THE UNIVERSITY  OF HONG KONG

**Department of Mathematics**

# Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

September 1, 2010 (Wednesday)
Rm 309, Run Run Shaw Bldg., HKU

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**Miss Chen Xi**
Department of Mathematics, HKU

***A Modified Entropy Approach for Construction of Probabilistic Boolean Networks***

**2:00 – 2:30pm**

Abstract: Boolean Network (BN) and its extension Probabilistic Boolean network (PBN) have received much attention in modeling genetic regulatory networks. In this paper, we consider the problem of constructing a PBN from a given positive stationary distribution. The problem can be divided into two subproblems: Construction of a PBN from a given sparse transition probability matrix and construction of a sparse transition matrix from a given stationary distribution. These are inverse problems of huge sizes and we proposed mathematical models based on entropy theory. To obtain a sparse solution, we consider a new objective function having an addition term of $L_\alpha$-norm. Newton's method in conjunction with CG method is then applied to solve the inverse problem. Numerical examples are given to demonstrate the effectiveness of our proposed method.

**Miss Jiang Hao**
Department of Mathematics, HKU

***Delay Discrete Dynamical Models for Genetic Regulatory Networks***

**2:30 – 3:00pm**

Abstract: In this talk, we study the problem of constructing a regulatory network of yeast in oxidative stress process. Discrete Dynamic System (DDS) model has been introduced in describing Gene Regulatory Networks (GRNs). However, delay effect was not taken into consideration within the model. A Time-delay DDS model composed of linear difference equations is developed to represent temporal interactions among significantly expressed genes. Interpolation and re-sampling are imposed to equalize the non-uniformity of sampling time points. Statistical significance plays an active role in obtaining the optimal interaction matrix of GRNs. The constructed gene network using linear multiple regression has a very good match with the original data. Simulation results are given to demonstrate the effectiveness of our proposed model.

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*All are welcome*