

NITMB Workshop Report, Authors: Moumita Das and Wallace Marshall Expanding the Palette of Mathematics in Biology, January 20–22, 2026

Workshop Overview

This workshop convened mathematicians working in areas not traditionally associated with mathematical biology and biologists interested in exploring their questions through new theoretical lenses. Mathematical biology has historically relied on a powerful—but limited—set of tools, primarily differential equations and dynamical systems. Meanwhile, large areas of mathematics, including group theory, category theory, algebraic topology, differential geometry, and number theory, remain seldom applied to biological problems. For many important questions, differential equations may not be the most natural representation, and alternative frameworks could open entirely new lines of inquiry. The workshop was organized by Moumita Das (Rochester Institute of Technology) and Wallace Marshall (UC San Francisco) and hosted at the NSF-Simons National Institute for Theory and Mathematics in Biology (NITMB) in Chicago. Approximately 60 participants attended, spanning career stages from graduate students and NITMB Fellows to senior faculty, and drawn from institutions across the United States and internationally. The goal was to foster genuine two-way exchange: mathematicians would leave with new, biologically motivated problems of mathematical interest, while biologists would gain perspectives on their research beyond the standard equation-based toolkit.

The workshop was structured as a hackathon style experiment in interdisciplinary engagement and ideation. Day 1 opened with 90-second lightning talks from every participant, followed by three rounds of structured pairwise conversations with partners pre-assigned based on abstracts, and then open discussion in which participants proposed topics on a shared blackboard and self-assembled into working groups. Day 2 featured five invited tutorials to build shared vocabulary: morphogenesis, category theory, ecology, network biology, and algebraic topology. Groups presented initial concepts, followed by a reorganization period. Day 3 was dedicated to sustained group work, final presentations, and planning for continued collaboration.

Breadth of Participant Expertise

The lightning talks revealed the exceptional breadth of expertise assembled for this workshop. On the biology side, participants presented research on topics including cell geometry and organelle size control, cytoskeletal mechanics, mitochondrial network dynamics, morphogenesis in organs and embryos, single-cell learning and cognition, microbial ecology and phycosphere dynamics, bacterial DNA–protein condensates, virus dynamics, wound healing, and collective behavior in organisms ranging from worm blobs to springtails to sled dogs. On the mathematics side, the workshop included researchers working in algebraic and geometric topology, higher algebra and homotopy theory, category theory, number theory and discrete dynamical systems, percolation theory, random matrix theory, algebraic statistics, nonlinear algebra, information theory, stochastic calculus, extremal graph theory, and complex networks. Several participants also brought expertise in computational approaches such as agent-based modeling, machine

learning, and data-driven reconstruction of dynamical equations from single-cell data. This diversity—deliberately cultivated by the organizers—was essential to the workshop’s design, ensuring that the pairwise interactions and group formation process could generate connections between fields that rarely intersect at conventional conferences.

Working Group Outcomes

By the final day, eight working groups had developed concrete research directions spanning a remarkable range of mathematical and biological territory.

A group on **category theory and biology** explored whether category theory captures aspects of biological systems that graph-based representations cannot—specifically composition, cross-scale relationships, and emergent properties. They examined test cases including intracellular transport and the central dogma, asking whether categorical representations enable transfer of theorems between analogous systems, and investigated category-theoretic framings of stochastic optimization in biology. A group on **formalizing teleological claims** tackled the pervasive but informal use of optimality arguments in biology, proposing a quantitative “Teleological Legitimacy Index” that penalizes claims based on the surprisal of the chosen objective function, providing a principled way to distinguish genuine biological optimization from post hoc fitting, with connections to statistical learning theory. A large group addressed **model building from data**, focusing on inverse problems in constructing interpretable mathematical models from biological data. They framed the challenge along top-down (data-driven) versus bottom-up (knowledge-driven) axes and formulated a concrete challenge problem using generalized Lotka–Volterra dynamics with eight species, exploring minimum data requirements for identifiability, surrogate neural networks for acceleration, and efficient inverse methods for PDEs. A related group on **high-throughput perturbation data**, motivated by datasets of 20,000 point mutations in the circadian clock protein KaiC, asked whether a generalized random matrix theory could predict the structure of the resulting phenotype cloud and be validated against experimental period–phase data from the Kai oscillator. A group on **information theory across biological scales** developed a research program around information theory as a unifying language for sensing, signaling, decision-making, and memory in biological systems, identifying frontier areas including cell fate decisions, immune activation, and high-dimensional omics data, and highlighting needs for new theory connecting information, irreversibility, and coarse-graining. A group on **phycosphere ecology** modeled bacterial community dynamics in phycospheres—microenvironments surrounding phytoplankton—using generalized Lotka–Volterra equations with spatially dependent interactions and random matrix theory, asking what maintains bacterial diversity and proposing future extensions with metapopulation models and number-theoretic tools. A group calling themselves “The Untanglers” worked on **mathematical invariants of living tangles**, applying knot theory and Khovanov homology to dynamic, reconfigurable biological systems such as worm blobs and DNA tangles during cell division. They mapped living tangles to mathematical tangles and tracked topological invariants—including linking numbers and knot polynomials—to detect tangling and untangling events over time, and proved a theorem showing that local arc additions produce predictable algebraic changes in the Poincaré polynomial, with applications to stochastically

tangling soft robots. Finally, a group on **quantifying structural differences at multicellular and subcellular scales** developed graph-theoretic and topological approaches for biological imaging data. At the multicellular scale, they applied persistent homology to histopathology images of osteosarcoma to distinguish normal, necrotic, and viable tumor tissue. At the subcellular scale, they used extremal graph theory and graph invariants to compare mitochondrial network architectures across cell states and species.

Emerging Themes and Future Directions

A clear synthesis emerging from the workshop is that biology offers a rich and largely untapped source of problems for areas of mathematics far beyond differential equations. Category theory attracted particular interest for its capacity to formalize relationships between biological processes across scales. Algebraic topology and knot theory found concrete applications in characterizing the shape of organelle networks and the dynamics of living tangles. Random matrix theory, information theory, extremal graph theory, and number theory all surfaced as having potential biological applications through the structured pairwise interactions and group work. Conversely, several biological challenges—including high-throughput perturbation data, inverse problems in model building, and the formalization of optimality claims—were reframed in terms that are mathematically interesting in their own right.

The unconventional workshop format was itself a successful experiment. The lightning talks democratized participation and made visible the full intellectual range of the group—from number theorists and higher algebraists to biophysicists studying worm collective behavior and researchers reconstructing whole-cell dynamics from single-cell data. The abstract-based pairwise interactions pushed participants into conversations they would not have initiated on their own, and the iterative presentation–feedback–reorganization cycle allowed ideas to be stress-tested in real time. The mix of career stages enriched the workshop, with graduate students and postdoctoral fellows bringing fresh perspectives alongside the depth of senior participants. Several groups indicated plans to pursue collaborative publications, joint grant proposals, or regular follow-up meetings. The consensus among participants was that much of mathematics remains unexplored territory for biology, and that workshops structured around active collaboration—rather than passive attendance—are an effective way to seed these new connections.

The organizers thank all participants for their energy and ideas. Special thanks go to NITMB leadership, particularly Tuca Auffinger and Joe Hibdon, and to Penelope Johnson for outstanding logistical support throughout the planning and execution of the event. The NITMB facility, with its exceptional collaborative spaces and striking views, provided an inspiring environment. This workshop was supported by grants from the NSF (DMS-2235451) and Simons Foundation (MPS-NITMB-00005320) to the NSF-Simons National Institute for Theory and Mathematics in Biology (NITMB).