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**Problem:**

Antibiotic Resistance is a huge problem plaguing clinical medicine. The implications of antibiotic resistance has been extensively reported on. Nearly, every major authority including the CDC and WHO have added their voices for the need for effective prevention, and further understanding of antibiotic resistance. One of the major problems is understanding how genetic information is passed from commensal bacteria and pathogens and how non-clinical environments can harbor antibiotic resistance genes. 1 Understanding this chain of events in bacteria will help us build better risk assessments that will enable better practices and limit the antibiotic resist-ome.

**Goal:**

Create a simple model that could incorporate experimental data that will serve as a foundation for risk assessment of antibiotic resistance gene reservoirs. With this foundation and adding more complexity we will be able to hopefully predict how different bacterial environments harbor specific genes in their environment whether that be soil, animal or the gut of humans.

**Description:**

The model is an object oriented program that tries to incorporate actual data on mutation rates, antibiotic concentration breakpoints and group dynamics of a bacterial population. The model considers three different populations a susceptible population, an intermediate population and a resistant population. This is based on the reporting mechanisms of antibiotic resistance by National Antimicrobial Resistance Motoring Systems (NARMS). It considers the chance for a susceptible population to turn to an intermediate and subsequently a resistant population. After exposure to an antibiotic the model incorporates the idea of the stress response. Where stressed bacteria (Susceptible populations) would increase their mutation rate, and natural competence to try and survive the stress. This is an opportunity to explore how each of these factors influence community dynamics; initial population size, rate of mutation between the populations, and horizontal gene transfer. This model is simple and does not account for multiple community dynamics such as multiple organisms, predation, non-motility bacteria, quorum sensing, biofilm formation, and assumes that there is one gene that attributes to the change of the bacterial behavior.

**Hypothesis:**

Each of the four factors being tested will influence the predominate-population and when it emerges. I predict that most of the scenarios will lead to resistant population being predominate. Also antibiotic concentration and mutation rate will be the most influential factors in the model. The below table illustrate some of the variables being tested and how I envision how interaction with an antibiotic will influence the predominate population over 10 000 “iterations”.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Time of Antibiotic** | **Initial Population Density** | **Iterations** | **Mutation Rate** | **Predominate Population** |
| Early | 0.1 | 10,000 | 0.05 | **Resistant** |
| Middle | 0.1 | 10,000 | 0.05 | **Resistant** |
| Late | 0.1 | 10,000 | 0.05 | **Intermediate/Resistant Mixed Resistant** |

**Conclusions:**

The above Hypothesis was tested – each of the four factors replication, death, mutation and horizontal gene transfer rate changed the predominate population. The rates seen in the program now reflect relevant information that could model some similar dynamics that have been reported on. Bacteria that are susceptible to antibiotic wouldn’t have any trade-offs therefore we see an increased replication rate, however their behavior changes after an antibiotic is added. Similarly, Intermediate bacteria have a similar replication rate and smaller step changes after antibiotic is added. The resistant population, however, has a lower replication rate (chance of replication), but are resistant to the stress after antibiotic is added to the system. The three examples in the Ipython Notebook show the results for the chart that was presented above. I assumed that the late antibiotic would lead to a mixed population, because the effect would be more gradual for the Intermediate bacteria. However, the parameters set as they are now, we see that there is a sharp decrease in the susceptible population after the antibiotic is added.

**References:**

1. Huijbers, Patricia MC, et al. "Role of the environment in the transmission of antimicrobial resistance to humans: A review." *Environmental science & technology* 49.20 (2015): 11993-12004.