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Descriptive and predictive analysis of gene co-expression networks

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Ample availability of gene co-expression data challenges researchers to find and apply unique approaches for extracting biological information to infer about gene functions or predict gene-disease relations. By means of reliable co-expression network construction techniques compiled networks exist and they require further predictive analysis to focus on the genes or groups of the genes exhibiting certain patterns reflected on the co-expression networks. We propose an integrated network analysis where social network descriptive analysis techniques are borrowed to summarize some structural features of the network. Then, the features are employed in optimization models to find groups of genes exhibiting certain patterns.

Biography

Harun Pirim received his PhD degree in Industrial and Systems Engineering (ISE) from Mississippi State University in May 2011. Harun worked on microarray data analysis in collaboration with Computer Science and Forestry departments. His research interests include mathematical programming and heuristic applications in biology, sociology, and supply chain fields focusing mainly on graph mining. He has several papers published in Computers and Operations Research, Computers in Biology and Medicine, conference proceedings, book chapters and a brief Springer book on supply chain optimization.

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