



Role of AI in Bio-chemistry

Samir Kumar Bandyopadhyay*

Professor, Distinguished Professor of Lincoln University, Malaysia

***Corresponding Author:** Samir Kumar Bandyopadhyay, Professor, Distinguished Professor of Lincoln University, Malaysia.

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The artificial algorithms have many researches in many computational chemistry applications. For example, computer-aided drug design, material property prediction, and quality analysis of molecular compounds and many more. The toxicity agents have been analyzed successfully. Most of recent Deep Learning algorithms established concentration on the notion of stacked layers of neural networks.

Deep learning offers a computational basis for the identification and priorities of bioactive compounds. It requires pharmacological effects and their enhancement as drug-like leads. Bio-target recognition and protein architecture are new fields of application [1].

Due to the rise in the biological data dimension and processing rate, it is challenging that traditional analytical strategies are difficult to tackle the problem. So, machine learning methods and also deep learning approaches are used to tackle high volume of data huge for identification of hidden patterns within them and to classify for prediction of proper drug related to the particular problem of patient.

The machine learning approaches can be used also in bioinformatics. The approach identifies different alveolar cells. These approaches are used now for predicting the secondary structure of protein.

Researchers combine traditional microscopy with deep neural networks for finding the accurate resolution of DNA and oncogene magnification at a single cell level.

For genome sequence data, bioinformatics used for a vast array of important tasks like analysis of gene variation, expression, analysis and prediction of gene and protein structure along with their function.

High blood pressure is now leading risk factor for morbidity and mortality worldwide. It causes a major public health challenge that needs interdisciplinary efforts.

The epigenetic modifications play a vital role in the biological pathway of hypertension. For this modification DNA methylation studied by researchers. The DNA methylation process adds a methyl group to the cytosine base at a region including repeated cytosine-guanine bonds. If a gene is highly methylated, the outcome remains in a transcriptionally silent state. Due to environmental factors, methylation level can change the structure dramatically. Promoter CpG island methylation is considered a potential type of biomarkers for disease detection, subtype classification, prognosis, and treatment response prediction.

In conclusion, it can predict now that the most challenging problems in computational biology is to transform the high volume of data into knowledge. Machine learning approaches have become an important tool to carry out this transformation. This letter tries to highlight that the machine learning plays an important role in biochemistry, bioinformatics and many others.

Bibliography

1. L David, *et al.* "Molecular representations in AI-driven drug discovery: a review and practical guide". *Journal of Cheminformatics* 12.1 (2020).