

New Expansions and Breakthroughs of the 21st Century AI Computing Life

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Abstract: This talk introduces the most widely used modern life science research, and its new developments in the 21st century, discovers the formation, breakthroughs, and developments of computing life science, discusses the carrier of computing life sciences, the ramification of biological mathematics, mathematical theory and its disciplinary characteristics, explores the research methodologies of computing life science. The study shows that while in the 21st century, the crossovers and intersections of mathematics, computational science, and the life science speed up. Computing life science methods are trying to interpret life sciences from a new perspective. It adopts a new research model and this will turn applied mathematics from non-life to life, thus greatly strengthens the interpenetration and connection of mathematics, computational science, and life sciences, which decisively advances the research of life science.

Keywords: Intelligent computing, Biological systems, Computational Life Sciences, New developments and breakthroughs

A new extension of modern life science research

In the 21st century when science and technology are rapidly developing, life science represents the frontier of natural sciences and is becoming one of the most impressive high-tech fields in the world with the fastest development, the most extensive application, the greatest potential, and the fiercest competition. Life science is an integrated and frontier discipline that combines multi-disciplinary, multi-information, and multi-information complex structures. Therefore, the method of studying the law of its motion change should be an innovative method of dynamic multidimensional and quantitative development [1-2].

It is no exaggeration to say that a complex biological system is a complex machine that involves the assembly of physics and chemistry. We can

understand the mysteries of life by identifying the structure and function of every part of the machine, which includes genes and proteins. However, due to the complexity, dynamics, and non-linearity of the living system, its overall not equal to the partial sum. Thus the behavior of the living system cannot simply constitute the overall behavior of the system component through superposition. The molecular basis of this non-linear feature is that there are extensive and complex interactions between various biomolecules, such as genes and proteins.

These complex connections may be physical or chemical. It is these complex interactions that lead to all kinds of networks of organisms. All the activities of life are based on the structure and function of these networks. Obviously, the use of experimental techniques alone is difficult to reveal the characteristics and nature of biological networks. To truly explore and understand the structure and function of each part in the complex machine of life, it must also be done through the intervention of computational biology.

Since the beginning of the 21st century, the methods and theories of computational life sciences have been continuously immersed in the research of life sciences at an unprecedented speed, especially in the frontier areas of modern life science research, such as molecular biology, immunobiology, and neurobiology. Science, developmental biology, and bioinformatics, environmental biology and many other frontier areas have brought a new look to the development of the entire modern life science. It

also have made new breakthroughs and new development to their research concepts, ideas, theories and methods [3].

Today, numerical calculations and simulations based on the basic principles of life sciences have become an important link between life science theory and scientific experiments. It has played a crucial role in the overall research of system life sciences. It also provides life science researchers with an important means of revealing the laws of life in a multi-layered and complex system.

In recent years, people have used computational biology to analyze biological complex networks and have explored a series of mathematical and computational methods for complex and variable network structures, such as matrix algorithms and network component analysis methods, to reveal biological complexity from the perspective of computational biology. The various organizational characteristics of the network, in turn, can establish a mathematical model of a biological complex network, which can further deepen people's understanding and understanding of the biological network topology structure.

In addition, because of the dynamic nature of the complex system of life, the metabolism of the biomolecules that make up the biological network makes the network inside the organism not a static structure, but always in motion. Therefore, how to develop the dynamic characteristics of biological complex systems has become an important topic for current mathematics and life science workers. Computational biology will also play a very important role in this area of research.

After the twenty-first Century, the bioinformatics, driven by the human genome project, has exploded rapidly with the development of the acquisition, processing, storage, networking, transmission, data mining, analysis and interpretation of biological information. The development of bioinformatics relies heavily on the development of computer technology and computational life sciences. It can be seen that the development of bioinformatics is closely related to the development of computational life sciences. Of course, the vigorous development of bioinformatics has provided enormous resources and development space for the development of computational life sciences. It can be predicted that the continuous development of computational life sciences will provide a reliable guarantee for the development of new theories, new methods, new technologies and new software for bioinformatics [4-5].

The branch content and mathematical theory of biological mathematics

Biomathematics is a new edge discipline between biology and mathematics in the rapid development of biology in the 20th century. Specifically,

Biological mathematics is an edge subject that applies mathematical theory and computer science to study the quantitative nature and spatial structure form of life science, analysis the inherent characteristics of complex biological systems, and reveal the biological information implied in a large number of biological experimental data. Since the beginning of the 21st century, biological mathematics has become very popular in the field of life science and mathematics research.

In 2004, Prof. Lan Stawart, a member of the Royal Society of England, predicted in the special issue of "Biological Mathematics" in Science magazine that in the 21st century one of the exciting and most advanced scientific fields is bound to be "biology mathematics."

If the branch of biology is regarded as a set and the different branches of mathematics are regarded as another set, then biological mathematics is a product space derived from the two sets. So the branch of biomathematics is very rich.

If it is divided by biological applications (biology as the object of study), there are quantitative taxonomy, quantitative genetics, quantitative biology, quantitative ecology, population ecology and quantum biology, biomechanics (biophysics and biomathematics Cross-overlapping fields), etc. If it is divided by the mathematical method used (that is, there is no clear biological research object), Biomathematics can be divided into branches such as biostatistics, bioinformatics, biological systems theory, biological cybernetics, and biological equations.

The scope of bio-mathematical research is very extensive. It had big huge influence in the fields of system ecology, bioinformatics, population biology, molecular biology, medical bio-mathematics, infectious disease dynamics, biomedical engineering and image processing, biophysics and biomechanics, biochemistry, agriculture, forestry biology, biostatistics, computational biology, evolution and system biology, environmental climate and applied meteorology, etc.

Mathematical theory for studying biological mathematics includes set theory, probability theory, statistical mathematics, stochastic processes, game theory, optimization of operations, calculus, differential equations, linear algebra, numerical calculations, matrix theory, and topology. It also includes some modern mathematics branches, such as information theory, graph theory, cybernetics, system theory and fuzzy mathematics, and gray system theory. Due to the complexity of life phenomena, the mathematical problems raised from biology are often very complicated and require a lot of scientific calculations. It can be seen that how important the development of computational life science is for the development of the whole biology mathematics ^[6-7].

Since entering the 21st century, computers have become an indispensable and important tool for researching and solving bio-mathematical problems. The rapid development of computer information processing technology effectively combines the quantitative analysis of established mathematic models in life sciences with the previous bioinformatics processing work.

As a result, the application of biological mathematics has been upgraded to a new stage. It further promotes the development of biometric mathematics in a new direction and then evolves into an edge discipline that combines biology, mathematics, and computer science.

Characteristics of mathematical biology discipline

Biological mathematics turns the application of mathematics from non-life to life. Its characteristics are:

1.As life activities occur in a large number of repeated and periodic cycles, they are disturbed by many random factors. Random phenomena are everywhere in the life world, and the study of random phenomena requires a probability and statistics method, which is the first characteristic of biological mathematics.

2.Because of the interrelated and interdependent phenomena in the life world, it is necessary to study with a comprehensive and comprehensive mathematical method, which is the second characteristic of biological mathematics;

3.Because the structure of life matter and the way of life activities are often discontinuous and intermittent, many discontinuous and discrete mathematical methods are often used in biological mathematics research. This is the third characteristic of biological mathematics.

4.The traditional mathematics (non-life phenomenon) has the following mathematical structure: $b=f(A)$. The mathematical structure of biomathematics is: $B=f(A)$.

Here A represents the set of data that is studied by the life phenomenon or reflects its own data. The set A is mapped by a generalized set function to a set of information that can reflect the essential attributes of the objective life phenomenon. It can be seen that information theory based on information quantity will be widely applied to biological mathematics.

Research on the method of computing life science

1.The quantification method of life phenomenon

Quantification of life phenomena is a quantitative description of life phenomena. It is worth mentioning that because of the existence of a large number of fuzzy phenomena in the biological field,

the fuzzy mathematical method based on the fuzzy set provides a new mathematical tool for the quantification of life phenomena. In addition, systems such as ecology, environment, and biomedicine have both some clear and unclear information. Thus, the prevalence of gray phenomena has made the gray system theory and method a new tool for studying the mathematicalization of life phenomena.

2. Probability and statistics method

Biostatistics is the earliest branch of biological mathematics. Today, various statistical methods have become a routine method in biological research. The application of probability and statistical methods is also reflected in the establishment and theoretical analysis of mathematical models of stochastic processes in biological mathematics research. The stochastic mathematical models are divided into two categories: continuous and discrete. Because of the discreteness of life phenomena, the Markov chain, as a discrete random mathematical model, has become an important tool in the study of biological mathematics, especially in population genetics. The Markov chain can clarify the laws of many groups of population genetics. In addition, Markov chains have many applications in ecology, environmental science and medicine.

3. The numerical calculation method

With the wide application of computer technology in modern life sciences, numerical calculations have increasingly shown their important role. The importance of scientific computing has been recognized by more and more life science workers. Numerical calculations in the research of life science include: numerical methods of nonlinear equations, numerical methods of linear equations, matrix method, interpolation, least squares and curve fitting, surface fitting, numerical calculus, numerical methods of ordinary differential equations and partial differential equations, and error analysis in numerical calculation, etc. Through the above numerical calculations, we can provide accurate, efficient and reliable scientific calculation methods and methods for related problems in life science [8].

4. Mathematical model method

In the study of biological mathematics, we often use mathematical models to transform a complex life matter movement into a mathematical problem. Then through the logical reasoning, solving and computing of the mathematical model, the relevant conclusions of objective facts are obtained, and the purpose of researching the phenomena of life is achieved. Mathematical models can be divided into deterministic and random types. The mathematical models of differential equations derived from the equations of mathematical physics are a very important class of determination models, including some important equations that we are familiar with, such as the Malthusian equation, the Logistic equation and the Lotka-Volterra equation. The process is very important for the study of the ecological relationship of population growth. In addition, the famous Hodgkin Huxley neural excitation transfer mathematical model is a two-order partial differential equation, which lays the foundation for the electrical neurophysiology. Because of this research, Hodgkin (Hodgkin) has also won the Nobel Prize.

5. Stochastic simulation method

Multi-information stochastic dynamic synthesis optimization simulation has become a new and important means and method in modern life science research. Compared with the traditional numerical interpolation, it can use modern random analysis, modern information quantification and random simulation methods in all directions and perspectives, to explore and fully dig out all kinds of biological information, and then establish a stochastic dynamic optimization model of biological information. In recent years, some new theories and new methods, such as fractal theory, random statistics theory, genetic coefficient method, optimal information entropy method, neural network technology, have not only enriched the stochastic simulation theory in the computational life science, but also widened the application range of the stochastic simulation. Its application effect was remarkable [9].

6. Comprehensive analysis method

Multivariate statistical analysis is the most practical and comprehensive mathematical method to study biology and medicine. Regression analysis, discriminant analysis, principal component analysis and canonical analysis are often used in multivariate statistical analysis.

System theory and Cybernetics whose core problem is optimal control is also one of the most effective mathematical methods for comprehensive analysis. The method of optimal control of biological systems is often based on the principle of the Behrman's dynamic programming. However, since the mathematical model of optimal control is usually a differential equation, other methods should be found for discrete cases.

7. Discrete mathematics methods

Because of the many discontinuities in biology, discontinuous mathematical methods play an important role in the study of biological mathematics.

The discrete models describing discontinuous life phenomena can be divided into two states and polymorphisms. Markov chain is a polymorphic discrete mathematical model. The two-state model is derived from the binary representation of biology. For example, The transfer of nervous excitement and the passage of excitement waves is a dual performance state. Boolean algebra is the basis for describing the two state discrete model of neural transmission. This model is constantly improved and realized with the help of computer. At present many complex neural functions can be simulated. It has become an important means to explore the mysteries of human brain.

Another kind of discontinuous mathematical method is to establish a mathematical model of multidimensional discontinuities by using the method of catastrophe theory. This model is a geometric model introduced by topology. Many of the discontinuous phenomena in the leap and critical state of biology can be qualitatively explained by the corresponding jump type [10].

Computer method

This is a new method put forward after the rapid development of computer technology. This method combines the software design of the computer with the design of the biological mathematical model. Data collection, data processing and data analysis can be completed by the software design system of the computer to achieve the goal of designing the complex biological mathematical model.

New needs generate new disciplines such as computational life science. New model creates new breakthroughs. Computational life science method helps us to understand life science from a new perspective. It greatly strengthens the mutual penetration and connection between mathematics, computational science and life sciences. The research process of modern life science is greatly accelerated by the new research model, that is, experimental data → mathematics and computational science theory and methods → computer simulation and prediction → biological experiment verification → mathematical model and post-validation theory.

Concluding remarks

The 21st Century is an information age with information technology and computing science technology as the core technology. The study of the intersection and integration of mathematics, computing science and life science is becoming increasingly close in the 21st century. Numerous facts indicate that the development trend and research direction of modern mathematics in the 21st century should be integrated, marginal, intersecting, and application-oriented in order to be more vigorous, more promising, and more promising.

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