Title：Gene regulatory network inference: from correlation to causality

Abstract:

Gene regulatory network inference aims to address the fundamental question: how gene expression is regulated? i.e., when, where, and how much a gene is controlled by the sequence of DNA bases located in the regulatory region of the gene and further interpreted by proteins called transcription factors that bind to those regions and increase or decrease gene expression. This induces a series of follow-up questions: Who is the regulators (cis-element, trans-element, cis-element interaction, trans-element interaction,…)? What is the quantitative function? How the tissue/condition specificity is achieved?

In this tutorial, we will treat the gene regulatory network inference as the modeling process to find out the best data generation network (knowledge or mechanism) to explain the observed high throughput data. We will review the ideas, models, and algorithms for network inference driven by the three data generation stages:

1. High-throughput gene expression experiments
2. Chromatin immunoprecipitation-based genome-wide mapping
3. Genome-wide measurement of chromatin accessibility

Reference

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