

ABSTRACT

THESIS: A Comparative Analysis on Computational Methods for Fitting an ERGM to Biological Network Data

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Understanding of a global biological network structure by studying its simple local properties through the well-developed field of graph theory is of interest. In particular, in this research an observed biological network was explored through a simulation study. However, one difficulty in such exploration lies on the fitting of graphical models on biological network data. An Exponential Random Graph Model (ERGM) was considered to determine estimations of the several network attributes of complex biological network data. We also compared the estimates of observed network to our random simulated network for both Markov Chain Monte Carlo Maximum Likelihood Estimation (MCMCMLE) and Maximum Pseudo Likelihood Estimation (MPLE) methods under ERGM. The motivation behind this was to determine how different the observed network could be from a randomly simulated network if the physical numbers of attributes were approximately same. Cut-off points of some common attributes of interest for different order of nodes were determined through simulations. We implemented our method to a known regulatory network database of *E. coli*.