Bacterial Game Dynamics

Cynthia Freeman
University of New Mexico
1 University of New Mexico
Albuquerque, New Mexico
cfreeman@mrn.org

1. INTRODUCTION

A two-dimensional, wrap-around cellular automaton (CA) is designed to simulate the dynamics of three interacting populations of bacteria using the game of Rock-Paper-Scissors. A simple implementation is first considered where varying initial conditions, neighborhoods, and update methods are tested. This implementation is then modified in an attempt to replicate the results in the Kerr et al. paper ([1],[2]) where the authors claim that diversity is preserved if dispersal and interaction are local and lost if global.

2. IMPLEMENTATION

The CA was implemented using Python and the MatPlotLib module. We will first consider a simple implementation and then move on to how the implementation is modified to replicate Kerr et. al's results.

An n by n wrap around cellular automata is considered where every square is a cell that can take a value of *rock* (blue square), *paper* (black square), or *scissors* (red square). Two methods of initiating the CA are tested. Each cell can be set randomly to one of the three possible states. This contrasts with the segregation method, where three solid, sectors of the grid (corresponding to *rock*, *paper*, and *scissors*) are generated, and each sector consists entirely of cells of one particular value. For each time step, all cells are updated at the same time. Thus, an old copy of the CA board is saved to create an updated version at each time step. To update itself, a cell i can choose one of its neighboring cells randomly and play a game of Rock-Paper-Scissors against it. The winner of the game occupies the position of the cell i. Another method is for the cell to play against *all* the cells in its neighborhood and adopt the state of the cell that beats it. In addition, different neighborhoods are considered: Moore and von Neumann neighborhoods. A Moore neighborhood of radius 1 consists of the 8 cells directly surrounding the central cell. A von Neumann consists of the cells that are at a Manhattan distance of 1 away from the central cell. Note that the Manhattan distance between two points (x_1, y_1) and (x_2, y_2) is $|x_1 - x_2| + |y_1 - y_2|$. Neighborhoods of radius 2 are also considered which for a von Neumann neighborhood, consists of the cells that are at a Manhattan distance of 2 away from the central cell.

For simplicity, n is set to a value of 21 and 500 time steps are considered. Choosing a multiple of 3 for n was a design choice that made the segregation method of initiating the CA board easier. All possible combinations of neighborhoods (von Neumann, Moore), neighborhood radii (1 and 2), initiation methods (random and segregation), and update methods (random and all) are considered.

Experiments with small n such as $n = 3$ were done to ensure the correctness of implementation. Consider the following CA board initiated randomly:

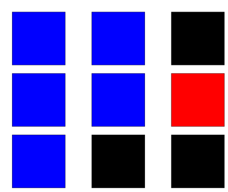

Figure 1: A CA board initiated randomly with $n = 3$. Blue squares represent rock cells, black squares represent paper cells, and red squares represent scissors cells.

With a Moore neighborhood of radius 1 and an update strategy where a cell competes with all cells in its neighborhood, the result of one time step changes the board to:

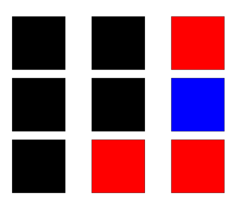

Figure 2: The CA board after 1 timestep with $n = 3$, a Moore neighborhood of radius 1, and an update strategy considering all cells in the neighborhood.

which can be easily verified. This process is repeated with various radii and neighborhood methods to ensure accuracy.

To replicate Kerr et. al's results, this implementation is modified. Although Kerr uses $n = 250$, in the interest of time, I use $n = 20$. Colicinogenic cells are represented as rock cells, colicin-sensitive cells as scissors, and resistant cells as paper. In addition to the three possible values, a cell can be empty. The CA board is always initiated randomly, and cells are updated asynchronously. In every time step, n^2 many random cells are updated sequentially. Kerr considers two different neighborhoods: a local one, which is identical to a Moore neighborhood of radius 1 and a global neighborhood consisting of every cell in the CA grid except the cell to be updated. Kerr uses 5000 time steps for a local neighborhood and 500 time steps for a global neighborhood, whereas I use 100 time steps for both. When a cell is to be updated, two situations occur depending on the value of the cell to be updated. If the cell is empty, the probability that it is updated to i is f_i, the fraction of its neighborhood that is of type i. If the cell is not empty (has value *rock*, *paper*, or *scissors*), it is killed with probability Δ_j where j is the value the cell currently has. Note that in this situation, the killed cell does not automatically adopt the state of a cell that would normally beat it. It is instead converted to an empty cell. This is a significant difference from the simple implementation above. Note that Δ_{rock} and Δ_{paper} are fixed but $\Delta_{scissors} = \Delta_{s,0} + \tau * f_{rock}$ where $\Delta_{s,0}$ is the probability of death of a *scissors* cell without any neighboring *rock* cells and τ measures the toxicity of neighboring *rock* cells. f_{rock} is simply the fraction of the cell's neigborhood that is of type *rock*.

Similar to Kerr, I use $\Delta_{rock} = \frac{1}{3}$, $\Delta_{paper} = \frac{10}{32}$, $\tau = \frac{3}{4}$, and $\Delta_{s,0} = \frac{1}{4}$.

3. RESULTS

We will first discuss the results of the simple implementation not involving Kerr et. al's methods.

Initiate	Nb	Radii	Update	CE
Random	Moore	1	Random	Y
Random	Moore	2	Random	N
Random	Moore	1	All	Y
Random	Moore	2	All	Y
Random	Neumann	1	Random	Y
Random	Neumann	2	Random	N
Random	Neumann	1	All	Y
Random	Neumann	2	All	Y
Seg	Moore	1	Random	Y
Seg	Moore	2	Random	N
Seg	Moore	1	All	Y
Seg	Moore	2	All	Y
Seg	Neumann	1	Random	Y
Seg	Neumann	2	Random	N
Seg	Neumann	1	All	Y
Seg	Neumann	2	All	Y

Let *Initiate* stand for how the CA board is initiated, *Nb* be the neighborhood, *Radii* represent the neighborhood's radius, and *Update* stand for the method chosen for updating a cell. Coexistence (*CE*) occurs when *all three* species exist after a specified number of time steps (500 in this case).

Consider the first two rows of the results table. Of interest is how a slight increase of a Moore neighborhood's radius from 1 to 2 wipes out the diversity of species (see Figure 4 and Figure 5).

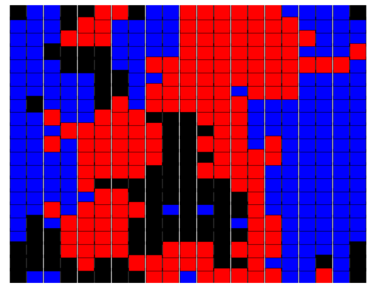

Figure 3: The CA board after 500 time steps, initiated randomly, with a Moore neighborhood of radius 1 and random update scheme. Blue squares represent rock cells, black squares represent paper cells, and red squares represent scissors cells.

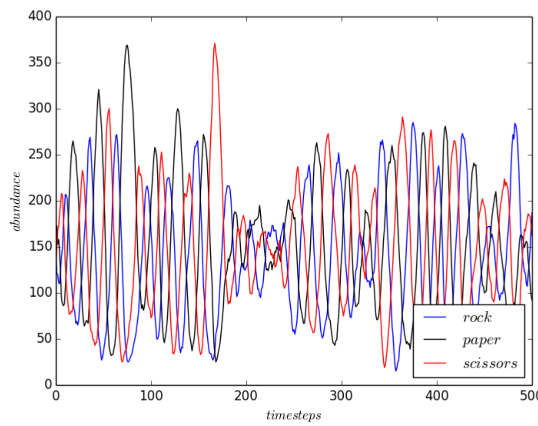

Figure 4: Community dynamics for 500 time steps, where the CA board is initiated randomly, with a Moore neighborhood of radius 1 and random update scheme.

This appears to reflect a concern of Kerr et. al's where increasing the neighborhood from a local to a global one decreases diversity. This similar type of behavior is exhibited with Neuman neighborhoods and increasing the radii (see rows 5 and 6 of the results table). Other interesting behavior can be discovered with parameter tuning. For example, periodic behavior in abundance plots (see Figure 6) is eventually reached with an update scheme involving all cells in a Neumann neighborhood of radius 1. With a segregation initiation method, there is a simple shift of the sectors after 500 time steps, and the numbers of each type of cell do not change (see Figure 7 and Figure 8).

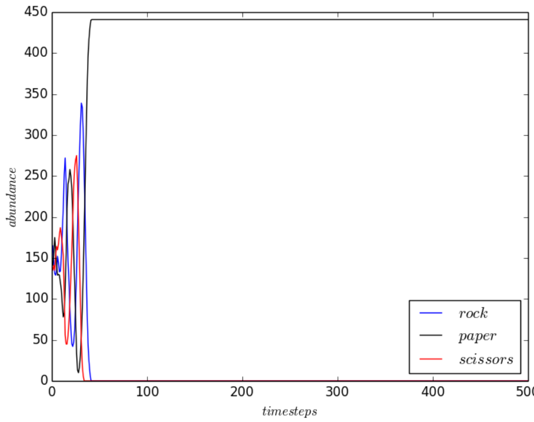

Figure 5: Community dynamics for 500 time steps, where the CA board is initiated randomly, with a Moore neighborhood of radius 2 and random update scheme. Only paper cells survive.

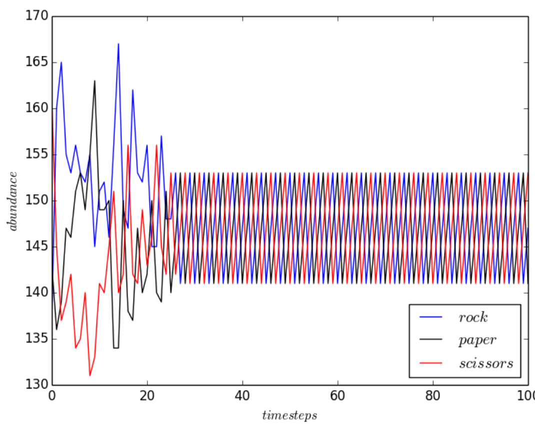

Figure 6: Periodic behavior is eventually reached with an update scheme involving all cells in a Neumann neighborhood of radius 1. The CA board is initiated randomly.

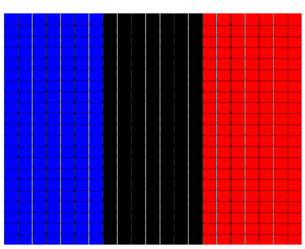

Figure 7: A CA board initiated with a segregation method. Blue squares represent rock cells, black squares represent paper cells, and red squares represent scissors cells.

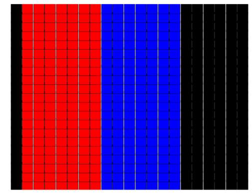

Figure 8: With a segregation initiation method involving a Moore neighborhood of radius 2 and an all update scheme, there is a simple shift of the sectors after 500 time steps.

4. REPLICATION OF KERR ET AL.

We now proceed with a discussion of how well the modified implementation replicates the results in Kerr et. al's paper. Colicinogenic cells are represented as rock cells, colicin-sensitive cells as scissors, and resistant cells as paper. An extra state of empty is also created. In the interest of time, $n = 20$ and only 100 time steps are considered for most plots.

Simulation results for the Kerr paper show that with a global neighborhood scheme, strains tend to die out. However, with a local neighborhood scheme, coexistence is kept. The modified implementation reflects these results (see Figure 10 where *scissors* die out and Figure 12 where all species still survive).

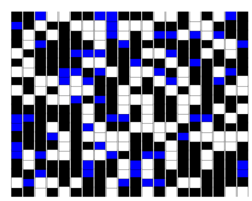

Figure 9: The CA board after 100 time steps with a global neighborhood.

Clumping occurs when cells of a certain type tend to stay close together in the CA board after after the specified number of time steps. Clumping tends to occur more strongly in a local neighborhood scheme than in a global scheme. This result is also reflective of the Kerr paper (see Figure 9 and Figure 11).

Sensitivity of dynamics to changes in a subset of parameter values are also mimicked in Figure 13. The neighborhood is set to local, the number of time steps is 1000, $\Delta_{rock} = \frac{1}{3}$, $\Delta_{s,0} = \frac{1}{4}$, and $n = 100$. For varying τ (toxicity of rock) and Δ_{paper}, 10 simulated runs are performed on each such τ, Δ_{paper} parameter combination. The probability of coexistence (where all 3 species survive after 1000 time steps) is measured. The higher the probability of coexistence, the lighter the square.

Interestingly, the coexistence color grids between this implementation and Kerr et. al's implmentation are similar although Kerr et. al's coexistence grid is more clear cut be-

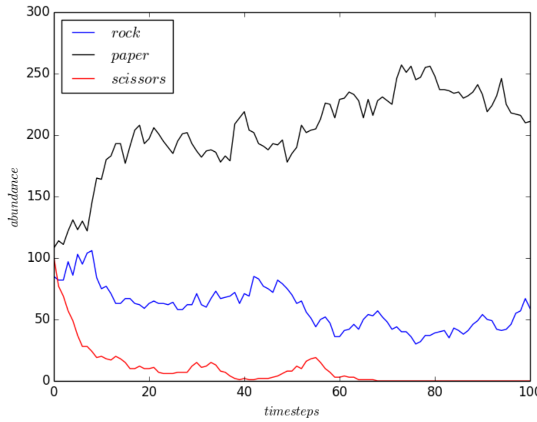

Figure 10: The abundance plot over 100 time steps under a global neighborhood. Scissors cells die out after around 60 time steps. Note that $\Delta_{rock} = \frac{1}{3}$, $\Delta_{paper} = \frac{10}{32}$, $\tau = \frac{3}{4}$, and $\Delta_{s,0} = \frac{1}{4}$.

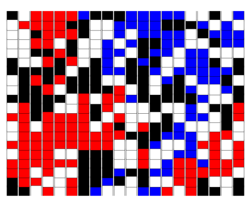

Figure 11: The CA board after 100 time steps with a local neighborhood. Clumping is more prominent. Blue squares represent rock cells, black squares represent paper cells, and red squares represent scissors cells.

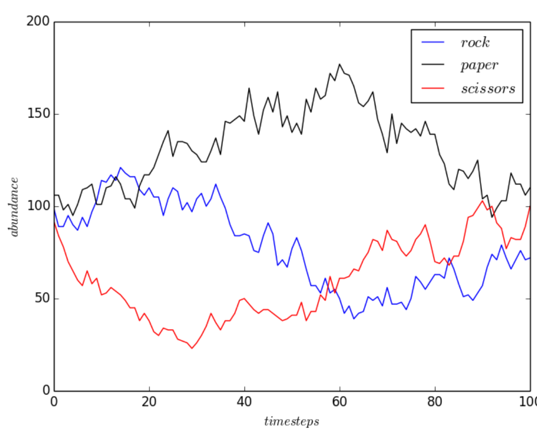

Figure 12: The abundance plot over 100 time steps under a local neighborhood. Note that $\Delta_{rock} = \frac{1}{3}$, $\Delta_{paper} = \frac{10}{32}$, $\tau = \frac{3}{4}$, and $\Delta_{s,0} = \frac{1}{4}$.

tween dark and light sections. Since 10 runs are simulated per τ, Δ_{paper} combination, n and the number of time steps

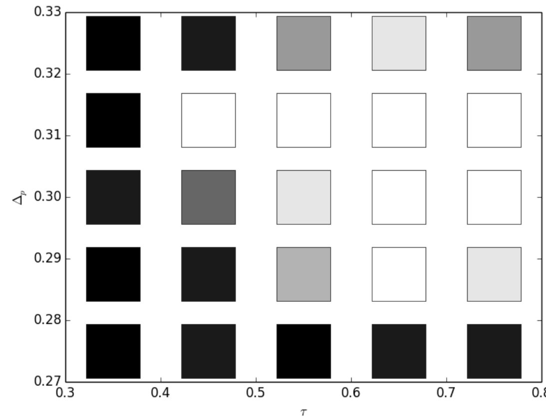

Figure 13: The coexistence color grid where a lighter square indicates a higher probability of coexistence. Parameters used: $n = 100$, time steps $= 1000$, $\Delta_{rock} = \frac{1}{3}$, $\Delta_{s,0} = \frac{1}{4}$. A local neighborhood is used and 10 runs are simulated per τ, Δ_{paper} combination.

are chosen to be quite low compared to Kerr et. al (where $n = 250$ and time steps $= 10000$) in the interest of time. This may have influenced the color grid to not be as distinct in coexistence and lack thereof.

Replicating Kerr et. al's methodologies was quite difficult considering certain techniques were not explained thoroughly in the paper. For example, it was not explicitly stated that an empty cell selected for update can still be empty with probability f_e, the fraction of its neighborhood consisting of empty cells. It was also assumed that when a cell is killed, it does not automatically adopt the value of the cell that would normally defeat it. Biologically, this models the behavior of cells better. A colicinogenic (C) cell releases a toxin (colicin) . Colicin sensitive (S) cells die due to the presence of this toxin. This does not mean that C cells automatically reproduce and take over space originally occupied S. C cells just released a toxin that happened to kill S. In addition, Kerr differentiates between interaction (killing and competition for space) and dispersal (birth). If killing automatically caused the cell to adopt the state of the killer, it would seem strange to distinguish the actions of interaction and dispersal.

5. DISCUSSION AND CONCLUSION

To simulate the dynamics of interacting populations of bacteria, a two-dimensional, wrap-around cellular automaton (CA) is designed. Both implementations, the simple one involving Moore and von Neumann neigborhoods and the modified one to better replicate Kerr et. al's results demonstrate that diversity is better preserved if dispersal and interaction are local and lost if more global. Clumping also tends to occur more strongly in a local neighborhoods than in global neighborhoods, reinforcing Kerr et. al's results. In the interest of time, n and time steps were not large, but further studies could increase such parameters and use parallel processing on determining the coexistence grid.

6. REFERENCES

[1] B. Kerr, M. A. Riley, M. W. Feldman, and B. J. Bohannan. Local dispersal promotes biodiversity in a real-life game of rock–paper–scissors. *Nature*, 418(6894):171–174, 2002.

[2] M. A. Nowak and K. Sigmund. Biodiversity: Bacterial game dynamics. *Nature*, 418(6894):138–139, 2002.