Role of Student vs. Mentor

I worked entirely on developing the mathematical model and implementing it in Python. My mentor helped me in the lab by explaining aseptic technique and going over dilutions and experimentation.

Equipment and Materials

This project utilizes both computational and laboratory resources. The mathematical model consisting of five ordinary differential equations was implemented in Python using NumPy and SciPy for computational analysis and simulations and Matplotlib and Seaborn for data visualization. All simulations were implemented and performed on a personal computer running Windows 11. For experimental validation, we used *E. coli*, T7 phages, and ampicillin, along with standard microbiological materials including sterile growth media, micropipettes, sterile pipette tips, a fume hood, and spectrophotometric methods to measure bacterial density. These combined computational and laboratory resources enable both computational and experimental study of the effects of phage-induced transduction on resistance.

Technique 1: Deterministic Mathematical Modeling

A system of five ordinary differential equations was constructed to model the interactions among susceptible bacteria, resistant bacteria, infected bacteria, bacteriophages, and antibiotic concentrations over time. The model incorporates bacterial logistic growth, phage infection and replication, antibiotic decay, and an antibiotic-dependent mutation rate for susceptible bacteria. Numerical integration was performed using NumPy and SciPy to simulate population trajectories under different treatment conditions. This technique was used to describe population-level dynamics and to predict how phages and antibiotics interact over time.

Technique 2: Stochastic Mathematical Modeling

To account for biological variability and randomness in infection and resistance processes, stochastic simulations were implemented by setting parameter values to normal distributions rather than set values and adding noise to the ordinary differential equation system. The libraries and implementation methods used for the deterministic model are used to implement the stochastic model. This technique was performed to analyze how random fluctuations in parameter values and noise influence bacteria-phage dynamics and to determine whether deterministic predictions were robust to biological noise.

Technique 3: In Vitro Validation

Preliminary *in vitro* experiments were conducted using *E. coli,* T7 bacteriophages, and ampicillin. Bacterial cultures were grown in media and exposed to phages and antibiotics in a controlled laboratory setting. Bacterial density was measured over time using spectrophotometry to compare experimental findings with model predictions.