Mini Review

Biological Computation

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Abstract

Computers and computer science are used in the field of computational biology to study and model the structures and functions of living things. It involves using computational techniques (such as algorithms) to model and simulate biological systems as well as to analyse experimental data, frequently on a very large scale (Liou TG et al., 2013).

INTRODUCTION

In order to comprehend biological systems and interactions, computational biology uses data analysis, mathematical modelling, and computer simulations. The area has roots in applied mathematics, chemistry, and genetics and is a nexus of computer science, biology, and big data. Biological computing, a branch of computer engineering that applies bioengineering to the construction of computers, is distinct from it. An interdisciplinary discipline known as computational biology and bioinformatics develops and uses computer techniques to evaluate massive volumes of biological data, such as genetic sequences, cell populations, or protein samples, in order to establish new hypotheses or uncover new biological processes. Analytical techniques, mathematical modelling, and simulation are all utilised in the computation (Siniscalco D et al., 2008).

Computational biology has its roots in the early days of computer science. Before his passing in the early 1950s, British mathematician and logician Alan Turing—often referred to as the "father of computing"—used primitive computers to put into practise a model of biological morphogenesis, or the emergence of pattern and shape in living things (Tzouvelekis A et al., 2013). A computer named MANIAC, which was developed at the Los Alamos National Laboratory in New Mexico for weaponry research, was used for modelling speculative genetic codes around the same period. (Even earlier, in the 1950s, population genetics calculations were performed on pioneering computers; nonetheless, Turing and the Los Alamos team's work represent the first instances of true computational modelling in biology).

Initially, computational biology concentrated on understanding the structure and sequence of biological molecules, frequently in the context of evolution (Ghaedi M et al., 2013). But it expanded steadily into the examination of function starting in the 1990s. Analysing the interactions between proteins and other molecules as well as their sequence and structural similarities between unknown and known proteins are necessary for functional prediction. Given the potential scope of such investigations, computational biology and systems biology—which aims to understand the functioning of sizable interacting networks of biological elements, particularly biological pathways—have grown to be intimately allied (Huang SXL et al., 2014). Due to their complexity, interdependence, and dynamic nature, biochemical, regulatory, and genetic pathways require advanced computational methods for modelling and analysis. Furthermore, modern technology platforms for the quick, automated (high-throughput) generation of biological data have enabled a shift from conventional hypothesis-driven experimentation to data-driven analysis, enabling computational experiments on unprecedentedly large genome-wide databases. As a result, many elements of biological research are now impractical without computers and computer science approaches (Williams MC 2003).

Even specialists frequently mix up the phrases bioinformatics and computational biology, and many people believe that the distinctions are pointless. Fundamentally, both

subjects are computational approaches to biology. However, computational biology is typically regarded as a branch of biology, in the same way that computational physics is a branch of physics, whereas bioinformatics tends to refer to data management and analysis using tools that are aids to biological experimentation and to the interpretation of laboratory results (Dahlin K et al., 2004). One area of biology that computation specifically facilitates is computational biology. In other words, the techniques computer science brought to the formulation and solution of difficult problems, to the representation and analysis of domain knowledge, and ultimately to the generation and testing of scientific hypotheses, defined its formation rather than the need to deal with scale (Kreda SM et al., 2001).

Despite certain commonalities, computational biology is more clearly distinguishable from mathematical biology. The focus of the earlier field of mathematical biology was on using numerical analysis, particularly differential equations, to study issues like population dynamics and enzyme kinetics. Later, it broadened to incorporate the use of sophisticated mathematical techniques in genetics, evolution, and spatial modelling. Computers were unavoidably helpful in these mathematical assessments, particularly for solving systems of differential equations that needed simulation. Computational biology is not automatically applied to such activities just because automated calculations are used. Computational biology and mathematical modelling of biological systems can, however, have certain similarities, particularly when simulation is a fundamental component of the model and used for prediction or hypothesis creation. Numerical analysis and discrete mathematics can be distinguished in this regard; the latter, which focuses on symbolic rather than numerical manipulations, is regarded as the basis of computer science, and generally, its applications to biology may be considered aspects of computational biology (DeMaio L et al., 2009).

Theoretical biology, which is also associated with mathematical biology at times, and computational biology may be differentiated from one another; however there are still important connections between them. The main focus of theoretical biology is frequently mathematical abstractions and speculative interpretations of biological processes, which may or may not be useful for analysis or adaptable to computational implementation. In general, computational biology is connected with practical application; in fact, publications and yearly meetings in the subject frequently actively urge the presentation of biological studies using real data in addition to theory. Theoretical parts of biology that has their roots in information theory, network theory, and nonlinear dynamical systems (among other fields) have, on the other hand, made significant contributions

to computational biology. For instance, advances in the mathematical study of complex networks have improved our understanding of how naturally occurring interactions between genes and gene products may have developed during the course of evolution and why characteristic network architectures tend to be robust in the face of perturbations such as mutations (Newman GR et al., 1999).

CONCLUSION

The goal of computational biology is to develop models for a variety of experimental data types, including concentrations, sequences, images, and biological systems, including molecules, cells, tissues, and organs. To do this, computational biology employs techniques from a variety of mathematical and computational fields, including complexity theory, algorithmic, machine learning, robotics, and others.

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