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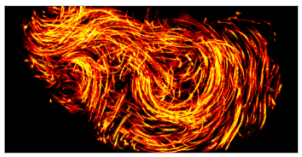
EDITORS: TRUNG (AVERAGE) V. PHAN, JONATHAN E. DAWSON, JACQUELINE ACRES

Highlights in Biological Physics, Physics Magazine



RESEARCH NEWS

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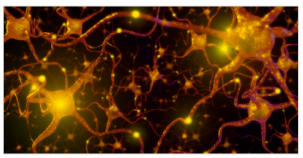

SYNOPSIS

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June 30, 2026

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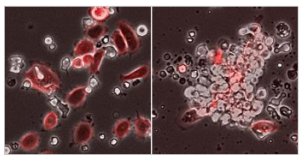
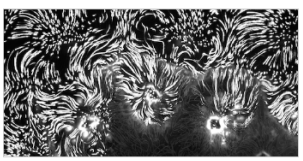


SYNOPSIS

Killer Cells Coordinate to Target Cancer

June 4, 2026

Experiments show how so-called natural killer cells adjust their dynamics depending on whether they face cancerous or healthy cells. Read More »

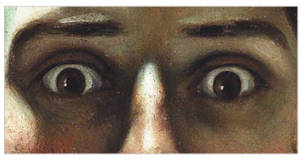


VIEWPOINT

How Corals Stir Seawater

Vivek N. Prakash – May 26, 2026

A new model explains how the microscopic hairs carpeting corals coordinate their beating to shape fluid flow. Read More »



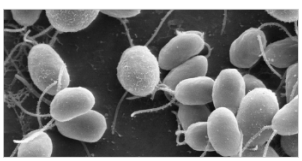
SYNOPSIS

Rapid Eye Movements Enhance Information Acquisition

April 28, 2026

A model captures how the retina avoids tuning out during a fixed gaze.

Read More »



FOCUS

3D Recordings of Swimming Algae

April 24, 2026

Measurements of the 3D fluid flow around a swimming microorganism could help researchers better understand the swimming dynamics of such microbes. Read More »

Meet our new Early Career Member-at-Large!

Jules Nde,
Postdoctoral Fellow,
University of Kansas

WHAT IS YOUR FAVORITE PAPER?

My favorite scientific paper is **Equation of State Calculations by Fast Computing Machines** (1953). Although the paper was written to study fluids in statistical physics, it profoundly shaped modern biophysics because it introduced the Metropolis algorithm, the foundation of Markov chain Monte Carlo (MCMC). Its importance lies not in the specific equation of state it computed but in the computational method it introduced. For example, before this method, physicists had to calculate thermodynamic properties by averaging over an astronomical number of molecular configurations. For a system of even 100 particles, the number of possible arrangements is so large that exhaustive computation is impossible. The challenge was as follows: How can we sample only the important molecular configurations instead of considering every possible one? The answer came from that paper. The authors proposed generating a sequence of configurations that preferentially visits those with low energy and high statistical weight instead of evaluating every configuration. This simple rule allows the simulation to reproduce the correct equilibrium distribution.

Then why biophysics? Protein folding, dynamics, and assembly have an enormous number of possible conformations. Metropolis sampling allows simulations to explore likely folded structures rather than searching every possible shape. This laid the groundwork for modern protein-folding simulations. Furthermore, simulations of protein dynamics and/or protein-complex assembly often alternate between deterministic molecular dynamics and Monte Carlo sampling inspired by the Metropolis algorithm. Metropolis sampling also enables the efficient estimation of free energy, which addresses many biological questions (including: Will a drug bind to a protein? Which protein conformation is more stable? How strongly do two biomolecules interact?) through calculations of free-energy differences. Last but not least, modern computational drug design frequently uses Monte Carlo methods to explore ligand conformations, binding orientations, solvent effects, protein flexibility, etc. Although many techniques have evolved, their conceptual framework traces back to the Metropolis algorithm.

The paper established a practical bridge between statistical mechanics and biological systems. It has become routine for researchers to apply Monte Carlo methods, for example, to study protein folding, membrane organization, chromosome structure, polymer physics, intrinsically disordered proteins, biomolecular phase separation, and many other topics.

... Continued from Page 2 ...

In summary, the paper introduced a remarkably general principle: *Don't solve the impossible problem directly; sample intelligently according to the governing probability distribution*. It marks one of the earliest examples of computational physics as a fundamental way of doing science, alongside theory and experiment. In biophysics, it made it possible to investigate systems whose complexity prevents exact analytical solutions. Its influence extends from molecular-scale simulations to modern AI-assisted molecular modeling. Even as methods such as molecular dynamics, enhanced sampling, and machine learning have advanced, many still rely on the core insight introduced in 1953: efficiently sampling the configurations that matter most rather than attempting to enumerate all possibilities. That idea remains central to computational biophysics today.

WHAT IS YOUR FAVORITE PAPER THAT YOU HAVE WRITTEN?

Coarse-Grained Modeling and Molecular Dynamics Simulations of Ca^{2+}-Calmodulin. This paper introduced me to the world of biophysics and showed me how to use physical principles to solve biological problems. Even though I knew how to utilize statistical mechanics to study the properties of materials, applying similar principles to protein folding and dynamics opened the door to the world of biophysics.

WHAT BIOLOGICAL PROBLEM DO YOU THINK MOST NEEDS A PHYSICAL-BASED APPROACH RIGHT NOW?

To me, the biological problem that most needs a physics-based approach right now is the study of protein folding, dynamics, assembly, and function. Proteins fold according to energy landscapes and molecular forces. The dynamics and assembly of proteins are also governed by the same principles. However, predicting the folding, dynamics, and assembly of proteins and protein complexes, which is necessary for predicting their functions, remains challenging despite advances in AI and machine learning. Statistical mechanics, thermodynamics, and quantum chemistry are the main areas of physics that explore these challenges.

IF YOU COULD INSTANTTLY MASTER ONE NEW TECHNIQUE OR TOOL, WHAT WOULD IT BE?

I know almost nothing about genetics, and I can do essentially nothing related to genetics other than politely ask other people to do things for me. If I could learn one new thing, I would learn all of modern genetics and its experimental tools. This is really more of an entire field than "one new technique or tool," as the question asks, but I think it is my biggest scientific weakness.

WHERE IS BIOPHYSICS HEADED?

This is an interesting question. Just as happened in well-established fields of physics, such as condensed matter physics or particle physics, several decades ago, biophysics researchers are moving toward not only understanding the large amount of available biological data but also defining normalized principles to study those data. This would take us from merely describing biological phenomena to defining predictive physical laws of living systems. Therefore, these laws can be employed in numerous areas of biology, such as active matter, whole-cell behavior, AI/ML in biology guided by physical principles, physics and mechanics applied to biology or mechanobiology, the physics of living systems, etc.

Creative Corner

IRIDESCENCE -- a visual poem contributed by Olivia M. Markowich, *SPS member*

B
e
n
d overlap,
and intertwine with others
like grass
with
strong
roots
t
luminous, standing tall in unison, c
e on what was taken, what was lost
pairs of eyes meeting l
f then keep shining anyway,
in recognition. e
R keep reaching for your share.

This piece uses iridescence as a bridge between physics, biology, and environmental harm. It is inspired by the shifting colors that appear when oil spreads across water, produced by thin-film interference as reflected light waves overlap. The effect is beautiful, but that beauty appears on a damaged surface.

Water is not merely a background for the physics; it is a living habitat. A thin contaminating layer can change how sunlight enters the water, how oxygen and carbon dioxide move across the surface, and how organisms interact with their environment, affecting life processes such as growth, movement, respiration, and survival. In this way, the author asks how physical processes at surfaces shape the conditions for life.

Meet our new Early Career Member-at-Large!

Linnea Lemma,
HHMI Hanna Gray Postdoctoral Fellow,
Princeton University

WHAT IS YOUR FAVORITE PAPER?

Reconfigurable self-assembly through chiral control of interfacial tension. Especially as postdocs, we are driven to chase high-impact science. It is a major motivating factor to think that my science will help us solve major problems in the world. However, in rereading this paper, I am reminded of another motivation for my work, which is to seek beauty and understanding. The stunning transition from a flat membrane to a chiral twisted ribbon, along with the corresponding physical framework, was a well-timed reminder for me to step back, think hard, and see what is beautiful in my own experiments (I share more thoughts in this episode of The Lemma Journal Club).

WHAT IS YOUR FAVORITE PAPER THAT YOU HAVE WRITTEN?

Kinase KEY1 controls pyrenoid size throughout the cell cycle by disrupting phase-separation interactions. On the science side, this paper was my first foray into biology and gave me a chance to connect my physics training to a biological problem. I'm proud of the insights we drew from the data, and I'm excited about active condensates as a source of both new physics and new biology. On the personal side, this was a joyful project resulting from a collaboration with my co-first author, Shan He, who is now a professor at UW–Madison. Through this work, Shan became one of my closest science friends, and we learned new techniques, new ways of thinking, and new ways of communicating from each other.

WHAT BIOLOGICAL PROBLEM DO YOU THINK MOST NEEDS A PHYSICAL-BASED APPROACH RIGHT NOW?

Intracellular organization: How does a cell organize its components to perform its functions? Researchers have largely focused on characterizing the components of cells and describing their interactions using the language of equilibrium physics, such as liquid–liquid phase separation. However, a cell must be out of equilibrium, or "active," to be alive, which limits what these equilibrium frameworks can tell us about cellular function. We need to study the interplay between equilibrium physical constraints and energy-consuming processes to uncover the principles behind intracellular organization.

IF YOU COULD INSTANTTLY MASTER ONE NEW TECHNIQUE OR TOOL, WHAT WOULD IT BE?

As an experimental scientist, it is part of my job to master any available techniques and tools that I need for my research, from multiphoton imaging to CRISPR. Looking beyond what is currently available, I look forward to new advances, particularly in live/liquid EM, confocal polarization microscopy, and genome manipulation techniques for studying non-model organisms. I am excited about the breadth of biology and hopeful that advances in tools for studying non-model organisms will expand basic research.

WHERE IS BIOPHYSICS HEADED?

We are at a crossroads as a field, facing a tension between the applications of bioengineering and the pursuit of the deeper laws of fundamental science. Both astrophysics and quantum mechanics have faced similar crossroads and chosen different paths, which have shaped their respective intellectual and funding landscapes. My hope is that biophysics is headed toward a quantitative understanding of living systems as a first-principles science.

Meet our Undergraduate Member!

Lucas Paul, *Senior Student*, Whitworth University

TELL US ABOUT YOURSELF

I am a senior undergraduate physics student at Whitworth University in Spokane, WA. I decided to study physics because I have always been fascinated by the idea that the world around us can be described through mathematics. I was especially drawn to how physics can mathematically predict results, even when the outcome may not seem intuitive, such as in statistical mechanics. That combination of mathematical structure and physical reality inspired me to pursue a degree in physics.

TELL US ABOUT YOUR APS GLOBAL PHYSICS SUBMIT 2026 EXPERIENCE

It was an excellent experience for me as an undergraduate student! It showed me the scale of a scientific conference on the world stage. It was very intriguing to hear talks from labs all over the world that focused on the same questions our lab was looking into. The work I found particularly interesting focused on biological physics modeling. Seeing the same models that our lab investigates applied to different systems, such as chemotaxis, and seeing the success achieved in that field through similar techniques demonstrated the strength and capabilities of these modeling techniques.

The work I presented focused on modeling cells under the influence of an applied electric field, which induces a directed motion known as electrotaxis. The system uses a random-walk model and stochastic parameters to determine the effect of the electric field on the system of cells. The most important skill I developed was how to communicate scientific research effectively and understand the process that goes into preparing a good presentation. I was most surprised by the fast pace of the conference between talks and by how researchers would pour into a small room for a single talk and then leave immediately afterward.

HOW HAS BIOPHYSICS RESEARCH PREPARED YOU FOR YOUR FUTURE?

The experience of conducting research in biological physics has been invaluable. I believe it has helped me think through complex problems and analyze results in ways that no class has taught me. The ability to analyze a complex stochastic system and interpret the results has made me a very effective problem-solver for large, dynamic systems across diverse physical domains. More importantly, it has convinced me that I enjoy research. I plan to apply to PhD programs this year and look forward to spending more of my time conducting research in the future.

Rage Against the Mean: Why Single-Phage Biophysics

This opinion article is based on a conversation with Dr. Jyot Antani, Yale University, whose work has advanced the biophysics of virus-host interactions by using microscopy to study how individual bacteriophages attach to bacterial cells.

Jyot Antani,
Associate Research Scientist,
Yale University

WHAT THE AVERAGE HIDES

A century after Felix d'Hérelle first described bacteriophages, most of what we know about these viruses still comes from measuring populations in bulk. The classic one-step growth curve, the adsorption assay, and the plaque count are foundational methods in phage biology, yet all report a single number that describes the average behavior of millions of particles. But according to Jyot D. Antani, that average hides the very thing that makes viruses interesting. "Much of the viral world is still effectively hidden from us because we usually can't measure how individual virus particles differ from one another. That particle-to-particle variation inside a single population is largely invisible in standard experiments," Antani says, highlighting the central question of his recent perspective on measuring fitness in individual phage particles. For a biophysicist, that invisible layer is not just a footnote, but it is where evolution, ecology, and the physics of infection can actually play out.

FROM POPULATION AVERAGES TO SINGLE PARTICLES

The problem, Antani explains, is that we lack the tools to see differences that almost certainly matter. "We still don't have practical, high-throughput ways to measure how individual phage particles differ -- especially in the properties that determine how well they succeed at infecting and reproducing." The lytic infection cycle, from diffusion to host binding, genome injection, replication, and lysis, is inherently noisy. Every individual step involves probabilities, and a phage particle that binds faster, injects sooner, or produces a few more progeny can have an outsized influence on the next generation. Yet for decades, these differences were simply averaged away as a one-step growth curve returns a mean burst size and an adsorption assay returns a single rate constant. " these average readouts can hide important particle-to-particle differences inside a phage population.," Antani notes. Such techniques may make it more difficult to learn about biological differences between particles and from there to determine which candidate phage may be ideal for problem-solving.

NEW TOOLS REVEAL HIDDEN HETEROGENEITY

What has changed is the arrival of measurement techniques sensitive enough to follow the single virions. Fluorescence microscopy, microfluidics, and machine learning enhanced particle tracking are now making individual phage phenotypes experimentally accessible. Antani points to his own work tracking single T4 phages as they interact with immobilized E. coli cells. When Antani and coworkers measured the dwell times (time that phages stay attached to bacterial cells) of thousands of fluorescently labeled particles, they saw something far from a single exponential decay.

... Continued from Page 6 ...

" We saw an extremely broad spread in how long phages stayed attached, which implies that binding is often reversible—much more so than people had assumed," Antani recounts. " Instead of one 'typical' binding strength, the data look like a whole distribution of binding affinities across particles—effectively a spread of dissociation constants within the same stock." A genetically uniform phage stock, in other words, behaves as though it contains a spectrum of binding affinities, which is a distribution that is completely invisible to what would be a classical adsorption assay.

These same principles appear further into the infection cycle. Using a microfluidic 'mother machine' to watch single T7 phage infections, other researchers have recorded genome translocation events at single particle resolution. " At the single-particle level, genome injection is highly variable—different phages transfer their DNA into cells at noticeably different rates and with different dynamics," Antani says. " Some particles got most of their genome into the cell within a few minutes, while others transferred only a small portion and then essentially stalled for several minutes before continuing." If two particles in the same population are able to differ by minutes in how long they take to commit to an infection, then the mean injection time tells only a fraction of the whole story.

THE PLAGU E ASSAY'S BLIND SPOT

Much of this heterogeneity has been hidden by the field's reliance on the double-layer agar plaque assay, which is a method that has essentially gone unchanged since the early twentieth century. Antani does not mince words about its limitations. " The 'gold-standard' plaque assay can be misleading: it can sometimes report plaques that don't reflect the process you think you're measuring, and even more often it misses real infections—especially in non model hosts—because successful replication doesn't always produce a visible plaque. Plaque formation requires a long chain of microscopic events, but the assay reports only the final macroscopic outcome." A phage that replicates just fine but fails to produce a visible clearing under particular conditions simply disappears from the data. Therefore, the measurement pipeline, by design, selects for what plaques, but that filter can systematically underestimate the true diversity of phage phenotypes and lead to false conclusions.

These consequences become stark when studying coinfection – infection of the same cell by two different phages. Antani's coworkers recently used flow cytometry to separate cells infected by two different phage species and then measured which species produced progeny. The outcome was unexpected, seeing as coinfected cells often released particles of only one parent as opposed to both. "Using this approach, my colleagues found that even a genetically uniform bacterial population can still support long-term coexistence of multiple phage species—contrary to what you'd expect from classic competitive-exclusion arguments," Antani explains. In other words, phenotypic variation at the level of individual infection events can determine whether phages either compete or coexist, which is a result that no bulk assay would have been able to reveal.

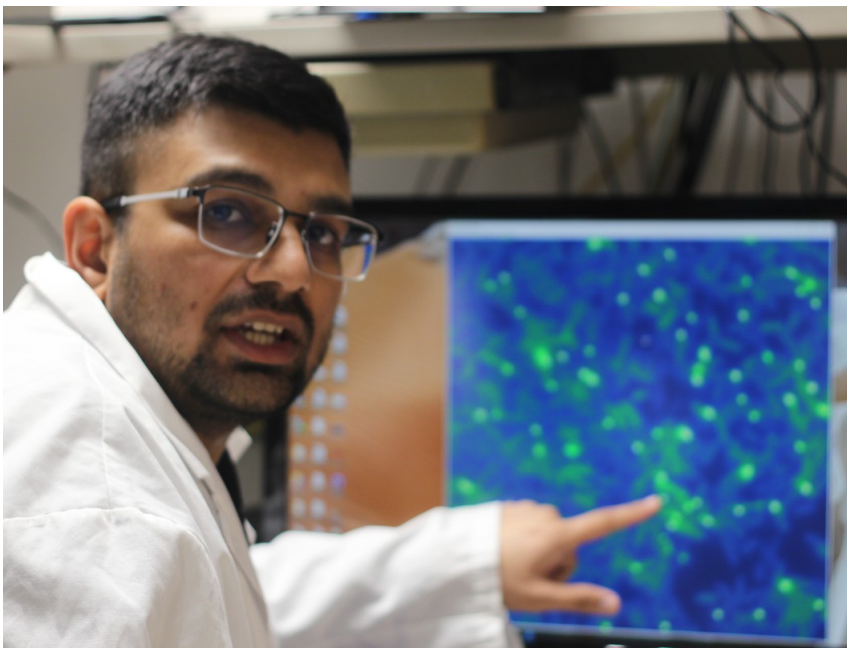
TOWARD A PREDICTIVE VIROLOGY

Even the stability of phage particles, which is a trait critical for therapeutic and biotechnological applications, shows variation that population averages obscure. " Even under relatively mild conditions, the vast majority—often 99% or more—of freshly produced phage particles quickly become noninfectious, especially in non-model phage species," Antani points out. Knowing the shape of that loss distribution and which particles degrade as well as why could be the difference between a shelf stable therapy and a completely failed treatment.

The article's bottom line is a call to treat phage infection as a stochastic, single particle process with measurable distributions, where improved measurement technology can enable tighter links between mechanistic theory and experiment. For the biophysics community, this represents an opportunity to bring the tools of single molecule physics to bear on one of the most abundant biological processes on Earth.

"The goal is to make that variability work for us," Antani concludes, " reduce the kinds of particles that cause failures, while keeping those with improved performance." The tools to do so are emerging, and the distributions that have long been hidden are finally coming into view. Whether the community will embrace them, he suggests, is the next crucial question.

By Luciana Sarabia,
SPS member



Courtesy of Michelle So, Yale Scientific Magazine.

Robophysics: Using Robots to Understand Living Systems

This opinion article is based on a conversation with Prof. Daniel I. Goldman, CRAB lab, Georgia Institute of Technology, whose work has helped shape robophysics as a field at the intersection of physics, biology, and robotics.

Daniel I. Goldman,
Dunn Family Professor,
Georgia Institute
of Technology

ROBOTS AS MODELS OF LIFE

Robots are often thought of as machines built to perform useful tasks. In robophysics, however, they serve a different purpose: they become physical models of living systems. For a biophysics audience, this distinction is important. Robophysics is not simply traditional robotics applied to biology, nor is it just biomechanics with machines added in. Instead of asking only how to build better robots, robophysics asks how robotic systems can help us understand the physical principles that shape biological motion, control, behavior, and collective organization.

Robots can also help us explore the "new physics" of active systems. Unlike ordinary materials, active systems are made of parts -- such as animals, cells, or robots -- that use energy to move and respond to their surroundings. By controlling how robots move and interact, researchers can study how simple individual actions produce collective motion, patterns, clustering, and other unexpected behaviors.

As Prof. Daniel Goldman explained, this idea goes back many years:

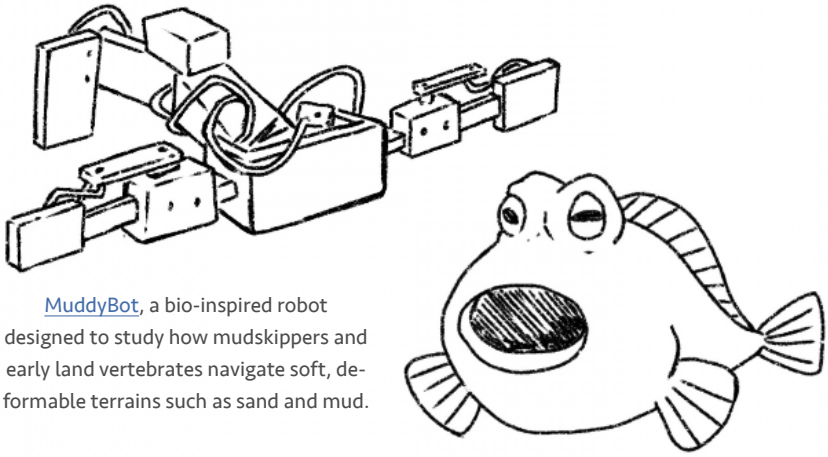
"I would first credit organismal biologists -- people like Bob Full, Barbara Webb, and others -- for having the idea that robots could act as models of living systems, as organisms."

FROM ORGANISMAL BIOMECHANICS TO ROBOPHYSICS

This origin matters. Robophysics did not arise only from the engineering goal of building better machines. It also grew out of organismal biomechanics, where researchers often use simplified mechanical systems to understand living organisms. In many cases, it is easier to test a physical or computational model than to vary every parameter in a real organism. For example, to understand how a tree branch responds when mass is added, a model allows researchers to change the mass, branch dimensions, or material properties in a controlled and repeatable way.

Robophysics builds on this tradition by making the model active. A robot can move, interact with the ground, collide with its surroundings, and respond to forces. It becomes not only a machine, but also a physical experiment.

For Prof. Goldman, this connection became especially clear during his postdoctoral work with Bob Full. At the time, he and others were working with engineers who wanted to learn from nature in order to build better robots. Robophysics emerged from the meeting of two motivations: the biologist's desire to model living systems and the engineer's desire to build better machines. When Prof. Goldman began his faculty career, he realized that these goals also aligned naturally with the interests of physicists studying living systems.



MuddyBot, a bio-inspired robot designed to study how mudskippers and early land vertebrates navigate soft, deformable terrains such as sand and mud.

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A CASE STUDY: LIZARDS SWIMMING THROUGH SAND

One of Prof. Goldman early interests was locomotion in granular media, such as lizards moving through sandy environments. To understand this system, one has to consider not only the animal, but also the thousands or even millions of grains surrounding it. This is a difficult problem because sand can behave in complicated ways: sometimes like a solid, sometimes like a fluid, and often like something in between.

"The most obvious example from our research is when we first started studying locomotion of a lizard running on sand or swimming in sand. We simply didn't have theoretical models of the kind that one would need for these kinds of interactions."

Computational simulations can help, but they are often time-consuming, especially when the environment involves millions of interacting granular particles. A robophysical model offers another route. If the goal is to understand how a lizard wiggles its body to move through sand, one can build a robot with controlled, repeatable motions and observe what happens. The goal is not necessarily to make a useful robot. The goal is to create a controlled physical model.

This is where robophysics differs from traditional robotics. A roboticist may focus on making a robot perform a task efficiently. A robophysicist may instead ask what the robot teaches us about an organism. In this sense, the robot becomes part of an experimental physics approach: create a system with reproducible movements, vary its parameters, and study the outcome.

ACTUATION AND BIOLOGICAL CONTROL

Robophysical models are especially useful for biological questions involving motion, actuation, and interaction with complex environments. Prof. Goldman pointed to organismal biology as one of the clearest areas where robophysics can contribute:

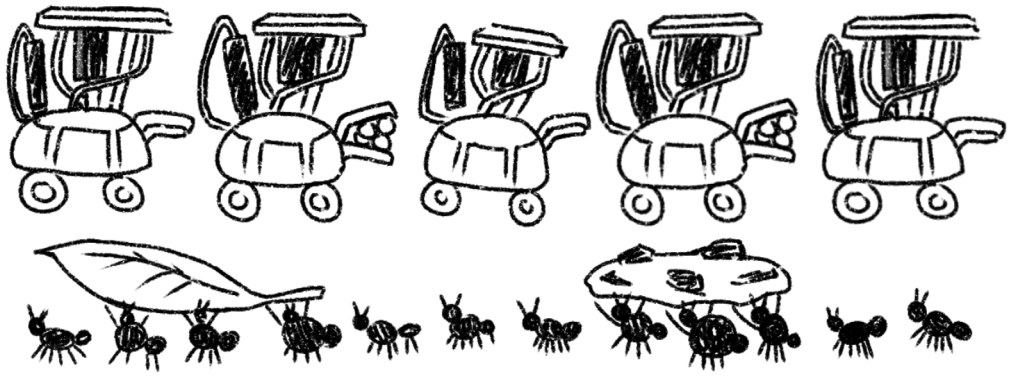
"I can speak to what I know, and that's organismal biology."

Beyond granular materials, his group has also studied systems such as the swimming of nematode worms. In these cases, the value of the robophysical model is that it includes actuation. The robot is not just a passive shape moving through an environment. It has internal driving, making it more analogous to the actuated bodies of invertebrate or vertebrate undulators. Living organisms are not simply objects pushed around by external forces. They generate motion through muscles, coordination, feedback, and interaction with their surroundings. A robophysical model therefore forces the researcher to think carefully about both the mechanics of the organism and the physics of the environment.

SWARMS, FIRE ANTS, AND ACTIVE MATTER SYSTEMS

Robophysics can also be useful for studying collective systems. At the APS Global Summit this year, for example, many studies focused on swarm robotics and active particle systems. The connection to biology is natural, since many living systems involve large numbers of individuals interacting with one another and with their environment.

Prof. Goldman's work on fire ants provides a good example. Fire ants excavate in tightly confined spaces, digging through granular material such as dirt. To study this behavior, his group developed robophysical models that allowed them to examine the roles of clogging, clustering, and jamming during excavation. These physical effects are difficult to isolate in real ants, but they can be explored more systematically in a robotic model.



Robotic excavator, a bio-inspired robot designed to mimic ant digging behavior and investigate how collective excavation strategies prevent clogging in confined granular environments.

... Continued from Page X ...

Swarm robots are especially useful because they allow researchers to study collective behavior through real physical interactions. In a purely computational model, agents may interact through simplified rules. In a robophysical model, the robots collide, block one another, jam, cluster, and respond to the physical constraints of the environment. This makes robophysics an important complement to computational approaches in active matter and swarm behavior.

A ROBOT IS STILL A MODEL

At the same time, robophysical models have limitations. The biggest pitfall is the same as in any modeling approach: mistaking the model for the real system. A robot is not an animal. It is usually much simpler than the organism it represents. Its materials, actuators, sensors, control systems, and environmental conditions all shape what it can and cannot reproduce.

But these limitations do not make robophysical models less valuable. All models sacrifice some accuracy in order to isolate what matters most. The value of a model is not that it captures everything, but that it helps us understand something specific. In some cases, especially when no good theoretical or computational model exists, robophysics may be the best available way to study a biological system..

FROM BIOLOGY TO USEFUL ROBOTS

Robophysical models can also lead to unexpected practical benefits. For example, Prof. Goldman's group has used robophysical models to study how centipedes coordinate their bodies and limbs to move effectively across diverse terrain. These models were originally designed to understand biological locomotion, but they also proved useful as robots in their own right, including in practical settings such as agriculture. This two-way relationship is one of the most interesting aspects of robophysics: biology inspires robots, and robots help us understand biology.

TRAINING THE NEXT GENERATION OF PHYSICISTS

For education, robophysics can also offer a valuable training ground. Prof. Goldman noted that physical models require students to engage directly with the real-world constraints of a system:

"Robophysical models are hard to cheat. If you want to try to understand something in the real world, you have to understand how it works in the real world."

This is an important lesson for students. To build a robophysical model, one must understand the phenomenon deeply enough to reproduce at least some of its essential features. The model has to move, interact, and respond to its environment. If the assumptions are wrong, the system often fails in a visible way.

Prof. Goldman also emphasized the value of hands-on experimentation:

"There are certain features for an experimental physicist where having your hands on the experiment leads to insight that you might not have gotten from more abstract processes — either analytic or computational."

This is especially useful for training the next generation of physicists. In American education, many students arrive at college with some robotics experience. Robophysics can build on that familiarity and use it as a gateway into deeper questions about living systems. By changing the parameters of a physical system and observing the results, students can quickly develop intuition for what matters and what does not.

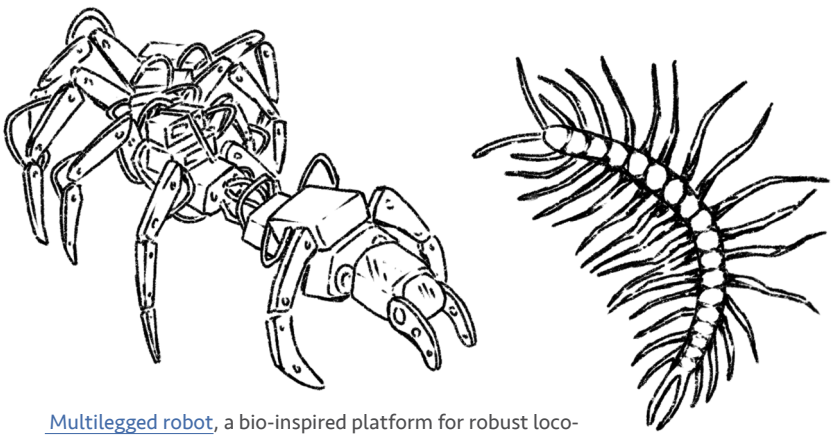
In this sense, robophysics is not only a research method, but also a teaching opportunity. It connects physics, biology, engineering, and computation through tangible experiments. It can help students see living systems not as mysterious exceptions to physics, but as physical systems whose behavior can be explored through models.

WHY ROBOPHYSICS MATTERS

Robophysics may also help shape future technology. Just as solid-state physics and superconductivity grew through the integration of physics, metallurgy, chemical engineering, and mathematics, robophysics may contribute to the development of more life-like machines. At the same time, those machines may teach us more about living systems. The promise of robophysics is therefore not simply that robots can imitate animals. Its deeper promise is that robots can help us think more clearly about biology. They make assumptions physical. They force ideas to interact with the real world. They reveal when a simplified mechanism is enough, and when something essential is missing.

A robot is not the organism itself. But when used carefully, it can become a powerful physical model of life.

By Kaitlyn S. Yasumura,
SPS member



Multilegged robot, a bio-inspired platform for robust locomotion and material transport on rough terrain.

An Invitation to Get Involved with Biological Physics Education

Our division, APS DBIO, is a growing community focused on biological physics, but determining a standard of approach for biological physics education, especially at the undergraduate level, remains an open question. While our division has begun to take action to address this, we argue that we should broaden participation and sustain engagement within our community to discuss what belongs in biological physics classes. Doing this will strengthen our community and further scientific innovation in the field.

These days, we are seeing challenges to higher education more broadly. In the United States, federal pressures have resulted in dialogues regarding the cost and return on investment of degrees. Students are also facing a future where they need to consider the impact of technologies such as artificial intelligence. Graduates in biological physics are well-suited to tackle the challenges of this changing world by using their understanding of fundamental principles to engage with and make sense of large amounts of noisy data.

Biological physics encompasses a wide range of phenomena and requires expertise in a variety of disciplines, including physics, biology, chemistry, mathematics, and engineering. While academic disciplines are arguably not as siloed as they may once have been, traditional physics majors tend to follow a set curriculum. Though the method of delivery may change or the order in which topics are presented, the major follows roughly the same broad ideas. A physics undergraduate degree has a backbone of requirements that institutions accepting students into physics graduate school expect their students to have. A graduate student in biological physics, however, must bridge the gap between various disciplines.

Our division has taken the initiative in addressing education in biological physics. We has hosted webinars on biological physics education at both the undergraduate and graduate levels as early as August 2022. There have been focus sessions at the APS Global Physics Summit in 2025 and 2026 with invited speakers and contributed talks. Mini-grants have brought together educators in biological physics for continued discussion. For the 2027 APS GPS, our division is partnering with GPER to host an invited session on education in biological physics. We invite the community to come and be a part of this discussion.

Educators have also worked to create online resources. The Center for Living Systems, through the Living Physics Portal, hosts a repository of curricular materials for upper-level and graduate-level courses in biological physics. The repository, partially funded by NSF, provides resources accessible to educators, including content slides, homework sets, detailed class notes, and instructions for the instructor. This was launched in March 2026, and we encourage the community to use it, discuss it, and contribute to it.

Members of our division can take action around education in biological physics. Some suggestions for this include discussing how to restructure traditional physics courses to include biological physics content, sharing curricular models across institution types (R1/R2/PUI), developing learning goals in biological physics courses, especially at the undergraduate level, developing graduate-level biological physics courses, promoting and contributing to the Center for Living Systems and the Living Physics Portal, and partnering with other scientific societies such as the Biophysical Society.

We encourage the community to use these resources and to share how they have helped or what challenges community members may still face. What skills define this discipline? How can we better prepare our future biological physicists for success in the workforce? We encourage our division to establish a community space for continuous discussion.

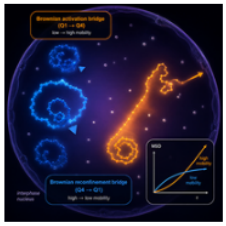
Simple Estimation

Human Germline Mutation Rates -- by Manh-Quan Nguyen, *PhD student*, Stanford University

Human population genetics depends on parameters such as mutation rate, recombination rate, effective population size, and selection coefficient. Because we cannot observe human populations over thousands of generations, these parameters must be inferred from genetic data. Here, we show how a simple comparison between species provides an estimate of the human germline mutation rate.

Consider **M** neutral sites in the human and chimpanzee genomes whose common ancestor lived **6.5×10^{6}-10^{7}** years ago (about **$T\approx3\text{-}5\times10^{5}$** generations) [1]. If both species have the same mutation rate **μ**, the expected number of differences is **$k\approx2\mu MT$**. A classica study found **$M\approx1.1\times10^{4}$** sites and differences in **$k\approx183$** non-functional, gene-resembling DNA segments [2]. Therefore, **$\mu\approx k/2MT\approx2\times10^{-8}$** mutations per base pair per generation. This simple estimate depends on uncertain fossil dates, generation times, ancestral genetic variation, and the assumption that the selected sites are neutral. Modern studies instead sequence parents and their children to identify mutations arising within a single generation. These studies estimate the human germline mutation rate to be approximately **1.00** to **1.30×10^{-8}** mutations per base pair per generation [3].

Highlights from PRX Life



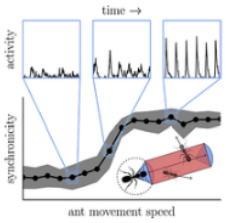
FEATURED IN PHYSICS

Brownian Bridging of Chromatin States in Leukemic Cells

M. Calero, E. del Arco, M. Amores-Sánchez, D. Herráez-Aguilar, E. García-Sánchez, A. González-Murillo, J. Lalchandani, N. Caselli, J. Fernández-Castillo, A. Caamaño, M. Ramírez-Orellana, I. Mora-Jiménez, and F. Monroy

PRX Life **4**, 033013 (2026) - Published 12 August, 2026

Rare chromatin mobility transitions uncover lineage-specific nonequilibrium dynamics of chromatin remodeling in acute lymphoblastic leukemia.



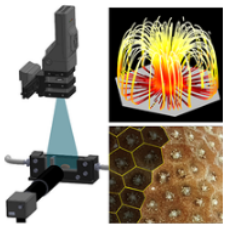
FEATURED IN PHYSICS

Nest-Level Phase Transition Drives Synchronized Activity Bursts in Ant Colonies

Michael Napoli, Simon Garnier, and Maurizio Porfiri

PRX Life **4**, 033010 (2026) - Published 5 August, 2026

Bursts of synchronized activity in ant colonies can be characterized as a phase transition, emerging as a balance between the responsiveness of the colony to the activation of a single ant and its ability to fully deactivate before the next burst.



FEATURED IN PHYSICS

Unravelling Three-Dimensional Active Transport by Ciliary Arrays on Coral Surfaces

Siluvai Antony Selvan, Cesar O. Pacherres, Michael Kühl, Angus Butler, Max S. Dhillon, Linda L. Blackall, Peter W. Duck, Draga Pihler-Puzović, and Douglas R. Brumley

PRX Life **4**, 023020 (2026) - Published 26 May, 2026

Experimental measurements of cilia distribution and fluid flow at the surface of reef-building coral uncover the crucial role of ciliary orientation in modulating nutrient transport.

Upcoming Event

16

APS DBIO Webinar is back!
Oct 2026: Setting up a Research Lab for Early Career Faculty

The APS DBIO Community Engagement Committee is kicking things off with a new webinar series featuring exciting topics and conversations! Our first webinar is **Setting up a Research Lab**, designed especially for new and incoming faculty. Experienced researchers will share practical advice on building a research program, purchasing equipment, recruiting and mentoring a team, and navigating the challenges of launching a lab.

Time: 10:00 AM Pacific Time, Friday, October 16

Registration Link