



Section on Statistical Genetics

School of Public Health, Department of Biostatistics

2nd Annual NSF-funded Short Course on Statistical Genetics & Statistical Genomics

Hyatt Regency Waikiki
Honolulu, Hawaii



Mon 7/13/2009

Mauka/Maloko Meeting Rooms

Time	Topic	Speaker
08:00 – 08:45 AM	Registration	
08:45 - 09:00 AM	Introductory Remarks	<i>Hemant K. Tiwari, Ph.D.</i>
09:00 - 10:30 AM	Introduction to Biostatistics	<i>Warren Ewens, Ph.D.</i>
09:00 - 10:30 AM	Introduction to Genetics & Genomics	<i>Bruce Walsh, Ph.D.</i>
10:30 – 10:45 AM	BREAK	
10:45 – 12:00 PM	Association Studies: GWAS & Haplotype Analysis	<i>Carl Langefeld, Ph.D.</i>
12:00 – 1:00 PM	Lunch	
01:00 – 02:15 PM	Binary TDT/ Quantitative TDT/PDT/FBAT	<i>Warren Ewens, Ph.D.</i>
02:15 – 2:45 PM	Open Discussion	<i>All Faculty</i>
02:45 – 03:00 PM	BREAK	
03:00 – 04:15 PM	Intro to software demo lab & ssglabvm	<i>Jelai Wang</i>
04:15 – 05:45 PM	PLINK (Demo & Hands-on)	<i>Hemant K. Tiwari, Ph.D.</i>

Tue 7/14/2009

Mauka/Maloko Meeting Rooms

Time	Topic	Speaker
08:00 – 09:15 AM	Structural Association Mapping	<i>David B. Allison, Ph.D.</i>
09:15 – 10:30 AM	Microarray Analysis I	<i>Guilherme Rosa, Ph.D.</i>
10:30 – 10:45 AM	BREAK	
10:45– 12:00 PM	Microarray Analysis II	<i>Rebecka Jörnsten, Ph.D.</i>
12:00 – 01:00 PM	Lunch	
1:00 – 1:30 PM	Open Discussion	<i>All Faculty</i>
01:30 – 03:00 PM	Haplotype Software Demo & Hands-on	<i>Hemant K. Tiwari, Ph.D.</i>
03:00 – 03:15 PM	BREAK	
03:15 – 05:45 PM	Microarray Software Demo & Hands-on	<i>Jelai Wang</i>

We would like to thank our sponsors for their support:



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AGENDA

Wed 7/15/2009

Mauka/Maloko Meeting Rooms

Time	Topic	Speaker
08:00 – 09:15 AM	Basic QTL Analysis	<i>Soledad Fernandez, Ph.D.</i>
09:15 – 10:30 AM	Multiple QTL analysis & R/qtlbim: Bayesian model selection approach	<i>Brian Yandell, Ph.D.</i>
10:30 – 10:45 AM	BREAK	
10:45 – 12:00 PM	Measuring fitness & detecting selection on multivariate phenotypes	<i>Bruce Walsh, Ph.D.</i>
12:00 – 01:00 PM	Lunch	
01:00 - 02:30 PM	Genome-wide Marker assisted selection (GWMAS)	<i>Guilherme Rosa, Ph.D.</i>
02:30 – 03:00 PM	Open Discussion	<i>All Faculty</i>
03:00 – 03:15 PM	BREAK	
03:15 – 05:45 PM	R/qtlbim Demo & Hands-on	<i>Brian Yandell, Ph.D.</i>

Thu 7/16/2009

Mauka/Maloko Meeting Rooms

Time	Topic	Speaker
08:00 – 09:15 AM	Copy Number Variations (CNVs)	<i>Hemant Tiwari, Ph.D.</i>
09:15 – 10:30 AM	Pathway Analysis	<i>L. Kelly Vaughan, Ph.D./David B. Allison, Ph.D.</i>
10:30 – 10:45 AM	BREAK	
10:45– 12:00 PM	Image Analysis & Proteomics	<i>Kimberly Sellers, Ph.D.</i>
12:00– 01:00 PM	Lunch	
01:00 - 02:15 PM	Methods, Examples, & Implications of Integrative Biology	<i>Atul Butte, Ph.D.</i>
02:15 – 02:30 PM	BREAK	
02:30 – 05:30 PM	CNV & Pathway Demo & Hands-on	<i>Faculty (led by Hemant K. Tiwari, Ph.D.)</i>

Fri 7/17/2009

Mauka/Maloko Meeting Rooms

Time	Topic	Speaker
09:00 - 12:00 PM	Roundtable Discussion	<i>Faculty (led by David B. Allison, Ph.D.)</i>
01:00 – 05:00 PM	Software Demo & Hands-on	

Course Website: <http://www.soph.uab.edu/ssg/nsfstatgen/nsfsecondannual>

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In response to feedback from last year's short course, we have also re-scheduled the relevant software demonstration and hands-on computer lab immediately after the lectures on each day. For example, the microarray software demo and hands-on lab will immediately follow the lectures on microarray analysis that day. In addition, the instructors will provide well-annotated slides and structure the software demonstration in such a way that students may follow each hands-on example on their own computers. Also, we have reserved four hours on the last day of the course for additional guided practice and to address remaining software questions.



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