Educational Issues in Biocomputing: Introduction to Session

†§Steven M. Thompson, †§Susan J. Johns, and §A. Keith Dunker

†Center for Visualization, Analysis, and Design in the Molecular Sciences, and

§Department of Biochemistry and Biophysics, Washington State University,

Pullman, WA, USA 99164-4660

{prcadams, thompson}@ribozyme.vadms.wsu.edu; dunker@mail.wsu.edu

Biocomputing, especially as applied to molecular biology, has two main historical branches: 1. biomolecule crystallographers and their cohorts began to develop computational approaches for gaining additional insights and understanding regarding the structures they had determined; and 2. with the advent of the massive databases of sequences of nucleotides and amino acids, molecular biologists, mathematicians, and computer scientists began to explore ways of discovering the biologically relevant organizations within these data fields. These two branches have not yet coalesced into a single field of study, though they are intimately intertwined and may someday merge; departments of biocomputing are not yet common. Nevertheless, a few scientists and university faculty, who are scattered across various departments, colleges, computer centers, and private companies, have begun to develop courses and workshops to teach, or to provide learning environments for, the use of the new tools of biocomputing.

Without a defined field or a formal departmental structure, and given the very brief history of biocomputing, special problems are encountered in the development of course and other educational materials. Even the most basic questions such as content and organization need to be answered.

In our informal (often e-mail) discussions with various individuals who, like ourselves, have been involved with the development of such educational materials, we have discovered a common thread of problems and experiences, repeated individually many times over. For this reason, we proposed that the Pacific Symposium on Biocomputing host an educational forum so new entrants into the educational arena could gain from all of our prior experiences and could also gain access to course materials that had been previously developed.

Educational issues at the Pacific Symposium on Biocomputing will be presented and discussed in three formats: oral presentation of papers, a poster session, and a workshop/panel discussion. The workshop will focus on several specific questions: 1. which students need formal training in biocomputing; 2. when should such courses be inserted into their curricula; 3. what core skills, and in what order, should be taught; 4. how can educators keep abreast of the rapid changes in this field; and 5. visualization, is it a necessary tool or merely window dressing? We intend to record and transcribe the discussions on these topics and to make them available to those interested on the World Wide Web at:

http://ribozyme.vadms.wsu.edu/~VADMS/PSB-edu.html

The paper by **Swanson and Lybrand,** "**Computational Biology Instruction at the University of Washington Center for Bioengineering**," is especially interesting because it describes courses in biocomputing implemented for students with backgrounds in physics and engineering. Their approach is quantitative and physics-based and assumes a high computer literacy for the students.

At the other end of the computer-skills spectrum, our paper (**Johns, Thompson, and Dunker**, "**An Introductory Course in Computational Molecular Biology: Rationale, History, Observations, and Course Description**") describes a course designed primarily for molecular biology students with little or no prior computing experience. This course provides a hands-on, "real-life" approach in which student-initiated projects are emphasized.

Whereas these first two papers focus on instruction leading to intelligent and correct usage of currently available algorithms in computational molecular biology, the paper by **Altman and Koza**, "**A Programming Course in Bioinformatics for Computer and Information Science Students**," describes a higher level course that strives to present a technical introduction to the field. This programming course initially focuses on fundamental representations and algorithms already in use in biocomputing, and then on current research by Stanford faculty in these areas.

The paper by **Gaëta, Bucholtz, Campbell, Huynh, Kim, and Reisner**, "**Biocomputing Education by the Australian National Genomic Information Service**," (ANGIS) describes their approach for addressing the needs of all of Australia; this is a particularly impressive goal. Details are given on a set of self-paced tutorials, a system-access recipe book, and various workshops by ANGIS.

A prototype course, which was sponsored by the Global Network Academy (GNA) using the World Wide Web and organized by the Biocomputing Division of the Virtual School of Natural Sciences (VSNS), is outlined in the paper by **De La Vega, Giegerich, and Fuellen**, "**Distance Education Through the Internet: the GNA-VSNS Biocomputing Course**." Offered in the summer of 1995, this course reached 34 students in 13 countries. This paper provides an illuminating and interesting discussion on the use of the World Wide Web to teach a course in computational molecular biology to the entire world.

We hope that the set of papers just described, and the workshop/panel discussion that will occur, will be found to be useful to the molecular biology community. We welcome your comments and long range participation, either through future meetings, which we hope will be a continual part of the Pacific Symposium on Biocomputing, or by comments sent to the WWW site given above.

Acknowledgments: We want to especially thank Lawrence Hunter and Teri Klein for administering the review of our own paper - many useful and helpful suggestions were provided - and for their tireless work on behalf of the entire conference. We also greatly appreciate the work of the several referees of the other papers in this session. Very thoughtful reviews were returned. These referees included David R. Bevan, David Haussler, Liz Howell, Diane Husic, Leslie Kuhn, Steven Meinhardt, Robert Murphy, and Thomas P. Quinn.