

On The Implementation of Artificial Neural Networks For Estimation Of Gene Regulatory Network Propensities

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This paper presents a fresh method for optimizing the state transition variability of gene regulatory networks (GRNs) due stochastic variation of propensity probabilities caused by internal noise at the molecular level. Using neural network modeling the state transition variability was measured to be within reasonable bounds. Results show promising agreement with theoretical predictions and significant improvement over previous efforts by Akman et al. The work presented here has profound implications for future studies of stochastic GRN modeling and may one day help solve the problem of cancer origination.