

## Abstract

One of the major challenges in the field of biology is modeling of gene regulatory networks. The genes, regulators and the regulatory connections between them, together with a semantic understanding of the existing structure form a gene network. In many cases, the perturbation in the regulation processes causes disease in person. So not only understanding the process of gene regulation is used for disease detection, but also to provide appropriate treatment. The Research in the field of gene regulatory networks is faced with many challenges such as noisy data and uncertainty in the gene expression. For this reason, the existing modeling methods are not sufficiently accurate and also are not significant in terms of biology.

In this thesis, to deal with the noisy and uncertainty data, learning networks especially Bayesian networks that have ability to use prior knowledge, have been used for gene regulatory networks modeling. Learning networks are methods that have the structure of the network and a learning process to obtain relationships. One method of measuring the relationship between genes is correlation metrics, but high correlation values between the genes does not necessarily mean that, there is a connection between genes. Common methods in inference of gene regulatory networks, haven't pay attention to this biological importance and therefore predictions by these methods have less accurate in terms of biology. Hence in the proposed method, genes that have high correlation, are located in one cluster using clustering, and not be allowed to exist edge between the genes in the cluster. Finally, after modeling Bayesian network based on knowledge gained from clustering, refining phase and improving regulatory relationships using biology correlation is done.

In order to show the efficiency, the proposed method has been compared with several common methods in this area including GENIE3 and BMALR. The results of the evaluation, indicate that the proposed method recognized regulatory relations in Bayesian modeling process well, due to using of biological knowledge that hidden in the data collection,. And is able to recognize gene regulatory networks align with important methods in this field, and at times better than them.

**Keywords:** gene regulatory networks, network modeling, learning networks, Bayesian network, clustering.