

**Day 1 – Mon, September 19<sup>th</sup>**

7:00 – 8:30	Dinner	
8:30-11:00	Welcome Reception – join us as you arrive	

**Day 2 – Tue, September 20<sup>th</sup>**

TIME	TOPIC	LECTURER/LEADER
8:00 – 9:00	Breakfast	
9:00 – 9:10	Administrative items: Welcome	David Allison
9:10 – 9:45	Designing microarrays for statistical analysis of gene expressions	Jane Chang
9:45 – 10:20	A probe level rank approach for gene selection in oligonucleotide arrays with a small number of replicates	Dung-Tsa Chen
10:20 – 10:40	Break	
10:40 – 11:10	Model building with microarray data	Lang Chen
11:10 – 11:40	Imputation of missing values and its effect of significance analysis of differential Expression	Rebecca Jornsten
11:40- 12:00	TBA/ Time Buffer	
12:00 – 1:30	Lunch	
1:30 – 6:30	Free Time	
6:30 – 8:00	Dinner	
8:00 – 8:30	Resample based inference	David Allison
8:30 – 9:00	Comparison of FDR methods	Gary Gadbury
9:00 – 9:30	Sources of Variation in microarray experiments	Stanislav Zakharkin

**Day 3 – Wed, September 21<sup>st</sup>**

TIME	TOPIC	LECTURER/LEADER
8:00 – 9:00	Breakfast	
9:00 – 9:35	Eigenspaces, cluster partition, facet structures, separating hyperplanes, and topographical mapping.	Bernie Gorman
9:35 – 10:10	Genetics of expression but deals with the use of dimension reduction techniques	Stephanie Monks
10:10 - 10:45	Dimension Reduction for Regressions with Categorical Variables	Xuerong (Meggie) Wen
10:45 – 11:05	Break	
11:05 – 11:40	Statistical power of expression QTLs for mapping of complex trait loci	Paul Shliekelman
11:40 – 12:00	TBA / Time buffer	
12:00 – 1:30	Lunch	
1:30 – 6:30	Free Time	
6:30 – 8:00	Dinner	
8:00 – 8:30	Error in genotype frequency estimates derived from pooled DNA using microarrays	Joanne Knight
8:30 – 9:00	Methods for Chip-chip data	Sunduz Keles
9:00 - 9:30	Heterologous competitive genomic hybridization	Susan Renn

**Day 4 – Thu, September 22<sup>nd</sup>**

TIME	TOPIC	LECTURER/LEADER
8:00 – 9:00	Breakfast	
9:00 – 9:35	Predicting microRNA genes using structural and sequence features and naive Bayes as a classifier.	Malik Yousef
9:35 – 10:10	Methodology for associating high-dimensional datasets (such as comparative genomic hybridization arrays) with censored and non-censored outcomes using piecewise constant estimation	Annette Molinaro
10:10 - 10:45	Equivalence studies	Xiangqin Cui
10:45 – 11:05	Break	
11:05 – 11:40	Inferring metabolic pathway connectivity in Arabidopsis using co-expression analysis and protein-protein interaction networks	Staffan Persson
11:40 – 12:00	TBA / Time buffer	
12:00-1:30	Lunch	
1:30 – 6:30	Free Time	
6:30 – 8:00	Dinner	
8:00 – 8:30	A spectral method for the analysis of microarray data	Mahyar Sabripour
8:30 – 9:00	Alpha spending	Jaap Brand
9:00 – 9:30	Statistical approach to a complex ecology problem	Mike Osier

**Day 5 – Fri, September 23<sup>rd</sup>**

TIME	TOPIC	LECTURER/LEADER
8:00 – 9:00	Breakfast	
9:00 – 9:30	HDBStat! and Power Atlas	Tapan Mehta
9:30 – 10:00	IGB	Ann Loraine
10:00 -10:30	ErmineJ and Class level analysis	Paul Pavlidis
10:30 – 10:45	Break	
10:45 - 12:00	Brain storming Integromics	Grier Page
12:00 – 1:30	Lunch	