TEACHING STATEMENT AND EVALUATIONS

As an undergraduate student, I was trained in biological sciences and engineering in a double-degree program designed to produce individuals conversant in the two diverse disciplines. This concurrent training provided me with an unusual mix of information and encouraged me to use the concepts of the biological sciences along with the problem-solving approach of engineering. The interdisciplinary nature of my background has been crucial in my research career as well as in my approach to teaching. In my courses, I provide students with fundamental interdisciplinary knowledge and with the opportunities to enhance their analytical skills to better tackle the new challenges posed by the on-going genomics revolution in Biology.

Since 1998, I have taught several undergraduate- and graduate-level courses, tailoring the material and instructional style of each course to the needs of the particular group. Each year, I co-teach a junior undergraduate class entitled "Organic Evolution" in which I introduce the fundamental concepts and theories of Evolutionary Biology, along with topics in earth history, phylogenetic reconstruction, divergence time estimation, patterns of species evolution of vertebrates, and the early evolution of eukaryotes and prokaryotes. In this class of 100 - 200 students, my co-teacher and I introduce facts, concepts, and theories through illustrated examples, and we attempt to encourage critical thinking in all facets of learning while de-emphasizing memorization. Student participation, comments made in the classroom, and their final evaluations clearly reflect their enthusiasm for this style of instruction.

At the senior-undergraduate/junior-graduate level, I have sporadically taught "Introduction to Computational Genomics," a course aimed at introducing the major concepts and practical aspects of comparative sequence analysis. The smaller class size (10 - 20 students) of this course makes it particularly amenable to the inquiry-based approach to teaching with which I became familiar in the HHMI workshop on more effective teaching techniques offered in 1999 at ASU. In this course, I act as a facilitator, enabling students to discover facts and to form concepts in Comparative Genomics themselves; this is done by giving students a data set at the beginning of each class period and prompting them to explore the data in order to make their own observations. The subject matter for the rest of the class period is based on what each student has discovered and how it relates to the present status of knowledge in Computational Genomics. I augment each discussion with additional pertinent information to ensure that each topic is covered in depth. The first class begins with the simplest case of one sequence, and subsequent classes proceed to analyze larger numbers of sequences and genomes. Student responses indicate that they are engaged for the entire class period and that they develop a deeper understanding of the concepts because they discover many of them on their own.

To the classroom environments of both graduate and senior undergraduate courses, I have added computational components that require students to complete exercises using computer programs popularly employed by researchers. This not only imparts a practical understanding of the subject matter, but also prepares them to use genetic and molecular evolutionary analysis methods in their own research. In the future, I plan to organize a seminar class that provides a platform for the critical evaluation of current literature bearing on the topics of molecular evolution, molecular systematics, quantitative genetics, the conservation and diversification of developmental evolutionary genes, and the evaluation of molecular clocks. This seminar will likely attract students with diverse interests, and will further their understanding about new avenues of research in Evolutionary Biology and the use of evolutionary analysis methodology in day-to-day molecular genetic research.

My evolutionary bioinformatics group at ASU provides opportunities for research training activities at undergraduate, graduate, and postgraduate levels. At the undergraduate level, I have trained many students who have been supported by my research grants and by undergraduate research grants to the biology department (MARC: Minority Access to Research Careers; HHMI: Howard Hughes Medical Institute). These experiences are likely to influence the decisions of undergraduate students to pursue higher degrees for research careers at the interface of biology and computer science. At the graduate level, I have trained many Masters and Professional Masters students (8), whose backgrounds are in life sciences, computer sciences, and engineering, but who want to work at the interface of the biological and computational sciences. Many of these students now enjoy successful careers in industry, whereas some others have joined the ranks of doctoral students. I am currently serving as chair or co-chair of six doctoral dissertation committees, with students from life sciences (4), electrical engineering (1) and computer sciences (1).

In an effort to prepare the next generation of faculty members, I am also engaged in the training of postdoctoral researchers. My research group has attracted and provided training for eight post-doctoral scholars, who will be good candidates for faculty positions at research/teaching institutions and who will help to supply the growing need for young faculty in genomics. Two of these postdoctoral fellows have already become tenure-track faculty, whereas the other three have been promoted to Assistant Research Professor. In order to enrich the educational and training experiences of everyone in my group, I routinely invite distinguished scholars from around the world to renew existing collaborations and to foster new ones.

I have contributed to university-wide efforts to begin the new Sloan Foundation-funded Professional Science Masters program in Computational Biosciences (ASU). I have also participated in a successful NSF-funded training grant proposal in the “Evolutionary, Computational, and Molecular Approaches to Genome Structure and Function” (University of Arizona), and I have contributed to the task of improving the participation of students from underrepresented minority groups in doctoral programs through a NSF-funded “Biodesigned Bridges for Doctorate” program (ASU) and an NIH-funded “Post-Baccalaureate Research Education Program in Biomedical Sciences” (ASU).

TEACHING EVALUATIONS

2005 BIO 345 [1.6]	Organic Evolution, 3 credits, 150 students (Jan–May)
2004 BIO 494 (1.3)	Intro to Comparative Genomics, 3 credits, 11 students (Jan–May)
2003 BIO 345 (1.4)	Organic Evolution, 3 credits, 185 students (Jan–May)
2003 BIO 494 (1.2)	Intro to Comparative Genomics, 3 credits, 12 students (Jan–May)
2001 BIO 445 (1.4)	Organic Evolution, 3 credits, 179 students (Jan–May)
2001 BIO 494 (1.3)	Computational Genomics, 3 credits, 7 students (Aug–Dec)
2000 BIO 445 (1.7)	Organic Evolution, 3 credits, 106 students (Jan–May)
2000 BIO 594 (1.3)	Molecular Evolutionary Genetics, 3 credits, 7 students (Aug–Dec)
1999 BIO 594 (1.5)	Molecular Evolutionary Genetics, 3 credits, 10 students (Jan–May)
1999 BIO 494 (1.2)	Advanced Evolution, 3 credits, 14 students (Aug–Dec)

Interpretation

The teaching evaluation score is the arithmetic mean from 13 individual scores (range 1 - 4). Lower scores are better, with a score of 1 being the best possible score. In both large (up to 200 students) as well as small (<30 students) classrooms, the scores are closer to the best possible. A survey of student comments also reflects this trend. A few excerpts include (from a class of 179 students): “Dr. Kumar is an excellent teacher who is interested and excited about material in class and relates information to relevant topics in other biology areas, and his attitude is excellent. One of the best Professors I have had in Biology at ASU.” “I would gladly take another class with Dr. Kumar: A+ Professor.” “He was great at making sure the material was understood.” “I enjoyed your teaching style and your lectures. I like the PowerPoint you used. The material was easy to understand due to bring clear. You’re a great teacher who is very knowledgeable and knows how to communicate to the class and see if people are struggling. I liked that you reviewed material every lecture also in beginning of class.”

BIO 494: Introduction to Comparative Genomics (Last Taught in 2004)

No.	Date	Topic
	Introduction	
1.		Introductory Comments
2.		Anatomy of Genomes
3.		Nature of Genes
	Calculating Basic Attributes of a Sequence	
4.		Quantitative Description of a Nucleotide Sequence
5.		Quantitative Description of a Protein Sequence
6.		Finding Genes in a Sequence
	Comparing Two Sequences	
7.		Comparison of Two Randomly Chosen Sequences
8.		Sequences of the Same Gene in Two Species
9.		Constructing Alignment of Two Sequences
10.		Nature of Observed Differences Between Nucleotide Sequences
11.		Simple Measurements of Nucleotide Sequence Divergence
12.		Complex Measurements of Nucleotide Sequence Divergence
13.		Measuring Sequence Divergence Codon-by-Codon
14.		Nature of Protein Sequence Differences
15.		Measures of Protein Sequence Divergence
16.		Computing Rates of Molecular Evolution
17.		Types of Selective Forces and Tests of Selection
	Analyzing a Set of Three Sequences	
18.		Applying Concepts to Three pairs of Two Sequences
19.		Constructing Evolutionary Trees of Three Sequences
20.		Testing for Steady Accumulation of Mutations (Molecular Clock)
21.	Exam	Applying Molecular Clock for Estimating Species Divergence Time
	Comparative Analysis of Four Sequences	
22.		Progressive Alignment of Multiple Sequences
23.		Reconstructing Evolutionary History of Four Sequences
24.		Testing Reliability of the Inferred Tree
25.		Estimating Patterns of Nucleotide/Protein Substitution
26.		Phylogenetic Molecular Clock Tests
27.		Linearized Trees
28.		Inferring Sequences of Extinct Ancestors and Genes
	Analyzing Larger Number of Sequences	
29.		Constructing Trees and Forests
30.		The Neighbor-Joining Method
31.		Sequences in Populations (Groups): Diversity Within and Between Groups
32.		Testing for Neutral Evolution and Positive Selection
	Evolutionary Dynamics of Multigene Families	
33.		Determining Orthology and Paralogy relations of sequences
34.		Evolutionary relationships of Genes and timing of gene duplications
35.		Computer predictions of genome content and gene function
36.		Comparative Sequence Profiles
	Evolution of Genomes and Species	
37.		Archaeology of Species from Genome Sequences
38.		Genome Evolution by Chromosomal Rearrangement
39.		Age of Gene Families and Chromosomal Segments
40.	Exam	Origin and Evolution of Introns and Other Non-Coding elements

BIO 345: Introduction to Comparative Genomics (Last Taught in 2005)

Date (Lecturer)	Topic	Reference[1]	TA schedule[2]
17 January (TED)	Introduction/History	Chapters 1-3	
22 January (TED)	Basic Genetics	Introductory text, Ch. 4	
24 January (TED)	Hardy-Weinberg equilibrium	5.1	
29 January (TED)	HW equilibrium and linkage	7.1	
31 January (TED)	Selection I	Chapter 5, 8	
5 February (TED)	Selection II	“	
7 February (TED)	Mutation	5.4	
12 February (TED)	Genetic drift	6.2, 6.3	
14 February (TED)	Nonrandom mating	6.4	
19 February	**1st Midterm Exam**		
21 February (TED)	Gene flow	6.1	
26 February (TED)	Interacting forces/Shifting balance		
28 February (TED)	Speciation I	Chapter 15	
5 March (TED)	Speciation II	“	
7 March (TED)	Genetics of speciation	“	
12 March 14 March	**Spring break**		*No office hours*
19 March (SK)	Evolutionary distances	Page 448	
21 March (SK)	Phylogenetic trees I	Chapter 13	
26 March	**2nd Midterm Exam**		
28 March (SK)	Phylogenetic trees II	Chapter 13	
2 April (SK)	Applications I	Chapter 13	
4 April (SK)	Applications II	Chapter 136	
9 April (SK)	Molecular clocks	Chapter 13	
11 April (SK)	Evolutionary tree of vertebrates		
16 April (SK)	Selection and Molecular Evolution	18.2	
18 April (SK)	Significance of Evolutionary Biology to Conservation	6.4, 15.5	
23 April	**3rd Midterm Exam**		
25 April (SK)	Precambrian evolution	Chapter 14	
28 April (SK)	Human evolution	16.1-16.3	

This course is co-taught with Dr. Thomas E. Dowling (TED).