Research and Application of Differential Equation System in Gene Regulation Network and Metabolic Pathway

Ming Cao

ABSTRACT

With the rapid increase in the number of organisms that complete sequencing and the wider understanding of gene functions, the study of biological networks has attracted more and more attention in bioinformatics. Moreover, due to the development of computer technology, more and more modelling models of regulatory networks and metabolic pathways are built. However, the evolution process of differential equation system is still in its infancy. There are some problems, such as large errors in structure and parameters, and too large amount of calculation in establishing models. Therefore, the author seeks solutions to related problems through the research and application of gene regulatory networks and metabolic pathways through differential equation systems. Studies have shown that a new optimization strategy is needed to obtain accurate differential equations in order to better solve practical problems in systems biology. At the same time, using a split idea can greatly reduce the search space in the process of equation optimization, and also combines the characteristics of the flexible tree model close to the form of differential equations.

KEYWORDS

Differential Equation System, Gene regulatory Network, Metabolic Pathway.

INTRODUCTION

In the early stage of bioinformatics, the main research object is sequence. Sequence analysis is used to discover genes, determine gene function, and analyze and predict protein structure[1]. It is the processing, storage and analysis of data obtained through biological experiments, thus revealing the biological significance implied by these biological data[2]. Therefore, genes interact with each other to form a network structure with complex regulatory relationships, namely Gene Regulatory Network (GRN)[3]. Functional genomics will not only promote the development of life sciences and biotechnology, but also have a major and far-reaching impact on the entire national economy, society and humanity itself. With the advancement of

Ming Cao
Faculty of Electronic and Information Engineering Xi'an Jiaotong University, Xi'an, 710049, China
School of Mathematics and Statistics Shaanxi Xueqian Normal University, Xi'an, 710100, China
molecular biology, advanced measurement techniques can provide a large amount of experimental data for network construction[4]. At the same time, the application of some related methods in mathematics, computer science and engineering also provides a powerful tool for the study of network structure, characteristics and regulation relations[5]. The research of gene regulatory network is established and analyzed from the molecular point of view, which can help us to understand the activities and functions of various factors in cells. And to study what causes the organism to change, help to understand the complex regulatory relationship between genes in the gene regulatory network, so as to systematically predict the process of organism life movement, and so on.

Bioinformatics is a new subject of applying computer science to manage bioinformatics. It is a subject that combines modern life science with computer science, mathematical science, chemical science and other fields[6]. The completion of human genome sequencing marks the gradual entry of biological research into the post-genome era, and the cost of gene sequencing has also decreased dramatically with the development of technology[7]. In recent years, the number of organisms that have completed sequencing has increased rapidly, and the focus of gene research has gradually shifted to the functional analysis of genes. With the completion of sequencing, functional genomics has become the mainstream of research. It clarifies the function of genome from the perspective of interaction between genome information and external environment[8]. The purpose of gene regulation network analysis is to establish a mathematical model of the regulatory network, and to study the interaction between genes through mathematical models[9]. In general, in the gene regulatory network, the expression of each gene may be affected by other factors, and the expression level of this gene may also affect the expression of other genes[10]. Molecular biology is a phenomenon of growth and development of graduate students at the molecular level. However, due to the limitations of the conditions at that time, scholars only studied the expression models of individual genes and some typical expression models of genomes. Based on the above problems, this study made a preliminary exploration and attempt on the construction of gene regulatory networks.

OVERVIEW OF GENE REGULATION NETWORK AND ITS RESEARCH STATUS

OVERVIEW OF GENE REGULATORY NETWORKS

Gene Regulator Network (GRN) refers to the process by which a group of regulatory factors regulate a set of gene expression. The commonly used method is to observe the phenotype of the organism after treatment by gene knockout, gene deletion, site-directed mutagenesis and the like. It is called “genetic particles” because during the reproduction process, the father copies a part of their own DNA and transmits them to the offspring, thus completing the propagation of the traits. Because in essence, the gene regulatory network is a complex dynamic system, which is somewhat similar to some research objects in physics. The methods in this field are worth learning. Gene regulatory networks reveal the complexity of life activities from the perspective of regulation between substances related to life activities. They are the focus of functional genomics and the frontier of bioinformatics. Gene expression can
be regulated at many stages, including transcriptional level, mature level of RNA processing and translation level, the most common of which is at the beginning of transcription. Generally speaking, the expression of one gene is affected by other genes, which in turn affect the expression of other genes. This interaction and mutual restriction constitutes a complex regulatory network of gene expression. Because time series microarray data can reflect the continuous changes of gene expression level, it has been widely used in the search of transcriptional regulation relationship between genes and the construction of gene regulation network in recent years.

The probability density can be calculated according to the distribution $I$ obeys. For convenience, it is unified into logarithmic form, and the unnecessary constant term is omitted to reduce the amount of calculation.

$$ I = I_{ph} - I_0 \left\{ \exp \left[ \frac{q \cdot (V + IR_s)}{AKT} \right] - 1 \right\} $$

(1)

The above formula is only for the maximum likelihood estimation formula of dimension $E$. To obtain the probability density of the whole time series, each dimension must be added up.

$$ I_n = DT^3 e^{\hat{\kappa} / x} $$

(2)

For a drift coefficient $I$ given by an algorithm, its fitness function is:

$$ V_c = \frac{AKT_c}{e} \ln \left( \frac{I_{ph} + I_0 - I_c}{I_0} \right) - R_s I_c $$

(3)

In theory, this is due to inadequate sampling, and the function generated randomly in the evolution process has only a very high accuracy in this very small interval. This interval is called effective interval in this paper.

$$ \alpha hv = A \left( hv - E_g \right)^n $$

(4)

The penalty term is introduced to subtract the measurement of system complexity from the original fitness function.

$$ LCA = f (\lambda_1) - f (\lambda_2) $$

(5)

The whole model is based on the theory of molecular collision, the so-called fast reaction, in which reactants are generated instantaneously. For example, the following reactions:

$$ y(h) = \phi \cdot y(h-1) + r $$

(6)
For a metabolic network containing $m$ substances and $H$ reactions, the dynamics of the system can be described by the following system equations:

$$h = \left(1 - \frac{\rho_A}{\rho_{A0}}\right) \cdot \left(\frac{3\eta \cdot m}{2\rho_{A0} \omega^2}\right)^{1/3}$$

(7)

CURRENT STATUS OF GENE REGULATORY NETWORKS

At present, there are two main research methods of gene regulatory networks: biological methods and computational intelligence methods. Biological methods are mainly based on biological experiments. Although data need to be processed, they are not very large. Random model can fit the network situation precisely, but it is difficult to apply to practice because of the difficulty of calculation. The aim of gene regulation network research is to reproduce the network structure of gene interaction by using the gene expression data obtained through experiments, so as to further study gene expression. In addition, with the help of mathematics and control theory, scientists have a more complete understanding of the composition of the gene regulatory network, the behavior of each molecule and the interaction relationship. The expression of each gene is assumed to be either on or off, that is, the intermediate state is not considered. Biologists can analyze the expression of genes in cells by observing the response of genes in cells under specific experimental conditions. At present, the research methods of gene regulatory networks have been greatly innovated, which has made the development of gene regulatory networks extremely rapid in recent years, and has also achieved many scientific research achievements in various fields. Mathematical tools for analyzing dynamic systems provide a detailed understanding of the nonlinear behavior of gene network performance.

In recent years, the number of researches related to gene regulatory networks is increasing, which indicates that the research of this project is being paid attention to by many scholars. Figure 1 shows the increasing and decreasing trend of related research in recent years.
GENE REGULATION NETWORK DIFFERENTIAL EQUATION MODEL

Stochastic Differential Equation, hereinafter referred to as SDE. Since the study of living organisms is a complicated process, we need to observe a lot of them and record the experimental data, and then analyze the sampling results. The ordinary differential equation model of the gene regulatory network does not contain a discussion of the spatial structure. Each variable in the model is defined by a single time effect concentration level, and at the spatial level, the regulatory system is considered to be uniform. By constructing and analyzing a gene regulatory network, we can understand the physiological activities and functions in cells at the molecular level and understand the interactions in the pathways. The process can be regarded as a parameterized random variable. After introducing the space formed by all second-order moment random variables, the distance, inner product and norm are defined in the space to define the limit. At this point, the stochastic process becomes a curve or sequence in the space. These models have different classification methods, such as discrete network and continuous network, deterministic network and stochastic network, qualitative network and quantitative network, etc. Although the continuous development of science and technology can provide experimental data for the construction of gene regulatory networks, this does not mean that all of its information can be fully obtained. It introduces the necessary nonlinearity and limits the upper limit of the rate of change of molecular concentration. By logarithmic transformation, the model can be transformed into a linear system and further solved by analytical method.

We assume that there are two genes A and B in the regulatory network, and A has an active regulatory effect on B. Their gene expression levels were continuously observed over a period of time, as shown in Figure 2.
Figure 2. Regulation of Gene A on Gene B.

The model can give a better explanation of the real situation of the system, but it is difficult to deal with mathematically. In most cases, the interaction between genes presents a complex non-linear relationship. This model is similar to the neural network model in many aspects. As a result of Taylor expansion and polynomial approximation, it has a wide range of approximation properties. With the development of expression profiling technology and gene sequencing, gene chips with high density can be used in organisms. Its advantage is that we can get a lot of information in a very short time, which can help us understand the relationship between genes more deeply. In addition, some assumptions and limitations can be made based on biological knowledge, which can greatly reduce the amount of computation in the network inference process. However, many biological processes rely on spatial structure and division, between different cells, or different parts of the same cell. For example, the concentration of molecules is different between the nucleus and the cytoplasm, and the spatial gradient of molecular concentration plays a very important role during development. Therefore, it is necessary to consider both the space and time factors in a network model. The time delay model in the above considers the spatial non-uniformity to some extent. But for the real situation, a more detailed fit is needed.

SUMMARY

In this paper, we mainly study a class of gene regulatory network models from the perspective of robust control theory. This work, like the problems we face in other areas of the natural sciences, such as physics and chemistry, is actually the simulation and analysis of complex systems. The gene regulatory network can be said to be inseparable from the lives of each of us. In-depth study of gene regulatory networks helps us understand the life processes of living things, which can help us better understand the activities between cells and how to treat certain diseases. Inferring the structure and parameters of gene regulatory networks by analyzing the collected gene expression data has become an important research topic in the field of biology. Of course, all reactions take place in organisms. At this time, we have to think about the difference of molecular concentration at the spatial level. The partial differential equation contains spatial variables, but it also makes the equation itself more complex. Therefore, the study of gene regulatory networks has attracted the attention of many research groups at home and abroad. However, we can also see that the progress of
molecular biology is changing with each passing day. More and more bioinformationists are also investing in this field. After hard exploration, gratifying discoveries will come out.

REFERENCES

1. Achdou Y, Porretta A. Convergence of a finite difference scheme to weak solutions of the system of partial differential equation arising in mean field games[J]. Computer Science, Vol. 7(2015) No. 7, pp. 73-77.
2. Wu Z, Yu Z. Probabilistic interpretation for a system of quasilinear parabolic partial differential equation combined with algebra equations[J]. Stochastic Processes & Their Applications, Vol. 124(2014) No. 12, pp. 3921-3947.
3. Kang W, Guo B Z. Stabilisation of unstable cascaded heat partial differential equation system subject to boundary disturbance[J]. Iet Control Theory & Applications, Vol. 10(2016) No. 9, pp. 1027-1039.
4. Mi X, Wang J, Wang R. Stochastic small disturbance stability analysis of nonlinear multi-machine system with Itô differential equation[J]. International Journal of Electrical Power & Energy Systems, Vol. 101(2018) pp. 439-457.
5. Caselli E, Ortega F, Santiago M, et al. A novel algorithm to solve the differential equation describing the non-interactive multiple-trap system model in thermoluminescence[J]. Radiation Effects and Defects in Solids, Vol. (2018) pp. 1-14.
6. Jiang Z, Ma W, Li D. Dynamical behavior of a delay differential equation system on toxin producing phytoplankton and zooplankton interaction[J]. Japan Journal of Industrial and Applied Mathematics, Vol. 31(2014) No. 3, pp. 583-609.
7. Ibrahim R W, Salih Y K. On a fractional multi-agent cloud computing system based on the criteria of the existence of fractional differential equation[J]. Mathematical Sciences, Vol. (2017) No. 1, pp. 1-7.
8. Kocayigit H, Sezer M, Cetin M. On the solution of differential equation system characterizing curve pair of constant breadth by the Lucas collocation approximation[J]. New Trends in Mathematical Sciences, Vol. 4(2016) No. 1, pp. 168-168.
9. Denisov, A. M. System of nonlinear integral equations for the unknown functions in a functional-differential hyperbolic equation[J]. Differential Equations, Vol. 53(2017) No. 9, pp. 1114-1120.
10. Wang, Xia Y. Discussion on the Complicated Topological Dynamic System of Ordinary Differential Equation (ODE)[J]. Applied Mechanics and Materials, Vol. 696(2014), pp. 30-37.