RECOMB REGULATORY GENOMICS, SYSTEMS BIOLOGY, AND DREAM4

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CONFERENCE CHAIRS:

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Wednesday, Dec 2

Session	Time	Program	#
	3pm	Conference check-in open, Poster session I set-up	
	5pm	Welcome Remarks	
RG1: U.Ohler/M.Brent. Post-transcriptional regulation and regulatory RNAs	5:15	Mark Biggin: Evidence for Quantitative Transcription Networks	1
	5:45	Sarah E. Calvo: Widespread translational repression by uORFs: implications for variation and disease	2
	6pm	Hilal Kazan: Binding Preferences of RNA-binding Prots from Noisy Affinity Data w/Physical Models	3
	6:15	Igor Ulitsky: Towards Computational Prediction of MicroRNA Function and Activity	4
	6:30	Break / light snacks	
	6:45	Clifford A. Meyer: Inferring Transcr Regulators using H3K4me2 Marked Nucleosome Occupancy Data	5
	7pm	Jason Ernst: Discovery and characterization of chromatin states from combinatorial histone marks	6
	7:15	Mattia Pelizzola: Human DNA methylomes at single-base resolution reveal widespread cell-specific epigenetic signatures	7
	7:30	Leonid Mirny: Fundamentally different strategies of gene regulation in bacterial and eukaryotes	8
	7:45	Bob Waterston: Deciphering the C. Elegans Embryonic Regulatory Network	9
	8:15-9:45p	Regulatory Genomics Poster Session I Regulatory Genomics Welcome Reception (hors-d'oeuvre, snacks, refreshments, wine, cash bar)	

Thursday, Dec 3

Session	Time	Program	#
	8am	Breakfast	
RG2: R.Shamir/T.Benos. Modeling and recognition of regulatory motifs and modules	9am	Rick Young: Programming Cell State	10
	9:30	Jesse M. Gray: Widespread Pol2 recruitment and transcription at enhancers during stimulus-dependent gene expression	11
	9:45	Yue Zhao: Inferring binding energies from selected binding sites	12
	10am	Guillaume Bourque: Extensive Binding Site Turnover in the Core Regulatory Network of Embryonic Stem Cells	13
	10:15	Coffee/Snacks/Fruit Break	
	10:45	Michael Brodsky: Identification and analysis of cis-regulatory regions based on pattern generating potential	14
	11am	Yang Ding: A Novel Algorithm for the Exact Calculation of Partition Function with respect to an Abstract Shape	15
	11:15	Sheng Zhong: A biophysical model for analysis of transcription factor interaction and binding site arrangement	16
	11:30	Pouya Kheradpour: Regulatory motifs associated with TF binding and chromatin dynamics in Drosophila & mammalian genomes	17
	11:45	Quan Zhong: Edgetic perturbation models of human inherited disorders	18
	12pm	Lunch Break / Networking Opportunities	
	1pm	Naama Barkai: Evolution of Nucleosome Positioning	19
	1:30	Pieter Meysman: Structural DNA properties for the prediction of regulator binding sites with conditional random fields	20
	1:45	Claes Wadelius: Nucleosomes are positioned in exons and have histone marks suggesting co-transcriptional splicing	21
	2pm	Eugene Bolotin: Integrated Approach for the Identification of Human HNF4α Target Genes Using Protein Binding Microarrays	22
	2:15	Coffee / Snacks / Fruit Break = Poster Set-Up for Session II	
	2:45	Damian Wojtowicz: Genome-wide mapping and computational analysis of non-B DNA structures in vivo	23
	3pm	Elizabeth A. Rach: Landscape of Transcr Initiation in Drosophila: Linking Initiation Patterns to Distinct Core Promoter Motifs	24
	3:15	Julia Lasserre: TSS detection helps unfold promoters' structure	25
	3:30	Ron Shamir : FSPIKE - Signaling Pathways Knowledge-base and Analysis Tool	26
	3:45	Regulatory Genomics Poster Session II DREAM Poster Session I (hors-d'oeuvre, snacks, refreshments)	
RG3: C.Leslie/N.Baliga. Regulatory networks	5:15	Nikolaus Rajewsky: Post-transcriptional Gene Regulation by Small RNAs and RNA Binding Proteins	27
	5:45	Stein Aerts : A transcriptional regulatory network for retinal differentiation in Drosophila	28
	6pm	Raja Jothi: Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture	29
	6:15	Andrew J. Gentles: A pluripotency signature predicts histological transformation/influences survival in follicular lymphoma patients	30
	6:30	Break / light snacks	
	6:45	Ferhat Ay: Scalable Steady State Analysis of Boolean Biological Regulatory Networks	31
	7pm	Lucia Marucci: How to turn a genetic circuit into a synthetic tunable oscillator, or a bistable switch	32
	7:15	Todd Wasson: An Ensemble Model of Competitive Multi-factor Binding of the Genome	33
	7:30	Jeremy Bellay: An efficient and exhaustive approach for modular decomposition of global genetic interaction networks	34
	7:45	Justin Kinney: Regulatory physics from DNA sequence data	35
	8pm	Erez Lieberman-Aidan - Consequences of the fractal globule model for chromatin dynamics in the nucleus	36
	8:15-9:45p	Dinner out on the town	

Friday, Dec 4

Session	Time	Program	#
	8am	Breakfast	
RG3 Continuation	9am	Kevin White: Transcriptional regulatory networks: from development to disease	37
	9:30	Zhi Xie: Global Analysis of Human Protein-DNA Interactions for Annotated and Unconventional DNA-Binding Proteins	38
	9:45	Manikandan Narayanan: Simultaneous clustering of multiple gene expression and physical interaction datasets	39
	10am	Andrei L. Turinsky: Literature Curation of Protein Interactions: Discrepancies Across Major Public Databases	40
	10:15	Welcome / DREAM Registration	
DR1: F.Roth. Modeling and Reverse Engineering Signaling Networks	10:45	Saez-Rodriguez: Discrete logic modeling to link pathway maps and functional analysis of mammalian signal transduction	41
	11am	Alexopoulos: Drug Effects via Pathway Alterations using Integer Linear Programming Optimization on Phosphoproteomic Data	42
	11:15	Wagner: Crosstalk among RTKinases from micro-Western phosphoprot. arrays using Bayesian networks, ARACNe, and CLR	43
	11:30	Garry Nolan: Single Cell Signaling & Pathology in Autoimmunity & Cancer	44
	12pm	Lunch Break / Networking Opportunities	
DR2: G. Stolovitzky. DREAM4 Challenges	1pm	Philip M. Kim: Peptide Recognition Domain (PRD) Specificity Prediction (DREAM 4 Challenge 1)	45
	1:15	Julio Saez-Rodriguez: Challenge 3: Predictive Signaling Network Modeling (DREAM 4 Challenge 3)	46
	1:30	Robert J. Prill: Challenges 1 and 3 overall results	
	1:45p	Best Prediction Teams 10 min Presentations - Peptide Recognition SH3 - PBIL: Kim, Hong, Chung - Peptide Recognition Kinase - Predikin: Ellis, Saunders, Kobe - Recognition PDZ - Chuck_Daly: Yanover, Zaslavsky, Bradley - Signaling Network - Giano4: DiCamillo, Corradin, Toffolo - Signaling Network - Team Steam: Schwacke	
	2:35	Short Break = RG poster take-down	
	2:45	Daniel Marbach: Generating realistic benchmarks for network inference: the DREAM4 in silico network challenge (Challenge 2)	47
	3pm	Robert J. Prill: Challenge 2 overall results	
	3:15-3:55p	In Sillico Network Best Prediction 10 min Presentations: Size 10 - Team amalia: Küffner, Erhard, Petri, Windhager, Zimmer Size 100 - Team ALF: Pinna, Soranzo, de la Fuente Size 100 - Bonneau: Greenfield, Madar, Ostrer, Bonneau Size 100 Multifact - ulg_biomod: Irrthum,Wehenkel,Geurts,Huynh-Thu	
DR3: P.Sorger. Modeling and Rev. Eng. Regulatory Networks.	3:55p	Short Break == SB registration open / Poster Set-up Systems Bio	
	4:15	Michael Yaffe: Systems Biology of DNA Damage and Repair	48
	4:45	Qian: Effective Identification of Conserved Pathways in Biological Networks Using Hidden Markov Models	49
	5pm	Marbach: Revealing strengths and weaknesses of methods for gene network inference	50
	5:15	Lefebvre: Human B Cell Interactome Identifies MYB and FOXM1 as Master Regulators of Proliferation in Germinal Centers	51
	5:30	Iorio: DRUg NETwork (DRUNET): a new and powerful approach to identify drug mode of action from gene expression profiles	52
	5:45	SB Welcome Remarks	
SB1: A.Ma'ayan/D.Vitkup. Rev. Eng. and Interrogation of Cellular Networks	6pm	Nevan J. Krogan: Functional Insights from Protein-Protein and Genetic Interaction Maps	53
	6:30	Tomer Benyamini: Metabolic Flux Balance Analysis with Context-dependant Biomass	54
	6:45	Yongjin Park: Dynamic networks from hierarchical Bayesian graph clustering	55
	7pm	Break / light snacks	
	7:15	Christina Chan: A dynamic analysis of IRS-PKR signaling in liver cells: a discrete modeling approach	56
	7:30	Doron Betel: Comprehensive modeling of microRNA targets: predicting functional non-conserved and non-canonical sites	57
	7:45	Franziska Michor: The Cell of Origin of Human Cancers	58
	8:15-9:45p	Systems Biology Poster Session I DREAM Poster Session II Systems Biology Welcome Reception (hors-d'oeuvre, snacks)	

Saturday, Dec 5

Session	Time	Program	#
	8am	Breakfast	
SB1 Continuation	9am	Jef D. Boeke: Building Saccharomyces cerevisiae v2.0: The Synthetic Yeast Genome Project	59
	9:30	Diogo Camacho: Decoding small RNA networks in bacteria	60
	9:45	Benjamin Logsdon: Regulatory network reconstruction from genome-wide gene expression and genotype data	61
	10am	Byung-Jun Yoon: Accurate and Reliable Cancer Classification Based on Probabilistic Inference of Pathway Activity	62
	10:15	Coffee / Snacks / Fruit Break	
SB2: J.Collins/D.di Bernardo. SB Applications: Development, Disease, and Drugs	10:45	Mark Brynildsen: Metabolic strategies to enhance antibiotics action	63
	11am	Andrej Bugrim: Integrated analysis of genomic/proteomic data reveals growth factor signaling network role in prostate cancer	64
	11:15	Antti Larjo: Simulating combined chemotactic and metabolic response using a visual formalism	65
	11:30	Manway Liu: Gene Network Analysis of Diabetes Susceptibility Models	66
	11:45	Arjun Raj: Expression variability underlies incomplete penetrance in C. elegans: single-molecule studies of single-cell development	67
	12pm	Lunch Break / Networking Opportunities	
	1pm	Ihor R. Lemischka: Pursuing Pluripotency: Systems Level Quantitative Approaches to Understand Stem Cell Fate Decisions	68
	1:30	Dennis Vitkup: Systems Biology Analysis and Prediction of Human Disease Genes	69
	1:45	Tomer Shlomi: Predicting Metabolic Engineering Knockout Strategies for Chemical Production w/ Competing Pathways	70
SB3: P.Tamayo/R.Sharan. Systems Biology analysis of physiologic and pathologic molecular signatures.	2pm	Jun Zhu: Characterizing dynamic changes in the Human blood transcriptional network	71
	2:15	Coffee / Snacks / Fruit Break == Poster Set-Up for Session II	
	2:45	Tal Peleg: Network-free Inference of Knockout Effects in Yeast	72
	3pm	Uri David Akavia: Conexic: A Bayesian framework to detect drivers and their function uncovers endosomal signature in Melanoma	73
	3:15	Aedin Culhane: Large Scale Gene Set Analysis of Stem Cell and Oncology Gene Expression Signatures	74
	3:30	Gang Fang: Subspace Differential Coexpression Analysis for the Discovery of Disease-related Dysregulations	75
	3:45	Systems Biology Poster Session II (hors-d'oeuvres, snacks, refreshments)	
	5:15	Edward Marcotte: Insights from Proteomics Into Cellular Evolution and Surprising Disease Models	76
	5:45	Kenzie MacIsaac: Novel methods for the discovery of condition specific master regulators of transcription	77
	6pm	Franck Rapaport: Determining frequent patterns of copy number alterations in cancer	78
	6:15	Guy Zinman: New insights into cross-species conservation of functional data	79
	6:30	Break / light snacks	
SB4: F.Michor/Y.Kluger. Modeling and Simulation	6:45	Theodore J. Perkins: Estimating the Stochastic Bifurcation Structure of Cellular Networks	80
	7pm	Önder Kartal: Ground State Robustness as an Evolutionary Design Principle in Signaling Networks	81
	7:15	Jonathan Bieler: Modeling 3D Flies: reconstructing the drosophila segmentation network on the embryo geometry	82
	7:30	John Reinitz: Finding the Rules by Asking the Right Questions: Lessons From Non-Modular Behavior of the eve Promoter	83
	8pm-11p	Conference Reception at the MIT Museum (Warm Food, Cash Bar, Jazz Band, Wild Robots)	

Sunday, Dec 6

Session	Time	Program	#
	8am	Breakfast	
SB4 Continuation	9am	Walter Fontana: Combinatorial Complexity in Systems Biology	84
	9:30	Elhanan Borenstein: Super-Metabolism and Functional Capacity in Microbial Communities	85
	9:45	Niels Klitgord: Predicting synthetic environments that induce microbial cross-feeding	86
	10am	Vebjorn Ljosa: Large-scale learning of cellular phenotypes from images	87
	10:15	Coffee / Snacks / Fruit Break	
	10:45	Sarah Richardson: Automated Design of Assemblable, Modular, Synthetic Chromosomes	88
	11am	Tamir Tuller: Reconstructing Ancestral Gene Content by Co-Evolution	89
	11:30	Business meeting and announcement of next year's venue	
	11:45	Closing remarks and adjourn == Poster Take-down	

Original Full Length Paper
Invited Speaker
Regulatory Genomics
DREAM
Systems Biology

REGULATORY GENOMICS KEYNOTES

MARK BIGGIN
BOB WATERSTON
RICK YOUNG
NAAMA BARKAI
NIKOLAUS RAJEWSKY
KEVIN WHITE

DREAM4 KEYNOTE SPEAKERS:

GARRY NOLAN
MICHAEL YAFFE

SYSTEMS BIOLOGY KEYNOTES

NEVAN J. KROGAN
FRANZISKA MICHOR
JEF D. BOEKE
IHOR R. LEMISCHKA
EDWARD MARCOTTE
JOHN REINITZ
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