Conclusion

The objective of this study was to evaluate how bacteriophages influence total and resistant bacterial populations under antibiotic treatment using a mathematical modeling framework. To accomplish this, a system of five ordinary differential equations was developed to represent concentrations of susceptible bacteria, resistant bacteria, infected bacteria, phages, and antibiotics. Deterministic simulations were performed to examine normal treatment dynamics, and stochastic simulations were used to assess the variability of the system. A parameter sweep across initial phage concentrations was conducted to evaluate optimal phage treatment.

Results demonstrated that phage treatment alone caused rapid and substantial suppression of total bacterial populations, while antibiotic treatment alone strongly selected for resistant bacteria as drug concentrations decayed. Combined phage-antibiotic treatment produced oscillatory dynamics and did not eliminate resistance populations. Analysis of phage dosing revealed a nonlinear relationship between initial phage concentration and resistant bacterial outcomes, with moderate phage levels minimizing resistance while maintaining effective bacterial control. Stochastic simulations further showed that population trajectories can vary significantly under identical initial conditions, emphasizing the importance of incorporating randomness into biological models.

Overall, this study demonstrates that phage therapy should be evaluated not only for its ability to reduce bacterial load, but also for its evolutionary consequences on resistance dynamics. By integrating ecological interactions and stochastic variability into a single framework, this work highlights the need for optimized, resistance-aware treatment strategies rather than simply increasing antibiotic intensity.