

Computational Methods in Analyzing MicroRNA Regulations in Cancer

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DATE 20 June 2017 (Tuesday)

TIME 2:30 pm - 3:30 pm

VENUE CS Seminar Room, Y6405, 6th Floor
Yellow Zone, Academic 1
City University of Hong Kong
83 Tat Chee Avenue
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ABSTRACT

MicroRNAs are a class of abundant small RNAs that can repress the translation of thousands of genes. They have critical regulatory functions in many essential cellular pathways, and perturbations in microRNA pathways often contribute to human diseases such as cancer. In this talk, I will describe some of the computational approaches that we have recently developed, which include (i) a target prediction method that can integrate sequence information with expression data, (ii) a framework that model the competition between mRNAs for common microRNA regulators, and (iii) a pan-cancer analysis of microRNAs in the TCGA dataset. I will further describe a new approach that can integrate multiple omics data sets to model the transcriptional regulation of human genes; I will use acute myeloid leukemia (AML) as an example to illustrate the performance of this approach.

BIOGRAPHY

Prof Zhaolei Zhang was trained in physics and biology (more the former than the latter) as an undergraduate in China, then attended graduate school at University of California, Berkeley, studying structure biology and protein crystallography under the supervision of Professor Sung-Hou Kim. While at Berkeley, Prof Zhang worked in the Physical Bioscience Division at the Lawrence Berkeley National Lab (LBNL). His doctoral research concerned the structure determination and functional mechanism of integral membrane protein complexes involved in cell respiration. He made key contributions in determining the crystal structure of cytochrome bc1 complex, a mitochondrial membrane protein machinery involved in cell respiration.

Prof Zhang was a post-doctoral fellow with Professor Mark Gerstein at the Department of Molecular Biophysics and Biochemistry (MBB) at Yale University from March, 2001 to 2004. While at Yale, he worked on a number of projects including genome annotation and data mining, pseudogene evolution and biological databases. His current research focuses on using computational informatics tools to understand the function and evolution of genes, proteins and genomes. He is also interested in the conservation and dynamics of biological pathways and networks.

All are welcome!



In case of questions, please contact Dr WONG Ka Chun at Tel: 3442 8618, E-mail: kc.w@cityu.edu.hk, or visit the CS Departmental Seminar Web at <http://www.cs.cityu.edu.hk/news/seminars/seminars.html>.

