Wednesday, January 2, 2013

Registration			
		Ballroom Prefunction	
Thursday, J	anuary 3, 2013		
Registration			
7:30-9:30am	Registration	Ballroom Prefunction	
12:00-2:00pr	12:00-2:00pm Registration Ballroom Prefunction		
6:00-7:30pm	Registration	Ballroom Prefunction	
Tutorials		Plaza Ballroom	
9:00-9:50:	Identification of Aberrant Pathway and Network Act	tivity from High-	
	Throughput Data		
	Computational Drug Repositioning		
-	Epigenomics		
Workshop		Salon 2&3	
9:00-12:00	Computational Biology in the Cloud: Methods and I	New Insights from	
	Computing at Scale		
Break	I all a second		
12:00-1:00	Lunch on own		
Tutorials	Developation of Madiaina, France County was and Mala	Plaza Ballroom	
1:00-1:50	Personalized Medicine: From Genotypes and Mole	cular Phenotypes	
2:00-2:50	Towards Therapy Phylogenomics and Population Genomics: Models, Algorithms, and		
2.00-2.50		, Algoriums, and	
3:00-3:50	Analytical Tools Post-NGS: Interpretation and Analysis of Next Generation Sequencing		
0.00 0.00	Data for Basic and Translational Science	icration ocquencing	
4:00-4:50	Text and Data Mining for Biomedical Discovery		
Workshop	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Salon 2&3	
1:00-4:00	Modeling Cell Heterogeneity: From Single-Cell Var		
	Populations		
Break	•		
4:00-6:30	Dinner on own		
Reception		& Ballroom Courtyard	
6:30-7:30	Opening Reception with Drinks and Desserts		
	(Posters to remain up for duration of conference.)		
Workshop	,	Salon 2&3	
7:30-10:30	Computational Challenges of Mass Phenotyping		

Friday, January 4, 2013

Dogiotrofica		
Registration	Desistation	Dallas and Dash washing
7:30-9:00	Registration	Ballroom Prefunction
10:15-11:00	Registration	Ballroom Prefunction Ballroom Prefunction
1:30-2:30	Registration	
Breakfast	DCD Draghfoot	Ballroom Courtyard
7:30-8:30	PSB Breakfast	0-1 000
Welcome 8:30-8:40	Welcome – Teri Klein	Salon 2&3
Session 1:	Personalized Medicine: From Genotypes and Mo	Novelor Phonotypes
Session 1.		Salon 2&3
8:40-8:50	Towards Therapy Introduction	Salon 2&3
8:50-9:05	Invited talk: Atul Butte, Stanford University	
9:05-9:20	Systematic Identification of Risk Factors for Alzh	eimer's Disease Through
3.00 3.20	Shared Genetic Architecture and Electronic Med.	
	Li Li, David Ruau, Rong Chen, Susan Weber, Atı	
9:20-9:35	Characterization of the Metabochip in Diverse Po	
0.20 0.00	International HapMap Project in the Epidemiolog	
	Linked to Environment (EAGLE) Project	
	Dana C. Crawford, Robert Goodloe, Kristin Brow	n-Gentry, Sarah Wilson,
	Jamie Roberson, Niloufar B. Gillani, Marylyn D. F	•
	William S. Bush	
9:35-9:50	AMP: Assembly Matching Pursuit	
	Surojit Biswas, Vladimir Jojic	
9:50-10:05	Spectral Clustering Strategies for Heterogeneous Disease Data	
	Grace T. Huang, Kathryn I. Cunningham, Panayi	otis V. Benos, Chakra S.
	Chennubhotla	
10:05-10:20	, , , , , , , , , , , , , , , , , , ,	
	Samuel Coulbourn Flores, Christina Waldsich	
Break		
10:20–10:50	Break	
Keynote		Salon 2&3
	Dan Roden, Vanderbilt University, with introducti	
Lunch	DODA	Orchid Court
12:00-1:30	PSB Lunch	
Session 2:	Computational Drug Repositioning	Salon 2&3
1:30-1:40	Introduction	
1:40-1:55	Drug Target Predictions Based on Heterogeneous Graph Inference	
1:55-2:10	Wenhui Wang, Sen Yang, Jing Li Protein chemical Interaction Prediction via Kerne	dized Sparce Learning
1.00-2.10	Protein-chemical Interaction Prediction via Kerne SVM	suzeu spaise Leaitiiig
	Yi Shi, Xinhua Zhang, Xiaoping Liao, Guohui Lin	Dale Schuurmans
	Troni, Allinua Zhang, Alaoping Liao, Guonui Lin	, Dale Ochuumans

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

Friday, January 4, 2013 (continued)

	0 (0 15 5 0 10 1 (0 1)	0 1 000
Session 2:	Computational Drug Repositioning (continued)	Salon 2&3
2:10-2:25	A Novel Multi-Modal Drug Repurposing Approach for Identific	ation of
	Potent ACK1 Inhibitors	
	Sharangdhar S. Phatak, Shuxing Zhang	
2:25-2:40	Evaluation of Analytical Methods for Connectivity Map Data	
2.20 2.40		Eroudonhora
	Jie Cheng, Qing Xie, Vinod Kumar, Mark Hurle, Johannes M.	rieudelibelg,
	Lun Yang, Pankaj Agarwal	
Discussion		Salon 2&3
3:00-4:00	Computational drug repositioning	
Discussion		Salon 2&3
4:00-5:00	Personalized medicine: from genotypes and molecular phenotypes	
	towards therapy	71
Meeting		Salon 2&3
5:00-5:30	International Society for Computational Biology (ISCB) Open	Meeting
Break		
5:30 -	Dinner and evening on own	

Saturday, January 5, 2013

Registration 7:30-9:00	Registration	Ballroom Prefunction
12:00-2:00	Registration	Ballroom Prefunction
Breakfast		Ballroom Courtyard
7:30-8:30	PSB Breakfast	
Announcem		Salon 2&3
8:30-8:40	Morning Announcements Russ Altman	
Session 3:	Post-NGS: Interpretation and Analysis of Next Gen	
0.40 0.50	Data for Basic and Translational Science	Salon 2&3
8:40-8:50 8:50-9:05	Introduction Invited Talk: Jason Moore, Dartmouth University	
9:05-9:20	ChIPModule: Systematic Discovery of Transcription	n Factors and Their
0.00 0.20	Cofactors from ChIP-seq Data	irr actors and rinch
	Jun Ding, Xiaohui Cai, Ying Wang, Haiyan Hu, Xia	oman Li
9:20-9:35	LSHPlace: Fast Phylogenetic Placement Using Loc	
	Daniel G. Brown, Jakub Truszkowski	_
9:35-9:50	Detecting Highly Differentiated Copy-Number Varia	ants from Pooled
	Population Sequencing	- le
Deselv	Daniel R. Schrider, David J. Begun, Matthew W. H.	ann
Break 9:50-10:10	Break	
Session 4:	Epigenomics	Salon 2&3
10:10-10:15	• •	001011 200
	Invited Speaker: Frank Pugh, Penn State Universit	V
	Using DNase Digestion Data to Accurately Identify Binding Sites	
	Kaixuan Luo, Alexander J. Hartemink	
10:50-11:05	Epigenomic Model of Cardiac Enhancers with Appl Wide Association Studies	lication to Genome
	Avinash Das Sahu, Radhouane Aniba, Yen-Pei Ch Hannenhalli	risty Chang, Sridhar
Discussion		Salon 2&3
11:05-12:05	Epigenomics with talk by Michael Snyder, Stanford	University
Poster Sess	ion Lunch Salon 1	& Ballroom Courtyard
12:30-2:30	Poster Session with Lunch	
	(A-L, last name of the first author presents from 12 (M-Z, last name of the first author presents from 1:	•
Workshop		Salon 2&3
2:30-5:30	The Future of Genome-Based Medicine	

Saturday, January 5, 2013 (continued)

Discussion	Plaza Ballroom	
4:30-5:30	Post-NGS: Interpretation and Analysis of Next Generation Sequencing	
	Data for Basic and Translational Science	
Break		
5:30 -	Dinner and evening on own	

Sunday, January 6, 2013

Breakfast		Ballroom Courtyard
7:30-8:30	PSB Breakfast	,
Announceme	ents	Salon 2&3
8:30-8:40	Morning Announcements Keith Dunker	
Session 5:	Text and Data Mining for Biomedical Discovery	Salon 2&3
8:40-8:50	Introduction	
8:50-9:05	Invited Talk: Lawrence Hunter, University of Colorad	
9:05-9:20	ATHENA: A Tool for Meta-Dimensional Analysis Ap and Gene Expression Data to Predict HDL Choleste	
	Emily R Holzinger, Scott M. Dudek, Alex T. Frase, F Marisa W. Medina, Marylyn D. Ritchie	
9:20-9:35	Statistical Epistasis Networks Reduce the Computa	tional Complexity of
	Searching Three-Locus Genetic Models	
	Ting Hu, Angeline S. Andrew, Margaret R. Karagas	
9:35-9:50	Evaluation of Linear Classifiers on Articles Containing	ng Pharamacokinetic
	Evidence of Drug-Drug Interactions	4. Daaba
0.50 10.05	Artemy Kolchinsky, Analia Lourenco, Lang Li, Luis N	
9:50-10:05	Detection of Protein Catalytic Sites in the Biomedica Karin Verspoor, Andrew MacKinlay, Judith D. Cohn	
Break	,	
10:05-10:15	Break	
Session 6:	Identification of Aberrant Pathway and Network Acti	vity from High-
	Throughput Data	Salon 2&3
	Introduction	
	Invited Talk: Nathan Price, Institute for Systems Bio	
10:45-11:00	Module Cover - A New Approach to Genotype-Pher	
11.00 11.15	Yoo-Ah Kim, Raheleh Salari, Stefan Wuchty, Teresa	
11.00-11.15	Identifying Master Regulators of Cancer and Their I by Integrating Genomic and Epigenomic Features	Jownstream rargets
	Olivier Gevaert, Sylvia Plevritis	
11:15-11:30		Mechanism-Scale
11.10 11.00	Profiling of RNA-seq Data	Woonamom Coare
	Alan Perez-Rathke, Haiguan Li, Yves A. Lussier	
Discussion	, , ,	Salon 2&3
11:30-12:30	Identification of Aberrant Pathway and Network Acti Throughput Data	
Discussion		Plaza Ballroom
11:30-12:30	Text and Data Mining for Biomedical Discovery	_

Sunday, January 6, 2013 (continued)

Break 12:30 – 5:30) Afternoon Free	
Dinner	7 Alternoon Free	Croquet Lawn
5:30-7:15	Dinner Party	
Keynote:		Salon 2&3
7:30-8:45	David Ewing Duncan with introduction by Larry Hunter	

Monday, January 7, 2013

Breakfast	Ballroom Courtyard
7:30-8:30	Breakfast
Closing	Salon 2&3
8:30-8:40	Closing Larry Hunter
Session 7:	Phylogenomics and Population Genomics: Models, Algorithms, and
	Analytical Tools Salon 2&3
8:40-8:50	Introduction
8:50-9:05	Evaluating Variations on the STAR Algorithm for Relative Efficiency and
	Sample Sizes Needed to Reconstruct Species Trees
	James H. Degnan
9:05-9:20	An Analytical Comparison of Multilocus Methods Under the Multispecies
	Coalescent: The Three-Taxon Case
0.00 0.05	Sebastien Roch
9:20-9:35	Maximum Likelihood Phylogenetic Reconstruction from High-Resolution
	Whole-Genome Data and a Tree of 68 Eukaryotes Yu Lin, Fei Hu, Jijun Tang, Bernard M.E. Moret
9:35-9:50	The Behavior of Admixed Populations in Neighbor-Joining Inference of
9.55-9.50	Population Trees
	Naama M. Kopelman, Lewi Stone, Olivier Gascuel, Noah A. Rosenberg
Discussion	Salon 2&3
9:50-10:50	Phylogenomics and Population Genomics: Models, Algorithms, and
ə.əu-10.əu	Analytical Tools

PSB over--see you next year!