

Potential Applications of Deep Learning in Bioinformatics Big Data Analysis



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1 Introduction

The rate of growth of biological data in recent years seems to be doubled in every 15 months. Substantial amounts of sequence, biomedical image and signal are being collected for use in medical and healthcare research. Such omics big data must be analysed for transformation into useful knowledge in bioinformatics research fields and thus remains as a key problem in computational biology.

Machine learning models have been used to find useful information from omics data. These algorithms utilize training data to reveal patterns and determine predictions. Machine learning approaches deals with learning relationships from data which does not require to be predefined [1–3]. The traditional machine learning algorithms depend on feature data, and thus its performance is determined. The intensive prediction task in the field of genomics [4, 5] and proteomics [6] as well as metabolomics research [7] depends on these machine learning techniques.

Deep learning technique is the evolving generation of artificial intelligence and advancement of machine learning that has exhibited exceptional prediction performance recently on big data analytics in image processing, signal processing and sequence analysis [8–10]. Deep learning has been inherited from artificial neural network with advanced features [11–17]. Deep learning neural networks (DNNs) are prominent for their fitness in analysing high-dimensional data. Since biological data appear to be high-dimensional and complex, hence DNN methods are suitable for bioinformatics research. DNNs can determine unknown abstract patterns and correlations to recognize the characteristics of data [18, 19]. The DNNs in bioinformatics will help to code raw data and study features effectively. The goal of this

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