Modeling the Effect of Bacteriophages on the Spread of Antibiotic Resistance

Richard Yan, Mass Academy

Research Question: How do bacteriophages quantitatively influence the population dynamics of resistant and susceptible bacteria under antibiotic pressure?

Hypothesis: Bacteriophages will reduce the overall bacterial population but will increase the resistant bacterial population through the spread of antibiotic resistance genes.

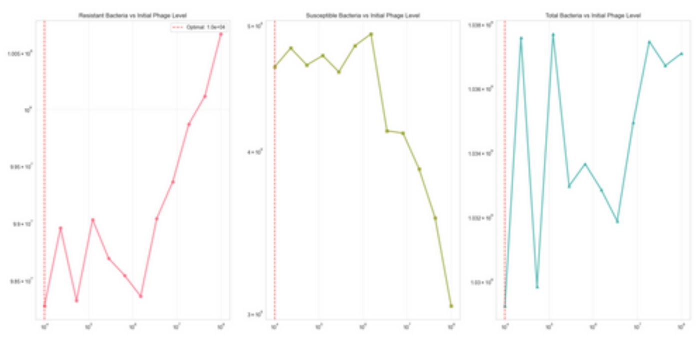
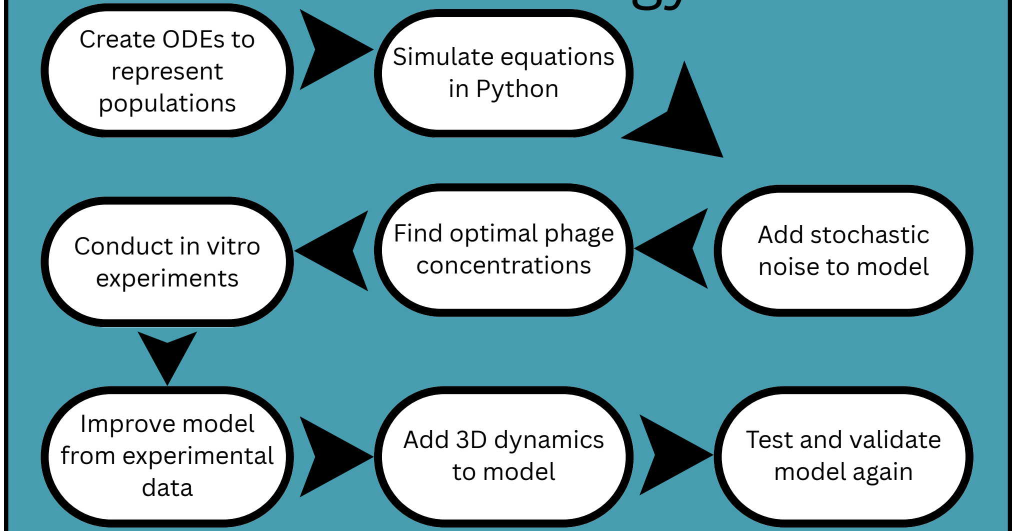


Figure 1: This graph shows how bacteria populations change in relation with initial phage populations. At each phage population, Monte-Carlo simulations were run, and the final bacteria populations were averaged to produce the results shown on the graph.

Moderate phage concentrations are best at balancing bacterial clearance and minimizing ARG spread.

Methodology



Create ODEs to represent populations

Simulate equations in Python

Add stochastic noise to model

Find optimal phage concentrations

Conduct in vitro experiments

Improve model from experimental data

Add 3D dynamics to model

Test and validate model again

Phage predation can reduce bacterial load, but resistance still emerges due to transduction of ARGs Monte-Carlo results show how final bacteria. populations can greatly vary while being put under similar conditions.

High initial phage populations lead to incredibly high resistant populations due to the transfer of antibiotic resistance genes