



COMPUTATIONAL MODELING FOR PREDICTING ANTIBIOTIC RESISTANCE RISK IN SOIL ECOSYSTEM

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ABSTRACT

Antibiotic contamination in soil ecosystems has emerged as a major environmental concern due to its role in accelerating antimicrobial resistance (AMR). This review aims to evaluate computational modeling approaches used to predict antibiotic behavior and resistance risk in soil environments. A structured literature review was conducted using peer-reviewed articles focusing on sorption, persistence, and toxicity modeling. Computational approaches such as QSAR, pedotransfer functions, and machine learning models were analyzed. The findings indicate that antibiotic fate in soil is strongly influenced by environmental factors such as pH and organic carbon content. Hybrid modeling approaches integrating molecular descriptors and environmental parameters showed improved predictive accuracy. Additionally, even low concentrations of antibiotics were found to contribute to resistance development through genetic mechanisms. Computational models are effective tools for predicting AMR risk in soil ecosystems. However, improved datasets and integrated modeling frameworks are required to enhance prediction reliability and environmental relevance.

KEYWORDS: Antibiotic residues; Antimicrobial resistance; Ecotoxicity; Persistence; Soil ecosystem; Sorption; Computational modelling.

1. INTRODUCTION

Antibiotics usage in clinical, agriculture, and veterinary applications has surged over time. As a result, antibiotics have entered environmental compartments such as soil ecosystems. Studies show that ~30–90% of consumed antibiotics are excreted in active form or partially metabolized forms and eventually reach the soil environment through various routes such as wastewater treatment plant effluents, agricultural runoff water and manure application.

In the environment, antibiotics are subjected to complex interactions with environmental matrices followed by various processes such as sorption, degradation, and transport mechanisms, which ultimately decide their fate, persistence, and bioavailability. Sorption interactions largely dictate mobility yet influence persistence and accumulation of antibiotics in soil systems.

Persistence of antibiotics in soil poses threats to antimicrobial resistance due to various selection pressures antibiotics impose on microbial communities leading to antibiotic resistance. Antibiotics concentrations below minimum inhibitory concentration (MIC) promote mutations and horizontal transfer of ARGs.

Experimentally determining the fate and effects of antibiotics is generally very expensive, time-consuming, and difficult to upscale. Therefore computational approaches such as QSAR, PTF, and machine learning have emerged as powerful alternatives for predicting environmental fate and toxicity endpoints.

This review aims to analyze QSAR modeling approaches for predicting antibiotic fate in soil ecosystems and implications for AMR risk assessment.

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

The current review was established by literature search using online available scientific databases and subsequently reviewing published articles from established scientific peer-reviewed journals like Environmental Sciences Europe, Environmental Science and Pollution Research, Frontiers in Environmental Science, Ecotoxicology and Environmental Safety, Toxicology Research, Environment International, Journal of Hazardous Materials, ACS Environmental Science & Technology, Oxford Academic (FEMSEC), PubMed and PMC.

The reviewed studies were selected to cover three distinct dimensions related to the environmental dimension of antibiotic resistance, namely antibiotic behaviour in soil environments, modelling approaches developed for antibiotic persistence in soil, and the environmental risk of antimicrobial resistance.

In complementary literature, Alhalabi et al. (2024) illustrated how pharmaceutically active compounds may enter the environment and interact with the soil and its properties. Neira-Albornoz et al. (2024), Li et al. (2026) and Barua et al. (2026) addressed modelling of sorption and development of machine learning/AI methods to predict the soil-related behaviour of PPCPs. Degradation and persistence was addressed by Banjare et al. (2024). These studies served as background to the present review.

2.2 Inclusion and Exclusion Criteria

Studies were selected on the basis of their relevance to the topic of the review as well as their methodological approach.

Inclusion Criteria

1. Alhalabi, A.; Fahrenholz, N.; Kaupenjohann, M.: Fate of selected pharmaceuticals in field soils— An empirical approach. In: Environmental Science and Pollution Research 25 (2018), S. 28991–29004. doi: 10.1007/s11356-018-3234-5, urn: FN: 676813151819918.

2. Neira-Albornoz, A. et al. 2024; Li, Z. et al. 2026; Barua, D. et al. (2016) Studies on environmental behavior such as sorption, persistence, toxicity or resistance (Banjare et al., 2024).

3. Peer-reviewed journal publications

Exclusion Criteria

1. Studies not focused on soil systems
2. Studies without computational modeling components
3. Studies not directly related to antibiotic fate or resistance

2.3 Study Selection and Screening Process

The study selection process involved the paper being read and then categorized according to primary purpose.

The studies were grouped into the following categories:

1. Mechanism of interaction between structure and surrounding soil, and structural behavior affecting the environment (Alhalabi et al.)
2. These computational modeling approaches are explored in Neira-Albornoz et al. (2024) and Li et al. (2026).
3. Toxicity (Banjare et al., 2024; Barua et al., 2026) and persistence (Banjare et al., 2024; Barua et al., 2026)

The studies were then assessed for the inclusion of specific details.

1. A computational modeling component
2. At environmental level measurable outputs of the compounds are found in processes such as sorption, degradation or toxicity.
3. Direct relevance to soil ecosystems

Studies that met the above inclusion criteria were selected for the final data analysis.

2.4 Data Extraction and Synthesis

Study characteristics were compiled from relevant sources of data and addressed in pre-defined study categories.

Model Type

These models were categorised.

1. QSAR and q-RASAR models (Banjare et al., 2024).
2. QSAR and PTF comparison (Neira-Albornoz et al., 2024).
3. Machine learning-based QSAR models (Li et al., 2026).
4. AI-based toxicity prediction models (Barua et al., 2026).

Molecular Descriptors

Studies on the behavior of antibiotics in aquatic environments and living organisms on the basis of their molecular properties such as hydrophobicity, molecular weight, degree of ionization, and structure etc.

Banjare et al. (2024) studied degradation influenced by molecular structure, while Li et al. (2026) used these descriptors as inputs for a machine learning model.

Soil Parameters

Soil parameters of importance include: soil organic carbon, soil pH, cation exchange capacity and surface properties.

The behavior of imazapire in soils was investigated by Alhalabi et al. (2024) and indicated that increase of sorption with organic carbon were observed while decrease of sorption with increase of pH were observed. In addition, Li et al. (2026) suggested that toxicities of imazapire to earthworms were influenced by several soil conditions.

Output Variables

The extracted outputs include:

- Sorption coefficients (Alhalabi et al., 2024)
- Degradation half-life (Banjare et al., 2024)
- Toxicity predictions (Li et al., 2026)
- Multi-endpoint toxicity assessments (Barua et al., 2026)

Synthesis Approach

The results obtained from column experiments were used as comparative data among studies to investigate the relationship between biodegradation characteristics and molecular properties, leaching potentials, and soil environmental changes.

5.5 Analytical Framework

The analytical framework of the review was organized around the themes present in the included studies, and presented in three key sections.

1. Soil–Antibiotic Interaction

The section is dedicated to discuss how antibiotics may enter the soil environment and interact with certain soil properties, primarily based on Alhalabi et al. (2024).

2. Computational Modeling Approaches

Different modelling methods such as QSAR, PTF and machine learning methods were reviewed for their application.

3. AMR Risk Prediction

This section discusses the relation between persistence and environmental behaviour of antibiotics, and how this relates to antimicrobial resistance, Banjare et al. (2024) and others.

3. REVIEW OF LITERATURE

Alhalabi and colleagues (2024) noted that you can't rely on a single model to predict the behaviour of antibiotics in soil, a series of studies suggests that the sorption of antibiotics could depend on multiple factors simultaneously including the chemical structure of the antibiotic, the amount of organic carbon in the soil, pH and aqueous solution factors. Sorption coefficients for the same antibiotic differed by orders of magnitude for different soils, offering a glimpse into the considerable variability involved.

Neira-Albornoz et al. (2024) performed an analysis of QSAR and PTF models for predicting leaching of chemical compounds which showed that both approaches have their

own limitations to model real-world scenarios by focusing on either molecular or soil properties. However, the study demonstrated that an integrated use of both methodologies results in improved predictions and usability for regulatory purposes.

Banjare et al. (2024) looked into persistence as a driver of antimicrobial resistance. They developed QSAR and q-RASAR models to predict antibiotic persistence/dissipation in soil and found good predictivity. Interestingly, the authors found that even sub-inhibitory concentrations of antibiotics can stimulate mutation and horizontal gene transfer events. This highlights that persistence is not an irrelevant parameter, but a parameter that is directly linked to AMR. Future models for predicting potential trends in resistance should thus include some measure of persistence.

Li et al. (2026) utilized machine learning approaches to develop QSAR models for soil toxicity prediction. It is noteworthy that besides the molecular structure of the tested chemicals, the QSAR models incorporated soil organic matter and pH as relevant factors influencing toxicity that were normally neglected by conventional QSAR models. SHAP (SHapley Values) values analysis revealed the major contributors responsible for toxicity prediction.

Barua et al. (2026) provide a broader perspective on the matter. Whilst noting that AI/machine learning approaches are going to be game changers for predicting environmental toxicology and enabling high-throughput prediction of multiple toxicity endpoints simultaneously with rapid modelling and prediction.

capabilities and reduction in animal testing etc., they emphasize that such potential can only be realized by development of clear guidelines regarding their regulated use in environmental toxicology.

4. RESEARCH GAPS IN EXISTING LITERATURE.

While significant advances have been obtained by using computational models for assessing the

risk of developing antibiotic resistance in soil ecosystems, relevant research gaps have been identified. A critical point is the lack of robust, high-quality, and sufficient datasets. As many available data are mostly related to controlled laboratory experiments, important variables, such as critical soil properties including pH, organic carbon and antimicrobial resistance genes (ARG), are generally not considered within model development, and their incorporation to build realistic models is highly recommended.

For instance, microbial dynamics such as gene mobilization, translocation and dispersal, community assembly and metabolic interactions (i.e., co- metabolic interactions) that control antibiotic-resistant bacteria ecology and the development of resistance are often hardly considered. Soil is a dynamic, multiphasic, complex and structured environmental medium that may alter, either temporarily or permanently, the properties of toxic substances, including antibiotics. It is thus common that several factors such as climate variability, seasonality and spatial variability within a single field, have been rarely integrated in existing predictive models.

Many existing environmental fate models for antibiotics lack environmental realism, as models do not account for in-field variability that may have measurable effects on environmental exposure, e.g., movement in irregular micro-porous media, spatial and temporal heterogeneity, non-equilibrium sorption/desorption. In addition, model development is generally uncoupled from validation, model parameter estimation and experimental design. A further significant gap is related to model reproducibility and the use of standardized modelling protocols and models validation approaches. In particular, only limited experiences of model validation at field scale have been reported. Indeed, while good results have been obtained in relating model predictions to experimental data collected in controlled laboratory conditions and in small-scale field experiments, very limited cases of model validation using long-term

monitoring data from real-field environments have been documented. Interpretation, transparency and predictive capabilities of novel data-driven AI/Machine Learning models also deserve special attention.

Furthermore, except for a few studies, little connection is currently made between model predictions, such as persistence, mobilization potential, toxicity, etc., and actual resistance outcomes (e.g., ARG copy numbers, mobile genetic elements abundance). Most predictive models are still focused on using single antibiotics. The effects of exposure to combinations of antibiotics and other pollutants such as heavy metals and mixtures of organic pollutants, that have the potential to synergistically increase the risk of generating resistance, have rarely been evaluated. Additional limitations relate to limited model scalability and transferability across different sites and soils. Finally, as a general rule, integration between models and existing risk assessment frameworks and environmental policies and management practices is highly recommended to increase their value and relevance in practical applications to manage the risk of developing AR.

5. DISCUSSION

The reviewed literature shows that computational modeling is essential for improving environmental AMR assessment. It allows for faster and more efficient predictions of antibiotic behavior in soil systems. Compared to traditional experimental methods, models like QSAR and machine learning offer better scalability and predictive power.

However, most models struggle to fully capture the complex interactions in soil, such as changes in pH, organic carbon levels, and microbial activity. Research indicates that relying on a single modeling approach often results in oversimplified predictions.

Hybrid modeling approaches that combine mechanistic and AI-based methods show improved accuracy and reliability. Additionally, antibiotic persistence has been recognized as a

key factor in antimicrobial resistance, even at low concentrations.

Despite progress, challenges remain. Issues such as the lack of real-world validation, limited datasets, and poor integration with treatment strategies hinder practical application.

6. CONCLUSION

Computational modeling has a significant role to play in predicting the risk of developing antibiotic resistance in the soil ecosystem. Antibiotic's behavior in the environment is largely determined by its sorption, persistence, and toxicity.

QSAR models can provide a strong basis for prediction, but typically only use molecular descriptors, in contrast Machine learning models are capable of integrating environmental variables to provide the most accurate and realistic predictions. Hybrid approaches also perform well.

We demonstrate that persistence of antibiotic concentrations in the environment drives the development of AMR, even at low exposure. To accurately predict this risk, predictive models must incorporate persistence as well as host-microbe and microbe-microbe interactions.

Future research could require the development and utilization of standardized datasets, the inclusion of explainable AI methods and a biological perspective to the current models.

7. FUTURE RESEARCH DIRECTIONS

Future studies should concentrate on these key areas:

- Integrated Soil–Aquatic Modeling

Develop frameworks that capture soil-water interactions, including leaching, runoff, and transport processes.

- Hybrid and Explainable AI Models

Merge machine learning with mechanistic models and enhance interpretability for better reliability and regulatory use.

- Real-World Validation and Scaling

Validate models with field-scale data and implement them in real environmental and agricultural systems.

- Standardized Environmental Data Platforms

Create shared datasets and standardized protocols to enhance data quality and model reproducibility.

- Optimization-Based Treatment Integration

Connect predictive models with treatment strategies, such as adsorption, AOPs, and biodegradation, to support effective decision-making.

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9. REFERENCES

1. Alhalabi.A.M.,Meetani.M.A.,Shabib.A.,Maraqa.M.A; Environ. Sci. Eur., 2024; 36, 161.
2. Banjare.P.,Singh.R.,Pandey.N.K.,Matore.B.W.,Murmua.A.,Singh.J.,Roy.P.P; Toxicol. Res., 2024; 13.
3. Li.S.,Zhang.P.,Zhou.R.,Bu.Y.,Zhang.H; Ecotoxicol. Environ. Saf., 2026; 311, 119804.
4. Barua.S.,Balaji.B.,Balaji.S; Environ. Sci. Pollut. Res., 2026.
5. Neira-Albornoz.A.,Martínez-Parga-Méndez.M.,González.M.,Spitz.A; Front. Environ. Sci., 2024; 12
6. 1379283.
7. ScienceDirect Study; J. Hazard. Mater., 2026.
8. Environmental fate study; Environ. Int., 2016.
9. Hazardous materials study; J. Hazard. Mater., 2024.
10. PMC Study; Toxicol. Res., 2024.
11. ACS Study; Environ. Sci. Technol., 2024.
12. ACS Ecosystem Study; Environ. Sci. Technol., 2017.
13. Oxford Academic Study; FEMS Microbiol. Ecol., 2016.
14. PubMed Study; Environ. Sci. Pollut. Res., 2018.