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On the use of Networks in Biomedicine

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Abstract

The concept of "neural network" emerges by electronic models inspired to the neural structure of human brain. Neural networks aim to solve problems currently out of computer's calculation capacity, trying to mimic the role of human brain. Recently, the number of biological based applications using neural networks is growing up. Biological networks represent correlations, extracted from sets of clinical data, diseases, mutations, and patients, and many other types of clinical or biological features. Biological networks are used to model both the state of a range of functionalities in a particular moment, and the space-time distribution of biological and clinical events.

The study of biological networks, their analysis and modeling are important tasks in life sciences. Most biological networks are still far from being complete and they are often difficult to interpret due to the complexity of relationships and the peculiarities of the data. Starting from preliminary notions about neural networks, we focus on biological networks and discuss some well-known applications, like protein-protein interaction networks, gene regulatory networks (DNA-protein interaction networks), metabolic networks, signaling networks, neuronal network, phylogenetic trees and special networks. Finally, we consider the use of biological network inside a proposed model to map health related data.

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Keywords: Biological Networks; Protein-Protein Interaction Networks (PPIn); Gene Regulatory Networks (GRN); Metabolic Networks; Signaling Networks; Neuronal Networks; Food Webs; Phylogenetic Trees, Special Networks and Hierarchies; Health Care Model.

1. Introduction

The human brain has the capacity of processing information and making decisions instantaneously. Many researchers have shown that human brain performs calculations in a different way than computers, hence the aspiration to solve problems whose complexity is beyond the current computing power, has prompted the scientific community to the neural networks. For biological network is meant any network applied to a biological systems.

A network, in a broad sense, identifies a system, which is characterized by interconnected sub-units. Biological networks are types of important applicable model in various contexts; complex biological systems can be represented and analyzed by computable networks. Like the computer networks, the high complexity degree of biological networks is generated by a simple mechanism. Bioinformatics really shifted its focus from individual genes, proteins, structures and search algorithms for large networks; even more biologists are discovering the links between Internet and metabolic pathways, interactions of proteins through a network topology or a scale-free network.

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A neural network is composed of a set of parallel and distributed processing units, referred as nodes or neurons; they are arranged in layers, and are interconnected by unidirectional or bidirectional connections (see Fig. 1). Typically, a neural network has a set of N input nodes, whose generic element is related with, and each node is interconnected to others through weighted arcs. The products of input and weight are simply summed and feed through (Activation Function) to generate the output (see Fig. 2).

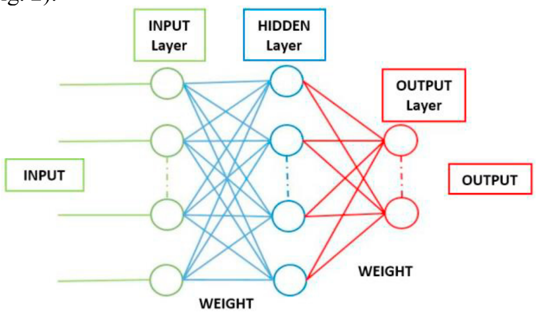

Fig. 1. Typical Structure of Neural Network

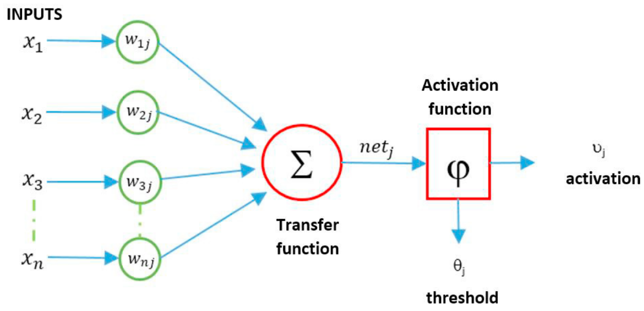

Fig. 2. Activation Functions

Neural network design typically consists of Topology, Transfer Function and Learning Algorithm. The neural network topologies are actually classified by the directions of interconnection in the layer; so the most referred topologies are, *Feed Forward Topology* and *Recurrent Topology*.

In *feed forward topology (FFT)* network, the nodes are "*hierarchically arranged*" in layers starting with the input layers and ending with output layers. The number of hidden layers provides most of the network computational power. In literature typical application of this topology are the *multilayer perception network* and *radial basic function network*. The nodes in each layers are connected to next layer through *unidirection* paths starting from one layer (source) and ending at the subsequently layer (sink). The output of a given layer feeds the nodes of the following layer in a forward direction and does not allow feedback flow of information[12].

Unlike the FFT, in the *recurring topology* (RNT) the flow of information between connected nodes is bidirectional. Typical applications of RNT, for example, are Hopfield Network[1] and time delay neural network (TDNN)[2]. A recurrent network structure has a sort of memory, which helps storing information in output nodes through dynamic states. Biological networks shapes both the state of a range of functionalities in a particular moment, and the space-time distribution of biological and clinical events[14].

In neural networks, the basic unit are the neurons that work like simple processors. Any neuron takes the weighted sum of its input nodes and thanks to the mapping function (activation function) delivers the output to the next neuron. In computational networks, the *activation function* of a node defines the output of that node given as an input or set of inputs. However *nonlinear* activation function allows such networks to compute nontrivial problems using only a small number of nodes. In artificial neural networks, this function is also called transfer function.

In training processes of the network, learning algorithm are used for updating the weight parameter of the input connections level of the neurons. Specifically, there are three types of algorithms: *Supervised*, *Unsupervised* and *Reinforcement*.

Supervised learning is the machine-learning task of inferring a function from *labeled training data*. The training data consist of a set of *training examples*. In supervised learning, each example is a *pair* consisting of an input object (typically a vector) and a desired output value (referred as *supervisory signal*). A supervised learning algorithm analyzes the training data and produces an inferred function that can be used for mapping new examples. Thus the learning algorithm is designed to generalize from the training data to unseen situations in a "reasonable" way. In *supervised learning* mechanism, the external source provides the network with a set of input stimuli for which the output is just known and during the running process the output results are continuously compared with the desired data. The gradient descent rule uses the error between the actual output and the target data for setting the connections weights to the closest match between the target output and the actual output. These types of learning algorithms are used in applications with feed forward networks[3].

Unsupervised machine learning is the machine-learning task of inferring a function to describe hidden structure from "unlabeled" data. In *unsupervised learning* algorithm, a classification or categorization is not included in the observations. The training data and input pattern are presented to the system that organizes data into clusters or categories. A set of training data is provided to the system at the input layer level; the network connection weights are then adjusted through a competition among the nodes of the output layer where the successful candidate will be the node with the highest value.

Reinforcement learning regards software agents ought to take *actions* in an *environment* so as to maximize some notion of cumulative *reward*. The problem, due to its generality, is studied in many disciplines, such as game theory, control theory, information theory, simulation-based optimization, statistics, and genetic algorithms. The *reinforcement learning* algorithm, is also called as graded learning. In this way the network connections are modified according to feedback information provided to the network by its environment. In case of correct response the corresponding connections leading to that output are strengthened otherwise they are weakened.