City University of Hong Kong
Department of Biomedical Sciences
presents a seminar

"INTEGRATIVE ANALYSIS OF MULTI-DIMENSIONAL OMICs DATA FOR GENE REGULATORY NETWORK CONSTRUCTION"

by

Dr. John Wang Junwen
Centre for Genome Sciences, Li Ka Shing Faculty of Medicine
The University of Hong Kong

Date : 21 January 2016
Time: 2pm to 3pm
Venue: Meeting room 2-130, 1/F, Block 2, To Yuen Building

About the speaker

Dr. John Wang Junwen is currently an Associate Professor at Centre for Genome Sciences, Li Ka Shing Faculty of Medicine, The University of Hong Kong. His research interest is in bioinformatics and computational genomics, focusing on developing bioinformatics tools to answer biological problems. He obtained his PhD from the University of Washington and MS from the University of Pennsylvania. He was a postdoctoral fellow at Center for Bioinformatics, the University of Pennsylvania, and a staff at the National Institute of Cancer, NIH, USA. He was the recipient of the outstanding young researcher award from HKU in year 2012, and was promoted to current position in 2014.

Abstract

The advent of OMICs technologies, such as microarray/RNA-seq, next generation sequencing (NGS) and proteomics, is revolutionizing the way we are doing biology. Biomedical research is transforming from a single candidate gene approach to systems biology. This transition is characterized by heavy use of genomics at DNA, RNA and protein levels, and by high demand of bioinformatics tools to process these data. I will introduce several bioinformatics tools developed in my lab for integrative analysis of genomic data, such as the web server ChIP-Array to infer gene regulatory networks from combined ChIP-seq and transcriptome data, and its application to collaborative research. I will also introduce our databases, GWASdb and GWAS3D that utilize data from ENCODE and 1000 genomes projects to annotate and prioritize genetic variants from NGS and GWAS studies. Finally, I will introduce our recent discovery on how GWAS can help in drug discovery, and computational methods to prioritize causal variants with regulatory roles. All the tools developed by the lab are freely available at http://jjwanglab.org/.

Contact
Dr. Yue Jianbo (Email: jianbyue@cityu.edu.hk; Tel: 3442-2812)

All are welcome