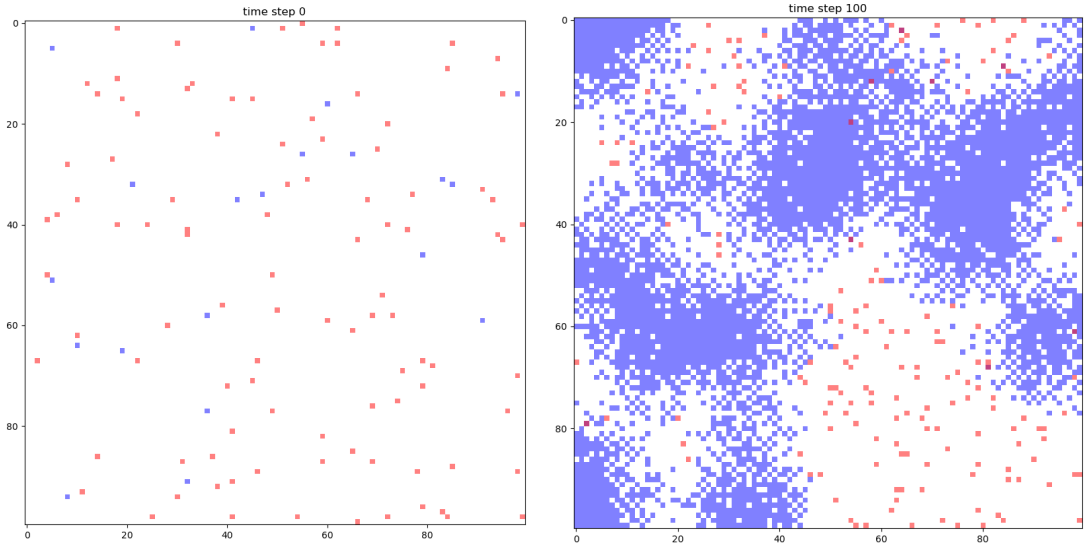
Since the last checkpoint, we have made significant progress in the implementation of our simulator. We have built a fully-functional cellular automaton in Python to model the interactions between bacteria and antibiotics. Our cellular automaton is 2xNxN dimensional with two size-N spatial dimensions and one size-2 dimension with a plane for the bacteria and a plane for the antibiotics. At time 0 these planes are randomly populated with antibiotics and bacteria.

Cell Division & Redosing

We also built a mechanism to model bacterial cell division in our cellular automaton. Our bacteria objects have an internal timer which ticks up as time advances in the simulation. When the timer reaches a predefined division interval value, the timer is reset and the bacterium attempts to divide. If there is space available the bacterium's offspring will be placed next to its parent, otherwise it will not divide. As a counterweight to cell division, we also implemented antibiotic redosing in our simulation. After a set interval, a predefined number of antibiotics will be randomly placed across the grid. This accurately models reality, where an individual might continually take antibiotics at a specific time of day for several weeks. Cell division and antibiotic redosing create an antagonistic relationship between bacteria and antibiotics each tries to dominate the other.



Phenotype Modeling for Antibiotic Susceptibility

For this checkpoint, we focused more on the interactions that would occur between the bacteria and antibiotics, and the mortality of the bacteria is based on the functionality of its structures. Therefore, we had to model the relationship between genes and phenotypic traits, using E. Coli as an example for this checkpoint. We identified and categorized genes based on their biological functions, like cell wall structure, respiration, and antibiotic resistance. Using these gene groupings, and additional research regarding gene mutations and resultant

phenotype outcomes, we were able to represent phenotypes for each structure as a one-hot vector, determined by boolean logic done with the gene groups. This boolean logic can be seen in the excel sheet *Gene_to_Phenotype_Logic* in our Github. Moving forward, this array will be used in evaluating the collisions between bacteria and antibiotics, allowing for varied antibiotic types to be used, since different phenotype presentations will result in different susceptibility of the bacteria to antibiotics.

Antibiotics

For the antibiotics, we added further functionality to check for bacteria that specific antibiotic types can kill. We designed a vector of features present in bacteria (e.g. cell wall type, number of efflux pumps, etc.) that antibiotics are able to kill. The bacteria vector is a 1x37 vector of phenotypes generated from a one-hot encoding of a 1x30 vector that represents bacteria genes. We also implement an antibiotic vector that is a 1x37 vector which represents the phenotypes that the antibiotic is capable of targeting. In the cellular automata, when bacteria come in contact with an antibiotic, the vector for the bacteria is checked against the vector for the antibiotic. Then, a probability vector is applied based on the type of antibiotic to determine whether the bacteria is killed.

Division of Work

Cellular Division and Redosing - Nick
Phenotype Modeling for Antibiotic Susceptibility - Ashley
Antibiotics - Seth

Remaining Work

Mutation Rates - Ashley
Verification - All
Possibility of Adding Additional Bacteria and Antibiotic Types - All

Repository

https://github.gatech.edu/ModSimFall2023Group22/bacterial-resistance-sim