Fractal dimension of protein–protein interactions: a tool for cancer protein identification

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Early cancer diagnosis is critical as it can help avoid the risks associated with long-term treatments and even prevent death. Identifying a defining trait of a cancer protein within its protein–protein interaction (PPI) network could lead to a significant breakthrough in accelerating early cancer detection. A systematic analysis of various topological properties of cancer proteins in the PPI network, focused on their fractal dimension, was conducted. It was observed that cancer proteins exhibit a high fractal dimension (with an average of 1.21). Those with the highest fractal dimension play a significant role in multiple mutation pathways. The observation that TP53 protein occupying high fractal dimension of 1.68, connected with 48 communities reaffirm the correctness of the approach. Further research in this area will provide valuable insights into the structural and functional complexity of cellular processes regulated by proteins, leading to the development of robust therapeutic approaches and enhancing our understanding of cancer biology.

Keywords: Betweenness centrality, cancer gene identification, degree centrality, eigenvector centrality, protein interaction network.

Cancer is a complex and heterogeneous disease. The dynamic nature of genetic changes in cancer cells adds complexity. The study of how genes contribute to dysregulated oncogenic pathways is crucial for advancing our understanding of cancer and developing more effective and personalized treatment approaches. Ivanov[3] developed a high-throughput screening platform, which allows access to and interprets a high-quality cancer-focused network of PPIs, and analyses mutual exclusivity of genomic alterations, cellular co-localization of interacting proteins, domain–domain interactions and therapeutic connectivity. Gulfidan *et al.*[4] presented a differential view of the human protein interactome among cancers. According to them, a certain fraction of proteins differentially interacts in various cancers, but they could not find a general protein interactome profile that applies to all cancers. Cutigi *et at.*[5] propose Discovering Significant Cancer Genes (DiSCaGe), a computational method for ranking possible cancer genes based on the type of mutation score. Integrating genes with coding and non-coding mutations, Paczkowska *et al.*[6] unveiled frequently mutated pathways and identified additional cancer genes with infrequent mutations. Their analysis of prognostic molecular pathways involved the integration of genomic and transcriptomic features from 1780 breast cancers, em-