**Commentary**

# BIOINFORMATICS: ANALYSIS, STRUCTURE AND NETWORK

**HEMAYET HOSSAIN***

Department of Biochemistry, Alumni La Trobe University, Australia.
**Email:** hossain23@gmail.com

## COMMENTARY

Bioinformatics is a multidisciplinary field that develops software tools to understand biological data, especially where data sets are large and complex. As a multidisciplinary science field, bioinformatics combines biology, chemistry, physics, computer science, information engineering and mathematics to analyze and interpret biological data. Bioinformatics was used to analyze the silico of biological questions using mathematical techniques. Bioinformatics incorporates biological studies using computer programs as part of their work, as well as analyzing specific "pipelines" that are used repeatedly, especially in the field of genomics. Often, such diagnoses are performed with the intention of better understanding the underlying cause of the disease, different habits, desirable structures, or differences between individuals. In a less formal way, bioinformatics also attempts to understand the principles of organization within the nucleic acid and protein sequences, called proteomics. To study how normal cellular functions are adapted to various disease conditions, biological data should be compiled to form a complete picture of these functions. Therefore, the field of bioinformatics has evolved to such an extent that the most stressful work now involves the analysis and interpretation of different types of data. These include nucleotide and amino acid sequences, protein domains, and protein structures. The most important processes within bioinformatics and computational biology include- development and implementation of computer programs that allow for effective access, management and use of a wide variety of information. Development of new algorithms and statistical measurements that examine relationships between members of large data sets. What makes it different from other methods, however, is its focus on developing and implementing powerful computer techniques to achieve this goal. Bioinformatics now integrates the creation and development of knowledge, algorithms, arithmetic and mathematical techniques, and the theory of solving legal and practical problems arising from the management and analysis of biological data. Evolutionary biology is the study of the origin and evolution of living things, as well as their evolutionary process over time. Informatics has helped evolutionary biologists by enabling researchers to track the evolution of large numbers of species by modifying their DNA, rather than by using the definitive taxonomy or biological analysis, to compare all genomes, allowing the study of more complex evolutionary events , such as genetic replication, horizontal gene transfer, and predictors of essential biological factors, create complex statistical models to predict system outcome over time, to track and share information on a growing number of species. The essence of genome analysis is the establishment of interactions between genes or other genomic genetic variants. It is these intergenomic maps that make it possible to trace the evolutionary processes responsible for the division of two genomes. At the highest level, the major chromosomal segments are duplicated, isolated, flexible, altered, removed and inserted. In cancer, affected genome cells are rearranged in complex or unexpected ways. Major follow-up efforts are used to identify mutations of previously unknown predisposition to a variety of cancer genes. Biologists continue to develop specialized automation systems to control the volume of sequential data generated, and to develop new algorithms and software to compare sequencing results with a growing collection of human genetic sequences and germline polymorphisms.

## ACKNOWLEDGMENT

## DECLARATION OF CONFLICTING INTERESTS

The authors declared no potential conflicts of interest for the research.