Nowak’s Punishment Study

written by Anoj Khadka | October 12, 2024



Nowak, a Harvard University mathematician and biologist, conducted an experiment with 100 students, who played a computer game involving dimes to reward or punish one another. Conventional wisdom held that costly punishment fosters cooperation between individuals, but Nowak’s findings contradicted this belief. He and his colleagues demonstrated that punishment often leads to retaliation, triggering a destructive spiral rather than encouraging cooperation.

“People who punish,” Nowak explained, “tend to escalate conflict, worsening their situation and, eventually, losing out.” Headlines summed it up with a twist on an old adage: “Nice guys finish first.”

Challenging established theories

This wasn’t the first time Nowak’s use of mathematical models had disrupted established theories. His contributions have continuously reshaped scientific understanding of complex phenomena. For instance, in 2002, Nowak developed equations to predict how cancer evolves and spreads. His models detailed how mutations occur within metastases and how chromosomes become unstable.

In the 1990s, Nowak tackled HIV, developing a model showing that the virus progresses to AIDS when it replicates fast enough to overwhelm the immune system with strain diversity. Immunologists later confirmed that he had accurately described the mechanism behind this process. Reflecting on his work, Nowak said, “Mathematics doesn’t just describe nature; it helps us understand the very mechanics that drive it.”

Evolutionary mathematics

Nowak, trained as a biochemist, firmly believes that mathematics is the “true language of science.” He considers it key to unlocking mysteries of the past, including the origin of life. As a graduate student at the University of Vienna, he worked with evolutionary game theorist Karl Sigmund, and from there, Nowak developed the field of evolutionary dynamics. This field involves creating mathematical formulas to describe essential evolutionary processes such as selection, mutation, random genetic drift, and population structure.

At Harvard, in the Program for Evolutionary Dynamics, Nowak’s blackboard is covered with chalked equations. His current work focuses on simplifying the origin of life into a basic chemical system that can be described mathematically. “We’re looking for the simplest chemical process that can show the transition from no life to life,” Nowak said. He uses zeros and ones to represent the fundamental building blocks of life, such as adenine, thymine, guanine, cytosine, or uracil—what he calls “monomers.”

Challenges of replicating life in the lab

Though his model is mathematically straightforward, recreating it in a laboratory setting poses significant challenges. “The difficulty,” Nowak admits, “is starting without enzymes or templates to guide the assembly of monomers.” David W. Deamer, a biomolecular engineer at the University of California, Santa Cruz, echoes this sentiment: “It’s hard to imagine an easy way to make nucleic acids in the lab. We don’t have solid ideas on how to get it to work using just chemistry and physics.”

In the 1980s, biochemist Leslie E. Orgel’s team at the Salk Institute demonstrated nonenzymatic template-directed polymerization—where an RNA strand acts as a template for making complementary RNA. Yet, figuring out how nucleotides might self-assemble without such templates has proven elusive. “We need a process that can comprise polymers,” Nowak explained, voicing his ambition.

Innovative ideas for Polymerization

Researchers like Irene Chen at Harvard propose solutions for facilitating the polymerization of RNA or DNA in the absence of enzymes. One potential approach involves adding a compound called imidazole to one end of monomers, making their polymerization easier and quicker. Others believe that lipids or clay may play a crucial role, as studies have shown that these substances can accelerate the reaction. For example, chemist James P. Ferris at Rensselaer Polytechnic Institute found that adenine nucleotides assembled into short RNA polymers on mineral clay—possibly replicating conditions in the prebiotic world.

Prelife: a system on the edge of life

Using his mathematical model, Nowak looks at the chemical reactions that lead to the formation of these strands and assigns rate constants to different reactions. He has observed that small differences in growth rates result in variations in abundance. Faster-growing sequences outcompete slower ones, demonstrating natural selection even before replication begins. “This is exciting,” Nowak exclaimed. “It shows that selection can occur prior to replication, which has huge implications for understanding the origin of life.”

Nowak calls this system “prelife” because it displays some of the essential characteristics of life—genetic diversity, selection, and mutation—but without replication. In this stage, some strands mutate and even cooperate with others to accelerate reaction rates, echoing Nowak’s long-held belief that cooperation is a fundamental aspect of evolution.

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Selection before replication

Typically, selection and mutation are seen as consequences of replication. For instance, if only large seeds were available on the Galápagos Islands, finches with stronger beaks would survive, passing their traits on to the next generation. Nowak’s model suggests that selection could exist before replication begins, potentially explaining how life first arose.

“All that’s needed is for a few strings to develop the ability to replicate themselves,” Nowak says, describing a scenario where replicating strings outcompete non-replicating ones. “Life destroys prelife,” he adds, hinting at the transformational process where life could emerge once replication crosses a critical threshold.

Nowak hopes his models will guide future experiments. He envisions a laboratory system where just two types of monomers self-assemble and replicate—“the simplest thing you can do,” he asserts. For Nowak, mathematics remains the guiding force in this exploration. “I don’t know what the ultimate understanding of biology will be,” he reflects, “but one thing is clear: it’s all about getting the equations right.”

References:

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