Institute for Pure and Applied Mathematics

Workshop II: Transcriptomics and Epigenomics

Tuesday October 25, 2011

8:00–9:00	*Check-In/Light Breakfast (Hosted by IPAM)*
9:00–9:15	*Welcome and Opening Remarks*
9:15–10:05	**Matteo Pellegrini** (University of California, Los Angeles (UCLA)) *Transgenerational Inheritance of DNA Methylation*
10:15–10:45	*Break*
10:45–11:35	**Joseph Ecker** (The Salk Institute for Biological Studies) *Transgenerational Epigenetic Instability is a Source of Novel Methylation Variants*
11:45–1:00	*Lunch (on your own)*
1:00–1:50	**Jigang Li** (Yale University) *Transcriptomes and Epigenomes in Specific Plant Developmental Processes*
2:00–2:30	*Break*
2:30–3:20	**Wei Li** (Baylor College of Medicine) *Transcriptome Instability in Prostate Cancer*
4:00–5:00	*Public Lecture by Michael Brenner at CNSI Auditorium <i>(Optional)</i> ”The Science of Cooking”*

Wednesday October 26, 2011

8:00–9:00	*Continental Breakfast*
9:00–9:50	**Alexander Hartemink** (Duke University) *Computational Advances in Elucidating Cell Cycle Transcriptional Regulation*
10:00–10:30	*Break*
10:30–11:20	**Nir Friedman** (Hebrew University) *Chromatin and Transcription: Adventures in Disentailing Complex Feedback Loops*
11:30–12:00	*Break*

(Wednesday schedule continued on next page)

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(Wednesday schedule continued from previous page)

12:00–12:50 **Tao Jiang** (University of California, Riverside (UC Riverside))
A Combinatorial Approach to the Inference of Isoforms from Short Sequence Reads

1:00–2:30 *Lunch (on your own)*

2:30–3:20 **Sandrine Dudoit** (University of California, Berkeley (UC Berkeley))
Normalization and Differential Expression in RNA-Seq

3:30–4:00 *Break*

4:00–4:50 **Christina Kendziorski** (University of Wisconsin-Madison)
Identifying DE Isoforms in an RNA-seq experiment

5:00–6:30 *Reception and Poster Session (Hosted by IPAM)*

Thursday October 27, 2011

8:00–9:00 *Continental Breakfast*

9:00–9:50 **Zhiping Weng** (University of Massachusetts Medical School)
Computational Analysis of Human Epigenome and Regulate

10:00–10:30 *Break*

10:30–11:20 **Yuval Kluger** (Yale University)

11:30–12:00 *Break*

12:00–12:50 **Zohar Yakhini** (Agilent Labs and the Technion)
Statistical Enrichment in Ranked Lists with Applications in Transcriptomics and Epigenomics

1:00–2:30 *Lunch (on your own)*

2:30–3:20 **Henrik Bengtsson** (University of California, San Francisco (UCSF))
Single-Pair Parent-Specific Copy Number Analysis

3:30–4:00 *Break*

4:00–4:50 **Orly Alter** (University of Utah)
Discovery of Mechanisms and Prognosis of Cancers from Matrix and Tensor Modeling of Large-Scale Molecular Biological Data

Friday October 28, 2011

8:00–9:00	*Continental Breakfast*
9:00–9:50	**Yi Xing** (University of Iowa) *Alternative Splicing in Evolution and Development*
10:00–10:30	*Break*
10:30–11:20	**Colin Dewey** (University of Wisconsin-Madison) *Enabling transcript quantification in non-model organisms with RNA-Seq and generative probabilistic models*
11:30–12:00	*Break*
12:00–12:50	**Adam Roberts** (University of California, Berkeley (UC Berkeley)) *eXpress*
1:00–2:30	*Lunch (on your own)*
2:30–3:20	**Hongkai Ji** (Johns Hopkins University) *Differential principal component analysis of ChIP-seq*
3:30–4:00	*Break*
4:00–4:50	**Ali Mortazavi** (University of California, Irvine (UCI)) *Integrating ChIP-seq and DNAse-seq ENCODE Data From from Multiple Cell Types Using Self-Organizing Maps*