Systems Biology: Global Regulation of Gene Expression

KEYNOTE SPEAKER

1	Aderem	A systems approach to dissecting immunity

Session 1 OVERTURE

THURSDAY 3/23/2006, 7:30 PM

J. Keene

#	lname	Title	Talk Length
2	Friedman	Reconstructing the yeast osmolarity regulatory network—Flexible processing by rewiring and cross-talk	15
3	Levine	Gene networks for fly gastrulation and sea squirt cardiogenesis	15
	Vidal	Title only: Towards a proteome-scale map of the human interactome network	15
	Barkai	Title only: Comparative analysis of gene expression data in closely related species	15
4	Tenenbaum	Computational tools for the genomic-scale identification of genomic regulatory	15

Session 2 COMPUTATIONAL APPROACHES TO IDENTIFYING CIS-

FRIDAY 3/24/2006, 9:00 AM

N. Friedman

#	lname	Title	Talk Length
5	Wasserman	Wet-dry cycles to link transcription factors with subsets of co-expressed genes	15
6	Benham	How DNA superhelicity affects strand separation events involved in regulation	15
7	Weng	Bidirectional promoters in the human genome	15
8	Segal	Genomes utilize a nucleosome positioning code to achieve biological function	15
9	Bussemaker	Quantifying the sequence specificity of transcription factors via statistical mechanical modeling of genome-wide occupancy data and structure-based prediction	15
10	Tanay	Extensive low-affinity transcriptional interactions in the yeast genome	15
11	Blanchette	Genome-wide computational prediction of transcriptional regulatory modules reveals new insights into human gene expression	15
12	Andrews	Phenotypic activation to explore gene toxicity and transcription factor functions	15
13	Williams	Systems genetics of gene expression and the use of reference populations to integrate across biological scales	15

Session 3 POSTER SESSION I

FRIDAY 3/24/2006, 1:30 PM

#	lname	Title	Talk Length
14	Agnew	Regulation of molecular rearrangements of alternatively spliced calcium channel structure during brain development—Profiling single-gene transcriptomes	
15	Andersen	A computational resource for the exploration of regulatory sequence variation	
16	Babak	Genome wide identification of conserved secondary structures in mammals	

17	Banerjee	Transcription factor centric discovery of regulatory elements in mammalian genomes using alignment-independent conservation maps
18	Barrera	Systematic characterization of promoters in mammalian tissues
19	Bengani	In silico approach to decipher mechanisms of regulation of homeotic genes in mammalian system
20	Berg	Functional alignment of biological networks
21	Berger	A compact, universal DNS microarray to determine the DNA binding specificities of transcription factors
22	Beyer	Revealing combinatorial regulation via an integrated quantification of transcription factor binding
23	Bezdan	Global identification of Hox response enhancers in *D. melanogaster*
24	Bieda	Unbiased location analysis of E2F1 binding sites suggests a widespread role for E2F1 in the human genome
25	Bolotin	High throughput approach for determination of HNF4α response elements
26	Boutros	Enhancing searches for molecular markers—Normalization and linear modeling improve the sensitivity of ChIP-chip studies
27	Brady	Transcriptional networks in the *Arabidopsis* root—A tissue-specific approach
28	Brauer	The metabolomic and transcriptional program of entry into quiescence in yeast and bacteria
29	Brauer	The yeast environmental stress response is primarily the results of decreased
30	Bristow	Systems level analysis of EGFR and BMP mediated gene expression in *Drosophila* oogenesis
31	Sandelin	Promoting mammalian transcription
32	Caudy	Genomic analysis of combinatorial and architectural DNA transcription codes mediating Notch signaling in a neural differentiation pathway
33	Chan	Comparative transcriptomics in vertebrates
34	Chechik	Temporal motifs in transcriptional control of metabolic transitions
35	Chen	Identify functional regulons by integrating heterogeneous data with Bayesian hierarchical modeling
36	Wang	Hierarchical organization of the yeast transcriptional regulatory network
37	Chen	Tissue-specific cis-regulatory modules prediction using Bayesian network and probability trees
38	Chesler	Combinatorial methods for systems genetics analysis
39	Clarke	Conservation of transcription factor binding potential in unaligned sequences—Prediction of co-regulation and a tool for the study of regulatory region
40	Newberg	Phylogenetic Gibbs Recursive Sampler—Finding transcription factor binding sites

41	Cui	A ChIP-chip approach to dissecting the transcriptional network underlying radial patterning in the *Arabidopsis* root
42	Dan	Identifying *Drosophila* transcription start site elements by comprehensive analysis of overrepresented sequences (CAOS)
43	Datla	Gene expression and network dynamics during embryo development in *Brassica* and *Arabidopsis*
44	Missero	p63 function in development and disease—A systems biology approach
45	Dieterich	Specifying the scope of action of micro RNAs
46	Dimitrova	Spectral analysis of CpG islands
47	Dinneny	Examining the effects of environmental stimuli on transcriptional profiles in the *Arabidopsis* root
48	Djordjevic	Search for transcription factor binding sites—Some principal limits and a novel
49	Doniger	Lineage specific loss and turnover of transcription factor binding sites
50	Doolan	Microarray and proteomics analysis of BrdU-DLKP—A systems biology approach to understanding differentiation in lung cancer cells
51	Oltvai	Topological basis of signal integration in the transcriptional-regulatory network of the yeast, *S. cerevisiae*
52	Farkash	Evidence for an instructive mechanism of de novo methylation in cancer
53	Foat	Inferring sequence specificity, condition-specific activity, and functional regulatory targets of yeast transcription factors by integrative modeling of mRNA expression data, ChIP-chip data, and genomic sequence
54	Fouquier d'Herouel	Transcription factor concentrations vs. binding site affinities in the yeast *S. cerevisiae*
55	Fujibuchi	Human cell type and morphology prediction by gene expression patterns
56	Gagneur	A compendium of gene expression time series of developmental transcription factor mutants in *D. melanogaster*
57	Gat-Viks	A computational methodology for improving the knowledge on biological networks
58	Buckley	Transcriptional programs and neuronal gene expression
59	Grosse	Reconstruction of Bayesian networks from mRNA and metabolic expression data
60	Guo	Characterization of human cytoglobin gene promoter region
61	Hanlon	Rap1 and meiosis—A model for activation and repression by a single transcription
62	Hollenhorst	Redundant and specific targets of ETS transcription factors
63	Prakash	Discovery of yeast regulatory elements by phylogenetic footprinting
64	Hughes	Towards explaining global regulation of vertebrate gene expression
65	Ito	Synthesis of artificial transcription cofactors mimicking HMG protein

66	Sato	Quantative analysis of circadian gene expression and signaling pathways in mammalian fibroblast cells
67	Jagalur	An information theoretic approach to constructing genetic regulatory networks of cis- and trans-acting loci
68	Johnson	Whole genome identification of coding and non-coding target genes of the transcriptional repressor, REST
69	Aburatani	An integrated map of p53-binding and histone modification in the human genome
70	Kao	Genome remodeling during real-time speciation
71	Kato	*Motifcombinator*—A web-based tool for identifying combinations of cis-regulatory motifs in mammalian genomes
72	Khavinson	Tetrapeptide induces gene expression in case of interaction with TATA-box site
73	Kim	Frequent localization of clustered YY1 binding sites in imprinting control regions
74	Kinney	Accurate models of protein-DNA interaction from simulated annealing
75	Kirova	Discovering genetic regulatory loci for gene expression using graph theory coupled with principal component and factor analysis
76	Kluger	Characterizing disease states from topological properties of transcriptional regulatory networks
77	Kolesov	The selfish gene cluster hypothesis cannot explain the widespread co-localization of transcription factors and their binding sites
78	Mirny	Physical constrains on reliable gene regulation, and genome organization that overcomes them
79	Konieczka	A comprehensive approach to elucidate the epithelial-mesenchymal transition system in chick gastrulation
80	KUNDAJE	Using predictive modeling to decipher the oxygen sensing and regulatory network in
81	Kusmider	Using "mouse neurotrophins & receptors" superarray GEArray Q series macroarray for rat brain tissue
82	Leandro-Garcia	The coevolution of muscle troponin gene isoforms in Drosophilids
83	Im	Identification and characterization of distal regulatory elements of the IL-10 locus in
84	Swiss	Understanding Msx1 homeoprotein DNA binding specificity
85	Halfon	Distinguishing regulatory from non-regulatory sequences—Insights from the *REDfly* database
86	Li	Model-based analysis of tiling-array (MAT) and its application towards the first definition of the nuclear receptor regulome
87	Li	Genome wide mapping of the in vivo DNA binding sites of transcriptional regulators of the *Drosophila* pregastrula gene network
88	Lawrence	Beyond HMMs—A hierarchical model for inhomogeneous tiled array observations

89	Siggia	Gene expression from random libraries of yeast promoters
90	Liu	Predicting DNA-binding sites of gene regulatory proteins by molecular simulation and homology modeling
91	Liu	*Motifmodeler*—Identification of transcription-factor binding sites using microarray
92	Long	Responses of root regulatory networks to iron deficiency
93	Macedo	A systems biology perspective of virus-host interactions
94	MacKenzie	5 dimensional biology—Bioinformatic and transgenic approaches to understanding gene regulatory systems
95	De Simone	Gene expression profile analysis by RNA microarrays in familial combined hyperlipidemia patients
96	Martinez	Computational prediction of novel components of the lung transcriptional network
97	Matilainen	Multiparameter model for the prediction of nuclear receptor target genes
98	Moreno	Hormonal and developmental regulation of micro-RNAs in prostate cancer cells
99	McCord	Predicting yeast transcription factor function from DNA binding specificities and expression data
100	McGettigan	Promoter analysis of genes involved in learning and memory
101	McKee	Genome scale identification of alternative exon use in neuroblastoma cells in response to membrane depolarization
102	Grosse	Identification of transcription factor binding sites in seed specific promoters in *A. thaliana*
103	Morohashi	Targets of the GLABROUS3 transcription factor during trichome initiation in *A. thaliana*
104	Morozov	Using rules of DNA mechanics and structural models to predict nucleosome positioning code in eukaryotic genomes
105	Murakami	InCeP—Intracellular pathway based on mKIAA protein-protein interactions
106	Murphy	Multiple transcriptional pathways are cross-regulated by insulin-like peptides to regulate longevity

Session 4 POSTER SESSION II and WINE & CHEESE PARTY

FRIDAY 3/24/2006, 4:00 PM

#	lname	Title	Talk Length
107	Ng	An integrative systems-wide network analysis of inflammatory responses	
108	Nibu	The dCtBP corepressor may prevent DNA-binding of an activator in the early *Drosophila* embryo	
109	Nie	SUMO'omics and fly development	
110	Niida	Integrative bioinformatics analysis that deconvolutes the changes of transcriptional regulatory programs during cancer progression	

111	Nordlund	Identification of novel in vivo binding sites for STAT6 in IL4/STAT6 co-regulated genes
112	Okada	Identification of genes specific for morphologically and embryologically distinct
113	Bina	Transcription factor binding and functional properties of conserved and not conserved DNA sequence elements in genomic DNA
114	Ray	A systems level analysis of links between the transcriptome and chromosome
115	Ray	MicroRNA regulatory network in keratinocyte differentiation
116	Philippakis	Expression-guided in silico evaluation of candidate *cis* regulatory codes in the developing *Drosophila* mesoderm
117	Polouliakh	Comparative genomic analysis of transcription regulation elements in higher eukaryotes with the motif discovery tool shoe
118	Ptitsyn	The true prominence of oscillating patterns in gene expression and its implications in modeling of biological pathways
119	Wadelius	The major epigenetic effect of the histone deacetylase inhibitor butyrate is a paradoxical decrease in promoter histone acetylation and decrease in gene activity
120	Radovic	*cis*-acting regulatory variation affecting maize gene expression
121	Reimers	Gene expression variation as a mark of interest in complex disease
122	Zhao	Identification of non-conserved transcriptional regulatory elements by histone acetylation islands
123	Cobellis	Identification of pathways involved in cell fate decision—The cardiomyocytes tale
124	Roni	Identification of transcription start sites of retinal expressed genes
125	Rozenberg	CREB is bound to specific motifs clustered 100 Bp upstream of transcription start
126	Ripatti	Comparative analysis of gene structure and gene expression in vertebrates
127	Sanges	Identification of shuffled conserved elements (SCEs) reveals much greater extent of functional conservation among vertebrate genomes than previously observed
128	Schones	Elucidating regulatory networks in adipose
129	Schug	Bounded collection grammars and the language of gene regulation
130	Seppänen	In silico promoter analysis of human V- and F-ATPase complexes
131	Sharov	Towards genome-wide analysis of transcription regulation in mouse
132	Shefi-Novershtern	Stochastic integrative modeling of transcription regulation
133	Sleumer	De novo detection of regulatory modules in *C. elegans*
134	Smith	DNA motifs in human and mouse proximal promoters predict tissue specific
135	Sprinzak	Reconstructing regulatory relations between pathways using logic analysis
136	Starkey	Intelligent searching algorithm for novel motif detection

137	Stoytcheva	In silico gene regulation study of human selenoproteins
138	Talukder	Seeking new *cis*-regulatory regions via the DNA-binding specificity of tissue specific transcription factors
139	Tepper	Pixel-derived quality metrics for cDNA microarrays
140	Thomas	Chromosomal domains of gene regulation—From yeast to mammals
141	Tsaih	Linear model genome scans for expression QTL analysis
142	Tsankov	Communication between levels of the transcriptional architecture improves robustness and adaptivity in eukaryotic cells
143	Tuomela	Characterization of a novel signaling pathway leading to Th2 cell differentiation
144	Van Loo	Computational detection of tissue- and process-specific *cis*-regulatory modules by a maximum specificity method
145	Journot	Identification of a network of imprinted genes that critically controls embryonic development
146	Vokes	Transcriptional interpretation of morphogen gradients—Identifying Gli targets of Hedgehog signaling
147	Vuorikoski	Transcriptional regulation in development of human osteoclast—The use of DNA microarray data with in silico binding site predictions and transcription factor
148	Wang	Identification of cis-regulatory sites in mammalian multi-species conserved
149	Warner	In silico analysis and discovery of cis regulatory modules in human skeletal muscle differentiation
150	Williams	Computational prediction of gene targets in yeast
151	SU	Knowledge-based transcriptional data mining on cold signal transduction pathway related to ABA catabolism in *Arabidopsis*
152	Yu	Inference of dynamic activity of transcriptional modules
153	Zhao	Boosting for predicting tissue specific non-CpG related promoters
154	Zhu	Similar sequence fragments within *Drosophila cis*-regulatory modules

Session 5 ADVANCES IN DETECTION OF TRANSCRIPTION FACTOR / DNA-

FRIDAY 3/24/2006, 7:30 PM

P. Farnham

#	lname	Title	Talk Length
155	Farnham	Suz12 silences large regions of the genom in a cell type-specific manner	15
156	Ren	Genome-wide location analysis of the RNA polymerase II pre-initiation complex in mouse embryonic stem cells and adult tissues	15
157	Myers	Systematic comparison of methylation, transcription factor binding and transcriptional activity of human promoters	15

158	Ng	Transcription regulatory circuitry in embryonic stem cells—Unbiased mapping of Oct4, Sox2 and Nanog binding sites using ChIP-PET technology	15
159	Buck	A chromatin-mediated mechanism for specification of environment-dependent transcription factor targets	15
160	Van Steensel	Hotspots of transcription factor colocalization in the genome of *D. melanogaster*	15
161	Walhout	Gene-centered protein-DNA interaction networks in the nematode *C. elegans*	15

Session 6 TRANSCRIPTIONAL AND POSTTRANSCRIPTIONAL NETWORK

SATURDAY 3/25/2006, 9:00 AM

P. Benfey

#	lname	Title	Talk Length
162	Keene	Dynamic remodeling of RNPs potentially representing post-transcriptional RNA operons in T cells	15
163	Dikstein	Computational and functional analysis of the human core promoter—Novel elements and a link to translation	15
164	Bailey-Serres	Genome-wide cell-type specific analysis of polysomal complexes	15
165	Zeller	Global mapping of c-Myc binding sites and target gene networks in a human B cell	15
166	Pe'er	Genetic variation and regulatory networks—Mechanisms and complexity	15
167	Rinn	Supra-anatomic organization of the fibroblast diversity by positional variation in gene expression programs	15
168	Snyder	Analysis of eukaryotic regulatory networks	15
169	Lécuyer	Genome-wide analysis of mRNA localization pathways	15

Session 7 COMPARATIVE GENOMICS OF GLOBAL GENE REGULATION

SATURDAY 3/25/2006, 2:00 PM

S. Mango

#	lname	Title	Talk Length
170	Mango	Genome-wide analysis of foregut development	15
171	Stubbs	Rapid expansion and divergence of zinc finger genes implies a selection for novelty in evolving vertebrate regulatory networks	15
172	Kellis	Regulatory motif discovery and evolution	15
173	Rubin	In vivo enhancer analysis of chromosome 16 conserved sequences or transgenic mouse enhancer survey of chromsome 16 conserved sequences	15
174	Ideker	Protein network comparative genomics	15
175	Gaul	Evolution of transcriptional control in the segmentation gene network of *Drosophila*	15
176	Lassig	Evolutionary innovations in regulatory DNA	15
177	Sperling	Genomic organization of transcriptomes—Coregulation and cofunctionality	15

Session 8 EMERGING TECHNOLOGIES AND CONCEPTS IN SYSTEMS BIOLOGY

SUNDAY 3/26/2006, 9:00 AM

P. Silver

#	lname	Title	Talk Length
178	Silver	Designing biological networks	15
179	Schwartz	Human genome structural variation discerned by single molecular analysis	15
180	Lim	Microarray analysis shows that microRNAs downregulate large numbers of target	15
181	Keränen	Spatio-temporal expression analysis at cellular resolution in the *Drosophila* embryo reveals new dynamics of morphology and gene expression	15
182	David	High-resolution transcriptional map indicates new functions for non-coding RNA in	15
183	Lee	Transcriptional and post-transcriptional regulation of transcription factor expression in *Arabidopsis* roots	15