Dynamic complexity in predator-prey models framed in difference equations

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Abstract

Predator prey interactions are a fundamental part of biological and ecological systems that have been modeled using mathematical models/equations to understand population dynamics over time. Continuous models can predict stable equilibria or regular population cycles throughout generations. However, discrete time models, such as the Nicholson-Bailey, which are based on host parasite systems, incorporate density dependent self regulation of the prey population. This model demonstrates that simple biological assumptions can generate stable equilibria, periodic cycles, and chaotic fluctuations. These findings are significant because they show that highly irregular population dynamics that are observed in nature may arise from intrinsic biological interactions. This is instead of the external environmental randomness. Being able to analyze and understand these dynamics can improve our ability to interpret biological patterns and predict long term species dynamics.

Introduction and Background

For a long time, scientists have used continuous mathematical models that predict either stable population levels or smooth, repeating cycles. However, more recent work with discrete time models has shown that population behavior can be a lot more complex. The paper, “Dynamic complexity in predator-prey models framed in difference equation”, explains that simple non linear difference equations can produce stable points, repeating cycles, chaotic and unpredictable behavior. This type of modeling is especially useful for insects and arthropods that have non overlapping generations. According to the paper, difference equation models give a more “realistic means of modeling the behavior of animal populations” compared to continuous models (Beddington). The most well known discrete model is the Nicholson-Bailey host parasite model which was designed to describe how insect parasitoids interact with their hosts.

The original Nicholson-Bailey model had major weaknesses, as it is biologically unrealistic due to the unstable parameter values. These caused unbounded population fluctuations. To alleviate this, researchers added density-dependent self-regulation in the prey population. This improved version of the model can now mimic and create more realistic outcomes. This paper highlights the complex and seemingly random population patterns that can appear even with no environmental randomness. It describes how the system can shift from stable behavior to limit cycles and eventually to chaotic dynamics purely due to internal predator prey interactions. Instead of assuming that strange population changes are always caused by weather or other outside factors, this model shows chaos can be built into the system itself. Studying the Nicholson-Bailey model will help show how real insect or arthropod populations might stay bound over time while still appearing random and unpredictable. This is useful for fields like pest control and conservation because it helps scientists understand why populations sometimes suddenly spike or reach even when the environment conditions seem stable.

Methods

In the new version of the model, prey populations are regulated through density dependent growth, which is what makes the system more biologically realistic than the original formulation. Unlike the original Nicholson-Bailey equations which produce unstable and unrealistic population trajectories, the modified model allows prey populations to self-regulate in the absence of predators. This adjustment creates the more realistic dynamic and allows the system to exhibit stable equilibria, periodic cycles, and complex oscillations depending on parameter values.

$$H_{t+1} = H_t \exp[\mathrm{r}(1 - H_t/K) - aP_t]$$

$$P_{t+1} = \alpha H_t[1 - \exp(- aP_t)]$$

The model equations used in this study are shown to the left. H_t represents the prey (host) population, P_t represents the predator (parasite) population, r is the intrinsic growth rate of the prey, K is the carrying capacity, and a is the predator attack rate.

To analyze stability, the study followed an approach where "analysis of the local stability properties of the model was performed" using linearization and characteristics equations (Beddington).

$$\lambda^2 - \lambda(1 - r + \varphi) + (1 - rq)\varphi + r^2 q(1 - q) = 0$$

$$\text{where} \qquad \varphi = r\,(1 - q)/\{1 - \exp[-\,r(1 - q)]\}$$

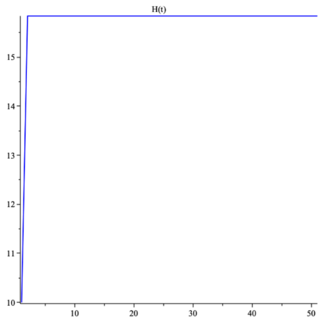
To analyze local stability of the predator prey system, the model was linearized around the equilibrium point and a characteristic equation was derived. The stability of the system was determined by examining the roots, eigenvalues, of the following characteristic equation. The parameter ϕ represents the equilibrium prey density relative to the carrying capacity. The roots of this equation were evaluated using the Schur Cohn stability criteria to determine whether they lay inside the unit circle in the complex plane. Parameters producing eigenvalues inside the unit circle were classified as stable, while the ones outside were unstable. This approach allowed the mapping of stable and unstable regions in parameter space, consistent with the methods described in the original study.

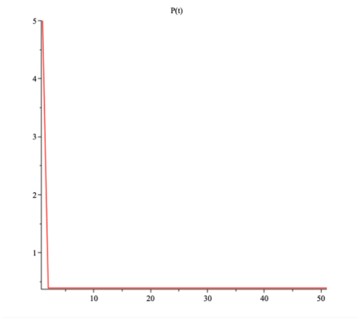
Results

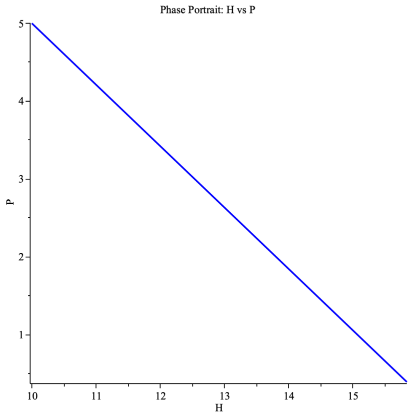
Using the Beddington and Nicholson-Bailey equations, three parameter sets were simulated with the Maple procedures NBH, ORB, and EvalNBH. Each produced distinct population dynamics.

Case 1: r = 1.2, a = 0.10, K =50

The host and predator populations showed stable oscillations that gradually settled into a repeating pattern. The EvalNBH eigenvalues were inside the unit circle, confirming the equilibrium was stable.

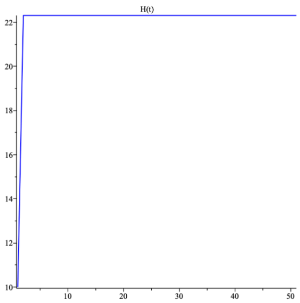


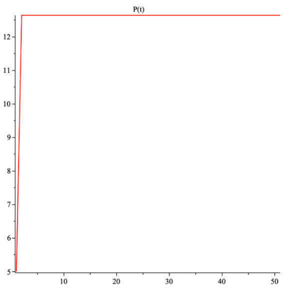


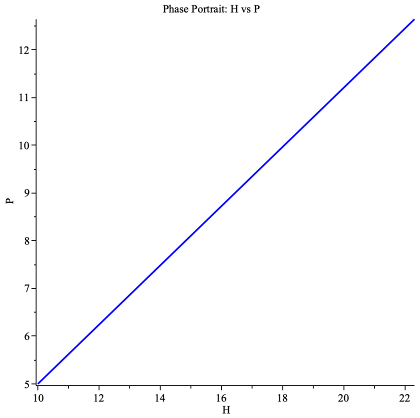


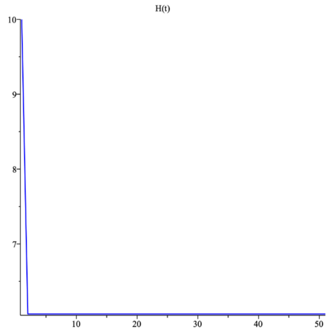
Case 2: r = 0.5, a = 0.20, K =50

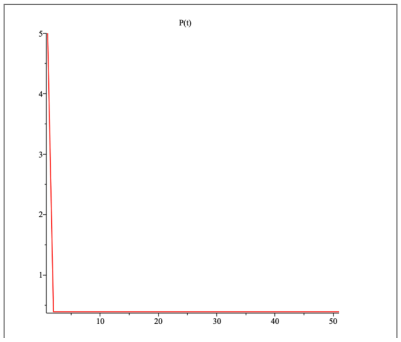
Both populations quickly converged to a stable fixed point. Oscillations were small and stability analysis again returned eigenvalues with magnitude < 1. This parameter set showed the strongest damping.





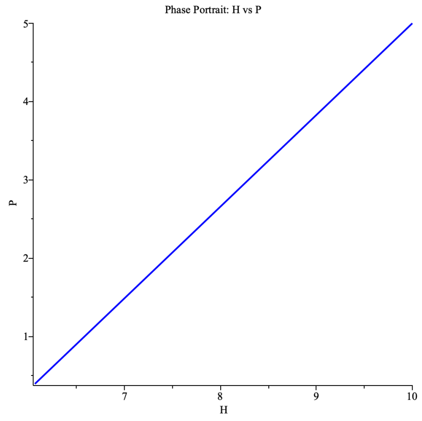






Case 3: r = 5, a = 1, K = 10

This simulation produced irregular, chaotic like fluctuations with no convergence. Populations repeatedly overshot and crashed, eigenvalues from EvalNMH exceeded 1 in magnitude, indicating an unstable equilibrium.



Across all simulations, changes in pre growth rate (r) and interaction strength (a) determined whether the system was stable, cyclic, or chaotic. This matches the behaviors described in the paper.

Conclusion

This project used code to implement and explore the modified Nicholson-Bailey predator prey model described in the paper, Dynamic complexity in predator-prey models framed in difference equations. The simulations and stability analysis showed that small changes in model parameters can shift the system from stable behavior to cycles and chaotic fluctuations. These results matched the paper's findings and demonstrated that complex population dynamics can arise from simple, deterministic biological interactions. Overall, this project showed how mathematical models and coding can be combined to better understand real world biological population patterns.