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A Survey Of Recent Trends And Developments In Networks In The Area Of Science

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Abstract : The field of networks has grown in recent years and still has scope to grow and create a lot of opportunities in this area. In this paper, we focus on the recent trends in networks and their developments in the area of sciences. A literature review was done on different topics and analyzed. The survey on recent trends in networks may depict the effectiveness of these technologies in present and future in simplifying the problems of mankind.
Key Words : OSI model, Graph Theory, Protein-protein interaction, Science

I. INTRODUCTION

A computer network is a system in which multiple computers are connected to each other to share information and resources. The computer networks use an open system interconnection (OSI) model. Protocol is the set of rules or algorithms which define the way how two entities can communicate across the network and there exist different protocols defined at each layer of OSI model [1,2].

Nowadays networks are widely used everywhere. It's observed that a lot of innovations are happening in the field of computer networking and the main goal being network security. The recent trends in the field of networking which are revolutionizing the digital world are Edge computing, Internet of Things (IoT), Cloud networking, Software Defined Network (SDN) Technology, Intent based learning, Artificial Intelligence, 4D Network, 5G, IPv6, automation and orchestration and many others. These technologies are being developed to have efficient and secured communication. In this paper, we perform literature surveys on recent trends and developments in the area of science.

A biological network is a method of representing systems as complex sets of binary interactions or relations between various biological entities.In general, networks or graphs are used to capture relationships between entities or objects. A typical graphing representation consists of a set of nodes connected by edges.This definition, figure1 was taken from wikipedia.

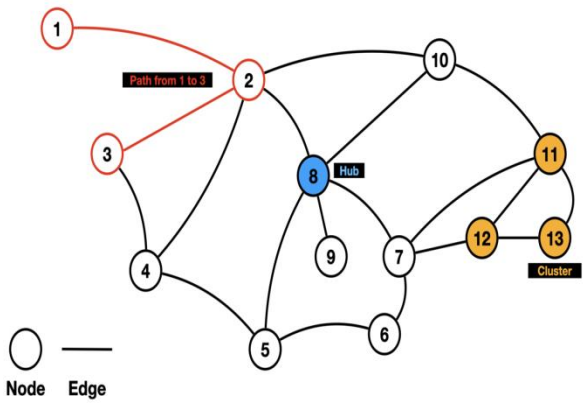

Figure 1

Graph theory: graph types and edge properties

Networks can represent many different types of data. The nodes represent different entities (e.g. proteins or genes in biological networks), and edges convey information about the links between the nodes. First we will concentrate on the edges. Depending on the nature of underlying edge information, different types of analysis can be performed. For this reason, it is useful to highlight the main types of edges that can be found in a network (Figure 2).

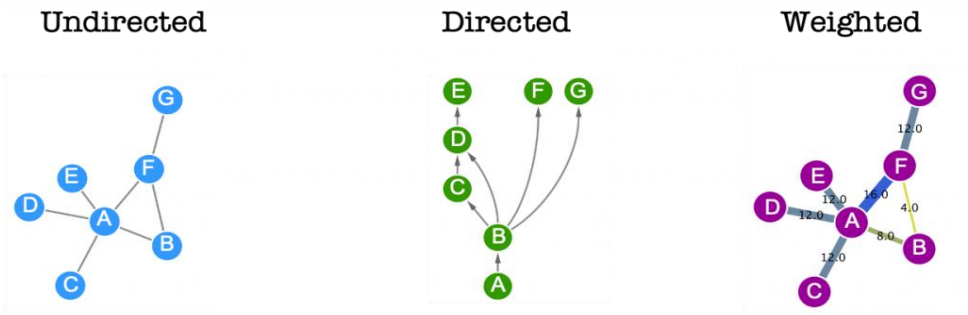

Figure 2

Types of network edges

Undirected edges

This type of edge is found in protein-protein interaction networks (PPINs). The relationship between the nodes is a simple connection, without a given 'flow' implied, since the evidence behind the relationship only tells us that A binds B.

Directed edges

This is the kind of connection found, for example, in metabolic or gene regulation networks. There is a clear flow of signal implied and the network can be organized hierarchically.

Weighted edges

Directed or undirected edges can also have weight or a quantitative value associated with them. This is used to depict concepts such as the reliability of an interaction, the quantitative expression change that a gene induces over another or even how closely related two genes are in terms of sequence similarity. Edges can also be weighted by their centrality values or several other topological parameters.

II MATERIALS AND METHOD

Different types of data will also produce different general network characteristics in terms of connectivity, complexity and structure, where edges and nodes potentially convey multiple layers of information.

Some of the most common types of biological networks are Protein-protein interaction networks, Metabolic networks, Genetic interaction networks, Gene / transcriptional regulatory networks, Cell signaling networks.

2.1 Protein-protein interaction networks

Protein-protein interactions (PPIs) are the physical contacts between two or more proteins and they represent complex biological functions. Nowadays, PPIs have been used to construct PPI networks to study complex pathways for revealing the functions of unknown proteins[4]. Figure 4, represents the physical relationships between proteins. They are central to practically every process that takes place in the cell. Proteins are represented as nodes that are linked by undirected edges.

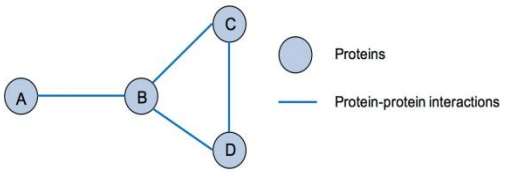

Figure 4

2.2 Metabolic networks

Metabolic networks describe the relationships between small biomolecules (metabolites) and the enzymes (proteins) that interact with them to catalyze a biochemical reaction [5]. Figure 5, represents the biochemical reactions that allow an organism to grow, reproduce, respond to the environment and maintain its structure. Metabolites and enzymes take the role of nodes and the reactions describing their transformations are represented as directed edges. Edges can represent the direction of metabolism flow or regulatory effects of a specific reaction.

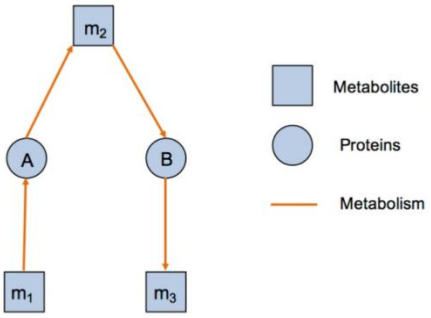

Figure 5

2.3 Genetic interaction networks

Genetic interaction networks represent the functional interactions between pairs of genes in an organism and are useful for understanding the relation between genotype and phenotype. The majority of genes do not code for particular phenotypes. Instead, phenotypes often result from the interaction between several genes [6]. Figure 6, represents the functional relationship between different genes, rather than a physical one. Genes are represented as nodes and their relationships as edges. Depending on the type of evidence behind the interaction, directionality can be inferred for the edges.

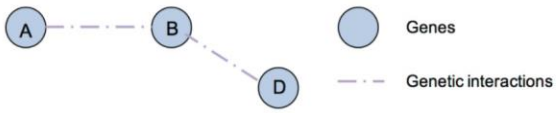

Figure 6

2.4 Gene / transcriptional regulatory networks

A gene regulatory network (GRN) is a collection of regulatory relationships between transcription factors (TFs) and TF-binding sites of specific mRNA to govern certain expression levels of mRNA and their resulting proteins [7].

Transcriptional regulatory networks (TRNs) encode instructions for animal development and physiological responses. Recent advances in genomic technologies and computational modeling have revolutionized our ability to construct models of TRNs [8]. Figure 7, represents how gene expression is controlled. Genes and transcription factors are represented as nodes, while the relationship between them is depicted by different types of directional edges. Regulatory RNAs and other mechanisms can also form part of this type of network. Usually generated via databases representing consensus knowledge of gene regulation (e.g., Reactome or KEGG), although large-scale experimental datasets are increasingly available.

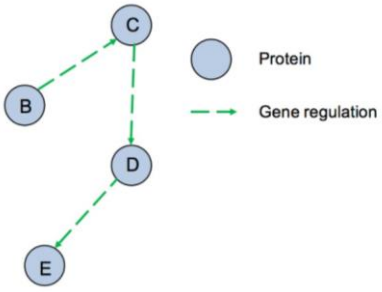

Figure 7

2.5 Cell signaling networks

Signaling pathways come together to form networks that connect receptors to many different cellular machines. Such networks not only receive and transmit signals but also process information. The complexity of these networks requires the use of computational models to understand how information is processed and how input–output relationships are determined [9]. Figure 8, represents the ordered sequence of events and models the information flow within the cell. Gene regulation networks can be considered as a subtype of cell signaling networks, focusing on a specific signaling event, which is often the final stage of a signaling cascade. Elements in the pathway (eg., proteins, nucleic acids, metabolites) are represented as nodes and the flow of information is represented by directed edges.

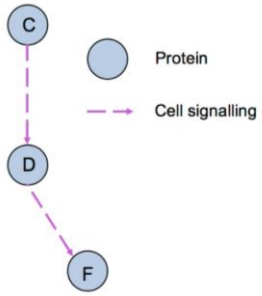

Figure 8

The below table 1, represents various recent developments that took place in various networks in the area of science.

S No	Name of the Network	Recent Developments	Aim	Source
1	Protein-protein interaction networks	High-throughput screening (HTS)	To discover classic drug targets	https://www.nature.com/articles/s41392-020-00315-3
		Fragment-based drug discovery (FBDD)	To identify molecular fragments from fragment libraries	
		Structure-based design	To rationally design the associate PPI modulators	
		Virtual screening	To screen out hits from compound libraries	
2	Metabolic networks	Parameter estimation	Models are fit to concentration data	https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/metabolic-network
		Flux estimation	Flux profiles are computed from fitting models	
		Model discrimination	Experimental design guides experiments	
3	Genetic Interaction Networks	CRISPR (clustered regularly interspaced short palindromic repeats)	Systematic functional genomics analysis	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6820710/
4	Gene / Transcriptional Regulatory Networks	Estimation of a global gene network	To understand cellular mechanisms	https://www.nature.com/articles/s41598-021-90556-1
		Extraction of context-specific core networks	To find a feasible flux distribution	
		Identification of a sample or patient-specific network	To design the correct personalized drugs	
5	Cell Signalling Networks	Cellular phenotypic diversity (CPD)	To govern differentiation during development or drug resistance in cancer	https://www.nature.com/subjects/cellular-signalling-networks
		CorALS (Correlation Analysis of Large-scale (biological) Systems)	The construction and analysis of large-scale parametric as well as non-parametric correlation networks for high-dimensional biological data	
		Critical transition in tumorigenesis	For achieving cancer reversion	
		Gene Ontology Biological Processes (GO:BP)	To represent the current state of knowledge in biology	

Table 1

III. CONCLUSION

The network technologies have increased efficiency. The applications of these networks are widespread and being used in every corner of the country. It is estimated that the above networks will conquer and the world is becoming smart by using these innovative developments. .

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