

Chapter 59

Protein–Protein Interactions (PPI) via Deep Neural Network (DNN)

Zizhe Gao

Columbia University, USA

Hao Lin

Northeastern University, USA

ABSTRACT

*Entering the 21st century, computer science and biological research have entered a stage of rapid development. With the rapid inflow of capital into the field of significant health research, a large number of scholars and investors have begun to focus on the impact of neural network science on biometrics, especially the study of biological interactions. With the rapid development of computer technology, scientists improve or perfect traditional experimental methods. This chapter aims to prove the reliability of the methodology and computing algorithms developed by Satyajit Mahapatra and Ivek Raj Gupta's project team. In this chapter, three datasets take the responsibility to testify the computing algorithms, and they are *S. cerevisiae*, *H. pylori*, and Human-B. Anthracis. Among these three sets of data, the *S. cerevisiae* is the core subset. The result shows 87%, 87.5%, and 89% accuracy and 87%, 86%, and 87% precision for these three data sets, respectively.*

INTRODUCTION

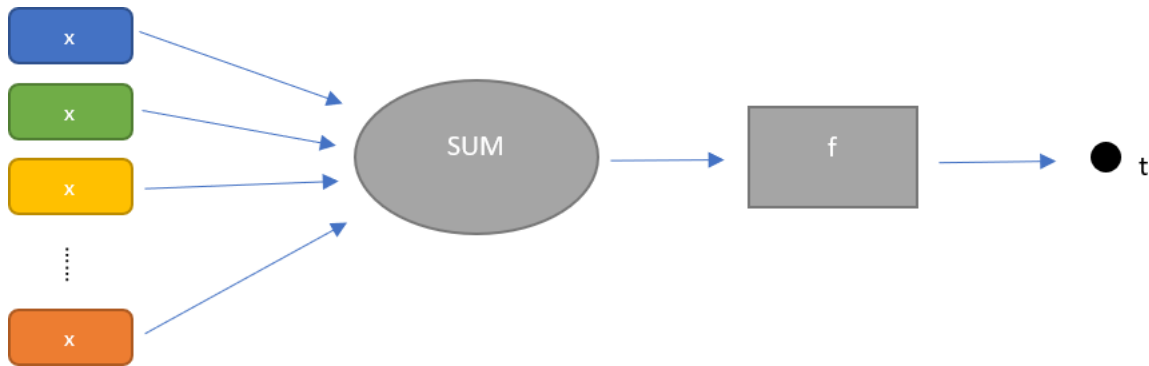
Neural network computing, as the name suggests, is to simulate the operation mode of the computer to achieve the simulation of human brain neural autonomous judgment ability, adaptability, and the ability of multi-project integration and parallel processing. From a biological perspective, the human cerebral cortex contains more than 10 billion neurons connected to form a neural network. Information is collected through the body's sense of touch, taste and other sensory organs. The collected data is transmitted

DOI: 10.4018/979-8-3693-3026-5.ch059

Protein-Protein Interactions (PPI) via Deep Neural Network (DNN)

to the central nervous system and the connection points of the neural network. Then the data collected will be screened, sorted out and cleaned by the nerve center system, and then transmitted to the whole body according to different analysis results to coordinate the functions of various organs in the body.

Figure 1. Neural network framework of inputs and functions to produce perceptron.



From a historical perspective, in the 1940s, McCulloch and Pitts discovered the work of turning logic devices into neurons (Palm, 1986); In the 1960s, Rosenblatt proposed the Perceptron model (Fig. 1), which utilizes simulated learning and recognition functions. It has several input terminals to represent the reception of signals from input or another perceptron. After summation of these signals, outputs or transmits them to other perceptrons through excitation functions. Nerve cells dendrites and axons, some close connection between neurons, some loose connection, and performance are high on the side of each connection weights on the perception of low, save the weight information is neural network acquisition of “knowledge”. However, due to the data dependence, use limitations and forced to end. Until recent years, modern high-tech approaches have provided a solid foundation for research into artificial intelligence, neural networks, deep learning, and other technologies, and the consumer market’s expectation of intelligent devices has fueled researchers’ enthusiasm for the development of neural networks and other related technologies (Admin, 2021).

Compared with the traditional computing methods, the deep neural network algorithm has the ability to self-adaptation and self-organization (Mahapatra, Gupta, Sahu, & Panda, 2021). The traditional computing methods rely on the knowledge and ability written by the programmers to the systematic program. Hence, it primarily depends on the early programmer to write the code, as well as the maintenance and update of the database. In this traditional model, the computing power and intelligence of the computer will be dramatically limited. They were looking at the new updated deep neuron network. The neural network algorithm provides machines with self-learning, self-identification and this specific ability can develop the computer beyond the capacity of its designer itself. Typically, the program designer sets up a learning method for the neural network algorithm or the content to imitate and periodically provides a sample standard for the computer to replicate. The other way is to let the algorithm learn on its own. In this case, the program designer only needs to build a learning instruction for the algorithm, and the algorithm will learn accordingly to the type and pattern of the imported data sets to achieve the goal of identifying the regularity and characteristics of the environment (Oja, 1994).

21 more pages are available in the full version of this document, which may be purchased using the "Add to Cart" button on the publisher's webpage:

www.igi-global.com/chapter/protein-protein-interactions-ppi-via/342577

Related Content

Pathway Analysis and Its Applications

Ravi Mathurand Alison Motsinger-Reif (2015). *Big Data Analytics in Bioinformatics and Healthcare* (pp. 215-239).

www.irma-international.org/chapter/pathway-analysis-and-its-applications/121460

Promoter Structures Conserved between Homo Sapiens, Mus Musculus and Drosophila Melanogaster

Boris R. Jankovic, John A. C. Archer, Rajesh Chowdhary, Ulf Schaeferand Vladimir B. Bajic (2013). *Bioinformatics: Concepts, Methodologies, Tools, and Applications* (pp. 1522-1534).

www.irma-international.org/chapter/promoter-structures-conserved-between-homo/76131

Crow-ENN: An Optimized Elman Neural Network with Crow Search Algorithm for Leukemia DNA Sequence Classification

Rehan Ullah, Abdullah Khan, Syed Bakhtawar Shah Abid, Siyab Khan, Said Khalid Shahand Maria Ali (2024). *Research Anthology on Bioinformatics, Genomics, and Computational Biology* (pp. 514-552).

www.irma-international.org/chapter/crow-enn-optimized-elman-neural/342542

Developing a Library Collection in Bioinformatics: Support for an Evolving Profession

Victoria Martin (2013). *Bioinformatics: Concepts, Methodologies, Tools, and Applications* (pp. 130-150).

www.irma-international.org/chapter/developing-library-collection-bioinformatics/76060

Chemosensitivity Prediction of Tumours based on Expression, miRNA, and Proteomics Data

I. Tsamardinos, G. Borboudakis, E. G. Christodoulouand O. D. Røe (2013). *Bioinformatics: Concepts, Methodologies, Tools, and Applications* (pp. 586-604).

www.irma-international.org/chapter/chemosensitivity-prediction-tumours-based-expression/76085