

## Jan 25-26<sup>th</sup>, 2010 HPC Workshop Tentative Schedule

### Day 1 – January, 25<sup>th</sup>, 2010

Introduction (9:00 am – 9:45 am)

Eddy Rubin – Joint Genome Institute

Rick Stevens – Argonne National Laboratory

Session I (9:45 am – 11:45 a.m.) Short Read Assembly

Chair : Alexy Sczyrba

Speaker	Affiliation	Title
David Jaffe & Sante Gnerre (combined)	Broad	Visualizing assembling everything
Srinivas Aluru	Iowa State	Parallel Assembly of Large Genomes from Paired Short Reads
Jarrold Chapman	JGI	Efficient short read assembly of eukaryotic genomes

Breakout session: 11:45 – 12:30

Lunch: 12:30 - 1:30

Session II (1:30 p.m. – 4:00 pm): Annotation and Knowledge Integration

Chair: Manolis Kellis

Speaker	Affiliation	Title
Ross Overbeek	FIG	Casting the Improvement of Annotations as an Optimization Problem
Bob Cottingham	ORNL	TBA
Chris Oehmen	PNNL	High performance computing for sequence analysis
Manolis Kellis	MIT	Large-scale integration of genomic and epigenomic datasets
Matteo Pellegrini	UCLA	Annotation of plant genomes using Illumina RNA-seq data

Breakout Session: 4:00pm to 4:45pm

### Day 2 – January 26<sup>th</sup>, 2010

Session III (9:00 am – 11:30 am): Evolutionary Analysis

Chair: Dan Rokhsar

Speaker	Affiliation	Title
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Ward Wheeler	AMNH	Heuristics for the General Tree Alignment Problem
Alexis Stamatakis	Tech. Univ. Munich	Rapid Evolutionary Placement of Short Sequence Reads
Cedric Notredame	CRG/Barcelona	New Challenges for the Computation of Multiple Sequence Alignments in the High-Throughput Era
Dan Rokhsar	JGI	Ancestral Genome Reconstruction
Richard Goldstein	MRC/NIMR	Interpreting Evolutionary Change: Hypothesis Testing in Phylogenetic Analysis

Breakout Session: 11:30 am to 12:15 pm

Lunch: 12:15 am to 12:45 pm

Session IV (12:45pm– 4:15 pm): Data Management, Visualization and Computing Infrastructure

Chair: Victor Markowitz

Speaker	Affiliation	Title
Victor Markowitz	JGI	Computational Challenges for Microbial Genome and Metagenome Data Analysis
Folker Meyer	ANL	Casting a wider net: Distributed Resources for Metagenomics
David Konerding	Google	From Molecular Dynamics to Bioformatics: Challenges in Scaling Computational Biology Using Commodity Computing
Jim Kent	UCSC	Visualizing distributed data with BigWig and BigBed at UCSC
Toby Bloom	Broad	Data Management and Scalability: Is Genomics different from other HPC applications?
Maya Gokhale	LLNL	Acceleration architectures for bioinformatics
Shane Cannon	NERSC	Running BLAST and the IMG Pipeline on HPC Systems

Breakout sessions: 4:15 pm to 5:00 pm

Wrap-up : 5:00 pm to 5:15 pm