Agenda

June 28, 2007（Thursday）

9:00~10:00	**Registration**
10:00~10:10	**Opening**
10:10~11:00	**Keynote speech** Peter McCullagh Department of Statistics, University of Chicago **Title : Sampling bias in binary random effects models**
11:00~12:30	**Invited Session I – Chair: Kuang-Fu Cheng**
11:00~11:30	Pak-Chung Sham Genome Research Centre, University of Hong Kong, Hong Kong **Title : Family-based and Genetically Stratified Association Analysis**
11:30~12:00	Zhaohai Li Department of Statistics, George Washington University **Title : The Impact of Population Stratification on Commonly Used Statistical Procedures in Population-based QTL Association Studies**
12:00~12:30	Chao A. Hsiung Division of Biostatistics and Bioinformatics, National Health Research Institutes **Title : Incorporating Endophenotypes into Family-based Allelic Association Studies**
12:30~13:30	**Lunch**
13:30~15:00	**Invited Session II- Chair: Yuh-Ing Chen**
13:30~14:00	Stephen Portnoy Department of Statistics, University of Illinois **Title : Censored Quantile Regression**
14:00~14:30	Weijing Wang Institute of Statistics, National Chiao-Tung University, Taiwan **Title : Regression Analysis for Semi-Competing Risks Data**
14:30~15:00	Xiao-Li Meng Department of Statistics, Harvard University **Title : Disparities in Measuring Disparities in Health Care: A Statistica Conceptual Framework**

15:00~15:20	Tea Break
15:20~17:20	**Invited Session III- Chair: Jing-Shiang Hwang**

15:20~15:50	Kwok Pui Choi Department of Statistics & Applied Probability, Department of Mathematics, National University of Singapore **Title : Statistics based computational methods for replication origin prediction in bacterial and viral genomes**
15:50~16:20	Anne Chao Institute of Statistics, National Tsing Hua University, Taiwan **Title : Estimating Biodiversity Indices**
16:20~16:50	Mendel Fygenson Marshall School of Business, University of Southern California **Title : Pessimistic Modeling and Inference in the Risk Evaluation of Carcinogens**
16:50~17:20	Chu-Chih Chen Division of Biostatistics and Bioinformatics, National Health Research Institutes **Title : Exterior exposure estimation using a one-compartment toxicokinetic model with blood sample measurements**

June 29, 2007（Friday）

9:00~10:30	**Invited Session IV - Chair: Yen-Feng Chiu**
09:00~09:30	Guan-Hua Huang Institute of Statistics, National Chiao Tung University, Taiwan **Title : Statistical validation of endophenotypes using a surrogate endpoint analytic analogue**
09:30~10:00	Hua Tang Department of Genetics, Stanford University **Title : Improving population-specific allele frequency estimates by adapting supplemental data: An Empirical Bayes Approach**
10:00~10:30	Mei-Chiung Shih Health Research and Policy-Biostatistics, Stanford University **Title : Test and confidence intervals for secondary parameters in sequential clinical trials**
10:30~10:50	**Tea Break**
10:50~12:20	**Invited Session V - Chair: Yun-Chan Chi**
10:50~11:20	Jane-Ling Wang Department of Statistics, University of California, Davis **Title : A New Approach to Model Longitudinal and Event-Time Data**
11:20~11:50	Mei-Cheng Wang Department of Biostatistics, Johns Hopkins University **Title : Bias-Correction Methods for Marker Data with Informative Terminal Events**
11:50~12:20	Chiung-yu Huang National Institute of Allergy and Infectious Diseases, National Institutes of Health **Title : Semiparametric analysis for recurrent event data with informative censoring**
12:20~13:30	**Lunch**
13:30~15:00	**Invited Session VI- Chair: Feng-Chi Chen**
13:30~14:00	Hongzhe Li Department of Biostatistics and Epidemiology, University of Pennsylvania School of Medicine **Title : Group SCAD Regression Analysis for Microarray Time**

14:00~14:30	**Course Gene Expression Data** Shili Lin Department of Statistics, Ohio State University **Title : A cross entropy Monte Carlo approach to aggregating results from microRNA and other genomic experiments**
14:30~15:00	Marc Coram Department of Health Research and Policy, Stanford University **Title : Statistical Challenges in Comparative Proteomics**
15:00~15:20	**Tea Break**
15:20~16:50	**Invited Session VII- Chair: I-Shou Chang**
15:20~15:50	Chuhsing Kate Hsiao Department of Public Health, National Taiwan University **Title : Evolutionary-based Haplotype Association Studies**
15:50~16:20	I-Ping Tu Institute of Statistical Science, Academia Sinica **Title : P-Value Approximation of Scan Statistics and its Application to Genomic Data**
16:20~16:50	Henry Horng-Shing Lu Institute of Statistics, National Chiao Tung University, Taiwan **Title : Is Less More? On Statistical Investigation for Large Biological Networks**