptor complex. The students were asked to design a chimeric protein using DNA from various RET co-receptors in hopes of determining regions of the co-receptor required for RET activation. The techniques required of the students included DNA isolation and digest analysis, bacterial transformation, PCR primer design, PCR, plasmid construction, DNA sequencing, protein expression, protein detection and transcriptional regulation assays. In addition to designing experiments and interpreting results, each group was required to write a summary of their results and conclusions in a scientific paper format. By providing a research project within a molecular laboratory course, students were able to prepare for future careers in molecular biology and learn how molecular research is conducted.

Wallack, D. L. W. (2000). “Molecular genetics: genes to genomes,” An undergraduate project-based course in yeast genomics. 2000 Education Committee Workshop, American Society for Cell Biology.

Through the support of GCAT, I offered a new course during the Fall semester of 2000 in the Biology Department at Muhlenberg College, entitled “Molecular Genetics: Genes to Genomes.” The course introduced students to genomics and microarray technology through reading, discussion, and design of individual student research projects that utilized microarray analysis to examine changes in gene expression for yeast grown under different conditions. Students presented their work in a poster session at the end of the semester and are in the process of writing about their findings in papers in the format of scientific journal articles.

Weiner, S. W., P. F. Cerpovicz, et al. (2000). “RasMol and mage in the undergraduate biochemistry curriculum.” Journal of Chemical Education 77(3): 401-406.

White, B., S. Kim, et al. (2002). “Evaluation of molecular visualization software for teaching protein structure.” Biochemistry and Molecular Biology Education 30(2): 130-136.

In this study we measured the learning outcomes resulting from using molecular visualization software in lecture and in the teaching laboratory of a large introductory-level undergraduate biology majors’ course. The study was initially carried out in the Fall semester of 1999; the results of this study were used to devise an expanded laboratory component that was evaluated in a second study carried out in the Fall of 2000. In both studies, students (n = 175 and 161) attended two 50-min lectures that used molecular visualization software to explain protein structure and function and the gene-protein connection. Students also used this software during one 3-h laboratory session as a tool for exploring these topics. Students completed open-ended pre- and post-surveys that involved a related but unfamiliar task. Survey responses were scored for correctness, as well as by the type(s) of explanations used in the response. We found the following eight types of responses that students employed to explain protein structure and function: genetics, protein structure, chemical interactions, amino acid sequence, purpose/teleology, extrinsic factors, miscellaneous, and none. In both studies, the frequencies of correct answers, as well as the frequencies of each response type, showed significant changes as a result of lecture and/or lab. The effects of lecture were highly similar in both studies. The changes in the expanded lab resulted in significant changes in outcome. Overall, the curriculum effectively communicated several core concepts in protein biochemistry and expanded the conceptual "toolkit" that students applied to problems of protein structure and function. Lecture increased students’ understanding of the role of amino acid sequence, whereas lab tended to increase their understanding of three-dimensional structure and the gene-protein connection. Our results demonstrate that exposure to molecular visualization, even for a relatively brief time, can improve students’ understanding of protein structure and function. In addition, we demonstrate the differing and largely non-overlapping effects of lecture and lab, suggesting that effective use of molecular visualization should involve both types of activities.

Whitehead, J. P. and H. E. Pence (2002). “Using computers to teach biochemistry.” Biochemistry and Molecular Biology Education 30(3): 206-297.

This paper describes a symposium entitled "Using Computers to Teach Biochemistry," which was presented at the fall, 2001 National Meeting of the American Chemical Society in Chicago, IL. The use of computers has increased in all areas of chemical education; however, the visualization capabilities needed to convey some aspects of biochemistry are quite complex, so the upward trend in the use of computers for this purpose has been especially significant. The various speakers in this symposium discussed the use of a wide range of instructional technologies, including presentation software, Chime, online data exercises, interactive visualization tools, self-designed tutorial programs, and bioinformatics.

Willian, K. R. (2002). “Using three-dimensional imaging of proteins: examples of class activities and subsequent assessments.” Biochemistry and Molecular Biology Education 30(3): 209-210.

This paper discusses the development of a new biochemistry course, "Biochemistry of Cellular Regulation," which is taught at the 300 level at Tuskegee University. The chemistry of cellular signaling and the subsequent cell regulation are discussed from a molecular viewpoint with emphasis on chemical structure, reactivity, and thermodynamics. Classroom lectures are composed almost entirely of PowerPoint lectures whereby figures from the textbook and figures from current research articles are incorporated directly into the lecture notes. The incorporation of supplemental materials from the textbook, i.e. the CD-ROM and websites from the CD-ROM was especially important. Three-dimensional images of proteins can be viewed and manipulated at these websites, which is critical for understanding the structural basis of protein function. Specific examples of class activities and subsequent assessments will be presented.

Yasar, O. and R. Landau (2002). Elements of computational science education: 1-12.

Education in computational science and engineering (CSE) has evolved through a number of stages, moving from recognition in the 1980s to its present early growth. Now a number of courses and degree programs are being designed and implemented at both the graduate and undergraduate levels, and students are beginning to receive degrees. This paper describes this development, including impact on faculty and students, nature of the job market, intellectual content of CSE education, and types of programs and degrees now offered. The descriptions of existing programs appear to lead to an accepted prescription for such programs.