Expression Arrays, Genetic Networks and Disease

Wednesday November 8, 2000

2:00	*Session On Pathways*
2:00–3:00	**Roland Somogyi** (Molecular Mining Corporation) *From Genes to Dynamic Molecular Networks*
3:00–3:20	*Break*
3:20–3:45	**Joel Bader** (CuraGen) *Deconvoluting gene expression profiles and overlaying gene expression networks with protein pathways*
3:45–4:15	**Amos Tanay** (Tel-Aviv University, Israel) *Biological hypothesis generation by pathway expansion*
4:15–4:45	**Monica Nicolau** (Stanford University / UC Berkeley) *A topological model for transcriptional gene interaction*
4:45–5:30	*Break*
5:30–7:00	*Mixer*

Thursday November 9, 2000

9:00	*Session On Medical Applications*
9:00–10:00	**Timothy Triche** (USC / CHLA) *Cancer biology applications of microarray technology*
10:00–10:20	*Break*
10:20–10:45	**Susan Hilsenbeck** (Baylor College of Medicine) *Design of expression array studies for translation to the clinic*
10:45–11:15	**Jeremy Taylor** (University of Michigan) *Regression modeling to assess association between gene expression data and clinical measures*
11:15–11:45	**Mei-Ling Lee** (Harvard University) *Issues in medical studies involving microarrays*
11:45–2:00	*Lunch (on your own)*
2:00	*Session On Classification & Clustering*
2:00–3:00	**Richard Olshen** (Stanford University) *Clustering, permutation testing, intermediate phenotypes and complex disease*
3:00–3:20	*Break*

(Thursday schedule continued on next page)

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3:20–3:45	**Amir Ben-Dor** (Agilent Technologies) *From gene expression data to cancer class discovery*
3:45–4:15	**Amy Peng** (The EMMES Corporation) *BRB Array Tools: an integrated package for the analysis of DNA microarray data*
4:15–4:45	**Steven Skiena** (SUNY Stony Brook) *Analysis techniques for microarray time-series data*
4:45–5:30	*Break*
5:30–7:00	*Mexican Buffet (by reservation only)*
7:00–8:00	**Jean-Michel Claverie** (CNRS, France) *From bioinformatics to computational biology*

Friday November 10, 2000

9:00	*Session On Biological Applications*
9:00–10:00	**Michael Eisen** (Lawrence Berkeley National Laboratory) *Computational approaches to making biological sense of genome-wide expression data*
10:00–10:20	*Break*
10:20–10:45	**Roland Stoughton** (Rosetta Inpharmatics, Inc.) *Determining gene function with microarrays*
10:45–11:15	**Francoise Seillier-Moiseiwitsch** (University of North Carolina) *Statistical methods in proteomics*
11:15–11:45	**Bud Mishra** (New York University/Courant Institute of Mathematical Sciences) *Genomics via microarrays*

Saturday November 11, 2000

9:00	*Session On Cancer*
9:00–10:00	**Michael Newton** (University of Wisconsin) *A simple network model for cancer genome abnormalities*
10:00–10:20	*Break*

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10:20–10:45	**Michael Radmacher** (National Cancer Institute) *Class prediction based on gene expression data: issues in the design and analysis of experiments*
10:45–11:15	**Jae Lee** (University of Virginia) *Analysis on gene expression data of the NCI's 60 cancer cell lines*
11:15–11:45	**Sandrine Dudoit** (Stanford University) *Statistical methods for cancer cluster validation in microarray experiments*
11:45–2:00	*Lunch (on your own)*
2:00	*Session On Statistical Methods*
2:00–3:00	**Mike West** (Duke University) *Bayesian binary regression modeling of outcomes based on microarray expression data*
3:00–3:20	*Break*
3:20–3:45	**Katie Kerr** (Jackson Laboratory)
3:45–4:15	**Thomas Kepler** (Santa Fe Institute) *Normalization and statistics for microarray data by self-consistency and local regression*
4:15–4:45	**Lue Ping Zhao** (University of Washington/Fred Hutchinson Cancer Research Center) *Statistical modeling of microarray data to discover cell cycle dependent transcripts*
4:45–5:30	*Break*
5:30–7:00	*BBQ (by reservation only)*

Sunday November 12, 2000

9:00	*Session On Classification & Clustering II*
9:00–10:00	**Kay Tatsuoka** (SmithKlineBeecham) *A comparison of error models for gene expression data with applications to clustering*
10:00–10:20	*Break*
10:20–10:45	**Laura Lazzeroni** (Stanford University) *Plaid models for two-way clustering of microarray data*
10:45–11:15	**William Noble** (Columbia University) *Support vector methods for functional genomic analysis*
11:15–11:45	**Yuhai Tu** (IBM Research) *Pattern discovery and statistics in gene expression analysis*