Pacific Symposium on Biocomputing (PSB) 2017 Schedule

January 3-7, 2017, Fairmont Orchid, Big Island of Hawaii

Monday, January 2, 2017
4:00 – 5:30 pm	Registration (Ballroom Prefunction)

Tuesday, January 3, 2017
7:30 – 9:30 am	Registration (Ballroom Prefunction)	
9:00 – Noon	Workshops	
9:00 – Noon	Harnessing Big Data for Presicistion Medicine: Infrastructure and Applications (Salon 2&3)	Organizers: Kun-Hsing Yu, Steven Hart, Rachel Goldfeder, Qiangfeng Cliff Zhang, Stephen Parker, and Michael Snyder
9:00 – Noon	The Making of Next Generation Data Scientists in Biomedicine (Plaza)	Organizers: Lana Garmire, Shamim Nemati, John D. Van Horn, Jason Moore, Carole Shreffler, and Michelle Dunn
Noon – 2:00 pm	Registration (Ballroom Prefunction)	
Noon – 1:30 pm	Break – Lunch on own	
1:30 – 4:30 pm	Workshops	
1:30 – 4:30 pm	Open Data for Discovery Science (Salon 2&3)	Organizers: Philip R.O. Payne, Kun Huang, Nigam H. Shah, and Jessica Tenenbaum
1:30 – 4:30 pm	No-Boundary Thinking in Bioinformatics (Plaza)	Organizers: Xiuzhen Huang and Jason H. Moore
4:30 – 5:30 pm	Working Group Meetings	
5:30 – 7:30 pm	Break – Dinner on own	
7:00 – 8:00 pm	Registration (Kilohana Room)	
7:30 – 8:30 pm	Reception – 22nd Anniversary Welcome Drink & Dessert Reception (Kilohana Room)	

Wednesday, January 4, 2017
7:30 – 9:00 am	Registration (Ballroom Prefunction)	
7:30 – 8:30 am	PSB Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Welcome (Salon 2&3)	
8:40 – 10:25 am	Session 1: Precision medicine: from genotypes and molecular phenotypes (Part 1) (Salon 2&3)	Co-chairs: Bruce Aronow, Steven Brenner, Dana Crawford, Josh Denny, Sean Mooney, Alexander Morgan
8:40 – 8:50 am	Introduction	
8:50 – 9:10 am	Invited Talk	**Joshua Denny**
9:10 – 9:25 am	Opening the Door to the Large Scale Use of Clinical Lab Measures for Association Testing: Exploring Different Methods for Defining Phenotypes	Christopher R. Bauer, Daniel R. Lavage, John Snyder, Joseph Leader, J. Matthew Mahoney, Sarah A. Pendergrass
9:25 – 9:40 am	Identifying Genetic Associations with Variability in Metabolic Health and Blood Count Laboratory Values: Diving into the Quantitative Traits by Leveraging Longitudinal Data from an HER	Shefali S. Verma, Anastasia M. Lucas, Daniel R. Lavage, Joseph B. Leader, Raghu Metpally, Sarathbabu Krishnamurthy, Frederick Dewey, Ingrid Borecki, Alexander Lopez, John Overton, John Penn, Jeffrey Reid, Sarah A. Pendergrass, Gerda Breitwieser, Marylyn D. Ritchie
9:40 – 9:55 am	Temporal Order of Disease Pairs Affects Subsequent Disease Trajectories: The Case of Diabetes and Sleep Apnea	Mette Beck, David Westergaard, Leif Groop and Soren Brunak
9:55 - 10:10 am	Strategies for Equitable Pharmacogenomic-Guided Warfarin Dosing Among European and African American Individuals in a Clinical Population	Laura Wiley, Jacob VanHouten, David Samuels, Melinda Aldrich, Dan Roden, Josh Peterson, Joshua Denny
10:10 – 10:25 am	De Novo Mutations in Autism Implicate the Synaptic Elimination Network	Guhan Ram Venkataraman, Chloe O'Connell, Fumiko Egawa, Dorna Kashef-Haghighi, Dennis Paul Wall
10:25 – 10:45 am	Break	
10:30 – 11:30 am	Registration (Ballroom Prefunction)	
10:45 – 11:45 am	Keynote: Neil Risch (Salon 2&3)	Introduction by Marilyn Ritchie

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

Wednesday, January 4 (cont.)

11:45 – 1:00 pm	PSB Hosted Lunch (Ballroom Courtyard)	
1:00 – 2:00 pm	Registration (Ballroom Prefunction)	
1:00 – 2:00 pm	Special Topics	
1:00 – 1:45 pm	Data Sharing in Clinical Trials	**Jeff Drazen**
1:45 – 2:00 pm	Research Parasite Awards	
2:05 – 3:50 pm	Session 2: Patterns in Biomedical Data - How do we find them? (Part 1) (Salon 2&3)	Co-chairs: Anurag Verma, Anna Okula Basile, Marta Byrska-Bishop, Christian Darabos, H. Lester Kirchner, and Sarah A. Pendergrass
2:05 – 2:15 pm	Introduction	
2:15 – 2:35 pm	Invited Talk	**Geoffrey H. Siwo**
2:35 – 2:50 pm	Predictive Modeling of Hospital Readmission Rates Using Electronic Medical Record-Wide Machine Learning: A Case-Study Using Mount Sinai Heart Failure Cohort	Khader Shameer, Kipp W. Johnson, Alexandre Yahi, Riccardo Miotto, Li Li, Doran Ricks, Jebakumar Jebakaran, Patricia Kovatch, Partho P. Sengupta, Annetine Gelijns, Alan Moskovitz, Bruce Darrow, David L. Reich, Andrew Kasarskis, Nicholas P. Tatonetti, Sean Pinney, Joel T. Dudley
2:50 – 3:05 pm	A New Relevance Estimator for the Compilation and Visualization of Disease Patterns and Potential Drug Targets	Modest von Korff, Tobias Fink, Thomas Sander
3:05 – 3:20 pm	Methods for Clustering Time Series Data Acquired from Mobile Health Apps	Nicole Tignor, Pei Wang, Nicholas Genes, Linda Rogers, Steven G. Hershman, Erick R. Scott, Micol Zweig, Yu-Feng Yvonne Chan, Eric E. Schadt
3:20 – 3:35 pm	Computer Aided Image Segmentation and Classification for Viable and Non-Viable Tumor Identification in Osteosarcoma	Harish Babu Arunachalam, Rashika Mishra, Bogdan Armaselu, Ovidiu Daescu, Maria Martinez, Patrick Leavey, Dinesh Rakheja, Kevin Cederberg, Anita Sengupta, Molly Ni'suilleabhain
3:35 – 3:50 pm	DeMo Dashboard: Visualizing and Understanding Genomic Sequences Using Deep Neural Networks	Jack Lanchantin, Ritambhara Singh, Beilun Wang, Yanjun Qi
4:00 – 4:30 pm	Meeting – ISCB Open Meeting (Salon 2&3)	
4:30 –	Break – Dinner on own	

Thursday, January 5, 2017

7:30 – 8:30 am	Registration (Ballroom Prefunction)	
7:30 – 8:30 am	PSB Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Morning Announcements (Salon 2&3)	
8:40 – 9:45 am	Session 2: Patterns in Biomedical Data – How do we find them? (Part 2) (Salon 2 & 3)	Co-chairs: Anurag Verma, Anna Okula Basile, Marta Byrska-Bishop, Christian Darabos, H. Lester Kirchner, and Sarah Pendergrass
8:40 – 8:45 am	Introduction	
8:45 – 9:00 am	Learning Attributes of Disease Progression from Trajectories of Sparse Lab Values	Vibhu Agarwal, Nigam H. Shah
9:00 – 9:15 am	Discovery of Functional and Disease Pathways by Community Detection in Protein-Protein Interaction Networks	Stephen J. Wilson, Angela D. Wilkins, Chih-Hsu Lin, Rhonald C. Lua, Olivier Lichtarge
9:15 – 9:30 am	Missing Data Imputation in the Electronic Health Record Using Deeply Learned Autoencoders	Brett K. Beaulieu-Jones, Jason H. Moore, The Pooled Resource Open-Access ALS Clinical Trials Consortium
9:30 – 9:45 am	Development and Performance of Text-Mining Algorithms to Extract Socioeconomic Status from De-Identified Electronic Health Records	Brittany M. Hollister, Nicole A. Restrepo, Eric Farber-Eger, Dana C. Crawford, Melinda C. Aldrich, Amy Non
9:45 – 10:00 am	Break	
10:00 – 11:05 am	Session 1: Precision Medicine: from Genotypes and Molecular Phenotypes (Part 2) (Salon 2&3)	Co-chairs: Bruce Aronow, Steven Brenner, Dana C. Crawford, Joshua Denny, Sean D. Mooney, Alexander Morgan
10:00 – 10:05 am	Introduction	

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

Thursday, January 5 (cont.)

10:05 – 10:20 am	MUSE: A Multi-locus Sampling-based Epistasis Algorithm for Quantitative Genetic Trait Prediction	Dan He, Laxmi Parida
10:20 -10:35 am	Human Kinases Display Mutational Hotspots at Cognate Positions Within Cancer	Jonathan Gallion, Angela D. Wilkins, Olivier Lichtarge
10:35 – 10:50 am	A Methylation-to-Expression Feature Model for Generating Accurate Prognostic Risk Scores and Identifying Disease Targets in Clear Cell Kidney Cancer	Jeffrey A. Thompson, Carmen J. Marsit
10:50 – 11:05 am	Differential Pathway Dependency Discovery Associated with Drug Response across Cancer Cell Lines	Gil Speyer, Divya Mahendra, Hai J. Tran, Jeff Kiefer, Stuart L. Schreiber, Paul A. Clemons, Harshil Dhruv, Michael Berens, Seungchan Kim
11:00 – 12:10 pm	Discussion Session	
11:00 – 12:10 pm	Precision medicine: from genotypes and molecular phenotypes (Salon 2&3) Patterns in Biomedical Data - How do we find them? (Plaza)	
12:10 – 2:15 pm	Poster Session with Lunch Salon1 and Ballroom Courtyard	ODD numbered boards presented from 12:45-1:30 EVEN numbered boards presented from 1:30-2:15
2:30 – 5:30 pm	Working Group Meetings	
2:30 –	Break – Afternoon, Dinner and evening on your own	

Friday, January 6, 2017

7:30 – 8:30 am	PSB Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Morning Announcements (Salon 2&3)	
8:40 – 10:05 am	Session 3: Methods to Ensure the Reproducibility of Biomedical Research (Salon 2&3)	Co-chairs: Konrad J. Karczewski, Nicholas Tatonetti, Chirag Patel, Arjun Manrai, C. Titus Brown, and John Ioannidis
8:40 – 8:50 am	Introduction	
8:50 – 9:05 am	Exploring the Reproducibility of Probabilistic Causal Molecular Network Models	Ariella Cohain, Aparna A. Divaraniya, Kuixi Zhu, Joseph R. Scarpa, Andrew Kasarskis, Jun Zhu, Rui Chang, Joel T. Dudley, Eric E. Schadt
9:05 – 9:20 am	Reproducible Drug Repurposing: When Similarity Does Not Suffice	Emre Guney
9:20 – 9:35 am	Empowering Multi-Cohort Gene Expression Analysis to Increase Reproducibility	Winston A. Haynes, Francesco Vallania, Charles Liu, Erika Bongen, Aurelie Tomczak, Marta Andres-Terrè, Shane Lofgren, Andrew Tam, Cole A. Deisseroth, Matthew D. Li, Timothy E.Sweeney, Purvesh Khatri
9:35 – 9:50 am	Rabix: An Open-Source Workflow Executor Supporting Recomputability and Interoperability of Workflow Descriptions	Gaurav Kaushik, Sinisa Ivkovic, Janko Simonovic, Nebojsa Tijanic, Brandi Davis-Dusenbery, Deniz Kural
9:50 – 10:05 am	Data sharing and clinical genetic testing: Successes and Challenges	Shan Yang, Melissa Cline, Can Zhang, Benedict Paten, Stephen E. Lincoln
10:10 –11:25 am	Session 4: Imaging Genomics (Salon 2&3)	Co-Chairs: Li Shen and Lee Cooper
10:10 –10:20 am	Introduction	
10:20 – 10:40 am	Invited Speaker	**Paul Thompson**
10:40 – 10:55 am	Integrative Analysis for Lung Adenocarcinoma Predicts Morphological Features Associated with Genetic Variations	Chao Wang, Hai Su, Lin Yang, Kun Huang
10:55 – 11:10 am	Identification of Discriminative Imaging Proteomics Associations in Alzheimer's Disease via a Novel Sparse Correlation Model	Jingwen Yan, Shannon L. Risacher, Kwangsik Nho, Andrew J. Saykin, Li Shen
11:10 – 11:25 am	Enforcing Co-expression in Multimodal Regression Framework	Pascal Zille, Vince D. Calhoun, Yu-Ping Wang

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

Friday, January 6 (cont.)

11:30 – 12:30 pm	Discussion Sessions	
11:30 – 12:30 pm	Methods to Ensure the Reproducibility of Biomedical Research (Salon 2&3)	
11:30 – 12:30 pm	Imaging Genomics (Plaza)	
12:30 – 2:00 pm	Break – Lunch on own	
2:00 – 5:00 pm	Working Group Meetings	
5:30 – 7:30 pm	Dinner Party (Coconut Grove)	
7:30 – 8:45 pm	Keynote: David Magnus (Salon 2&3)	Introduction by Russ Altman

Saturday, January 7, 2017

7:30 – 8:30 am	Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Closing Announcements (Salon 2&3)	
8:40 – 9:55 am	Session 5: Single-cell analysis and modelling of cell population heterogeneity (Salon 2&3)	Co-chairs: Nikolay Samusik, Sean Bendall, and Nima Aghaeepour
8:40 – 8:50 am	Introduction	
8:50 – 9:10 am	Invited Speaker	**Nikesh Kotecha**
9:10 – 9:25 am	Production of a Preliminary Quality Control Pipeline for Single Nuclei RNA-Seq and Its Application in the Analysis of Cell Type Diversity of Post-Mortem Human Brain Neocortex	Brian Aevermann, Jamison Mccorrison, Pratap Venepally, Rebecca Hodge, Trygve Bakken, Jeremy Miller, Mark Novotny, Danny N. Tran, Francisco Diez-Fuertes, Lena Christiansen, Fan Zhang, Frank Steemers, Roger S. Lasken, Ed Lein, Nicholas Schork, Richard H. Scheuermann
9:25 – 9:40 am	An Updated Debarcoding Tool for Mass Cytometry with Cell Type-Specific and Cell Sample-Specific Stringency Adjustment	Kristin I. Fread, William D. Strickland, Garry P. Nolan, Eli R. Zunder
9:40 – 9:55 am	Tracing Co-Regulatory Network Dynamics in Noisy, Single-Cell Transcriptome Trajectories	Pablo Cordero, Joshua M. Stuart
10:00 – 11:25 am	Session 6: Computational approaches to understanding the evolution of molecular function (Salons 2&3)	Co-chairs: Yana Bromberg, Matthew Hahn, and Predrag Radivojac
10:00 – 10:10 am	Introduction	
10:10 – 10:30 am	Invited Speaker	**Joe Thorton**
10:30 – 10:45 am	Identification and Analysis of Bacterial Genomic Metabolic Signatures	Nathan Bowerman, Nathan Tintle, Matthew DeJongh, Aaron A. Best
10:45 – 11:00 am	When should we NOT transfer functional annotation between sequence paralogs?	Mengfei Cao, Lenore J. Cowen
11:00 – 11:10 am	ProSNet: integrating homology with molecular networks for protein function prediction	Sheng Wang, Meng Qu, Jian Peng
11:10 – 11:25 am	On the power and limits of sequence similarity based clustering of proteins into families	Christian Wiwie, Richard Röttger
11:30 – 12:30 pm	Discussion Sessions (Salon 2&3)	
11:30 – 12:30 pm	Single-cell analysis and modelling of cell population heterogeneity (Plaza)	
11:30 – 12:30 pm	Computational approaches to understanding the evolution of molecular function (Salon 2&3)	

PSB over—see you next year!!

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.