

# An Investigation of Gene Regulatory Network State Space Variability

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Genes are segments of DNA that provide a blueprint for cells and organisms to effectively control processes within individuals. There have been many attempts to quantify these processes, as a greater understanding of how genes operate could have large impacts on both personalized and precision medicine. Gene interactions are of particular interest, however, current biological methods can not easily reveal the details of these interactions. Therefore, we infer networks of interactions, which we call a gene regulatory network, or GRN, from gene expression data. Due to the robust behavior of genes and the inherent variability within interactions, models incorporating stochasticity are more realistic than those that are only deterministic. In this work, we extend previous work investigating ways to incorporate stochasticity into gene regulatory networks. First, we use a transition function and investigate its inherent variation, then we use a statistical distribution for activating and degrading the states of genes, and finally, we use a new method incorporating spectral density to incorporate stochasticity within a GRN.