

# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

January 3-7, 2017, Big Island of Hawaii

## Monday, January 2, 2017

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### Registration

4:00-5:30pm Registration

Ballroom Prefunction

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## Tuesday, January 3, 2017

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### Registration

7:30-9:30am Registration

Ballroom Prefunction

12:00-2:00pm Registration

Ballroom Prefunction

7:00-8:00pm Registration

Kilohana Room

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### Workshops

9:00-12:00 Harnessing Big Data for Precision Medicine: Infrastructure and Applications [Salon 2&3](#)

Organizers: Kun-Hsing Yu, Steven Hart, Rachel Goldfeder, Qiangfeng Cliff Zhang, Stephen Parker, and Michael Snyder

9:00-12:00 The Making of Next Generation Data Scientists in Biomedicine [Plaza](#)

Organizers: Lana Garmire, Shamim Nemat, John D. Van Horn, Jason Moore, Carole Shreffler, and Michelle Dunn

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### Break

12:00-1:30 Lunch on own

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### Workshop

1:30-4:30 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 No-Boundary Thinking in Bioinformatics [Plaza](#)  
Organizers: Xiuzhen Huang and Jason H. Moore

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### Working Group Meetings

4:30-5:30

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### Break

5:30-7:30 Dinner on own

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### Reception

7:30-8:30 22<sup>nd</sup> Anniversary Reception with Drinks and Desserts

Sponsored by the Institute for Computational Biology, a collaborative effort of Case Western Reserve University, the Cleveland Clinic, and University of Hospitals of Cleveland and the Rxight Pharmacogenetics Program

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

16 December 2016

# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

January 3-7, 2017, Big Island of Hawaii

## Wednesday, January 4, 2017

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### Registration

7:30-9:00	Registration	Ballroom Prefunction
10:30-11:30	Registration	Ballroom Prefunction
1:00-2:00	Registration	Ballroom Prefunction

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### Breakfast

7:30-8:30	PSB Breakfast	Ballroom Courtyard
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### Welcome

8:30-8:40	Welcome	Salon 2&3
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### Session 1: Precision medicine: from genotypes and molecular phenotypes (Part 1)

Co-chairs: Bruce Aronow, Steven Brenner, Dana Crawford, Josh Denny, Sean Mooney, Alexander Morgan

8:40-8:50	Introduction	
8:50-9:10	Invited Talk: Josh Denny	
9:10-9:25	<i>Opening the Door to the Large Scale Use of Clinical Lab Measures for Association Testing: Exploring Different Methods for Defining Phenotypes</i> Christopher R. Bauer, Daniel Lavage, John Snyder, Joseph Leader, J. Matthew Mahoney, Sarah A. Pendergrass	
9:25-9:40	<i>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</i> 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	<i>Temporal Order of Disease Pairs Affects Subsequent Disease Trajectories: The Case of Diabetes and Sleep Apnea</i> Mette Beck, David Westergaard, Leif Groop and Soren Brunak	
9:55-10:10	<i>Strategies for Equitable Pharmacogenomic-Guided Warfarin Dosing Among European and African American Individuals in a Clinical Population</i> Laura Wiley, Jacob VanHouten, David Samuels, Melinda Aldrich, Dan Roden, Josh Peterson, Joshua Denny	
10:10-10:25	<i>De Novo Mutations in Autism Implicate the Synaptic Elimination Network</i> Guhan Ram Venkataraman, Chloe O'Connell, Fumiko Egawa, Dorna Kashef-Haghighi, Dennis Paul Wall	

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### Break

10:25-10:45

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### Keynote

10:45-11:45	Neil Risch with introduction by Marylyn Ritchie	Salon 2&3
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### Lunch

11:45-1:00	PSB Hosted Lunch	Ballroom Courtyard
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# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

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## Wednesday, January 4, 2017 (continued)

<b>Special Topics</b>		<b>Salon 2&amp;3</b>
1:00-1:45	Jeff Drazen, <i>Data Sharing in Clinical Trials</i>	
1:45-2:00	Research Parasite Awards	
<b>Session 2:</b>	<b>Patterns in Biomedical Data - How do we find them? (Part 1)</b>	<b>Salon 2&amp;3</b>
	Co-chairs: Anurag Verma, Anna Okula Basile, Marta Byrska-Bishop, Christian Darabos, H. Lester Kirchner, and Sarah Pendergrass	
2:05-2:15	Introduction	
2:15-2:35	Invited Talk: Geoffrey H. Siwo	
2:35-2:50	<i>Predictive Modeling of Hospital Readmission Rates Using Electronic Medical Record-Wide Machine Learning: A Case-Study Using Mount Sinai Heart Failure Cohort</i> Khader Shameer, Kipp W. Johnson, Alexandre Yahy, 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	<i>A New Relevance Estimator for the Compilation and Visualization of Disease Patterns and Potential Drug Targets</i> Modest von Korff, Tobias Fink, Thomas Sander	
3:05-3:20	<i>Methods for Clustering Time Series Data Acquired from Mobile Health Apps</i> 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	<i>Computer Aided Image Segmentation and Classification for Viable and Non-Viable Tumor Identification in Osteosarcoma</i> 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	<i>DeMo Dashboard: Visualizing and Understanding Genomic Sequences Using Deep Neural Networks</i> Jack Lanchantin, Ritambhara Singh, Beilun Wang, Yanjun Qi	
<b>Meeting</b>		<b>Salon 2&amp;3</b>
4:00-4:30	ISCB Open Meeting	
4:30	Dinner on own	

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# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

January 3-7, 2017, Big Island of Hawaii

## Thursday, January 5, 2017

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### Registration

7:30-8:30 Registration Ballroom Prefunction

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### Breakfast

7:30-8:30 PSB Breakfast Ballroom Courtyard

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### Announcements

8:30-8:40 Morning Announcements Salon 2&3

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### Session 2: Patterns in Biomedical Data - How do we find them? (Part 2) Salon 2&3

8:40-8:45 Introduction

8:45-9:00 *Learning Attributes of Disease Progression from Trajectories of Sparse Lab Values*

Vibhu Agarwal, Nigam H. Shah

9:00-9:15 *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 *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 *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

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### Break

9:45-10:00

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### Session 1: Precision medicine: from genotypes and molecular phenotypes (Part 2) Salon 2&3

10:00-10:05 Introduction

10:05-10:20 *MUSE: A Multi-locus Sampling-based Epistasis Algorithm for Quantitative Genetic Trait Prediction*

Dan He, Laxmi Parida

10:20-10:35 *Human Kinases Display Mutational Hotspots at Cognate Positions Within Cancer*

Jonathan Gallion, Angela D. Wilkins, Olivier Lichtarge

10:35-10:50 *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 *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

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# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

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## Thursday, January 5, 2017 (continued)

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### Discussion Session

11:10-12:10 Precision medicine: from genotypes and molecular phenotypes [Salon 2&3](#)

11:10-12:10 Patterns in Biomedical Data - How do we find them? [Plaza](#)

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### Poster Session Lunch

[Salon 1 and Ballroom Courtyard](#)

12:10-2:15 Poster Session with Lunch

(Posters on ODD numbered boards presented from 12:45-1:30)

(Posters on EVEN numbered boards presented from 1:30-2:15)

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### Working Group Meetings

2:30-5:30

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### Break

2:30- Afternoon, Dinner & Evening on own

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# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

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## Friday, January 6, 2017

<b>Breakfast</b>		<b>Ballroom Courtyard</b>
7:30-8:30	PSB Breakfast	
<b>Announcements</b>		<b>Salon 2&amp;3</b>
8:30-8:40	Morning Announcements	
<b>Session 3:</b>	<b>Methods to Ensure the Reproducibility of Biomedical Research</b>	<b>Salon 2&amp;3</b>
	Co-chairs: Konrad J. Karczewski, Nicholas Tatonetti, Chirag Patel, Arjun Manrai, C. Titus Brown, and John Ioannidis	
8:40-8:50	Introduction	
8:50-9:05	<i>Exploring the Reproducibility of Probabilistic Causal Molecular Network Models</i>	
	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	<i>Reproducible Drug Repurposing: When Similarity Does Not Suffice</i>	
	Emre Guney	
9:20-9:35	<i>Empowering Multi-Cohort Gene Expression Analysis to Increase Reproducibility</i>	
	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	<i>Rabix: An Open-Source Workflow Executor Supporting Recomputability and Interoperability of Workflow Descriptions</i>	
	Gaurav Kaushik, Sinisa Ivkovic, Janko Simonovic, Nebojsa Tijanic, Brandi Davis-Dusenbery, Deniz Kural	
9:50-10:05	<i>Data sharing and clinical genetic testing: Successes and Challenges</i>	
	Shan Yang, Melissa Cline, Can Zhang, Benedict Paten, Stephen E. Lincoln	
<b>Session 4:</b>	<b>Imaging Genomics</b>	<b>Salon 2&amp;3</b>
	Co-chairs: Li Shen and Lee Cooper	
10:10-10:20	Introduction	
10:20-10:40	Invited Speaker: Paul Thompson	
10:40-10:55	<i>Integrative Analysis for Lung Adenocarcinoma Predicts Morphological Features Associated with Genetic Variations</i>	
	Chao Wang, Hai Su, Lin Yang, Kun Huang	
10:55-11:10	<i>Identification of Discriminative Imaging Proteomics Associations in Alzheimer's Disease via a Novel Sparse Correlation Model</i>	
	Jingwen Yan, Shannon L. Risacher, Kwangsik Nho, Andrew J. Saykin, Li Shen	
11:10-11:25	<i>Enforcing Co-expression in Multimodal Regression Framework</i>	
	Pascal Zille, Vince D. Calhoun, Yu-Ping Wang	
<b>Discussion Sessions</b>		
11:30-12:30	Methods to Ensure the Reproducibility of Biomedical Research	<b>Salon 2&amp;3</b>
11:30-12:30	Imaging Genomics	<b>Plaza</b>

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# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

January 3-7, 2017, Big Island of Hawaii

## Friday, January 6, 2017 (continued)

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### Break

12:30-2:00 Lunch on Own

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### Working Group Meetings

2:00-5:00

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### Dinner

5:30-7:30 Dinner Party

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Coconut Grove

### Keynote

7:30-8:45 *David Magnus with introduction by Russ Altman*

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Salon 2&3

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# Pacific Symposium on Biocomputing (PSB) 2017 Schedule

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## Saturday, January 7, 2017

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Breakfast		Ballroom Courtyard
7:30-8:30	Breakfast	
Closing		Salon 2&3
8:30-8:40	Closing Announcements	
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	Introduction	
8:50-9:10	Invited Speaker: Nikesh Kotecha	
9:10-9:25	<i>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</i> Brian Aevertmann, 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, <u>Richard H. Scheuermann</u>	
9:25-9:40	<i>An Updated Debarcoding Tool for Mass Cytometry with Cell Type-Specific and Cell Sample-Specific Stringency Adjustment</i> Kristin I. Fread, William D. Strickland, Garry P. Nolan, <u>Eli R. Zunder</u>	
9:40-9:55	<i>Tracing Co-Regulatory Network Dynamics in Noisy, Single-Cell Transcriptome Trajectories</i> Pablo Cordero, Joshua M. Stuart	
Session 6:	Computational approaches to understanding the evolution of molecular function	Salon 2&3
	Co-chairs: Yana Bromberg, Matthew Hahn, and Predrag Radivojac	
10:00-10:10	Introduction	
10:10-10:30	Invited Speaker: Joe Thornton	
10:30-10:45	<i>Identification and Analysis of Bacterial Genomic Metabolic Signatures</i> Nathan Bowerman, Nathan Tintle, Matthew DeJongh, <u>Aaron A. Best</u>	
10:45-11:00	<i>When should we NOT transfer functional annotation between sequence paralogs?</i> Mengfei Cao, <u>Lenore J. Cowen</u>	
11:00-11:10	<i>ProSNet: integrating homology with molecular networks for protein function prediction</i> <u>Sheng Wang</u> , Meng Qu, Jian Peng	
11:10-11:25	<i>On the power and limits of sequence similarity based clustering of proteins into families</i> Christian Wiwie, Richard Röttger	
Discussion Sessions		
11:30-12:30	Single-cell analysis and modelling of cell population heterogeneity	Plaza
11:30-12:30	Computational approaches to understanding the evolution of molecular function	Salon 2&3

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**PSB over--see you next year!**

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