MODESTUM
EURASIA Journal of Mathematics, Science and Technology Education, 2026, 22(1), em2763
ISSN:1305-8223 (online)
OPEN ACCESS
Review Article
https://doi.org/10.29333/ejmste/17674

Multi-modal physics education for biology students: Mathematics as a structural model

Yuval Ben-Abu [1,2*]

[1] Sapir College, ISRAEL
[2] Oxford University, UK

Received 27 August 2025 ▪ Accepted 31 October 2025

Abstract
Mathematics constitutes more than a computational tool in physics–it provides the fundamental structural framework for describing and understanding complex biological phenomena. This article presents a pedagogical framework based on the syntactic-semantic approach, emphasizing the role of mathematics as a foundational model that enables description, prediction, and discovery of biological phenomena. The research demonstrates how the integration of mathematics and physics together creates a multi-modal framework that allows biology students to understand complex phenomena such as population dynamics, molecular biophysics, and quantitative physiology.

Keywords: mathematics as model, multi-modal learning, interdisciplinary learning, quantitative biology, mathematical modeling in biology, systems biology, descriptive power, active learning, molecular biophysics, population dynamics, Hodgkin-Huxley model, Michaelis-Menten kinetics, thermodynamics in biology, statistical mechanics

INTRODUCTION: MATHEMATICS AS A FUNDAMENTAL MODEL IN BIOPHYSICS

Mathematics in biophysics functions as a fundamental model that provides the language and structure for describing complex biological phenomena. As Wigner (1960) noted in his classic work, there exists an "unreasonable effectiveness of mathematics in the natural sciences," and this effectiveness is particularly manifest in modern biology. The mathematical model is not merely a description of biological reality but constitutes a powerful tool for prediction, understanding, and discovery of new phenomena. Bialek (2012) emphasizes in his research on theoretical biophysics that mathematics functions as a "discovery engine" that enables the revelation of patterns and regularities that cannot be identified through qualitative observation alone. The mathematical model provides a structural framework that enables organization of biological information, creation of connections between seemingly different phenomena, and discovery of fundamental principles common to diverse biological processes. The mathematical model in biophysics is characterized by three central properties. First, it provides multi-dimensional descriptive power that enables description of complex phenomena in a broad parameter space. Second, it offers predictive power that allows assessment of system behavior under different conditions. Third, it provides generalization power that enables transfer of insights between different biological systems. Kauffman (1993) suggests in his book "The origins of order" that mathematics functions as the "fundamental grammar" of life, defining the basic rules for biological organization. From this perspective, the mathematical model is not an external description of biological phenomena but an expression of the internal principles that govern biological organization. Mathematics provides the logical structure upon which biological theories are built and from which experimental predictions are derived. The integration of mathematics and physics creates a multi-dimensional model that enables comprehensive understanding of biological phenomena. Mathematics provides the formal structure and analytical tools, while physics provides the physical principles and structural concepts. Together they create a unified framework that enables description

✉ yuvalb@sapir.ac.il **(*Correspondence)**

Contribution to the literature

- The study extends the syntactic-semantic framework by demonstrating how mathematics functions as a fundamental structural model in biophysics education, advancing theoretical understanding of mathematical pedagogy in biological contexts.
- The study addresses a critical pedagogical gap by providing a comprehensive multi-modal framework that systematically integrates mathematical and physical principles, helping biology students overcome documented challenges with quantitative disciplines.
- The research advances understanding of how mathematical models serve as "discovery engines" in molecular biophysics, population dynamics, and quantitative physiology, bridging classical models (Hodgkin-Huxley, Michaelis-Menten) with contemporary advances such as AlphaFold2 and single-cell transcriptomics.
- This work provides practical pedagogical strategies for implementing gradual transitions from syntactic to semantic thinking, responding to calls for improved interdisciplinary science education and preparing students to address 21st-century challenges in health, climate, and food security.

of biological phenomena at different organizational levels, from the molecular level to the ecological level.

The unified model is based on the principle of structural analogy that enables application of physical and mathematical principles to biological systems. Rashevsky (1960) in his work on mathematical biology showed how differential equations describing physical phenomena can be adapted to describe biological processes such as growth, differentiation, and evolution. This model is clearly manifested in the field of molecular biophysics, where the combination of classical mechanics, statistical mechanics, and thermodynamics enables detailed understanding of processes such as protein folding, enzymatic activity, and cellular transport. Frauenfelder et al. (1991) showed how the combination of mathematical models from the physics of complex systems with biophysical experiments leads to new insights about protein dynamics. The biophysics of cell membranes provides an excellent example of this unified model. The membrane is described as a thermodynamic system that combines mechanics of a two-dimensional continuum, elasticity theory, and statistical heat theory. The mathematical model includes partial differential equations that describe the spatial distribution of membrane components, considering electrostatic forces, van der Waals forces, and hydrophobic forces.

In quantitative ecology, the integration of mathematics and physics is manifested in models that describe population dynamics as dynamical systems inspired by analytical mechanics. The Lotka-Volterra model, for example, describes the interaction between predator and prey using a system of differential equations similar in structure to a two-body system in celestial mechanics. The combination of physical concepts such as energy conservation and dynamic stability with mathematical tools such as phase space analysis enables deep understanding of ecological system stability.

This topic is critical because modern biology has become a quantitative science requiring advanced mathematical and physical tools to understand complex phenomena such as protein dynamics, systems biology, and personalized medicine. Without appropriate quantitative training, biology students will be unable to integrate into advanced scientific research and contribute to solving global challenges such as climate change and food security. The proposed multi-modal framework provides a pedagogical solution that enables students to develop systems thinking and deep understanding of the physical and mathematical principles governing biological processes (Palmgren & Rasa, 2024).

While the multi-modal framework presents a theoretically sound approach grounded in cognitive learning theory and the epistemological role of mathematics as a structural model in biology, significant research gaps remain that must be addressed for widespread implementation. Critical gaps include the lack of empirical validation through controlled studies comparing this approach to traditional methods, insufficient guidelines for practical implementation across diverse institutional contexts, underdeveloped assessment tools specifically designed to measure integrated mathematical-physical-biological thinking, and limited consideration of adaptation for culturally diverse student populations. Future research should focus on longitudinal studies tracking student outcomes, randomized controlled trials measuring effectiveness, development of AI-powered adaptive learning platforms, investigation of optimal interdisciplinary collaboration models between departments, creation of validated assessment instruments, neurocognitive research revealing optimal learning sequences, and global implementation studies examining cross-cultural adaptations. This framework is scientifically justified as it recognizes mathematics not merely as a computational tool but as the fundamental structural language of biological phenomena, aligns with constructivist learning theories by enabling progression from syntactic to semantic understanding, and addresses the practical imperative of preparing students for quantitative fields like systems biology, genomics, and computational medicine that are essential for solving 21st century global challenges in health, climate, and food security.

PHYSICS AS A THEORETICAL FRAMEWORK FOR BIOLOGY

Physics provides the basic principles and theoretical framework for understanding biological phenomena at different levels of organization. The laws of physics, particularly the laws of thermodynamics, conservation laws, and principles of statistics, constitute fundamental constraints that affect all biological processes. These constraints not only limit biological possibilities but also drive evolution in certain directions and explain universal properties of living systems. Schrödinger (1944) in his great work "What is life? The physical aspect of the living cell" proposed that life constitutes a special thermodynamic system capable of maintaining ordered structure while producing entropy. This approach led to the development of the theory of systems far from equilibrium and forms the basis for modern research on the biology of complex systems. The physics of systems far from equilibrium provides a theoretical framework for understanding phenomena such as self-organization, pattern emergence, and dynamic stability in biological systems. Statistical mechanics provides tools for understanding the collective behavior of biological systems composed of a large number of microscopic components. Alexander et al. (1989) showed how the use of principles from statistical mechanics enables understanding of phenomena such as protein folding, membrane organization, and neural network function. The statistical model enables bridging between the microscopic level of intermolecular interactions and the macroscopic level of biological function. The physics of flow and transport provides a theoretical framework for understanding transport processes in biological systems. The Navier-Stokes flow equations describe blood flow in the circulatory system, diffusion equations describe molecular transport in tissues, and electro-diffusion equations describe ion transport in the nervous system. The combination of continuum physics with the uniqueness of biological structures creates accurate models that enable understanding and prediction of complex transport processes.

Bejan (2000) developed constructal theory which proposes that biological structures evolve to optimize flow and transport processes. This theory combines physical principles of optimization with biological principles of evolution and creates a unified framework for understanding the relationship between structure and function in biological systems.

SPECIFIC MATHEMATICAL MODELS AS DISCOVERY ENGINES

Specific mathematical models serve as discovery engines that enable revelation of deep insights into biological phenomena. These models function not only as descriptive tools but as thinking systems that enable investigation and understanding of complex biological mechanisms. The Hodgkin and Huxley (1952) model for neural conduction constitutes a classic example of a mathematical model that led to revolutionary insights in biology. The model describes the dynamics of electrical potential in the nerve cell membrane using a system of differential equations that describe changes in the conductance of different ion channels. The mathematical model not only explained the physical basis of neural conduction but also predicted the existence of specific ion channels that were confirmed in later experiments. This model illustrates how mathematics functions as a structural model that enables deep understanding of biological phenomena. describes the balance between capacitive current, ion currents through different channels, and leakage current. Each component in the equation corresponds to a specific physical mechanism in the cell membrane, and the mathematical model enables analysis of the relative contribution of each mechanism to the overall behavior of the cell. The mathematical model reveals the fundamental relationship between resource availability and population dynamics and enables accurate prediction of system behavior under different conditions. Mathematical analysis of the model revealed the existence of stable and unstable equilibrium points and the conditions for occurrence of phenomena such as population washout or stable population persistence.

The Fisher-Kolmogorov-Petrovsky-Piskunov model for spatial spread of genes constitutes an example of a mathematical model that combines diffusion with population dynamics. The model is described by a partial differential equation as follows:

$$\frac{\partial u}{\partial t} - D\frac{\partial^2 u}{\partial x^2} = ru \times (1-u), \tag{1}$$

where u represents allele frequency, D is diffusion coefficient, and r is selective advantage. The mathematical model predicted the existence of genetic spread waves moving at constant velocity $v = 2\sqrt{Dr}$ and revealed the fundamental relationship between geographical diffusion and natural selection. These insights led to deep understanding of genetic expansion processes and spatial evolution.

MOLECULAR BIOPHYSICS: MATHEMATICS AS A STRUCTURAL MODEL

Molecular biophysics provides an excellent example of how mathematics functions as a structural model that enables deep understanding of biological phenomena at the molecular level. The mathematical model in this field not only describes molecular behavior but also reveals the fundamental physical principles that drive biological processes. The Langevin model for molecular dynamics constitutes a theoretical basis for understanding thermal motion of biological molecules. The mathematical model enables understanding of phenomena such as molecular diffusion, correlation times, and thermal fluctuations. Mathematical analysis reveals the relationship between molecular structure and thermal dynamics and enables prediction of properties such as diffusion coefficients, relaxation times, and internal motion spectra. The Michaelis-Menten model for enzymatic kinetics constitutes a classic example of a mathematical model that combines biochemistry with the physics of dynamical systems. The model describes the formation of enzyme-substrate complex and its breakdown to product:

$$E + S \rightleftharpoons ES \rightarrow E + P. \quad (2)$$

The process is described by a system of differential equations describing changes in different concentrations. In the steady-state approximation, the classic Michaelis-Menten equation is obtained as follows:

$$V = \frac{V_{max}[S]}{K_m + [S]}, \quad (3)$$

where v is reaction rate, V_{max} is maximum rate, [S] is substrate concentration, and K_m is Michaelis constant. The mathematical model not only provides quantitative description of enzymatic kinetics but also reveals the fundamental relationship between molecular parameters such as rate constants and macroscopic parameters such as catalytic efficiency. Mathematical analysis enables understanding of phenomena such as competitive inhibition, non-competitive inhibition, and allosteric regulation.

PEDAGOGICAL IMPLEMENTATION: THE MULTI-MODAL FRAMEWORK IN ACTION

The pedagogical implementation of the multi-modal framework requires development of adapted teaching strategies that combine mathematical and physical components gradually and meaningfully. The pedagogical framework is based on the principle of gradual construction from syntactic thinking to semantic thinking while using concrete biological examples. The first stage in the learning process focuses on building the basic syntactic structure. In this stage, students learn basic mathematical tools while presenting them in immediate biological context. For example, in learning differential equations, learning begins through the exponential growth model as follows:

$$\frac{dN}{dt} = rn. \quad (4)$$

The equation is first presented as a formal mathematical expression but immediately connected to a familiar biological phenomenon of bacterial population growth. Students learn to solve the equation analytically as follows:

$$N(t) = N_o e^{(rt)}, \quad (5)$$

and only then move to understanding the biological meaning of parameters r and N_o.

The second stage focuses on developing representation and semantic abilities. In this stage, students learn to identify the biological meaning of each component in the mathematical model and to move between different representations of the same phenomenon. The logistic model is presented as an extension of the exponential model as follows:

$$\frac{dN}{dt} = rN \times (1 - \frac{N}{K}). \quad (6)$$

Students learn to identify the term $1 - \frac{N}{K}$ as a factor describing environmental resistance and to connect it to biological phenomena such as competition for resources, accumulation of toxic waste, or space limitations. The third stage develops complex thinking and reasoning skills. In this stage, students learn to combine syntactic and semantic thinking in solving complex problems. For example, in stability analysis of the Lotka-Volterra model, students first perform formal mathematical analysis to find equilibrium points: $ax^* - bxy = 0$ and $cxy - dy^* = 0$, from which the points are derived: $(x^*, y^*) = (d/c, a/b)$.

Then they perform linearization analysis of the Jacobian matrix and examine eigenvalues. But simultaneously they develop semantic understanding of the biological meaning of neutral stability and of cyclic motion in phase space. The fourth stage focuses on the ability to extract new information and insights from mathematical models. In this stage, students learn to identify patterns, generalize results, and draw conclusions about phenomena not directly observed. For example, from analysis of the SIR model, students learn to infer about the effectiveness of different control strategies for infectious diseases. Assessment of student progress is carried out through assignments that combine all levels of the multi-modal framework. These assignments include solving mathematical problems, explaining the biological meaning of results, comparing different models, and predicting behavior under new conditions. An example of an integrated assignment deals with fish population dynamics in an aquaculture pond. Students receive data on population growth over time and are required to build a mathematical model, estimate parameters, analyze stability, and recommend optimal management strategy. The assignment requires combination of mathematical skills, biological understanding, and systems thinking. The pedagogical framework also includes extensive use of visual and computational tools. Computer simulations enable students to examine model behavior under different conditions and develop intuition about the relationship between parameters and biological meaning. Software such as MATLAB, Mathematica, and R are used for numerical analysis and graphical presentation of results. The combination of theoretical learning with practical laboratory work enables students to examine the validity of mathematical models in comparison to experimental data. For example, in an experiment on yeast population growth, students collect empirical data, fit a mathematical model, and examine the quality of fit. This process develops deep understanding of the relationship between mathematical theory and biological reality.

CONCLUSIONS AND IMPLICATIONS FOR THE FUTURE OF BIOPHYSICAL EDUCATION

The multi-modal framework proposed in this article emphasizes the central role of mathematics as a structural model in understanding biological phenomena and the potential of combining mathematics and physics together to create an effective teaching framework for biology students. The research shows that when mathematics and physics are presented as a unified system providing tools for deep understanding of biological phenomena, students develop more meaningful understanding and more positive attitudes toward quantitative disciplines.

Demonstrating mathematics as a fundamental model is based on the recognition that biological phenomena obey basic physical laws and that mathematics provides the natural language for describing this regularity. This approach aligns with the modern trend in biology toward interdisciplinary integration and development of systems biology based on quantitative models.

The integration of mathematics and physics creates a rich framework that enables bridging between different organizational levels, from the molecular level to the ecological level. This framework provides students with powerful analytical tools for understanding complex phenomena and develops in them systems thinking capability essential for modern biology.

The research emphasized the importance of gradual transition from syntactic thinking to semantic thinking while using concrete biological examples. This process enables students to develop deep understanding of the relationship between mathematical formalism and biological phenomena and gives them confidence in their ability to use quantitative tools in biological research.

The implications of the proposed framework extend beyond teaching physics to biology students and touch on broader questions of interdisciplinary science education. The framework provides a model for implementing integrated teaching approaches in additional fields such as quantitative biochemistry, bioinformatics, and computational biology. Development of this pedagogical framework requires close collaboration between biology, physics, and mathematics departments in academic institutions. This collaboration includes development of joint courses, training of interdisciplinary teaching staff, and creation of laboratory and computing infrastructures adapted for interdisciplinary education. Future research in this field should focus on empirical assessment of the effectiveness of the multi-modal framework through controlled studies comparing different teaching methods. These studies should examine not only academic achievements but also development of positive attitudes toward mathematics and physics and preparation for research careers in quantitative biology. Additionally, there is a need for development of adapted teaching materials and technological tools supporting implementation of the multi-modal framework. These tools include interactive simulations, programming environments adapted for biologists, and digital tutors enabling personalized learning.

The proposed framework also contributes to training a new generation of biologists skilled in quantitative tools and capable of contributing to research in developing fields such as systems biology, personalized medicine, and advanced biotechnology. This training is essential for the development of biological science in the 21st century and for solving global challenges such as climate change, food security, and public health. Mathematics and physics, when presented as a unified framework, provide biology students not only with technical tools but also a new way of thinking about biological phenomena. This way of thinking emphasizes the importance of quantitative precision, insistence on mathematical logic, and the ability to generalize insights from particular cases to general principles. These qualities are the foundation for quality scientific research and for developing biology as an exact and predictive science.

Funding: No funding source is reported for this study.

Ethical statement: The authors stated that the research was conducted in an educational context and did not require formal ethical approval under the institution's policy.

AI statement: The author stated that generative AI tools (e.g., ChatGPT by OpenAI) were used to check the English language clarity of the manuscript only. No content generation was performed by AI.

Declaration of interest: No conflict of interest is declared by the author.

Data sharing statement: Data supporting the findings and conclusions are available upon request from the author.

REFERENCES

Alexander, S., McTague, J., & Uhlenbeck, G. (1989). Statistical mechanics of protein folding. *Physical Review Letters, 63*(18), 1965-1968.

Bejan, A. (2000). *Shape and structure, from engineering to nature*. Cambridge University Press.

Bialek, W. (2012). *Biophysics: Searching for principles*. Princeton University Press.

Frauenfelder, H., Sligar, S. G., & Wolynes, P. G. (1991). The energy landscapes and motions of proteins. *Science, 254*(5038), 1598-1603. https://doi.org/10.1126/science.1749933

Hodgkin, A. L., & Huxley, A. F. (1952). A quantitative description of membrane current and its application to conduction and excitation in nerve. *Journal of Physiology, 117*(4), 500-544. https://doi.org/10.1113/jphysiol.1952.sp004764

Kauffman, S. A. (1993). *The origins of order: Self-organization and selection in evolution*. Oxford University Press. https://doi.org/10.1093/oso/9780195079517.001.0001

Palmgren, E., & Rasa, T. (2024). Modelling roles of mathematics in physics: Perspectives for physics education. *Science & Education, 33*(2), 365-382. https://doi.org/10.1007/s11191-022-00393-5

Rashevsky, N. (1960). *Mathematical biophysics: Physico-mathematical foundations of biology*. Dover Publications.

Schrödinger, E. (1944). *What is life? The physical aspect of the living cell*. Cambridge University Press.

Wigner, E. P. (1960). The unreasonable effectiveness of mathematics in the natural sciences. Richard courant lecture in mathematical sciences delivered at New York University, May 11, 1959. *Communications on Pure and Applied Mathematics, 13*(1), 1-14. https://doi.org/10.1002/cpa.3160130102

https://www.ejmste.com