The present paper proposes a fuzzy GRN model for searching activator / repressor regulatory relationship between gene triplets in the microarray data of plasma RNA from colon cancer patients. Here a novel hybrid clustering algorithm is proposed as a preprocessing step and the cluster centroid was used as an input to fuzzy GRN model. Our approach uses fuzzy membership function to transform gene expression values into three fuzzy set HIGH, MEDIUM, and LOW which are evaluated using a set of heuristic rules, bringing together the advantage of the high level human like reasoning of the fuzzy system. The present model is designed to find triplets of activators, repressors and target among the set of selected genes. This approach saves significant amount of time while building the model since it uses cluster centers to identify genes which are likely to interact. This approach makes it feasible to build complex regulatory networks including co-activators and repressors. Using this method, it may be possible to identify the cellular function of unknown genes by examining known genes associated with the set.

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