

Genome Informatics [2007]

Session 1 REGULATION, PATHWAYS AND NETWORKS

THURSDAY 11/1/2007, 7:30 PM

M. Kellis / Z. Weng

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
1	Weng	Identification and characterization of cell type-specific and ubiquitous chromatin regulatory structures in the human genome	15
2	Meynert	Regulatory switches—Multiple weak transcription factor binding sites explain the ultra conserved regions in mammalian genomes	15
3	Singh	Functional diversification of paralogous transcription factors—An inverse correlation between expression divergence and DNA binding	15
4	Kellis	Regulatory network inference using 12 <i>Drosophila</i> genomes	15
5	Li	fdrMotif—Identifying cis-elements by an EM algorithm coupled with false discovery rate control	15
6	Reimand	Graph-based methods for mining functional and regulatory modules from heterogeneous data	15
7	Flannick	Automatic parameter learning for network alignment	15

Session 2 PATHOGENIC MICROBE GENOMICS

FRIDAY 11/2/2007, 9:00 AM

J. Carlton / J. Parkhill

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
8	Carlton	The current status of parasite genomics—Progress, issues and future directions	15
9	Silva	IDEA—The sugarcoat for PAML	15
10	Prochnik	Comparative genomics of related green algae— <i>V. carteri</i> and <i>C. reinhardtii</i>	15
11	Stajich	Comparative genomics of the fungal kingdom—A deep view from chytrid fungi	15
12	Parkhill	Variation detection in highly monomorphic bacteria using new sequencing technologies	15
13	Francke	The identification of transcription factor specific operator sequences in bacteria	15
14	Livny	High-throughput prediction and annotation of putative non-coding RNAs in bacterial replicons using automated workflow management and distributed computing	15
15	Pickett	CovarView—A program for visual display of genome-wide covariance analyses	15

Session 3 POSTER SESSION I

FRIDAY 11/2/2007, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
16	Abbott	WebACT—Online visualization of genome comparisons	
17	Aken	Improving the Ensembl genebuild	

18	Bhanot	In breast cancer, the oncogene IKBKE is overexpressed only in HER2+ with lymphocytic infiltrate and basal-like subtypes
19	Avraham	The role of plant ontology in comparative plant genomics and gene discovery
20	Blankenberg	Making the analysis of multiple-species whole-genome alignments accessible to everyone
21	Bono	YUZ—An environment for integration and analysis of gene regulatory networks
22	Sinclair	Mouse Genome Informatics (MGI)—The ever-expanding resource
23	Cain	A complete system for community genome annotation
24	Chen	Orthology detection through finding consensus
25	Cherry	Scripting language interfaces to the NCBI C++ toolkit
26	Cherukuri	Patterns of diversity across the human genome
27	Clements	Digesting the genome glut—Promoting the use and extension of GMOD to emerging model organisms
28	Cruz	MethylMeasure—Quantification of DNA methylation in bisulfate-modified sequence traces
29	Dewal	Analyzing somatic copy-number and genetic variation in different types of cancer using the amplification distortion test
30	Dong	Large-scale analysis of the <i>Daphnia</i> transcriptome under stress, based on expressed sequence tags
31	Dong	Exploring a simple topology-based computational method to detect genome mis-assemblies caused by repeats
33	Taschner	Facilitating DNA diagnostics by collecting human disease gene variation using an Open Source LSDB-in-a-box platform—LOVD 2.0
34	Washietl	Accurate background models for comparative genomic screens and their application to RNA gene prediction
35	Gilbert	Tandem genes lost and found
36	Godfrey	Comparative genomics of <i>P. aeruginosa</i>
37	Soliman	Interspecies data mining to predict novel protein-protein interactions in human
38	Hansen	Functional analysis of the mammalian genome by large scale gene trap mutagenesis
39	Hansen	Assessing the accuracy of software for the detection of deletions/insertions in fluorescence-based sequencing traces
40	Harris	Exploring community annotation of a mature model organism database
42	Hauser	Pattern formations in tumors, precursors, and metastases along clinical segmentation
43	Heiges	Integrated online resources for apicomplexan and amitochondrial parasite genomes
44	Ho	A computational pipeline for the identification of novel essential genes, including non-coding RNAs, in <i>P. aeruginosa</i>
45	Hurwitz	Reconstructing phylogenies using gene trees for the genus <i>Oryza</i>

46	Issac	Demonstration of ChiP-Seq method to study different chromatin marks associated with differential gene expression in imprinted loci
47	Joseph	The <i>D. discoideum</i> actinome
48	Kaczanowski	Discovering biologically significant information by automatic literature mining
49	Kawaji	Independent layers of small RNAs from HepG2
50	King	Cladistic motifs—Models for motif conservation and turnover in lineage-specific erythroid regulatory elements
51	Koche	A computational framework for the identification of modified chromatin domains from ChIP-sequencing data
52	Krishnan	James Watson genotype viewer
53	Lancaster	In silico detection of structural variation in the human genome
54	Leung	Exploring differences in chromatin packaging using comparative analysis of dot chromosome sequences from <i>D. melanogaster</i> and <i>D. virilis</i>
55	Carvunis	Revisiting the yeast orfeome—From comparative genomics to functional genomics
56	Batalov	Genomic annotation of the human E3 ubiquitin ligases leads to a mitochondrial E3 that controls the organelle's dynamics
57	Li	A method of gene pathway involvement prediction using profiles of evolutionary divergence
58	Liang	Evidence based gene build in Gramene
59	Liu	Re-ranking candidate gene models for improved gene annotation

Session 4 ASSEMBLY, ANNOTATION AND RESOURCES I

FRIDAY 11/2/2007, 7:00 PM

E. Birney / J. Kent

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
60	Birney	EBI Genomes	15
61	Zerbino	Velvet—Complete mammalian genome assembly using very short paired reads	15
62	Ning	Assembly of paired-end Solexa reads by kmer extension using base qualities	15
63	Havlak	Next-generation sequencing improves BAC-based assembly of comparative sequence data	15
64	Zhang	AB SOLiD resequencing alignment software suite—Matching, pairing and indel finding	15
65	Raetsch	mGene—A novel discriminative gene finder	15
66	Taylor	Galaxy—The platform for accessible, large-scale, integrated genomic analysis	15
67	Stein	The Generic Genome Browser—Faster, more flexible	15

Session 5 EPIGENOMICS

SATURDAY 11/3/2007, 9:00 AM

R. Martienssen / T. Mikkelsen

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
68	Martienssen	Epigenetic natural variation in <i>A. thaliana</i>	15
69	Peterson	MEM (Multi Experiment Matrix)—Web tool for global expression analysis	15
70	Flicek	Whole genome functional annotation	15
71	Mikkelsen	Sequencing mammalian epigenomes	15
72	Schmid	ChIP-seq data reanalyzed—Unprecedented precision for nucleosomes mapping	15

73	Schuler	A pipeline for managing epigenomic data	15
74	Bock	Epigenome data analysis and prediction made easy—Public release of the EpiGRAPH software for biologist-friendly (epi-)genomic data mining	15

Session 6 BIRDS OF A FEATHER

SATURDAY 11/3/2007, 2:00 PM

KEYNOTE SPEAKER: Michael Ashburner, University of Cambridge

SATURDAY 11/3/2007, 4:30 PM

Session 7 ASSEMBLY, ANNOTATION AND RESOURCES II

SUNDAY 11/4/2007, 9:00 AM

E. Birney / J. Kent

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
75	Kent	Displaying associations, and improving alignments at the gene set at UCSC	15
76	Searle	Using new types of sequence evidence to improve Ensembl gene annotation	15
77	Tatusova	A combined approach for gene prediction in eukaryotic genomes	15
78	Huala	Genome annotation at TAIR (The <i>Arabidopsis</i> Information Resource)	15
79	Yandell	New measures for management and comparison of annotated genomes	15
80	Shrivastava	The multi genome annotation tool (MGAT)	15
81	Khatun	Proteogenomic mapping for the human genome—Identifying protein-coding sequences	15
82	Sperling	Translational control of splicing in eukaryotes	15

Session 8 POSTER SESSION II

SUNDAY 11/4/2007, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
83	Swedlow	Toward the Usable Image—New approaches to the design of image informatics software	
84	Mujica	Manual annotation of the mouse genome—The groundwork for high throughput conditional knock-out vector design	
85	Ni	The comprehensive functional annotation of mouse genes and gene products using the gene ontology (GO)	
88	Cunningham	Customizing Ensembl	
89	Peterson	Regulatory SNPs in <i>S. cerevisiae</i> —Characterization and analysis	
90	Jubin	Mekano—A program for analyzing whole genome shotgun assemblies	
91	Greene	ERIC—Enteropathogen Resource Integration Center, an NIAID Bioinformatics Resource Center for Biodefense	
92	Ratan	Comparative genome assembly	

93	Rosenfeld	Differentiation of heterochromatin and euchromatin based on histone modifications
94	Rotmistrovsky	Oligo-FAR—A tool to map short nucleotide sequences to genome or mRNA
95	Mozes	Learning signaling pathway structures from single cell measurements of network subsets
96	Saha	Targeted data mining of spatial proximity relationships of repetitive regions in genomes
97	Sanders	Prospecting for new genes in the chicken genome using proteomics
98	Sebastian	Multiple genome analysis and annotation mapping via mummer_remap and cog alignments
99	Silverstein	Small cysteine-rich peptides resembling antimicrobial peptides have been under-predicted in plants
100	Raetsch	Accurate large scale genomic signal detection
101	Maglott	Genome annotation at NCBI—The products
102	Syed	Genome assembly visualization tool for short read data
103	Taylor	Leveraging deep comparative sequence data to understand mammalian gene regulatory elements
105	Tress	Determining principal gene products
106	Tyekucheva	Human-macaque comparisons illuminate variation in neutral substitution rates
107	Varuzza	Significance indexes for differential expression
108	Vogel	Analysis of gene annotations in Ensembl using comparative genomics
109	Von Kuster	Galaxy as the analysis medium for Mart/Gbrowse-based resources
110	Wang	Identification of <i>Drosophila</i> microRNA cis-regulatory elements by phylogenetic footprinting
111	Whitney	Prediction of overlapping protein complexes with CLOVER
112	Brudno	BioFlock—Virtual machine technology for bioinformatics software development
113	Wortman	The <i>C. muris</i> genome project
114	Wu	A pathway-based system to understand the functional relationships among a gene set
115	Xuan	Mapping reads from the Solexa/Illumina 1G sequencer
116	Elnitski	Computational identification of bidirectional promoters and consequent biological inferences
117	Yeremian	Tractable algorithms for realistic large-scale biophysics and bioinformatics models—Structure-based genomic analyses
118	Zeller	Detecting polymorphic regions with resequencing microarrays
119	Zeng	Comparative analysis of <i>F. tularensis</i> genomes
120	Zhang	Dual-specificity splice sites function alternatively as 5' and 3' splice sites
121	Zhang	Motifs that discriminate functions in genomic regions

Session 9 IMAGES, ATLASES AND RECONSTRUCTION

SUNDAY 11/4/2007, 7:00 PM

R. Murphy / R. Waterston

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
123	Waterston	Beyond the genome—Automated, continuous analysis of embryonic gene expression with cellular resolution in <i>C. elegans</i>	15
124	Verbeek	Spatio-temporal analysis of gene expression in zebrafish	15
125	Knowles	Berkeley <i>Drosophila</i> Transcription Network Project—Morphology and gene expression atlas	15
126	Murphy	Automated image analysis for proteome-wide determination of subcellular location	15
127	Glory	Automated subcellular location analysis from tissue atlas images	15
128	Lewis	The strategy we've employed and the architecture we've used to capture phenotypic descriptions in a computable manner	15
129	Swedlow	The Open Microscopy Environment—Informatics and quantitative analysis for biological microscopy	15

Session 10 COMPARATIVE AND EVOLUTIONARY GENOMICS

MONDAY 11/5/2007, 9:00 AM

R. Hardison / E. Margulies

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
130	Margulies	Evaluation of sequence quality/quantity for comparative genomic analyses	15
131	Sanchez-Herrero	ENREDO, PECAN and ORTHEUS, accurate and realistic genome wide alignment and ancestor reconstruction	15
132	Nagarajan	Chromhome—A web application for comparative genomics	15
133	Chen	Orthocluster—A depth-first search algorithm for identifying syteny blocks and genomic structural variants	15
134	Hardison	Comparative genomics and high throughput binding assays illuminate cis-regulatory modules	15
135	Thorisson	HGVbase-G2P—A central genetic association study database	15
136	Yang	Comparative analysis of chicken chromosome 28 provides new clues to the evolutionary fragility of gene-rich vertebrate regions	15
137	Makova	The genome-wide determinants of microsatellite evolution	15