Department of Biomedical Sciences

presents a seminar

Developing experimental and computational methods to study the non-coding genetic basis of cancer and complex diseases

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Chinese Academy of Agricultural Sciences

Date : 24 Jun 2019
Time : 14:00 - 16:00
Venue : TYB-1B-G04, To Yuen Building

Abstract

Genome-wide association studies have identified many non-coding genetic variants associated with cancer and complex diseases. However, we lack efficient experimental tools to understand the biological functions of these variants. We also lack computational methods to integrate information encoded in non-coding regions to explore the genetic basis of cancer and complex diseases. In my talk, I will present two experimental methods and one computational method that we have built/extended in the past. First, we used a human prostate cancer cell line, LNCaP as a model to perform whole human genome STARR-Seq (WHG-STARR-Seq) to reliably obtain an assessment of enhancer activity. Compared to the original STARR-Seq, our approach greatly increases the library complexity per unit of starting material, making it feasible and cost-effective to explore the landscape of regulatory activity in the much larger human genome. Second, we adapted STARR-Seq with DNA-capture strategy to systematically identify the cancer GWAS SNPs that affect gene expression by modulating activities of distal regulatory elements. Third, we built a statistical method (TADA-Annotations) to analyze non-coding functional annotations with de novo mutations from whole genome sequencing studies of nuclear families. This method learns from data which annotations are informative of pathogenic mutations, and combines both coding and non-coding mutations at the gene level to detect risk genes.

About the Speaker

Yuwen Liu is a principal investigator at Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences. He obtained his Ph.D. from the University of Chicago, and B.S. from Tsinghua University. His research focuses on developing experimental and computational methods to unlock the mystery of noncoding regions in the genomes of both humans and other animals.

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All are welcome!