Research Seminar

Inferring Aging Regulation and Intervention from Big Data

Date: 13 November 2017 (Monday)
Time: 12:00pm – 01:00pm
Venue: Workshop, MD9 Level 1



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Abstract

New high-throughput technologies, such as microarrays and deep sequencing technologies, have provided unprecedented opportunities for mapping mutations, transcripts, transcription factor binding and histone modifications at high resolution and at genome-wide level. This has revolutionized the way regulations of diseases and other biological processes are studies and generated a large amount of heterogeneous data, which is begging to be unbiasedly and efficiently integrated. How to integrate these data still remains a big challenge. We have explored to ab initio predict or reconstruct regulatory networks based on heterogeneous data on gene expression, histone modification and genomic changes. We find that innovative integrations of these data can lead to not only global pictures of the complex biological processes, such as aging, but also key regulatory events of these processes. We have also developed new computational algorithms to facilitate mapping of epigenetic features from the deep sequencing data, and mapped various transcriptome changes during aging and dietary interventions. I will highlight our new methods and results for the integrative analyses of multi-dimensional heterogeneous large datasets to infer regulatory events on aging and dietary intervention induced transcriptome changes.

Biography

Prof. Jing-Dong Jackie Han obtained Ph.D. degree from Albert Einstein College of Medicine. She had her postdoctoral training at The Rockefeller University and Dana-Farber Cancer Institute. In 2004, she became an investigator/professor at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences. She is currently a director of the CAS-Max Planck Partner Institute for Computational Biology. Her research focuses on the structure and dynamic inference of molecular networks, using a combination of large-scale experiments and computational analysis to probe the networks and to integrate functional interaction data in order to explore the design principles of the networks and to find how the complex phenotypes, such as aging, cancer and stem cell development are regulated through molecular networks. She was awarded the Chinese Academy Sciences Hundred Talent Plan and NSFC Outstanding Young Scientist Award in 2006, and the Hundred Talent Plan Outstanding Achievement Award in 2009, selected as a Max Planck Follow in 2011 and a MaxNetAging Fellow in 2014, F1000 faculty in developmental biology in 2016.

Convener: Dr. Tsai Shih-Yin