

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2003

These are the proceedings of the eighth Pacific Symposium on Biocomputing (PSB), held on the island of Kauai, Hawaii. The proceedings for this and previous PSB meetings are also available in electronic form at <http://psb.stanford.edu/psb-online/> and are indexed in the Medline resource provided by the National Library of Medicine of the U.S. The online proceedings offer more than 350 manuscripts presented since 1996 at PSB. Because PSB sessions are organized in a grass roots fashion, the intellectual challenges of our field can be chronicled by an analysis of the sessions presented each year. Early conferences were dominated by protein structure, HMMs and sequence analysis. More recently, natural language processing, human genetic variation, and comparative genomics have emerged. It is particularly gratifying to note that the impact of PSB papers has been growing, and our published corpus in certain niches (such as natural language processing for biology and reconstruction of metabolic networks) has become influential in these subdisciplines.

PSB is sponsored by the International Society for Computational Biology (<http://www.iscb.org/>). Meeting participants benefit once again from travel grants from the ISCB, U.S. Department of Energy, National Library of Medicine/National Institutes of Health, and Applied Biosystems. In addition, GeneticXchange is a corporate affiliate.

We thank Dr. Marvin Cassman for his plenary address on the future of computational biology, and Dr. Latanya Sweeney for her plenary address on issues of database privacy and confidentiality. Tiffany Jung, the newest member of our PSB editorial team, has created the printed and online proceedings, while also administering the meeting. We would especially like to acknowledge the contributions of the session organizers who solicited papers and reviews, and ensured that the quality of the meeting remains high. The session organizers (and their associated sessions) are:

Serafim Batzoglou and Lior Pachter (Gene Regulation)

*Peter Karp, Pedro R. Romero, Eric Neumann, Alexander J. Hartemink
(Genome, Pathway, and Interaction Bioinformatics)*

Sean D. Mooney and Patricia C. Babbitt (Informatics Approaches in Structural Genomics)

Liping Wei, Inna Dubchak, and Victor Solovyev (Genome-wide Analysis and Comparative Genomics)

Lynette Hirschman, Carol Friedman, Robin McEntire, and Cathy Wu (Linking Biomedical Language, Information and Knowledge)

Francisco M. De La Vega, Kenneth K. Kidd, and Isaac S. Kohane (Human Genome Variation: Haplotypes, Linkage Disequilibrium, and Populations)

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

We are also happy to host two discussion panels on “Graduate and Undergraduate Bioinformatics Education” (moderated by Richard Hughey) and “Genetic Diversity and DNA-based Identification” (moderated by James Sikela and Eric Juengst). The latter topic is particularly relevant in light of a special report at the end of these proceedings that describes the informatics tools that helped catalog and identify the remains of victims of the World Trade Center collapse on September 11, 2001.

As usual, the PSB organizers and session leaders relied on the assistance of those who capably reviewed the submitted manuscripts. A partial list of reviewers is provided in the following pages, and we also thank those who have been left off this list inadvertently or who wished to remain anonymous.

We encourage participants to consider submitting proposals for future PSB sessions and tutorials in order to ensure that the meeting continues to provide a forum for the early discussion and publication of new directions in biocomputing.

Aloha!

Pacific Symposium on Biocomputing Co-Chairs

October 1, 2002

Russ B. Altman

Department of Genetics & Stanford Medical Informatics, Stanford University

A. Keith Dunker

Department of Biochemistry and Biophysics, Washington State University

Lawrence Hunter

Department of Pharmacology, University of Colorado Health Sciences Center

Teri E. Klein

Department of Genetics & Stanford Medical Informatics, Stanford University