

THE UNIVERSITY



OF HONG KONG

Department of Mathematics

Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

Computational Systems Bioinformatics for Pathway Analysis and Optimal Drug Therapy

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in Room 309, Run Run Shaw Building, HKU

Abstract

The premise of today's drug development is that the mechanism of a disease is highly dependent upon underlying signaling and cellular pathways. Such pathways are often composed of complexes of physically interacting genes, proteins, or biochemical activities coordinated by metabolic intermediates, ions, and other small solutes and are investigated with molecular biology approaches in genomics, proteomics, and metabonomics. Nevertheless, the recent declines in the pharmaceutical industry's revenues indicate such approaches alone may not be adequate in creating successful new drugs. Our observation is that by combining methods of genomics, proteomics, and metabonomics with techniques of bioimaging will systematically provide powerful means to decode or better understand molecular interactions and pathways that lead to disease and potentially generate new insights and indications for drug targets. The former methods provide the profiles of genes, proteins, and metabolites, whereas the latter techniques generate objective, quantitative phenotypes correlating to the molecular profiles and interactions. In this talk, I will describe pathway reconstruction and target validation based on the proposed systems biologic approach and show microenvironment based in-silico modeling for pathway analysis and optimal drug selection.

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All are welcome
