A Review on the Role of Machine Learning in Predicting the Spread of Infectious Diseases

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Abstract

AI and the development of the ML system are expected to play a crucial role in preventing and controlling infectious diseases as part of global health issues. Typically, conventional epidemic models give a narrow perspective of the distribution of diseases and their causes, which leads to the use of AI/ML solutions. Some of these tools utilize genomic data and environmental and patient information to boost forecasts' accuracy and facilitate real-time disease surveillance. The human-driven models of pandemic identification were replaced by sophisticated artificial intelligence models such as deep learning and advanced neural networks indicating patterns, the possibility of future outbreaks, and driving the concept of public health interventions. Many examples can be provided to support the efficiency of ML's approaches to combating antimicrobial resistance, tuberculosis relapse, and the spatial-temporal modeling of an alternative disease such as measles or COVID-19; nonetheless, data standardization, scaling, ethics, and bias issues are limitations to the application of such solutions. Controlling unfairness consists of the problem of transparency, patient data confidentiality, and disparities in the deployment of AI systems. However, practical and comparable implementations of these systems require cross-sector cooperation and global data sharing for varied conditions in the broader healthcare environment. Future developments point to the opportunity to enrich epidemic prediction models by blending genomic precision systems, explainable artificial intelligence, and interdisciplinary studies. This review provides evidence for how AI/ML has revolutionized infectious disease management, calls for responsible innovation and ethical deployment of AI, and encourages international collaborations to safeguard the global health sector against new and emerging diseases. Subsequently, unexpected events with high fatality rates and global impact, such as disease outbreaks, epidemics and pandemics, are still a threat to life; therefore, the ability of AI and ML to advance epidemic preparedness and response in the future is promising to enhance global health protection to future pandemics.

Keywords: Artificial intelligence; Machine learning; Epidemic prediction; Infectious diseases; Public health; Data integration

1. Introduction

The context of epidemics and pandemics has created considerable challenges to the health systems across the globe and has incurred a huge imprint on global health dynamics. COVID-19, Zika, and Ebola are examples of diseases that require proper models for predicting how to control their spread. Standard methods of

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studying the spread of disease, based on linear epidemiology models, have resulted in limitations in elucidating how diseases evolve. As a result, authors introduced more efficient technologies, such as AI, ML, and mathematical modeling, to predict further trends of epidemics. As complex systems analyze communities and simulate disease trends, these methods open fresh avenues for early identification and stronger, more adaptive social health interventions to reduce the effects of disease outbreaks. This literature review explores the use of AI and ML in forecasting infectious diseases, emphasizing the success rates of AI and ML in predicting threats to global health from diseases.

1.1 Introduction to Epidemic Forecasting and AI Integration

Epidemic forecasting is one of the areas in healthcare that has greatly benefited from the use of artificial intelligence (AI) from the large volume of data available in the field. AI increases the potential of the prognosis of the occurrence and advancement of diseases based on data from previous years and days. These are disease history, environment, social movement, and health sectors. For example, recurrent neural networks and graph-based algorithms help AI estimate disease dissemination and resource distribution. Such tools are useful in advising public policies and initiatives, mainly in new emerging cases such as COVID-19 and influenza epidemics. Similarly, AI-driven models can model massive datasets with spatiotemporal resolution, allowing for detailed epidemic monitoring in space and time across regions [1].

A significant advantage of AI applied to epidemic forecasting is its ability to handle new diseases using data revisions, real-time monitoring, and uncertainty characterizations. This is in contrast to most traditional models, which rely on endogenous parameters, equations, and sometimes-underlying assumptions that are proactively incorporated when building the model. For example, in the era of COVID-19, AI models were used to predict and estimate the number of hospitalizations and mortality to facilitate rationing and planning. Nevertheless, some issues remain important, including data normalization, data protection, and the requirement for domain knowledge. Overcoming these barriers will remain crucial in enabling AI to deliver future improvements and reduce the effects of new emergencies on public health [2].

1.2 Application of Machine Learning and Big Data in Disease Prediction

Big data analytics and machine learning have significantly contributed to disease prediction and management because they make it possible to identify diseases earlier and manage stages and decisions. Small sample data analysis is often employed to provide qualitative analysis, and data analysts use a variety of advanced Machine Learning techniques and tools, including random forests, support vector machines, and deep neural networks, to analyze large and complex datasets to discover implicit patterns and relations beyond the abilities of traditional statistical procedures. These methods bring about the ability to forecast a range of disease incidences, their development, and their prognosis based on various sources of inputs like EMR, genomics, and data from wearable devices. Big data platforms allow social data storage and processing, simultaneously providing the big picture of diseases and health risks. For example, the use of ML in predictor-based health of the masses has demonstrated its ability to handle diseases such as diabetes, cardiovascular ailments, and epidemics by controlling risk factors for many populations [3].

Some of the main unresolved issues relate to confidence in reliability, interpretability and ability to scale up these methods. The integration of ML and big data has potential for equity in the utilization of the health care setup and disparities in health outcomes since the data can guide the use of resources for the services of the deprived groups. However, contemporary advancement pays much attention to ethical issues such as patients' privacy and the algorithms' fairness in deploying these technologies. The methods like federated learning and the application of explainable artificial intelligence are presented as solutions to the question of privacy protection. In particular, it is crucial for data scientists, clinicians, and policymakers to work together on an ongoing basis to apply these gains to clinical practice and improve people’s health in individual countries and around the world [4].

1.3 Case Studies of Epidemic Prediction Models

Various methodologies of epidemic predicting models have been discussed in different cases and how these are useful in handling epidemics. One study used a spatiotemporal heterogeneity model called GTNNWR to forecast COVID-19 deaths and then model prevention scenarios in the United States. The study also showed better fits with measured natural data than basic SEIR models and the incorporation of measures such as

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wearing masks, vaccinations, and social distancing. Supplementary approaches achieved a 45 % cut in the winter mortality rate, thus underscoring their usefulness in the pandemic management strategies [5].

Another special case examined the application of machine learning in epidemic prediction by considering big data analysis. It described using CNNs to predict outbreaks of dengue fever in tropical regions based on climatic and demographic data to produce reasonably accurate results. This approach demonstrates the role of AI models in efficiently deploying scarce resources for health delivery and averting the epidemic [6].

1.4 Challenges in Modeling Disease Dynamics

There are profound difficulties in modeling the disease dynamics due to numerous factors related to the biological system on the one hand and the need for more suitable methods on the other. An issue, of course, is that the simple transmission models that inform traditional epidemiological output are grossly biased and oversimplified, do not capture history, and hence do not represent the actual process of spread. Such models need to help quantify population parameters such as infection rates and recovery periods since they base their analysis on assumptions of random population mixing or constant infection rates. This oversimplification can lead to significant aberrations when used on real-world models, as disease, like most things, is not a function of one variable but the social environment, biology, and other factors. To overcome these problems, novel approaches that history-dependent models are being developed, which include time-specific changes in the dynamics of an epidemic for better predictions and optimal management strategies to be implemented [7].

A significant issue arises with the attempt to incorporate spatial and temporal aspects into prediction models. Traditional models are confined to time-series data and fail to incorporate space-based sectional changes of the disease in different districts. This may result in a poor portrayal of transmission patterns and hold back the formulation of efficient containing measures. To this end, recent developments that have been made to address the mentioned gap include graph-based spatial-temporal models. These models entail operations such as graph attention networks to perform dynamic learning of the spatial dependencies and heterogeneous influence of regions. _issues persist, such as computation costs, the requirement for a sizable and diverse dataset and the ability to implement these models for various diseases and regions [8].

1.5 Future Directions and Implications for Public Health

Future trends identified for public health modeling include integration and precision medicine-related models. Specifically, modern approaches such as machine learning, genomic surveillance, and real-time data integration outlooks the future reformation of disease prediction and response methods. For instance, genomic precision systems can improve the sensitivity of alarms for the early identification of a pathogen's source and spread. In combination with enhanced public health systems, such Technologies allow preventive outcomes to be conducted. However, to enact these strategies, issues of equity in technology distribution must be solved, and citizens and organizations must integrate cross-border data sharing. Greater integration at the subnational and transnational level, in line with principles maintained within the One Health concept, is crucial for tracking zoonoses and managing environmental processes that condition the emergence of pathogens.

Relations to public health are critical, as complex simulations enhance the system’s effectiveness in epidemic prevention and supply management. Approaches such as the One Health approach propose broad consultation between sectors in the fight against related health problems concerning human beings, animals and the environment. This method is cost-effective in the end and improves pandemic planning by accounting for ESP in decision-making. Subsequent steps to the COVID-19 pandemic should be aimed not only at increasing the capacity of the healthcare networks in the most deprived parts of the world but also at harnessing AI for fair distribution of health benefits around the world and overall preparedness of the healthcare systems for future challenges [9], [10].

2. Literature Review

Global epidemics and pandemics have highlighted the necessity of developing a well-organized control system with effective prediction techniques at its core for ensuring public health. In this respect, an accurate understanding of how infectious diseases will emerge and spread is crucial in formulating intervention strategies to reduce the social and economic impacts and burdens of such diseases. The accuracy and efficiency of epidemic prediction models have recently improved significantly with advances in artificial

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intelligence (AI) and machine learning. Combining these innovations, big data, and mathematical modeling gives an excellent advantage in tackling the complexities of the parameters involved in infectious disease dynamics. This literature review will discuss AI and machine learning applications toward epidemic and pandemic predictions, with examples of COVID-19, Zika, and Ebola.

AI in [11] has brought advances to the field of infection prediction, especially with the emergence of ML and DL approaches. These advances present new strategies that could be applied to impose control over disease emergence and spread. Yet, much remains to be done about which data are used, their analysis methodology, and possible exploitations. This contribution is thus divided into three main categories: public health data on prevention against regional disease spread, patient medical data for infection detection, and combined public and patient data to estimate disease propagation within populations.

According to [12], the global health consequence induced by multidrug-resistant gram-negative bacteria (MDR-GNB) necessitates innovations concerning treatment in the face of high mortality rates resulting from improper antimicrobial use. The study introduced an AI-clinical decision-support system (CDSS) that augments machine learning (ML) through matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). The applicability of 165,299 bacterial specimens and 11,996 KP isolates as the database for advanced ML applications to predict the resistance of these bacteria against some key antibiotics (levofloxacin and ciprofloxacin, among others) showed effectiveness. Among the models tested, a random forest classifier performed exceedingly well, with an area under the curve (AUC) of 0.95, validating its predictive accuracy. This ingenious fusion of MALDI-TOF MS with ML can provide notable improvements in diagnosis speed and accuracy, offering a critical tool in solving what is increasingly seen as an impending global healthcare disaster in antibiotic resistance.

According to [13], Tuberculosis (TB) continues to be one of the most common respiratory diseases. It is reported to be responsible for more than a million deaths throughout the year, with Mycobacterium tuberculosis (MTB) as the causative agent, being easily contagious and disseminated by air. Types of multidrug-resistant TB are hugely challenging; among them are lengthy duration of treatment, lack of tolerability, and high costs, all of which call for shorter and more efficacious cure regimens. This work studies the application of machine learning techniques, such as logistic regression, random forests, and boosting, to predict relapse rates from different experimental and treatment-specific variables and recurrence outcomes without resource-demanding experimental assays. This approach proposes the derivation of T90 values from four Relapsing Mouse Model (RMM) trials, which reflect effective treatment regimen ranking based on efficacy and represent treatment durations required to achieve a 90% probability of cure. The approach would provide an efficient and resource-efficient alternative to classical procedures of recurrence evaluation in line with the 3R principles (Replacement, Reduction and Refinement.

State-of-the-art [14] infectious diseases continue to challenge global health significantly. Such modern crises as the COVID-19 pandemic and the recent Ebola outbreaks emphasize the importance of infectious disease modeling in public health policy-making and response. Basic models such as SIR (susceptible-infectious-recovered) and SEIR (susceptible-exposed-infectious-recovered) laid down foundations for the original development of the field of modeling; stochastic modeling, networked approaches, and big data analytics have further taken it into a completely new class of predictive capacities. The study emphasizes incorporating machine-learning techniques to improve model accuracy and responsiveness while dealing with other challenges like parameter estimation, model validation, and use of real-time data. Ethical considerations, including privacy concerns and risk communication, are also addressed in the discussion, stressing the urgent need for interdisciplinary effort and integration of data into the advancement of the field of infectious disease modeling.

As mentioned earlier in the paper [15], Epidemics have been redefined for real-time detection and prediction of outbreaks using artificial intelligence and cloud computing. This AI-enabled framework collects large amounts of data from hospitals, wearable devices, health public records, security, and environmental sensors to monitor any abnormal health pattern that may indicate the onset of an epidemic. Epidemiologists have tied machine-learning models learned from historical data for prediction accuracy enhancement and early detection of outbreaks compared to traditional methods. In doing so, Auspices uses geographic data and epidemiological models to forecast the future of disease transmission and to develop proper containment strategies. The cloud-based system ensures scalability and high availability and compiles large amounts of

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health data quickly in emergency scenarios. Among various challenges being addressed are data privacy and security issues, for which several measures have been factored into the system, such as encryption and role-based access controls under regulations like HIPAA and GDPR, in addition to other legal structures. The case studies thus reveal how outbreak prediction and its reduced propagation could be made possible by using this framework, thus making it invaluable as part of global health preparedness strategies.

While measles is noted in [16] as the most critical case study for studying nonlinear spatio-temporal dynamics in infectious diseases, it is also challenging to model mechanistically. To model and predict measles transmission based on the limitations of the mechanistic models, researchers constructed a high-dimensional feed-forward neural network model with spatial features (SFNN) that forecast measles outbreaks and relate its performance with traditional mechanistic modeling TSIR using England and Wales data from 1944 through 1965. The results indicate that, generally, SFNN performed better than TSIR across the multiple forecasting windows and exposed spatial hierarchies in disease spread driven by major cities through consistently lower root mean squared error values. Hybrid TSIR-PINN approaches were introduced, demonstrating that TSIR could recover latent susceptible dynamics while increasing forecast accuracy in mean absolute error. The study shows the impossibility of mechanistic approaches in predicting public health responses to measles or similar diseases compared with their approaches based on neural models.

As detailed in [17], climate change drives complex eco-evolutionary dynamics in marine pathogens, with *Vibrio* bacteria exemplifying climate-sensitive species undergoing global expansion. This study developed a methodological framework integrating genomic and environmental data to investigate the population dynamics of *Vibrio parahaemolyticus* (VpST3). This clone successfully adapted to Latin America after expanding beyond its endemic region in tropical Asia. The findings highlighted the role of El Niño events as marine corridors, revealing nonlinear lagged effects that increased *Vibrio* detection 3–4 months post-event and identifying gene-level dispersal mechanisms via marine organisms. Using machine learning, the study predicted environmentally driven *Vibrio vulnificus* infections in the USA with 0.971 sensitivity, uncovering complex environmental drivers. These insights emphasize the need for risk models, expanded surveillance systems, and a deeper understanding of human exposure pathways to improve predictive capacity and manage the effects of climate change on marine pathogens.

As reported in [18], it is the act of rapid worldwide spreading of the SARS-CoV-2 virus (which is the cause of COVID-19) that brings damage socially and economically, including in Indonesia. For the Medan area, changes are caused mainly by increased human interaction and the death rate. In general, the transmission dynamics of COVID-19 are modeled by deterministic epidemiological approaches that classify persons into susceptible, infectious, and recovered groups. Therefore, this study aims to develop a dynamic transmission model for Medan, Indonesia, for COVID-19 and incorporate isolation measures through a deep learning approach. The object of this research is DEEPCOV; data taken from the Medan COVID-19 task force consisting of exposed, infected, recovered, and deceased individuals will be used to improve the prediction of disease spreading. This deep learning model is developed to improve predictions and influence public health responses to the pandemic.

As stated in the study reference [19], the early detection of communicable diseases, especially COVID-19, significantly reduces their transmission and prevents them from becoming global pandemics. This study presents Early Detect, a framework that does end-to-end passive monitoring of health information such as heart rate and step data from consumer health trackers into early prediction of COVID-19. However, a central challenge in early detection is identifying the right amount of historical data to analyze for a precise result as to whether or not infection has occurred. EarlyDetect employs Reinforcement Learning for Early Time Series Classification by extracting 45 digital biomarkers and feeding them into a multi-layer perceptron deep network trained using Double Deep Q-Network to address this. EarlyDetect automatically decides to wait for more data or classify the observed data window at every iteration. A novel rewarding mechanism ensures early and accurate classification, even with a highly imbalanced class distribution. With a 72-hour lookback window, the framework has achieved 0.8 in accuracy, 0.73 in AUC-ROC, and 0.07 in earliness while requiring up to 86% less data than existing methods and making predictions 50% earlier for confirming COVID-19 status. EarlyDetect identified 61% and 46% of positive cases before peak transmissibility on two COVID-19 data sets, showing that it could be a vital step forward in early screening for infectious diseases.

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As outlined in [20], Tuberculosis (TB), the second leading infectious killer globally, resulted in 1.3 million deaths in 2022, surpassing even HIV and AIDS. With an estimated 10.6 million new cases reported worldwide in the same year, the urgency to address this ongoing public health crisis remains critical. This study focuses on employing predictive modeling techniques to forecast TB incidence, utilizing various machine-learning models to enhance the accuracy and timeliness of predictions. The research also incorporates impactful visualizations to facilitate comprehensive data exploration and analysis. The optimal model developed in this study aims to forecast TB incidence and customize a user-defined function for enhanced applicability. By examining key determinants influencing TB spread, the study contributes valuable insights for formulating strategies to prevent the further transmission of this deadly disease.

In the research presented in [21], AI and ML techniques have advanced a lot in predicting infectious diseases and their spread, as shown in the research output in [*]. Deep learning, the current frontier in artificial intelligence development, has improved these capabilities even further, presenting innovative alternatives for disease prediction. However, challenges still exist regarding the kinds of data collected and the different methodologies employed in studying and analyzing such data. This paper aims to present developments in the domain while addressing some of these issues of data types and methods for each specific research objective. The contributions fall into three categories: predictions using Public Health Data in preventing the spread of transmissible diseases in a region, predictions from Patients' Medical Data to detect infections, and predictions combining both Public and Patient Medical Data in estimating the reach of a disease. A critical evaluation of the promise of AI in managing infectious diseases is included within the paper, together with its limitations and the need for future efforts.

When infectious diseases like Covid-19 are detected early, further transmission and pandemics can be mitigated. Reference [22] presents Early Detect, an all-in-one framework designed for early detection of COVID-19 using passive heart rate and step count data collected from consumer-grade health trackers. This framework solves the problem of figuring out how much historical information to consider achieving accurate, early detection of infections. The study extends Reinforcement Learning Early Time Series Classification to decide in real-time the optimal lookback period that balances having early detection of infection and accuracy. It reduced data requirements by a whopping amount, requiring even under 14% of similar existing techniques. It also predicted COVID-19 status at 50%, representing the best early infectious disease detection progress.

Emerging scientific research faces the daunting task of predicting disease outbreaks, perhaps prompted by worldwide threats and irreparable effects of the COVID-19 pandemic. As discussed in [23], the current study applies the Susceptible-Infectious-Recovered Mathematical (SIR) model in understanding India's multifaceted COVID-19 scenario. The study investigates various lockdown scenarios and evaluates the impacts on the infection rate and other important aspects using Microsoft Excel simulations. Results from the study showed that with longer lockdowns, the basic reproduction number, as well as the rate of infections, went down, where it was reduced from 9.19 to 2.66. Thus, susceptibility has decreased from 97.69% to 48.59%, indicating prolonged locking-in. In conclusion, these results could work toward a paradigm shift in how modern countries and societies handle pandemics.

The discipline of epidemiology has witnessed a significant leap in its courtesy of artificial intelligence (AI). Numerous research as enumerated in [24], have employed machine learning (ML) and deep learning (DL) approaches for early detection, monitoring, and prediction of future outbreaks, as well as drug and vaccine development during the COVID-19 pandemic. Nonetheless, its actual application in health institutions remains limited due to the "black box" nature of AI algorithms. Explainable AI (XAI) aims to overcome this hurdle by making AI decisions less opaque. It traces the development and subfields of historical AI, addresses its introduction in disease management through AI's contribution, and advocates that XAI can augment the prediction and management of infectious diseases.

For public health, the new Roueche virus (OROV) outbreak from 2023 to 2024 is the outbreak with the highest-ever confirmed cases. As discussed in [25], Bolivia, Brazil, Peru, Colombia, and Cuba all suffer from the outbreak, with confirmed cases acquired through travel to the USA and Europe. Although the outbreak is extensive, the most pertinent questions revolve around the specific factors responsible for this epidemic's propagation. The study by Tiago Gräf et al. investigated the ecology of the outbreak considering the influence of small agricultural communities, particularly those cultivating bananas or cassava, as conducive for the

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significant vector, Culicoides biting midges. Ecological factors with possible contributions toward the outbreak, including changes in agricultural practices, deforestation, and landscape modification, were suggested through findings resembling previous studies. The definition of good fits between ecological predictors and OROV transmission is smudged because predictors are highly autocorrelated and deviously interrelated. The paper concludes with the urgent need for sophisticated methodologies and continuing data to increase model accuracy, with possible future extensions to study factors such as climate, loss of biodiversity, and socioeconomic indicators.

Exposure to pathogenic infections due to food leads people to threaten their health. It makes the detection of foodborne diseases significant to limit the possibilities of transmission. The study in [26] presents an AI model constructed for identifying foodborne pathogenic bacteria based on their single-cell Raman spectrum data. It uses self-transfer deep learning with an ensemble prediction algorithm to enhance the training efficiency and predictive performance for high prediction accuracy. With this model, over 99.99% accurate classification can be attained in gram-negative and gram-positive bacterial identification, as the material can further be brought to genus and species identification and strain recognition with an accuracy of over 99.49%. Such advancement can have significant practical applications in medical detection and diagnosis and possibly have higher significance in reducing false negatives from foodborne disease- identification.

Climate change is inducing some very complex ecological changes worldwide that have troubling consequences for pathogens likely to be sensitive to environmental changes, particularly those associated with waterborne diseases. As described in the paper [27], this study will concentrate on Vibrio, a group of marine epidemiological pathogens- the gastroenteritis caused by those which have gone on to other parts of the world in an evolving change associated with climate. They include the $V.$ cholerae and $V.$ parahaemolyticus pathogens that have caused worldwide epidemics in the East and West of the Pacific. These are excellent cases for studying various possible eco-evolutionary driving forces in climate-sensitive pathogens. It also describes a methodological approach to combining genomic and environmental data to study how an influential $V.$ parahaemolyticus clone ($VpST3$) has spread from its endemic tropics in Asia. The research reveals the role of El Niño events as marine corridors for Vibrio bacteria. In this context, it also uncovers nonlinear lagged effects in their identification, revealing simultaneously a gene-level dispersal mechanism related to marine organisms. Finally, it achieves a sensitivity of 0.971 by incorporating machine learning techniques to forecast the number of $V.$ Vulnificus infections expected in the USA, thus representing valuable insight into the eco-evolutionary dynamics that drive the global spread of Vibrio pathogens.

Measles is an important infectious disease not only because of its burden on public health but also because of the opportunity, it provides for studying the nonlinear spatial-temporal dynamics of the disease. The current study, as detailed in [28], develops a high-dimensional feed-forward neural network model with spatial features (SFNN) to forecast endemic measles outbreaks. It then compares that model's performance with a classical mechanistic model, the TSIR. Using England and Wales data (1944-1965), the study addresses some modeling challenges, particularly the interplay between metapopulations, seasonal trends, and the implications of demography on nonlinear dynamics. While the TSIR model gives accurate short-term forecasts for the most populous cities, the SFNN consistently demonstrates lower root mean squared error (RMSE) in a longer forecast horizon. The SFNN model identifies a gravity-model-like spatial hierarchy in the spread of measles, emphasizing the role of major metropolitan areas in driving regional outbreaks. It also examines how the mechanistic and the machine learning worlds can be bridged. An example of this is to show how TSIR can improve the performance of Physics-Informed-Neural-Networks (PINN) through better parameter inference and forecast accuracy.

The year 2020 saw the appearance of a new virus called Coronavirus (COVID-19). The SARS-CoV-2 virus caused it. Now, in the study referenced under the cited text [29], the research speaks of the dynamic transmission of COVID-19 in Medan City, Indonesia. The city has been quite affected by the social and economic changes the virus has inflicted. This study introduces an advanced deep learning model termed DEEPCOV to forecast the spread of COVID-19 with data collected from the Medan City COVID-19 task force on the number of exposed, infected, recovered, and deceased counts. The model improves the understanding of how COVID-19 spreads by considering the heterogeneity of human social contacts through the intensity of isolation meant to curb spread. This study gives a transmission model that could improve forecasting and responses in any pandemic scenario.

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Epidemics and pandemics have left quite a negative imprint on the globe's population in terms of health owing to the unprecedented proportion of deaths of the vulnerable. This research outlined in [30] has focused on artificial intelligence, machine learning algorithms, and mathematical approaches to predict and control epidemic diseases such as Zika virus, HIV/AIDS, Ebola virus, COVID-19, SARS, and MERS. Predictive modeling predicts highly contagious diseases early instead of relying only on detection and analysis, making it an important addition to the intervention arsenal. It is thus pertinent to increase and improve control measures for outbreaks and deter further spread in nations. The paper emphasizes the importance of mathematical models and big data for predicting and forecasting the dynamics of infectious diseases during pandemic and epidemic outbreaks.

The overview of the literature review on the application of Artificial Intelligence and Machine Learning in predicting and managing infectious diseases is presented in Table 1 below. It covers significant works, approaches and results, from high-level predictive methods such as deep learning and reinforcement learning to the combination of genomic and environmental data for assessing the nature of diseases. Hair highlighted that AI and ML have made considerable strides in protecting and improving the public's health through early detection systems, better resource allocation and better models of disease transmission. Further, it reveals a wide range of working areas in terms of disease control and prevention, from combating antimicrobial resistance and TB relapse rates to early volumetric prediction of epidemics such as COVID-19 and measles. These lessons stress the disruption that AI/ML technologies hold for global health and support significant problems such as data protection, the ethical implications of AI advancements and the cross-disciplinary cooperative framework.

Table 1: Summary of Literature Review

Reference Number	**Study Focus**	**Methodology/Technology Used**	**Key Findings/Contributions**
[11]	AI and ML applications in infection prediction	AI, ML, DL, public health data, patient data	AI/ML improved disease prediction and public health interventions.
[12]	AI-based CDSS for antimicrobial resistance prediction	ML with MALDI-TOF MS; Random Forest	High accuracy in predicting antibiotic resistance; Random Forest AUC 0.95.
[13]	ML techniques for TB relapse prediction	Logistic regression, Random Forests, Boosting	Efficient prediction of TB relapse with less resource use.
[14]	Role of AI in infectious disease modeling	SIR, SEIR, stochastic models, big data analytics	Enhanced predictive capacity for epidemics; ethical considerations highlighted.
[15]	Real-time epidemic prediction using AI and cloud computing	Cloud computing, wearable device data, epidemiological models	Improved real-time outbreak predictions and resource allocation.
[16]	Spatial-temporal modeling of measles transmission	High-dimensional neural networks, TSIR model	SFNN outperformed TSIR in long-term forecasting; spatial hierarchies were observed.

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[17]	Climate-driven dynamics of marine pathogens	Genomic and environmental data integration	Revealed climate influence on Vibrio spread; predicted infections with high sensitivity.
[18]	Dynamic COVID-19 transmission modeling in Medan, Indonesia	DEEPCOV, deep learning, transmission modeling	Enhanced forecasting and public health responses to COVID-19 in Medan.
[19]	Early detection of COVID-19 via health tracker data	Reinforcement Learning, multi-layer perceptron	Reduced data needs, improved early detection, balanced timeliness and accuracy.
[20]	ML techniques for predicting TB incidence	Predictive modeling, visualization, ML techniques	Accurate TB incidence prediction; data visualization enhanced insights.
[21]	AI and ML advancements in infectious disease prediction	Public health data, patient data, combined datasets	Promising AI/ML applications in managing disease spread.
[22]	Early COVID-19 Detection Using Reinforcement Learning	Reinforcement Learning, time-series classification	Reduced data needs for COVID-19 detection; earlier predictions achieved.
[23]	SIR modeling for COVID-19 lockdown effects in India	SIR modeling, simulation, Microsoft Excel	Lockdowns reduced infection rates; SIR modeling demonstrated scenario impacts.
[24]	Explainable AI for infectious disease prediction	Explainable AI, deep learning, historical AI contributions	XAI can make AI predictions transparent and applicable in health systems.
[25]	Ecological factors in Roueche virus outbreak	Ecological predictors, Culicoides midges, landscape changes	Ecological factors influence disease spread; the need for improved models is emphasized.
[26]	AI for detecting foodborne pathogens	Self-transfer deep learning, Raman spectrum data	Accurate foodborne pathogen detection; high practical significance.
[27]	Eco-evolutionary dynamics of Vibrio pathogens	Machine learning, genomic-environmental data, sensitivity analysis	El Niño effects on Vibrio dynamics; integrated genomic-environmental modeling.
[28]	SFNN model for measles forecasting	Feed-forward neural networks, mechanistic models	SFNN identified drivers of measles spread; hybrid models were proposed for better accuracy.

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[29]	Deep learning for COVID-19 transmission in Medan	DEEPCOV model, isolation measures, task force data	Advanced modeling enhanced understanding of COVID-19 dynamics in Medan.
[30]	AI/ML for predicting global epidemics and pandemics	Predictive modeling, mathematical models, big data analytics	AI/ML-enabled better prediction and control of infectious disease outbreaks.

Artificial intelligence, machine learning, and mathematical models have entered our definition of understanding and predicting infectious disease outbreaks. More precise forecasting could trigger a release of pre-emptive activities to control disease transmission. One benefit these technologies could provide would be to help in early detection, response strategy improvement, and outbreak management. Although the potential of these technologies is great, some optimization challenges remain to be addressed in real-life scenarios, especially concerning the environment's diversity and dynamics. Future research should concentrate on predictive algorithm refinement and data integration improvements to strengthen the global response against infectious disease threats.

3. Discussion

The analysis of genomics, environmental data, and novel ML algorithms democratizes the next level in epidemic prediction and control. These approaches work well when different data sets are involved where features that cause diseases are complex, and those identified provide a more transparent and compelling picture. Besides, it also improves the realities of the models in question and allows mobility for the public health authorities to implement the correct measures. Nevertheless, all these advancements can only be realized with strong multi-sectorial cooperation, ethical practices and responsible data sharing. This section focuses on the critical issues, constraints, and prospects of applying AI and ML to build fair and efficient epidemic prediction models.

3.1 Integration of AI and ML in Epidemic Predictions

AI and ML are the most crucial tools for improving the forecast and control of infectious diseases. Machine learning has demonstrated impressive performance in early identification, utilization of resources, and near real-time disease surveillance using deep learning (DL). For example, the advances in infectious disease control have shown how AI has dramatically improved essential disease control processes, such as diagnosis, early detection of the disease, disease prediction/forecasting, and disease treatment [31].

However, they need problems like data normalization, fine-grained identity information protection, and the learning structure's interpretability. AI technology in disease surveillance and outbreak identification completely transforms how we can watch over and investigate episodes of contagion. In essence, harnessing sophisticated technology enhances the healthcare system's capability to approach illness detection, tracking and containment to protect public health infrastructure and enhance the general health of the populace [32].

3.2 Key Achievements in Forecasting Accuracy

Many works have managed to get record-high accuracy in predicting AMR and have used machine-learning approaches. For instance, a study using Random Forest algorithms found that it could perform better than traditional methods in AMR detection, which mitigates the problems with long cycles of bacterial culture and helps make timelier clinical decisions [33].

Regarding spatial-temporal disease modeling, deep learning, particularly neural networks, has proved to be associated with promising results. The innovation of Forecast Net, a time-variant deep feed-forward neural network, has improved the model's capacity for accurate time-varying dynamical feature representations in data, extending the prior work for multi-step-ahead time series forecasts. This development emphasizes the possibilities of such models in capturing more intricate temporal patterns of disease transmission and

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transmission rates for enhanced precision in stochastic modeling and additionally guides public health approaches to managing the disorder [34].

3.3 Challenges and Ethical Considerations

Despite the advances spurred by artificial intelligence (AI) and machine learning (ML) in healthcare, important issues still need to be addressed concerning bias in AI datasets and the scaling-up and fairness of AI applications. Much bias is usually introduced in the systems through the dataset used to train them, distorting the outcome of treatments given to patients so that the disadvantaged groups in society are even further disadvantaged. Other challenges that crop up are the scalability problems that crop up when an AI model used in the labs fails to perform well when it is moved to other clinical settings. Algorithm bias must be avoided during the application process to avoid discriminating against patients and to give all patients an equal chance in the healthcare system [35].

In the case of the use of AI in healthcare systems, the following key areas of consideration arise. One major issue pertains to patient anonymity, which is important because most AI applications involve deep examination of integrated patient records containing separately identifiable health information. AI accountability enables healthcare providers and patients to trust the decisions made by such AI and to assess whether the provision of such decisions is reasonable. Mitigating these ethical issues is relevant to achieving responsible deployment of AI in healthcare programs [36].

3.4 Future Directions for AI in Public Health.

External factors, genomes, and new-generation ML must be amalgamated to predict epidemic outbreaks and create an accurate alert system. Integrating all scalar data like genetic data, climate data and socioeconomic data into an ML model makes it possible to capture all the interrelationships that contribute to disease transmission dynamics. This approach improves the reliability of the estimations and allows the targeted actions to be performed in the sphere of public health. For example, the R-package learn MET helps integrate genomic and environmental data, thereby providing possible applications of such combined analysis for predicting phenotypic end-point readouts [37].

Nevertheless, utilizing these innovative approaches to predictive systems requires solid cooperation across industry sectors, high levels of ethical compliance, and excellent international data-sharing programs. To have comprehensive data sets that will form the basis for effective Machine Learning, there is the need to share data across sectors to reduce cases of fragmented data sets solely cultivated by a specific department or organization such as the healthcare, environment, and research institutions. Essential issues that should be addressed include data ethical issues about privacy and acquisition of informed consent, equity, and justice, which would help distribute the benefits from the new technologies in artificial intelligence. As the case may show where the Urban Institute argues strongly that dismantling the hurdles that hinder cross-sector data sharing can only be done if there are good relationships between the parties and there should be trust between the parties involved. For that reason, the promotion of global collaboration, as well as the enhancement of AI and ML guidelines, are critical measures in the fight against future pandemics [38].

4. Conclusion

AI and ML have become revolutionary methodologies in infectious disease forecasting and therapy. These technologies have facilitated detecting, tracking and managing outbreaks more accurately through state-of-art computational procedures. Hence, AI/ML models can extract important information from genomic and environmental data, health monitoring systems, etc., which is imperative to determining the proper method for public health intervention. Applying these technologies to solve problems such as antimicrobial resistance, tuberculosis relapses, and the nature of the pandemic suggests that they can transform disease control models.

However, adopting the AI or ML system has its drawbacks. This indicates that problems as far as data standardization, scalability, and inherent bias of the data are still critical and can lead to a compromise in the reliability of the predicted results; however, due to some ethical constraints that include issues to do with patient privacy, transparency of the algorithms, and issues to do with equity in access, and integration of such technologies in health care facilities. Moreover, the nature of infectious disease transmission necessarily requires models that are update-friendly, easy to interpret, and able to accommodate data from multiple

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sources and types. It is important to overcome these limitations to fulfill the pledge of AI/ML capability in epidemic forecasting and prevention.

These are multifaceted issues, but the most important solutions are interdisciplinary teamwork, strict compliance with ethical rules, and the dissemination of large databases worldwide. Credible collaboration between governments, healthcare institutions, researchers, and technology providers can help to build sound, fair, and sustainable AI/ML systems. Furthermore, utilizing regional and specialist databases reporting by standardized procedures will also become critical for compatibility. AI standards based on transparency, fairness and the inclusion of all demographic groups must be in the foreground to counteract loss of public trust and gain widespread adoption.

Moving to the future, the development of epidemic prediction depends on improving AI/ML solutions in terms of accuracy and applicability at a broad scale and for adherence to ethical and fair use. Genomic precision systems will continue to improve to enhance disease tracking, while spatial-temporal modeling and explainable AI will improve approaches to disease prevention. So, to adapt to new changes in world health threats and to unleash the potential of AI and machine learning approaches further, improved multi-sectoral research, policy advancements, and global cooperation will be needed. This review seeks to demonstrate these technologies' revolutionary advancement to the health sector without dismissing the need for technology's continuous enhancement and proper use to attain global health security.

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