

Name of Candidate: Ravins
Name of Supervisor: Prof. Pankaj Sharan
Centre: Centre for Interdisciplinary Research in Basic Sciences
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ABSTRACT

The interaction of objects can be seen everywhere and every system. The interaction of Biomolecules represents biological networks. The object or Biomolecules or others may be dynamic unit of complex system. The properties of network can be graph theory is a branch of discrete mathematics and this is triple of two non-empty sets, say Graph $G = (V, E)$ where V is called set of vertex or nodes, another one E is a set of pairs of nodes is called set of Edges. The interactions of objects in any system which gives the system complex can be represents by a Graph. We also capture the global properties of system and model in Graph whose nodes are dynamical objects of system and from the model network we can determine unifying properties and structural characteristic of graph.

In chapter 2 we study the influence of elements diffusing in and out of a network to the topological changes of the network and characterize it by investigating the behavior of probability of degree distribution ($\Gamma(k)$) with degree k . The local memory of the incoming element and its interaction with the elements already present in the network during the growing process significantly affect the network stability which in turn reorganize the network properties. We found that the properties of $\Gamma(k)$ of this network are deviated from scale free type, where the power law behavior contains a exponentially decay factor supporting earlier reported results of Amaral et.al. (2000) and Newman (2001, 2003) and recent statistical analysis results on degree distribution data of some scale free network (R. Khanin and E. Wit, 2006). Our numerical results also support the behavior of this network. However, we found numerically the contribution from exponential factor to the $\Gamma(k)$ to be very weak as compared to the scale free factor showing that the network as a whole carries the scale free properties approximately.

Most of empirical networks having some type of pattern of subgraph in the network those patterns are deviated from random networks and those special patterns of subgraph are called networks motif. Network motifs are small over represented reoccurring pattern having specific function and statistical significance in the different biological networks such as transcriptional regulatory network, protein- protein interaction etc. and they occur in significantly higher frequencies than would be expected in random networks.

So, in the chapter 3 we discussed the network motifs of three and four nodes motifs of transcriptional regulatory network and neural networks and by studying their different properties and analysed them on the basis of Z-Score and Original Frequency individually.

Then by comparing and analysing different transcriptional regulatory networks and neural network among themselves respectively and also between the two of these networks on the basis of Z-Score and Original Frequencies of all the three node motifs, we show that some network motif are fundamentally more versatile than others and are of higher significance. One of such motif is FFL which is very important. For all this we have used various experimental works available in the literature and other useful resources of databases. Our work will be very helpful for better understanding of various undefined principles and dynamical behaviour of Biomolecules.

Network motifs are sub-network or modules having different characteristics and they depict various kind properties of network at fundamental level. There are plenty of Empirical data available of such motifs and of enormous application in diagnosis of the interaction mechanism and also in better refinement of available knowledge to proceed further. There are quite strong association between various topological properties and behavioural pattern of a network. The interaction pattern between network motifs and their topological properties show that many of these transcription regulatory networks and some neural networks also display the phenomenon of small world and scale-free network topologies.

In the chapter 4 we discussed a comparative analysis of the transcriptional regulatory network and some Neural Networks using various network properties like centrality measures, Modularity, clustering coefficient, Degree distributions, and some more. For further detailed analysis, network motifs are calculated for the complex network of few organisms. When we diagnose the relationship between these properties and network motifs, we are surprised to get some useful interconnection among networks motifs and topological behaviours of networks.

As we have discussed in chapter 1 and chapter 2, the most of realistic networks either follows power law probability of degree distribution or they approximated power law with some exponential part in the probability of degree distribution. The degree distribution of biological networks we analysed follows approximately power-law scale-free behaviour of networks.

In the chapter 5 we discussed the interaction of chemical oscillators in the scale-free networks and brain networks where every node works as chemical oscillators. The oscillators are diffusively couple with a certain coupling constant. We found that the nodes start clustering with different sizes as a function of coupling constant. In scale-free network, the number of cluster decreases as coupling constant increases. This gives the clear signature of community formation in the network due to the strength of signal processing among them. However in brain network a single cluster is formed when coupling constant is large enough.

We them conclude based on the result we obtained that the possibility of deviation of scale-freeness in some real networks. Community formation could be possible if the rate of information processing is varied. Investigation of network properties at various system levels may open up various new opening of ideas and principles governing the network at fundamental level.