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Interdisciplinary applications of mathematics in biological sciences

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Abstract

Quantitative modeling, analysis, prediction and interpretation are valuable interdisciplinary tools for understanding complex biological systems that can be provided by mathematics. This study is dedicated to the application of mathematics in biology and is based on an interplay of differential equations, dynamical systems, graph theory, network mathematics and computational modeling. Both the temporal (time) changes of population sizes, interaction between cells, and physiological processes can be modeled as differential equations, and graph-based models can be used to capture the overall structure of complex biological networks and their connectivity. Biological processes which involve growth, regulation, competition and interaction are also represented using mathematical models. The behavior of gene expression is investigated with quantitative formulations, in order to understand the molecular dynamics and regulation. Estimation of disease transmission, development and the effects of interventions are also performed using disease progression models. The interdisciplinary approach shows the advantages of a mathematical literacy in enhancing biological interpretations, enabling prediction, and also the development of systematic mathematical tools for exploring and understanding complex biological mechanisms at several spatial and temporal scales.

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1. Introduction

Mathematics is now an integral part of many disciplines to gain insights into the structure, behaviour and evolution of complex biological systems. The interactions between cells, genes, organisms, populations, and the environment in biological processes often have interconnections, dynamic, and nonlinear features [1, 2]. Mathematical tools offer methods to describe the interactions in a systematic manner, uncover hidden patterns, and quantify biological relationships or predict system behaviours in response to varying conditions [3, 4]. Population growth, ecology, model of cellular dynamics, biochemical reaction and physiological processes are among the applications that use differential equations and dynamical systems [5], [6]. The biological systems and analysis are connected by mathematical modelling as shown in Figure 1.

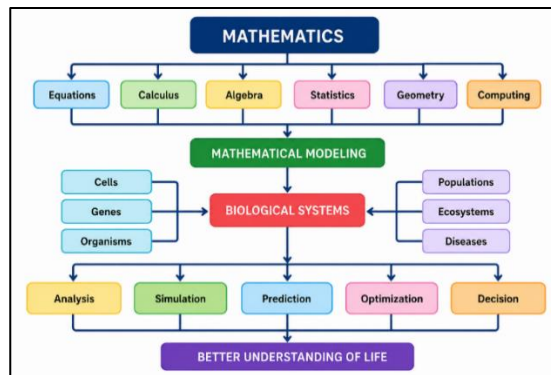


Figure 1
Mathematical Modeling Framework for Interdisciplinary
Analysis of Biological Systems

It is possible to study temporal changes, equilibrium conditions, stability and sensitivity to external interventions by using these techniques. Networks of various kinds are also used in biology, such as the interconnections of genes and proteins, metabolic networks, and ecological communities, and are called graph theory or network mathematics [7, 8, 9]. Mathematical models can also be used to describe the regulation of transcription, interactions between molecules, and changes in expression levels to quantitatively investigate gene expression [10, 11].

2. Differential Equations and Dynamical Systems

Biological changes over time can be modeled by differential equations and/or dynamical systems, and can be analyzed quantitatively with respect to population growth, cellular interactions, ecological dynamics, equilibrium behavior, stability and biological responses [12, 13].

Population Growth Dynamics

$$\frac{dN}{dt} = rN \left(1 - \frac{N}{K}\right) \quad (1)$$

Equation (1) is logistic growth in which the intrinsic growth rate generates population growth but when resources are limiting population growth is capped to obtain biologically realistic population stabilization.

General Dynamical System

$$\frac{dx_i}{dt} = f_i(x_1, x_2, \dots, x_n, t) \quad (2)$$

Equation (2) represents the temporal evolution of biological state variables in a functional form that allows representation of interconnected processes, nonlinear interactions, environmental influences and changing biological conditions – through time.

Cumulative Population Change

$$N(t) = N_0 + \int_0^t rN(\tau) \left(1 - \frac{N(\tau)}{K}\right) d\tau \quad (3)$$

The cumulative population variation over time in equation (3) is an integral of the instantaneous growth effects, and thus offers a continuous perspective of the population development from given values of biological conditions and parameters.

Root Mean Square State Deviation

$$D_{RMS} = \sqrt{\left[\left(\frac{1}{n}\right) \sum_{i=1}^n (x_i - x_i^*)^2\right]} \quad (4)$$

The average deviation of the biological states from the equilibrium state is measured by equation (4), and is used as a quantitative metric for measuring the system's variability, convergence, stability and overall system prediction accuracy.

Stability Measure

$$S = \sqrt{\left[\sum_{i=1}^n \lambda_i^2\right]} \quad (5)$$

Equation (5) brings together the characteristic stability components in one quantity, which allows for a quantitative analysis of the behavior of the system, its sensitivity to perturbations, its convergence properties and overall dynamical stability under varying conditions.

3. Graph Theory and Network Mathematics

The graph is used to represent the biological entities which are interconnected by the nodes and the edges and can be used for analysis of the biological networks including gene networks, protein interactions, neural systems, metabolic pathways, connectivity, centrality and regulatory relationships.

$$G = (V, E) \quad (6)$$

An equation in the form of (6) is a biological network consisting of vertices and edges, each vertex represents a biological entity and each edge

represents interaction, relationship or functional connections between the system elements.

$$k_i = \sum_{j=1}^n A_{ij} \quad (7)$$

Equation (7) is used to calculate the degree of each biological node and is a measure of the local connectivity of each node, giving an indication of the highly connected components within the overall biological network structure.

$$\bar{k} = \left(\frac{1}{n}\right) \sum_{i=1}^n k_i \quad (8)$$

Average network connectivity, shown in equation (8), is based on the individual node degrees and represents a global measure of interaction intensity and/or structural organization within the network of investigated biological network systems.

$$D = \frac{2|E|}{[|V|(|V|-1)]} \quad (9)$$

The fraction of existing biological connections to all possible connections (Eq. 9) is a measure of the compactness of the network, the richness of interactions and overall connectivity among the biological entities represented.

$$C_R = \sqrt{\left[\left(\frac{1}{n}\right) \sum_{i=1}^n k_i^2\right]} \quad (10)$$

The connectivity measure calculated by Equation (10) is based on the roots of the node degree, which highlights strongly connected nodes and quantitatively measures connectivity variation and structural complexity of biological networks effectively.

$$I(t) = \int_0^t \sum_{i=1}^n \sum_{j=1}^n A_{ij} x_{i(\tau)} x_{j(\tau)} d\tau \quad (11)$$

The equation (11) is a time integral over interactions between the connected biological nodes, which quantifies a total activity of a network in the time frame of interest, and shows how the strength of interactions between the biological nodes change over time in dynamically evolving biological network systems.

4. Mathematical Modeling of Biological Processes

The mathematical modelling of biological processes converts the biological mechanism into a quantitative formulation so that the growth, competition, regulation, biochemical reactions, cellular behaviour, interaction with the environment and reaction to different biological conditions can all be simulated.

$$\frac{dB}{dt} = \alpha B - \beta B^2 \quad (12)$$

For biological growth, the intrinsic growth is balanced by density-dependent limitation in the equation (12). This allows the quantitative

representation of population expansion, the competition between resources and the stabilization of a population under environmental limitation over time.

$$\frac{dx}{dt} = ax - bxy \quad (13)$$

The interactions between the biological species are defined by equation (13); and can be interpreted as competition, predation, cooperation and changes of population over time quantitatively.

$$\frac{dy}{dt} = cy \left(1 - \frac{y}{K}\right) - dxy \quad (14)$$

The model of population growth described in equation (14) takes into account interspecies interaction as well as limited resources, showing how both biological relationships and carrying capacity can affect the development of populations and trends of long-term sustainability.

$$B(t) = B_0 + \int_0^t [\alpha B(\tau) - \beta B^2(\tau)] d\tau \quad (15)$$

Equations (15) give integrated response to the growth of the biological system, thereby giving a cumulative information on the development of the system and allowing to quantify the temporal changes caused by growth and regulation.

$$E_B = \sqrt{\left[\left(\frac{1}{m}\right) \sum_{i=1}^m (B_i^{obs} - B_i^{pred})^2\right]} \quad (16)$$

The prediction error between observed and modeled biological values is calculated by Equation (16) to effectively assess the accuracy, reliability and prediction ability of models.

$$A_B = \sqrt{\alpha^2 B^2 + \beta^2 R^2 + \gamma^2 C^2} \quad (17)$$

Multiple weighted biological variables are integrated in a root based equation (17), which is used to quantitatively assess the collective biological response, interaction and system behavior.

5. Mathematical Analysis of Gene Expression

Mathematical analysis of gene expression quantifies the transcriptional and regulatory dynamics, and is used to identify the patterns of expression, molecular interactions, regulatory feedback, temporal variations, and relationships between the expression of genes under biological conditions.

Gene Expression Dynamics

$$\frac{dG}{dt} = \alpha - \beta G \quad (18)$$

The change of expression over time, as described by equation (18), balances the production and destruction of the gene, allowing for a quantitative understanding of the stability of expression, its molecular regulation, and dynamic responses of cells to be effectively analysed.

Regulated Gene Expression

$$\frac{dG}{dt} = \left[\frac{\alpha X^n}{(K^n + X^n)} \right] - \beta G \quad (19)$$

This equation (19) is a model of the controlled expression of a gene, it is nonlinear (transcriptional response) and the regulatory molecules affect gene activity depending on the biological state.

Gene Interaction Model

$$\frac{dG_i}{dt} = \sum_{j=1}^m w_{ij} G_j - \delta_i G_i \quad (20)$$

In equation (20), multiple genes are connected by weighted regulatory relations which describe how temporal gene expressions are determined in complex gene networks dynamically, due to the interaction of activation, inhibition and degradation.

Cumulative Gene Expression

$$G_{c(t)} = \int_0^t G(\tau) d\tau \quad (21)$$

By integrating the gene expression levels over time as shown in equation (21), a total measure of the transcriptional activity is calculated and it is possible to assess the molecular response over long time periods and during specific biological observation periods effectively.

Gene Expression RMSE

$$E_G = \sqrt{\left[\left(\frac{1}{n} \right) \sum_{i=1}^n \left(G_i^{\text{exp}} - G_i^{\text{model}} \right)^2 \right]} \quad (22)$$

Root mean square error between experimental and modeled gene expression values (Equation 22) is a quantitative estimation of the prediction accuracy, reliability of the model and overall estimation performance.

Normalized Expression Magnitude

$$G_N = \sqrt{\left[\frac{\left(\sum_{i=1}^n G_i^2 \right)}{\left(\sum_{i=1}^n R_i^2 \right)} \right]} \quad (23)$$

Using equation (23) to calculate the magnitude of gene expression normalized to reference expression values allows for a standard comparison of expression level, molecular variability and regulatory activity according to different biological conditions effectively.

6. Mathematical Modeling of Disease Progression

Mathematical models help define the progression of diseases by providing quantitative and dynamic representations of the disease process, allowing for the estimation of disease development, transmission, treatment response, disease pattern and the effectiveness of interventions.

Susceptible Population Dynamics

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \quad (24)$$

Equation (24) represents reduction in susceptible individuals by disease transmission, and relates the rate of infection, susceptible population and infected population with total population to quantify epidemic spread over time in susceptible individuals.

Infected Population Dynamics

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \quad (25)$$

Changes in infected people are described in equation (25) which is used throughout to balance new infections and recovery so that the intensity of disease transmission, extent of the epidemic and time course of infections can be assessed quantitatively.

Cumulative Disease Burden

$$D(t) = \int_0^t I(\tau) d\tau \quad (26)$$

The integral for the infected population level shown in equation (26) is a measure of disease burden that can be used to evaluate the impact of the epidemic over time on the population observed during this time.

Disease Prediction Error

$$E_D = \sqrt{\left[\left(\frac{1}{n} \right) \sum_{i=1}^n (I_i^{obs} - I_i^{pred})^2 \right]} \quad (27)$$

The root mean square differences between observed and predicted infection values (infection errors) is calculated for equation (27) which provides a quantitative measure of the accuracy of the disease model, its predictive reliability, and its performance in estimating infection values well.

Disease Progression Index

$$P_D = \sqrt{\left[\left(\frac{I}{N} \right)^2 + \left(\frac{\beta}{\gamma} \right)^2 + \left(\frac{D}{N} \right)^2 \right]} \quad (28)$$

Equation (28) integrates the infection prevalence, transmission-recovery relationships and cumulative disease burden in a root based formulation to provide an integrated quantitative measure of overall patterns of disease progression and disease burden.

7. Result and Discussion

Results show that integrated mathematical solutions can provide a characterization of the complexity of biological systems, unveil dynamic interactions, enhance the predictive interpretation of results and provide quantitative information on gene regulation, disease processes, and biological processes.

Table 1
Comparative Performance of Mathematical Models for Biological Applications

Mathematical Approach	Prediction Accuracy (%)	RMSE	Stability Index	Computational Efficiency (%)
Differential Equation Model	91.24	0.128	0.89	88.42
Dynamical System Model	92.86	0.114	0.92	86.75
Graph-Based Model	90.47	0.139	0.87	91.36
Biological Process Model	93.58	0.102	0.93	89.64
Gene Expression Model	94.21	0.094	0.95	87.82

Table 1 shows a comparison of the biological applications of different mathematical methods. The best prediction accuracy of Gene Expression Model is 94.21% with the lowest RMSE value of 0.094 which proves that the model has a better predictive capability.

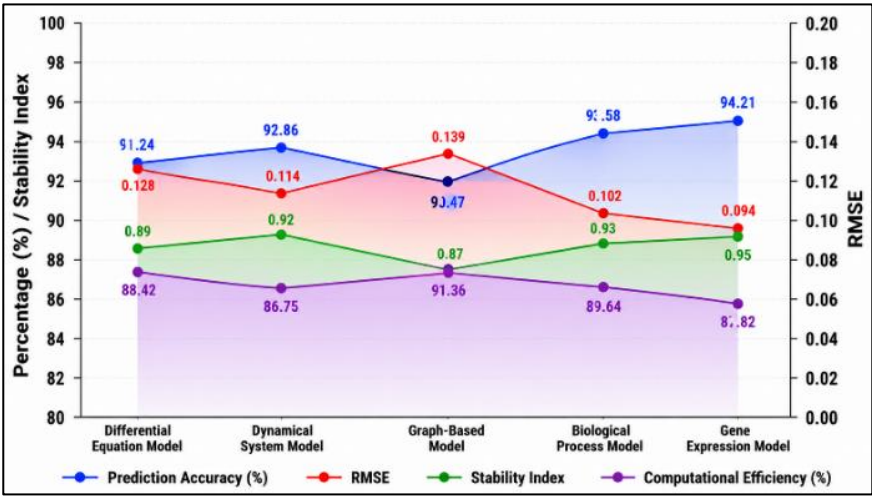


Figure 2
Comparative Performance Analysis of Mathematical Modeling Approaches

The comparisons of predictive performance, stability, errors and computational efficiency are illustrated in Figure 2. It also has the highest stability index (SI) of 0.95. The Graph Based Model has a comparatively low accuracy, but the highest computational efficiency at 91.36%.

Table 2
Quantitative Analysis of Biological Modeling Scenarios

Scenario	Growth Rate	Interaction Coefficient	Equilibrium Value	Prediction Error (%)	Sensitivity Index
S1	0.42	0.18	72.45	6.84	0.81
S2	0.48	0.21	76.82	5.93	0.84
S3	0.53	0.24	81.36	5.12	0.87
S4	0.57	0.27	85.74	4.46	0.90
S5	0.61	0.29	89.28	3.81	0.93
S6	0.65	0.32	93.16	3.24	0.95

Table 2 shows progressive changes over six different biological modeling scenarios. As for the growth rate, it is 0.42 for S1 and 0.65 for S6, both of which are increasing, as are the interaction coefficients and equilibrium values.

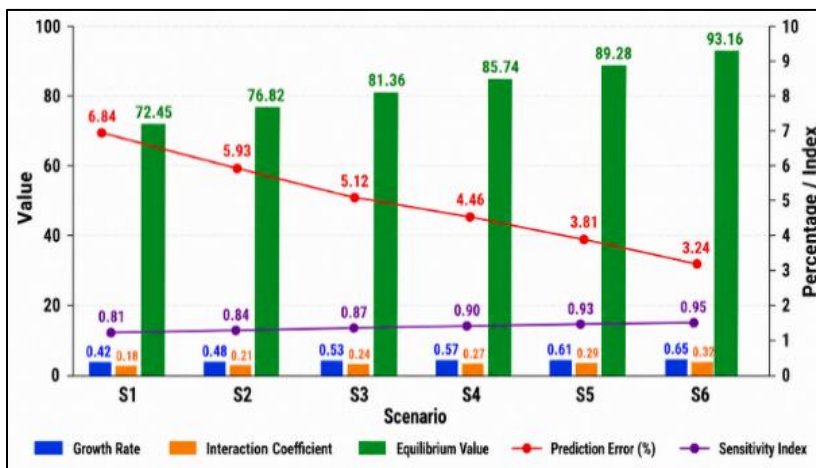


Figure 3
Comparative Analysis Across Biological Modeling Scenarios

This Figure 3 shows a comparison of growth, equilibrium, prediction error and sensitivity to scenarios. In the meanwhile, the prediction error consistently reduces from 6.84% to 3.24%, showing increased predicting reliability.

8. Conclusion

This study underscores the importance of mathematics in a complex understanding and analysis of biological systems. The use of differential equations and dynamical systems is a useful way of modelling temporal biological behaviour; graph theory may be used to study a network of

interconnected biological systems. Mathematical modeling allows quantitative depiction of biological processes, gene expression and disease development under different conditions. These methods enhance the understanding of mechanism, prediction and measurement of biological mechanisms by combining theory and measurable biological data. Mathematics and biology are used in an interdisciplinary way, which enhances the investigation of phenomena using computational tools and enables evidence-based scientific analysis. Adopting advanced numerical techniques, data-driven modelling, and AI can further improve biological predictions in future research.

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