9:30 **Frederick Leung**, Dean, Faculty of Science
Opening Remarks

Chair: D. Cheung

9:35 – 10:30 **Kei-Hoi Cheung**, Center for Medical Informatics, Yale, USA
Database and software tool interoperation for microarray data analysis

Tea Break

Chair: N. Mok

10:45 – 11:40 **I-Shou Chang**, National Health Research Institute, Taipei, Taiwan
Normalization and analysis for cDNA microarray experiments having many differential expressed genes

11:45 – 12:40 **Horng-Shing Lu**, Statistics, National Chiao Tung U., Taiwan
Visualization, screening and classification of cell cycle-regulated genes in yeast by multi-dimensional scaling, nonlinear dimension reduction and wavelet transform

Lunch Break

Chair: T.L. Lai

14:15 – 15:10 **Jonathan Taylor**, Statistics, Stanford, USA
Multiple comparisons in functional magnetic resonance imaging (fMRI)

15:15 – 16:10 **Sung Nok Chiu**, Mathematics, HKUB
New quantitative description for spatial point patterns

Tea Break

Chair: N.K. Tsing

16:30 – 17:25 **Antoine Danchin**, HKU-Pasteur Research Centre
Living Turing machines

Chair: T.W. Ng

9:30 − 10:25   **Tony W.K. Fung**, Statistics & Actuarial Sciences, HKU and
Xinsheng Zhang, Statistics, Fudan U.
Some statistical problems in gene finding and gene mapping

10:30 − 11:25   **Ming-Ying Leung**, Management Science and Statistics, U. Texas at San Antonio, USA
Prediction of replication origins in DNA viruses

Tea Break

Chair: A. Danchin

11:45 − 12:40   **Kwok-Pui Choi**, Mathematics, NUS, Singapore
Efficient homology search: consecutive seed versus spaced seeds

12:45   **Ngaiming Mok**, Director, Institute of Mathematical Research
Closing Remarks