Importance of Computational Biology in Biology

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Editorial

Computational biology, which includes many aspects such as bioinformatics, is the science of using biological data to develop algorithms or models for understanding biological systems and relationships. Until recently, biologists did not have access to very large amounts of data. This data has become particularly common in molecular biology and genomics. Researchers were able to develop analytical methods for interpreting biological information, but could not immediately share it with colleagues.

Bioinformatics was considered to be the science of analyzing computer science processes in various biological systems. At that time, artificial intelligence research used a network model of the human brain to generate new algorithms. With this use of biological data to explore other areas, biological researchers have rethought the idea of using computers to analyze and compare large datasets. Information was exchanged between researchers using punch cards. In the late 1980s, the amount of data shared began to grow exponentially. This required the development of new computational methods to enable rapid analysis and interpretation of relevant information.

Since the late 1990s, computational biology has become an important part of the development of new biology technologies. The terms computational biology and evolutionary computation have similar names, but should not be confused. In contrast to computational biology, evolutionary computation does not deal with the modeling and analysis of biological data. Instead, build algorithms based on the idea of trans-species evolution. Research in this area, sometimes referred to as genetic algorithms, which can be applied to computational biology. Evolutionary computation is not essentially part of computational biology, but computational evolutionary biology is. Computational biology has been used to assist in sequencing the human genome.

Software and tools

Computational biologists use a wide variety of software. These range from command line programs to graphic and web-based programs.

Open source software provides a platform for developing computational biology techniques. In particular, open source means that all individuals and / or entities have access to and benefit from research-developed software. PLOS lists four main reasons for using open source software:

Reproducibility: This allows researchers to use the exact method used to calculate the relationships between biological data.

Faster development: Developers and researchers do not have to reinvent existing code for smaller tasks. Instead, you can leverage your existing programs to save time developing and implementing larger projects.

Proprietary Software

Standard modeling and scientific software used on an industrial scale also provides an excellent foundation for the rapid development of computational biology. This software also provides isolation against code errors through aggressive development by a large number of collaborative experts in areas specially developed for algorithm development. It also speeds up the internal development of computational biology by eliminating the need to code features from scratch and ensuring compatibility and easy learning through consistent syntax guidelines and documentation practices. The libraries used in it can be cross-validated to get the same (or better) results as an open source project. Since the software is a closed source, there is little public monitoring and the lack of verifiable scientific data is less obvious throughout the process.

Proprietary scientific computer software used in mathematics, statistics, data analysis, and numerical methods includes Mathematica (Wolfram Language), Matlab, and SAS.

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How to cite this article: Qiang Chen. "Importance of Computational Biology in Biology." *J Microbiol Pathol* 5 (2021): 137.