

Simulating Gene Regulatory Networks to Estimate Stochastic Transition Variation

Abstract

Genes are segments of DNA that provide a blueprint for cells and organisms to effectively control processes and regulations within individuals. Current biological methods cannot easily reveal the details of gene interactions. Therefore, we use Markov Chains to simulate gene expression data to infer networks of interactions, which are called gene regulatory networks or GRNs. In this work, we extend previous work by Liesman et al. (2021) to incorporate stochasticity into gene regulatory networks.