

Modeling Escherichia Coli Dynamics in Multi-Stage Wastewater Treatment Systems

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ABSTRACT

Sustainable Development Goal 6 on clean water and sanitation is threatened by Escherichia coli (E. coli) contamination in wastewater, which poses grave dangers to the environment and public health. Microbial and chemical contaminants are present in wastewater from various sources, and treatment difficulties are growing due to urbanization. While biofilm formation, disinfectant resistance, and particle attachment increase bacterial survival, pathogenic E. coli strains can cause serious illness. To explain the dynamics of E. coli in wastewater systems, this study develops a deterministic mathematical model. MATLAB solvers and uncertainty and sensitivity techniques based on Latin hypercube sampling and partial rank correlation coefficients are used to analyze the model. The findings promote more effective wastewater treatment and microbial risk management by identifying key drivers of persistence.

INTRODUCTION

Achieving Sustainable Development Goal 6 (SDG 6) on clean water and sanitation is severely hampered by Escherichia coli (E. coli) contamination in wastewater, which poses a serious environmental and public health hazard. Urbanization and rapid population growth have increased wastewater generation, placing significant strain on existing treatment facilities and exacerbating freshwater scarcity (Yezli et al., 2021).

Wastewater from residential, commercial, agricultural, and stormwater sources contains several pollutants, including pathogens and chemical contaminants. (Fida et al., 2023; Rodriguez-Pere Abdelbasir et al., 2019). Inadequate treatment has significant adverse effects on the environment and society, including eutrophication, groundwater pollution, fecal contamination, and elevated risks of waterborne illnesses (Fida et al., 2023).

A standard indicator of fecal contamination in aquatic environments is Escherichia coli, a Gram-negative bacterium belonging to the Enterobacteriaceae family (Coxon, 2023). Pathogenic variants, such as E. coli O157:H7, can cause severe illness even though most strains are benign. Leaking sewage systems, agricultural runoff, and inadequately treated wastewater are the primary sources of contamination (Tang et al., 2020; Abdelbasir & Shalan, 2019; Prakasha & Veerasha, 2020)—biofilm formation and resistance to disinfectants such as chlorine increase E. coli's persistence.

Because they have a significant ecological role in regulating E. coli populations and frequently display a Type II functional response, bacteriophages are promising biological control agents in wastewater treatment (Savini et al., 2017)(Savini et al., 2017). However, existing models provide limited insight into multi-stage therapeutic systems and bacteriophage-based regulation.

This study develops a deterministic mathematical model based on Monod kinetics to investigate E. coli dynamics (Luong, 1987), bacteriophage predation, and resistance within a multi-stage wastewater treatment framework, thereby providing quantitative support for improved treatment procedures.

Bacteriophages are promising biological control agents in wastewater treatment because they play a significant ecological role in controlling *E. coli* populations and typically exhibit a Type II functional response (Savini et al., 2017). Nevertheless, current models offer little understanding of bacteriophage-based control and multistage therapy systems.

To provide quantitative support for improved treatment approaches, this study develops a deterministic mathematical model based on Monod kinetics to examine *E. coli* dynamics (Luong, 1987), bacteriophage predation, and resistance within a multi-stage wastewater treatment framework.

Model Formulation

The dynamics of *E. coli* and bacteriophages during various wastewater treatment stages are described in this paper using a deterministic compartmental model based on Monod kinetics. The suggested architecture includes seven interacting compartments to represent treatment-stage structure, biological predation, and resistance, in contrast to earlier models that mainly concentrate on lake or single-compartment pollution systems.

Bacteriophages are divided into two compartments, whereas the *E. coli* population is split into five groups based on treatment stage and resistance status. Pre-primary, primary, secondary, tertiary, resistant *E. coli*, and bacteriophage populations are thus represented by a seven-dimensional framework. Biological growth, recruitment, treatment, predation, and natural mortality processes are all represented by model parameters. When needed, suitable estimates were added to parameter values taken from the literature (Tables 1 and 2).

The model assumes that bacteriophage and *E. coli* concentrations can be measured per unit volume and that competition, natural mortality, treatment-induced mortality, and bacteriophage predation affect population dynamics. Additionally, it is believed that bacteriophages are primarily active during the pre-primary and primary treatment stages, advection and diffusion are low, and evaporation is insignificant.

A system of nonlinear ordinary differential equations describes the temporal evolution of each compartment. Monod growth kinetics (Luong, 1987), density-dependent effects, treatment terms, and predator-prey interactions are all included in these equations.

Section 2.4 presents the complete set of governing equations.

Model Structure

- **E. coli compartments:** Five classes representing different states of bacterial population, including susceptible, resistant, and biofilm-forming cells.
- **Bacteriophage compartments:** Two classes representing free and bound phages.

The compartments interact through growth, predation, resistance development, and biofilm formation.

Variables

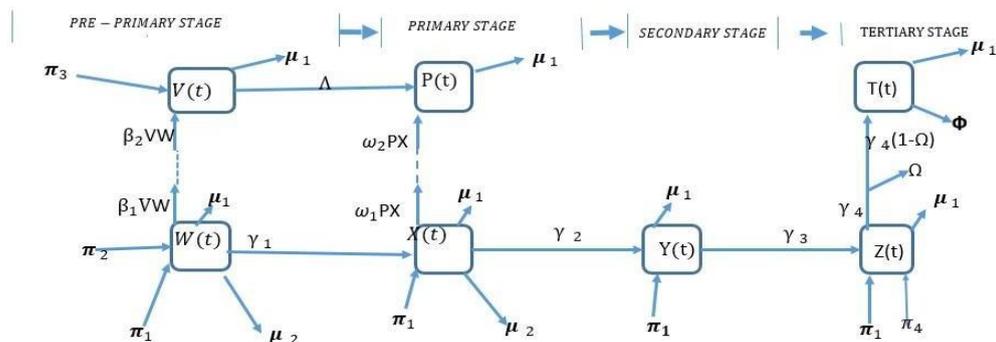
Variable	Description
$W(t)$	Represent the <i>E. coli</i> population in the pre-primary stage of water treatment.
$X(t)$	Represent the <i>E. coli</i> population in the primary stage of water treatment.
$Y(t)$	Represent the <i>E. coli</i> population in the secondary stage of water treatment.

Z(t)	Represent the E. coli population in the Tertiary stage of water treatment
T(t)	Represent the E. coli population in a tertiary stage that resists
V(t)	Represent the bacteriophage population in the primary stage of water treatment.
P(t)	Represent the bacteriophage population in the primary stage of water treatment.t

Assumptions

1. E. coli growth follows Monod kinetics with resource-limited growth.
2. Bacteriophage predation follows a Type II functional response.
3. Disinfectants may not eliminate resistant E. coli, leading to a resistant compartment.
4. Wastewater is well-mixed, and spatial heterogeneity is ignored.

Model Flowchart



A conceptual flowchart illustrates interactions between E. coli compartments and bacteriophage populations, highlighting growth, predation, and resistance pathways.

Model Equations

The system of differential equations describes the dynamics of each compartment. These equations are implemented and solved using MATLAB ODE solvers.

$$\frac{dW}{dt} = (\pi_1 + \pi_2 - \mu_1 W - \mu_2 W - \beta_1 WV + \frac{\pi_m WS}{K_2 + S} - \gamma_1 W) \left(1 - \frac{N}{A}\right) \quad (1)$$

$$\frac{dX}{dt} = (\gamma_1 W + \pi_1 - \mu_1 X - \mu_2 X - \omega_1 XP + \frac{\pi_m XS}{K_2 + S} - \gamma_2 X) \left(1 - \frac{N}{A}\right) \quad (2)$$

$$\frac{dY}{dt} = (\gamma_2 X + \pi_1 - \mu_1 Y + \frac{\pi_m YS}{K_2 + S} - \gamma_3 Y) \left(1 - \frac{N}{A}\right) \quad (3)$$

$$\frac{dZ}{dt} = (\gamma_3 Y + \pi_1 + \pi_4 - \mu_1 Z + \frac{\pi_m ZS}{K_2 + S} - \gamma_4 Z) \left(1 - \frac{N}{A}\right) \quad (4)$$

$$\frac{dT}{dt} = (\gamma_4 Z(1 - \Omega) - \mu_1 T + \frac{\pi_m TS}{K_2 + S} - \Phi T) \left(1 - \frac{N}{A}\right) \quad (5)$$

$$\frac{dV}{dt} = \left(\beta_2 WV + \pi_3 - \mu_1 V + \frac{\pi_m VS}{K_2 + S} - \Lambda V\right) \left(1 - \frac{B}{A}\right) \quad (6)$$

$$\frac{dP}{dt} = \left(\Lambda V + \omega_2 XP - \mu_1 P + \frac{\pi_m PS}{K_2 + S}\right) \left(1 - \frac{B}{A}\right) \quad (7)$$

The following are conditions incorporated in the above system (1-7) of equations

$$0 \leq \omega_1 \leq 1, 0 \leq \omega_2 \leq 1, 0 \leq \beta_1 \leq 1, 0 \leq \beta_2 \leq 1, N \leq A, \text{ and } B \leq A.$$

Model analysis

Analytical analysis

The above model equations were qualitatively analysed by determining the model's feasible region, critical points (equilibrium points), and bifurcations.

Differential and integral calculus were used as analytical tools to demonstrate the Positivity and bounded nature of the solutions within the feasible region. The solution to the system with non-negative initial conditions exists and is unique.

The state variables that did not change with time in this study were considered as critical points. These vital points were obtained by equating all the differential equations to zero.

The study had five cases (critical points), which were denoted as $E^0 = \{0,0,0,0,0,0\}$,

$E^1 = \{0,0,0,0,0, V^1, P^1\}$, $E^2 = \{W^2, X^2, Y^2, Z^2, T^2, 0,0\}$, $E^3 = \{W^3, X^3, Y^3, Z^3, T^3, V^3, P^3\}$,

and $E^4 = \{W^4, X^4, Z^4, 0, V^4, P^4\}$

E^0 represent Case 1; In the absence of E. coli and resistance in the system.

E^1 represent Case 2: In the absence of E. coli only.

E^2 represent Case 3. In the extinction of the predator only

E^3 represent Case 4. In the absence of resistance

E^4 represent Case 5: Coexistence of the system

Both local and global stability were considered. The nature of its eigenvalues determined the local stability of the system (1-7); the Routh-Hurwitz criterion was used to assess stability, yielding a characteristic polynomial.

$a_7\lambda^7 + a_6\lambda^6 + a_5\lambda^5 + a_4\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda^1 + a_0 = 0$. The system (1-7) was locally asymptotically stable at the critical point by the Routh-Hurwitz criterion for stability $a_0 > 0, a_1 > 0, a_2 > 0, a_3 > 0, a_4 > 0, a_5 > 0$ and $a_6 > 0$ are satisfied and unstable (Ngari, C. G., Muthuri, G. G., & Kitavi, D. M., 2022)

A global stability was the stability of a critical point away from the equilibrium point. One common approach used in studying the global asymptotically stable state of this study was by use of Lyapunov function (Odhiambo et al., 2023), and it is globally asymptotically stable since $\frac{dV}{dt} < 0$ if

$$V = \frac{(W-W^*)}{2} + \delta_1 \frac{(X-X^*)}{2} + \delta_2 \frac{(Y-Y^*)}{2} + \delta_3 \frac{(Z-Z^*)}{2} + \delta_4 \frac{(T-T^*)}{2} + \delta_5 \frac{(V-V^*)}{2} + \delta_6 \frac{(P-P^*)}{2}$$

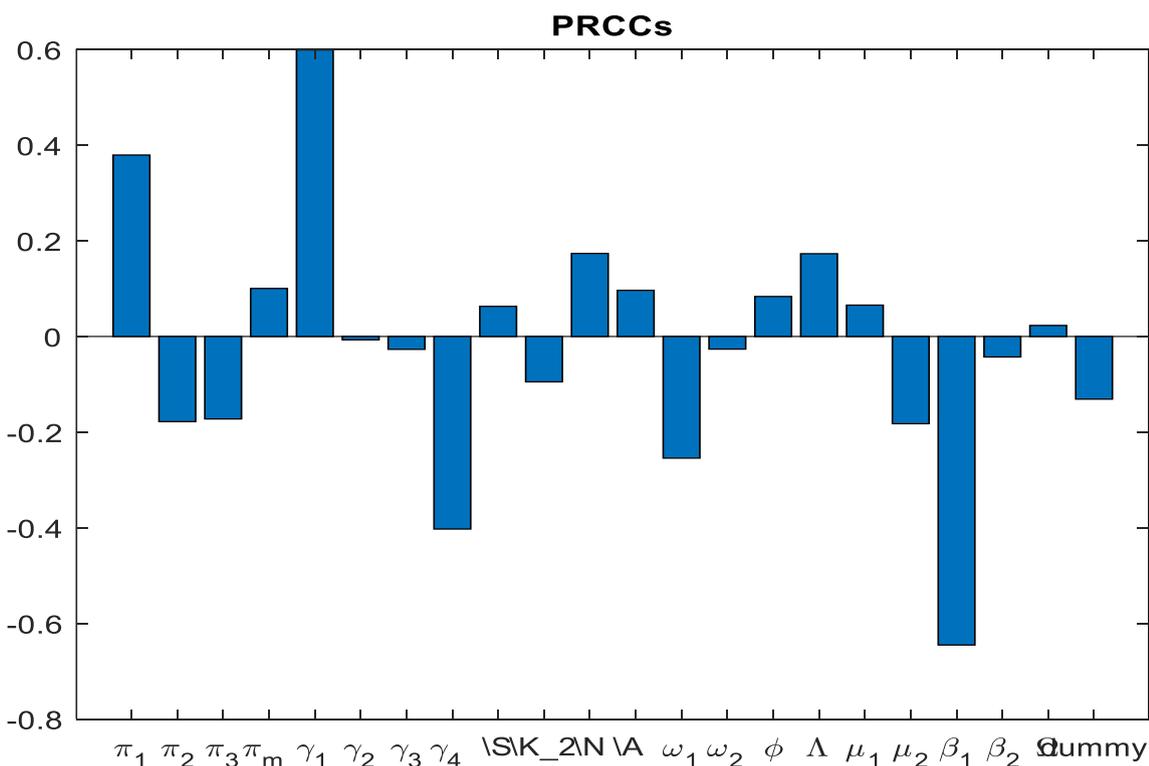
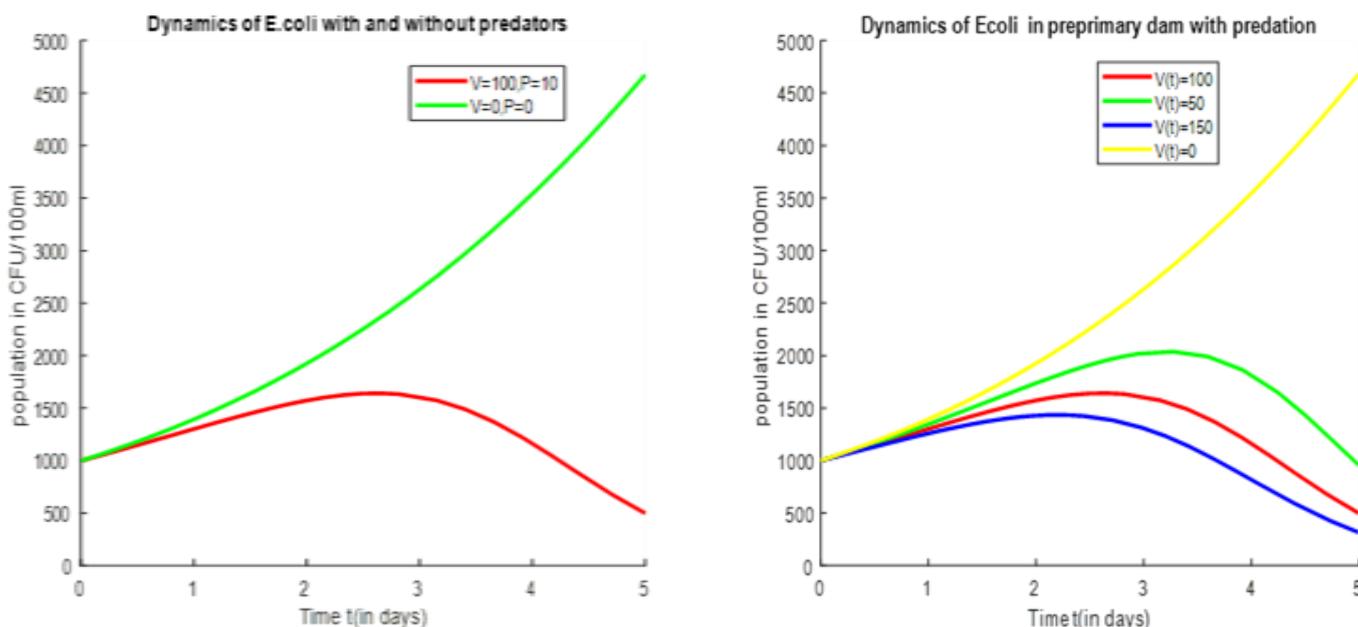
A Hopf bifurcation occurred where the system had a non-hyperbolic equilibrium point and had purely imaginary eigenvalues, and β_1, ω_1 were considered as the bifurcation parameters and β_1^*, ω_1^* as the turning point for values of the bifurcation parameters (Odhiambo et al., 2023).

Numerical analysis

Numerical simulations demonstrate that bacteriophage predation is the most influential mechanism for reducing *E. coli* populations. A 50% increase in bacteriophage predation parameters resulted in reductions of up to approximately 76% in *E. coli* concentrations, whereas algae-induced mortality produced comparatively minor effects. The results further show that resistant *E. coli* populations persist despite conventional treatment, consistent with known biofilm formation, disinfectant resistance, and stress-response mechanisms.

Sensitivity analysis confirms that bacteriophage-related parameters are among the most significant contributors to uncertainty and control, highlighting the potential of integrating bacteriophage-based strategies into wastewater treatment systems.

Simulations



Uncertainty and Sensitivity Analysis

Parameter Symbol	PRCC	p-values
π_1	0.4466	3.2021e-06
π_2	-0.036901	0.71549
π_3	0.14363	0.15398
π_m	0.047649	0.63781
γ_1	0.40187	3.4085e-05
γ_2	0.16649	0.09782
γ_3	-0.23424	0.018992
γ_4	-0.065812	0.51533
S	0.047082	0.64182
K_2	0.040344	0.69024
N	0.12048	0.23249
A	-0.03593	0.72267
ω_1	-0.088145	0.38317
ω_2	-0.012077	0.90508
ϕ	0.154	0.12607
Λ	-0.041982	0.67834
μ_1	-0.19124	0.056648
μ_2	-0.047424	0.63939
β_1	-0.65831	9.8345e-14
β_2	0.076511	0.44929
Ω	0.14255	0.15712

Uncertainty analysis was performed using Latin Hypercube Sampling (LHS) combined with Partial Rank Correlation Coefficients (PRCC). This approach explores the parameter space efficiently and quantifies the relative influence of parameters on model outputs (Bidah et al., 2020). PRCC values range from -1 to $+1$, with larger absolute values indicating greater influence.

The LHS/PRCC analysis identifies bacteriophage-related parameters as dominant drivers of *E. coli* dynamics. In particular, bacteriophage-induced mortality parameters exhibit strong negative PRCC values, indicating that increased predation substantially reduces *E. coli* concentrations. These findings confirm the critical role of biological control in enhancing wastewater treatment efficiency.

RESULTS

Simulation results reveal that:

Predation by bacteriophages is the most influential factor controlling the *E. coli* population, as confirmed by sensitivity analysis using Partial Rank Correlation Coefficient (PRCC = -0.65831) with Latin Hypercube Sampling (LHS).

Resistance development reduces the effectiveness of chemical disinfectants, necessitating complementary biocontrol strategies.

Numerical outcomes illustrate population dynamics across compartments, but results are interpreted separately to avoid conflating data with conclusions.

DISCUSSION

- The study demonstrates the utility of mathematical models in predicting *E. coli* behaviour in wastewater, particularly in exploring predation and resistance dynamics.
- Comparison with previous studies (Prakasha & Veerasha, 2020; Hurdoganoglu et al., 2022; Fauzi & Jamil, 2021) shows that our compartmental model captures additional interactions, such as bacteriophage predation and resistance development, which are often overlooked.
- Policy relevance is framed as theoretical guidance, highlighting that increased biocontrol strategies could improve wastewater management but require empirical validation before implementation.
- Limitations include reliance on estimated parameters without experimental calibration and omission of spatial heterogeneity. Future work should focus on multi-species modelling and empirical validation.

CONCLUSION

Effective wastewater management is critical for public health and SDG6. This study provides a mathematical framework for understanding *E. coli* dynamics under biotic and abiotic influences. Bacteriophage predation emerges as a key factor in controlling bacterial populations, suggesting avenues to enhance treatment efficiency. The model enriches scientific knowledge, guiding future research and policy while emphasizing the need for empirical data to strengthen predictions.

Detailed analytical derivations and supporting calculations are provided in the Supplementary Material.

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