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Subject: Doctoral Seminar by Mr Charlie Lee

SCHOOL OF COMPUTING,NUS

DOCTORAL SEMINAR BY

Mr. Charlie LEE Wah Heng

Supervisor: A/P Ken Sung

Recombination Breakpoint Detection and Phylogenetic Network Construction among Viruses

18 February 2009, 9am

Meeting Room 1 (COM1 03-43)

Abstract:

Viruses are one of the main classes of microscopic agents which cause infectious disease in humans. Apart from the common cold, mumps, chickenpox, influenza, polio, rabies and smallpox, viruses cause long term diseases which can be life threatening, for example HIV seriously damages or destroys the immune system, hepatitis B and hepatitis C viruses can severely damage and eventually destroy the liver. Combating the different virus diseases requires long term research for vaccines and antiviral drugs. However, this is difficult as viruses evolve rapidly to become drug-resistant. The emergence of new viruses through recombination or from animals to humans may also render current treatments useless. Phylogenetics is an important research area in computational biology involving the study of evolutionary relationships among a set of organisms that will enable us to better understand viral pathogenicity and the role of recombination in achieving drug-resistance. Specifically, the research will focus on two aspects of phylogenetic analysis, namely recombination detection and phylogenetic network construction. Recombination detection identifies regions involved in recombination and reveals the mosaic organization of recombinant viruses, thus improving the accuracy of subsequent phylogenetic analysis. Phylogenetic network construction then serves to better represent complex evolutionary events and provide insights on the origin of viral pathogens. No doubt, the continual research in detecting and reconstructing evolutionally processes in viruses will play a major role in developing effective treatments and bears a great impact on human health.

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