

Machine Learning in Epidemic Modelling: A Literature Review

1. Introduction

Epidemic modelling plays a vital role in public health by providing insights into disease transmission dynamics and guiding effective intervention strategies. Classical frameworks such as the Susceptible-Exposed-Infectious-Recovered (SEIR) model and agent-based simulations are valued for their theoretical clarity and mechanistic structure (Kermack and McKendrick, 1927; Kerr et al., 2021). However, these models often rely on simplifying assumptions, such as homogeneous mixing and fixed parameters, limiting their ability to represent the complexity of real-world outbreaks marked by diverse behaviours and rapid change. Such rigidity may reduce their usefulness in fast-evolving epidemic contexts where adaptability is crucial (Wang et al., 2015).

Machine learning (ML) offers a flexible, data-driven alternative capable of detecting nonlinear patterns within high-dimensional, heterogeneous datasets (Mooney and Pejaver, 2018; Wang et al., 2021). Its capacity to adapt to incoming data has led to rapid uptake during the COVID-19 pandemic, using methods such as Random Forests, XGBoost, Long Short-Term Memory (LSTM) networks, and hybrid models that integrate ML with traditional epidemiological frameworks (Zheng et al., 2023; Zhou et al., 2023; Baccega et al., 2024; Delli Compagni et al., 2022).

Despite these advances, several challenges remain. The “black-box” nature of many ML models undermines interpretability, which is essential for trust and decision-making in public health (Topol, 2019; Ribeiro et al., 2016). Additionally, inconsistent validation methods and limited benchmarking against classical models raise questions about their generalisability and reliability (Dautel et al., 2023; Gaskin et al., 2024).

This review synthesises recent secondary research on the integration of ML into epidemic modelling, with a focus on methodological robustness, predictive performance, and interpretability. It aims to highlight key limitations, explore emerging opportunities, and outline best practices for future forecasting frameworks.

2. Overview of Machine Learning Techniques in Epidemic Modelling

ML has quickly expanded the range of methods used for epidemic forecasting, supported by diverse data sources and the urgent needs of global public health. These models in epidemic contexts broadly fall into three categories: supervised learning, time-series deep learning, and hybrid approaches that combine ML with mechanistic models from epidemiology (Shakeel et al., 2021).

Supervised learning remains a foundational approach, with algorithms such as Random Forest (RF), Gradient Boosting Machines (e.g., XGBoost), and Support Vector Machines (SVMs) favoured for handling nonlinearities and mixed data types, while offering some interpretability through feature importance measures (Zheng et al., 2023; Shakeel et al., 2021). These models typically rely on structured tabular inputs such as demographics, clinical indicators, and environmental factors (Ramírez del Real et al., 2022; Vaid et al.,

2020). However, their reliance on static features and limited temporal context constrains adaptability, potentially overlooking evolving epidemic dynamics and interactions (Feng et al., 2022; Kim et al., 2025).

Deep learning models, notably recurrent neural networks (RNNs) like LSTM and Gated Recurrent Units (GRUs), excel at capturing temporal dependencies in epidemic time-series data (Zhou et al., 2023; Feng et al., 2022). CNN-LSTM hybrids extend this by extracting spatial and contextual patterns, thereby enhancing predictive accuracy (Alizadeh et al., 2025). Nevertheless, these models suffer from interpretability deficits and susceptibility to overfitting, particularly when trained on noisy or limited datasets, emphasizing the necessity for rigorous validation (Kim et al., 2025; Wang et al., 2021).

Hybrid models attempt to reconcile the interpretability of compartmental epidemiological frameworks, such as SEIR, with the flexibility of ML by embedding machine learning for parameter estimation or incorporating genomic variant data (Baccega et al., 2024; Li et al., 2023; Delli Compagni et al., 2022). While promising, this integration amplifies complexity in validation, requiring well-defined frameworks to ensure reliability across diverse epidemic scenarios (Dautel et al., 2023).

ML applications extend beyond COVID-19 to diseases like influenza and dengue, demonstrating adaptability across pathogens and contexts (Rama et al., 2025; Smith et al., 2025). These models leverage multimodal inputs such as case data, hospital admissions, electronic health records, mobility, wastewater, and social media signals. This offers a richer predictive scope but also introduces challenges in data harmonisation, noise management, and generalisability (Vaid et al., 2020; Adiga et al., 2020; Vaughan et al., 2023; Ward et al., 2022; Gaskin et al., 2024).

A notable gap remains in standardised validation and benchmarking. Many studies lack rigorous evaluation against traditional epidemiological models and often overlook uncertainty quantification. This limits confidence in the generalisability and practical usefulness of ML forecasts (Shakeel et al., 2021; Dautel et al., 2023; Gaskin et al., 2024).

In summary, while ML techniques substantially advance epidemic forecasting capabilities, their true efficacy hinges on methodological rigor in data handling, validation, and interpretability. The following sections delve deeper into these critical implementation considerations.

3. Implementation and Methodological Approaches

The performance and credibility of ML-based epidemic forecasting models depend fundamentally on rigorous implementation, encompassing data preparation, model training, evaluation, and transparency. Considerable variation exists across the literature in how these stages are conducted, affecting both scientific robustness and practical applicability (Shakeel et al., 2021; Dautel et al., 2023). This inconsistency complicates direct comparisons and may erode confidence in model outputs. Without standardised validation and transparent reporting, even promising models risk overfitting or producing misleading forecasts, limiting their reliability for guiding urgent public health decisions. (Shakeel et al., 2021; Dautel et al., 2023).

Data preprocessing is a critical initial step. Common practices include removing anomalies, imputing missing values, and applying transformations to improve data

distribution. Techniques such as log-scaling and smoothing are frequently used to stabilise volatile case counts, while feature selection, guided by statistical or epidemiological criteria, helps reduce dimensionality and enhance interpretability (Lucas et al., 2021). However, transparency in reporting these steps is often inadequate, impeding reproducibility and introducing potential bias (Zhou et al., 2023). Moreover, data augmentation strategies like rolling windows and synthetic data generation can expand training datasets but risk embedding artificial patterns, which may mislead models if not carefully validated (Gaskin et al., 2024).

Model training methodologies also vary widely. The commonly used 80:20 train-test split is convenient but often fails to preserve the temporal dependencies that are critical in epidemic data. More robust validation techniques such as k-fold cross-validation and walk-forward validation are underutilised, despite their importance in assessing generalisability and mitigating data leakage (Vaid et al., 2020; Smith et al., 2025). External validation on independent populations or regions remains rare, though it is critical to evaluate model applicability across diverse epidemic contexts (Dautel et al., 2023). Many hybrid models incorporate ongoing retraining to adapt to evolving outbreaks, yet often lack transparency about retraining frequency and convergence criteria. (Li et al., 2023; Alizadeh et al., 2025).

Evaluation metrics predominantly focus on Root Mean Squared Error (RMSE), Mean Absolute Error (MAE), and Area Under the Curve (AUC) for classification. Yet, these metrics alone are insufficient, as they fail to capture forecast uncertainty or assess the practical implications of predictions for public health decision-making (Shakeel et al., 2021; Wang et al., 2021). Probabilistic methods for expressing forecast confidence are

emerging but remain inconsistently applied and lack standardisation (Gaskin et al., 2024). Furthermore, benchmarking against traditional epidemiological models or across ML techniques is inconsistently performed, which limits reproducibility, hampers comparability, and hinders practical adoption (Saleem et al., 2022).

Reproducibility is a pressing concern. Open-source platforms like Covasim exemplify best practice by providing transparent code, data, and detailed methodology, supporting peer review and real-world use (Kerr et al., 2021). In contrast, many ML studies rely on proprietary datasets or omit critical methodological details, undermining replicability and scientific integrity (Dautel et al., 2023). There is an urgent need for standardised validation protocols, reproducibility checklists, and documentation standards, including model cards and data provenance, to foster trust among researchers and public health practitioners (Ueda et al., 2024; de Manuel et al., 2023). Benchmark resources such as the Johns Hopkins COVID-19 dataset (Dong et al., 2020) and Covasim (Kerr et al., 2021) support reproducibility, yet remain inconsistently used, limiting comparability across studies.

A notable tension exists between the development of innovative deep learning architectures and the necessity for methodological clarity. Novel models may deliver superior predictive performance but often at the cost of interpretability and replicability, increasing the risk of overfitting and limiting usability in public health settings (Kim et al., 2025). Striking a balance between experimental innovation and rigorous validation with transparent reporting is essential for the successful integration of ML into epidemic response.

In summary, without transparent and rigorous implementation, along with comprehensive evaluation that includes ethical considerations and uncertainty quantification, even the most advanced ML models risk failing to provide reliable and actionable forecasts for epidemic management.

4. Interpretability and Practical Use

Interpretability is a critical consideration when applying ML to public health, where decisions based on model outputs can have profound consequences. Many high-performing models, particularly deep neural networks, function as opaque systems that offer limited insight into how predictions are made (Topol, 2019; Ribeiro et al., 2016). This lack of transparency raises accountability concerns, reduces stakeholder trust, and obstructs practical adoption in policy contexts. It may also worsen health inequities by concealing biases embedded in training data and algorithmic design, emphasising the ethical importance of interpretable frameworks (de Manuel et al., 2023).

Deep learning models such as LSTM networks and Convolutional Neural Networks (CNNs) can identify complex temporal and spatial patterns in epidemic data. However, their internal processes often remain unclear. This lack of clarity can undermine the justification of interventions like mobility restrictions or vaccination strategies, which require trust and transparency (Kim et al., 2025). To improve understanding, post hoc tools such as LIME and SHAP have been introduced. These techniques aim to explain individual predictions by quantifying feature contributions, providing insights into how variables like population density, mobility, and social behaviours influence outcomes.

However, the consistency and reliability of these tools remain debated (Ribeiro et al., 2016; Zheng et al., 2023).

Interpretability is not only a technical requirement but also a foundation for public confidence. In healthcare, responsible AI must be accurate, understandable, and justifiable to enable equitable and targeted action (Topol, 2019; Ueda et al., 2024). Yet many current practices treat interpretability as a secondary consideration rather than a design priority. Models that identify key risk factors such as vaccination rates or socioeconomic indicators can help address disparities and improve resource allocation. However, their value is reduced if the rationale behind predictions is not clearly communicated (Alkhanbouli et al., 2025). Building interpretability into the design process from the outset is increasingly seen as best practice, but implementation remains inconsistent and often superficial, undermining intended transparency (Alkhanbouli et al., 2025).

Literature continues to reflect these inconsistencies. Tree-based models like Random Forest and XGBoost offer some transparency through feature importance scores, supporting their use in public health discussions (Zheng et al., 2023). In contrast, many deep learning methods favour performance over interpretability, limiting trust when used to inform large-scale decisions (Kim et al., 2025). This gap also raises ethical concerns, particularly when models risk reinforcing social inequities without offering clear causal explanations (de Manuel et al., 2023).

The absence of interpretability continues to limit model adoption at the national policy level. While some applications have proven helpful in hospital planning and clinical forecasting (Delli Compagni et al., 2022; Vaid et al., 2020), few have meaningfully

shaped national policy, exposing a real-world disconnect. Public health authorities need both accurate forecasts and transparent reasoning to ensure accountability. Without clarity, even effective models remain confined to research settings.

Traditional epidemiological models such as SEIR retain an advantage due to their simple structure and understandable parameters (Kermack and McKendrick, 1927).

Hybrid models that embed ML into mechanistic systems offer a promising balance, but still require advanced techniques to ensure outputs are clear and actionable (Baccega et al., 2024; Li et al., 2023).

In conclusion, advancing interpretability alongside accuracy is essential for making ML a trusted component of epidemic forecasting. Incorporating explainability tools into the development process will improve transparency, foster trust, and support more effective public health decision-making.

5. Challenges, Gaps, and Opportunities

Despite many recent advances, ML in epidemic forecasting still faces important challenges. A major issue is data quality and availability. High-resolution, timely, and representative data are often lacking, particularly in low-resource settings, which limits fair and effective model application (Srivastava, 2023). Underreporting, delays in reporting, and inconsistent case definitions undermine reliability and make it difficult to compare results across locations or time periods (Vaughan et al., 2023; Adiga et al., 2020). In addition, combining and cleaning data from diverse sources such as clinical records, mobility reports, social media, and wastewater surveillance introduces

substantial methodological complexity. These challenges require transparent and robust approaches to ensure data integrity (Mohammed et al., 2022).

A critical gap remains in methodological standardisation. Variation in data preprocessing, model development, validation protocols, and reporting metrics limits comparability and restricts the accumulation of generalisable knowledge. The absence of benchmark datasets and consistent validation frameworks exacerbates this fragmentation, reducing confidence in model robustness and hindering broader applicability (Shakeel et al., 2021; Saleem et al., 2022).

Ethical and fairness concerns are often overlooked. Models trained on unrepresentative datasets risk reinforcing healthcare disparities related to socioeconomic status, ethnicity, and geographic location (Ueda et al., 2024; Gu et al., 2025). Addressing these risks requires the integration of bias mitigation strategies that include fairness-aware objectives and inclusive data collection practices (Gu et al., 2025). Furthermore, privacy concerns involving sensitive health and behavioural data require clear consent procedures, strong data security, and accountability mechanisms. These safeguards remain insufficiently developed in many current applications (Ueda et al., 2024).

Nevertheless, there are significant opportunities for progress. Hybrid models that combine mechanistic epidemiological knowledge with data-driven ML can support interpretable and adaptive forecasting (Li et al., 2023). Advances in explainable artificial intelligence, federated learning, and privacy-preserving methods offer ways to improve transparency and security without reducing data utility (Vaughan et al., 2023).

Participatory approaches that involve public health experts, data scientists, and

ethicists can help align technical developments with societal needs and policy priorities (Chharia et al., 2024).

Investments in open data initiatives, standardised ontologies, and collaborative platforms can enhance reproducibility and promote cumulative progress (Mohammed et al., 2022). Continued model evaluation and transparent reporting will also be essential for building trust and scaling ML solutions across diverse public health contexts (Vaughan et al., 2023; Chharia et al., 2024; Smith et al., 2025).

6. Conclusion

Machine learning has significantly broadened the capabilities of epidemic forecasting by enabling the analysis of complex, high-dimensional datasets and uncovering nonlinear relationships often missed by traditional models. The current literature underscores ML's strong potential to improve outbreak predictions, guide public health interventions, and complement classical epidemiological approaches.

Nonetheless, effective deployment of ML models requires more than technical sophistication. Methodological rigor, transparency, interpretability, and ethical considerations are equally vital for fostering public trust, ensuring scientific credibility, and securing policy relevance. While some studies exemplify high standards, persistent gaps remain in reproducibility, bias mitigation, and practical usability.

To fully harness ML's promise in epidemic modelling, the field must prioritize robust validation frameworks, transparent reporting, ethical safeguards, and user-centered design principles. Achieving this will demand collaborative efforts that integrate domain

expertise, governance structures, and technological innovation. Such integration is essential for advancing ML as a trusted, impactful tool for managing current and future public health crises.

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