Pacific Symposium on Biocomputing 1998

By now the world-wide sequence and structure databases contain more than one billion ordered base pairs, more than one hundred thousand protein sequences and more than ten thousand nucleic acid or protein structures. These notable milestones were all surpassed in the past year. Achievement of these milestones emphasizes the need to advance the field of bioinformatics or biocomputing. The Pacific Symposium on Biocomputing (PSB) was established precisely to meet this need.

The goal of the PSB is to bring computer scientists together with biologists to discuss and debate mutual interests in a productive environment. Perhaps inevitably, PSB has developed a primary focus on the data-rich area of molecular biology.

Another milestone reached during the past year was the establishment of the International Society for Computational Biology (ISCB). We are pleased that PSB is to be one of two international meetings sponsored by ISCB; the other is Intelligent Systems in Molecular Biology. Watch for instructions for joining ISCB at our website: www.cgl.uscf.edu/psb/.

PSB reached an important milestone of its own. Starting with the spring of 1998, the PSB proceedings will be indexed by MEDLINE, including retroactive inclusion of PSB-96 and PSB-97. To facilitate the indexing process, these proceedings will be identified by volume numbers, with these proceedings, PSB-98, corresponding to volume 3. PSB-96, volume 1, and PSB-97, volume 2, can be viewed at www.cgl.ucsf.edu/psb/. The manuscripts herein and the sessions into which they are organized presage another vibrant and exciting PSB. Once again, all manuscripts were examined by at least two reviewers, and in many cases more. Kudos to the session chairs for soliciting an exciting group of papers. Sessions and organizers for PSB-98 include:

Gene Expression and Genetic Networks (Barbara Bryant, Aleksandar Milosavljevic & Roland Somogyi)

Molecules to Maps: Tools for Visualization and Interaction (Tom Ferrin & Eileen Kraemer)

Gene Structure Identification in Large-scale Genomic Sequence (Edward Uberbacher & Ying Xu)

Molecular Modeling in Drug Design and Biotechnology (Jurgen Bajorath, Teri Klein & Terry Lybrand)

Protein Structure Prediction (Richard Lathrop)

The Relationship Between Protein Structure and Function: How Have Proteins Over Time Diverged in Function? (Patricia Babbitt)

Computing with Biomolecules (Peter Clote, Masami Hagiya, & Tom Head)

Complexity and Information Theoretic Approaches to Biology (David Dowe & Klaus Prank)

Distributed and Intelligent Databases (Dmitrij Frishman)

Building Bioinformation Infrastructure in the Pacific Rim (Tin Wee Tan, S. Subbiah, Tim Littlejohn and Hideaki Sugawara)

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Thanks to reviewers...

The meeting chairs and session organizers would like to thank the following individuals for their efforts in reviewing submissions. We also thank those who are not listed here.

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