

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2008

This year, PSB returns to its most common venue, the Fairmont Orchid on the Big Island of Hawaii. We are now in our thirteenth year, and had a record number of both proposed sessions (we accepted 9) as well as submissions to the conference this year (150). Many sessions at PSB have a lifetime of approximately three years. The first year is a test of the interest in the field, and the ability to attract a critical mass of papers. With success, the second year is usually a larger, more competitive session. The third (and rarely fourth years) usually come as the subdiscipline is recognized at the general biocomputing meetings such as ISMB, RECOMB and others, and often this is when the PSB organizers conclude that their work is done, and the session can be “retired.” PSB aficionados will notice new sessions this year in next-generation sequencing, tiling array analysis, multiscale modeling, small regulatory RNAs, and other areas. The richness of exciting new areas has led us to have more total sessions, and thus the average session size is smaller. We consider this an experiment, and look forward to seeing how it goes.

We would like to thank our keynote speakers. Dr. Andrew McCulloch, Professor and Chair, Department of Bioengineering, University of California, San Diego, will talk about “Systems biology and multi-scale modeling of the heart.” Our keynote in the area of Ethical, Legal and Social implications of technology will be John Dupre, Director of Egenis (ESRC Centre for Genomics in Society) and Professor of Philosophy of Science, University of Exeter.

PSB provides sessions focusing on hot new areas in biomedical computation. These sessions are usually conceived during earlier PSB meetings, as emerging fields are identified and targeted. The new sessions are lead by relatively junior faculty members trying to define a scientific niche and bring together leaders in these exciting new areas. Many areas in biocomputing have first been highlighted at PSB. If you have an idea for a new session, contact the organizers at the meeting or by e-mail.

Again, the diligence and efforts of a dedicated group of researchers has led to an outstanding set of sessions, with associated introductory tutorials. These organizers provide the scientific core of PSB, and their sessions are as follows:

Michael Brudno, Randy Linder, Bernard Moret, and Tandy Warnow. *Beyond Gap Models: Reconstructing Alignments and Phylogenies Under Genomic-Scale Events*

Doron Betel, Christina Leslie, and Nikolaus Rajewsky. *Computational Challenges in the Study of Small Regulatory RNAs*

Francisco De La Vega, Gabor Marth, and Granger Sutton. *Computational tools for next-generation sequencing applications*

Michael Ochs, John Quackenbush, and Ramana Davuluri. *Knowledge-Driven Analysis and Data Integration for High-Throughput Biological Data*

Atul Butte, Maricel Kann, Yves Lussier, Yanay Ofran, Marco Punta, and Predrag Radivojac. *Molecular Bioinformatics for Diseases: Protein Interactions and Phenomics*

Jung-Chi Liao, Peter Arzberger, Roy Kerckhoffs, Anushka Michailova, and Jeff Reinbolt. *Multiscale Modeling and Simulation: from Molecules to Cells to Organisms*

Martha Bulyk, Ernest Fraenkel, Alexander Hartemink, and Yael Mandel-Gutfreund. *Protein-Nucleic Acid Interactions: Integrating Structure, Sequence, and Function*

Antonio Piccolboni and Srinka Ghosh. *Tiling Microarray Data Analysis Methods and Algorithms*

Kevin Bretonnel Cohen, Philip Bourne, Lynette Hirschman, and Hong Yu. *Translating Biology: Text Mining Tools that Work*

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Aloha! Pacific Symposium on Biocomputing Co-Chairs,
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