Simulating Social Interaction of Bacterial Communities using Agent-Based Models

Department of Mathematics;
Florida State University

Roshu Senthil
Dr. Mohammad Nooranidoost

ABSTRACT

The behavior of bacterial communities is dependent on many factors such as the availability of resources, the rate of mutation, and the presence of antibiotics. The social interaction between bacteria determines their population dynamics and survival rates. In our research project, we sought to model these behaviors using an agent-based modeling software, NetLogo. NetLogo allowed us to create our own bacterial community with varying levels of each predetermined factor to then test how each of them affects the growth and interaction of the bacteria. We tested different amounts of resources, rates of genetic mutation, and the presence of antibiotics. From these results, we were able to observe different mathematical models that fit the growth (or decay) of the community. Once we had a basic understanding of the behavior of these bacterial communities, we set out to modify a previous NetLogo model to incorporate more genetic mutant agents. With this research, we will learn more about the complexities of bacterial communities and how we can use agent-based modeling as well as mathematical models to properly simulate and represent the behaviors and interactions of these communities.

METHODS

CODING

- Used NetLogo software to create environment that replicates a bacterial community
- Pre-existing model – "Bacterial Growth and Antibiotic Resistance" from Kyle Harston and Ashok Prasad
  - In our research, we are ignoring antibiotic resistance
- Changed NetLogo code to accommodate new genetic mutant
  - Created new mutant agent within the environment (Mutant 2)
  - Created new mutation rate (Mutation Rate 2)
  - Calculated and implemented new mathematical formula for population limiting factor that includes the factor of another mutant

IMPLEMENTING

- Ran code and viewed results through interface of NetLogo
  - Fixed and changed different variables (Initial Bacteria Population, Carrying Capacity, Mutation Rate 1 and 2, and every agents Birth Rate)each time
- Recorded results into Excel
- Used R software to code line plots of the changing variable against the counts of each agent (Wild-Type, Mutant 1, Mutant 2)

RESULTS

- Figure no.1. – the population of the wild-type bacteria rises the greater the initial bacteria population, and the population of each mutant gradually decreases
- Figure no.2. – the population of the mutants follows a linear growth graph with increases in the carrying capacity while the population of the wild-type bacteria stays at a relatively low level
- Figure no.3. – the population of wild-types drastically decreases the larger the mutation rate gets, while the population of the mutants increases and then eventually plateaus
- Figure no.4. – this graph shows us the relationship between the 2 mutants with respect to their mutation rate, while the wild-type population stays at a somewhat constant level because mutation rate 1 is .5
- Figures no.5., no.6., and no.7. – show us how each agent acts in accordance with a change in the birth rate of another agent

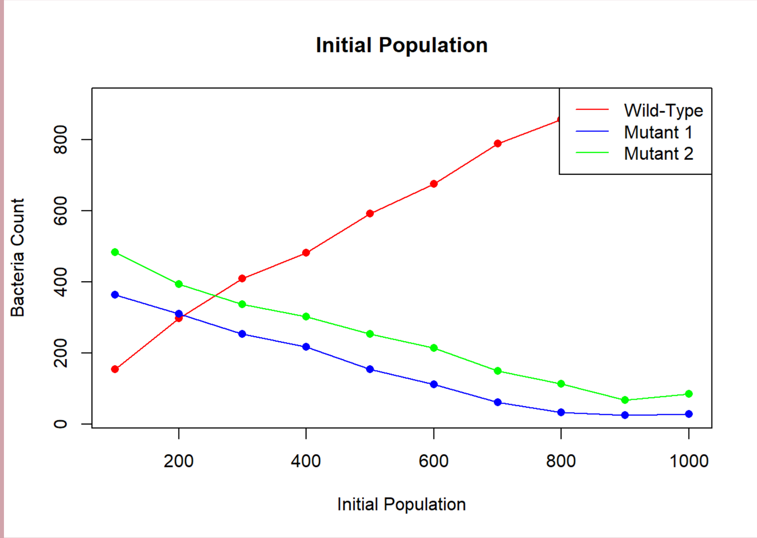

Figure no.1. Initial Bacteria Population vs Bacterial Population of each agent

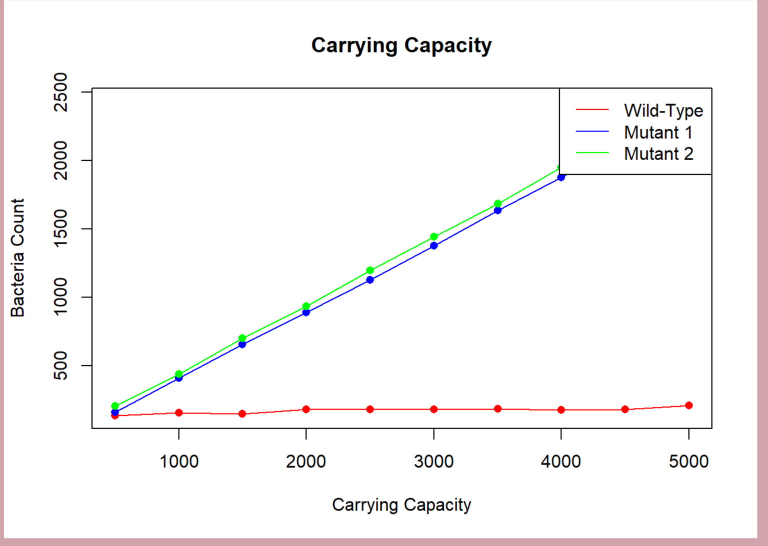

Figure no.2. Carrying Capacity vs Bacterial Population of each agent

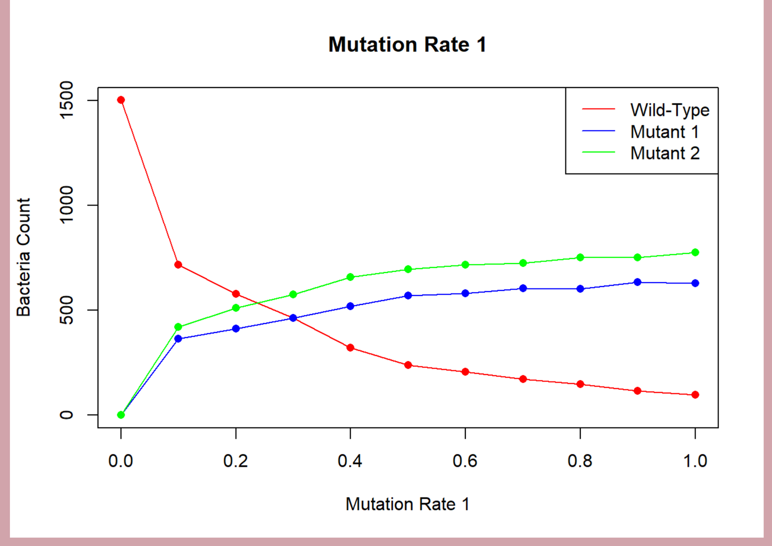

Figure no.3. Mutation Rate 1 vs Bacterial Population of each agent

Figure no.4. Mutation Rate 2 vs Bacterial Population of each agent

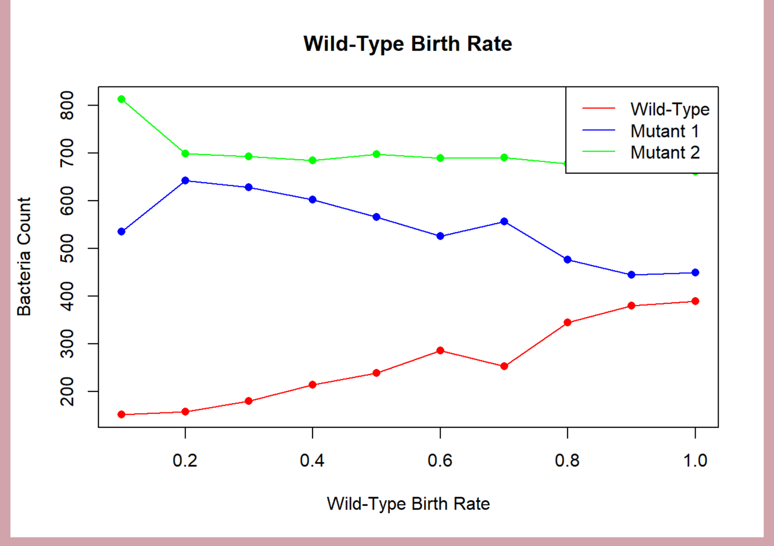

Figure no.5. Birth Rate of Wild-Type vs Bacterial Population of each agent

Figure no.6. Birth Rate of Mutant 1 vs Bacterial Population of each agent

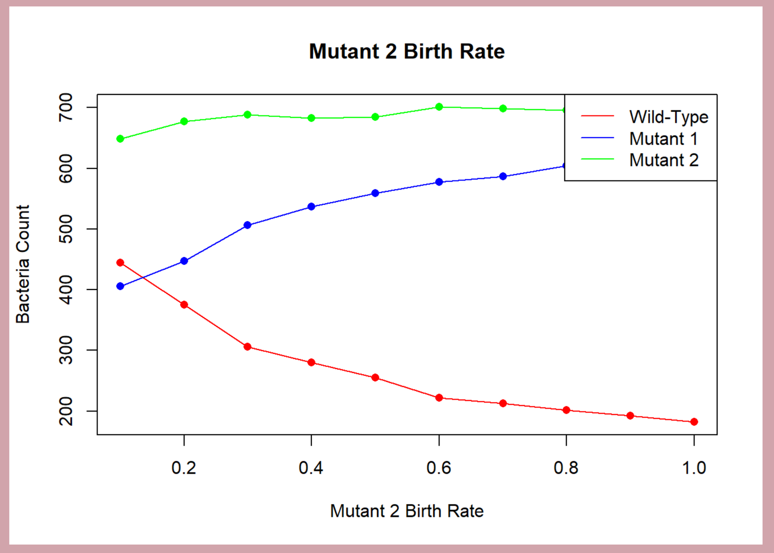

Figure no.7. Birth Rate of Mutant 2 vs Bacterial Population of each agent

DISCUSSION

These are the values of the variables that we fixed in each graph:

- Initial Population – 0.1
- Carrying Capacity – 1.5
- Mutation Rate 1 – 0.5
- Mutation Rate 2 – 0.1
- Birth Rate WT – 0.2
- Birth Rate M1 – 0.4 (0.5 in Birth Rate graphs)
- Birth Rate M2 – 0.6 (0.5 in Birth Rate graphs)

We can see that introducing a new genetic mutant has created more competition between the wild-type bacteria and the mutants and even between the 2 mutants. In general, the mutant population will always surpass the wild-type population because the wild-type bacteria is allowed to either birth a new bacteria or die, and within that birth function, it must choose between mutating or staying a wild-type. The mutants, however, are only given the choice of birthing another mutant or dying. This allows the mutants to grow far more than the wild-types, however, we can see in the initial bacteria population graph that this does not always have to be the case. Given that the initial population of the wild-types is greater than around 250, the wild-type bacteria will have enough strength in numbers to outgrow the mutants and create an environment in which the competition is too strong for the mutants to grow.

Most of the graphs produce outputs that align with our assumptions based on what we know about bacteria and how they respond to their environment. Controlling the amount of resources available (carrying capacity) allows the mutants to grow in a linear function because they are the only agents strong enough to compete for the resources available, and more resources lead to more mutants.

The mutation rate graphs show us how powerful the mutation rate variable is in controlling the population of each agent. Compared to the birth rate graphs, they definitely take more precedence and have a larger impact on the probability of a wild-type bacteria mutating and whether it mutates to mutant 1 or mutant 2. The birth rate graphs show even if the mutation rate 2 favors the growth of mutant 2, mutant 1 and the wild-types still respond in likeness to their respective birth rates, which seems to be a symmetrical reflection of one another.

As these graphs show, each factor plays a crucial role in the social interaction and survival of bacteria in a community. Introducing a new genetic mutant creates a more competitive environment, however, there are key factors (such as the initial bacteria population, carrying capacity, and mutation rate) that we can control to produce a desired outcome in the bacterial population of each different agent.

ACKNOWLEDGEMENTS

I would like to thank Dr. Nooranidoost for allowing me to work on this project and guiding me throughout the course of this year. Thank you for helping me delve into this project and allowing me the creative space to make it great. I would also like to the Florida State University Department of Mathematics for giving me the opportunity to make this project a reality.

REFERENCES

SCAN ME