AMENDMENT

The Hong Kong University of Science & Technology
Computational Science Initiative
Department of Mathematics

JOINT SEMINAR

Topological deep learning of biomolecular data

By

Prof. Guo-Wei WEI
Department of Mathematics, Michigan State University

****

Date: ** 15 Dec 2016 (Thur)
Time: ** 11:00am – 12:30pm
Venue: Room 5510

****

Abstract

The exponential growth of biological data has offered a revolutionary opportunity for mathematically driven advances in biological sciences. Conventional geometric analysis is frequently inundated with too much structural detail to be computationally tractable for massive biomolecular data, while traditional topological tools often incur too much reduction of the original data to be practically useful. Persistent homology, a new branch of algebraic topology, is able to bridge the gap between geometry and topology. I will discuss how to combine persistent topology with cutting edge machine learning and deep learning to arrive at the state of the art predictions of a vast variety of biomolecular data, including solvation free energies, partition coefficients, protein-drug binding affinities, and protein mutation impacts.

ALL ARE WELCOME

***** Please note the change in Date & Time***