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Mining functional modules in cancer protein interaction networks

Protein-protein interaction (PPI) networks are embedded with vital information about proteins' functions. Analysis of PPI networks associated with specific disease systems including cancer helps us in the understanding of the complex biology of the diseases. Specifically, identification of the similar and distinct subgraphs across PPI networks will provide useful clues on functional modules involved in the diseases. In this study, we compared PPI networks associated with 9 cancer diseases to identify their common and distinct functional modules. We used gene lists from Oncomine database and mapped them against known interacting proteins to build cancer-specific PPI networks. Subgraphs are abstracted to patterns based on their graph topology and nodes' properties. From these networks we discovered frequent patterns that occur in all networks and at each sub-graph size level. These patterns represent the common functional modules of cancer diseases. The distinct patterns are those appearing only in a specific network and they represent functional modules that are characteristic of a given cancer type. We believe that this work would allow us to identify functionally-relevant subgraphs in cancer networks which can be advanced to experimental validation to further our understanding of the complex biology of cancer.

Biography

Dr. Chittibabu (Babu) Guda is the Director of Center for Bioinformatics and Systems Biology and an Associate Professor in the department of Genetics, Cell Biology and Anatomy at the University of Nebraska Medical Center. He completed his Ph.D. from Auburn University, and post-doctoral training from University of California at San Diego. He has published over 40 research articles in reputed journals, and serving as an editorial board member for peer-reviewed journals and as a panelist for grant reviewing. His research interests lie in the area of Computational Systems Biology, particularly on protein-protein and domain-domain interaction networks and protein subcellular localization.