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Deep Learning Augmented with Hybrid Non-linear Cellular Automata Platform for Addressing Open Problems in Bioinformatics

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Abstract and Introduction

Most of the grand challenges in Bioinformatics can be addressed my Deep Learning and Cellular Automata [1]. We have developed various classifiers to address essential problems in Bioinformatics. After that, we have done a literature survey, which indicates that many computer algorithms are used to solve open issues like Protein Coding Region (PCR), Promoter prediction (PR), and Chronic Disease Prediction (CDP) individually [2,3]. After thorough research, we conclude that many of the chronic diseases, homology searches, gene finding, and genomic sequence finding could be addressed quickly with a combination of deep learning augmented with cellular automata [4-6].

We understood when a deep learning model is augmented with non-linear cellular automata, and we can have the following advantages.

1. These give the best performance in several domains Bioinformatics in particular
2. This combination reduces the purpose of feature engineering, as this is the most typical part of most of the classifiers.
3. The architectures designed can be easily adapted to solve many problems also as we can make a single platform to address many issues.
4. The augmentation of NLCA

a) Gives more dynamism making the training less expensive.

b) Learning quickly with fewer examples.

c) Understanding of theoretical foundations.

d) Processing with fewer hyper parameters

e) Easy to understand the process as to what is happening and what is going to happen next.

Keywords

Deep learning ; Bioinformatics ; Cellular automata ; Non-linear rules

Abbreviations

PCR: Protein Coding Regions

CDP: Chronic Disease Prediction

NLCA: None Linear Cellular Automata

CA: Cellular Automata

DNN: Deep Neural Network

CNN: Convolution Neural Network

NL-MACA: Non-Linear Multiple Attractor Cellular Automata

System Design

Based on the above intuition, the design applicable for various problems was given below in (Figure1). This system design is vital in addressing these problems as the input can be any sequence. Hybrid non-linear CA [7] rules are used to process the data either in the number of three or six or nine.

PCR [8] prediction process the DNA sequence in terms of three as Codons are identified in three in number, and so on. A deep learning technique DNN (Deep Neural Network) [9] is used to classify the sequence into many classes from which once classes are predicted by NL-MACA (Non-Linear Multiple Attractor Cellular Automata). The classes or the prediction analysis can be the result of the entire design.

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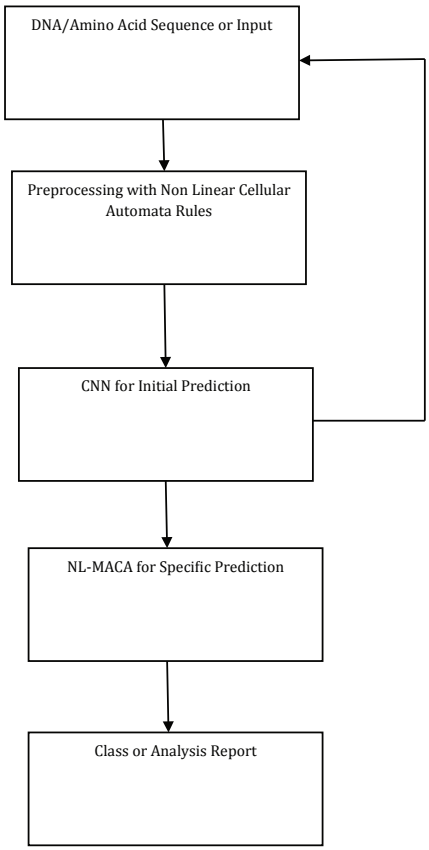

Figure 1: Design of a common platform to address various problems in Bioinformatics

Conclusion

We have done a thorough literature survey to find a common platform to address various problems in Bioinformatics and are successful in this regard. The strength of the classifier lies in the adaptability, less overhead, more sensitivity, specificity, more accuracy, less computing time, and processing large datasets [10]. Complex problems like secondary, quaternary protein structure prediction can be carried within 0.7 Nanoseconds.

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