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Subject: Doctoral Seminar by Mr Melvin Zhang

SCHOOL OF COMPUTING,NUS

DOCTORAL SEMINAR BY

Mr Melvin Zhang

Conserved Gene Clusters Discovery and Applications in Comparative Genomics

Meeting Room1 (COM1 03-43)

9 February 2009, 10.00am

Abstract:

It is well known that the differences between the genomes of extant species can be attributed to both small and large-scale mutations. Large-scale mutations or rearrangements, are relatively rare but they affect the content and order of the genomes thereby obscuring the relationship between species. Comparison of multiple genomes based on their gene orders --- the sequence of genetic markers --- reveal segments with homologous gene content. These segments are commonly referred to as conserved gene cluster.

Max-gap clusters limit the maximum distance between adjacent genes and it is commonly used in practice. In this talk, we describe our recent work on the Gene Team Tree (GTT), which is a compact representation of max-gap clusters over all gap lengths.

We propose two applications of our GTT in comparative genomics, 1) detecting segmental duplications via self comparison and 2) identifying positional homologs.

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