Wednesday, January 3, 2018

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Registration			-
7:30-9:30	3		Prefunction
12:00-2:00	Registration	Ballroom	Prefunction
7:30-8:30	Registration		Kilohana
Workshops			
9:00-12:00	Machine Learning and Deep Analytics for Biocomputin for Better Explainability	ng: Call	Salon 2&3
	Organizers: Dragutin Petkovic, Lester Kobzik, Christo	pher Re	
Break			
12:00-1:30	Lunch on own		
Workshop			
1:30-4:30	Integrating Community-level Data Resources for Prec	ision	Salon 2&3
	Medicine Research		
	Organizers: Dana C. Crawford, William S. Bush		
1:30-4:30	Methods for Examining Data Quality in Healthcare Into	egrated	Plaza
	Data Repositories	- 9: -::- ::	
	Organizers: Vojtech Huser, Michael Kahn, and Jeffrey	Brown	
Break	, , , , , , , , , , , , , , , , , , , ,		
4:30-7:30	Dinner on own		
Reception			Kilohana
7:30-8:30	23 rd Anniversary Reception		

Thursday, Jar	ıuary 4	, 2018
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i nursuay,	January 4, 2018		
Registration			
7:30-9:00	Registration	Ballroom	Prefunction
10:30-11:30	Registration	Ballroom	Prefunction
12:00-1:00	Registration	Ballroom	Prefunction
Breakfast	<u> </u>		Courtyard
7:30-8:30	PSB Breakfast		
Welcome			Salon 2&3
8:30-8:40	Welcome		
Session 1:	Applications of Genetics, Genomics and Bioinformati	cs in	Salon 2&3
	Drug Discovery		
	Co-chairs: Richard Bourgon, Rick Dewey, Zhengyan	Kan, Dan I	_i
8:40-8:50	Introduction	,	
8:50-9:10	Invited Talk: Rick Dewey		
9:10-9:25	Large-scale integration of heterogeneous pharmacog	genomic da	ta for
	identifying drug mechanism of action		
	Yunan Luo, Sheng Wang, Jinfeng Xiao, Jian Peng		
9:25-9:40	Cell-specific prediction and application of drug-induced	ed gene ex	pression
	profiles		
	Rachel Hodos, Ping Zhang, Hao-Chih Lee, Qiaonan	Duan, Zic	hen Wang,
	Neil R. Clark, Avi Ma'ayan, Fei Wang, Brian Kidd, Ji	anying Hu,	David
	Sontag, Joel Dudley		
9:40-9:55	Characterization of drug-induced splicing complexity	in prostate	cancer
	cell line using long read technology		
	Xintong Chen, Sander Houten, Kimaada Allette, Robert P. Sebra,		ra,
	Gustavo Stolovitzky, <u>Bojan Losic</u>		
9:55-10:10	Chemical Reaction Vector Embeddings: Towards Predicting Drug		
	Metabolism in the Human Gut Microbiome		
	Emily K. Mallory, Ambika Acharya, Stefano E. Rens	i, Peter J T	urnbaugh,
	Roselie A. Bright, Russ B. Altman		
10:10-10:25	Extracting a Biologically Relevant Latent Space from	Cancer	
	Transcriptomes with Variational Autoencoders		
	Gregory P. Way, Casey S. Greene		
Break			
10:25-10:45			
Keynote			Salon 2&3
10:45-11:45	Improving Healthcare through Biomedical Data Scien	псе	
	Carlos Bustamante with introduction by Russ Altman		
Lunch		Ballroom	Courtyard
11:45-1:00	PSB Hosted Lunch		

Thursday, January 4, 2018 continued

Session 2:	Imaging Genomics	Salon 2&3
	Co-chairs: Heng Huang, Junzhou Huang, Kun Huang, Li She	en, Paul M.
	Thompson, Lin Yang	
1:00-1:10	Introduction	
1:10-1:30	Invited Talk: Mert Sabuncu	
1:30-1:45	Codon Bias Among Synonymous Rare Variants Is Associate	d 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	Deep Integrative Analysis for Survival Prediction	
	Chenglong Huang, Albert Zhang, Guanghua Xiao	
2:00-2:15	Discriminative Bag-of-Cells for Imaging-Genomics	
	Benjamin Chidester, Minh N. Do, Jian Ma	
2:15-2:30	Genotype-Phenotype Association Study via New Multi-Task	Learning
	Model	
	Zhouyuan Huo, Dinggang Shen, <u>Heng Huang</u>	
Special Top	ics	
2:30-3:00	Parasite & Symbiont Awards	Salon 2&3
Discussion	Sessions	
3:00-4:00	Imaging Genomics	Salon 2&3
4:00-5:00	Applications of Genetics, Genomics and Bioinformatics in	Salon 2&3
	Drug Discovery	
Meeting		
5:00-5:30	ISCB Meeting	Salon 2&3
Break		
5:30	Dinner on own	

Friday, January 5, 2018

Friday, Jan	uary 5, 2018		
Registration 7:30-8:30	Registration	Ballroom	Prefunction
Breakfast		Ballroor	n Courtyard
7:30-8:30	PSB Breakfast		•
Announceme	ents		Salon 2&3
8:30-8:40	Morning Announcements		
Session 3	Precision Medicine: from diplotypes to disparities tow improved health and therapies		Salon 2&3
0.40 0.45	Co-chairs: Bruce Aronow, Steven E. Brenner, Dana C. Denny, Alexander A. Morgan	C. Crawfor	d, Joshua
8:40-8:45	Introduction		
8:45-9:05 9:05-9:20	Invited Talk: Vence Bonham	inical mata	halia
9.05-9.20	Considerations for automated machine learning in cliprofiling: altered homocysteine plasma concentration		
	metformin exposure	associate	Willi
	Alena Orlenko, Jason H. Moore, Patryk Orzechowsk	ki, Randal	S. Olson,
	Junmei Cairns, Pedro J. Caraballo, Richard M. Weir		
	Wang, Matthew K. Breitenstein		
9:20-9:35	Analyzing metabolomics data for association with ge	notypes us	sing two-
	component gaussian mixture distributions	01	
	<u>Jason Westra</u> , Nicholas Hartman, Bethany Lake, Gr Nathan Tintle	egory She	earer,
9:35-9:50	Single subject transcriptome analysis to identify func	tionally sic	ined dene
0.00 0.00	set or pathway activity	donany dig	nou gono
	Joanne Berghout, Qike Li, Nima Pouladi, Jianrong L	i, Yves A	Lussier
9:50-10:05	Emergence of pathway-level composite biomarkers to		
	set signals of heterogeneous transcriptomic respons		
	Samir Rachid Zaim, Qike Li, A. Grant Schissler, Yve		
10:05-10:20	Coalitional game theory as a promising approach to autism genes	identify ca	ndidate
	Anika Gupta, Min Woo Sun, Kelley M. Paskov, Nate Yoon Jung, Dennis P. Wall	T. Stockh	am, Jae-
10:20-10:35	Using simulation and optimization approach to impro	ve outcom	e through
	warfarin precision treatment		
	Chih-Lin Chi, Lu He, Kourosh Ravvaz, John Weisse		
10:35-10:50	Addressing vital sign alarm fatigue using personalize Sarah Poole, Nigam Shah	d alarm th	resholds
Discussion S			Salon 2&3
	Precision Medicine: from diplotypes to disparities tow	vards	Calon 200
. 1.00 12.00	improved health and therapies phenotypes		
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Friday, January 5, 2018 continued

Poster Session Li	unch Salon 1 and Ballroom Courtyard
	ter Session with Lunch
	sters on ODD numbered boards presented from 12:30-1:30)
•	sters on EVEN numbered boards presented from 1:30-2:30)
	nocratizing Health Data for Translational Research Salon 2&3
	chairs: Philip Payne, Nigam Shah, Jessie Tenenbaum,
	a Mangravite
	oduction
2:40-3:00 Invit	ted Talk: Joe Corkery
3:00-3:20 Invit	ted Talk: John Wilbanks
3:20-3:35 Clin	Gen Cancer Somatic Working Group – Standardizing and
Den	nocratizing Access to Cancer Molecular Diagnostic Data to Drive
Trai	nslational Research
	bha Madhavan, Deborah Ritter, Christine Micheel, Shruti Rao,
	gshumoy Roy, Dmitriy Sonkin, Matthew McCoy, Malachi Griffith, Obi L
	ffith, Peter Mcgarvey, Shashikant Kulkarni on Behalf of the ClinGen
	matic Working Group
	t Practices and Lessons Learned from Reuse of 4 Patientderived
	abolomics Datasets in Alzheimer's Disease
	ssica D. Tenenbaum, Colette Blach
	euristic Method for Simulating Open-Data of Arbitrary Complexity that
	Be Used to Compare and Evaluate Machine Learning Methods
	son H. Moore, Maksim Shestov, Peter Schmitt, Randal S. Olson
Discussion Session	
•	nocratizing Health Data for Translational Research
Break	
5:10- Dini	ner & Evening on own

Saturday, January 6, 2018

Saturuay, J	alluary 0, 2010
Breakfast	Ballroom Courtyard
7:30-8:30	PSB Breakfast
Announceme	ents Salon 2&3
8:30-8:40	Morning Announcements
Session 5:	Challenges of Pattern Recognition in Biomedical Data Co-chairs: Anurag Verma, Anna Basile, Marta Byrska-Bishop, Christian Darabos, Shefali Setia Verma
8:40-8:50	Introduction
8:50-9:10	Invited Talk: Larry Smarr
9:10-9:25	Functional Network Community Detection Can Disaggregate and Filter Multiple Underlying Pathways in Enrichment Analyses <u>Lia X. Harrington</u> , Gregory P. Way, Jennifer A. Doherty, Casey S. Greene
9:25-9:40	Large-Scale Analysis of Disease Pathways in the Human Interactome Monica Agrawal, Marinka Zitnik, Jure Leskovec
9:40-9:55	Data-driven Advice for Applying Machine Learning to Bioinformatics Problems
	Randal S. Olson, <u>William La Cava</u> , Zairah Mustahsan, Akshay Varik, Jason H. Moore
9:55-10:10	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	Mapping Patient Trajectories using Longitudinal Extraction and Deep Learning in the MIMIC-III Critical Care Database Brett K. Beaulieu-Jones, Patryk Orzechowski, Jason H. Moore
10:25-10:40	Causal 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	How Powerful Are Summary-Based Methods for Identifying Expression- Trait Associations Under Different Genetic Architectures? Yogasudha Veturi, Marylyn D. Ritchie
Keynote:	Salon 2&3
11:00-12:15	Data Disparities: Discrimination & Equity in Big Data Jennifer Wagner with introduction by Marylyn Ritchie
Break	
12:15-1:30	Lunch on Own
Workshop	Salon 2&3
1:30-4:30	Diversity and Disparity in Biomedical Informatics Organizers: Philip R.O. Payne, William M. Southerland, S. Joshua Swamidass, Laura Wiley, and ClarLynda Williams-DeVane

Saturday, January 6, 2018 continued

Discussion	Session	Salon 2&3
4:30-5:30	Challenges of Pattern Recognition in Biomedical Data	
Dinner		Plantation Estate
5:30-7:30	Hawaii Loa Luau PSB's dinner will be held at the Fairmont's Hawaii Loa I Luau Schedule: 5:30 pm Check-In & Seating Begins 6:00 pm Luau Dinner Buffet 7:00 pm Performance Begins / Bar Closed	Luau this year.

Sunday, January 7, 2018

Sulluay, January 7, 2010
Breakfast Ballroom Courtyard
7:30-8:30 Breakfast
Closing Salon 2&3
8:30-8:40 Closing Announcements
Session 6: Advances in Text Mining and Visualization for Precision Salon 2&3
Medicine
Co-chairs: Graciela Gonzalez, Casey Greene, Hongfang Liu, Abeed Sarker
8:40-8:50 Introduction
8:50-9:10 Invited Talk: Jason Moore
9:10-9:30 Invited Talk: Sophia Ananiadou
9:30-9:45 VisAGE: Integrating External Knowledge into Electronic Medical Record
Visualization
Edward W. Huang, Sheng Wang, ChengXiang Zhai
9:45-10:00 Annotating gene sets by mining large literature collections with protein
networks
Sheng Wang, <u>Jianzhu Ma</u> , Michael Ku Yu, Fan Zheng, Edward W Huang
Jiawei Han, Jian Peng,Trey Ideker
10:00-10:15 Improving Precision in Concept Normalization
Mayla Boguslav, K. Bretonnel Cohen, William A. Baumgartner Jr.,
Lawrence E. Hunter
Session 7: Reading Between the Genes: Computational Models to Salon 2&3
Discover Function and/or Clinical Utility from Noncoding DNA
Co-chairs: Yves Lussier, Maricel Kann, Jason Moore, Kenneth Ramos,
Joanne Berghout, Francesca Vitali
10:20-10:30 Introduction
10:30-10:50 Invited Talk: Martha Bulyk
10:50-11:05 Network analysis of pseudogene-gene relationships: from pseudogene
evolution to their functional potentials Travia S. Johnson, Sibona Li, Johnston B.Kho, Kun Huang, Van Zhang,
<u>Travis S Johnson</u> , Sihong Li, Johnathan R Kho, Kun Huang, Yan Zhang 11:05-11:20 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
11:20-11:35 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
Discussion Sessions
11:40-12:40 Reading Between the Genes: Computational Models to Salon 2&3
Discover Function and/or Clinical Utility from Noncoding DNA
11:40-12:40 Text Mining and Visualization for Precision Medicine Kilohana
PSB oversee you next year!