PACIFIC SYMPOSIUM ON BIOCOMPUTING 2004

Last spring the PSB organizers engaged in an e-mail conversation on the origins of our field. This led to the following brief study. According to the Oxford English Dictionary, *biocomputing* is defined as the application of computing in biological research, especially the analysis of statistical data and molecular structures, and the modeling of biological processes, while *bioinformatics* is defined as the science of information and information flow in biological systems, especially the use of computational methods in genetics and genomics. Furthermore, the same dictionary indicates that an advertisement in *Science,* December 2, 1977, contained the first documented use of biocomputing and that a biographical sketch in *Simulation* volume 31, 1978, contained the first documented use of bioinformatics. The sketch referred to Paulien Hogeweg of the University of Utrecht as having her main field of research in bioinformatics. To this day, this university maintains a research group described as "Theoretical Biology/Bioinformatics," and Professor Hegeweg continues to publish in this field.

For the period up until the eve of the first PSB, biocomputing was, by a slight margin, the most widely used term for our field. For example, for the period up until December 31, 1995, PubMed searches give 27 hits for the term *computational biology*, 14 hits for *bioinformatics*, and 32 hits for *biocomputing*. The picture is quite different now: on the eve of the ninth PSB, *computational biology* gives 4,452 hits, *bioinformatics* gives 4,773 hits, and *biocomputing* a mere 147 hits.

An e-mail conversation with Jean Michel Claverie provides an interesting hypothesis regarding the popularity of the term *bioinformatics.* Being unaware of Professor Hogeweg's use of "bioinformatics," Professor Claverie independently coined the term "la bioinformatique molecularie" [Claverie, J. M., Caudron, B., and Gerard, O. (1984) Le systeme d'analyse de sequences de l'Institute Pastuer (S.A.I.S.P) *Biofutur*, Juin 35-37]. In the following years, the term picked up quite well in France. Professor Claverie tells that

> "It became increasingly difficult for me and my French colleagues, when giving seminars in English, to switch back to the accepted English terms of the time: "computational biology" or "biocomputing." During seminars, my tongue slipped many times, such as "I am going to present some of our new developments in Bioinformatics -sorry- Biocomputing…" One of the clearest instances of this happening many times over, was in one of the first Waterville Valley meetings [Macromolecules, Genes and Computers. These important meetings were organized by Temple Smith. The first one was in August of 1986], where I first met with people like Lipman, Wilbur, Temple Smith, Staden, well, all the people from the early NAR special issues,

> but that was also well attended (for the first time) by Europeans (Saccone, Gautier, Grantham, myself, and a few others). I remember some of the attendance asking me the exact meaning and origin of "Bioinformatics"… (Also because I had such a bad French accent!) I think I remember (this is SOOO old), some Americans being quite enthusiastic about it, AND THIS IS IMPORTANT, as a way to distinguish the computational use of computers (when you do calculus and compute things) from the more "textual" use of them (sequence text analysis, sequence alignment, databases, etc), and thus, a great way to denote the 'new wave' from the old computer application (computational biology, biocomputing, theoretical biology). I think it is this new ecological niche that made the term quickly popular in English."

Despite the gaining popularity of the term *bioinformatics*, PSB will retain the use of biocomputing: its definition conveys the breadth of topics embraced by this meeting. *– A. Keith Dunker*

PSB 2004 has again been supported by grants from the U.S. Department of Energy and the National Library of Medicine/National Institutes of Health. The International Society for Computational Biology and Applied Biosystems continue to sponsor PSB, and as a result, meeting participants will once again benefit from travel grants from their generous support.

We look forward to the key addresses by Debbie Nickerson and by Henry T. Greely. Tiffany Jung again carried out a yeoman's work of creating the printed and online proceedings while also providing the backbone for the administration of the meeting.

Each year we thank the session organizers. Their unselfish and tireless work gives PSB its special flavor.

Trey Ideker, Eric Neumann, and Vincent Schachter
Computational and Symbolic Systems Biology

Alexander Hartemink and Eran Segal
Joint Learning from Multiple Types of Genomic Data

Hui Wang, Ueng-cheng Yang, and Chris Lee
Alternative Splicing

Francisco de la Vega, Kenneth Kidd, and Andrew Collins
Computational Tools for Complex Trait Gene Mapping

Olivier Bodenreider, Joyce A. Mitchell, and Alexa T. McCray
Biomedical Ontologies

Sean D. Mooney, Philip E. Bourne, and Patricia C. Babbitt
Informatics Approaches in Structural Genomics

PSB 2004 will also host four tutorials *Systems Biology Host/Pathogen and Other 'Community' Interactions* by Christian Forst, *Creating Web Services for Bioinformatics* by Michael D. Jensen, Timothy B. Patrick, and Joyce A. Mitchell, *Network (Reticulated) Evolution: Biology, Models, and Algorithms* by C. Randal Linder, Bernard M.E. Moret, and Tandy Warnow, and *Modeling Genetic and Metabolic Networks: Design of High Throughput Experiments* by Kenneth Kauffman, Babatunde A. Ogunnaike, and Jeremy S. Edwards

Again we acknowledge the crucial assistance of those who capably reviewed the submitted manuscripts. The partial list on the following pages does not include those who have been left of the list inadvertently or who wished to remain anonymous.

Participants and those who haven't yet attended PSB are encouraged to submit proposals for sessions and tutorials for future meetings. Well-conceived submissions are vital to the continuing success of PSB.

Aloha!

Pacific Symposium on Biocomputing Co-Chairs *October 1, 2003*

Russ B. Altman
Department of Genetics & Stanford Medical Informatics, Stanford University

A. Keith Dunker
Center for Computational Biology & Bioinformatics, Indiana University School of Medicine

Lawrence Hunter
Department of Pharmacology, University of Colorado Health Sciences Center

Teri E. Klein
Department of Genetics & Stanford Medical Informatics, Stanford University