Pacific Symposium on Biocomputing (PSB) 2018 Schedule

January 3-7, 2018, Fairmont Orchid, Big Island of Hawaii

Wednesday, January 3, 2018

7:30 – 9:30 am	Registration (Ballroom Prefunction)	
9:00 – Noon	Workshop	
9:00 – Noon	Machine Learning and Deep Analytics for Biocomputing: Call for Better Explainability (Salon 2&3)	Organizers: Dragutin Petkovic, Lester Kobzik, Christopher Re
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	Integrating Community-level Data Resources for Precision Medicine Research (Salon 2&3)	Organizers: Dana C. Crawford, William S. Bush
1:30 – 4:30 pm	Metods for Examining Data Quality in Healthcare Integrated Data Pepositories (Plaza)	Organizers: Vojtech Huser, Michael Kahn, and Jeffrey Brown
4:30 – 7:30 pm	Break – Dinner on own	
7:30 – 8:30 pm	Registration (Kilohana Room)	
7:30 – 8:30 pm	Reception – 23rd Anniversary Welcome Drink & Dessert Reception (Kilohana Room)	

Thursday, January 4, 2018

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: Applications of Genetics, Genomics and Bioinformatics in Drug Discovery (Salon 2&3)	Co-chairs: Richard Bourgon, Rick Dewey, Zhengyan Kan, Dan Li
8:40 – 8:50 am	Introduction	
8:50 – 9:10 am	Invited Talk	**Rick Dewey**
9:10 – 9:25 am	Large-scale integration of heterogeneous pharmacogenomic data for identifying drug mechanism of action	Yunan Luo, Sheng Wang, Jinfeng Xiao, Jian Peng
9:25 – 9:40 am	Cell-specific prediction and application of drug-induced gene expression profiles	Rachel Hodos, Ping Zhang, Hao-Chih Lee, Qiaonan Duan, Zichen Wang, Neil R. Clark, Avi Ma'ayan, Fei Wang, Brian Kidd, Jianying Hu, David Sontag, Joel Dudley
9:40 – 9:55 am	Characterization of drug-induced splicing complexity in prostate cancer cell line using long read technology	Xintong Chen, Sander Houten, Kimaada Allette, Robert P. Sebra, Gustavo Stolovitzky, Bojan Losic
9:55 - 10:10 am	Chemical Reaction Vector Embeddings: Towards Predicting Drug Metabolism in the Human Gut Microbiome	Emily K. Mallory, Ambika Acharya, Stefano E. Rensi, Peter J Turnbaugh, Roselie A. Bright, Russ B. Altman
10:10 – 10:25 am	Extracting a Biologically Relevant Latent Space from Cancer Transcriptomes with Variational Autoencoders	Gregory P. Way, Casey S. Greene
10:25 – 10:45 am	Break	
10:30 – 11:30 am	Registration (Ballroom Prefunction)	
10:45 – 11:45 am	Keynote: Carlos Bustamante (Salon 2&3)	Introduction by Russ Altman
11:45 – 1:00 pm	PSB Hosted Lunch (Ballroom Courtyard)	
12:00 – 1:00 pm	Registration (Ballroom Prefunction)	
1:00 – 2:30 pm	Session 2: Imaging Genomics (Salon 2&3)	Co-chairs: Heng Huang, Junzhou Huang, Kun Huang, Li Shen, Paul M. Thompson, Lin Yang
1:00 – 1:10 pm	Introduction	
1:10 – 1:30 pm	Invited Talk	**Mert Sabuncu**
1:30 – 1:45 pm	Condon Bias Among Synonymous Rare Variants is Associated with Alzheimer's Disease Imaging Biomarker	Jason E. Miller, Manu K. Shivakumar, Shannon L. Risacher, Andrew J. Saykin, Seunggeun Lee, Kwangsik Nho, Dokyoon Kim
1:45 – 2:00 pm	Deep Integrative Analysis for Survival Prediction	Chenglong Huang, Albert Zhang, Guanghua Xiao
2:00 – 2:15 pm	Discriminative Bag-of-Cells for Imaging-Genomics	Benjamin Chidester, Minh N. Do, Jian Ma
2:15 – 2:30 pm	Genotype-Phenotype Association Study via New Multi-Task Learning Model	Zhouyuan Huo, Dinggang Shen, Heng Huang

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Thursday, January 4 (cont.)

2:30 – 3:00 pm	Special Topics: Parasite & Symbiont Awards (Salon 2&3)	
3:00 – 5:00 pm	Discussion Topis:	
3:00 – 4:00 pm	Imaging Genomics (Salon 2&3)	
4:00 – 5:00 pm	Applications of Genetics, Genomics and Bioinformatics in Drug Discovery (Salon 2&3)	
5:00 – 5:30 pm	Meeting - ISCB Meeting (Salon 2&3)	
5:30 –	Break – Dinner on own	

Friday, January 5, 2018

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 – 10:50 am	Session 3: Precision Medicine: from diplotypes to disparities towards improved health and therapies (Salon 2 & 3)	Co-chairs: Bruce Aronow, Steven E. Brenner, Dana C. Crawford, Joshua C. Denny, Alexander A. Morgan
8:40 – 8:45 am	Introduction	
8:45 – 9:05 am	Invited Talk	**Vence Bonham**
9:05 – 9:20 am	Considerations for automated machine learning in clinical metabolic profiling: altered homocysteine plasma concentration associated with metformin exposure	Alena Orlenko, Jason H. Moore, Patryk Orzechowski, Randal S. Olson, Junmei Cairns, Pedro J. Caraballo, Richard M. Weinshilboum, Liewei Wang, <u>Matthew K. Breitenstein</u>
9:20 – 9:35 am	Analyzing metabolomics data for association with genotypes using two-component gaussian mixture distributions	<u>Jason Westra</u>, Nicholas Hartman, Bethany Lake, Gregory Shearer, Nathan Tintle
9:35 – 9:50 am	Single subject transcriptome analysis to identify functionally signed gene set or pathway activity	<u>Joanne Berghout</u>, Qike Li, Nima Pouladi, Jianrong Li, Yves A Lussier
9:50 – 10:05 am	Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses	Samir Rachid Zaim, Qike Li, A. Grant Schissler, <u>Yves A. Lussier</u>
10:05 – 10:20 am	Coalitional game theory as a promising approach to identify candidate autism genes	Anika Gupta, Min Woo Sun, Kelley M. Paskov, Nate T. Stockham, Jae-Yoon Jung, <u>Dennis P. Wall</u>
10:20 – 10:35 am	Using simulation and optimization approach to improve outcome through warfarin precision treatment	<u>Chih-Lin Chi</u>, Lu He, Kourosh Ravvaz, John Weissert, Peter J. Tonellato
10:35 – 10:50 am	Addressing vital sign alarm fatigue using personalized alarm thresholds	<u>Sarah Poole</u>, Nigam Shah
11:00 – Noon	Discussion Session Precision Medicine: from diplotypes to disparities towards improved health and therapies phenotypes (Salon 2&3)	
Noon – 2:30 pm	Poster Session with Lunch Salon1 and Ballroom Courtyard	ODD numbered boards presented from 12:30-1:30 EVEN numbered boards presented from 1:30-2:30
2:30 – 4:05 pm	Session 4: Democratizing Health Data for Translational Research (Salon 2&3)	Co-chairs: Philip Payne, Nigam Shah, Jessie Tenenbaum, Lara Mangravite
2:30 – 2:40 pm	Introduction	
2:40 – 3:00 pm	Invited Talk	**Joe Corkery**
3:00 – 3:20 pm	Invited Talk	**John Wilbanks**
3:20 – 3:35 pm	ClinGen Cancer Somatic Working Group – Standardizing and Democratizing Access to Cancer Molecular Diagnostic Data to Drive Translational Research	<u>Subha Madhavan</u>, Deborah Ritter, Christine Micheel, Shruti Rao, Angshumoy Roy, Dmitriy Sonkin, Matthew McCoy, Malachi Griffith, Obi L Griffith, Peter Mcgarvey, Shashikant Kulkarni on Behalf of the ClinGen Somatic Working Group

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Friday, January 5 (cont.)

3:35 – 3:50 pm	Best Practices and Lessons Learned from Reuse of 4 Patientderived Metabolomics Datasets in Alzheimer's Disease	Jessica D. Tenenbaum, Colette Blach
3:50 – 4:05 pm	A Heuristic Method for Simulating Open-Data of Arbitrary Complexity that Can Be Used to Compare and Evaluate Machine Learning Methods	Jason H. Moore, Maksim Shestov, Peter Schmitt, Randal S. Olson
4:10 – 5:10 pm	Discussion Session: Democratizing Health Data for Translational Research (Salon 2&3)	
5:10 -	Break – Dinner & Evening on own	

Saturday, January 6, 2018

7:30 – 8:30 am	PSB Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Morning Announcements (Salon 2&3)	
8:40 – 10:55 am	Session 5: Challenges of Pattern Recognition in Biomedical Data (Salon 2&3)	Co-chairs: Anurag Verma, Anna Basile, Marta Byrska-Bishop, Christian Darabos, Shefali Setia Verma
8:40 – 8:50 am	Introduction	
8:50 – 9:10 am	Invited Talk	**Larry Smarr**
9:10 – 9:25 am	Functional Network Community Detection Can Disaggregate and Filter Multiple Underlying Pathways in Enrichment Analyses	Lia X. Harrington, Gregory P. Way, Jennifer A. Doherty, Casey S. Greene
9:25 – 9:40 am	Large-Scale Analysis of Disease Pathways in the Human Interactome	Monica Agrawal, Marinka Zitnik, Jure Leskovec
9:40 – 9:55 am	Data-driven Advice for Applying Machine Learning to Bioinformatics Problems	Randal S. Olson, William La Cava, Zairah Mustahsan, Akshay Varik, Jason H. Moore
9:55 – 10:10 am	Automated disease cohort selection using word embeddings from Electronic Health Records	Benjamin S. Glicksberg, Riccardo Miotto, Kipp W. Johnson, Khader Shameer, Li Li, Rong Chen, Joel T. Dudley
10:10 –10:25 am	Mapping Patient Trajectories using Logitudinal Extraction and Deep Learning in the MIMIC-III Critical Care Database	Brett K. Beaulieu-Jones, Patryk Orzechowski, Jason H. Moore
10:25 –10:40 am	Casual Inference on Electronic Health Records to Assess Blood Pressure Treatment Targets: An Application of the Parametric G Formula	Kipp W. Johnson, Benjamin S. Glicksberg, Rachel Hodos, Khader Shameer, Joel T. Dudley
10:40 – 10:55 am	How Powerful Are Summary-Based Methods for Identifying Expression-Trait Associations Under Different Genetic Architectures?	Yogasudha Veturi, Marylyn D. Ritchie
11:00 – 12:15 pm	Keynote: Jennifer Wagner (Salon 2&3)	Introduction by Marylyn Richie
12:15 – 1:30 pm	Break – Lunch on own	
1:30 – 4:30 pm	Workshop: Diversity and Disparity in Biomedical Informatics (Salon 2&3)	Organizers: Philip R.O. Payne, William M. Southerland, S. Joshua Swamidass, Laura Wiley, and ClarLynda Williams-DeVane
4:30 – 5:30 pm	Discussion Session: Challenges of Pattern Recognition in Biomedical Data (Salon 2&3)	
5:30 – 7:30 pm	Hawaii Loa Luau (Plantation Estate)	

Sunday, January 7, 2018

7:30 – 8:30 am	Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Closing Announcements (Salon 2&3)	Co-chairs: Graciela Gonzalez, Casey Greene, Hongfang Liu, Abeed Sarker
8:40 – 10:15 am	Session 6: Advances in Text Mining and Visualization for Precision Medicine (Salon 2&3)	
8:40 – 8:50 am	Introduction	
8:50 – 9:10 am	Invited Talk	**Jason Moore**
9:10 – 9:30 am	Invited Talk	**Sophia Ananiadou**
9:30 – 9:45 am	VisAGE: Integrating External Knowledge into Electronic Medical Record Visualization	Edward W. Huang, Sheng Wang, ChengXiang Zhai
9:45 - 10:00 am	Annotating gene sets by mining large literature collections with protein networks	Sheng Wang, Jianzhu Ma, Michael Ku Yu, Fan Zheng, Edward W Huang, Jiawei Han, Jian Peng,Trey Ideker

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Sunday, January 7 (cont.)

Time	Title	Presenters
10:00 – 10:15 am	Improving Precision in Concept Normalization	Mayla Boguslav, K. Bretonnel Cohen, William A. Baumgartner Jr., Lawrence E. Hunter
10:20 – 11:35 am	Session 7: Reading Between the Genes: Computational Models to Discover Function and/or Clinical Utility from Noncoding DNA (Salon 2&3)	Co-chairs: Yves Lussier, Maricel Kann, Jason Moore, Kenneth Ramos, Joanne Berghout, Francesca Vitali
10:20 – 10:30 am	Introduction	
10:30 – 10:50 am	Invited Talk	**Martha Bulyk**
10:50 – 11:05 pm	*Network analysis of pseudogene-gene relationships: from pseudogene evolution to their functional potentials*	Travis S Johnson, Sihong Li, Johnathan R Kho, Kun Huang, Yan Zhang
11:05 – 11:20 pm	Convergent downstream candidate mechanisms of independent intergenic polymorphisms between co-classified diseases implicate epistasis among noncoding elements	Jiali Han, Jianrong Li, Ikbel Achour, Lorenzo Pesce, Ian Foster, Haiquan Li, Yves A. Lussier
11:20 – 11:30 am	*Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in type 2 diabetes GWAS*	Elisabetta Manduchi, Alessandra Chesi, Molly A. Hall, Struan F. A. Grant, Jason H. Moore
11:40 – 12:40 pm	Discussion Sessions (Salon 2&3) Reading Between the Genes: Computational Models to Discover Function and/or Clinical Utility from Noncoding DNA (Salon 2&3) Text Mining and Visualization for Precision Medicine (Kilohana)	

PSB over—see you next year!!

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