

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2000

The fifth Pacific Symposium on Biocomputing (PSB) begins on the fourth day of the year 2000. The numerics of biocomputing are nearly as convoluted as those of calendrics: four bases, twenty amino acids, three bases per codon, three billion bases per human, one hundred thousand genes per human, and so on. As calendrics endeavors to summarize the quirky behavior of celestial bodies, so biocomputing endeavors to capture the mysteries of biological systems. As we approach the new millennium, we are ready to reap the benefits of the dual revolutions in digital computing and biology. The PSB continues to provide a home for emerging subdisciplines within biocomputing. This year, new sessions are introduced in the analysis of single nucleotide polymorphisms, structural genomics, natural language processing and cheminformatics. There is a growing interest in gene expression analysis and molecular networks, and continued progress in the areas of protein structure prediction, information theory, data mining and visualization.

Many PSB participants benefit from travel grants from the U.S. Department of Energy, the National Library of Medicine, the International Society for Computational Biology, and PE Biosystems. Once again, Silicon Graphics, Compaq and Cisco have generously donated machines, shipping and insurance to allow live demonstrations and internet connectivity during the meeting. Zymogenetics and Partek provided general support for the meeting.

Dr. Wah Chiu is thanked in advance for his plenary address. Kevin Lauderdale has expertly created the printed proceedings and the electronic version. Al Conde has ensured that the donated hardware is actually assembled, powered-up and functional.

The largest debt for effort in ensuring the high scientific quality of PSB goes to the session chairs. Their work in soliciting papers, moderating the review, recommending outcomes and then chairing discussion sessions is crucial. We therefore gratefully acknowledge their efforts:

Identification of Coordinated Gene Expression and Regulatory Sequences

(Jean-Michel Claverie, Minoru Kanehisa, Dan Prestridge, Gary Stormo & Michael Q. Zhang)

Molecular Network Modeling and Data Analysis (Roland Somogyi, Hiroaki Kitano, Satoru Miyano & Qiang Zheng)

Analysis, Management, and Application of SNP Data (Francisco M. De La Vega & Martin Kreitman)

Protein Evolution and Structural Genomics (Dmitrij Frishman, Richard A. Goldstein & David D. Pollock)

Natural Language Processing for Biology (Tatsuhiko Tsunoda & Limsoon Wong)

Protein Structure Prediction in Biology and Medicine (Roland Dunbrack, Keith Dunker & Adam Godzik)

Computer-Aided Combinatorial Chemistry and Cheminformatics (Alexander Tropsha & Robert S. Pearlman)

Applications of Information Theory to Biology (T. Gregory Dewey & Hanspeter Herzel)

Data Mining and Discovery in Molecular Databases (Janice Glasgow, Igor Jurisica & Raymond Ng)

Tools for Visualization and Interaction (Eileen Kraemer & Thomas Ferrin)

We also thank those who reviewed submitted manuscripts. A partial list is given elsewhere in this volume, and we also thank those who have been left off this list inadvertently or who wish to remain anonymous.

We encourage you to consider submitting proposals for future PSB sessions in order to ensure that the meeting maintains its tradition of hosting sessions on the most exciting new challenges within biocomputing. The prospects for progress in biocomputing during the next one thousand years are reasonably good. Aloha!

Pacific Symposium on Biocomputing Co-Chairs

October 1, 1999

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