

A Spatial Model of the Red Queen Effect

Jules Ottino-Loffler, William Rand and Uri Wilensky

Center for Connected Learning & Computer-Based Modeling (CCL) / Northwestern Institute on Complex Systems (NICO)

600 Foster St., Evanston, IL, USA 60208

julesol2002@yahoo.com, {wrand, uri}@northwestern.edu

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1. ABSTRACT

Van Valen first discovered the “Red Queen Effect” (RQE), where two species can dramatically co-evolve their phenotypes over time but never gain a relative advantage [2]. In the ideal version of the RQE, regardless of the actual values that the species evolve to obtain, they have not moved in relation to each other. Though previous models of the RQE exist, we developed an agent-based model (ABM) which has a base ontology more similar to real world coevolutionary systems than equation-based models (EBMs). For instance, this model contains spatial information and an individual-level reproduction mechanism. Yet this model recreates traditional EBM results. For instance Dieckmann et al show that there are three possible outcomes of competitive coevolution: predator dominance, prey dominance and evolutionary cycling (RQE) [1]. By reconceptualizing this EBM using an ABM, we make it easier for students and researchers to understand, manipulate, and modify this model [4].

The model is written in the NetLogo agent-based modeling environment [3]. The model is initialized with 150 predator and 150 prey agents. Predator agents have a resistance level r and prey agents have a poison p . The agents are initially randomly distributed on a toroidal real-valued 35 by 35 grid. The initial resistance and poison values for the predators and prey are drawn from normal distributions with means μ_r and μ_p and a standard deviation of 1.

During a model timestep, each agent moves one unit at a random heading. If at the end of its move a predator is within 1 unit of a prey, then it will challenge the prey. The predator will compare its resistance value to the prey’s poison value and which ever agent has the larger value will win the challenge and the other agent will be killed. At the end of an agent’s turn if the total number of agents is less than the maximum carrying capacity the agent will reproduce with a 50% probability. The new agent’s initial poison / resistance will be drawn from a normal distribution with the parent’s poison / resistance as the mean value and a standard deviation of 1.

Our goal was to investigate whether this ABM would repli-

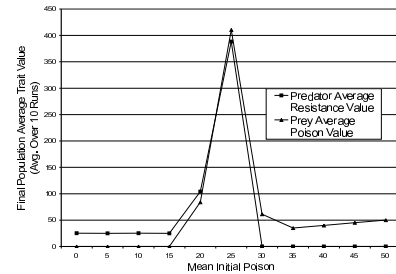


Figure 1: Final trait values.

cate the results of the EBM of [1]. Our parameter of interest was μ_p ; we held μ_r constant at 25 and varied μ_p from 0 to 50 at increments of 5. For each value we ran the model 10 times for 5000 timesteps. Figure 1 illustrates the final average values of both the resistance and the poison for the various initial values. If there are no predators or prey then a value of 0 is plotted for the respective final trait. In most cases, one species drives the other to extinction, and there is little change in the initial trait values. However when the value of μ_p is similar to μ_r then neither species is completely destroyed, but if there is any significant difference between μ_r and μ_p then one species will die off. The highest final trait values are found when $\mu_p = \mu_r$, in this case we see the results of the RQE since the final trait values are much higher than the initial values. These final values are more than 1.5 orders of magnitude larger than the initial values.

This model reproduces classical models of the RQE, but has two different mobile species interacting on a spatial grid over time which is a closer representation of reality than traditional models. This closer representation makes ABMs excellent teaching and experimental tools because their basic assumptions can easily be manipulated and explored.

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2. REFERENCES

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