

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2001

The sixth Pacific Symposium on Biocomputing (PSB) marks the first PSB held after the completion of the "rough draft" of the Human Genome Sequence. Whereas the early days of bioinformatics were characterized by the development of methods to support the sequencing effort (assembling the sequence, performing preliminary annotations, storing the sequence, and creating tools for its retrieval), the days to come will focus on making sense of this "parts list" for human biology. Our task now becomes one of assigning the molecular functions of genes (and all their variants), placing these functions in the context of pathways and interaction graphs within the cell, understanding how these pathways create a network of interactions that allow a cell to live, and then decoding the language used by cells to communicate during organismal development and growth. The PSB once again offers a cutting-edge view of all these activities in a set of sessions that have arisen from grass-roots proposals about how to focus the meeting.

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

We thank Dr. David Haussler in advance for his plenary address on creation and analysis of the working draft of the human genome. Kevin Lauderdale has once again expertly created the printed and online proceedings. Al Conde has ensured that the hardware and network systems are functional. 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:

Francisco De La Vega, Martin Kreitman and Isaac Kohane (Human Genome Variation: Linking Genotypes to Clinical Phenotypes)

Limsoon Wong and Junichi Tsujii (Natural Language Processing for Biology: Term extraction, Information retrieval, Information extraction, and Corpus annotation)

Peter Karp, Eric Neumann and Pedro Romero (Genome, Pathway and Interaction Bioinformatics)

Jennifer Steinbachs and Paul Kearney (Phylogenetics in the Post-Genomic Era)

Thomas Ferrin, Bruce Foster and Richard Hughey (High performance computing for computational biology)

Clay Bracken, A. Keith Dunker and Malin Young (Disorder and Flexibility in Protein Structure and Function)

Richard Lathrop and Pierre Baldi (DNA Structure, Protein-DNA Interactions, and DNA-Protein Expression)

Richard Goldstein and David Pollock (Structures, Phylogenies, and Genomes: The Integrated Study of Protein Evolution)

Pierre Baldi and Soren Brunak (Bioethics, Fiction Science, and the Future of Mankind)

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 elsewhere in this volume, and we also thank those who have been left off this list inadvertently or who wish to remain anonymous.

Once again, 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

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