

## Information Technology (IT) in Teaching

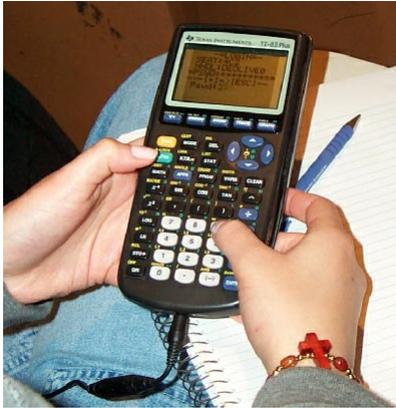
The latest "buzz" in improving teaching is IT. Some efforts are aimed at replacing teachers and books, but others are aimed at improving teacher/student interactions. Projects of both types are being pursued within the Biology Department.

**Randy Phillis**, who teaches introductory biology using ClassTalk Technology, just returned from delivering a presentation at a [Pew Center for Academic Transformation](#) conference on IT in teaching. At the conference both of the aforementioned aims of IT in teaching were presented. Randy returned with many new ideas and a reassurance that the Biology Department is at the forefront of thinking with regard to IT and teaching.

The Massachusetts Board of Higher Education recently published a mandate on IT in higher education. An included target is laptop ownership by every undergraduate. While this may seem like a dream at the moment, the Biology Department is anticipating that eventuality.

**Randy Phillis** and **Elizabeth Connor** from Biology, **Steve Goodwin** from Microbiology and **Adam Porter** from Entomology have combined forces to use an innovative cluster of technologies in their teaching of Biology 100 and 101. In this endeavor they are supported by our teaching technology expert **Steve Brewer** and the ClassTalk expertise developed in the Physics Education Research Group, headed by **Bill Gerace**. Students come to class with their personal \$100 TI calculators

which they plug into the ClassTalk network. During the lecture, small student groups are given problems to solve and the answers, accompanied by class results, are projected for the entire class to see and discuss. Students are also encouraged via an online daily-updated web page to read the relevant chapters in the required text prior to lecture and to earn credits by successfully completing short online quizzes before class. This allows class



time to be spent in clarifying the information rather than exposing students to it for the first time. In Biology 100 and 101, the use of IT does not result in a dilution of course content; the same amount of material is covered with more time spent clarifying concepts. The ClassTalk approach will be extended in spring 2002 when **Elsbeth Walker** will use it to teach genetics. Genetics would seem a natural course for this approach; it would be helpful to provide students the opportunity to solve genetics problems with the instructor at hand to help analyze responses and to provide reasons for the inappropriateness of certain solutions.

Randy reports that, at the Pew Conference, courses were described in which 50 or 100 laptops were connected with wireless technology to the course hub. If groups of two or three students were to use one computer, then classes of 200 to 300 students could be accommodated. The key to developing IT-supplemented pedagogy is to enhance rather than eliminate the role of the teacher.

Several other faculty have introduced IT into their courses. **Dennis Searcy** has experimented with the use of an online textbook in his Cell Biology course. This requires that every student have access to an online computer or terminal. Currently, about 85% of UMass students own computers. **Pat Wadsworth** reports that she has ceased to use paper handouts in her 400 student course, Biology of Social Issues; all visual materials are on the course website. Use IT and save a tree!

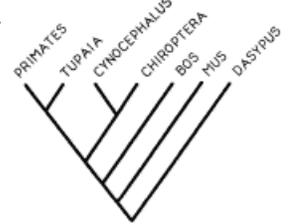
## Genes: New High Fashion on Campus?

The year 2001 marks the beginning of a new era in which we know the entire genome sequence for several organisms, including our own species, *Homo sapiens*. We are now faced with making sense and use out of the vast assemblage of information about our genome. Molecular biology once pursued the understanding of gene structure and expression. Now, the field of bioinformatics has the task of organizing and understanding the design and evolution of the large databases we know as genomes. The sheer vastness of the data will require new approaches to handling databases and accessing the data therein. This opportunity to develop new technology and methodology might be likened to the challenge of landing a human on the moon. One approach will be to compare our genome architecture to that of closely and distantly related species - not comparing gene structure but rather the clusters and orderings of genes on the chromosomes on which they lie. The evolution of gene patterns may teach us about the function of the large amount of "junk" DNA that lies between the transcribed DNA that codes for proteins and structural RNAs. The Biology Department has joined the cadres of scientists who will be exploring genome organization in a variety of species.

In 1998 **The University of Massachusetts Automated DNA Sequencing Facility** was established with Biology faculty member **Ron Adkins** as Director. Since its opening,



the facility has applied its machinery to the sequencing of DNA of over 200 different species. The facility services the sequencing needs of 60 laboratories in the 5-College community. Each year sees its usage increasing with a 6,400 sequence throughput in the past year, representing 3.2 million nucleotide pairs identified. Facility director **Ron Adkins** is interested in the deep structure of mammalian phylogenetic divergence as exemplified by this tree of mammalian evolutionary branching, excerpted from one of his earlier publications, which includes primates, tree shrews (*Tupaia*), flying lemurs (*Cynocephalus*), bats (Chiroptera), mice (*Mus*), cows (*Bos*) and armadillos (*Dasypus*). Ron's current research is exploring the evolution of the deep structure of the speciose group of mammals which includes mice and rats. Another Biology faculty member **Yin-Long Qiu** uses the facility to study plant genomics. Microbiology Professor **Derek Lovley** used the facility extensively to contribute to the *Geobacter* genome project. Biology courses use the facility to provide training in the application of the tools of molecular biology. In addition to genomics research per se, the facility is being used by university geneticists in a variety of ways.



Geneticist **Randy Phillis** explains typical scenarios: "Once we have induced a mutation in our organism of choice, we can identify the locus of the mutation and sequence the gene. Then we can compare that gene to the worldwide database of gene sequences and perhaps find homologous genes whose properties have been identified previously. This gives us clues to how our gene works. Second, we can engineer a mutation in a known gene in order to explore the effects of such a mutation. The sequencing facility can quickly allow us to check that our engineering created the mutation we desired."

The Sequencing Facility is an indicator of the serious commitment the University and its biology faculty have made to support modern genomics research and teaching.