

Development and Application of Biomathematics

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Abstract. At present, mathematics has been widely used in biology, and biomathematics, the combination of biology and mathematics, has become an entirely separate discipline, but also gotten good development and application. Biomathematics is widely applied, has various branches, and the new branch is still appearing and developing. This paper reviews the development process of biomathematics, elaborates specific applications among the various fields, and proposes the development prospect of biomathematics.

Introduction

Biomathematics is an interdisciplinary subject between biology and mathematics, mainly using mathematical ways to study and analyze related problems in the biological field, also exploring biological related mathematical methods. Biomathematics may be said to be a collection of biology and mathematics, fully applying mathematical knowledge to biology, thus able to better reflect the prominent role of biology and mathematics. Today, mathematics has been well used in biology, for example, application in environmental studies, epidemiological studies and ecological studies or other areas has high value. Although biomathematics started relatively late, but it has a bright prospect, worth to be further explored.

Development Process of Biomathematics

Biological research often will use observation and experiment methods to explore the nature of the living body, but these observations and experiments usually require large amounts of data as a precondition. How to use data to investigate the nature of life is extremely important. In view of the experimental data showing an geometric-level increasing trend, the practical value of mathematics in biology becomes increasingly prominent. In the past, the focus of applying mathematics in the study of life is the population problem, and the dynamics method is the most typical and most successful example of early application. In early twentieth century, the Italian mathematician, Volterra, in a lecture first mentioned in exploration on application of mathematics in biology, which laid the foundation for integration of mathematics into biological science. Thereafter, the British scholar, Pearson, started "Biometry" magazine, which can be said the milestone in the development process of biomathematics. In the twenties of the last century, mathematician, R. A. Fisher, and biologist, Dean Koala, jointly explored the relationship model of predation and prey, to in theory explain why volatility occurs in the fish school, and get the viewpoint that real-time predation is more advantageous for prey, which has also become an important basic theory in ecology among. Application of mathematics in biology is not just a static description of life, but an exploration on the complex process and law, and application of mathematical tools to create all kinds of mathematical models so as to integrate the differential equation model into biology. After that, due to the continued development of electronic technology, electronic products began to appear, and constantly upgraded, so as to promote the development of biomathematics into a new stage. Based on the use of computer technology, promote reasonable explanation for part of biomathematics class difficult to analyze to be, and also the formation of a lot of branches. In view of the rapid development of information technology, application areas of biomathematics have also been unprecedentedly extended, thereby making biomathematics research facilitated and more efficient.

Specific Application of Biomathematics in Various Fields

Currently, branches of biomathematics have penetrated into the life science, and are closely related to development of the national economy system. Biomathematics research has a great relationship with various industries, including from agriculture, forestry, animal husbandry, fishery to health care development, and from crop cultivation, animal and poultry species breeding to pest control, etc. With the continuous development of new technologies, bioengineering, human genome group, brain function simulation and computer technology and others remain to be deeply studied by biomathematics. Currently, humanity is facing increasing scarcity of energy, severe environmental pollution, sharp expansion of the population and other difficult issues. Biomathematics research should focus on these issues. Next, the paper focuses on the specific application in main branches of biomathematics, including biological cybernetics, infectious disease dynamics, animal breeding and genetics, population ecology, and molecular ecology.

Application in biological cybernetics

In recent years, people found many biological phenomena appeared, and control on the life phenomena is carried out continuously, so that we cannot solely use differential equations or difference equations for description. For example, based on pharmacodynamics studies, absorption, metabolism and excretion of drug in human body is a sustainable development process, able to be described by the dynamics model. However, oral drugs and intravenous injection are transient behaviors of impulse. The mathematical model to combine the transient behavior and flowing of drugs in vivo is the impulse differential equation model. This requires the use of the impulse differential equation theory and method to explore the best methods of rational drug use. Like this, in fish farming and forest management process, breeding, harvesting and deforestation programs can be optimized and improved, so as to be effectively protected, to ensure its continued production and good benefit. Plant protection research can make the best countermeasures for prevention and treatment of pests, mainly including the rational use of all types of pesticides or specific programs for culture of natural pest enemies. Environmental protection work can further study how to better protect diversified features of creatures. Theory and practice of impulsive differential equations have been well applied in life science and many other fields, so the application in improvement of biochemical products also has a higher value.

Application in infectious disease dynamics

For the last two decades, in the world, the research on infectious disease dynamics classroom has made great progress, and a number of mathematical models are used in the analysis of various infectious diseases. Most of the above mathematical models are also suitable for the study on universal laws of various infectious diseases. Some are specific to measles, tuberculosis or sexually transmitted diseases, AIDS and others and such models involve various infectious forms, including contact transmission, vertical transmission and arthropod-borne transmission. Given the variety of diseases have a certain incubation period, so for isolation of patients, immunity obtained due to illness or vaccination and immunity loss, illness associated mortality and cross infection between various types of populations, different increase laws of populations, age structure of populations, spatial migration or diffusion and other related factors. Compared to previous epidemic model, research models in recent years have more emphasis on being close to the reality, and there are three main directions. Model-related factors increase continuously; model dimension increase continuously; based on some specific symptoms of infectious diseases, carry out more detailed and deeper studies. Because the model is more consistent with facts, so it is even more complex, and theoretical research will face the new difficulty. In the study, in addition to necessary classical methods, dynamics method, degree theory and semigroup theory of operators are also integrated recently, especially computer simulation technology has been widely used in western countries.

Application in animal breeding and genetics

Animal breeding and genetics is an important branch of biomathematics, mainly studying the transmission of life information and coding theory, focusing on describing the relationship between information process, information and material carrier. Life information can be divided into major

genotype information and memory-type information. Genetic information stored in the biological macromolecules mainly determines various types of genetic information of the life entity and activity characteristics. First, create various genomic databases associated with animal elite breeding. Because livestock economy traits are usually controlled by micro-effect polygene, and also there is the presence of the major gene in this context. Then we can use the sequence alignment and homology analysis, to find and position major genes and homology genes related to livestock economy traits in the existing organism database, so as to form the new genomic database associated with animal elite breeding, in order to optimize and improve livestock breeds. Meanwhile, in the gene fragment sequences of the non-coding region, among we should really combine with molecule genetic markers to early monitor each gene fragment of major genes, differences of genotypes, channels of alleles inherited to offspring from the parental generation, and unknown information, in order to more precisely identify differences in genes between individuals. So we can make subdivision from the individual phenotype and formation causes, naturally, able to more effectively obtain genetic model, thus enhancing the standard line and efficiency of farm animal genetic evaluation. Second, explore livestock functional group, to allow the livestock sequence for homology recognition and sequence alignment, detect characterized fragments, build data model, identify functional sites, and predict possible related structures, so as to show its corresponding various functions. Currently, we have been able to apply the DNA chip technology in the nucleic acid layer, using two-dimensional gel electrophoresis and mass spectrometry sequencing in the protein layer, and conduct large-scale genetic map construction. Third, form animal genetic resource database. The essence of breed conservation is to scientifically preserve existing livestock resource gene pool currently, and effectively stabilize gene frequencies among the various groups. Breed conservation means retaining the most complete genome of a species, therefore the form of animal genetics and breeding can be used to conduct population genome detection in order to develop new characteristic genes and form the characteristic gene pool. From a macro perspective, we can build normative geographic information system, and begin to improve the relevant database of animal genetic resource.

Application in population ecology

Currently, the population ecology has become an important part of modern ecological theory development. Based on placing the population growth into the environment closer to the reality, the effect of noise interference originating in and out of population, and individual behaviors within heterogeneous environment and population on population dynamics has become an important issue. In particular, appropriately integrate above three aspects, to form a model with more extensive biological basis, and the most important is the emergence of a large number of individual-based models. Today, related research has further combined spatial heterogeneity, differences in behavior between individuals, and other random environmental disturbances to fully explore the population dynamics. The main method is to use biological relevant tests to obtain the life history information with individual differences, in order to further add various types of random noises into the model, and use computer simulations to obtain the dynamic model of the assumed ecology, so as to make corresponding analysis and comparison with reality results to obtain the exact information.

Application in molecular ecology

Today, molecular ecology has become a new study growing point crossing between mathematics and biology, which covers the now hotspots, including mathematical model of spatial variables, ecology-level trait changes, behavior and gene flow conversion and change. The author thinks that, there are three main aspects getting the biggest concern. Firstly, use mathematical models to create repeatable tiny organism unit for differentiation and simulation process, wherein, most researches focus on dissemination, expansion, expression and response of biological signals during differentiation and other aspects. Secondly, use molecular techniques to mark the population at different time and space, and analyze the biological relationship in accordance with statistics, so as to provide excellent basis for judging part of macro ecology. Thirdly, use mathematical models to build the spatial structure at the molecular level, to get related knowledge of basic biological unit form and functions.

Prospect of Biomathematics

American scholar, Friedman, in 1998, presented “Reflections on Future Mathematics” at the International Congress of Mathematicians, indicating the point of view that mathematics will occupy a very prominent position in the important areas, including material science, life science and digital technology, in particular, differential equations will have a great progress in the field of cardiac mechanics and immunology. In 2004, the magazine, “Science”, published a special edition of biomathematics, in which, the British scholar, Ian Stewart, predicted biomathematics research area would be a paramount research concern of the present century. Jim Austin, the American scholar, also believed that biomathematics research could facilitate the reconstruction of mathematical ecology, epidemiology and genetics, and many other disciplines. American famous ecology mathematician, Carlos Castlillo-Chavez, wrote in 2004 and pointed that the huge impact of globalization will lead to many problems, including the progress of biomathematics research and emphasized the very important role of mathematicians in biopharmaceutics research.

Conclusions

In summary, with the continuous development of society, biomathematics has been widely used in all areas, and in which biomathematics also has been continuously improved and optimized, able to be more comprehensively applied. At the same time, due to the continuous development of modern information technology, the efficient combination of biomathematics and information technology can more effectively enhance the actual role of biomathematics. Thus, the future development of biomathematics is promising, definitely able to provide strong support for the research work of multiple disciplines.

Acknowledgments

Topic in this paper: research on multigroup discrete time model, university-level research project, talent-introduction project.

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