

IS-1: Comparison of propensity and spectral density approaches for estimating transition variability of gene regulatory networks

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In gene regulatory networks (GRN), variability can be used as a measure of the stability of a GRN. The state transition variability of gene regulatory networks (GRNs) due stochastic variation of propensity probabilities caused by internal noise at the molecular level. We obtain the state transition variability based on two methods; using propensities and using spectral density of gene expression. A precision estimate is obtained by comparing the results of each method with that of a known network.