

Microarray data analysis is one of data mining tool which is used to extract meaningful information hidden in biological data. One of the major focuses on microarray data analysis is the reconstruction of gene regulatory network that may be used to provide a broader understanding on the functioning of complex cellular systems. Since cancer is a genetic disease arising from the abnormal gene function, the identification of cancerous genes and the regulatory pathways they control will provide a better platform for understanding the tumor formation and development. The major focus of this thesis is to understand the regulation of genes responsible for the development of cancer, particularly colorectal cancer by analyzing the microarray expression data.

In this thesis, four computational algorithms namely fuzzy logic algorithm, modified genetic algorithm, dynamic neural fuzzy network and Takagi Sugeno Kang-type recurrent neural fuzzy network are used to extract cancer specific gene regulatory network from plasma RNA dataset of colorectal cancer patients. Plasma RNA is highly attractive for cancer analysis since it requires a collection of small amount of blood and it can be obtained at any time in repetitive fashion allowing the analysis of disease progression and treatment response.

The approaches proposed in this study extend the previous state of the art by incorporating clustering and some statistical techniques to reduce the computational complexity and processing time. The unpaired t-test has been employed to identify the genes that are differentially expressed in cancerous tissues and normal ones. The fuzzy logic algorithm models gene