

## Genome Informatics

### Session 1 HIGH THROUGHPUT GENOMICS

FRIDAY 10/28/2005, 7:30 PM

J. Harrow / B.F.F. Ouellette

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
1	Brudno	Efficient assembly with string graphs	15
2	Messina	<i>semblance</i> —A whole-genome-shotgun assembly assessment tool	15
3	Tenney	Base calling for traces derived from multiple templates	15
4	Kasahara	Draft genome sequence of medaka	15
5	Mackey	GLEAN—Improved eukaryotic gene prediction by statistical consensus of gene	15
6	Nekrutenko	Galaxy2—On-line genome analysis system for geeky and not-so-geeky types—Making experimental and computational tails of user distribution happy	15
7	Harrow	Multi-genome annotation	15
8	Sachidanandam	GeneSeer—A genomic sage for gene names and families	15

### Session 2 PATHWAYS AND PROTEOMICS I

SATURDAY 10/29/2005, 9:00 AM

P. Thomas / R. Sharan

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Sharan	No Abstract	15
9	Singh	Interrogating protein interaction networks to uncover functional modules and	15
10	Ouellette	Integrating interaction databases	15
11	Khadake	IntAct database—Working towards interaction network development and	15
12	Rachlin	Context-dependent biological networks and the emergence of scale-free properties	15
13	Novak	NUKE—Fast and scalable multiple alignment of protein interaction networks	15
14	Caudy	Whole genome analysis of combinatorial and architectural transcription codes mediating Notch signaling in a neural differentiation pathway	15
15	McKay	Loose clustering of genes encoding metabolic pathways in the reactome database	15

### Session 3 PATHWAYS AND PROTEOMICS II

SATURDAY 10/29/2005, 2:00 PM

P. Thomas / R. Sharan

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Thomas	No Abstract	15
16	Suthram	Comparative analysis of protein—Protein interaction networks	15
17	Nachman	Realistic reconstruction of regulatory networks—Cell cycle regulation in fission yeast	15
18	Lawrence	On the futility of optima in genomic and other high dimensional inferences	15

**Session 4 EPIGENOMICS**

SUNDAY 10/30/2005, 9:00 AM

A. Ferguson-Smith / R. Martienssen

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Ferguson-Smith	INTRO ONLY	
19	Greally	Identification of DNA sequence motifs that direct epigenetic organization	15
20	Schulz	A quantitative evaluation of imprinted gene detection in mice using uniparental chromosomal duplications and microarrays	15
21	Taylor	Phylogeny-based encoding of genomic sequence alignments to investigate functional elements	15
22	Ciccarelli	Evolutionary history of overlapping genes in higher eukaryotes	15
23	Buisine	Towards the definition of transposable element reference sequences---Dream or	15
24	Barbazuk	Reduced representation sequencing in maize	15
25	Vaughn	Epigenomic profiling of <i>A. thaliana</i>	15
26	Flicek	Histone modification patterns from HMM analysis of ChIP-chip data	15

**Session 7 BIRDS OF A FEATHER**

SUNDAY 10/30/2005, 12:30 PM

**Session 6 POSTER SESSION I**

SUNDAY 10/30/2005, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
27	Adlem	Tools for comparative genome analysis and annotation	
28	Albert	UNIVERSE framework for integration of biological data and analysis tools	
29	White	Sybil—Comparative analysis system	
30	Arikawa	A genome-wide and comprehensive gene expression profiling database	
31	Arumugam	Pairagon—Program for accurate cDNA to genome alignment	
32	Avraham	Plant ontology—Organizational principles and computational tools	
33	Batalov	Analysis of ten animal genomes reveals the evolutionary history of ion channel genes	
34	Dicks	ComparaGRID—Enabling technologies for comparative genomics	
35	Ochs	Identifying changes in signaling from high-throughput transcription data	
36	Sajot	POGO—A tool to query gene and plant ontology	
37	Biro	Protein folding information in nucleic acids which is not present in the genetic code	
38	Braun	Pseudogene identification and prediction of gene conversion	
39	Blankenberg	G2EMBOSS—Web-based implementation of EMBOSS tools featuring user history system, statistical tools and multiple data sources	
40	Brudno	FLARE—Progressive aligner for rearranged sequences via network flow	

41	Bruynseels	i-Lims—Managing heterogeneous geno- and phenotypical information in plants
42	Budrul	Genome annotation with 5'SAGE
43	Bult	Database-driven disease gene discovery in the laboratory mouse
44	Cain	The generic model organism database project
45	Canaran	An interactive web-based multiple sequence alignment viewer with polymorphism analysis support
46	Chen	Creation of a genome-wide high-density SNP map and development of high-throughput SNP genotyping tools for <i>D. melanogaster</i>
47	Chen	Comparative analysis of X-box gene battery in multiple nematode species
48	Davuluri	Integrative systems biology approach reveals combinatorial association of <i>c-MYC</i> and <i>ER<math>\alpha</math></i> in <i>ER<math>\alpha</math></i> activated promoters
49	Cheng	Deconvolute transcription regulation and genome organization by integrated analysis of chromatin IP and RNA expression using high-density tiling arrays
50	Dabrowski	Cis-regulatory features associated with a mode of expression common to neuronal differentiation and hippocampal development
51	Dasgupta	Conservation and clustering of ribosomal proteins
52	Dicks	From microarray to phylogeny using gene content
53	Dong	Transforming full-text literature to formalized facts
54	Dupuy	The <i>C. elegans</i> localizome project—High-throughput analysis of transgenic strains
55	Mäser	Can you tell a parasite from its genome sequence?—Comparative genomics between parasitic and free-living eukaryotes
56	Fiedler	WormBook—A paradigm for online biological review articles
58	Bussemaker	Profiling condition-specific, genome-wide regulation of mRNA stability in yeast
59	Ghosh	Exploring differential regulation patterns across the genome
60	Wortman	PASA-2—Improved automated incorporation of full-length cDNA and EST data into gene structure annotation
61	Hannick	Automated annotation pipeline for the mosquito <i>A. aegypti</i>
62	Holm	One thousand clans of protein families
63	Helt	The Integrated Genome Browser
64	Hepler	A flexible software model for event based LIMS
65	Blake	Ontological representation of complex biological systems
66	Hofmann	Comparing mouse to man—The next step in understanding the regulation of development and cancer in mammals
67	Hornischer	Promoter evolution of signal transduction pathways

68	Hurwitz	Rice gone wild—Large-scale detection of rearrangements in the genomes of wild rice in the Oryza Map Alignment Project (OMAP)
69	ITO	Protein expression pattern analysis of maternal mRNAs in <i>C. elegans</i>
70	Ivanov	Comparative analysis of U12 introns
71	Just	Dictybase—A case study of an existing genome resource adopting GMOD tools
72	Kapranov	Hidden complexities of the human transcriptome
73	Yoon	Determining transcription factors that trigger non-housekeeping genes of various human tissues
74	Keibler	An algorithm for simultaneous, parallel, optimal gene prediction on all combinations of alleles
75	King	Dissection of evolutionary constraint within a strictly defined set of ENCODE regulatory elements
76	Kirkpatrick	Genomics studies in the grapevine
77	Krishnan	Exploring HapMap with HapMart
78	Kumar	Identification and bioinformatic characterization of novel mammalian transcripts expressed in bovine placenta
79	LaFramboise	An expectation-maximization approach to determining allelic dosage in cancer from SNP array data
80	Lee	Genes involved in complex regulatory processes tend to have highly conserved upstream regions
81	Li	Pseudogene prediction in human, mouse and rat genomes
82	Durbin	TreeFam—A curated database of phylogenetic trees of animal gene families
83	Zhao	An empirical multipoint method for identifying haplotype blocks and haplotype-tagging SNPs
84	Liang	Gramene Ensembl—A tool for comparative analysis in cereal genomes
85	Spier	Design and validation of resequencing primer sets for 16,336 human genes for analyses of sequence variation and SNP discovery
86	Liu	Comparative analyses of genomic variation among mammalian genomes—Recent genome expansions and substitution patterns
87	Huang	A streaming dynamic programming model for accelerating sequence alignment
88	Loveland	Annotation challenges of the zebrafish genome
89	Lussier	Computational approaches for genome scale analyses of phenotypes—Bridging the phenotypic gap between clinical repositories and model organism databases

**Session 7 IMAGES, ATLASES AND PHENOTYPES**

SUNDAY 10/30/2005, 7:00 PM

J. Swedlow / Z. Bao

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Swedlow	INTRO ONLY	
90	Bao	Automated cell lineage tracing in <i>C. elegans</i>	15
91	Moerman	An interactive database of <i>C. elegans</i> promoter::GFP constructs	15
92	Fraser	RNAi screens to examine genetic interactions in <i>C. elegans</i> development	15
93	Hall	WormAtlas and wormImage—Two web-based resources for exploring <i>C. elegans</i> anatomy	15
94	Knowles	Berkeley <i>Drosophila</i> Transcription Network Project—3D blastoderm gene expression atlas	15
95	Burger	The Edinburg Mouse-Atlas gene expression database	15

**Session 8 GENETIC REGULATION**

MONDAY 10/31/2005, 9:00 AM

T. Down / C. Burge

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Burge	INTRO ONLY	
96	Adams	Evolution of transcription factor genes on the human lineage	15
97	Brody	Identification of conserved interlocking transcription factor DNA binding sites in coordinately regulated genes	15
98	Chan	Master regulator or methodological confounder?—Searching for multiple loci effects in genetical genomics studies	15
99	Dike	High resolution mapping of sites of transcription across the euchromatic genome through <i>D. melanogaster</i> embryonic development reveals a large number of time specific unannotated 5' start sites	15
100	Down	Computational prediction of transcription factor binding sites in <i>Drosophila</i>	15
101	Lunter	Positive selection on human non-coding functional elements	15
102	Voelker	Exonic splicing enhancers are associated with specific intronic motifs—Indication of two distinct classes of human major-spliceosomal introns	15

**Session 9 POSTER SESSION II**

MONDAY 10/31/2005, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
103	Ma	Reconstructing contiguous regions of an ancient genome	
104	Maeshiro	Structural properties of knowledge infrastructure for genome informatics	
105	Maher	Evolution of plant microRNA families through duplication events	
106	McLeod	The generic utility for research unification—Application to large genome projects	

107	Merchant	An architectural overview of a secure, robust and cross-platform integration of the Apollo genome annotation tool into a Perl web application
108	Miller	Power-law distribution of sequence lengths in the ultraconservation regime and
109	Mohler	A preliminary collection of multidimensional movies of <i>C. elegans</i> embryonic gene-expression
110	Nishikawa	Construction of cell cycle regulatory network using literature mining
111	Nishimura	Visualization for finding copy number polymorphism regions using genotyping
112	Okayasu	Cluster analyses of bacteria and archaea based on amino acid compositions and codon usages
113	Braun	Optimization and evaluation of high-throughput mutation screening
114	Orvis	Workflow/CRAM—A data management system for automated genome annotation and comparative analysis
115	Hamilton	The TIGR Rice Genome Annotation database
116	Paten	PECAN—Consistency alignment at a genome scale
117	Piccolboni	An HSMM-based algorithm for expression detection in tiling DNA microarray data
118	Pleasance	A method for genome-wide <i>cis</i> -regulatory element discovery in <i>D. melanogaster</i>
119	Popescu	Statistical algorithm for breakpoint estimation and detection of changes in chromosome copy number from comparative genomic hybridization data
120	Portales-Casamar	RegDB—Framework for collection and dissemination of <i>cis</i> -regulatory sequence annotation
121	Prendergast	Chromatin structure is implicated in genomic patterns of mutation and selection
122	Quon	Quantifying the discriminatory power of information content for transcription factor binding site discovery in yeast
123	Rassoulzadegan	RNA-mediated non-Mendelian inheritance of epigenetic changes in the mouse
124	Ren	Utilizing controlled vocabularies within Gramene
125	Stupka	Uncovering large hidden portions of the mammalian transcriptome—Lessons from insertional mutagenesis
126	Roy	This is how PAM and BLOSSUM matrices are interdependent on each other
127	Sakai	Molecular evolutionary analysis of processed pseudogenes in the human and mouse genomes
128	Sanges	Fragmentation and mobility of conserved non-coding sequences (CNSs) in vertebrate genomes
129	Ouellette	High-quality annotation from twelve vertebrates for genes orthologous to a focused region of study in the human genome
130	Shimoyama	Disease and phenotype data in the context of the genome

131	SHIN	Identification of alternate isoforms of a common gene with dual mitochondrial and cytoplasmic localization
132	Siddiqui	A fine-scale dissection of developing mouse tissues for gene expression profiling
133	Stojanovic	Computational analysis of short degenerate repeated motifs in DNA sequences
134	Smith	Genome-wide distribution of genes and sequence features in the context of linkage disequilibrium values
135	Sorimachi	Simulation analysis reveals the chronological precedence of protein formation over codon formation
136	Srinivasan	Integrated protein interaction networks for 230 microbes
137	Srinivasan	Comparative genomics of two cyprinid species
138	Stein	DAS/2 next generation distributed annotation system
139	Stevens	RTDB—An RT-PCR experimental database
140	Davuluri	Bioinformatics tools for modeling epigenetic changes in cancer genomes
141	Sundquist	Short read assembly
142	Taschner	In silico identification of transcription factors involved in cellular differentiation by promoter analysis of co-regulated genes
143	Terry	Automated annotation of a large eukaryotic genome <i>S. tropicalis</i>
144	Miller	Short "ultraconserved" sequence among vertebrate genomes is highly enriched for microRNAs
145	Miller	MicroRNAs are a major component of short "ultraconserved" sequence among insect genomes
146	Twigger	Flash GViewer—A Flash-based visualization tool providing an overview of genomes and their data
147	Wang	A fine-scale linkage disequilibrium measure based on length of haplotype sharing
148	Warren	Real-time contiguity improvement of whole-genome shotgun assemblies using physical maps
149	Ge	Toward a system-level view on <i>C. elegans</i> embryonic development
150	White	Annotation of non-coding genes in Ensembl
151	Williams	Seeing the forest and the trees—Detection of biological functionality in high-throughput experiments
152	Wu	Reactome software tools for annotating and visualization biological pathways
153	Xing	Protein modularity of alternatively spliced exons is associated with tissue-specific regulation of alternative splicing
154	Xu	Massively parallel, cost-effective <i>de novo</i> sequencing of complete microbial
155	Xu	Promiscuous and dynamic evolution of symbiotic species in the human intestine

- 156 Yi ArrayBlast—Data-mining for gene expression signatures  
 157 Youens-Clark CMap—A software application for displaying comparative genetic and physical  
 158 Zhao Panzea—A database and resource for molecular and functional diversity in the maize genome

**Session 10 COMPARATIVE AND EVOLUTIONARY GENOMICS I**

MONDAY 10/31/2005, 7:00 PM

W. Miller / L. Stubbs

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Stubbs	No Abstract	15
159	Taylor	Mammalian promoter evolution	15
160	Hughes	Comparison of the structure and function of the $\alpha$ globin cluster throughout evolution	15
161	McEwen	Duplicated conserved non-coding elements associated with vertebrate paralogues	15
162	Kumar	Signatures of higher level phylogeny and evolutionary rate differences in noncoding regions of mammalian genomes	15
163	Rasmussen	Whole-genome phylogeny across multiple species for ortholog and paralog detection	15
164	Drummond	Why highly expressed proteins evolve slowly	15
165	Schattner	Hotspots of synonymous-codon conservation in mammalian genomes	15

**Session 11 COMPARATIVE AND EVOLUTIONARY GENOMICS II**

TUESDAY 11/1/2005, 9:00 AM

W. Miller / L. Stubbs

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
166	Dehal	Phylogenomic timing of the two rounds of whole genome duplication in vertebrates	15
167	Qu	Evolution of genes and genome of medaka ( <i>O. latipes</i> )	15
168	Wapinski	A genome-wide reconstruction of orthologous groups of genes in fungi	15

**Session 12 EXPECT THE UNEXPECTED**

TUESDAY 11/1/2005, 10:30 AM

*Speakers to be announced during the session*