

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Thursday, January 3, 2019

Registration

7:30-9:30	Registration	Ballroom Prefunction
12:00-2:00	Registration	Ballroom Prefunction
7:00-8:00	Registration	Kilohana

Workshop

9:00-12:00	Merging Heterogeneous Data to Enable Knowledge Discovery Organizers: Tina Hernandez-Boussard, Michael Kahn	Salon 2&3
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Break

12:00-1:30	Lunch on own	
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Workshop

1:30-4:30	Translational informatics of population health: How large biomolecular and clinical datasets Organizers: Yves Lussier, Atul Butte, Jason Moore, Rong Chen, Haiquan Li	Salon 2&3
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Break

4:30-7:00	Dinner on own	
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Reception

7:00-8:00	24 th Anniversary Reception Sponsored by the Cleveland Institute for Computational Biology	Kilohana
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Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 18, 2018

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Friday, January 4, 2019

Registration

7:30-9:00	Registration	Ballroom Prefunction
10:30-11:30	Registration	Ballroom Prefunction
12:00-1:00	Registration	Ballroom Prefunction

Breakfast

7:30-8:45	PSB Breakfast	Ballroom Courtyard
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Welcome

8:30-8:40	Welcome	Salon 2&3
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Session 1

Salon 2&3

Pattern recognition in biomedical data: challenges in putting big data to work

Co-chairs: Shefali Setia Verma, Anurag Verma, Dokyoon Kim, Christian Darabos

8:40-8:50	Introduction
8:50-9:10	Invited Talk: Barbara Engelhardt
9:10-9:25	<i>The Effectiveness of Multitask Learning for Phenotyping with Electronic Health Records Data</i> <u>Daisy Yi Ding</u> , Chloe Simpson, Stephen Pfohl, Dave Kale, Kenneth Jung, Nigam Shah
9:25-9:40	<i>ODAL: A one-shot distributed algorithm to perform logistic regressions on electronic health records data from multiple clinical sites</i> Rui Duan, Mary Regina Boland, Jason Moore, <u>Yong Chen</u>
9:40-9:55	<i>PVC Detection Using a Convolutional Autoencoder and Random Forest Classifier</i> <u>Max Gordon</u> , Cranos Williams
9:55-10:10	<i>Removing Confounding Factors Associated Weights in Deep Neural Networks Improves the Prediction Accuracy for Healthcare Applications</i> <u>Haohan Wang</u> , Zhenglin Wu, Eric Xing
10:10-10:25	<i>DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM</i> <u>Yuexu Jiang</u> , Duolin Wang, Dong Xu
10:25-10:40	<i>Res2s2aM: Deep residual network-based model for identifying functional noncoding SNPs in trait-associated regions</i> <u>Zheng Liu</u> , Yao Yao, Qi Wei, Benjamin Weeder, Stephen Ramsey

Break

10:40-10:50

Keynote

Salon 2&3

10:50-12:00	Informatics for understanding drug response Russ Altman with introduction by Steven Brenner
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Lunch

Ballroom Courtyard

12:00-1:00	PSB Hosted Lunch
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Pacific Symposium on Biocomputing (PSB) 2019 Schedule

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Friday, January 4, 2019 (continued)

Session 1 (continued)

Salon 2&3

Pattern recognition in biomedical data: challenges in putting big data to work

Co-chairs: Shefali Setia Verma, Anurag Verma, Dokyoon Kim, Christian Darabos

1:00-1:10 Introduction to second half of session

1:10-1:25 *Bi-directional Recurrent Neural Network Models for Geographic Location Extraction in Biomedical Literature*

Arjun Magge, Davy Weissenbacher, Abeed Sarker, Matthew Scotch, Graciela Gonzalez-Hernandez

1:25-2:40 *PLATYPUS: A Multiple-View Learning Predictive Framework for Cancer Drug Sensitivity Prediction*

Kiley Graim, Verena Friedl, Kathleen E. Houlahan, Joshua Stuart

2:40-2:55 *Computational KIR copy number discovery reveals interaction between inhibitory receptor burden and survival*

Rachel Pyke, Raphael Genolet, Alexandre Harari, George Coukos, David Gfeller, Hannah Carter

2:55-3:10 *Implementing and Evaluating A Gaussian Mixture Framework for Identifying Gene Function from TnSeq Data*

Kevin Li, Rachel Chen, William Lindsey, Aaron Best, Matthew DeJongh, Christopher Henry, Nathan Tintle

3:10-3:25 *Extracting allelic read counts from 250,000 human sequencing runs in Sequence Read Archive*

Brian Tsui, Michelle Dow, Dylan Skola, Hannah Carter

3:25-3:40 *Semantic workflows for benchmark challenges: Enhancing comparability, reusability and reproducibility*

Arunima Srivastava, Ravali Adusumilli, Hunter Boyce, Daniel Garijo, Varun Ratnakar, Rajiv Mayani, Thomas Yu, Raghu Machiraju, Yolanda Gil, Parag Mallick

Discussion Session

Salon 2&3

3:40-4:40 **Pattern recognition in biomedical data: challenges in putting big data to work**

Working Group Meeting (all invited)

Salon 2&3

Writing bio-computational manuscripts with Manubot

Organizer: Daniel Himmelstein

Manubot is an open source tool for writing manuscripts on GitHub in markdown format. Attendees are encouraged to bring a laptop if they would like assistance setting up a manuscript during the last 40 minutes of the workshop.

Break

6:00- Dinner & Evening on own

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Saturday, January 5, 2019

Registration		Ballroom Prefunction
7:30-8:30	Registration	
Breakfast		Ballroom Courtyard
7:30-8:45	PSB Breakfast	
Announcements		Salon 2&3
8:30-8:40	Morning Announcements	
TERI Talks		Salon 2&3
8:40-9:10	Dennis Wall, Stanford University	
9:10-9:40	Marylyn Ritchie, University of Pennsylvania	
Session 2		Salon 2&3
	When biology gets personal: hidden challenges of privacy and ethics in biological big data	
	Co-chairs: Gamze Gürsoy, Arif Harmanci, Haixu Tang, Erman Ayday, Steven Brenner	
9:45-9:55	Introduction	
9:55-10:15	Invited Talk: Greg Hampikian	
10:15-10:30	<i>Leveraging summary statistics to make inferences about complex phenotypes in large biobanks</i>	
	Angela Gasdaska, Derek Friend, Rachel Chen, Jason Westra, Matthew Zawistowski, William Lindsey, <u>Nathan Tintle</u>	
10:30-10:45	<i>Protecting Genomic Data Privacy with Probabilistic Modeling</i>	
	<u>Sean Simmons</u> , Bonnie Berger, Cenk Sahinalp	
10:45-11:00	<i>Evaluation of patient re-identification using laboratory test orders and mitigation via latent space variables</i>	
	Kipp Johnson, <u>Jessica De Freitas</u> , Benjamin Glicksberg, Jason Bobe, Joel Dudley	
Discussion Session		Salon 2&3
11:00-12:00	When biology gets personal: hidden challenges of privacy and ethics in biological big data	
Poster Session Lunch		Salon 1 and Ballroom Courtyard
12:00-2:30	Poster Session with Lunch (Posters on ODD numbered boards presented from 12:30-1:30) (Posters on EVEN numbered boards presented from 1:30-2:30)	
Workshop		Salon 2&3
2:30-5:30	Text Mining and Machine Learning for Precision Medicine Organizers: Graciela Gonzalez, Hongfang Liu, Zhiyong Lu, Robert Leaman	
Meeting		Salon 2&3
5:30-6:00	ISCB Meeting	
Break		
6:00-	Dinner & Evening on own	

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Pacific Symposium on Biocomputing (PSB) 2019 Schedule

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Sunday, January 6, 2019

Breakfast		Ballroom Courtyard
7:30-8:45	PSB Breakfast	
Announcements		Salon 2&3
8:30-8:40	Morning Announcements	
Session 3		Salon 2&3
	Precision medicine: improving health through high-resolution analysis of personal data	
	Co-chairs: Steven Brenner, Martha Bulyk, Dana Crawford, Jill Mesirov, Alexander Morgan, Predrag Radivojac	
8:40-8:50	Introduction	
8:50-9:10	Invited Talk: John Witte	
9:10-9:25	<i>CrowdVariant: a crowdsourcing approach to classify copy number variants</i> <u>Peyton Greenside</u> , Justin Zook, Marc Salit, Madeleine Cule, Ryan Poplin, Mark DePristo	
9:25-9:40	<i>A repository of microbial marker genes related to human health and diseases for host phenotype prediction using microbiome data</i> <u>Wontack Han</u> , Yuzhen Ye	
9:40-9:55	<i>AICM: A Genuine Framework for Correcting Inconsistency Between Large Pharmacogenomics Datasets</i> <u>Zhiyue Tom Hu</u> , Yuting Ye, Patrick A. Newbury, Haiyan Huang, Bin Chen	
9:55-10:10	<i>Outgroup Machine Learning Approach Identifies Single Nucleotide Variants in Noncoding DNA Associated with Autism Spectrum Disorder</i> <u>Maya Varma</u> , Kelley Marie Paskov, Jae-Yoon Jung, Brianna Sierra Chrisman, Nate Tyler Stockham, Peter Yigitcan Washington, Dennis Paul Wall	
10:10-10:25	<i>Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network</i> <u>Xinyuan Zhang</u> , Yogasudha Veturi, Shefali Verma, William Bone, Anurag Verma, Anastasia Lucas, Scott Hebring, Joshua C. Denny, Ian Stanaway, Gail Jarvik, David Crosslin, Eric Larson, Laura Rasmussen-Torvik, Sarah A. Pendergrass, Jordan W. Smoller, Hakon Hakonarson, Patrick Sleiman, Chunhua Weng, David Fasel, Wei-Qi Wei, Iftikhar Kullo, Daniel Schaid, Wendy Chung, Marylyn Ritchie	
10:25-10:40	<i>Integrating RNA expression and visual features for immune infiltrate prediction</i> Derek Reiman, Lingdao Sha, Irvin Ho, Timothy Tan, Denise Lau, <u>Aly Khan</u>	
10:40-10:55	<i>Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms</i> <u>Francesca Vitali</u> , Joanne Berghout, Jungwei Fan, Jianrong Li, Qike Li, Haiquan Li, Yves Lussier	

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Sunday, January 6, 2019 (continued)

Session 3 (continued)		Salon 2&3
10:55-11:10	<i>An Optimal Policy for Patient Laboratory Tests in Intensive Care Units</i> Li-Fang Cheng, Niranjani Prasad, Barbara Engelhardt	
Discussion Session		Salon 2&3
11:10-12:10	Precision medicine: improving health through high-resolution analysis of personal data	
Break		
12:10-1:30	Lunch on Own	
Workshop		Salon 2&3
1:30-4:30	Reading between the genes: interpreting non-coding DNA in high-throughput Organizers: Joanne Berghout, Yves Lussier, Francesca Vitali, Martha Bulyk, Maricel Kann, Jason Moore	
Special Topics		
4:30-5:00	Parasite & Symbiont Awards	Salon 2&3
Break		
5:00-5:30	Break	
Dinner		Coconut Grove
5:30-7:15	PSB Dinner Banquet	
Keynote		Salon 2&3
7:30-8:30	Sex, Race, Nature, Genomics & AI: A values-laden hour in Hawaii Lawrence Hunter with introduction by Russ Altman	

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Monday, January 7, 2019

Breakfast		Ballroom Courtyard
7:30-8:30	Breakfast	
Closing		Salon 2&3
8:30-8:40	Closing Announcements	
TERI Talks		Salon 2&3
8:40-9:10	Graciela Gonzalez, University of Pennsylvania	
9:10-9:40	Keith Dunker, University of Indiana	
Session 4		Salon 2&3
	Single cell analysis, what is in the future?	
	Co-chairs: Lana X. Garmire, Guo-Cheng Yuan, Rong Fan, Gene Yeo, John Quackenbush	
9:45-9:55	Introduction	
9:55-10:15	Invited Talk: Zemin Zhang	
10:15-10:30	<i>LISA: Accurate reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data</i> Yang Chen, Yuping Zhang, <u>Zhengqing Ouyang</u>	
10:30-10:45	<i>Topological Methods for Visualization and Analysis of High Dimensional Single-Cell RNA Sequencing Data</i> <u>Tongxin Wang</u> , Travis Johnson, Jie Zhang, Kun Huang	
10:45-11:00	<i>Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics</i> <u>Qiwen Hu</u> , Casey Greene	
Discussion Session		Salon 2&3
11:00-12:00	Single cell analysis, what is in the future?	

PSB over--see you next year!

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