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		Salon 2&3
9:00-12:00	**Merging Heterogeneous Data to Enable Knowledge Discovery** Organizers: Tina Hernandez-Boussard, Michael Kahn	
Break		
12:00-1:30	Lunch on own	
Workshop		Salon 2&3
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	
Break		
4:30-7:00	Dinner on own	
Reception		Kilohana
7:00-8:00	24th Anniversary Reception Sponsored by the Cleveland Institute for Computational Biology	

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

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 — Ballroom Courtyard

7:30-8:45 PSB Breakfast

Welcome — Salon 2&3

8:30-8:40 Welcome

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 *The Effectiveness of Multitask Learning for Phenotyping with Electronic Health Records Data*
Daisy Yi Ding, Chloe Simpson, Stephen Pfohl, Dave Kale, Kenneth Jung, Nigam Shah

9:25-9:40 *ODAL: A one-shot distributed algorithm to perform logistic regressions on electronic health records data from multiple clinical sites*
Rui Duan, Mary Regina Boland, Jason Moore, Yong Chen

9:40-9:55 *PVC Detection Using a Convolutional Autoencoder and Random Forest Classifier*
Max Gordon, Cranos Williams

9:55-10:10 *Removing Confounding Factors Associated Weights in Deep Neural Networks Improves the Prediction Accuracy for Healthcare Applications*
Haohan Wang, Zhenglin Wu, Eric Xing

10:10-10:25 *DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM*
Yuexu Jiang, Duolin Wang, Dong Xu

10:25-10:40 *Res2s2aM: Deep residual network-based model for identifying functional noncoding SNPs in trait-associated regions*
Zheng Liu, 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

Lunch — Ballroom Courtyard

12:00-1:00 PSB Hosted Lunch

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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
1:25-1:40	*PLATYPUS: A Multiple–View Learning Predictive Framework for Cancer Drug Sensitivity Prediction* Kiley Graim, Verena Friedl, Kathleen E. Houlahan, Joshua Stuart
1:40-1:55	*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
2:55-2:10	*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
2:10-2:25	*Extracting allelic read counts from 250,000 human sequencing runs in Sequence Read Archive* Brian Tsui, Michelle Dow, Dylan Skola, Hannah Carter
2:25-2:40	*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

2:40-3:40	**Pattern recognition in biomedical data: challenges in putting big data to work**

Working Group Meeting (all invited) — Salon 2&3

3:45-5:00	**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

5:00-	Dinner & Evening on own

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	*Leveraging summary statistics to make inferences about complex phenotypes in large biobanks* Angela Gasdaska, Derek Friend, Rachel Chen, Jason Westra, Matthew Zawistowski, William Lindsey, Nathan Tintle	
10:30-10:45	*Protecting Genomic Data Privacy with Probabilistic Modeling* Sean Simmons, Bonnie Berger, Cenk Sahinalp	
10:45-11:00	*Evaluation of patient re-identification using laboratory test orders and mitigation via latent space variables* Kipp Johnson, Jessica De Freitas, 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		
5:30-6:00	~~ISCB Meeting~~ Cancelled	Salon 2&3
Break		
6:00-	Dinner & Evening on own	

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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	*CrowdVariant: a crowdsourcing approach to classify copy number variants* Peyton Greenside, Justin Zook, Marc Salit, Madeleine Cule, Ryan Poplin, Mark DePristo	
9:25-9:40	*A repository of microbial marker genes related to human health and diseases for host phenotype prediction using microbiome data* Wontack Han, Yuzhen Ye	
9:40-9:55	*AICM: A Genuine Framework for Correcting Inconsistency Between Large Pharmacogenomics Datasets* Zhiyue Tom Hu, Yuting Ye, Patrick A. Newbury, Haiyan Huang, Bin Chen	
9:55-10:10	*Outgroup Machine Learning Approach Identifies Single Nucleotide Variants in Noncoding DNA Associated with Autism Spectrum Disorder* Maya Varma, Kelley Marie Paskov, Jae-Yoon Jung, Brianna Sierra Chrisman, Nate Tyler Stockham, Peter Yigitcan Washington, Dennis Paul Wall	
10:10-10:25	*Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network* Xinyuan Zhang, Yogasudha Veturi, Shefali Verma, William Bone, Anurag Verma, Anastasia Lucas, Scott Hebbring, 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	*Integrating RNA expression and visual features for immune infiltrate prediction* Derek Reiman, Lingdao Sha, Irvin Ho, Timothy Tan, Denise Lau, Aly Khan	
10:40-10:55	*Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms* Francesca Vitali, Joanne Berghout, Jungwei Fan, Jianrong Li, Qike Li, Haiquan Li, Yves Lussier	

Sunday, January 6, 2019 (continued)

Session 3 (continued) — Salon 2&3

10:55-11:10 *An Optimal Policy for Patient Laboratory Tests in Intensive Care Units*
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

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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

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 *LISA: Accurate reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data*
Yang Chen, Yuping Zhang, Zhengqing Ouyang
10:30-10:45 *Topological Methods for Visualization and Analysis of High Dimensional Single-Cell RNA Sequencing Data*
Tongxin Wang, Travis Johnson, Jie Zhang, Kun Huang
10:45-11:00 *Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics*
Qiwen Hu, 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!