

Emergent Behavior of Bacteria in a Multiagent System

(Extended Abstract)

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ABSTRACT

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I.2.11 [Distributed Artificial Intelligence]: Multiagent systems

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1. INTRODUCTION

Bacteria forming clusters in a Petri dish is a common example of emergent behavior, i.e. many seemingly simple bacteria, when under stress, form clusters through basic rules of interaction. Under suitable conditions, the clusters form spectacular patterns [1]. Those properties of bacteria have inspired a lot of modeling work, attempting to reproduce the patterns and make sense of them.

The goal of the research presented in this abstract is to show that bacteria and the emergent behavior of bacteria can be accurately modeled using a multi-agent framework. The bacteria model was designed to closely reflect the rules of interaction obtained from empirical studies. The bacteria modeled are *Escherichia coli*, commonly referred to as *E. coli*. The novelty of this effort stems from modeling bacteria as bacteria actually behave. Most previous efforts to model the complex patterns of bacteria use partial differential equations (pde's). These pde's are used to produce a pattern as an end result. In contrast, the multi-agent approach allows for a time sequence that shows the formation of the patterns.

Bacteria movement is composed of *runs* and *tumbles*. A *run* is the forward movement of bacteria in a straight line,

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and a *tumble* is the reorientation of a bacterium so that it may change direction. As the bacteria move, they both excrete and sense aspartate, a chemical attractant. The bacteria change their tumble frequency based on the sensed amount of aspartate in such a way that they move up a chemoattractant gradient, thereby forming into clusters.

We wish to accurately model bacteria, because they are some of the most simple biological organisms. Accurately modeling the behavior of these very simple organisms will provide a strong stepping stone from which research can model more complex organisms, and provide a form of validation for the mapping of simulated experimental results to real world empirical results.

The self-organization of bacteria into clusters for higher resistance to stress has been acquired presumably because it provides an evolutionary advantage to the bacteria. Similar behavior exists in other species, but bacteria may be the simplest organisms displaying such behavior.

The results presented in this abstract show bacteria-agents forming clusters and moving swarm rings in a simulated Petri dish. The work presented in this abstract strives to accurately model bacteria, but does not model all aspects of bacterial behavior. However, the results gained from the approach shown in this abstract offer a significant advancement in the modeling of bacteria, as the results show that it is possible to reproduce the self-organization in clusters of a population of bacteria observed empirically, using what is known of their movement in runs and tumbles.

2. RESULTS AND DISCUSSION

Since an abstract cannot display movies, we show time series images of the simulation. Figure 1 shows the time series of six stages of a clustering experiment over a 10 minute period. Each of the six images displays the bacteria in the Petri dish. The lighter colors within the dish represent higher concentrations of bacteria. The number in the upper-left hand corner of each image displays the time step in the form minutes : seconds. The first image in the figure displays the initial condition at time step 0. The second image shows the bacteria after 2 minutes. In this image we can see that some areas are darker than others, meaning the distribution of bacteria is no longer uniform. After 6 minutes distinct clusters can be seen. The clusters become more pronounced

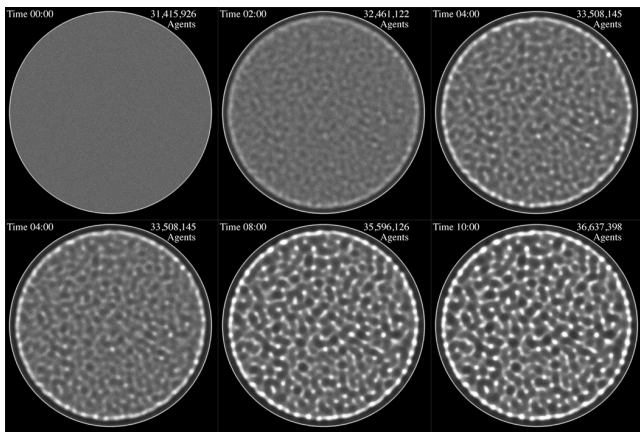


Figure 1: Simulation of *E. coli* bacteria in a 20mm Petri dish over a 10 minute time period. Agent density was set to $100,000 \text{ Agents}/\text{mm}^2$. Time step 0 shows the initial setup of bacteria agents with locations and directions randomly sampled from uniform distributions. The beginnings of clustering can be seen at minute 4, and are clearly visible at minute 6. Agents were exposed to trigger levels of $5mM$.

after 8 and 10 minutes. Figure 3 shows a side by side comparison of the simulated bacteria clusters (left) to that of the real world empirical results (right).

The results of the swarm ring are presented in Figure 2. The swarm ring in the upper left hand corner is a snapshot of the Petri dish after 3 hours of simulation time. The remaining five images are also snapshots of the swarm ring and were taken in one hour time increments from left to right from 4 hours to 8 hours.

Using only runs and tumbles for movement the simulated bacteria were able to form clusters similar to that of real-world bacteria. By observing the images of clusters from the simulation results on the left-hand side of Figure 3 to the real-world results shown on the right-hand side of Figure 3 we can compare the results. The real-world result has very dense clusters (in white) and not as dense regions (in gray). Similarly, in the simulation results, we can observe that the bacteria density of the bacteria differ between clusters and other regions. Some clusters appear to be darker (more dense) than others. The simulation can also reproduce the variation in size and distance between the clusters, as they depend on the amount of aspartate/chemoattractant secreted by the bacteria, which is an adjustable parameter in the simulation.

The swarm ring grew at roughly the same pace as the initial growth of the empirical swarm rings provided by Budrene and Berg in [1]. The growth rate of the simulated swarm ring falls between the growth rate of the empirical results with initial succinate amounts of $2mM$ and $3mM$.

These simulations show that it is possible with very few inputs to reproduce important properties of population of bacteria. From the perspective of random walks, the aspartate concentration dependent movement in “runs” and “tumbles” is a case of “biased random walk”. Those simulations also shed light on important aspects of the parallel mathematical modeling inspired by the emergence of the clusters. In the related work, to reproduce the patterns from diffusion equations, an aspartate concentration dependent chemotactic term had to be added. These simulations

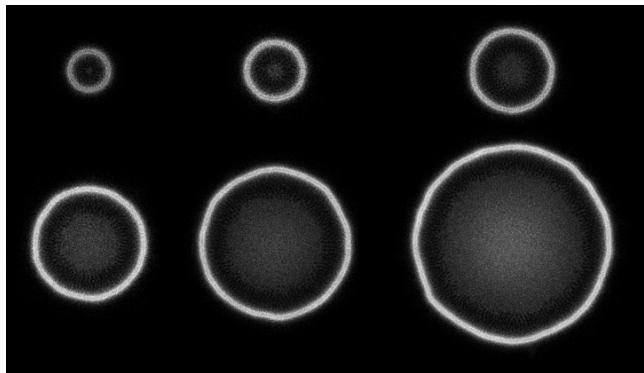


Figure 2: Simulation of *E. coli* bacteria over an 8 hour time period. At time 0, 10,000 bacteria agents were placed in the middle of the Petri dish. Initial succinate was set to $2mM$. The upper left hand swarm ring is a snapshot of the swarm ring after 3 hours of simulation time. The remaining five images are also snapshots of the swarm ring and are in one hour time increments from left to right from 4 hours to 8 hours.

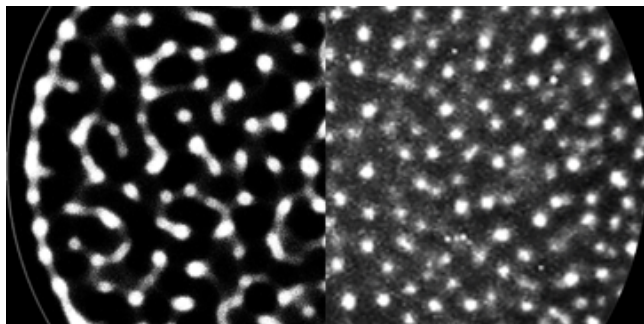


Figure 3: Clustering result of *E. coli* in a 12mm Petri dish after 10 minutes.

show that the non linear dependence of the chemotaxis of the bacteria does not conceal any mysterious property not yet known of the bacteria. It is a natural consequence of the way a multi-agent population of bacteria measure concentration gradients: by successive measurements of concentration. The study of the emergence of clusters has triggered a few theoretical questions on the response function of bacteria, among other things bacteria simulations may potentially be used to answer questions using simulations, as it is possible to change the conditions in which the bacteria are put.

3. ACKNOWLEDGMENTS

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4. REFERENCES

- [1] E. Budrene and H. Berg. Dynamics of formation of symmetrical patterns by chemotactic bacteria. *Nature*, 376:49–53, July 1995.