

## PACIFIC SYMPOSIUM ON BIOCOMPUTING 2009

This year, PSB remains at its most common venue, the Fairmont Orchid on the Big Island of Hawaii. We are now in our fourteenth year. A brief review of our field shows a clear trend: sequence analysis is back! The introduction of “next generation” sequencing technologies has taken many by surprise. These technologies are creating volumes of data that are amazing, and that stress out most existing software and hardware infrastructures. Reports of the demise of sequence analysis as an active research area are premature. Some say that bioinformatics is like waves on the beach—a new wave hits the beach regularly, but only some of the water actually sinks into the sand and stays a while—most of it goes back into the sea. So it is for bioinformatics, where waves of scientists arrive as exciting new data sets emerge (e.g. sequence data brought combinatorial algorithms and microarray data brought statisticians), some of these remain in the field, while others recede after the initial thrill wears out. Well, for those who do sequence analysis, the second wave has broke. More importantly, these data promise to enrich our ability to measure genotype, ask important questions about its relationship to phenotype, and bring the \$1000 genome into view.

We would like to thank our keynote speakers. Dr. Drew Endy, Department of Bioengineering, Stanford University, will talk about “Post-Synthesis Genetics & Engineering Biological Simplicity.” Our keynote in the area of Ethical, Legal and Social implications of technology will be Greg Hampikian, Professor of Biology and Criminal Justice Director of the Idaho Innocence Project, Boise State University, who will talk about “DNA Don't Lie: How Bioinformatics freed some of my best friends, and sent the guilty to prison.”

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 sessions often define a new scientific niche and bring together leaders in these exciting new areas. If you have an idea for a new session, contact the organizers at the meeting or by e-mail.

The diligent 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:

**Gil Alterovitz, Judith A. Blake, Jonathan M. Dreyfuss, Drew Endy, and Marco F. Ramoni.** *Biomolecular Networks: From Analysis To Synthesis*

**Bernard Moret, Webb Miller, Pavel Pevzner, and David Sankoff.** *Computational Challenges in Comparative Genomics: Gene Family Evolution, Ancestral Genome Reconstruction, and Applications to Human Genetics*

**Tanya Berger-Wolf, Teresa Przytycka, and Mona Singh.** *Dynamics of Biological Networks*

**Roy Kerckhoffs, James Bassingthwaight, Jeff Reinbolt, and Peter Arzberger.** *Emerging Challenges in Multi-Scale Modeling in Biology*

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

**Yves A. Lussier, Younghee Lee, Predrag Radivojac, Yanay Ofran, Atul Butte, and Maricel Kann.** *Molecular Bioinformatics for Disease*

PSB 2008 will also feature two workshops: *Open Science: Developing tools and approaches to facilitate open exchange between scientists and data* by Cameron Neylon and Shirley Wu and *Post-transcriptional gene regulation: RNA-protein interactions, RNA processing, mRNA stability and localization* by Benjamin Blencowe, Steven Brenner, Timothy Hughes, and Quaid Morris.

Tiffany Murray provided outstanding support of the peer review process, assembly of the proceedings, and meeting logistics. We thank the National Institutes of Health, National Science Foundation, and the International Society for Computational Biology for travel grant support. We also acknowledge the many busy researchers who reviewed the submitted manuscripts on a very tight schedule. The partial list following this preface does not include many who wished to remain anonymous, and of course we apologize to any who may have been left out by mistake.

Aloha! Pacific Symposium on Biocomputing Co-Chairs,  
September 30, 2008

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