

Chapter 30

Principles and Analysis of Biological Networks: Biological Pathways and Network Motifs

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ABSTRACT

The biological network complexity is growing enormously and in order to reveal confined properties of these intricate networks, detection of crucial network components may assist in gaining effortless perceptive on the underlying biological processes. Analyzing complex biological pathways for their disease association is still a drawn-out process and requires an integrative approach for comprehensive examination of proteins and interactions to identify candidate markers underlying major malignancies and genetic disorders. There is a need for an amalgamated approach to annotate all the sub-components and their associated interactions in a biological system. It is anticipated that analysis of biological pathways would serve as a valuable accompaniment for analyzing biomarkers in disease pathways and will also contribute scientific knowledge towards their better understanding.

INTRODUCTION

In present era, the advent of human genome sequence, high-throughput techniques and massive generated information has revolutionized the biomedical research (Bentley D. R., 2006). This huge amalgamation of genomic data is rising exponentially due to employment of next generation technologies and application of modern biology (Bentley D. R. 2006; Voelkerding. K. V et al., 2009; Mamanova L, et al. 2010). However, less emphasis is remunerated on the obligatory genomic analysis; subsequently there is a need to apply extensive computational approaches that could deal abreast with the remarkable

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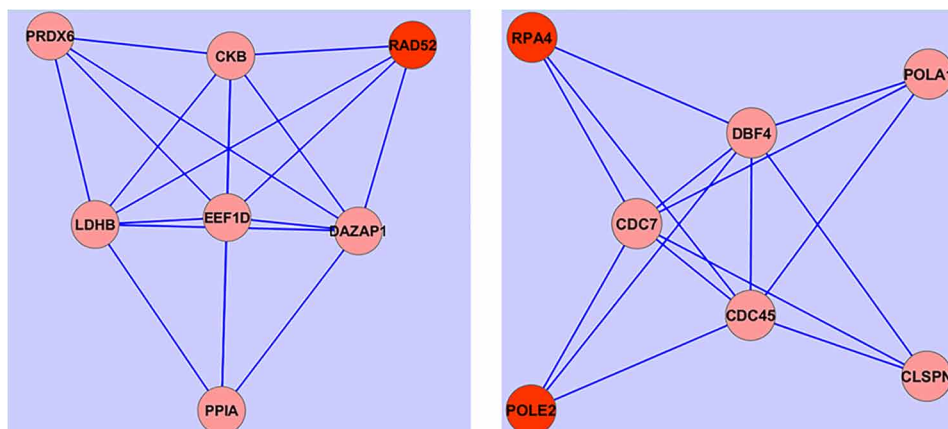
growth in generated biological data (Barabasi A. L. & Oltvai Z.N. 2004; Jeong H., et al. 2000, Jeong H. et al. 2001). Since, the human system is very complex and the ultimate challenge is to decipher numerous multifaceted processes involved in its regulation therefore biological network analysis has major relevance which assists in wide-ranging understanding of an entire system as a whole (Jeong H., et al. 2001). These biological networks present several processes such as cellular mechanisms, signaling cascades, transcriptional regulation, expression profiles and protein-protein interactions (Barabasi A. L. & Oltvai Z. N. 2004; Jeong H. et al., 2000). In Figure 1, these networks comprise of nodes as entities and edges as relationships among them. In general terms a network may be any social interaction, electric circuits, internet and food chain, etc. In biological context, these nodes may vary from a range of macromolecules for instance DNA, RNA, proteins and metabolites. The applications of networks can be observed in ecological networks, expression networks, gene regulatory networks, metabolic networks, protein interaction networks.

Recently, pathway analysis and reconstruction has also gained a lot of attention as it assists in unravelling unknown parameters concerning many precarious diseases. Therefore, the study of networks, their modelling, visualization and simulation are an important aspect for extensively understanding the underlying processes to make sense of the complex available data. Biological networks can be broadly classified into following types:

1. Protein-Protein Interaction (PPI) Networks

The PPI networks form the basis for a vast majority of cellular events, including signal transduction and transcriptional regulation. An extensive understanding of a biological system is feasible only once all the interactions are characterized. These interactions are very well deduced from numerous high-throughput experiments such as protein arrays, co-immunoprecipitation, microarrays and predicted from computational resources developed over time. These *in silico* tools and databases include Search Tool for the Retrieval of Interacting Genes/proteins (STRING), Biomolecular Interaction Network Database (BIND), Molecular INteraction database (MINT) and Database of Interacting Proteins (DIP). These PPI databases help us effortlessly access the existing information for biological interactions among a

Figure 1. Representation of a sub-network comprising of nodes as entities and edges as relationship/ association with nodes



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