PACIFIC SYMPOSIUM ON BIOCOMPUTING 2017

2017 marks the 22nd Pacific Symposium on Biocomputing (PSB)! Biocomputing, biomedical informatics and data science have become high profile activities in recent years. The associated emphasis on the need for policies and technologies for effective data sharing has also received quite a bit of attention. In a series of editorials, the New England Journal of Medicine (Longo & Drazen, N Engl J Med 2016; 374:276-277. 1/21/2016. DOI: 10.1056/NEJMe1516564 and Drazen, N Engl J Med 2016; 374:e24. 5/12/2016. DOI: 10.1056/NEJMe1601087) discussed the particular challenges for data sharing in the context of clinical data, generating much discussion about the proper approaches for these activities. Most notable, however, was the introduction of the phrase "research parasite" to describe "people who had nothing to do with the design and execution of the study but use another group's data for their own ends, possibly stealing from the research productivity planned by the data gatherers, or even use the data to try to disprove what the original investigators had posited." Of course, this perfectly describes (although in somewhat more negative terms than are typically used by data scientists) the motivation behind data sharing in genomics and molecular biology—and the potential value of secondary analysis of public data sets, including the occasional disproof of an incorrect scientific finding or conclusion—thus saving time, resources and potentially lives. The depiction of secondary analyses and the potential refutation of primary analyses as a negative surprised many, but points to the special challenges of sharing sensitive clinical data. Nonetheless, "I am a research parasite" became a refrain among biomedical data analysts who felt strongly that these analyses are indeed quite positive and exactly what is needed. In that vein, the PSB organizers were approached with an idea to host an award to recognize those who have made substantial scientific contributions by analyzing data collected by others. These "Research Parasite Awards" quickly attracted financial support and will be presented for the first time at this meeting. To his credit, Dr. Jeffrey Drazen, the Editor-in-Chief of the New England Journal of Medicine, has also agreed to give a talk about the challenges in clinical data sharing, particularly from his vantage point as an editor of an influential clinical journal. Dr. Drazen has no connection with the Research Parasite Awards, but is fully aware that they have been created and will be awarded at the meeting this year.

The mission of PSB is to provide a forum for the best *emerging* science in Biocomputing, providing both formal and informal mechanisms for scientific communication. PSB depends on the community to define emerging areas in biomedical computation. Its sessions are usually conceived at the previous PSB meeting as people discuss trends and opportunities for new science. The typical program includes sessions that evolve over two to three years as well as entirely new sessions. This year we revisit new dimensions of precision medicine, ranging from single cell measurements to populations.

In addition to being published by World Scientific and indexed in PubMED, the proceedings from all PSB meetings are available online at http://psb.stanford.edu/psb-online/. PSB has published more than 800 papers. These papers are often cited in journal articles and represent early contributions in emerging subfields—many times before there is an established literature in more traditional journals; for this reason, many papers have garnered hundreds of citations. The Twitter handle PSB 2017 is @PacSymBiocomp and the hashtag this year will be #psb17.

The efforts of a dedicated group of session organizers have produced an outstanding program. The sessions of PSB 2017 and their hard- working organizers are as follows:

Computational approaches to understanding the evolution of molecular function
Yana Bromberg, Matthew Hahn, and Predrag Radivojac

Imaging Genomics
Li Shen and Lee Cooper

Methods to Ensure the Reproducibility of Biomedical Research
Konrad J. Karczewski, Nicholas P. Tatonetti, Chirag J. Patel, Arjun K. Manrai, C. Titus Brown, and John P.A. Ioannidis

Patterns in Biomedical Data - How do we find them?
Anurag Verma, Anna Okula Basile, Marta Byrska-Bishop, Christian Darabos, H. Lester Kirchner, and Sarah Pendergrass

Precision medicine: from genotypes and molecular phenotypes towards improved health and therapies
Bruce Aronow, Steven E. Brenner, Dana C. Crawford, Joshua C. Denny, Sean D. Mooney, and Alexander A. Morgan

Single-cell analysis and modelling of cell population heterogeneity
Nikolay Samusik, Sean Bendall, and Nima Aghaeepour

We are also pleased to present four workshops in which investigators with a common interest come together to exchange results and new ideas in a format that is more informal than the peer-reviewed sessions. For this year, the workshops and their organizers are:

Harnessing Big Data for Precision Medicine: Infrastructures and Applications
Kun-Hsing Yu, Steven Hart, Rachel Goldfeder, Qiangfeng Cliff Zhang, Stephen Parker, and Michael Snyder

The Making of Next Generation Data Scientists in Biomedicine
Lana Garmire, Shamim Nemati, John D. Van Horn, Jason Moore, Carole Shreffler and Michelle Dunn

No-Boundary Thinking in Bioinformatics
Xiuzhen Huang and Jason H. Moore

Open Data for Discovery Science
Philip R.O. Payne, Kun Huang, Nigam H. Shah, and Jessica Tenenbaum

We thank our keynote speakers Neil Risch (Science keynote) and David Magnus (Ethical, Legal and Social Implications keynote). We also thank Jeffrey Drazen for his talk.

We look forward to a great meeting once again. Aloha!

Pacific Symposium on Biocomputing Co-Chairs,
October 15, 2016

Russ B. Altman
Departments of Bioengineering, Genetics & Medicine, Stanford University

A. Keith Dunker
Department of Biochemistry and Molecular Biology, Indiana University School of Medicine

Lawrence Hunter
Department of Pharmacology, University of Colorado Health Sciences Center

Marylyn D. Ritchie
Department of Biomedical and Translational Informatics, Geisinger Health System

Teri E. Klein
Department of Genetics, Stanford University

Thanks to the reviewers...