

Biostatistics Symposium and Short Course Program, last updated 11/03/05

Short Courses

Saturday, November 19, 2005, 8:30 am - 5:30pm

“Design and Analysis of Microarrays”

Kathleen Kerr, John Storey, and Rob Tibshirani
Metropolitan Ballroom, Third Floor

- 7:30 – 8:30 Continental Breakfast & Check In
- 8:30 – 10:00 Short Course
- 10:00 – 10:30 **Break**
- 10:30 – 12:00 Short Course
- 12:00 – 1:30 Lunch, Buffet in the Cirrus Room, 35th Floor
- 1:30 – 3:00 Short Course
- 3:00 – 3:30 **Break**
- 3:30 – 5:30 Short Course

Sunday, November 20, 2005, 8:30 am – 5:30pm

“Analysis of Population Genetic Data”

Jonathan Pritchard and Matthew Stephens
Metropolitan Ballroom, Third Floor

- 7:30 – 8:30 Continental Breakfast & Check In
- 8:30 – 10:00 Short Course
- 10:00 – 10:30 **Break**
- 10:30 – 12:00 Short Course
- 12:00 – 1:30 Lunch, Buffet in the Cirrus Room, 35th Floor
- 1:30 – 3:00 Short Course
- 3:00 – 3:30 **Break**
- 3:30 – 5:30 Short Course

Other Sunday items -

6:30 pm -

Poster room, West Ballroom, Second Floor, available for set up. Posters must be removed by 9:30 pm on Monday.

5:00 pm – 7:00 pm

Early Symposium registration check in, Metropolitan Ballroom Foyer, Third Floor

7:00 pm – 9:00pm

Speakers Dinner at the Space Needle, Skyline level, Seattle Room.

Third Seattle Symposium in Biostatistics: Statistical Genetics and Genomics

Grand Ballroom A, Second Floor

Monday, November 21, 2005

7:00 – 8:00 Continental Breakfast
Registration Check In

8:00 – 8:15 Formal Welcome –
Opening Remarks

Session 1, “*Analysis of Population Based Genetic Data*”

8:15 – 9:15	David Cox Perlegen Sciences Inc.	<i>Keynote Address: Statistical Analysis of Whole Genome Association Studies of Complex Human Traits</i>
9:15 – 9:45	Lon Cardon University of Oxford	<i>Using Genomic Patterns of Linkage Disequilibrium to Help Locate Complex Disease Genes</i>
9:45 – 10:15	David Altshuler Harvard Medical School	<i>Humane Genome Sequence Variation and the Inherited Basis of Disease</i>
10:15 – 10:40	Break	
10:40 – 11:30	Robert Temple Food and Drug Administration	<i>Keynote Address: Use of Genetic and Proteomic Information to Select Patients for Trials</i>
11:30 – 12:00	Jun Liu Harvard University	<i>Bayesian Models for Haplotype Inference and Fine-Mapping</i>
12:00 – 12:30	David Clayton Cambridge University	<i>Characterization of Linkage Disequilibrium and its Implications for Association Studies</i>

12:30 – 1:45 **Lunch in the Grand Ballroom C, Second Floor**

Session 2, “Analysis of Family Based Genetic Data”

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| 1:45 – 2:45 | Elizabeth Thompson
University of Washington | <i>Keynote Address: Uncertainty in Inheritance:
Assessing Evidence for Linkage</i> |
| 2:45 – 3:15 | Augustine Kong
deCODE Genetics | <i>Recombination, Fertility and Selection</i> |
| 3:15 – 3:45 | Robert Elston
Case Western
Reserve University | <i>Genetic Associate Tests Based on Family
Data</i> |
| 3:45 – 4:15 | Break | |
| 4:15 – 4:45 | Laura Almasy
Southwest Federation for
Biomedical Research | <i>Identifying the Genetic Variants that Account
for a Linkage Signal</i> |
| 4:45 – 5:15 | Stephanie Monks
Oklahoma State University | <i>Genetic Inheritance of Gene Expression in
Humans</i> |
| 5:15 - 5:30 | Closing remarks | |
| 6:00 – 7:00 | Poster Question and Answer Session in the West Ballroom, Second Floor | |
| 7:00 – 8:30 | Mixer in the Second Floor Pre-function Area | |

Tuesday, November 22, 2005

Session 3, “Analysis of Microarrays and Functional Genomic Data”

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| 7:00 – 8:00 | Coffee and Tea | |
| 8:00 – 9:00 | Wing Hung Wong
Stanford University | <i>Keynote Address: An Approach to the Study of
Cis-Regulatory Elements in Mammalian
Genomes</i> |
| 9:00 – 9:30 | Gary Churchill
The Jackson Laboratory | <i>Modeling and Inference in Complex Genetic
Systems</i> |
| 9:30 – 10:00 | Eric Schadt
Merck-Rosetta | <i>Forward Genetics in Reverse: Novel Methods
to Reconstruct Genetic Networks Underlying
Complex Human Diseases</i> |

10:00 – 10:30 Terry Speed
UC Berkeley Gene Expression Over Time: Data, Questions
and Partial Answers

10:30 – 11:00 **Break**

Session 4, “Analysis of Genome Sequences”

11:00 – 11:30 Chris Burge
Massachusetts Institute
of Technology *Computational and Experimental Analysis of
RNA Splicing*

11:30 – 12:00 Simon Cawley
Affymetrix *Exploring the Genome with Exon Tiling Arrays*

12:00 – 12:30 Phil Green
University of Washington *Signal and Noise in Genome Structures*

12:30 – 12:45 Closing Remarks