

Workshop I: Next-generation Sequencing Technology and Algorithms for Primary Data Analysis

Monday October 3, 2011

- 8:00–9:00 *Check-In/Light Breakfast (Hosted by IPAM)*
- 9:00–9:30 *Welcome and Opening Remarks by Jay Shendure*
- 9:30–10:20 **Radoje Drmanac** (Complete Genomics, Inc.)
Complete Genomics' approach for sequencing thousands of human genomes and determining accurate genome variant lists
- 10:30–10:45 *Break*
- 10:45–11:35 **Chris Saunders** (Illumina, Inc.)
Illumina Sequence Analysis: From Imaging to Somatic Variant Discovery
- 11:45–12:00 *Break*
- 12:00–12:50 **Jim Kent** (University of California, Santa Cruz (UC Santa Cruz))
Visualizing large data sets from next generation sequencing.
- 1:00–2:30 *Lunch (on your own)*
- 2:30–3:20 **David Haussler** (University of California, Santa Cruz (UC Santa Cruz))
Cancer and Evolutionary Genomics
- 3:30–4:00 *Break*
- 4:00–4:50 **Rafael Irizarry** (Johns Hopkins University)
- 5:00–6:30 *Reception and Poster Session (Hosted by IPAM)*

Tuesday October 4, 2011

- 8:00–9:00 *Continental Breakfast*
- 9:00–9:50 **Daniel Zerbino** (University of California, Santa Cruz (UC Santa Cruz))
- 10:00–10:15 *Break*
- 10:15–11:05 **Srinivas Aluru** (Indian Institute of Technology, Bombay)
Error Correction Algorithms for Next Generation Sequencing
- 11:15–11:30 *Break*

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- 11:30–12:20 **Moran Yassour** (Broad Institute)
Characterizing transcriptomes from high throughput sequencing data: from yeast to mammals
- 12:30–2:00 *Lunch (on your own)*
- 2:00–2:50 **Phil Green** (University of Washington)
- 3:00–3:15 *Break*
- 3:15–4:05 **Christopher Lee** (University of California, Los Angeles (UCLA))
Phenotype sequencing: identifying the genes that cause a phenotype directly from pooled sequencing of independent mutants

Wednesday October 5, 2011

- 8:00–9:00 *Continental Breakfast*
- 9:00–9:50 **Elaine Mardis** (Washington University in St.Louis - School of Medicine)
Charting tumor genome evolution from massively parallel sequencing data
- 10:00–10:15 *Break*
- 10:15–11:05 **Mark Depristo** (Broad Institute)
Data processing and analysis of genetic variation using next-generation DNA sequencing
- 11:15–11:30 *Break*
- 11:30–12:20 **Can Alkan** (University of Washington)
Next-generation sequence characterization of complex genome structural variation
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:20 **Jonas Korf** (Pacific Biosciences)
Harnessing Kinetic Information in Single-Molecule, Real-Time (SMRT™) Sequencing
- 3:30–4:00 *Break*

Thursday October 6, 2011

- 8:00–9:00 *Continental Breakfast*
- 9:00–9:50 **David Jaffe** (Broad Institute)
High-quality draft assemblies of large and small genomes from massively parallel DNA sequence data
- 10:00–10:15 *Break*

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10:15–11:05 **Ruiqiang Li** (Novogene)

11:15–11:30 *Break*

11:30–12:20 **Cristina Pop** (Stanford University)

12:30–2:30 *Lunch (on your own)*

2:30–3:20 **Steven Jones** (BC Cancer Agency)
Identification of recurrent mutational events in human cancers

3:30–4:00 *Break*

4:00–4:50 **Earl Hubbell** (Life Technologies)
Computational Challenges for Scalable Semiconductor Sequencing

