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Commentary

Descriptive Study on Biological Modeling System

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DESCRIPTION

In biomedical science, system biology is an approach to understanding the greater picture by bringing its parts together, whether at the level of the organism, tissue, or cell. It is in stark contrast to the reductionist biology of decades, which requires separating the pieces. In order to analyze biological data, bioinformatics and systems biology use computer methods. System biology is a field of study that focuses on understanding whole biological processes, such as protein complexes, metabolic pathways, or gene regulation networks, in comparison to the previous emphasis on single genes or proteins [1-10].

Computational biology is an interdisciplinary field in which computational methods are created and applied in order to analyze large biological data sets, such as genetic sequences, cell populations or protein samples, to make new predictions or to discover new biology.

About 2000, when the Institute for Systems Biology was founded in Seattle in an attempt to attract "computational" style individuals who were not drawn to the university's academic settings, Systems Biology was started as a new area of science. In 2003, a Department of Systems Biology was launched at Harvard Medical School. Work on CytoSolve, a technique to model the entire cell by combining several molecular pathway models, was initiated in 2003 at the Massachusetts Institute of Technology.

In 2006, it was predicted that the hype created by the "very fashionable" new concept would cause all major universities to need a department of systems biology, so that graduates with a minimum of computer programming and biology skills would have careers available. The National Science Foundation put out a challenge in 2006 to create a mathematical model of the entire cell.

The Karr Laboratory at the Mount Sinai School of Medicine in New York obtained the first whole-cell model of Mycoplasma genitalium in 2012. The whole-cell model is capable of predicting M's viability. In response to genetic mutations and genitalia cells.

Study of bioinformatics and data

In systems biology, other elements of computer science, informatics, and statistics are also included. These include new types of computational models, such as the use of process calculus to model biological processes (notable approaches include stochastic π-calculus, BioPEPA, and Brane calculus) and modeling based on constraints; incorporation of literature information, using information extraction techniques and text mining. Online database and repository creation for data and model sharing, database incorporation approaches and software interoperability by loose coupling of software, websites and databases or commercial suits; network-based approaches for high-dimensional genomic data sets analysis.

Biological models formation

Researchers begin by selecting a biological pathway and diagramming all interactions with proteins. Mass action kinetics is used to characterize the speed of the reactions in the system after evaluating all the interactions of the proteins. Differential equations to model the biological system are given by mass action kinetics as a mathematical model in which experiments can decide the parameter values to be used in differential equations.

Modeling biological systems

In systems biology and mathematical biology, modeling biological systems is an important activity. Biology of computational systems seeks to build and use powerful algorithms, data structures, visualization and communication tools in order to model biological systems on computers.

Visualizing biological data

Visualization of biological data is a branch of bioinformatics which focuses on the application of computer graphics, and visualization of information to various areas of the life sciences. This includes sequence visualization, genomes, alignments, phylogenies, macromolecular structures, biology of systems, microscopy, and evidence from magnetic resonance imaging.

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The software tools used for biological data visualization vary from basic, independent programs to complex, integrated systems.

We are witnessing a rapid growth in the volume and diversity of biological data today, providing biologists with a growing challenge. Visualization is a crucial step in understanding and learning from this data. There has thus been a related rise in the number and diversity of biological data visualization systems.

An evolving trend is the blurring of boundaries between atomic resolution visualization of 3D structures, cryo-electron microscopy visualization of larger complexes, and visualization of the position of proteins and complexes within entire cells and tissues.

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