

Poster presentation

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## Modelling of time series microarray data using dynamic Bayesian network

KG Srinivasa\*, S Seema and Manoj Jaiswal

Address: Department of computer science and engineering, M.S. Ramaiah institute of technology, Bangalore, India

\* Corresponding author

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Gene Regulatory Network represents how the genes interact with each other. Using genetic network modelling, it is possible to explain the cell functions at molecular level. DNA microarrays can measure the expression levels of thousands of genes simultaneously. Two steps method adapted to model large-scale Gene Regulatory Networks using time series microarray data. Firstly, genes are clustered based on existing biological knowledge (Gene Ontology annotations) and then a dynamic Bayesian network applied in order to model causal relationships between genes in each cluster. Finally the learned sub-networks are integrated to make a global network. This project aims at inferring the regulatory network that provides us the interaction between the various genes. Our aim is to apply data mining technique to gene expression data and infer regulatory network for various experiments, which include experiments in good and bad conditions using the information available in Gene Ontology.