Review Article

Artificial Intelligence Approach for Identification of Diseases through Gene Mapping

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Abstract

Biotechnology and information technology have been in a continuous and nearly parallel phase of development since last few decades. With time these two fields, with information technology having more emphasis, have started integrating each other at very many places, the outcome too is definitely good. Artificial intelligence has also emerged as a very advanced field related to information technology and finding varied space in biotechnology, hopefully the hybrid will arrive as a promising combination in resolving many issues of biotechnology. Present work highlights a preliminary insight of combination of artificial intelligence in identification of diseases at the genetic level.

Keywords: Artificial intelligence, diseases, Gene Mapping.

I. Introduction

In artificial intelligence (AI), machine learning is an application that provides systems the ability to automatically learn and improve from existing experiences without being explicitly programmed. It is a technology developed with the help of computer programs that make the use of data that they can access, to learn for themselves. Machine learning algorithms take part in the development and application of computer algorithms that improve with experience. Genetic mapping is based on the use of Genetic techniques to construct maps showing the positions of genes and other sequence features of the chromosomes. Although measuring the transcription of a single gene is not new, it is new to measure at once the transcription of all the genes in an organism. The past applications of machine learning to population genetics demonstrate that they outperform traditional approaches. Potentially important disease biomarkers have been revealed by the use of various method of machine learning on gene expression data, where algorithms learn to differentiate between different disease phenotypes. Today agency like the National Institutes of Health is documenting many ways that artificial intelligence and artificial intelligence simply can contribute towards the better understanding of genetics as well as genomics [1-5].

II. Conceptual definitions

Artificial Intelligence: - Artificial intelligence (AI) refers to the simulation of human intelligence in machines that are programmed to think like humans

and mimic their actions. The term may also be applied to any machine that exhibits traits associated with a human mind such as learning and problem-solving.

Machine learning: - Machine learning is an application of artificial intelligence (AI) that provides systems the ability to automatically learn and improve from experience without being explicitly programmed. Machine learning focuses on the development of computer programs that can access data and use it to learn for themselves.

Gene mapping:- Gene mapping describes the methods used to identify the locus of a gene and the distances between genes. The essence of all genome mapping is to place a collection of molecular markers onto their respective positions on the genome.

III. Need and importance

In the post-genomic era, it is one of the most challenging tasks is to identify disease causing genes from a vast amount of genetic data. Also, complex diseases present highly heterogeneous genotype, which makes biological marker identification difficult. These markers are identified widely with the help of machine learning methods. While identifying disease genes, we come across some challenges such as, extracting the location and structure of genes, identifying regulatory elements, identifying non-coding RNA genes, gene function prediction, RNA secondary structure prediction etc. These have all been tackled using machine learning approaches. Machine learning models are found to be very useful in neurological diseases. It is helpful in facilitating precision medicine and neuroscience research. The genes of an organism are expressed through the production of proteins, the building blocks of life. The method by which the genes of an organism are expressed is through the production of proteins, the building blocks of life. A specific protein is encoded by each gene, and various proteins are being produced at each point in the life of a given cell. The production of specific proteins that an organism responds to environmental and biological situation, such as stress, and to different developmental stages, such as cell division, is done through it turning on and off. It is made possible to simultaneously measure the rate at which a cell or tissue is expressing and translating into a protein each of its thousands of genes, through the use of gene-expression microarrays, commonly called as gene chips[1-8].

IV. Limitations

A. Machine learning algorithms require massive stores of training data.
B. Machines cannot explain themselves.
 C. When machine learning algorithms are deployed, there may be more instances in which potential bias finds its way into algorithms and data sets.
D. Machine learning is to high error susceptible.
E. There is bias in data
F. It requires a lot of time and resources

V. Conclusion

The utilization of machine learning algorithms and techniques in genomics is increasingly extensive. It is an alternative to the traditional genome-wide association studies (GWAS). Recent successful application includes cancer research, where crucial information regarding patient genotypes, gene-expression-related phenotypes, and patient outcomes has been revealed. The applications of machine learning are nearly endless. The scientists have taken the help of machine learning in activities like analyzing DNA, decoding the human genome, assessing disease phenotypes, understanding gene expression, processes such as gene editing (a process which splices the DNA into an organism's genetic code).

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