**Archives of Pharmaceutical Sciences and Research** E-ISSN 0975-2633 | PRINT ISSN 0975-5284
Vol 16 Issue 2 51-56 June 2026 Review Article

# COMPUTATIONAL OPTIMIZATION STRATEGIES FOR MITIGATION OF ANTIBIOTIC RESISTANCE IN ECOSYSTEMS

**Pravardhana Prabhu, Swathi, Nithya, Deepika, Sai Lekhana D S**

International Institute of Medical Science and Technology Council, Bengaluru, Karnataka

## ABSTRACT

Antibiotic resistance has emerged as a global environmental and public health concern, with soil and aquatic ecosystems acting as critical reservoirs for antibiotic-resistant bacteria and antibiotic resistance genes. Continuous inputs of antibiotics from agricultural practices, wastewater discharge, and industrial effluents promote the persistence and dissemination of resistance across environmental compartments. Traditional mitigation approaches relying on experimental studies and regulatory frameworks often face limitations due to ecosystem complexity, resource constraints, and spatiotemporal heterogeneity. In this context, computational modeling and optimization strategies provide powerful tools for analyzing antimicrobial resistance dynamics and designing effective mitigation interventions.

This review presents a comprehensive synthesis of computational optimization strategies applied to mitigate antibiotic resistance in soil and aquatic ecosystems. The study examines a wide range of modeling approaches, including statistical models, machine learning techniques, simulation frameworks, and network-based analyses, highlighting their roles in understanding resistance evolution and transmission pathways. Furthermore, optimization methods such as evolutionary algorithms, multi-objective optimization, and hybrid AI-driven approaches are critically reviewed with respect to their applications in wastewater treatment optimization, pollution control, and intervention planning. Comparative assessments are provided to evaluate the strengths, limitations, and practical applicability of existing methods.

The review also identifies key challenges, including data scarcity, limited real-world implementation, and inadequate integration of soil-water interaction dynamics. Finally, future research directions are outlined, emphasizing the potential of digital twins, data-driven decision-support systems, and interdisciplinary frameworks for sustainable environmental antimicrobial resistance mitigation.

**KEYWORDS:** Antibiotic resistance, Computational optimization, Soil ecosystems, Aquatic environments, Environmental modeling, AMR mitigation, Decision-support system.

## 1.INTRODUCTION

Antibiotic resistance (AMR) is widely recognized as one of the most severe global health and environmental challenges of the twenty-first century. While the clinical dimensions of AMR have been extensively investigated, increasing evidence highlights the environment as a critical component in the emergence and dissemination of resistance (Larsson & Flach, 2021). Soil and aquatic ecosystems function as dynamic reservoirs of antibiotic-resistant bacteria (ARB) and ARGs, enabling their persistence, amplification, and transfer across ecological and biological boundaries (Sassi et al., 2025).

Soil ecosystems receive antibiotic inputs primarily through agricultural practices such as manure application, irrigation with treated or untreated wastewater, and land disposal of biosolids. These inputs exert selective pressure on native microbial communities, promoting the enrichment and horizontal transfer of ARGs (Cycon et al., 2019). Aquatic environments, including rivers, groundwater, lakes, and coastal systems, are similarly impacted by pharmaceutical residues and resistant microorganisms originating from wastewater treatment plants, hospital effluents, industrial discharge, and surface runoff (Meradji et al., 2025). The interconnectedness of soil and water systems further accelerates the spread of resistance across environmental compartments.

Despite growing awareness, mitigation of environmental AMR remains challenging. Conventional strategies are often limited by high costs, experimental constraints, and the inability to account for complex, nonlinear interactions within ecosystems (Patra & Dubey, 2025). Consequently, there is increasing interest in computational modeling approaches capable of integrating large-scale environmental, microbial, and genomic datasets to predict resistance dynamics and assess intervention outcomes

(Sutradhar et al., 2021).

Recent advances in computational intelligence, including machine learning, simulation-based modeling, and network analysis-have demonstrated considerable potential for AMR prediction, risk assessment, and decision support (Sakagianni et al., 2023). When coupled with optimization techniques such as evolutionary algorithms and multi-objective optimization, these models can identify optimal mitigation strategies under competing environmental and operational constraints. However, existing studies often remain fragmented, focusing on prediction rather than integrated mitigation, and rarely address soil-water interactions in a unified framework.

The objective of this review is to systematically analyze computational optimization strategies employed for mitigating antibiotic resistance in soil and aquatic ecosystems. Specifically, this study synthesizes existing modeling approaches, evaluates optimization-based intervention strategies, identifies critical research gaps,

and highlights future directions for developing scalable, data-driven, and sustainable solutions to environmental AMR.

## 2.REVIEW METHODOLOGY

This review adopts a structured and transparent literature review methodology to systematically analyze computational optimization strategies for mitigating antibiotic resistance in soil and aquatic ecosystems. The methodology was designed to ensure comprehensive coverage, reproducibility, and alignment with established best practices for environmental and interdisciplinary review studies.

### 2.1 Literature Search Strategy

A comprehensive literature search was conducted across major scientific databases known for high-quality peer-reviewed publications, including Scopus, Web of Science, PubMed, and IEEE Xplore. These databases were selected to capture relevant studies spanning environmental science, microbiology, computational modeling, and optimization methodologies. The search was performed for articles published between January 2015 and February 2026, reflecting recent developments in environmental antimicrobial resistance research and computational intelligence.

### 2.2Inclusion and Exclusion Criteria

To ensure relevance and quality, articles were selected based on predefined inclusion and exclusion criteria.

Studies were included if they

- Focused on antibiotic resistance or ARGs in soil and/or aquatic environments.
- Employed computational, modeling, or optimization-based approaches.
- Were published in peer-reviewed journals or reputable conference proceedings indexed in Scopus.

Excluded studies included purely clinical investigations without environmental relevance, non-computational experimental studies, non-English publications, editorials, and short communications lacking methodological detail.

### 2.3 Study Selection and Screening Process

The screening process was conducted in multiple stages following principles commonly recommended for structured environmental reviews. Initially, titles and abstracts were screened to eliminate irrelevant studies. Subsequently, full-text screening was performed to assess methodological rigor, computational relevance, and applicability to soil and aquatic ecosystems. Reference lists of selected articles were also examined to identify additional relevant studies, a practice frequently adopted in environmental AMR scoping and systematic reviews.

### 2.4 Data Extraction and Synthesis

From each selected article, key information was extracted, including ecosystem type (soil or aquatic), antibiotic or ARG focus, computational modeling technique, optimization strategy employed, application domain, and reported outcomes. The extracted information was synthesized using a qualitative thematic analysis. Studies were grouped into thematic categories such as predictive modeling, simulation-based analysis, optimization of treatment processes, and decision-support systems. Comparative synthesis approaches similar to those used in recent computational AMR modeling studies were adopted.

## 2.5 Analytical framework

An analytical framework was developed to compare computational optimization strategies based on their objectives, modeling assumptions, scalability, and practical applicability. Emphasis was placed on identifying strengths, limitations, and research gaps, particularly regarding real-world implementation and integrated soil-water system modeling. This framework supports a critical evaluation of existing methodologies and provides a structured basis for identifying future research directions.

## 3. REVIEW OF LITERATURE

Early investigations into antimicrobial resistance (AMR) largely focused on clinical and hospital settings. However, over the past decade, growing evidence has established the environmentparticularly soil and aquatic ecosystemsas a critical reservoir and transmission pathway for antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs). Larsson and Flach (2021) provided one of the most comprehensive environmental perspectives, emphasizing that antibiotic pollution in water and soil creates sustained selective pressure even at sub-inhibitory concentrations, thereby accelerating resistance evolution.

Soil ecosystems have been extensively reported as long-term reservoirs of ARGs due to repeated exposure from manure applications, biosolids, and reclaimed wastewater. Cycoń et al. (2019) demonstrated that antibiotic residues significantly alter soil microbial diversity and enzymatic activity, facilitating horizontal gene transfer among indigenous microbial populations. Their findings highlighted soil not as a passive sink but as an active evolutionary interface for resistance development.

Aquatic systems, especially wastewater treatment plants (WWTPs), rivers, and sediments, have been identified as resistance amplification hotspots. Meradji et al. (2025) showed that WWTP effluents remain major contributors of ARG dissemination, despite significant microbial load reduction during treatment. These findings reinforce the notion that conventional treatment processes are often insufficient to mitigate environmental AMR risks.

Recent literature increasingly adopts the One Health framework, recognizing the interconnectedness of human, animal, and environmental health. Sassi et al. (2025) emphasized that resistance transmission occurs across soil, water, and air compartments, driven by anthropogenic pressures such as agricultural runoff, pharmaceutical effluents, and untreated sewage.

Cheung et al. (2025) further highlighted fecal pollution as a key driver for AMR spread in aquatic environments, demonstrating strong spatial heterogeneity influenced by sanitation infrastructure, climatic variables, and population density. Collectively, these studies underscore the inadequacy of compartment-specific investigations and the need for integrated environmental assessments.

Jiang et al. (2024) proposed a rapid MLbased framework for quantifying AMR burden in aquatic environments using easily accessible environmental indicators, reducing computational time while maintaining high predictive accuracy. Similarly, Tong et al. (2024) developed a holistic hybrid modeling framework that integrates statistical and process-based models to predict spatiotemporal AMR hotspots in reservoirs, demonstrating improved reliability over single-method approaches.

Evolutionary algorithms and multi-objective optimization approaches are widely applied to wastewater treatment optimization, enabling trade-off analysis among ARG removal efficiency, operational cost, and environmental impact. Lu et al. (2024) reviewed biological treatment systems optimized for simultaneous antibiotic and ARG removal, highlighting the role of microbial community engineering and process parameter optimization.

## 4. RESEARCH GAPS IN EXISTING LITERATURE.

Despite rapid advancement, significant challenges continue to limit the real-world application of computational AMR mitigation strategies:

- Data scarcity and fragmentation, particularly for coupled soil–water systems
- Limited real-world validation beyond laboratory or pilot-scale studies
- Lack of standardized surveillance and modeling protocols, hindering comparability (Cheung et al., 2025)
- Model interpretability and regulatory acceptance, especially for AI-based approaches
- Scalability issues in transitioning from academic models to operational systems
- Weak integration with environmental policy and governance frameworks

Addressing these gaps requires interdisciplinary collaboration, harmonized monitoring frameworks, and closer alignment between computational research and environmental regulation

## 5. DISCUSSION

The reviewed literature clearly demonstrates that computational modeling and optimization are transforming environmental AMR assessment from reactive monitoring to proactive management. Advanced AI-based models enable rapid identification of resistance hotspots, while optimization strategies provide structured pathways for intervention planning.

However, most existing studies remain fragmented, focusing on either prediction or treatment optimization in isolation. The lack of integrated soil–water modeling and limited validation under real operational conditions represent major barriers to implementation. Hybrid frameworks combining mechanistic understanding with AI-driven prediction and optimization-based decision support are therefore essential.

Emerging concepts such as digital twins, AI-enabled surveillance platforms, and One Health-aligned decision frameworks represent promising future directions for scalable and sustainable AMR mitigation.

## 6. CONCLUSION

Antimicrobial resistance (AMR) in soil and aquatic ecosystems represents a critical and complex challenge at the interface of environmental science, public health, and sustainability. This review has systematically examined recent advances in computational modeling and optimization strategies developed to understand, predict, and mitigate the environmental dissemination of antibiotic resistance. The synthesis of statistical, mechanistic, machine learning , and hybrid modeling approaches demonstrates that computational tools are increasingly capable of capturing nonlinear, multiscale AMR dynamics that traditional experimental methods alone cannot adequately address.

Optimization strategies, including evolutionary algorithms, multi-objective optimization, and hybrid AI-driven frameworks, play a pivotal role in translating predictive insights into actionable mitigation strategies, particularly in wastewater treatment, nature-based remediation, and decision-support systems. Comparative analysis across approaches reveals that integrated modeling–optimization frameworks provide superior performance in terms of scalability, adaptability, and practical relevance. However, the review also highlights persistent challenges, such as data scarcity, limited real-world validation, and insufficient integration of soil–water interactions.

Overall, this review underscores that computational optimization represents a transformative pathway for advancing environmental AMR management. By bridging predictive modeling with intervention planning, these approaches enable a shift from reactive monitoring to proactive, data-driven mitigation. Continued interdisciplinary research and closer alignment between computational innovations, field validation, and policy frameworks are essential to realize their full potential in addressing the environmental dimension of antimicrobial resistance.

## 7. FUTURE RESEARCH DIRECTIONS

Future studies should focus on the following key directions to advance the field:

1.Integrated Soil–Aquatic Modeling: Develop unified modeling frameworks that explicitly capture soil-water interactions, including runoff, leaching, sediment transport, and microbial exchange pathways.

2.Hybrid and Interpretable AI Models: Combine machine learning with mechanistic modeling and explainable AI techniques to improve model transparency, reliability, and regulatory acceptance.

3.Real-World Validation and Scaling: Move beyond laboratory and pilot-scale studies by validating computational and optimization frameworks in full-scale wastewater treatment plants and agricultural systems.

4.Standardized Environmental AMR Data Platforms: Establish harmonized protocols and open data repositories to improve data availability, comparability, and reproducibility across regions and studies.

5.Optimization-Driven & Decision-Support Systems: Develop user-friendly, optimization-enabled decision-support tools for stakeholders, integrating environmental, economic, and policy constraints.

## 8. ACKNOWLEDGEMENT

The authors express their sincere gratitude to the International Institute of Medical Science and Technology Council (IIMSTC) for providing valuable internship support and research exposure. We also acknowledge Visvesvaraya Technological University (VTU) and the affiliated institutions of the authors, including Sir M Visvesvaraya Institute of Technology and Bapuji Institute of Engineering and Technology, for their academic support and guidance.

## 9. REFERENCE

1.Cycoń, M., Mrozik, A. and Piotrowska-Seget, Z. (2019) Antibiotics in the soil environment-degradation and their impact on microbial activity and diversity. Frontiers in Microbiology, 10, 338. https://doi.org/10.3389/fmicb.2019.00338

2.Larsson, D.G.J. and Flach, C.F. (2021) Antibiotic resistance in the environment. Nature Reviews Microbiology, 20(5), pp. 257–269. https://doi.org/10.1038/s41579-021-00649-x.

3.Meradji, S., Basher, N.S., Sassi, A., Ibrahim, N.A., Idres, T. and Touati, A. (2025) The role of water as a reservoir for antibiotic-resistant bacteria. Antibiotics, 14(8), 763. https://doi.org/10.3390/antibiotics14080763

4.Patra, M. and Dubey, S.K. (2025) Antimicrobial resistance transmission in environmental matrices: current prospects and future directions. Reviews of Environmental Contamination andToxicology, 263, Article 20. https://doi.org/10.1007/s44169-025-00096-2.

5.Sakagianni, A., Koufopoulou, C., Feretzakis, G., Kalles, D., Verykios, V.S. and Myrianthefs, P. (2023) Using machine learning to predict antimicrobial resistance-A literature review. Antibiotics, 12(3), 452. https://doi.org/10.3390/antibiotics12030452

6.Sassi, A., Basher, N.S., Kirat, H., Meradji, S., Ibrahim, N.A., Idres, T. and Touati, A. (2025) The role of the environment (water, air, soil) in the emergence and dissemination of antimicrobial resistance A one health perspective 14(8),764. https://doi.org/10.3390/antibiotics14080764

7.Sutradhar, I., Ching, C., Desai, D., Suprenant, M., Briars, E., Heins, Z., Khalil, A.S. and Zaman,M.H. (2021) Computational model to quantify the growth of antibiotic-resistant bacteria in wastewater. mSystems, 6(3), e00360-21. https://doi.org/10.1128/mSystems.00360-21.

8.Calero-Cáceres, W., Tavella, R. A., Sellera, F. P., Balcazar, J. L., Rodriguez-Manzano, J., Lincopan, N., … Furlan, J. P. R. (2026). Artificial intelligence for early detection and risk prediction of antimicrobial resistance in aquatic ecosystems. npj Antimicrobials and Resistance, 4, Article 20. https://doi.org/10.1038/s44259-026-00192-w

9.Cheung, C., Naughton, P. J., Dooley, J. S. G., Corcionivoschi, N., & Brooks, C. (2025). The spread of antimicrobial resistance in the aquatic environment from faecal pollution: A scoping review. Environmental Monitoring and Assessment, 197, 467. https://doi.org/10.1007/s10661-025-13860-7

10.Jiang, P., Sun, S., Goh, S. G., Tong, X., Chen, Y., Yu, K., & Gin, K. Y. H. (2024). A rapid machine learning approach for quantifying antimicrobial resistance burden in aquatic environments. Water Research, 262, 122079. https://doi.org/10.1016/j.watres.2024.122079.

11.Lu, Z., Liu, G., Xie, H., Zhai, Y., & Li, X. (2024).

Advances and solutions in biological treatment for antibiotic wastewater with resistance genes: A review. Journal of Environmental Management, 368, 122115. https://doi.org/10.1016/j.jenvman.2024.122115

12. Mukhopadhyay, R., Drigo, B., & Sarkar, B. (2024). Mitigation potential of antibiotic resistance genes in water and soil by clay-based adsorbents. npj Materials Sustainability, 2, Article 26. https://doi.org/10.1038/s44296-024-00030-y.

13. Tong, X., Goh, S. G., Mohapatra, S., Tran, N. H., Zhang, J., He, Y., & Gin, K. Y. H. (2024). Predicting antibiotic resistance and assessing environmental risk using a holistic modeling framework. Environmental Science & Technology, 58(15), 6781–6792. https://doi.org/10.1021/acs.est.3c10467.