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# A Study to Signify the Application of Biomathematics: Mathematical Models in Biology and Beyond

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**Abstract**

Mathematical tools are currently ubiquitous in the biological sciences, and the field that emerged from the merging of the two, biomathematics, has not only flourished but also seen substantial growth and practical use. Biomathematics has many different subfields, each with its own set of applications; new subfields are constantly emerging and expanding. Applying mathematical tools and procedures to tackle issues in the biological sciences is the essence of mathematical biology, a multidisciplinary field. Important models covered include logistic growth and Lotka-Volterra models for population dynamics, SIR and SEIR models for epidemiology, the Michaelis-Menten equation for biochemical reaction kinetics, the Hodgkin-Huxley model for neural networks, and the Wright-Fisher model for evolutionary dynamics.

**Keywords:** Biology, Models, Biomathematics, Ecology, Applications

## I.Introduction

Numerous areas of biology, biotechnology, and medicine draw from the multidisciplinary study of mathematical and theoretical biology. For a more mathematical focus, the discipline is known as biomathematics or mathematical biology; for a more biological focus, it is known as theoretical biology. Using a wide range of applied mathematical methods and tools, mathematical biologists seek to represent, analyze, and model biological processes mathematically. In the fields of biology, medicine, and biotechnology, it finds use in both theoretical and practical contexts. For instance, "cartoon" models of protein interactions are common in cell biology; they're simple to draw but fail to capture the complexities of the systems under investigation. This can only be accomplished with the use of exact mathematical models. It is possible to anticipate traits that may not be obvious to the researcher by providing a quantitative description of the systems, which allows for better simulation of their behavior.

I find the most fascinating contemporary use of mathematics in mathematical biology, a rapidly expanding field that is well-known yet poorly defined. As the field of biology moves towards a more quantitative approach, the usage of mathematics will inevitably increase. Collaboration across disciplines is crucial in the biological sciences due to their inherent complexity. Both mathematicians and biologists can benefit from mathematical modeling; the former can explore new avenues of study in biology, while the latter can take advantage of a powerful new laboratory technique—within reason—by understanding how to apply it correctly and acknowledging its limitations. Unfortunately, the crucial interdisciplinary involvement is hindered by mathematicians' haughty

application of arcane mathematics to biological problems and by their unfounded assertions about the significance of such theories.

Research in mathematical biology needs to have some sort of biological relevance if it is to be both practical and engaging. Optimal models not only illustrate the process's operation but also provide predictions about its potential outcomes. If the predictions pan out and these aren't already apparent to the biologists, they'll be paying attention. Mathematics from many branches is finding new uses in biology, including calculus, statistics, probability, abstract algebra, graph theory, combinatorics, algebraic geometry, topology, dynamical systems, differential equations, and coding theory. Research into mathematical biology led to the development of tools in some fields of mathematics, such as specific statistical approaches. Mathematical considerations are now integral to every step of the process, from conceptualizing the experiment to analyzing the results for patterns and underlying mechanisms. It goes without saying that the early stages of physics are significantly simpler than biology at every point of this caricature. Computers have allowed us to explore and, at times, grasp things that were unimaginable even 50 years ago, thanks to their incredible potential that has doubled every 18 months for the previous few decades.

**Reviews of related studies**

Murray, J.. (2012). Mathematics models have a lengthy history of use in the medical and biological sciences. After a small number of articles and a few of scientists were engaged in the area in the early 1900s, there are now thousands of dedicated researchers and the discipline has expanded greatly. Our overview of the field's evolution and the shifts in research methods is concise but by no means exhaustive. We discuss in further depth just two instances of particular models that are pertinent to actual biological issues: the patterning of animal coats and the development and improvement of images of glioblastoma brain tumors.

Jungck, John. (2011) The work of fifteen groups at as many different institutions has produced stunning biological applications of mathematics that differ in three ways from most of what is currently available. These contributions are shared in this special issue of Mathematical Modelling of Natural Phenomena on biomathematics education. To start, instead of using famous examples from textbooks that are at least fifty years old, several of these choices use more recent work in biomathematics. Secondly, the chosen modules are those that may be quickly and easily adapted and used in the classroom. Rather than delving into the difficulties of integrating biology into mathematics or vice versa, or conducting educational research on the efficacy of a single small implementation, the writers concentrate on creating individual biological models that are adaptable enough to be used in mathematics and biology classes. Discrete mathematics and novel pedagogies are included in this collection, which is a third difference. It may come as a surprise that discrete models are being prioritized, given that most of the biomathematics modeling work has been on calculus-based models up until recently. Nanostructures in DNA, viral capsids, neurological processes, and ecological issues are only a few examples. In addition, modern biomathematics curricula place modeling as an independent practice and a taxonomy of quantitative reasoning in its proper context.

Allman, Elizabeth & Rhodes, John. (2005) This mathematical biology introduction textbook covers discrete models in many different branches of the biological sciences. Population models (both linear and non-linear), genetics, infectious disease models, phylogenetic tree construction, Markov models of molecular evolution, and other biological issues are covered. Among books at this level, this one covers molecular evolution models and how to build phylogenetic trees from DNA sequence data. Exercises and more elaborate projects involve computer investigations with MATLAB throughout to provide readers with hands-on experience with the mathematical models produced. Accompanying the material are MATLAB programs. There is a low bar for entry in terms of mathematics knowledge because mathematical techniques like matrix algebra, eigenvector analysis, and fundamental probability are inspired by biological models and developed independently.

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## II.History Of Relation Between Mathematics And Biology

### The Past

Mathematics and biology have interacted for the past 500 years, and their current interactions are a direct result of those connections. Around 500 years ago, Europeans found the New World, which led to the description of numerous biological species not seen in religious texts. This led to significant conceptual advancements in biology.

For a significant period of time, it was widely believed that there were distinct types of blood in the body: arterial blood and venous blood. This concept originated with the ancient Greek physician Galen (131–201 C.E.) and persisted until William Harvey's medical studies in Padua (1600–1602), which coincided with Galileo's time in the same city. Both kinds of blood were believed to be synchronized with the liver's function, similar to the moon's correlation with the earth's tides. Harvey served as the physician to the monarch of England. He executed criminals and performed dissections on deer from the king's deer park, both of which were rights granted to him. Harvey states that human arm veins include unidirectional valves, which facilitate the flow of blood from the outside to the inside of the heart, but prevent it from flowing in the other direction. Consequently, the notion that blood flows in an uninterrupted cycle via the veins and arteries is not valid. Harvey saw the heart, a muscular organ that contracts and has one-way valves linking its chambers. Based on his findings, the left ventricle of a deceased human heart may have a volume ranging from 1.5 to 3 ounces (60 ml). He determined that with each ventricular contraction, the left ventricle expelled a minimum of one-quarter of its blood. He calculated that the heart rate was between 60 and 100 beats per minute. Therefore, the left ventricle pumped out roughly 27 liters of blood each hour, which was determined by multiplying 60 ml by 1/8, then multiplying by 60 beats per minute, and finally multiplying by 60 minutes per hour. However, an analysis of a blood sample from a deceased body would show that the average person had just 5.5 liters of blood. In light of this, the blood might be likened to a theatrical army that enters the stage from one side, proceeds behind the scenes, and then reappears from the other side. The prevailing idea at that time, which posited that blood originated from the ingestion of food, failed to account for the substantial volume of blood being pumped every hour. Unfortunately, Harvey was unable to see the tiny vessels that carried blood from the arteries leading out to the veins leading back in, so he had to make do with his best guess. Marcello Malpighi's remarkable confirmation of his theoretical prediction, which was based on his exacting mathematical calculations and careful anatomical observations, occurred almost fifty years later, when the capillaries were examined under a microscope. The tremendous power of using common, readily available mathematics in conjunction with meticulous observation and logical reasoning is demonstrated by Harvey's finding. For all subsequent applications of mathematics in biology, it was a benchmark.

### The Present

Assume a person is diagnosed with cancer. Could cancer-treatment medication selection be guided by knowledge of gene activity in cancer cells, allowing for the avoidance of less effective medications and the use of more effective ones? In their brilliant use of commercially available mathematics, by using these direct approaches, they successfully combined extensive datasets on gene expression and molecular pharmacology for the first time and extracted useful insights from them. We employed two kinds of data from the National Cancer Institute's drug development program. The original dataset consisted of descriptions of gene expression patterns for 1,375 genes in 60 distinct human cancer cell lines. The target matrix T included the quantitative representation of gene g's mRNA transcript abundance in cell line c. This information was stored as a numerical value in row g and column c. The drug activity matrix A contains information on the pharmacology of 1,400 drugs, including 118 that have a "known mechanism of action". These medications were discovered to have an effect on the same set of 60 human cancer cell lines. The value in row d and column c of drug activity matrix A shows the efficacy of drug d in suppressing the proliferation of cell line c, or in other words, the responsiveness of cell line c to drug d. The drug activity matrix A had 82,500 entries, whereas the target matrix T for gene expression contained 84,000 entries.

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An indicator of which tumor cells are likely to be suppressed successfully by a treatment might be a gene with high expression in a patient's cancer cells and a very positive association between that gene and drug activity. The marker gene may signal whether it is not safe to use a medicine if there is no association with its activity. There are still many unanswered significant scientific problems regarding this method, but it certainly helps with coming up with theories to test in future research. It is a brilliant strategy for arranging and making sense of a large number of separate observations.

**The Future**

In order to fully harness the potential benefits of the symbiotic relationship between biology and mathematics, it is crucial to navigate possible obstacles and capitalize on potential advantages.

## III.Application Of Biomathematics In Various Fields

Currently, biomathematics subfields are permeating the life sciences and have strong ties to national economic system development. The fields of agriculture, forestry, animal husbandry, fisheries, health care development, crop cultivation, insect control, animal and poultry species breeding, and many more are all greatly impacted by biomathematics study. Bioengineering, the human genome project, brain function simulation, computer technology, and many more areas will continue to be extensively studied by biomathematics as new technologies emerge. Energy is becoming increasingly scarce, pollution is at an all-time high, and the world's population is growing at an alarming rate, among other pressing problems. Questions like these ought to be the center of biomathematics studies. The specific application in important disciplines of biomathematics, such as infectious disease dynamics, population ecology, molecular ecology, animal breeding and genetics, and biological cybernetics, is then the emphasis of the article.

**Application in biological cybernetics**

Because of the constant regulation of biological events in recent years, it is no longer sufficient to describe them using differential or difference equations alone. Take drug absorption, metabolism, and excretion as an example. These processes can be characterized by the dynamics model, according to pharmacodynamics studies. Nevertheless, injecting medicines intravenously and taking medications orally are both impulsive behaviors. In vivo drug flow and transient behavior can be captured mathematically using an impulse differential equation model. To do this, we must investigate the most effective means of rational drug use by applying the theory and method of impulse differential equations. To guarantee its continuous production and good profit, it is possible to enhance and improve the breeding, harvesting, and deforestation programs as part of the forest management process and fish farming. Research into plant protection can lead to the most effective methods of pest treatment and prevention, such as the most efficient use of pesticides in general or targeted initiatives to cultivate natural enemies of pests. The field of environmental conservation can go deeper into the question of how to safeguard species' varied characteristics. Because impulsive differential equations have found widespread use in the biological sciences and beyond, their potential use in the enhancement of biochemical products is highly valuable.

**Application in infectious disease dynamics**

Infectious disease dynamics This research has come a long way in the past 20 years, with the use of several mathematical models applied to the study of different infectious illnesses. Research on the underlying universal rules of different infectious diseases can also make use of the majority of the aforementioned mathematical models. There are models that focus on certain infectious diseases, such as AIDS, tuberculosis, or measles; these models incorporate several modes of transmission, such as vertical transmission, arthropod-borne transmission, and contact transmission. Isolation of patients, immunity gained through illness or vaccination and immunity lost, illness-associated mortality and cross-infection between different types of populations, different population growth laws, age structures, spatial migration, diffusion, and other related factors are all important considerations when considering the incubation periods of various diseases. There have been three major shifts in recent years in

the emphasis of research models relative to their resemblance to reality, as compared to earlier epidemic models. More in-depth research should be conducted based on certain specific symptoms of infectious diseases as model-related features and model dimensions continue to grow at a steady rate. This new challenge will arise in theoretical study as a result of the model's increased complexity brought about by its increased consistency with the facts. Aside from the required classical approaches, the research also incorporates the dynamics method, degree theory, and semigroup theory of operators. Computer simulation technology, in particular, has been extensively utilized in western countries.

**Application in animal breeding and genetics**

The field of biomathematics known as animal breeding and genetics primarily deals with the study of life information transmission and coding theory, with an emphasis on explaining the connection between information process, information, and material carrier. Important genetic information and memory-type information are two main categories of life information. Different kinds of genetic information about a living thing and its activity traits are mostly determined by the genetic information kept in biological macromolecules. The first step is to establish a number of genetic databases linked to selective breeding of animals. Due to the presence of the primary gene and the fact that micro-effect polygene typically controls economic features in cattle. In order to enhance and optimize livestock breeds, we can utilize sequence alignment and homology analysis to identify and place important genes and homology genes linked to economic traits in the current organism database. This will allow us to create a new genomic database linked to elite animal breeding.

**Application in population ecology**

In recent years, population ecology has grown in prominence as a branch of contemporary ecological theory. An important issue that has arisen as a result of bringing population growth into closer contact with reality is the impact of noise interference, both internal and external to the population, as well as individual behaviors within a diverse population and environment, on population dynamics. Most importantly, a great number of individual-based models must be developed by properly integrating the aforementioned three components in order to create a model with a more complete biological foundation. More recent studies in the field have integrated regional heterogeneity, individual behavioral differences, and other forms of random environmental disruption to go even further into population dynamics. The primary strategy involves collecting data on individuals' life histories through biologically relevant tests; then, adding different kinds of random noises to the model; and finally, using computer simulations to get a dynamic model of the assumed ecology; finally, comparing the results with real-world data allows for accurate information extraction.

**Application in molecular ecology**

Molecular ecology, which bridges mathematics and biology, is a relatively young field that is rapidly expanding to include these areas of current interest. Conversion and change in behavior and gene flow as well as changes in traits at the ecological level are all included in this mathematical model. There are three key areas that the author feels are receiving the most attention. In the first step, researchers utilize mathematical models to build a reproducible microorganism unit for the differentiation and simulation process. During this stage, researchers primarily study the spread, growth, expression, and reaction to biological signals. Secondly, to offer a great foundation for evaluating a portion of macroecology, employ molecular techniques to tag the population at various times and locations, and then assess the biological link using statistics. Thirdly, to learn about the shape and function of fundamental biological units, employ mathematical models to construct their spatial organization at the molecular level.

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## IV.Mathematical Models In Biology

### Population Dynamics Models

**1. Logistic Growth Model:** For population ecologists, the logistic growth model—which accounts for population expansion in the face of finite resources—is an essential tool. The following differential equation represents the model:

$\frac{dN}{dt} = r\ N\ (1 - \frac{N}{K})$

Where:

- $N$ is the population size
- $r$ is the intrinsic growth rate
- $K$ is the carrying capacity of the environment

**2. Lotka-Volterra Model:** Ecosystem interactions between predator and prey populations are described by the Lotka-Volterra model. Two differential equations that are coupled make it up:

$\frac{dS}{dt} = rS - \alpha SI$

$\frac{dI}{dt} = \beta SI - \gamma I$

Where:

- $S$ and $I$ are the prey and predator populations respectively
- $r$ is the prey growth rate
- $\alpha$ is the predation rate
- $\beta$ is the conversion efficiency of prey to predator
- $\gamma$ is the predator death rate

### Epidemiological Models

**1. SIR Model:** One compartmental model that attempts to capture the dynamics of illness transmission in a population is the SIR model. The population is split into three groups: those who are susceptible ($\bar{S}$), those who are infectious ($\bar{I}$), and those who have recovered (R). They are the model equations:

$\frac{dS}{dt} = -\frac{\beta SI}{N}$

$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$

$\frac{dS}{dt} = \gamma I$

Where:

- $\beta$ is the transmission rate
- $\gamma$ is the recovery rate
- $N$ is the total population size

**JOURNAL OF ALGEBRAIC STATISTICS**
Volume 13, No. 1, 2022, p.1026-1035
https://publishoa.com
ISSN: 1309-3452

**2. SEIR Model:** The SEIR model extends the SIR model by adding an exposed (latent) compartment ($E$), representing individuals who are infected but not yet infectious. The model equations are:

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dE}{dt} = -\frac{\beta SI}{N} - \sigma E$$

$$\frac{dI}{DT} = \sigma E - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Where:

- $\sigma$ is the rate of progression from exposed to infectious

**Biochemical Reaction Kinetics**

**1. Michaelis-Menten Kinetics:** The Michaelis-Menten equation describes the rate of enzymatic reactions, where an enzyme ($E$) catalyzes the conversion of a substrate ($S$) to a product ($P$). The equation is given by:

$$v = \frac{V_{max}[S]}{K_m + [S]}$$

Where:

- $v$ is the reaction rate
- $Vmax$ is the maximum reaction rate
- $Km$ is the Michael is constant
- $[S]$ is the substrate concentration

**2. Enzyme Inhibition Models:** Enzyme inhibition models describe the effects of inhibitors on enzyme activity. The simplest form is the competitive inhibition model, where the inhibitor competes with the substrate for binding to the enzyme. The rate equation is modified to:

$$v = \frac{V_{max}[S]}{K_m\left(1 + \frac{[I]}{K_i}\right) + [S]}$$

Where:

- $[I]$ is the inhibitor concentration
- $Ki$ is the inhibition constant

**Neural Network Models**

**1. Hodgkin-Huxley Model:** The Hodgkin-Huxley model describes the generation and propagation of action potentials in neurons. It consists of a system of ordinary differential equations that describe the dynamics of ion channels:

$$C_m \frac{dV}{dt} = I - gNa\, m^3 h\, (V - V_{Na}) - gKn^4\, (V - V_K) - gL\, (V - V_L)$$

Where:

**JOURNAL OF ALGEBRAIC STATISTICS**
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- $Cm$ is the membrane capacitance
- $V$ is the membrane potential
- $I$ is the injected current
- $gNa$ and $gK$ are the conductance's of sodium and potassium channels
- $m$, $h$, and $n$ are gating variables
- $VNa$, , and $VL$ are the reversal potentials for sodium, potassium, and leak channels respectively.

**Evolutionary Dynamics Models**

**1. Wright-Fisher Model:** The Wright-Fisher model is a stochastic model used to simulate genetic drift in finite populations. It assumes non-overlapping generations and random mating. The probability of allele frequencies changing from $p$ to $p'$ in one generation is given by the binomial distribution:

$$P(p'|p) = \binom{N}{P'} p'^{p} (1 - p')^{(N-P)}$$

Where:

- $N$ is the population size
- $p$ and $p'$ are the initial and final allele frequencies

## V.Selection Of Mathematical Model For Biology

**A Note on Notation**

We are considering models, f(x; θ), describing the state x ∈ Ω ⊆ R $^{N}$ of a biological system; the states x are confined to the state space, Ω, of the system. Here θ ∈ Θ ⊆ R $^{d}$ is the d-dimensional vector of model parameters (e.g. reaction rate parameters) in the parameter space Θ. We denote by xi and θi the ith components of the state and parameter vectors, respectively.

When f(x; θ) represents a dynamical system, for example an ordinary differential equation dx/dt = f(x; θ), we use $x_0$ ∈ Ω to denote the initial conditions. Alternative models will be represented by subscripts, j, therefore fj (x; θ).

We represent any experimental observations or data by D = {d1, d2, . . . , dm}; here di is a vector with number of coordinates possibly less than N to account for observations that do not capture the whole state space, therefore where dim(di) < dim(x).

**Inverse Problems and Parameter Sensitivity**

At least its structure, or a potential model, f(x; θ), is available in numerous cases. In the next step, we need the parameters, θ, and sometimes the initial conditions, x0 = x (0). If we wish to compare the model's output with observed behavior or data D, parameter choice is critical. Parameters are frequently selected by reviewing the literature, but, this method is not without its risks. Parameters may have been determined under different circumstances than those actually considered in the literature; for instance, if the ambient pH is not equivalent, the reaction rate may not be what was expected. If the experimental conditions were not similar or at least equivalent, it becomes challenging to combine response rate parameters from diverse sources.

We typically have three options to delimit the range for the parameter θ. We can identify the value of θ that produces model output that is most similar to the observed data. The likelihood,

$$L(\theta) = \Pr(D|\theta), \quad (1)$$

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Volume 13, No. 1, 2022, p.1026-1035
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is the probability of the data for a given parameter θ. The maximum-likelihood estimate (MLE), $\hat{\theta} = \text{argmax}_{\theta}(L(\theta))$, corresponds to the parameter that has the highest probability of producing the observed data, and it can be obtained through optimization. We usually use optimization to estimate $\hat{\theta}$. In addition to this point-estimate we can determine confidence intervals for the value of θ.

In a Bayesian framework we determine the posterior probability of a parameter,

$$Pr(\theta|D) = \frac{\Pr(D|\theta)\pi(\theta)}{Pr(D)} \quad (2)$$

Where the prior, π (θ), represents our knowledge (or assumptions) about the parameter value prior to looking at any data. The posterior is thus determined from both prior information and the available data, D, via the likelihood, Pr(D|θ). The probability distribution over parameters rather than a single estimate tends to be the focus of Bayesian inference. Both frequentist and Bayesian inference are vast areas of research in their own right.

What really drives inference, irrespective of the framework, is the information content of the data (assuming that the model structure, that is the functional form of f(x; θ), is sufficiently close to the truth). One measure of this is how much varying θ changes the probability of observing the data, therefore the likelihood or the posterior probability. Information geometry arguably provides the most rigorous way of assessing certainty in an estimate, especially the so called Fisher information. Under mild regularity conditions the Fisher information matrix is given by

$$[I(\theta)]i,j = -E\left[\frac{\partial^2}{\partial\theta_i\partial\theta_j}\log L(\theta)|\ \theta\right] \quad (3)$$

For uni-modal likelihoods, a suitable measure of certainty is the curvature of the posterior function, which is the log-likelihood, or another cost function. Although ad hoc metrics for multi-modal likelihoods and posteriors have been suggested, there is currently no simple or widely accepted answer.

In many real-world scenarios, we discover that given a dataset and a model, we can only infer a subset of the parameters (or, more generally, a subset of parameter combinations). The remaining parameters are either not inferable at all or have very similar marginal posteriors to the posteriors. When parameterizing big models, such as whole cell models, it will be essential to determine which parameter combinations may be learned from both data and prior knowledge. For now, we can determine which parameters may be inferred from the data by doing sensitivity and robustness analyses, which include changing the parameters and then comparing the model's output.

## VI.Conclusion

Throughout the annals of biological study, mathematics has been an indispensable tool. The strength of mathematics in biology, however, needs to be encapsulated in a short list of accomplishments. A lot has occurred in the previous ten years in mathematical biology, and most of the changes have been positive. As a result of its success, it is now increasingly integrated into fields of application, whereas twenty years ago it was peripheral to many sub disciplines of biology.

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