

7th Annual RECOMB Satellite on

SYSTEMS BIOLOGY

6th Annual RECOMB Satellite on

REGULATORY GENOMICS

4th Annual Dialogue on

DREAM4

Reverse Engineering Challenges

Dec 2-6, 2009
Broad Institute of MIT and Harvard

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The Joint RECOMB Satellite meeting on Regulatory Genomics, Systems Biology, and DREAM4 will be at MIT, jointly held by the Broad Institute of MIT and Harvard, and the MIT Computer Science and Artificial Intelligence Lab (CSAIL). The goal of the meeting is to bring together computational and experimental scientists in the area of regulatory genomics and systems biology, to discuss current research directions, latest findings, and establish new collaborations towards a systems-level understanding of gene regulation and cellular systems. Welcome to all!

Invited Keynote Speakers

REGULATORY GENOMICS:

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

DREAM4:

GARRY NOLAN
MICHAEL YAFFE

SYSTEMS BIOLOGY:

NEVAN J. KROGAN
FRANZISKA MICHOR
JEFF D. BOEKE
IHOR R. LEMISHCHKA
EDWARD MARCOTTE
JOHN REINITZ
WALTER FONTANA

CONFERENCE CHAIRS:

MANOLIS KELLIS
ZIV BAR-JOSEPH
ANDREA CALIFANO
GUSTAVO STOLOVITZKY

Wednesday, Dec 2	
3pm	Conference check-in open, Poster session I set-up
5pm	Welcome Remarks
5:15	Mark Biggin: Evidence for Quantitative Transcription Networks
5:45	Sarah E. Chuang: Widespread transcriptional repression by uORFs: implications for variation and disease
6pm	Tal Katz: Binding Preferences of RNA-binding Proteins from Noisy MicroRNA Data
6:15	Matteo Pellegrini: Human DNA methylation at single-base resolution reveals widespread cell-specific epigenetic signatures
6:30	Break / light snacks
6:45	Clifford A. Meyer: Inferring Transcription Regulators using H3K4me2 Marked Nucleosome Occupancy Data
7pm	Jason Erwin: Discovery and characterization of chromatin states from combinatorial histone marks
7:15	Matteo Pellegrini: Human DNA methylation at single-base resolution reveals widespread cell-specific epigenetic signatures
7:30	Leandro Morán: Fundamentals of different strategies of gene regulation in bacterial and eukaryotes
7:45	Bob Waterston: Deciphering the C. Elegans Embryonic Regulatory Network
8:15-9:45p	Regulatory Genomics Poster Session I Regulatory Genomics Welcome Reception (hors-d'oeuvre, snacks, refreshments, wine, cash bar)

Thursday, Dec 3		Friday, Dec 4		Saturday, Dec 5		Sunday, Dec 6	
8am	Breakfast	8am	Breakfast	8am	Breakfast	8am	Breakfast
9am	Blick Young: Programming Cell State	9am	Kevin White: Transcriptional regulatory networks: from development to disease	9am	Jeff D. Boeke: Building Saccharomyces cerevisiae v2.0: The Synthetic Yeast Genome Project	9am	Walter Fontana: Combinatorial Complexity in Systems Biology
9:30	Jesse M. Gray: Widespread Pu2 recruitment and transcription at enhancers during stimulus-dependent gene expression	9:30	Zhi-Xie: Global Analysis of Human Protein-DNA Interactions for Annotated and Unannotated DNA-Binding Proteins	9:30	Diego Camacho: Decoding small RNA networks in bacteria	9:30	Ethan Borenstein: Super-Metabolism and Functional Capacity in Microbial Communities
9:45	Yue Zhao: Inferring binding energies from selected binding sites	9:45	Mankandan Narayanan: Simultaneous clustering of multiple gene expression and physical interaction datasets	9:45	Benjamin Lounsbury: Regulatory network reconstruction from genome-wide gene expression and genotype data	9:45	Nees Kilian: Predicting synthetic environments that induce microbial cross-feeding
10am	Gaillaume Bourque: Extensive Binding Site Turnover in the Core Regulatory Network of Embryonic Stem Cells	10am	Andrei L. Turinsky: Literature Curation of Protein Interactions: Discrepancies Across Major Public Databases	10am	Bing-Jian You: Accurate and Reliable Cancer Classification Based on Probabilistic Inference of Pathway Activity	10am	Yablon Lissa: Large-scale learning of cellular phenotypes from images
10:15	Coffee / Snacks / Fruit Break	10:15	Welcome / DREAM Registration	10:15	Coffee / Snacks / Fruit Break	10:15	Coffee / Snacks / Fruit Break
10:45	Michael Brody: Identification and analysis of cis-regulatory regions based on pattern generating potential	10:45	Saez Rodriguez: Discrete logic modeling to link pathway maps and functional analysis of mammalian signal transduction	10:45	Mark Brylinski: Metabolic strategies to enhance antibiotics action	10:45	Sarah Richardson: Automated Design of Assemblable, Modular, Synthetic Chromosomes
11am	Yanqing Ding: A Novel Algorithm for the Exact Calculation of Partition Function with respect to an Abstract Shape	11am	Atsushi Ogino: Drug Effects via Pathway Alterations using Integer Linear Programming Optimization on Phosphoproteomic Data	11am	Andrei Buzgari: Integrated analysis of genomics/proteomic data reveals growth factor signaling network role in prostate cancer	11am	Lars Tjell: Reconstructing Ancestral Gene Content by Co-Evolution
11:15	Sheng Zhang: A biophysical model for analysis of transcription factor interaction and binding site arrangement	11:15	Wagner, Christakos among RTKinases from micro-Western spotarrays: arrays using Bayesian networks, ARACNe, and CLR	11:15	Antti Lahti: Simulating combined chromatin and metabolic response using a visual formalism	11:30	Business meeting and announcement of next year's venue
11:30	Rouay Choudhury: Regulatory motifs associated with TF binding and chromatin dynamics in Drosophila & mammalian genomes	11:30	Garry Nolan: Single Cell Signaling & Pathology in Autoimmunity & Cancer	11:30	Manhua Liu: Gene Network Analysis of Diabetes Susceptibility Models	11:45	Closing remarks and adjourn + Poster Take-down
11:45	Shan Zhang: Edgetic perturbation models of human inherited disorders	12pm	Lunch Break / Networking Opportunities	12pm	Lunch Break / Networking Opportunities		
12pm	Lunch Break / Networking Opportunities	12pm	Lunch Break / Networking Opportunities	12pm	Lunch Break / Networking Opportunities		
1pm	Naama Barkai: Evolution of Nucleosome Positioning	1pm	Philip M. Kim: Peptide Recognition Domain (PRD) Specificity Prediction (DREAM 4 Challenge 1)	1pm	Ihor R. Lemishchka: Pursuing Pluripotency: Systems Level Quantitative Approaches to Understand Stem Cell Fate Decisions		
1:30	Rieder Maysman: Structural DNA properties for the prediction of regulator binding sites with conditional random fields	1:30	Robert J. Pridi: Challenges 1 and 3 overall results	1:30	Dennis Vilup: Systems Biology Analysis and Prediction of Human Disease Genes		
1:45	Giles Westhead: Nucleosomes are positioned in exons and have histone marks suggesting co-transcriptional splicing	1:45	Best Prediction Teams 10 min Presentations - Peptide Recognition SH3 - DIBL, Kim, Hong, Chung - Peptide Recognition Kinase - Preskitt, Ellis, Saunders, Kobe - Recognition POZ - Chuck, Daly, Yanover, Zaslavsky, Bradley - Signaling Network - Ganou, DiCamillo, Corradin, Toffolo - Signaling Network - Team Sileas, Schwabe	1:45	Imanet Ozbun: Predicting Metabolic Engineering Knockout Strategies for Chemical Production via Compelling Pathways		
2pm	Eugene Biolinski: Integrated Approach for the Identification of Human HNF-1c Target Genes Using Protein Binding Microarrays	2pm	Short Break = RD poster take-down	2pm	Jun Zhu: Characterizing dynamic changes in the Human blood transcriptional network		
2:15	Coffee / Snacks / Fruit Break = Poster Set-Up for Session II	2:15	Short Break = RD poster take-down	2:15	Coffee / Snacks / Fruit Break = Poster Set-Up for Session II		
2:45	Bertram Wollberg: Genome-wide mapping and computational analysis of non-B DNA structures in vivo	2:45	Robert J. Pridi: Challenge 2 overall results	2:45	Tal Peleg: Network-free Inference of Knockout Effects in Yeast		
3pm	Elizabeth A. Rugh: Landscape of Transcription Initiation in Drosophila: Uniform Initiation Patterns to Distinct Core Promoter Motifs	3pm	Robert J. Pridi: Challenge 2 overall results	3pm	Uli David Alexander: Context: A Bayesian framework to detect drivers and their functional uncovers endosomal signature in Melanoma		
3:15	Lidia Lassone: TSS detection helps unfold promoters' structure	3:15	In Silico Network Best Prediction 10 min Presentations: - Size 10 - Team anika: Kuffner, Erhard, Peck, Windhager, Zimmer - Size 100 - Team ALP: Eliza, Soriano, de la Fuente - Size 100 - Bonneau: Greenfield, Madar, Ocher, Bonneau - Size 100 Multifit - uig, diomond, jtrumb, Wehenkel, Geurts, Huyhng-Thu	3:15	Andin Cuhance: Large Scale Gene Set Analysis of Stem Cell and Oncology Gene Expression Signatures		
3:30	Ron Sharm: TSPiKE - Signaling Pathways Knowledge-base and Analysis Tool	3:30	Short Break = SB registration open / Poster Set-up Systems Bio	3:30	Jonathan Eisler: Modeling 3D Free-convection Analysis for the Discovery of Disease-related Dysregulations		
3:45	Regulatory Genomics Poster Session II (DREAM Poster Session I) (hors-d'oeuvre, snacks, refreshments)	3:45	Systems Biology Poster Session II (hors-d'oeuvre, snacks, refreshments)	3:45	Edward Marcotte: Insights from Proteomics into Cellular Evolution and Surprising Disease Models		
5:15	Nikolaus Rajewsky: Post-transcriptional Gene Regulation by small RNAs and RNA Binding Proteins	5:15	Michael Yaffe: Systems Biology of DNA Damage and Repair	5:15	Kenzie McIsaac: Novel methods for the discovery of condition specific master regulators of transcription		
5:45	Steen Aertj: A transcriptional regulatory network for retinal differentiation in Drosophila	5:45	Qian: Effective Identification of Conserved Pathways in Biological Networks Using Hidden Markov Models	5:45	Frank Rappaport: Determining frequent patterns of copy number under Karlin: Ground State Robustness as an Evolutionary Design Principle in Signaling Networks		
6pm	Raja Subh: Genomic analysis reveals a link between transcription factor dynamics and regulatory network architecture	6pm	Leahure: Human B Cell Interactions identifies MYB and FOXM1 as Master Regulators of Proliferation in Germinal Centers	6pm	Guo Zhen: New insights into cross-species conservation of functional data		
6:15	Andrew J. Gentles: A pluripotency signature predicts histological transformation/influences survival in follicular lymphoma patients	6:15	Tomer Benayahu: Metabolic Flux Balance Analysis with Context-dependent Biomass	6:15	Break / light snacks		
6:30	Break / light snacks	6:30	Yongxin Pei: Dynamic networks from hierarchical Bayesian graph clustering	6:30	Theodore J. Perkins: Estimating the Stochastic Bifurcation Structure of Cellular Networks		
6:45	Erithal Av: Scalable Steady State Analysis of Boolean Biological Regulatory Networks	6:45	Tomer Benayahu: Metabolic Flux Balance Analysis with Context-dependent Biomass	6:45	Order Karlin: Ground State Robustness as an Evolutionary Design Principle in Signaling Networks		
7pm	Lidia Lassone: How to turn a genetic circuit into a synthetic tunable oscillator, or a stable switch	7pm	Break / light snacks	7pm	Jonathan Eisler: Modeling 3D Free-convection Analysis for the Discovery of Disease-related Dysregulations		
7:15	Lidia Lassone: An Ensemble Model of Competitive Multi-factor Binding of the Genome	7:15	Christina Chan: A dynamic analysis of IRS-PKR signaling in liver cells: a discrete modeling approach	7:15	John Beitzel: Finding the Rules by Asking the Right Questions: Lessons From Non-Monotonic Behavior of the eve Promoter		
7:30	Jeremy Bellay: An efficient and exhaustive approach for modular decomposition of global genetic interaction networks	7:30	Robert J. Pridi: Challenge 3 overall results	7:30	Conference Reception at the MIT Museum (Warm Food, Cash Bar, Jazz Band, Wild Robots)		
7:45	Justin Kimmerly: Regulatory physics from the DNA sequence data	7:45	Erithal Av: Scalable Steady State Analysis of Boolean Biological Regulatory Networks				
8pm	Erez Lieberman-Aidan: Consequences of the fractal globule model for chromatin dynamics in the nucleus	8pm	Systems Biology Poster Session I (DREAM Poster Session II)				
8:15-9:45p	Dinner out on the town	8:15-9:45p	Systems Biology Welcome Reception (hors-d'oeuvre, snacks)				

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