Teaching Statement

Teaching Philosophy

My teaching philosophy is centered on the notion of learning by discovery. In my research, which I consider a form of learning, I am strongly motivated by the drive to discover, and I believe that by inspiring the same drive in students and providing discovery opportunities, a deeper, more comprehensive understanding of the material is attained.

This philosophy is implemented by building a solid foundation of basic results, including concrete examples, to establish an initial understanding and intuition for the algorithm or problem at hand, followed by a discussion of real-world details. With this basis, the students are then tasked with real-world problems and projects that force them to confront and resolve the gaps in their understanding of theoretical concepts. This approach to learning by doing drives students to go beyond syntax and rote to understanding and intuition, while providing valuable experience in problem solving, application domains, such as bioinformatics, and software implementation.

Further, teaching benefits the teacher as well as student. Teaching requires the ability to distill the most important aspects of a large body of knowledge into few key concepts, and to present these concepts in a way that hints to the larger picture. As such, striving to teach well leads the teacher to a deeper understanding of the material.

Teaching Experience

My recent teaching experience includes a graduate level computer science theory course “Algorithms in Biosequence Analysis” in Fall 2005, and a graduate level elective in biochemistry “Biological Mass Spectrometry,” which I co-teach with Dr. Catherine Fenselau (Spring 2005, 2006, 2007). Materials from each of these courses is available from [http://www.umiacs.umd.edu/~nedwards](http://www.umiacs.umd.edu/~nedwards).

The computer science theory course on bioinformatics algorithms was developed from scratch, to cover exact and inexact string matching, string indexes, hidden Markov models, and haplotype phasing. The teaching evaluations for this course are attached. This was a powerful learning experience for me and served to reinforce the teaching philosophy above. In particular, the problem sets and projects were extremely valuable.

A mid-semester problem set asked the students to implement Ukkonen’s suffix tree construction algorithm to achieve the asymptotic linear running time and memory footprint. Students were asked to demonstrate correctness by comparison with slower alternative construction algorithms, and by comparison of intrinsic sequence properties computed with and without using the suffix tree datastructure. Students gained a much better understanding of suffix trees and the difficulties in developing good, robust, correct scientific software. Students chose class projects in a molecular biology area of interest, including mRNA folding, gene finding, haplotype phasing, consensus multi-alignments, multi-core sequence alignment, the Burrows-Wheeler transform, and subpopulation detection in genotyping data. In each case, students had to not only implement and demonstrate correctness of appropriate algorithms, but also use their implementations to answer specific biological questions.

The graduate biochemistry elective on biological mass spectrometry has been taught for a number of years by Dr. Catherine Fenselau from the Biochemistry department. My contribution to the course adds an introduction to the bioinformatics of proteomics by way of lectures to introduce...
the material, a computer lab using bioinformatics tools to analyze a real proteomics experiment, and homework exercises requiring the analysis of real mass spectra. This phase of the course has proven to be very helpful in making the course lectures and readings more concrete. It has also helped to teach students with little prior bioinformatics exposure a degree of critical thinking in the interpretation of computational analyses.

In addition to this formal teaching experience, I have given numerous presentations in formal and informal business contexts, presenting to colleagues and management at all levels; guest lectured in many graduate and undergraduate courses at local universities; and co-taught the Bioinformatics for Proteomics short-course, with Dr. Akilesh Pandey, offered in conjunction with the 2005 and 2006 US Human Proteome Organization (HUPO) annual symposium.

My experience has prepared me for teaching at all levels, in a variety of styles. In each case, where practical, I try to incorporate exercises or labs to help the students learn by doing, rather than listening; and to bring abstract concepts to life with examples that resonate for each distinct audience.

Teaching Interests

I am particularly interested in teaching courses in algorithms and combinatorial optimization, where my own interests and research lie. Bioinformatics and computational biology provide a rich source of motivating problems and clear examples of modeling trade-offs, and I would very much like to reprise my graduate level “Algorithms in Biosequence Analysis” course from 2005. My graduate school background in operations research brings familiarity, at varying depths, with non-linear, linear, and combinatorial optimization, scientific computing, discrete mathematics, and probability and statistics. My collaborations with molecular biologists and analytical biochemists has also prepared me well for teaching bioinformatics tools and techniques to non-computer scientists. In particular, I would be interested in developing a course, for non-computer science undergraduates, in basic bioinformatics scripting using Python.

— Nathan J. Edwards, Ph.D.