

# Current and Future Challenges in Mathematical and Computational Biology

By  
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New mathematical and computational tools have become important in every area of biological investigation. The modern life sciences relies on quantitative concepts to analyze phenomena, explain mechanisms, and describe the state of our knowledge of complex biological systems. Given the importance of dynamics in fields as diverse as biochemical reaction kinetics, fluid flow associated with vascular tissue, population dynamics, epidemiology, immunology, and evolutionary theory, the basic mathematical methods to describe and analyze time-dependent phenomena are now just as essential for life scientists as laboratory training. Similarly, the use of discrete mathematics in such disparate fields as DNA sequence analysis, demography, bioinformatics, evolutionary game theory, and time-series of animal behavior indicates that diverse mathematical concepts are needed for application in the life sciences.

Summarizing the expanse of current mathematical biology would require far more than the brief time of my presentation, so I will merely plan to tantalize the attendees with some of the ways that mathematics and computational science have contributed to our knowledge of biological systems. I will start by discussing biocomplexity, illustrating with audience participation how simple models can lead to non-intuitive results. I will then proceed to show using ongoing research in ecology how models can summarize data, contribute to understanding, enhance success in managing natural systems, and promote an open scientifically-based approach to public policy decisions. Examples will wend through Everglades restoration, black-bear/human interactions, control of antibiotic resistance, ramps (wild leeks), the Florida panther, and tie these all together as examples of spatial control.

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