

THE UNIVERSITY



OF HONG KONG

Department of Mathematics

**Numerical Mathematics and
Applied Analysis Group Seminar
(NMAA)**

**Contrasting Patterns of Context-Dependent
Mutation in Eukaryotic Lineages**

Dr. James J. Cai

Department of Microbiology, HKU

on Wednesday, May 3, 2006 at 2:00p.m.
in Room 309, Run Run Shaw Building, HKU

Abstract

Context-dependent mutation processes manifests specific patterns of dinucleotide frequencies in the genomes of most organisms. The CpG-methylation–deamination process, for example, is such a prominent mutation process in vertebrates (CpG effect). Other kinds of such processes, often with unknown mechanistic origins, need to be incorporated in order to make more realistic models of nucleotide substitutions. Based on a general framework of nucleotide substitutions, we developed a method to identify the most relevant dinucleotide substitutions and to estimate their relative frequencies. Our method starts from a model of context-independent nucleotide substitution, then context-dependent substitution parameters are successively added to increase the likelihood of the model in describing given data. We applied the method on the dataset from major eukaryotic lineages and revealed contrasting patterns in dinucleotide substitution.

All are welcome
