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ARTIFICIAL IMMUNE ARTIFICIAL DEEP LEARNING IN IMAGE PROCESSING & BIOMETRIC APPLICATIONS

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ABSTRACT

Artificial Deep Learning Mechanism (CA) is a computing model which provides a good platform for performing complex computations with the available local information. In recent years, Artificial Deep Learning Mechanism (DLM) study as a potential modeling tool has gained importance. Some researchers and scientists have used DLM in image processing, data compression, pattern recognition, encryption, VLSI design and language recognition. This article depicts the importance of DLM in the applications of bioinformatics.

INTRODUCTION

A DLM displays three basic characteristics- simplicity, vast parallelism, and locality.

The basic unit of Artificial Deep Learning Mechanism (DLM) is a cell that has a simple structure evolving in discrete time and space. One of the most important milestones in the history of development of the simple homogeneous structure of DLM is due to Wolfram. Solutions to complex problems demand parallel computing environment. Most parallel computers contain more than a few dozen processors. DLM can achieve parallelism on a scale larger than massively parallel computers. DLM is characterized by local connectivity of its cells. All interactions take place on a purely local basis. A cell can only communicate with its neighboring cells. Further, the interconnection links usually carry only a small amount of information. One implication of this principle is that no cell has a global view of the entire system.

COMPLEXITY OF DLM

DLM performs computations in a distributed fashion on a spatially extended grid. It differs from the conventional approach to parallel computation in which a problem is split into independent sub-problems, each solved by a different processor; the solution of sub-problems are subsequently combined to yield the final solution.

The evolution process is directed by the popular Genetic Algorithm (GA) with the underlying philosophy of survival of the fittest gene. This GA framework can be adopted to arrive at the desired CA rule structure appropriate to model a physical system. The goals of GA formulation are to enhance the understanding of the ways DLM performs computations and to learn how DLM may be evolved to perform a specific computational task and to understand how evolution creates complex global behavior in a locally interconnected system of simple cells.

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The task of pattern recognition is encountered in a wide range of human activity. In a broader perspective, the term could cover any context in which some decision or forecast is made on the basis of currently available information.

The problem deals with the construction of a procedure to be applied to a set of inputs; the procedure assigns each new input to one of a set of classes on the basis of observed attributes or features. The construction of such a procedure on an input dataset is defined as pattern recognition.

DLM IN PATTERN RECOGNITION

Pattern recognition algorithm has two phases, the learning or training phase and the testing phase. In the training phase, the algorithm is trained with some patterns. Based upon the nature of training, there are two broad categorization of pattern classifications.

This model is built describing a predefined set of data classes. A sample set from the database, each member belonging to one of the predefined classes, is used to train the model. The training phase is termed as supervised learning of the classifier. Each member may have multiple features. The classifier is trained based on a specific metric. Subsequent to training, the model performs the task of prediction in the testing phase. Prediction of the class of an input sample is done based on some metric, typically distance metric.

WORKING OF DLM

A DLM consists of a number of cells organized in the form of a lattice. It evolves in discrete space and time. The next state of a cell depends on its own state and the states of its neighboring cells. In a 3-neighborhood dependency, the next state $q_i(t+1)$ of a cell is assumed to be dependent only on itself and on its two neighbors (left and right), and is denoted as

$$q_i(t + 1) = f\,(q_{i-1}(t), q_i(t), q_{i+1}(t)) \tag{1}$$

where $q_i(t\ )$ represents the state of the i^{th} cell at t^{th} instant of time, f is the next state function and is referred to as the rule of the automata. The decimal equivalent of the next state function, as introduced by Wolfram, is the rule number of the DLM cell. In a 2-state 3-neighborhood DLM, there are total 223 that is, 256 distinct next state functions. Out of 256 rules, two rules 85 and 238 are illustrated below:

$$\text{Rule 85: } q_i(t + 1) = q_{i+1}(t) \tag{2}$$

$$\text{Rule 238: } q_i(t + 1) = q_i(t) + q_{i+1}(\mathrm{t}) \tag{3}$$

CONCLUSION

We have worked on the feasibility to test the Artificial Deep Learning mechanism over Bioinformatics and after a thorough experiment, we conclude that DLM can be applied on bioinformatics for obtaining an accuracy of more than 84%.

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