

Expression Arrays Technologies and Methods of Analysis

Wednesday October 11, 2000

- 2:00 *Inspirational Stories From Biology*
- 2:00–2:50 **Bruce Conklin** (University of California at San Francisco)
Defining the Genomic Responses to G Protein Signals by Engineering Receptors and G Proteins in Transgenic Mice
- 2:50–3:40 **Leena Peltonen** (UCLA)
Finding Disease Genes: Lessons from Population Isolates
- 3:40–4:00 *Break*
- 4:00–5:00 **Barbara Wold** (California Institute of Technology)
Defining Regulatory Networks - Pitfalls and Progress from the Array-world
- 5:00–7:00 *Wine/Cheese Reception (Hosted by IPAM)*

Thursday October 12, 2000

- 9:00 *Databases I*
- 9:00–10:00 **Christopher Lee** (UCLA)
Genome-Wide Analysis of Human Sequence Diversity
- 10:00–10:30 **Alan Perelson** (Los Alamos National Laboratory)
Immune System Modeling: Influenza Vaccination
- 10:30–10:50 *Break*

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- 10:50–11:20 **Eugene Spier** (Celera Genomics)
Celera: Genomic Databases & Gene Expression Services
- 11:20–12:00 **Alan Roter** (Iconix Pharmaceuticals, Inc.)
Chem Express - Facilitating Drug Discovery with an Integrated Database
- 12:00–2:00 *Lunch (on your own)*
- 2:00 *Analysis of Expression Data I*
- 2:00–2:30 **Richard Simon** (National Cancer Institute)
Statistical Aspects of the Design and Analysis of DNA Microarray Experiments
- 2:30–3:00 **Rob Tibshirani** (Stanford University)
Some Methods for the Analysis of Microarray Data
- 3:00–3:30 **Carsten Rosenow** (Affymetrix)
Large Scale Expression Monitoring Using GeneChip & #61666; Probe Arrays: Applications in Microbiology
- 3:30–4:00 *Break*
- 4:00–4:30 **Glenn Albrecht** (Lynx Therapeutics, Inc.)
How to Score, Differentially, 50,000 to 250,000 SNP's, Against Two Populations of 100 to 1,000 Genome Each, in One Experiment, without Genotyping
- 4:30–5:00 **Avi Shoshan** (Compugen.com)
DNA Chips Designed to Detect Alternative Splicing
- 5:00–5:30 *Break*
- 5:30–7:00 *Italian Buffet (reservation only)*
- 7:00 *New Technologies/Expression Arrays*
- 7:00–8:00 **Stanley Nelson** (UCLA)
Microarray Analysis for the Classification of Human Brain Tumors
- 8:00–8:30 **Stephen Laderman** (Agilent Technologies)
Flexible Expression Analysis Methods in the Context of Biomedical Research
- 8:30–9:00 **Richard Glynn** (Phenomix)
The Genome, Microarrays, and Cancer

Friday October 13, 2000

- 9:00 *New Technologies/SNP'S*
- 9:00–10:00 **Paul Heaney** (Sequenom)
Genomic Applications of Automated High Throughput Mass Spectrometry
- 10:00–10:30 **Michael Heller** (Nanogen)
Microelectronic Arrays for DNA Diagnostic, Pharmacogenomic and Drug Discovery Applications
- 10:30–11:00 **Deane Little** (Hyseq)
Sequencing & SNP Detection by HyChip Array
- 11:00–11:15 *Break*
- 11:15–11:45 **Luis Allegri** (Motorola)
Oligonucleotide Microarray Platform for Gene Expression and SNP Analysis
- 11:45–12:15 **Rolf Swenson** (Orchid Biosciences)
The SNPStream 100K: An Ultra-High Throughput Genotyping Platform
- 12:15–12:45 **Krishnan Nandabalan** (Genaissance Pharmaceuticals)
Patterns of Variation and Linkage Disequilibrium in Key Pharmaceutical Genes

Saturday October 14, 2000

- 9:00 *Image Analysis/Data Compression*
- 9:00–10:00 **Tony Chan** (UCLA)
Using Partial Differential Equations for Image Restoration and Segmentation
- 10:00–10:30 **Stuart Kim** (Stanford University)
*Gene Expression Profiles in *C. Elegans**
- 10:30–11:00 *Break*

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- 11:00–11:30 **Bin Yu** (University of California at Berkeley)
Compressing Gene Expression Data
- 11:30–12:00 **Matthew Coleman** (Lawrence Livermore National Laboratory)
Image Analysis of Customized Expression cDNA Microarrays
- 12:00–2:00 *Lunch (on your own)*
- 2:00 *Analysis of Expression Data II*
- 2:00–3:00 **Christian Burks** (Exelixis, Inc.)
Target Discovery: Model Organism Genetics and Functional Synteny
- 3:00–3:30 **M. Michael Shabot** (Cedars-Sinai Medical Center)
A Large Scale Oracle-Based Severity and Outcomes Database for Intensive Care
- 3:30–3:50 *Break*
- 3:50–4:15 **Jane Staunton** (Massachusetts Institute of Technology, Whitehead Institute)
Expression Analysis Environment at the Whitehead: Tools for Molecular Classification
- 4:15–4:45 **Heiko Mueller** (Monsanto / Pharmacia)
Statistically Robust E2F Induced Gene Expression Patterns in Functional Gene Expression Data Mining (Target Gene Bias Analysis)
- 4:45–5:30 *Break*
- 5:30–7:00 *Barbeque (by reservation only)*

Sunday October 15, 2000

- 9:00 *Final Session*
- 9:00–10:00 **Ron Shamir** (Tel-Aviv University, Israel)
DNA Chips and Algorithms: A Spectrum of Opportunities
- 10:00–10:30 **Charles Sugnet** (University of California at Santa Cruz)
Detection of Splicing Events in Yeast with Oligonucleotide Microarrays
- 10:30–10:50 *Break*
- 10:50–11:20 **Martin Ringwald** (Jackson Laboratory)
GXD: Integrated Access to Gene Expression Data from the Laboratory Mouse