Pacific Symposium on Biocomputing (PSB) 2018 Schedule January 3-7, 2019, Fairmont Orchid, Big Island of Hawaii

Thursday, January 2, 2010		
Thursday, January 3, 2019 7:30 – 9:30 am	Registration (Ballroom Prefunction)	
9:00 – Noon	Workshop – Merging Heterogeneous Data to	Organizers: Tina Hernandez-Boussard,
9.00 - 110011	Enable Knowledge Discovery (Salon 2&3)	Michael Kahn
Noon – 1:30 pm	Break – Lunch on own	Michael Kalili
Noon – 2:00 pm	Registration (Ballroom Prefunction)	
		Organizers: Yves Lussier, Atul Butte, Jason
1:30 – 4:30 pm	Workshop – Translational informatics of population	
	health: How large biomolecular and clinical	Moore, Rong Chen, Haiquan Li
4:20 7:00 :- :	datasets (Salon 2&3)	
4:30 – 7:00 pm	Break – Dinner on own	
7:00 – 8:00 pm	Registration (Kilohana Room)	
7:00 – 8:00 pm	Reception – 24th Anniversary Welcome Drink &	
F:1 1 4 0040	Dessert Reception (Kilohana Room)	
Friday, January 4, 2019	B 14 (1 (B II	
7:30 – 9:00 am	Registration (Ballroom Prefunction)	
7:30 – 8:45 am	PSB Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Welcome (Salon 2&3)	
	Session 1: Pattern recognition in biomedical data:	Co-chairs: Shefali Setia Verma, Anurag
	challenges in putting big data to work	Verma, Dokyoon Kim, Christian Darabos
8:40 – 8:50 am	Introduction	
8:50 – 9:10 am	Invited Talk	Barbara Engelhardt
9:10 – 9:25 am	The Effectiveness of Multitask Learning for	Daisy Yi Ding, Chloe Simpson, Stephen Pfohl,
	Phenotyping with Electronic Health Records Data	Dave Kale, Kenneth Jung, Nigam Shah
9:25 – 9:40 am	ODAL: A one-shot distributed algorithm to perform	Rui Duan, Mary Regina Boland, Jason Moore,
	logistic regressions on electronic health records	Yong Chen
	data from multiple clinical sites	
9:40 – 9:55 am	PVC Detection Using a Convolutional Autoencoder	Max Gordon, Cranos Williams
	and Random Forest Classifier	
9:55 - 10:10 am	Removing Confounding Factors Associated	Haohan Wang, Zhenglin Wu, Eric Xing
	Weights in Deep Neural Networks Improves the	
	Prediction Accuracy for Healthcare Applications	
10:10 – 10:25 am	DeepDom: Predicting protein domain boundary	Yuexu Jiang, Duolin Wang, Dong Xu
	from sequence alone using stacked bidirectional	
	LSTM	
10:25 – 10:40 am	Res2s2aM: Deep residual network-based model	Zheng Liu, Yao Yao, Qi Wei, Benjamin
	for identifying functional noncoding SNPs in trait-	Weeder, Stephen Ramsey
	associated regions	resource, etoperon realises,
10:30 – 11:30 am	Registration (Ballroom Prefunction)	
10:40 – 10:50 am	Break	
10:50 – Noon	Keynote: Russ Altman (Salon 2&3)	Introduction by Steve Brenner
12:00 – 1:00 pm	PSB Hosted Lunch (Ballroom Courtyard)	maddadan by Glove Bronner
12:00 – 1:00 pm	Registration (Ballroom Prefunction)	
12.00 – 1.00 pm	Session 1 (continued) Pattern recognition in	Co-chairs: Shefali Setia Verma, Anurag
	biomedical data: challenges in putting big data to	Verma, Dokyoon Kim, Christian Darabos
	work (Salon 2&3)	Verma, Dokyoon Kim, Chinstian Darabos
1:00 – 1:10 pm	Introduction to second half of session	
1:10 – 1:10 pm 1:10 – 1:25 pm	Bi-directional Recurrent Neural Network Models	Arjun Magge, Davy Weissenbacher, Abeed
1.10 = 1.25 pm		
	for Geographic Location Extraction in Biomedical	Sarker, Matthew Scotch, Graciela Gonzalez-
1.05 1.40	Literature	Hernandez
1:25 – 1:40 pm	PLATYPUS: A Multiple–View Learning Predictive	Kiley Graim, Verena Friedl, Kathleen E.
4.40 4.55	Framework for Cancer Drug Sensitivity Prediction	Houlahan, Joshua Stuart
1:40 – 1:55 pm	Computational KIR copy number discovery reveals	Rachel Pyke, Raphael Genolet, Alexandre
	interaction between inhibitory receptor burden and	Harari, George Coukos, David Gfeller, Hannah
4.55 0.40	survival	Carter
1:55 – 2:10 pm	Implementing and Evaluating A Gaussian Mixture	Kevin Li, Rachel Chen, William Lindsey, Aaron
	Framework for Identifying Gene Function from	Best, Matthew DeJongh, Christopher Henry,
0.40	TnSeq Data	Nathan Tintle
2:10 – 2:25 pm	Extracting allelic read counts from 250,000 human	Brian Tsui, Michelle Dow, Dylan Skola, Hannah
	sequencing runs in Sequence Read Archive	Carter

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Friday, January 4 (cont)		
2:25 – 2:40 pm	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
2:40 – 3:40 pm	Discussion Session (Salon 2&3) Pattern recognition in biomedical data: challenges in putting big data to work	, 0
3:45 – 5:00 pm	Working Group Meeting: Writing bio-computational manuscripts with Manubot (Salon 2&3)	Organizer: Daniel Himmelstein
5:00 –	Break – Dinner & evening on own	
Saturday, January 5, 2019		
7:30 – 8:30 am	Registration (Ballroom Prefunction)	
7:30 – 8:45 am	PSB Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Morning Announcements (Salon 2&3) TERI Talks (Salon 2 & 3)	
8:40 – 9:10 am	Dennis Wall, Stanford University	
9:10 – 9:40 am	Marylyn Ritchie, University of Pennsylvania	
	Session 2: 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 am	Introduction	
9:55 – 10:15 am	Invited Talk	Greg Hampikian
10:15 – 10:30 am	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 am	Protecting Genomic Data Privacy with Probabilistic Modeling	Sean Simmons, Bonnie Berger, Cenk Sahinalp
10:45 – 11:00 am	Evaluation of patient re-identification using laboratory test orders and mitigation via latent space variables	Kipp Johnson, <u>Jessica De Freitas</u> , Benjamin Glicksberg, Jason Bobe, Joel Dudley
11:00 – Noon	Discussion Session (Salon 2&3) When biology gets personal: hidden challenges of	
	privacy and ethics in biological big data	
Noon – 2:30 pm	Poster Session with Lunch Salon1 and Ballroom Courtyard	ODD numbered boards presented from 12:30-1:30
	Salom and Ballioon Soungala	EVEN numbered boards presented from 1:30-2:30
2:30 – 5:30 pm	Workshop: Text Mining and Machine Learning for Precision Medicine (Salon 2&3)	Organizers: Graciela Gonzalez, Hongfang Liu, Zhiyong Lu, Robert Leaman
5:30 – 6:00 pm	Meeting: ISCB Meeting (Salon 2&3)	
6:00 -	Break – Dinner & Evening on own	
Sunday, January 6, 2019		
7:30 – 8:45 am	PSB Breakfast (Ballroom Courtyard)	
8:30 – 8:40 am	Morning Announcements (Salon 2&3)	
8:40 – 11:10 am	Session 3: Precision medicine: improving health	Co-chairs: Steven Brenner,, Martha Bulyk,
0.40 0.50	through high-resolution analysis of personal data (Salon 2&3)	Dana Crawford, Jill Mesirov, Alexander Morgan, Predrag Radivojac
8:40 – 8:50 am	Introduction	John Witte
8:50 – 9:10 am 9:10 – 9:25 am	Invited Talk CrowdVariant: a crowdsourcing approach to	John Witte Peyton Greenside, Justin Zook, Marc Salit,
9. 10 — 9.25 aiii	classify copy number variants	Madeleine Cule, Ryan Poplin, Mark DePristo
9:25 – 9:40 am	A repository of microbial marker genes related to human health and diseases for host phenotype	Wontack Han, Yuzhen Ye
9:40 – 9:55 am	prediction using microbiome data AICM: A Genuine Framework for Correcting Inconsistency Between Large Pharmacogenomics	Zhiyue Tom Hu, Yuting Ye, Patrick A. Newbury, Haiyan Huang, Bin Chen
	Datasets	

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Sunday, January 6 (cont.)		
9:55 – 10:10 am	Outgroup Machine Learning Approach Identifies	Maya Varma, Kelley Marie Paskov, Jae-Yoon
	Single Nucleotide Variants in Noncoding DNA	Jung, Brianna Sierra Chrisman, Nate Tyler
	Associated with Autism Spectrum Disorder	Stockham, Peter Yigitcan Washington, Dennis Paul Wall
10:10 –10:25 am	Detecting potential pleiotropy across	Xinyuan Zhang, Yogasudha Veturi, Shefali
	cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on	Verma, William Bone, Anurag Verma, Anastasia Lucas, Scott Hebbring, Joshua C.
	43,870 individuals from the eMERGE network	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 am	Integrating RNA expression and visual features for	Derek Reiman, Lingdao Sha, Irvin Ho, Timothy
10:40 – 10:55 am	immune infiltrate prediction Precision drug repurposing via convergent eQTL-	Tan, Denise Lau <u>, Aly Khan</u> <u>Francesca Vitali,</u> Joanne Berghout, Jungwei
10.40 – 10.55 am	based molecules and pathway targeting	Fan, Jianrong Li, Qike Li, Haiquan Li, Yves
	independent disease-associated polymorphisms	Lussier
10:55 – 11:10 pm	An Optimal Policy for Patient Laboratory Tests in	Li-Fang Cheng, Niranjani Prasad, Barbara
11:10 12:10 nm	Intensive Care Units	Engelhardt
11:10-12:10 pm	Discussion Session (Salon 2&3) Precision medicine: improving health through high-	
	resolution analysis of personal data	
12:10 – 1:30 pm	Break – Lunch on own	
1:30 – 4:30 pm	Workshop: Reading between the genes:	Organizers: Joanne Berghout, Yves Lussier,
	interpreting non-coding DNA in high-throughput (Salon 2&3)	Francesca Vitali, Martha Bulyk, Maricel Kann, Jason Moore
4:30 – 5:00 pm	Parasite & Symbiont Awards (Salon 2&3)	Success Moore
5:00 – 5:30 pm	Break	
5:30 – 7:15 pm 7:30 – 8:30 pm	PSB Dinner Banquet (Coconut Grove) Keynote: Lawrence Hunter (Salon 2&3)	Introduction by Duca Altman
7.30 – 8.30 pm	Reynote: Lawrence number (Salon 2&3)	Introduction by Russ Altman
Monday, January 7, 2019	Production (Pollmann County and)	
7:30 – 8:30 am 8:30 – 8:40 am	Breakfast (Ballroom Courtyard) Closing Announcements (Salon 2&3)	
0.00 0.10 am	TERI Talks (Salon 2&3)	
8:40 – 9:10 am	Graciela Gonzalez, University of Pennsylvania	
9:10 – 9:40 am	Keith Dunker, University of Indiana Introduction	On the size of the V. Onessien Over Observ Verse
9:45 – 11:00 am	Session 4: Single cell analysis, what is in the future? (Salon 2&3)	Co-chairs: Lana X. Garmire, Guo-Cheng Yuan, Rong Fan, Gene Yeo, John Quackenbush
9:45 - 9:55 am	Introduction	-
9:55 – 10:15 am	Invited Talk	Zemin Zhang
10:15 – 10:30 am	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 am	Topological Methods for Visualization and Analysis	Tongxin Wang, Travis Johnson, Jie Zhang, Kun
	of High Dimensional Single-Cell RNA Sequencing	Huang
10.15 11.00	Data	0: 11 0 0
10:45 – 11:00 pm	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for	Qiwen Hu, Casey Greene
	single cell RNA transcriptomics	
11:00 – 12:00 pm	Discusstion Session (Salon 2&3)	
<u>-</u>	Single cell analysis, what is in the future?	

PSB over—see you next year!!