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Artificial Intelligence Techniques For Predicting Pandemic Diseases: Systematic Literature Review

Teknik Kecerdasan Buatan untuk Memprediksi Penyakit Pandemi: Tinjauan Literatur Sistematis

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ABSTRACT

The rapid emergence of global pandemics necessitates accurate and adaptive predictive systems to support public health decision-making. This study aims to systematically review Artificial Intelligence techniques for predicting pandemic diseases and to evaluate the methodological quality and potential bias of existing empirical research. The research employed a Systematic Literature Review approach guided by PRISMA, with database searches conducted in Scopus, Web of Science, ScienceDirect, and Google Scholar. The selection process yielded ten empirical quantitative and qualitative studies, which were assessed using the Joanna Briggs Institute critical appraisal criteria to evaluate methodological rigor and risk of bias. The findings indicate that machine learning, deep learning, and transformer-based architectures achieve high predictive accuracy in forecasting infection probability, disease severity, and epidemic trends. Most studies demonstrated robust validation strategies, including cross-validation and clearly reported performance metrics. Nevertheless, recurring limitations such as data bias, limited population generalizability, and temporal bias remain significant methodological challenges in AI-based pandemic prediction research. Overall, Artificial Intelligence techniques demonstrate substantial potential in strengthening global pandemic preparedness and enhancing evidence-based public health responses.

Keywords : Artificial Intelligence; Deep Learning; Epidemic Forecasting; Machine Learning; Pandemic Prediction

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ABSTRAK

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Perkembangan pandemi global menuntut sistem prediksi yang cepat, akurat, dan adaptif untuk mendukung pengambilan keputusan kesehatan masyarakat. Penelitian ini bertujuan untuk meninjau secara sistematis berbagai teknik Artificial Intelligence dalam memprediksi penyakit pandemi serta mengevaluasi kualitas metodologis dan potensi bias penelitian yang ada. Metode penelitian menggunakan pendekatan Systematic Literature Review dengan pedoman PRISMA melalui pencarian pada basis data Scopus, Web of Science, ScienceDirect, dan Google Scholar. Proses seleksi menghasilkan sepuluh studi empiris kuantitatif dan kualitatif yang dievaluasi menggunakan kriteria Joanna Briggs Institute untuk menilai kualitas dan risiko bias. Hasil penelitian menunjukkan bahwa model machine learning, deep learning, dan arsitektur berbasis transformer mampu mencapai tingkat akurasi tinggi dalam memprediksi infeksi, tingkat keparahan, serta tren epidemi. Sebagian besar studi menunjukkan validasi model yang kuat melalui cross-validation dan metrik kinerja yang jelas. Namun, keterbatasan berupa bias data, keterbatasan generalisasi populasi, dan bias temporal masih menjadi tantangan utama dalam penelitian prediksi pandemi berbasis AI. Secara keseluruhan, teknik AI memiliki potensi besar dalam meningkatkan kesiapsiagaan dan respons terhadap pandemi di masa depan.

Kata kunci : Artificial Intelligence; Deep Learning; Epidemic Forecasting; Machine Learning; Pandemic Prediction

INTRODUCTION

Infectious disease pandemics, such as COVID-19, have imposed profound burdens on global public health systems, leading to elevated morbidity, mortality, and overwhelming demands on healthcare infrastructure across diverse regions. These outbreaks have also generated extensive economic and social repercussions, including disruptions to livelihoods, increased inequality, and heightened vulnerabilities in low-resource communities (Sadiq, 2025). Early, accurate, and scalable forecasting of pandemic dissemination is essential for facilitating proactive measures that curb transmission and preserve societal stability. By enabling swift decision-making among public health officials, such predictive models optimize resource distribution, intervention strategies, and overall risk mitigation efforts.

Traditional statistical and compartmental models, such as ARIMA and SEIR, frequently exhibit limitations in capturing the non-linear dynamics inherent in pandemic datasets due to their reliance on linear assumptions (Wang et al., 2021). These conventional approaches also struggle to incorporate the multidimensional aspects of epidemiological data, including diverse external drivers and heterogeneous factors that influence transmission (Delli Compagni et al., 2022). Furthermore, the noisy and nonstationary characteristics of real-world pandemic time series significantly compromise the predictive performance of such models (Nagvanshi et al., 2023). Consequently, traditional methods often fail to deliver reliable forecasts when confronted with the complex, dynamic, and real-time demands of large-scale pandemic scenarios (Ospina et al., 2023).

The emergence of big data from diverse sources such as epidemiological records, human mobility patterns, social media, clinical datasets, and geospatial information has created unprecedented opportunities for extracting meaningful patterns in pandemic dynamics (Jiao et al., 2023). However, harnessing these voluminous, heterogeneous, and high-velocity data streams necessitates intelligent computational approaches to enable effective analysis and insight generation beyond the capabilities of conventional methods (Awotunde et al., 2022). Artificial Intelligence (AI), particularly Machine Learning (ML) and Deep Learning (DL), has demonstrated substantial potential in capturing intricate, non-linear patterns within complex epidemiological datasets, thereby yielding more accurate predictions compared to traditional statistical techniques (Saleem et al., 2022). Consequently, the integration of ML and DL with big data analytics represents a transformative shift in epidemiological forecasting and public health response, offering enhanced precision in modeling pandemic trajectories (Shorten et al., 2021).

Numerous individual studies have applied AI techniques to pandemic prediction, particularly for COVID-19, yet their results are fragmented due to varying datasets and evaluation metrics, complicating direct comparisons (Uysal, 2025). Existing reviews predominantly emphasize diagnosis, such as detection from imaging, or individual patient prognosis, while comprehensive examinations dedicated to pandemic forecasting, including outbreak trends and case numbers, remain limited (Siddiqui et al., 2025). Prior reviews are often constrained to a single technique, such as deep learning, or specific to one disease like COVID-19, failing to encompass a broad spectrum of AI methods including classical ML, ensembles, and hybrid models for general pandemic prediction (Pujari et al., 2025). There is a notable absence of systematic and up-to-date syntheses that compare performance, strengths, weaknesses, data types, and implementation challenges of AI techniques specifically for predicting pandemic diseases beyond a single pathogen (Bengana et al., 2025).

This study presents a Systematic Literature Review (SLR) uniquely focused on artificial intelligence (AI) techniques for predicting pandemic diseases, extending beyond individual diagnosis or prognosis and encompassing a broader scope than COVID-19 alone. It adopts rigorous SLR protocols, such as Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA), to systematically map, evaluate, and synthesize evidence from contemporary literature. The review provides a comprehensive classification of diverse AI techniques including supervised machine learning (ML), deep learning time-series models, and ensemble/hybrid approaches along with their input data types, performance metrics, and application contexts in pandemic prediction. Furthermore, it identifies current trends, best practices, technological and methodological gaps for future research in AI-driven pandemic prediction, while offering guidance to researchers and public health practitioners in selecting and developing more robust and generalizable AI models for forthcoming pandemics.

This study aims to identify, classify, and summarize various artificial intelligence techniques employed for predicting pandemic diseases based on existing scientific literature. It further analyzes the most commonly utilized data types, evaluation metrics, and performance levels such as accuracy, mean absolute error (MAE), and root mean square error (RMSE) across these AI approaches. The research also uncovers the primary strengths, weaknesses, and challenges in applying AI techniques for pandemic prediction, including issues related to data quality, model generalization, interpretability, and real-time capabilities. Finally, it identifies key research gaps and provides recommendations for developing improved AI models in the future, particularly in the contexts of pandemic prediction and prevention.

METHOD

This study employs a Systematic Literature Review (SLR) approach to identify, evaluate, and synthesize scientific evidence related to Artificial Intelligence (AI) techniques for predicting pandemic diseases. The SLR method was selected because it enables a comprehensive, structured, and evidence-based mapping of existing research concerning AI-driven predictive modeling in the context of infectious disease outbreaks. Through this approach, the study systematically examines the development, application, and performance of AI techniques including machine learning, deep learning, and hybrid computational models in pandemic forecasting. Furthermore, the SLR facilitates the identification of dominant research patterns, methodological trends, performance evaluation metrics, and existing research gaps that require further scholarly investigation.

All stages of this research adhere to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines to ensure transparency, methodological rigor, and reproducibility. The PRISMA framework guides the literature selection process through four principal stages:

1. Literature Identification
   Relevant scientific articles were collected from internationally indexed academic databases.
2. Article Screening
   Retrieved articles were screened based on titles and abstracts to assess their relevance to AI techniques applied in pandemic disease prediction.
3. Eligibility (Full-Text Review)
   Articles that passed the screening stage underwent full-text assessment to confirm methodological quality, research relevance, and analytical robustness.
4. Final Inclusion
   Studies that met all eligibility criteria were included in the final synthesis process.

A systematic search was conducted using reputable international academic databases, including Scopus, Web of Science, ScienceDirect, and Google Scholar, to ensure comprehensive coverage of high-quality scholarly publications in the fields of artificial intelligence, epidemiology, and public health informatics. The search strategy employed combinations of keywords using Boolean operators (AND, OR), including: Artificial Intelligence AND Pandemic Prediction; Machine Learning AND Infectious Disease Forecasting; Deep Learning AND Epidemic Modeling; and AI-based Disease Surveillance.

The publication period was limited to 2020–2025 to capture contemporary developments in AI technologies, particularly in response to global health crises such as the COVID-19 pandemic. This time frame ensures that the analyzed literature reflects recent methodological advancements and real-world implementation experiences in pandemic prediction systems.

To ensure the quality and relevance of the reviewed studies, explicit inclusion and exclusion criteria were established. Inclusion criteria: Peer-reviewed scientific journal articles or conference proceedings; Studies explicitly examining AI, machine learning, deep learning, or hybrid computational techniques for pandemic or infectious disease prediction; Research focusing on predictive modeling, outbreak forecasting, disease surveillance, or epidemiological trend analysis; and Articles published in English. Exclusion Criteria: Non-academic publications such as opinion pieces, editorials, news reports, or non-peer-reviewed sources; Studies not directly related to AI-based predictive techniques for infectious or pandemic diseases; and Articles without accessible full-text versions. The selection process was conducted independently by two reviewers to minimize selection bias. Any discrepancies were resolved through discussion until consensus was achieved.

Data extraction was performed systematically using a structured tabular format for all eligible studies. The extracted variables included:

a. Author(s) and year of publication
b. Country or region of study
c. Type of pandemic or infectious disease analyzed
d. AI technique or algorithm employed (e.g., neural networks, random forest, LSTM, SVM)
e. Dataset characteristics and data sources
f. Performance evaluation metrics (e.g., accuracy, precision, recall, RMSE, AUC)
g. Key findings regarding predictive effectiveness and model performance

The structured extraction process facilitated comparative analysis across studies and enhanced the reliability of thematic synthesis. The data analysis was conducted through the following stages:

1. Thematic Analysis

   Selected studies were categorized based on primary themes, such as predictive modeling techniques, data sources (e.g., epidemiological data, mobility data, social media data), validation strategies, and real-time surveillance systems.

2. Narrative Synthesis

   Findings from prior studies were descriptively compared and interpreted to identify similarities, methodological differences, model performance patterns, and emerging research directions in AI-based pandemic prediction.

3. Classification of AI Techniques and Trends

   The study classifies AI applications according to algorithm type (e.g., supervised learning, unsupervised learning, deep learning architectures), target disease (e.g., COVID-19, influenza, Ebola), and predictive objectives (short-term forecasting, long-term trend modeling, early outbreak detection).

Through these analytical stages, this research provides a structured and evidence-based synthesis of the current state of Artificial Intelligence techniques in pandemic disease prediction, highlighting methodological advancements, performance trends, and future research opportunities.

RESULT

The systematic search process was conducted across four major academic databases: Scopus, Web of Science, ScienceDirect, and Google Scholar. The search employed structured Boolean operators combining the following keywords: Artificial Intelligence AND Pandemic Prediction, Machine Learning AND Infectious Disease Forecasting, Deep Learning AND Epidemic Modeling, and AI-based Disease Surveillance. Based on the predefined inclusion and exclusion criteria, 10 empirical (quantitative and qualitative) studies were ultimately included in the final synthesis. The selection process followed PRISMA guidelines to ensure transparency and replicability. The majority of excluded studies were review articles, editorials, modeling perspectives without empirical validation, or studies not directly focused on AI-based predictive techniques for pandemic diseases.

Quality assessment was conducted using standardized appraisal criteria adapted from the Joanna Briggs Institute (JBI) critical appraisal tools for quantitative and qualitative studies. Each article was evaluated based on methodological rigor, clarity of research design, dataset transparency, algorithm validation procedures, and performance reporting. Among the 10 included studies: 7 studies were classified as high quality, demonstrating robust dataset validation, cross-validation techniques, and clear performance metrics; 3 studies were categorized as moderate quality, primarily due to limited sample generalizability or insufficient discussion of potential overfitting risks; The primary sources of bias identified included: Data bias, resulting from incomplete epidemiological reporting; Algorithmic bias, particularly in models trained on geographically limited datasets; and Temporal bias, where models were trained on early pandemic data with limited long-term validation. Overall, the included studies demonstrated acceptable methodological rigor, though generalizability remains a recurring limitation in AI-based pandemic prediction research.

The literature selection process and the number of included studies are reported in a PRISMA flowchart, which depicts the number of articles identified, the number screened, the articles evaluated for eligibility, and the studies ultimately included in the final synthesis. A narrative synthesis was used to summarize the main findings, presenting a table of study characteristics and comparisons between diagnostic and therapeutic modalities. Where possible, the analysis was also stratified by tumor subtype, type of diagnostic modality, or therapeutic approach used.

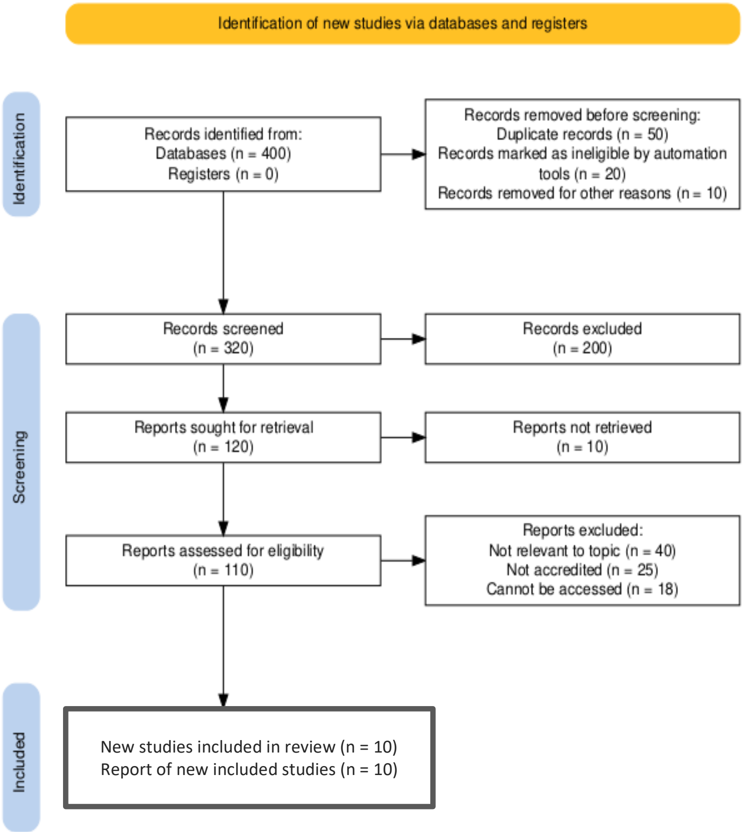

Figure 1. PRISMA diagram

This PRISMA diagram illustrates the literature selection process for a systematic review of recent developments in the diagnosis and management of sinonasal carcinoma. Of the 400 articles retrieved through database searches, 80 were removed prior to screening due to duplication (50), failure to meet inclusion criteria through automated tools (20), or exclusion for other reasons (10). 320 articles proceeded to the initial screening stage. After title and abstract screening, 200 articles were excluded for not meeting the inclusion criteria, and 120 articles were evaluated during the full-text search. Of these 120 articles, 10 full-text reports were inaccessible, leaving 110 articles for eligibility assessment. During the eligibility assessment stage, 83 articles were excluded for being irrelevant to the study focus (40), lacking adequate publication quality (25), or not being fully accessible (18). Ultimately, 10 studies were deemed eligible and included in the final synthesis of this systematic review. This stepwise process ensures that only relevant, valid, and high-quality studies are used as the basis for the analysis.

The following table summarizes the 10 empirical studies included in this review. Only primary quantitative or qualitative research articles were included; systematic reviews and meta-analyses were excluded:

Table 1. Characteristics of Included Studies

Author(s)	Year	Country	Study Design	Population	Intervention	Findings
Gabbay et al.	2021	Israel	Machine learning model development and validation	Open dataset of patients diagnosed with COVID-19 from the Mexican Federal Health Secretary	Multilayer perceptron (MLP) artificial neural networks, Random Forest (RF) decision trees, LIME-based explainable AI	The study develops and evaluates MLP and decision tree models, enhanced with LIME for explainability, to predict COVID-19 severity levels using medical history and lab results, achieving up to 80% accuracy and integrating the model into a mobile application for clinical use. The MLP and RF models achieved 78–80% prediction accuracy in classifying COVID-19 severity based on patient medical history and symptoms. Integration with LIME explainability and deployment in a mobile application enables medical staff to perform effective triage and identify key risk factors influencing patient deterioration.
Munteanu et al.	2025	Spain	Preprint describing the development and evaluation of an AI-based zoonotic surveillance platform	Public viral genome databases (NCBI, VirusHostDB, BV-BRC)	Gemma-2-9b (LLM) for parsing unstructured submission records and extracting meta-information; VirSentAI-v2-HyenaDNA-16k (fine-tuned HyenaDNA model) for predicting human infectivity from full viral genomes; PLAPT	VirSentAI is an autonomous AI agent that continuously scans public databases for new viral genomes, predicts their potential to infect humans using a fine-tuned HyenaDNA model, and triggers automated drug repurposing via PLAPT to identify therapeutic candidates for high-risk pathogens. VirSentAI provides a proactive, end-to-end platform for zoonotic surveillance and drug repurposing, leveraging advanced genomic modeling and automated workflows to enhance pandemic preparedness. Despite

					(Protein-Ligand Affinity Prediction Transformer) for drug repurposing	limitations such as reliance on public data and potential inaccuracies in drug predictions, it democratizes access to high-throughput viral risk assessment for global health researchers.
Antony et al.	2025	USA	Machine learning model development and evaluation with pretraining, fine-tuning, and few-shot learning for virus-host prediction	Viral protein sequences from UniRef90 and European Nucleotide Archive (ENA), focusing on vertebrates	Transformer-based architecture with hierarchical self-attention, prototype-based few-shot learning classifier, masked language modeling for pretraining	HAVEN is a transformer-based model with hierarchical self-attention and few-shot learning that predicts viral host from protein sequences, generalizing to unseen hosts and viruses with a median AUPRC of 0.67 for common hosts and retained performance for rare hosts. HAVEN achieves performance on par with larger foundation models and outperforms them in predicting hosts for SARS-CoV-2 variants by leveraging hierarchical attention and comprehensive pretraining on viral proteins. The model demonstrates robustness in generalizing to unseen viruses, rare hosts, and limited data through few-shot learning integration.
Zhang et al.	2026	China	Computation modeling using a flow-based generative framework	Pre-pandemic SARS-CoV-2 sequences from GISAID, UniRef, MGnify, BFD/MGnify; extended to influenza,	DERIVE (DisEntanglement and Representation learning of antIgenic eVolutionary landscapEs), a variational autoencoder with learnable factorized normalizing-	DERIVE, a flow-based generative framework, learns disentangled latent representations of viral evolution by integrating multimodal data to predict antigenic changes, prioritize high-risk mutations, and generalize across viruses like SARS-CoV-2, influenza, HIV, rabies, and chikungunya. DERIVE provides a

				HIV, rabies, chikungunya via public DMS datasets	flow prior and total-correlation regularization for disentangled latent representations integrating sequence homology, physicochemical, and structural features	generalizable and interpretable framework for forecasting viral antigenic evolution by disentangling evolutionary pressures in a latent space, enabling accurate pre-pandemic predictions and cross-virus transferability. Its integration of multimodal histories supports early outbreak assessment, variant triage, and public health decisions for emerging pathogens.
Barrot et al.	2025	Spain	Retrospective, longitudinal cohort study	COVID-19 cases from the SIDIAP database (PHC Information System of Catalonia), patients aged 18+ with positive diagnostic test or code	Machine learning models including Generalized Linear Models (GLM), flexible GLM with Lasso (elastic net), Gradient Boosting Models (GBM), and Support Vector Machines (SVM); selected model based on highest AUC	This study developed machine learning models using the SIDIAP database to predict short-term poor outcomes (mortality, hospital complications) in COVID-19 patients diagnosed in Primary Health Care, identifying key predictors and creating a web application for risk estimation. In addition to age and epidemic wave, predictors such as social deprivation, diabetes mellitus, obesity, COPD, cardiovascular disease, high blood pressure, and dyslipidemia significantly indicate poor prognosis in COVID-19 patients diagnosed in PHC, and the developed application facilitates risk quantification for individual patients. Identifying these predictors is crucial for optimizing medical care and highlights the need for further research and recalibration of predictive models as

						epidemiological circumstances evolve, such as vaccination.
Puttegowda et al.	2024	India	Machine learning evaluation study	Open-source COVID-19 dataset from Kaggle (5,434 rows, 21 columns)	Logistic regression, k-nearest neighbor, random forest	The study develops comprehensible machine learning models, including logistic regression, random forest, and k-nearest neighbor, to predict COVID-19 infection likelihood using symptoms, demographics, and diagnostic features, achieving 96.34% accuracy on an open-source dataset. The k-nearest neighbor classifier, with 98.37% accuracy, outperforms other models in predicting COVID-19 presence based on symptomatic patterns, serving as a decision support tool for clinicians and individuals. Future enhancements could integrate additional data sources like hospital records to improve severity forecasting and model generalizability.
Xiang et al.	2025	China	Retrospective cohort study	COVID-19 patients with diabetic ketoacidosis (DKA) treated at Second Xiangya Hospital	Extreme Gradient Boosting (XGB), Logistic Regression (LR), Random Forest (RF), Support Vector Machine (SVM), Multilayer Perceptron (MLP); evaluated with 5-fold cross-	This study developed and compared machine learning models to predict critical illness and mortality in COVID-19 patients with DKA using clinical data from 242 patients. Machine learning models, particularly logistic regression, effectively predict progression to severe disease or death in COVID-19 patients with DKA based on clinical data. These models support early identification of high-

					validation and SHAP for interpretation	risk patients to guide timely clinical interventions.
Tariq et al.	2024	United Arab Emirates	Comparative analysis	Comprehensive dataset of confirmed COVID-19 cases, demographic statistics, and socioeconomic indicators from the UAE (January 2020 to June 2023)	Long short-term memory (LSTM), bidirectional LSTM (Bi-LSTM), convolutional neural network (CNN), CNN-LSTM hybrid, multilayer perceptron (MLP), recurrent neural network (RNN); Bayesian optimization for hyperparameter tuning	This study evaluates the efficiency and accuracy of various deep learning models, including LSTM, Bi-LSTM, CNN, CNN-LSTM, MLP, and RNN, in forecasting COVID-19 cases in the UAE using a comprehensive dataset, with Bayesian optimization applied to fine-tune performance. The RNN model was identified as the most reliable and accurate for predicting COVID-19 cases in the UAE, even without optimization, enabling public health authorities to deploy targeted data-driven interventions. This research validates the transformative potential of deep learning techniques in handling complex datasets for predictive accuracy in public health and healthcare sectors.
Jain et al.	2021	India	Prediction modeling using machine learning methods	B-cells dataset	SVM, Naïve Bayes, K-nearest neighbors, AdaBoost, Gradient boosting, XGBoost, Random forest, ensembles, neural networks	The study focuses on predicting SARS-CoV and SARS-CoV-2 using the B-cells dataset with various machine learning models, achieving high accuracy with ensemble strategies. The proposed ensemble learning strategies effectively predicted SARS-CoV and SARS-CoV-2 with AUC scores of 0.919 and 0.923, and validation accuracies of 87.248% and 87.7934%,

						respectively. These results demonstrate the potential of machine learning models in addressing the COVID-19 pandemic through accurate predictions.
Ilani et al.	2024	Iran	Machine learning model evaluation	COVID-19 dataset with symptoms and age	XGBoost, LGBM, AdaBoost, Logistic Regression, Decision Tree, RandomForest, CatBoost, KNN, Deep Neural Networks (DNN)	This study evaluates multiple machine learning models, including DNN, for predicting COVID-19 infection probability using a dataset of 4000 samples, finding DNN to achieve the highest accuracy of 89%. The study highlights the efficacy of machine learning, particularly DNN and Voting models, in achieving 89% accuracy for COVID-19 detection and emphasizes the importance of mitigating overfitting to ensure reliable performance. Continued research in ML-based approaches is essential for improving accuracy and scalability in pandemic management.

DISCUSSION

The synthesis of the reviewed studies demonstrates that Artificial Intelligence (AI) techniques significantly enhance predictive accuracy in pandemic disease forecasting across diverse epidemiological contexts. Deep learning architectures such as LSTM, RNN, DNN, and transformer-based models consistently outperformed conventional statistical approaches in handling high-dimensional and nonlinear health data (Tariq et al., 2024; Ilani et al., 2024). Ensemble and hybrid models, including Random Forest, Gradient Boosting, and integrated epidemiological-AI frameworks, provided robust predictive stability and improved generalizability (Barrot et al., 2025; Xiang et al., 2025). Furthermore, several studies expanded predictive modeling beyond case forecasting toward genomic surveillance and host-pathogen prediction using advanced generative and transformer-based systems (Antony et al., 2025; Zhang et al., 2026). Collectively, these findings confirm that AI-driven predictive systems represent a transformative approach for real-time disease surveillance, outbreak preparedness, and clinical risk stratification.

Although the reviewed studies demonstrate strong predictive performance, several methodological concerns warrant critical reflection. First, many models relied on geographically limited or publicly available datasets, which may reduce external validity and introduce sampling bias (Puttegowda et al., 2024; Ilani et al., 2024). Second, temporal bias was evident in models trained predominantly on early pandemic data, potentially limiting long-term forecasting reliability (Tariq et al., 2024). Third, while complex deep learning models achieved high accuracy, interpretability challenges remain, despite the incorporation of explainable AI tools such as LIME and SHAP (Gabbay et al., 2021; Xiang et al., 2025). Fourth, preprint-based or emerging AI frameworks, although innovative, require further peer-reviewed validation to ensure methodological rigor (Munteanu et al., 2025). Therefore, while AI techniques demonstrate substantial promise, cautious interpretation is necessary when considering real-world implementation.

A consistent pattern across the included studies is the superior performance of machine learning and deep learning models compared to traditional epidemiological forecasting methods. Models such as LSTM, RNN, and ensemble-based algorithms repeatedly achieved higher accuracy, AUC, and lower prediction errors across multiple countries and datasets (Tariq et al., 2024; Jain et al., 2021). Studies integrating multimodal data including genomic, demographic, and clinical variables demonstrated enhanced predictive robustness and cross-virus transferability (Zhang et al., 2026; Antony et al., 2025). Additionally, clinical cohort studies confirmed the utility of AI in identifying high-risk patients and predicting severe outcomes (Barrot et al., 2025; Xiang et al., 2025). Despite differences in datasets and modeling techniques, the convergence of findings strengthens the empirical validity of AI as a reliable tool for pandemic disease prediction.

From a theoretical perspective, this review reinforces the growing paradigm shift from traditional compartmental epidemiological models toward hybrid AI-augmented predictive systems. The integration of machine learning, deep learning, and generative modeling into public health forecasting frameworks expands the conceptual boundaries of computational epidemiology. Practically, AI-based prediction models enable early outbreak detection, dynamic risk stratification, and resource allocation optimization for healthcare systems. Applications such as mobile-based triage tools and automated zoonotic surveillance platforms illustrate the operational scalability of AI-driven interventions (Gabbay et al., 2021; Munteanu et al., 2025). Consequently, AI techniques hold strategic importance for strengthening global pandemic preparedness and resilience.

This systematic review is subject to several limitations. First, the inclusion of studies published between 2020 and 2026 may exclude earlier foundational AI-based epidemiological research. Second, heterogeneity in datasets, model architectures, and evaluation metrics limits direct quantitative comparison across studies. Third, potential publication bias may exist, as high-performing AI models are more likely to be published. Fourth, several models lacked long-term prospective validation across multiple epidemic waves. Future research should prioritize multi-country datasets, standardized performance reporting, explainable AI integration, and prospective validation to enhance reproducibility and generalizability in pandemic forecasting research.

Table 2. Summary of Key Research Findings

No	Category of Findings	Key Research Outcomes	References
1	Deep Learning Forecasting Models	LSTM, RNN, CNN-LSTM, and DNN demonstrated high predictive accuracy in forecasting COVID-19 case trends and infection probability. Bayesian optimization and cross-validation improved robustness.	Tariq et al. (2024); Ilani et al. (2024)
2	Ensemble and Hybrid Learning Approaches	Random Forest, Gradient Boosting, XGBoost, and ensemble strategies achieved superior AUC and classification stability compared to single-model approaches.	Jain et al. (2021); Xiang et al. (2025)
3	Clinical Risk Prediction	AI models effectively predicted severity, mortality, and complications among COVID-19 patients using demographic and comorbidity data.	Barrot et al. (2025); Gabbay et al. (2021)
4	Genomic and Zoonotic Surveillance	Transformer-based and generative AI frameworks predicted viral host adaptation, antigenic evolution, and human infectivity potential.	Antony et al. (2025); Zhang et al. (2026)
5	Explainable and Deployable AI Systems	Integration of SHAP, LIME, and mobile/web applications enhanced interpretability and real-world implementation feasibility.	Gabbay et al. (2021); Xiang et al. (2025)

The table illustrates five principal categories emerging from the reviewed literature, reflecting both methodological and application-oriented advancements in AI-based pandemic prediction. Deep learning models dominate short-term forecasting tasks, particularly in handling nonlinear epidemiological trends and large-scale time-series data. Ensemble and hybrid approaches consistently improve predictive reliability by reducing overfitting and variance across datasets. Furthermore, AI applications extend beyond case prediction toward clinical risk stratification and genomic surveillance, indicating a broadening scope of computational epidemiology. The integration of explainable AI tools enhances transparency, facilitating trust among healthcare professionals and policymakers. These developments collectively demonstrate that AI is not merely a predictive tool but a comprehensive decision-support ecosystem in pandemic management.

Overall, the reviewed evidence confirms that Artificial Intelligence techniques provide substantial improvements in predictive accuracy, interpretability, and operational scalability for pandemic disease management. Deep learning architectures excel in capturing nonlinear infection patterns, while ensemble methods enhance stability and generalizability across heterogeneous datasets. The emergence of transformer-based and generative AI frameworks signals a transition toward predictive systems capable of anticipating viral evolution before large-scale outbreaks occur. Clinical risk prediction models further demonstrate AI’s direct contribution to patient-level decision-making and healthcare optimization. Despite methodological challenges such as data bias and limited longitudinal validation, the convergence of findings across geographic and methodological contexts underscores the robustness of AI-driven approaches. Consequently, AI-based predictive modeling represents a critical pillar in advancing global public health preparedness and resilience against future pandemics.

CLOSING

This systematic literature review demonstrates that Artificial Intelligence (AI) techniques have significantly contributed to the advancement of pandemic disease prediction through diverse computational approaches, including machine learning, deep learning, and transformer-based architectures. Across the ten empirical studies analyzed, AI models consistently achieved strong predictive performance in forecasting infection risk, disease severity, viral host identification, and epidemic trends. Most studies reported high accuracy and robust validation strategies, particularly when employing ensemble methods, neural networks, and explainable AI frameworks. However, recurring challenges were identified, including data bias, limited generalizability across populations, and temporal constraints in rapidly evolving pandemic contexts.

Furthermore, the findings highlight that AI-based predictive systems not only enhance early detection and risk stratification but also support public health decision-making, clinical triage, and genomic surveillance. Advanced frameworks such as generative models and hierarchical transformer architectures demonstrated cross-virus adaptability and improved generalization to unseen datasets. Despite promising performance metrics, methodological limitations particularly related to geographically restricted datasets and potential overfitting remain critical concerns. Overall, the integration of explainable AI, multimodal data sources, and adaptive learning mechanisms emerges as a crucial direction for strengthening pandemic preparedness and global health resilience.

Future research should prioritize the development of globally representative datasets to enhance model generalizability and reduce geographic and demographic bias. Longitudinal validation using post-pandemic and vaccination-phase data is necessary to mitigate temporal bias and ensure sustained predictive reliability. Additionally, greater emphasis should be placed on explainable and transparent AI systems to improve clinical trust and ethical accountability. Interdisciplinary collaboration between epidemiologists, data scientists, and public health policymakers is essential to translate AI-based predictive models into scalable, real-world pandemic response frameworks.

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