



Yijie Wang

National Institutes of Health
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Luddy Hall, Rm. 3166

Reconstructing gene regulatory networks --- moving from tissue level toward cell level

Abstract: Understanding how organisms regulate gene expression is one of the most important and complex challenges in biology. Existing computational methods to infer gene regulatory networks (GRNs) either cannot generate reliable predictions by only using gene expression data or lose tissue/context-specificity by integrating data from different tissue/conditions. In this talk, I will first present Network Reprogramming using EXpression (NetREX), a method I developed to reconstructs a tissue/context-specific GRN given tissue/context-specific expression data and a context-agnostic prior network. Then, I will talk about my ongoing research on cell sub-population alignment for single-cell RNA-seq data from different experiments, which is a fundamental step for collecting cell-level expression data that can be used for building and analyzing cell-level GRNs. In the end, I will describe my future research on reconstructing cell-level GRNs and comparative analysis of cell-level GRNs under different conditions.

Biography: I am a research fellow in the National Center for Biotechnology Information (NCBI) at the National Institutes of Health (NIH) working with Dr. Teresa M. Przytycka. Before joining NCBI/NIH in 2015, I was a graduate student under the supervision of Prof. Xiaoning Qian and obtained my Ph.D. in Electrical Engineering from Texas A&M University. I received my B.S. and M.S. from Dalian University of Technology, China. I worked on developing a parallel particle movement simulation algorithm with Dr. Allen McPherson at Los Alamos National Laboratory in 2012.

