

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2010

This year marks the 15th year of PSB. Started in 1996 by Teri Klein and Larry Hunter, the meeting was a session within the Hawaii International Conference on Systems Sciences Conference (HICSS) for a couple of years. The interest in biocomputing was great and was threatening to alter the balance of attendees within the HICSS meeting, and so the organizers asked Teri and Larry to find an alternative. Taking advantage of the nice meeting opportunities in Hawaii immediately following New Year's Day, they created PSB with a simple formula: oral presentation of peer reviewed papers in emerging areas of biocomputing, interactive poster sessions, and lively discussion sessions on these topics. They invited Keith Dunker and Russ Altman to join the team for the second PSB, and we have been working together ever since.

In fifteen years, we have had some papers that have made remarkable impact. Using Google Scholar, the top 15 papers, in terms of citations over the last 15 years are listed below (with number of citations listed as of September 2009, followed by the reference). Obviously, there are other great papers, especially ones that have been written in the last few years, that have not yet had time to rise to the top of this list. Nevertheless, the list provides highlights of the last 15 years in biocomputing challenges.

(573) [REVEAL, A General Reverse Engineering Algorithm for Inference of Genetic Network Architectures](#) S. Liang, S. Fuhrman and R. Somogyi; Pacific Symposium on Biocomputing 3:18-29 (1998).

(457) [Modeling Gene Expression with Differential Equations](#) T. Chen, H. L. He, and G.M. Church; Pacific Symposium on Biocomputing 4:29-40 (1999).

(422) [Principal Components Analysis to Summarize Microarray Experiments: Application to Sporulation Time Series](#) S. Raychaudhuri, J.M. Stuart, and R.B. Altman; Pacific Symposium on Biocomputing 5:452-463 (2000).

(419) [The Spectrum Kernel: A String Kernel for SVM Protein Classification](#) Leslie, E. Eskin, and W.S. Noble; Pacific Symposium on Biocomputing 7:566-575 (2002).

(294) [EDGAR: Extraction of Drugs, Genes and Relations from the Biomedical Literature](#) T.C. Rindfleisch, Lorraine Tanabe, John N. Weinstein, and L. Hunter; Pacific Symposium on Biocomputing 5:514-525 (2000).

(270) [Mutual Information Relevance Networks: Functional Genomic Clustering Using Pairwise Entropy Measurements](#) A. J. Butte and I. S. Kohane; Pacific Symposium on Biocomputing 5:415-426 (2000).

(245) [Biobibliometrics: Information Retrieval and Visualization from Co-Occurrences of Gene Names in Medline Abstracts](#) B.J. Stapley and G. Benoit; Pacific Symposium on Biocomputing 5:526-537 (2000).

(218) [Hybrid Fold Recognition: Combining Sequence Derived Properties with Evolutionary Information](#) D. Fischer; Pacific Symposium on Biocomputing 5:116-127 (2000).

(215) [Hybrid Petri Net Representation of Gene Regulatory Network](#) H. Matsuno, A. Doi, M. Nagasaki, and S. Miyano; Pacific Symposium on Biocomputing 5:338-349 (2000).

(198) [Discovery of Regulatory Interactions Through Perturbation: Inference and Experimental Design](#) T.E. Ideker, V. Thorsson, and R.M. Karp; Pacific Symposium on Biocomputing 5:302-313 (2000).

(152) [Cluster Analysis and Data Visualization of Large-Scale Gene Expression Data](#) G.S. Michaels, D.B. Carr, M. Askenazi, S. Fuhrman, X. Wen and R. Somogyi; Pacific Symposium on Biocomputing 3:42-53 (1998).

(191) [ANN-Spec: A Method for Discovering Transcription Factor Binding Sites with Improved Specificity](#) C.T. Workman and G.D. Stormo; Pacific Symposium on Biocomputing 5:464-475 (2000).

(137) [Development of a System for the Inference of Large Scale Genetic Networks](#) Y. Maki, D. Tominaga, M. Okamoto, S. Watanabe, and Y. Eguchi; Pacific Symposium on Biocomputing 6:446-458 (2001).

(130) [A Comparison of Genetic Network Models](#). L.F.A. Wessels, E.P. Van Someren, and M.J.T. Reinders; Pacific Symposium on Biocomputing 6:508-519 (2001).

(126) [Detecting Gene Relations from MEDLINE Abstracts](#). M. Stephens, M. Palakal, S. Mukhopadhyay, R. Raje, and J. Mostafa; Pacific Symposium on Biocomputing 6:483-496 (2001).

We have seen PSB papers cited in the other “high impact journals” and it is satisfying to know that the work presented here is making a real difference. We have spoken with scientists who hesitate to submit their work to PSB for fear that it will not be subsequently considered eligible for a journal. This is an understandable concern, but is mitigated by the excellent penetration of PSB paper as they are listed in Medline and clearly generate some attention, if they are good.

We would like to thank our keynote speakers. Dr. Stanley Nelson, Professor of Human Genetics and Psychiatry at the David Geffen School of Medicine at UCLA will talk about “Whole genome sequencing: issues and progress towards common application.” Our keynote in the area of Ethical, Legal and Social implications of technology will be Dr. Isaac Kohane, Professor of Pediatrics and Medicine, Harvard Medical School, who will discuss issues related to the ethical application of emerging technical capabilities.

PSB provides sessions focusing on emerging areas in biomedical computation. These sessions are frequently conceived at the meeting itself, during the discussion times. Again, the 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:

Bernard Moret, Webb Miller, Pavel Pevzner, and David Sankoff

[*Computational Challenges in Comparative Genomics*](#)

Rolf Backofen, Hamidreza Chitsaz, Ivo Hofacker, S. Cenk Sahinalp, and Peter F. Stadler

[*Computational studies of non-coding RNAs*](#)

Tanya Berger-Wolf, Teresa Przytycka, Mona Singh, and Donna Slonim

[*Dynamics of Biological Networks*](#)

Julie Bernauer, Samuel Flores, Xuhui Huang, Seokmin Shin, and Ruhong Zhou

[*Multi-resolution Modeling of Biological Macromolecules*](#)

Can Alkan, Michael Brudno, Evan E. Eichler, Maricel G. Kann, S. Cenk Sahinalp

[*Personal Genomics*](#)

Gil Alterovitz, Silvio Cavalcanti, May Wang, and Marco F. Ramoni

[*Reverse Engineering and Synthesis of Biomolecular Systems*](#)

In addition, we welcome three satellite workshops to PSB this year:

Richard Goldstein, Phil Husbands, Chrisantha Fernando, and Dov Stekel

[*In silico biology*](#)

Dawn Field, Lynette Hirschman, Peter Sterk, and John Wooley

[*Metagenomics, Metadata and Metaanalysis \(m3\)*](#)

Adrien Coulet, Nigam Shah, Larry Hunter, Chitta Baral and Russ B. Altman

[*GPD-Rxn Workshop: Genotype-Phenotype-Drug Relationship Extraction from Text*](#)

Tiffany Murray continues to run the peer review process and assembly of the proceedings. We thank the National Institutes of Health, the International Society for Computational Biology (ISCB) for travel grant support. We are particularly grateful to BJ McKay-Morrison at ISCB for her assistance. 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.

We look forward to a great meeting once again.

Aloha!

Pacific Symposium on Biocomputing Co-Chairs,
September 28, 2009

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Thanks to the reviewers...

Finally, we wish to thank the scores of reviewers. PSB requires that every paper in this volume be reviewed by at least three independent referees. Since there is a large volume of submitted papers, paper reviews require a great deal of work from many people. We are grateful to all of you listed below and to anyone whose name we may have accidentally omitted or who wished to remain anonymous.

Gil Alterovitz	Andreas Hildebrandt	Eric K. Neumann
Nice-Sophia Antipolis	Ivo Hofacker	Bill Noble
Zafer Aydin	Fereydoun Hormozdiari	Ruth Nussinov
Rolf Backofen	David Hsu	Yuko Okamoto
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