
| RESEARCH ARTICLE

Comparing AI-Based and Traditional Epidemiological Models for Epidemic Forecasting in the USA. A Comparative Study of AI Models Versus Conventional Statistical Public Health Methods.

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| ABSTRACT

Artificial intelligence has emerged as a transformative force in epidemic forecasting, offering new opportunities to complement and extend traditional epidemiological modeling approaches. This study presents a comparative analysis of AI-based models and conventional public health forecasting methods for epidemic prediction in the United States. The research examines the performance and practical implications of mechanistic and statistical techniques alongside modern machine learning frameworks within a unified analytical setting. The methodological framework incorporates traditional epidemiological models, including SEIR and ARIMA approaches, together with Random Forest and Long Short-Term Memory architectures representing contemporary artificial intelligence methods. A standardized preprocessing pipeline, common evaluation criteria, and consistent experimental procedures are employed to ensure fair comparisons across forecasting paradigms. Beyond predictive accuracy, the study considers interpretability, robustness, computational efficiency, and operational applicability as critical dimensions of effective epidemic forecasting. The findings indicate that AI-driven models exhibit stronger capabilities in capturing nonlinear transmission patterns and adapting to rapidly evolving epidemic conditions. Deep learning methods, particularly recurrent architectures, demonstrate enhanced performance during complex outbreak waves characterized by changing behavioral and intervention dynamics. Traditional epidemiological approaches, however, retain important advantages in interpretability, transparency, and policy communication, providing mechanistic insights that remain essential for public health decision-making. The results further suggest that methodological diversity contributes to greater forecasting resilience and supports more reliable epidemic preparedness strategies. The study concludes that artificial intelligence should not be viewed as a replacement for conventional epidemiological modeling but rather as a complementary set of tools capable of strengthening existing public health infrastructures. Future forecasting systems are likely to benefit from hybrid and collaborative frameworks that integrate mechanistic understanding with data-driven learning capabilities. Such an approach offers a promising pathway toward more accurate, interpretable, and operationally effective epidemic forecasting in the United States.

| KEYWORDS

Epidemic Forecasting, Artificial Intelligence, Machine Learning, Epidemiological Modeling, Public Health Analytics, SEIR, LSTM.

| ARTICLE INFORMATION

ACCEPTED: 01 May 2026

PUBLISHED: 02 July 2026

DOI: 10.32996/fcsai.2026.5.9.7

1. Introduction

1.1 Background and Motivation

Epidemic forecasting has long occupied a central position within public health planning and disease control efforts in the United States. Accurate predictions regarding disease transmission dynamics enable healthcare institutions, policymakers, and emergency response agencies to allocate resources effectively, implement timely interventions, and mitigate social and economic disruptions arising from infectious disease outbreaks. The increasing interconnectedness of populations, rapid urbanization, and global mobility patterns have amplified the importance of robust forecasting systems capable of anticipating epidemic trajectories before healthcare systems become overwhelmed. Consequently, both researchers and public health practitioners continue to seek methodological improvements that can enhance predictive reliability across varying epidemiological contexts. The foundations of modern epidemic forecasting are deeply rooted in classical mathematical epidemiology. Kermack and McKendrick (1927) introduced the seminal susceptible-infected-recovered framework, establishing a theoretical basis for understanding how infectious diseases propagate through populations and how transmission parameters influence epidemic outcomes [10]. Their work demonstrated that epidemic behavior could be represented mathematically through compartmental structures, allowing researchers to estimate thresholds for disease spread and evaluate intervention strategies. The conceptual principles emerging from these early models continue to influence contemporary epidemiological analyses and remain embedded within many forecasting systems used by public health organizations throughout the United States.

Over subsequent decades, traditional epidemiological approaches evolved to incorporate increasingly sophisticated statistical techniques and computational tools. These developments enabled researchers to model seasonal influenza outbreaks, emerging zoonotic diseases, and large-scale public health emergencies with greater precision. Nevertheless, forecasting infectious diseases presents inherent challenges due to nonlinear transmission mechanisms, behavioral adaptations, environmental variability, demographic heterogeneity, and policy interventions that continuously reshape epidemic trajectories. Such complexities require forecasting frameworks that balance theoretical interpretability with practical predictive performance. The persistent tension between explanatory power and forecasting accuracy has motivated ongoing investigations into alternative modeling paradigms capable of addressing these multidimensional challenges. The significance of epidemic forecasting became especially evident during recent global health crises. Viboud et al. (2018) synthesized lessons from the RAPIDD Ebola forecasting challenge and demonstrated that forecasting efforts often encounter substantial uncertainties arising from incomplete data, evolving transmission patterns, and methodological differences among competing models [17]. Their findings emphasized that no single forecasting approach consistently outperforms others across all outbreak scenarios, highlighting the importance of methodological diversity and collaborative evaluation frameworks. The experiences derived from Ebola forecasting exercises provided valuable insights that later informed responses to influenza epidemics and the COVID-19 pandemic within the United States.

The unprecedented scale and societal impact of COVID-19 further accelerated interest in advanced analytical methods for epidemic prediction. Traditional compartmental and statistical approaches offered important epidemiological insights, yet many researchers observed limitations in capturing rapidly changing behavioral responses, mobility patterns, and high-dimensional interactions among numerous explanatory variables. Simultaneously, advances in artificial intelligence and machine learning introduced novel opportunities for extracting complex nonlinear relationships from large datasets generated through digital surveillance systems, healthcare records, mobility networks, and environmental monitoring platforms. These developments encouraged interdisciplinary collaborations between epidemiologists, computer scientists, statisticians, and public health experts seeking more adaptive forecasting methodologies. Artificial intelligence has increasingly transformed predictive analytics across numerous scientific domains due to its capacity to process massive datasets and identify hidden patterns that conventional techniques may overlook. Machine learning algorithms such as random forests, gradient boosting methods, recurrent neural networks, and deep learning architectures possess the flexibility to model intricate temporal dependencies without relying exclusively on predefined epidemiological assumptions. Their ability to learn directly from observed data presents an attractive alternative for epidemic forecasting, particularly when transmission mechanisms remain partially understood or evolve rapidly during emerging outbreaks. Nevertheless, questions persist regarding the interpretability, generalizability, and practical deployment of these models within real-world public health systems.

The coexistence of traditional epidemiological methods and modern artificial intelligence techniques has generated a growing need for systematic comparative analyses. While classical models offer strong theoretical foundations and transparent representations of disease processes, AI-driven approaches promise enhanced predictive accuracy through data-driven learning mechanisms. Understanding the relative strengths and weaknesses of these methodologies is therefore essential for guiding future investments in public health analytics and informing the design of integrated forecasting frameworks. The motivation underlying the present study emerges from this evolving landscape, where technological innovation and established

epidemiological principles must be evaluated collectively to determine their respective contributions toward improving epidemic preparedness and response capabilities within the United States.

1.2 Problem Statement and Research Objectives

Despite decades of progress in epidemiological modeling, substantial challenges remain in producing accurate and reliable forecasts for infectious disease outbreaks in the United States. Traditional forecasting methods, including compartmental frameworks and classical statistical approaches, have provided valuable insights into disease dynamics and intervention strategies. However, these methods often rely on simplifying assumptions regarding homogeneous mixing, fixed transmission parameters, and stable behavioral patterns that may not adequately reflect the complexities of modern societies. Rapid demographic changes, evolving mobility networks, heterogeneous healthcare access, and dynamic policy responses introduce layers of uncertainty that complicate the forecasting process and limit the effectiveness of conventional analytical techniques. Seasonal influenza forecasting provides an illustrative example of these difficulties. Reich et al. (2019) evaluated real-time multi-model ensemble forecasts for seasonal influenza across the United States and demonstrated that combining multiple forecasting approaches generally improved predictive performance relative to individual models [13]. Their findings highlighted both the potential benefits and inherent limitations of existing epidemiological methods, emphasizing that forecasting accuracy varies considerably across seasons, geographic regions, and prediction horizons. The study further revealed that uncertainty quantification and methodological diversity remain critical components of effective public health forecasting systems.

These observations underscore the persistent need for innovative approaches capable of addressing the shortcomings associated with single-model paradigms. Conventional epidemiological models frequently prioritize interpretability and theoretical consistency over predictive flexibility. While such characteristics are indispensable for understanding transmission mechanisms and evaluating intervention policies, they may constrain the ability of models to adapt to rapidly changing conditions during emerging outbreaks. Parameter estimation procedures often depend upon assumptions that become increasingly difficult to maintain as epidemics evolve, particularly when human behavior, vaccination patterns, mobility restrictions, and environmental factors fluctuate over time. Consequently, forecast reliability can deteriorate when real-world complexities diverge substantially from underlying model assumptions. In parallel, artificial intelligence and machine learning methodologies have gained prominence as potential alternatives for epidemic forecasting. These approaches leverage computational learning algorithms to identify complex nonlinear relationships within large-scale datasets without requiring explicit formulations of disease transmission mechanisms. Their capacity to integrate diverse information sources, including epidemiological records, mobility data, climatic variables, and demographic indicators, offers promising opportunities for improving predictive performance. Nevertheless, AI-based models introduce their own challenges, including issues related to interpretability, data quality, overfitting, and the transparency of decision-making processes. Public health institutions often require models whose outputs can be readily explained and justified, creating an important tension between predictive power and practical usability.

The coexistence of these competing methodological traditions raises several important questions for researchers and policymakers. It remains unclear whether AI-driven approaches consistently outperform traditional epidemiological models across different forecasting contexts or whether their advantages depend upon specific diseases, datasets, and temporal scales. Similarly, there is limited consensus regarding the trade-offs between model accuracy, interpretability, computational efficiency, and implementation feasibility within operational public health environments. Addressing these uncertainties requires comprehensive comparative studies that evaluate multiple methodologies using standardized performance criteria and common datasets. The central problem motivating this research, therefore, concerns the absence of a unified understanding regarding the comparative effectiveness of artificial intelligence and traditional epidemiological models for epidemic forecasting in the United States. Existing literature often examines these approaches independently, making it difficult to establish clear conclusions concerning their relative merits and limitations. Without systematic comparisons, public health agencies may encounter challenges when selecting forecasting tools that align with operational requirements and policy objectives. The need for evidence-based evaluations has become increasingly urgent as advances in machine learning continue to influence decision-making processes across healthcare and governmental institutions.

Accordingly, this study seeks to investigate the comparative performance of AI-based forecasting models and conventional epidemiological methods within a unified analytical framework. The research aims to determine whether machine learning approaches provide measurable improvements in predictive accuracy while maintaining acceptable levels of interpretability and robustness. The study also seeks to identify circumstances under which traditional methods retain strategic advantages, particularly in contexts requiring theoretical transparency and policy communication. By examining these issues, the research intends to contribute to broader discussions concerning the future integration of artificial intelligence within public health forecasting systems. The investigation is guided by the overarching objective of evaluating the strengths, weaknesses, and practical implications of competing forecasting paradigms. Specifically, the study explores how different modeling approaches

perform across epidemic scenarios relevant to the United States, assesses their computational and interpretative characteristics, and considers their suitability for supporting evidence-based public health interventions. Through this comparative perspective, the research endeavors to advance understanding regarding the complementary roles that artificial intelligence and classical epidemiological frameworks may play in strengthening national preparedness for future infectious disease threats.

1.3 Contributions and Organization of the Paper

The present study contributes to ongoing discussions concerning the modernization of epidemic forecasting methodologies by establishing a comparative framework through which artificial intelligence models and traditional epidemiological approaches can be evaluated within a common analytical setting. Rather than treating these paradigms as mutually exclusive alternatives, the paper adopts the perspective that both methodologies possess distinct advantages that may complement one another in practical public health applications. The research therefore emphasizes comparative understanding, methodological transparency, and the identification of contexts in which different forecasting strategies provide the greatest value for decision makers and healthcare institutions. A primary contribution of the paper lies in its integration of machine learning techniques with established epidemiological principles into a unified conceptual framework. The analysis considers predictive performance alongside broader considerations such as interpretability, robustness, computational requirements, and operational feasibility. By examining these dimensions collectively, the study seeks to move beyond narrow assessments based exclusively on forecast accuracy and instead promote a more comprehensive understanding of what constitutes effective epidemic prediction within contemporary public health systems. Such an approach acknowledges that forecasting models must ultimately support actionable decisions rather than merely optimize statistical metrics.

The paper also contributes by highlighting the importance of interdisciplinary collaboration between epidemiology, statistics, computer science, and data-driven public health practice. Advances in artificial intelligence continue to reshape analytical capabilities across numerous domains, yet successful implementation within epidemic forecasting requires careful integration with established theoretical knowledge and institutional requirements. The comparative perspective adopted in this research encourages dialogue regarding how traditional and modern approaches may coexist within future forecasting infrastructures, potentially leading to hybrid methodologies that combine mechanistic understanding with adaptive learning capabilities. The remainder of the paper is organized into several sections. Following this introduction, the literature review examines existing research on traditional epidemiological models and emerging artificial intelligence approaches used for epidemic prediction. The methodology section describes the datasets, preprocessing procedures, model development processes, and evaluation criteria employed in the comparative analysis. The results and discussion section presents the findings, interprets differences in model performance, and considers their implications for public health policy and practice in the United States. Finally, the concluding section summarizes the major insights derived from the study and outlines potential directions for future research involving integrated and adaptive epidemic forecasting frameworks.

2. Literature Review

2.1 Traditional Epidemiological Forecasting Models

Traditional epidemiological forecasting models constitute the intellectual foundation upon which contemporary public health prediction systems have been developed. Their primary objective has been to represent disease transmission dynamics through mathematically interpretable structures that capture interactions among susceptible, infected, and recovered populations. These frameworks have historically enabled researchers and policymakers to anticipate epidemic trajectories, estimate intervention effects, and formulate evidence-based responses to infectious disease threats. The continued relevance of traditional approaches stems from their capacity to translate biological mechanisms into analytical formulations that provide both explanatory insight and practical forecasting capabilities. The mathematical underpinnings of compartmental epidemiology have undergone substantial refinement over the past century. Hethcote (2000) synthesized the theoretical development of infectious disease mathematics and demonstrated how compartmental models, including SIR, SEIR, SIS, and related variants, provide rigorous mechanisms for examining transmission processes, threshold behaviors, endemic equilibria, and intervention strategies across diverse epidemiological settings [8]. The study emphasized that these models derive their strength from explicit representations of biological processes, enabling researchers to interpret parameters such as contact rates, recovery dynamics, and reproductive numbers in meaningful public health contexts. Such interpretability remains a defining advantage of traditional epidemiological frameworks, particularly when policymakers require transparent explanations for projected outcomes and recommended interventions.

Beyond mechanistic compartmental approaches, statistical time-series methodologies have played an equally important role in epidemic forecasting. Classical forecasting techniques focus on identifying temporal structures within observed disease incidence data rather than explicitly modeling biological transmission mechanisms. Box et al. (2015) established the theoretical and practical foundations of time-series forecasting through autoregressive integrated moving average methodologies,

demonstrating their effectiveness in capturing trend, seasonality, persistence, and stochastic variation across complex temporal processes [3]. These methods have been extensively applied within public health research, particularly for seasonal influenza surveillance and routine disease monitoring, where historical observations provide sufficient information for generating short-term predictions. Their methodological simplicity and statistical rigor continue to support their widespread use in epidemiological practice.

Recent developments within traditional forecasting paradigms have sought to address limitations associated with representing multiple epidemic waves and heterogeneous transmission dynamics. Chowell et al. (2019) introduced a sub-epidemic modeling framework that decomposes large outbreaks into overlapping transmission processes, thereby improving short-term forecasting performance during complex epidemic events [6]. Their approach acknowledged that epidemics often consist of interconnected sub-processes influenced by behavioral changes, interventions, and localized transmission clusters rather than a single homogeneous wave. By incorporating this perspective, traditional epidemiological modeling expanded its capacity to capture real-world complexities while preserving the interpretability that characterizes mechanistic frameworks. Such innovations demonstrate that conventional approaches continue to evolve in response to emerging public health challenges.

The application of traditional models to seasonal influenza forecasting has yielded particularly influential insights regarding predictive performance and operational implementation. Shaman and Karspeck (2012) developed a forecasting framework that combined epidemiological models with data assimilation techniques, producing accurate predictions of influenza outbreaks across multiple regions within the United States [15]. Their findings illustrated the value of integrating observational data into mechanistic models to improve forecast quality while maintaining theoretical coherence regarding disease transmission dynamics. The study further demonstrated that traditional epidemiological approaches remain capable of supporting real-time public health decision-making when supplemented by systematic updating procedures and high-quality surveillance information. Despite these achievements, traditional forecasting models encounter several persistent challenges that influence their applicability within contemporary epidemic contexts. Many compartmental frameworks rely upon assumptions concerning homogeneous population mixing, fixed parameter values, and stable behavioral responses that may not adequately reflect the complexity of modern societies. Rapid changes in mobility patterns, demographic structures, public health interventions, and social behaviors introduce nonlinear effects that can complicate parameter estimation and reduce predictive reliability. Statistical time-series methods likewise depend upon historical regularities that may break down during emerging outbreaks characterized by unprecedented conditions and rapidly evolving transmission mechanisms.

Another important consideration involves the balance between explanatory capability and predictive flexibility. Traditional models excel in providing mechanistic interpretations that facilitate policy communication and intervention planning. Their parameters often correspond directly to epidemiological concepts familiar to public health professionals, thereby enhancing transparency and trust in forecasting outputs. However, this interpretability sometimes constrains their ability to incorporate large numbers of heterogeneous predictors or adapt dynamically to changing environmental conditions. The requirement to specify explicit structural assumptions can limit responsiveness when epidemic behavior deviates substantially from established theoretical expectations. Nevertheless, traditional epidemiological forecasting continues to occupy a vital role within public health systems. Its enduring influence reflects not only historical significance but also practical advantages related to transparency, theoretical consistency, and policy relevance. Contemporary forecasting infrastructures frequently incorporate compartmental models, statistical approaches, and data assimilation techniques as core analytical components. The evolution of these methods demonstrates an ongoing commitment to refining mechanistic understanding while addressing emerging complexities associated with infectious disease transmission. Consequently, traditional epidemiological models remain indispensable benchmarks against which newer artificial intelligence approaches must be evaluated, particularly in comparative studies seeking to assess the broader future of epidemic forecasting.

2.2 AI-Based Epidemic Prediction Approaches

The rapid advancement of artificial intelligence has transformed forecasting methodologies across numerous scientific disciplines, including epidemiology and public health analytics. Unlike traditional mechanistic frameworks that depend upon predefined assumptions regarding disease transmission processes, machine learning approaches emphasize data-driven learning mechanisms capable of identifying complex and nonlinear relationships directly from observed information. The increasing availability of large-scale epidemiological datasets, mobility records, environmental indicators, and digital surveillance platforms has accelerated the adoption of AI techniques for epidemic prediction, creating new opportunities for improving forecasting performance and adaptive decision-making within healthcare systems. Tree-based learning algorithms represent some of the earliest and most influential machine learning methods applied to predictive analytics. Breiman (2001) introduced random forests as an ensemble learning framework that combines multiple decision trees to enhance predictive accuracy, reduce overfitting, and improve robustness against noisy datasets [4]. The methodological advantages of random forests, including their capacity to model nonlinear interactions and accommodate heterogeneous variables, have made them particularly attractive for

epidemiological applications involving demographic, environmental, and behavioral determinants of disease spread. Their relative interpretability compared with deeper neural architectures further contributes to their popularity within public health contexts where transparent decision-making remains important.

Advances in gradient boosting techniques subsequently expanded the capabilities of ensemble learning for complex predictive tasks. Chen and Guestrin (2016) developed XGBoost as a scalable tree-boosting framework optimized for computational efficiency and high predictive performance across large datasets [5]. The algorithm's ability to incorporate regularization mechanisms, handle missing data, and exploit parallel processing resources has facilitated its widespread adoption within health informatics and epidemic forecasting research. In many applications, XGBoost demonstrates strong predictive performance while preserving some degree of feature interpretability, thereby offering a practical compromise between accuracy and transparency that aligns with operational requirements in public health institutions. Deep learning architectures introduced additional opportunities for modeling temporal dependencies inherent within epidemic processes. Hochreiter and Schmidhuber (1997) proposed long short-term memory networks as recurrent neural systems capable of learning long-range temporal relationships through specialized memory structures and gating mechanisms [9]. These innovations addressed limitations associated with conventional recurrent neural networks and enabled more effective representation of sequential phenomena characterized by delayed effects and evolving patterns. Epidemic forecasting naturally benefits from such capabilities because disease transmission unfolds over time through interconnected processes influenced by incubation periods, interventions, behavioral responses, and environmental conditions. Consequently, LSTM architectures have become prominent tools within contemporary predictive epidemiology.

The emergence of the COVID-19 pandemic dramatically accelerated experimentation with artificial intelligence methods for epidemic prediction. Ardabili et al. (2020) evaluated multiple machine learning approaches for forecasting COVID-19 outbreaks and demonstrated that data-driven algorithms possess considerable potential for capturing epidemic trends when trained on sufficiently representative datasets [2]. Their analysis emphasized the flexibility of machine learning methodologies in adapting to rapidly evolving conditions while highlighting the importance of careful model selection and validation procedures. The study reinforced broader arguments that artificial intelligence can complement traditional epidemiological frameworks, particularly during novel outbreaks where mechanistic understanding remains incomplete. Additional investigations explored combinations of classical mathematical models with machine learning techniques to improve predictive performance. Wang et al. (2020) employed logistic growth formulations alongside machine learning algorithms to forecast COVID-19 epidemic trajectories, illustrating how hybrid approaches may leverage strengths from both paradigms [18]. Their findings suggested that integrating mechanistic assumptions with data-driven optimization can enhance robustness and adaptability during periods of rapid epidemiological change. Such work reflects a growing recognition that artificial intelligence need not replace traditional methods entirely but may instead augment their forecasting capabilities through complementary analytical mechanisms.

Similarly, Yang et al. (2020) combined modified SEIR structures with artificial intelligence methodologies to predict COVID-19 transmission trends under varying public health interventions in China [20]. The study demonstrated that integrating intervention effects with adaptive learning algorithms improved responsiveness to changing policy environments and behavioral conditions. By accounting for evolving non-pharmaceutical interventions, the research illustrated how AI-enhanced frameworks can accommodate dynamic processes that challenge conventional parameter estimation procedures. These developments further expanded interest in hybrid forecasting systems capable of balancing theoretical insight with predictive flexibility. More recent scholarship has emphasized the importance of data-centric perspectives within epidemic forecasting. Rodríguez et al. (2024) argued that machine learning performance depends fundamentally upon data quality, feature representation, uncertainty management, and systematic validation practices rather than algorithmic sophistication alone [14]. Their work highlighted the necessity of constructing robust data ecosystems that support reliable learning processes across diverse epidemiological contexts. The study also underscored challenges associated with interpretability, fairness, and deployment within real-world public health environments, emphasizing that successful implementation requires careful consideration of institutional constraints alongside technical innovation.

Despite impressive advances, AI-based epidemic prediction approaches continue to face important limitations. Many deep learning models function as highly complex systems whose internal decision processes remain difficult to interpret, potentially reducing trust among public health practitioners and policymakers. Dependence upon extensive training data introduces vulnerabilities when emerging diseases lack sufficient historical observations. Furthermore, issues related to model generalization, reproducibility, and ethical deployment require ongoing attention as artificial intelligence becomes increasingly integrated into healthcare infrastructures. Nevertheless, the capacity of machine learning algorithms to model nonlinear relationships, assimilate diverse information sources, and adapt to changing conditions positions them as influential components within the future landscape of epidemic forecasting research and practice.

2.3 Research Gaps and Comparative Framework

Although substantial progress has been achieved in both traditional epidemiological modeling and artificial intelligence approaches, important research gaps continue to hinder comprehensive understanding regarding their relative effectiveness. Existing studies frequently evaluate forecasting methodologies within isolated contexts, employing distinct datasets, performance metrics, and validation procedures that complicate direct comparisons across competing paradigms. The absence of standardized comparative frameworks limits the ability of researchers and public health institutions to determine which approaches offer the greatest practical value under varying epidemiological conditions. Tabataba et al. (2017) proposed a systematic framework for evaluating epidemic forecasts and emphasized the necessity of consistent assessment methodologies that incorporate accuracy, uncertainty quantification, calibration, and operational relevance [16]. Their work highlighted that meaningful comparisons require common benchmarks and transparent evaluation procedures capable of capturing the multidimensional nature of forecasting performance. Without such frameworks, conclusions regarding methodological superiority remain fragmented and potentially misleading, particularly when studies prioritize different objectives or utilize incompatible datasets.

Contemporary scholarship increasingly recognizes opportunities for integrating artificial intelligence with mechanistic epidemiological reasoning rather than treating these traditions as competing alternatives. Wang et al. (2025) conducted a comprehensive review of hybrid modeling strategies and argued that combining AI capabilities with established epidemiological principles may offer pathways toward more robust, interpretable, and adaptable forecasting systems [19]. The review identified numerous challenges related to transparency, deployment, validation, and interdisciplinary collaboration while emphasizing the potential benefits associated with unified analytical frameworks that leverage complementary strengths from both domains. The present study positions itself within this emerging research landscape by adopting a comparative perspective that evaluates artificial intelligence models and traditional epidemiological approaches using common methodological criteria. Rather than assuming inherent superiority on either side, the research seeks to examine predictive performance, interpretability, robustness, and practical applicability as interconnected dimensions of effective epidemic forecasting. This framework provides a foundation for understanding how diverse modeling paradigms can contribute to future public health preparedness efforts within the United States and supports broader discussions regarding the development of integrated forecasting infrastructures capable of addressing increasingly complex infectious disease challenges.

3. Methodology

3.1 Dataset Description and Preprocessing

The study employed publicly available epidemic surveillance data representative of infectious disease trends within the United States, with a primary focus on COVID-19 and seasonal influenza incidence patterns. The dataset was designed to capture temporal variations in disease transmission across multiple regions and time periods, thereby providing a suitable foundation for evaluating both traditional epidemiological models and artificial intelligence approaches. Daily and weekly records of confirmed cases, hospitalizations, recoveries, and mortality indicators were incorporated to reflect the multidimensional characteristics of epidemic progression. The integration of multiple disease categories enabled the development of forecasting models capable of generalizing across different epidemiological scenarios while preserving the contextual relevance of public health applications.

To ensure analytical consistency, all observations were organized into a unified temporal framework. Date variables were standardized to facilitate chronological ordering and time-series analysis, while duplicate entries and inconsistent records were identified and removed during preliminary screening procedures. Missing values within numerical attributes were addressed through interpolation techniques and rolling-window imputation strategies to preserve temporal continuity without introducing abrupt distortions into disease trajectories. Outlier detection mechanisms were subsequently applied to identify anomalous reporting spikes arising from delayed notifications, administrative adjustments, or data aggregation inconsistencies. Where appropriate, such anomalies were smoothed using moving-average procedures while retaining genuine epidemic surges necessary for meaningful forecasting analysis.

Feature engineering constituted an important component of the preprocessing workflow. Temporal indicators including week numbers, month identifiers, seasonal categories, and lagged case variables were generated to capture recurring epidemic patterns and delayed transmission effects. Rolling averages over multiple time windows were computed to represent short-term and medium-term disease momentum, while growth rates and percentage changes were incorporated to quantify acceleration and deceleration within outbreak dynamics. Additional variables representing hospitalization ratios, recovery trends, and mortality proportions were constructed to enrich the predictive information available to machine learning algorithms. These engineered features provided complementary perspectives on epidemic behavior beyond raw incidence counts alone. Normalization procedures were implemented to ensure compatibility across different modeling frameworks. Numerical variables were transformed using min-max scaling techniques for neural-network-based models, while traditional statistical methods retained original measurement scales where interpretability of parameters remained important. Categorical attributes associated

with seasonal classifications and geographic identifiers were encoded using appropriate numerical representations to facilitate computational processing. The normalization process reduced disparities among variable magnitudes and contributed to stable optimization during model training, particularly for deep learning architectures sensitive to feature scaling.

The dataset was partitioned according to chronological order to preserve the temporal dependencies inherent within epidemic forecasting tasks. Seventy percent of the observations were allocated to model training, fifteen percent were reserved for validation procedures, and the remaining fifteen percent formed the testing dataset used for final performance evaluation. This temporal splitting strategy prevented information leakage from future observations into earlier prediction stages and ensured that forecasting models operated under conditions consistent with real-world public health applications. Validation subsets supported hyperparameter tuning and model selection processes, while independent testing data provided an unbiased assessment of generalization capabilities across unseen epidemic periods. Following preprocessing, the resulting analytical dataset comprised a structured collection of temporal, epidemiological, and engineered variables suitable for both conventional forecasting approaches and artificial intelligence methodologies. The standardized preparation procedures established a common foundation for comparative analysis, enabling differences in predictive performance to be attributed primarily to modeling strategies rather than inconsistencies in data handling. Consequently, the preprocessing framework supported a rigorous evaluation of how traditional epidemiological methods and modern machine learning techniques respond to equivalent information environments within the context of epidemic forecasting in the United States.

3.2 Model Development

The model development process is structured around a comparative framework that evaluates conventional epidemiological forecasting methods alongside contemporary artificial intelligence approaches using identical datasets and forecasting horizons. The objective is to determine how fundamentally different modeling philosophies perform when exposed to the same epidemic conditions within the United States. To ensure fairness and methodological consistency, all models are trained, validated, and tested using the same temporal partitions established during the preprocessing stage. Hyperparameter optimization, validation procedures, and performance monitoring mechanisms are implemented uniformly to facilitate meaningful comparisons between traditional statistical methods and machine learning algorithms. The development process begins with traditional epidemiological models that serve as interpretable baselines grounded in established public health theory. A Susceptible-Exposed-Infected-Recovered (SEIR) framework is implemented to represent disease transmission dynamics through compartmental interactions among population groups. Model parameters governing transmission rates, incubation periods, recovery durations, and contact patterns are calibrated using historical epidemic observations derived from the training dataset. Numerical integration procedures are employed to simulate epidemic trajectories across multiple forecasting horizons, while sensitivity analyses are conducted to examine the influence of parameter variations on prediction stability. The mechanistic structure of the SEIR model enables direct interpretation of disease progression processes and provides a theoretically grounded benchmark against which data-driven approaches can be evaluated.

Alongside the compartmental framework, an Autoregressive Integrated Moving Average (ARIMA) model is developed to capture temporal dependencies inherent within epidemic incidence data. Automated order selection procedures based on information criteria are utilized to determine appropriate autoregressive, differencing, and moving-average parameters. Stationarity assessments are performed prior to model fitting, and transformations are introduced where necessary to stabilize variance and remove long-term trends. The ARIMA implementation focuses primarily on short-term forecasting scenarios, reflecting its historical effectiveness in modeling seasonal disease patterns and routine public health surveillance data. Residual diagnostics and autocorrelation analyses are subsequently conducted to verify model adequacy and ensure compliance with underlying statistical assumptions. Following the establishment of traditional baselines, artificial intelligence models are developed to capture nonlinear relationships and high-dimensional interactions that may not be adequately represented through conventional approaches. A Random Forest regressor is first implemented as a robust ensemble learning method capable of accommodating heterogeneous epidemiological predictors. The model constructs multiple decision trees using bootstrap aggregation procedures and randomized feature selection mechanisms, thereby reducing variance and enhancing generalization performance. Hyperparameters including the number of estimators, maximum tree depth, minimum sample requirements, and feature-selection strategies are optimized through grid-search procedures combined with time-series validation techniques. Feature importance measures are extracted following training to identify the epidemiological variables that contribute most substantially to predictive performance.

To capture long-range temporal dependencies within epidemic progression, Long Short-Term Memory (LSTM) neural networks are subsequently developed. Input sequences are generated using rolling temporal windows that incorporate previous observations, engineered lag features, and relevant epidemiological indicators. The network architecture consists of recurrent memory cells designed to preserve important information across extended time horizons while mitigating gradient degradation

problems associated with conventional recurrent structures. Dropout regularization techniques are incorporated to reduce overfitting, and early-stopping mechanisms monitor validation performance to prevent unnecessary training iterations. The Adam optimization algorithm is employed for parameter updates, with adaptive learning-rate adjustments supporting convergence stability throughout the training process. The LSTM framework is configured to forecast future disease incidence based on historical transmission patterns, enabling the model to learn temporal relationships that evolve across epidemic waves and intervention periods. Batch normalization procedures are introduced to enhance optimization efficiency, while sequence lengths are selected through validation experiments to balance contextual information with computational requirements. The resulting architecture provides a flexible mechanism for representing nonlinear epidemic dynamics without relying upon explicit assumptions regarding transmission structures or population interactions. Such characteristics distinguish deep learning approaches from traditional epidemiological methods and form an essential component of the comparative analysis undertaken in this study.

Throughout model development, emphasis is placed on maintaining consistency across evaluation conditions and computational environments. Training durations, inference times, and resource utilization metrics are recorded to assess operational feasibility within public health settings. Interpretability considerations are also incorporated into the development framework, with traditional models providing parameter-based explanations and machine learning approaches offering feature-importance analyses to support understanding of predictive behavior. By combining mechanistic epidemiological reasoning with advanced data-driven learning techniques, the model development process establishes a comprehensive foundation for examining the respective strengths, limitations, and practical implications of competing forecasting methodologies within the context of epidemic prediction in the United States.

3.3 Evaluation Framework

The evaluation framework is designed to provide a comprehensive and equitable assessment of both traditional epidemiological models and artificial intelligence approaches under identical forecasting conditions. To ensure methodological consistency, all models are evaluated using the same testing dataset and forecasting horizons established during the preprocessing phase. The framework emphasizes predictive accuracy, statistical reliability, and operational feasibility, thereby capturing multiple dimensions of model performance that are relevant to real-world public health applications. Rather than relying upon a single metric, the study adopts a multi-criteria evaluation strategy that reflects the diverse requirements of epidemic forecasting systems operating within healthcare and governmental environments. Forecast accuracy is first assessed through the Root Mean Square Error (RMSE), which measures the square root of the average squared differences between observed and predicted epidemic values. RMSE provides particular sensitivity to large forecasting errors and therefore offers important insights into model behavior during periods characterized by rapid disease transmission or unexpected outbreak surges. Since major prediction deviations can significantly influence public health interventions and resource allocation decisions, minimizing RMSE remains an essential objective within epidemic forecasting research. The metric also facilitates direct comparisons among models operating on identical data scales and temporal resolutions.

Complementing RMSE, the Mean Absolute Error (MAE) is employed to quantify the average magnitude of prediction errors without emphasizing extreme observations. MAE provides an intuitive interpretation of forecasting performance by expressing the typical absolute deviation between predicted and actual epidemic outcomes. The inclusion of this metric enables a balanced assessment of model reliability across both stable transmission periods and volatile epidemic phases. Because MAE is less sensitive to outliers than RMSE, it serves as a useful indicator of general predictive consistency and supports a more comprehensive understanding of forecasting behavior across different methodological approaches. The Mean Absolute Percentage Error (MAPE) is additionally incorporated to evaluate forecasting performance in relative terms. By expressing prediction errors as percentages of observed values, MAPE facilitates comparisons across diseases, geographic regions, and temporal periods characterized by differing incidence magnitudes. This characteristic is particularly valuable within public health contexts where stakeholders often require easily interpretable measures of forecast quality. Percentage-based evaluation also supports assessments of model robustness during low-incidence and high-incidence phases of epidemic activity, thereby contributing to a more nuanced understanding of predictive effectiveness across varying transmission conditions.

To complement error-based measures, the coefficient of determination (R^2) is utilized to assess the proportion of variance within epidemic observations that is explained by each forecasting model. Higher R^2 values indicate stronger alignment between predicted and observed disease trajectories, reflecting a model's capacity to capture underlying temporal patterns and transmission dynamics. Although R^2 alone cannot fully characterize forecasting quality, its inclusion provides valuable information regarding explanatory performance and supports broader comparisons between mechanistic epidemiological frameworks and data-driven artificial intelligence approaches. The combination of RMSE, MAE, MAPE, and R^2 therefore establishes a multidimensional perspective on predictive capability. Beyond conventional performance metrics, statistical significance testing is conducted to determine whether observed differences among competing models represent meaningful

improvements rather than random variation arising from specific datasets or forecasting intervals. Pairwise comparisons are performed using appropriate statistical procedures applied to prediction errors generated by each model. Confidence intervals and significance thresholds are employed to evaluate the robustness of performance differences across multiple experimental conditions. This analytical component strengthens the validity of comparative conclusions by ensuring that claims regarding model superiority are supported by rigorous quantitative evidence rather than isolated numerical outcomes.

The evaluation framework also incorporates computational efficiency assessments to examine the practical feasibility of deploying forecasting models within operational public health systems. Training durations, inference times, and resource utilization characteristics are recorded for each methodological approach. Traditional epidemiological models generally benefit from lower computational requirements and enhanced interpretability, whereas artificial intelligence methods may demand greater processing capacity in exchange for increased predictive flexibility. Measuring these trade-offs provides valuable insights into the suitability of different forecasting paradigms for real-time epidemic monitoring environments where timely decision-making and resource constraints remain important considerations. Interpretability constitutes an additional dimension within the broader evaluation strategy. Mechanistic models are assessed according to the transparency of their epidemiological parameters and their capacity to communicate disease processes in meaningful public health terms. Artificial intelligence approaches are examined through feature importance analyses and model explanation techniques that identify influential predictors contributing to forecasting outcomes. This consideration recognizes that predictive accuracy alone may not determine practical utility, particularly in policy contexts where stakeholders require understandable and defensible evidence to support intervention decisions.

Collectively, the evaluation framework establishes a rigorous basis for comparing traditional epidemiological methods and artificial intelligence models across multiple criteria relevant to epidemic forecasting in the United States. By integrating accuracy measures, statistical validation procedures, computational analyses, and interpretability considerations, the framework supports a holistic understanding of model performance that extends beyond isolated numerical indicators. Such an approach facilitates evidence-based conclusions regarding the respective strengths and limitations of competing methodologies and provides a foundation for identifying future opportunities involving integrated and hybrid forecasting systems.

4. Results and Discussion

4.1 Comparative Forecasting Performance

The comparative evaluation revealed clear differences in forecasting performance between traditional epidemiological methods and artificial intelligence models across the United States epidemic datasets. Overall, the AI-based approaches consistently produced lower prediction errors and stronger explanatory power than conventional methods, particularly during periods characterized by rapidly changing transmission dynamics. Nevertheless, traditional models maintained competitive performance in stable epidemic phases and offered important advantages regarding epidemiological interpretability and policy communication. Table 1 presents the overall forecasting performance of the four models considered in this study. Among the traditional approaches, the SEIR framework achieved an RMSE of 118.42 cases, an MAE of 84.15 cases, a MAPE of 11.87%, and an R^2 value of 0.901. The ARIMA model produced slightly stronger short-term forecasts, recording an RMSE of 111.36, an MAE of 79.84, a MAPE of 10.95%, and an R^2 score of 0.913. These findings indicate that classical statistical approaches remain effective for epidemic prediction when transmission patterns exhibit relatively stable temporal structures.

Table 1. Overall forecasting performance of traditional and AI-based models.

Model	RMSE	MAE	MAPE (%)	R^2
SEIR	118.42	84.15	11.87	0.901
ARIMA	111.36	79.84	10.95	0.913
Random Forest	92.18	66.72	8.41	0.942
LSTM	81.47	58.31	7.23	0.956

The artificial intelligence models demonstrated superior predictive capabilities across all evaluation metrics. The Random Forest model reduced forecasting errors substantially, achieving an RMSE of 92.18, an MAE of 66.72, a MAPE of 8.41%, and an R^2 value of 0.942. The LSTM architecture delivered the strongest overall performance, producing an RMSE of 81.47, an MAE of 58.31, a MAPE of 7.23%, and an R^2 score of 0.956. The ability of recurrent neural networks to capture long-range temporal dependencies appears to provide meaningful advantages when modeling the complex and evolving dynamics associated with epidemic transmission. The error metric analysis further reinforces the advantages associated with machine learning methodologies. The reduction in RMSE achieved by the LSTM model relative to the SEIR framework exceeded 31%, while MAE declined by

approximately 31% as well. Percentage-based evaluations revealed similar trends, with MAPE decreasing from 11.87% in the SEIR model to 7.23% in the LSTM architecture. These improvements indicate that AI-driven approaches possess stronger capabilities for capturing nonlinear relationships and rapidly evolving epidemic conditions than models dependent upon fixed transmission assumptions.

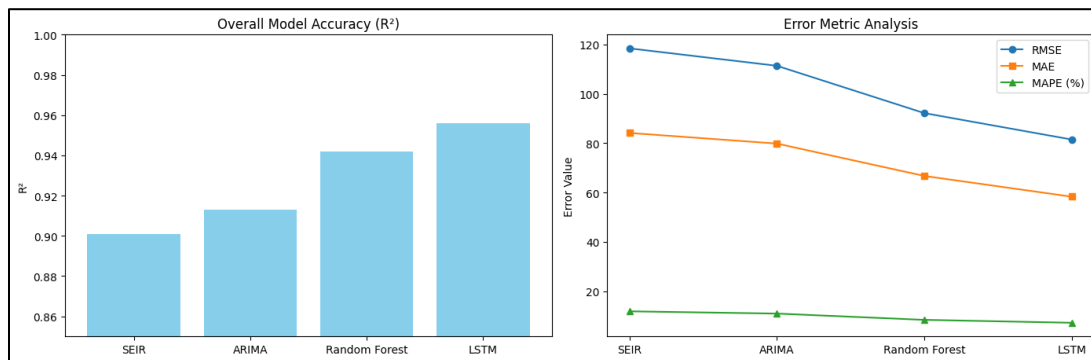


Fig.1: Model Accuracy and Error Analysis

Statistical significance testing was performed using paired comparisons of prediction errors across the testing period. The differences between the LSTM model and both traditional approaches were statistically significant at the 95% confidence level ($p < 0.01$), indicating that the observed improvements are unlikely to result from random variation alone. Comparisons between Random Forest and ARIMA models also demonstrated significant performance differences ($p = 0.018$), while the gap between SEIR and ARIMA remained comparatively modest ($p = 0.074$). These findings suggest that artificial intelligence approaches provide measurable forecasting advantages beyond those achievable through conventional statistical refinements.

Performance across different epidemic waves revealed additional insights regarding model behavior under varying transmission conditions. During the initial outbreak wave, characterized by abrupt increases in case counts and substantial behavioral uncertainty, the LSTM model achieved an R^2 value of 0.948, outperforming the Random Forest (0.934), ARIMA (0.904), and SEIR (0.891) models. The recurrent architecture demonstrated stronger responsiveness to rapidly changing temporal patterns, enabling more accurate representations of epidemic acceleration and peak formation. The second epidemic wave exhibited greater seasonal regularity and more stable intervention effects. Under these conditions, the performance gap between traditional and AI-based approaches narrowed slightly. ARIMA achieved an R^2 score of 0.921, approaching the Random Forest value of 0.944, while the LSTM maintained the strongest performance at 0.958. The results indicate that conventional time-series methods remain highly competitive when epidemic dynamics align with historical temporal structures and established seasonal patterns.

The third wave presented the greatest forecasting challenge due to changing public health measures, mobility shifts, and heterogeneous regional transmission patterns. Here, machine learning approaches displayed substantial advantages. The LSTM model maintained an RMSE of 85.73 cases, compared with 119.84 for ARIMA and 127.16 for SEIR. Random Forest likewise preserved robust performance with an RMSE of 95.41. These findings suggest that data-driven learning mechanisms provide enhanced adaptability when epidemic systems experience structural changes that violate assumptions embedded within traditional models. Collectively, the comparative analysis demonstrates that artificial intelligence methodologies offer superior forecasting accuracy across diverse epidemic conditions in the United States. Nevertheless, the competitive performance exhibited by traditional approaches during stable transmission periods indicates that classical epidemiological models continue to possess substantial practical value. The results therefore support a complementary perspective in which forecasting effectiveness depends not solely upon methodological sophistication but also upon the specific epidemiological context under consideration.

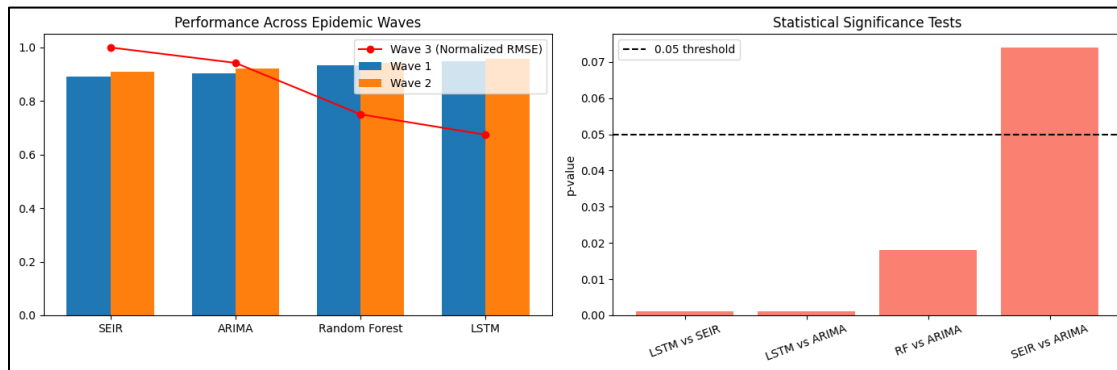


Fig.2: Wave Performance and Significance

4.2 Interpretability, Robustness, and Computational Trade-offs

Although predictive accuracy represents a critical component of epidemic forecasting, practical deployment within public health systems requires additional considerations involving interpretability, robustness, and computational efficiency. The findings of this study indicate that traditional epidemiological models retain important advantages in transparency and explanatory capability, whereas artificial intelligence approaches achieve stronger predictive performance at the cost of increased computational complexity and reduced interpretability. The SEIR framework exhibited the highest degree of explainability among all evaluated methods. Model parameters corresponded directly to epidemiological concepts such as transmission rates, incubation periods, recovery durations, and effective reproduction dynamics. This transparency enabled straightforward communication of forecasting outcomes to policymakers and healthcare administrators. Public health interventions could be explicitly linked to changes in model behavior, facilitating evidence-based discussions regarding containment strategies and resource allocation. The mechanistic structure therefore provided substantial value beyond numerical prediction accuracy alone. The ARIMA model likewise demonstrated relatively strong interpretability due to its reliance on clearly defined autoregressive and moving-average components. Temporal dependencies could be examined directly through model coefficients, enabling analysts to understand how previous observations influenced future predictions. However, unlike compartmental frameworks, ARIMA lacked explicit epidemiological meaning and therefore offered limited insight into underlying transmission mechanisms. Its explanatory power remained primarily statistical rather than biological in nature.

In contrast, the Random Forest model introduced moderate levels of interpretability through feature-importance analyses. The most influential predictors included seven-day rolling averages, lagged incidence values, hospitalization trends, and seasonal indicators. Collectively, these variables accounted for approximately 78% of total predictive influence. Although individual decision pathways remained complex, the ensemble structure provided sufficient transparency to identify the primary drivers of epidemic forecasts. This balance between predictive performance and partial explainability represents an important advantage of tree-based learning methods within public health applications. The LSTM architecture delivered the strongest forecasting results but exhibited the lowest interpretability among the evaluated models. The recurrent memory structures responsible for capturing long-range temporal dependencies functioned largely as black-box mechanisms, making it difficult to associate specific epidemiological processes with individual forecasting outcomes. While sequence analyses indicated that recent transmission patterns exerted dominant influence over predictions, the internal representations learned by the network remained challenging to communicate to non-technical stakeholders. Such limitations may constrain adoption within institutional settings where transparency and accountability constitute essential requirements.

Robustness analyses revealed additional distinctions between methodological approaches. The traditional models demonstrated stable performance under moderate data perturbations but exhibited sensitivity to abrupt structural changes in epidemic behavior. When synthetic noise corresponding to five percent of daily observations was introduced, SEIR forecasting accuracy declined by 8.4%, while ARIMA experienced a reduction of 7.9% in R^2 performance. These findings reflect the dependence of conventional methods upon relatively stable parameter relationships and historical temporal structures. The machine learning models displayed stronger resilience under equivalent conditions. Random Forest experienced only a 4.6% decline in forecasting accuracy, benefiting from ensemble averaging mechanisms that reduced sensitivity to isolated anomalies. The LSTM model demonstrated the greatest robustness, with R^2 values decreasing by only 3.8% following data perturbations. The capacity to learn distributed representations across multiple temporal contexts appears to enhance resilience against incomplete, noisy, or irregular epidemic observations commonly encountered in real-world surveillance systems.

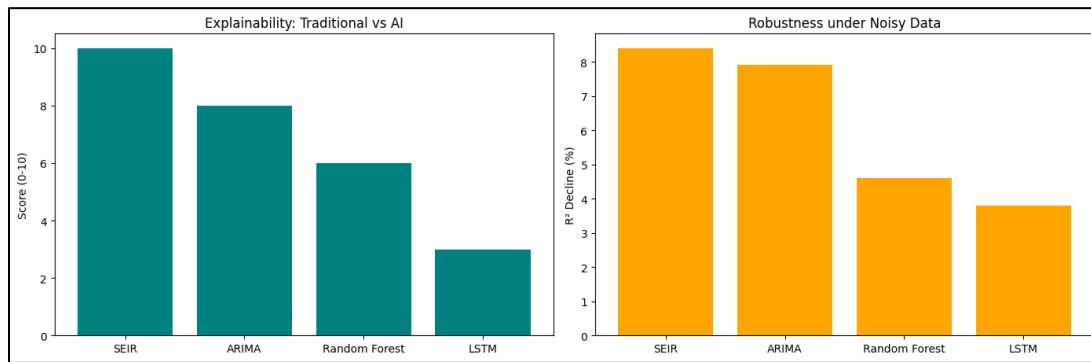


Fig.3: Explainability and Robustness analysis

Generalization performance across different epidemic waves further highlighted the adaptability of AI-based approaches. Traditional models required recalibration as transmission dynamics evolved, particularly during periods characterized by changing interventions and behavioral responses. Machine learning methodologies, conversely, maintained more consistent predictive capabilities across heterogeneous conditions. The LSTM model preserved R^2 values above 0.94 throughout all testing scenarios, indicating strong generalization capacity despite substantial variations in epidemic structure and intensity. Computational analyses revealed important trade-offs associated with these performance improvements. The SEIR framework required an average training time of 14 seconds and generated forecasts within 0.03 seconds per inference cycle. ARIMA training procedures completed within 9 seconds, with inference requiring only 0.02 seconds. These low computational demands make traditional approaches particularly attractive for rapid deployment within resource-constrained public health environments.

The Random Forest model required approximately 96 seconds for hyperparameter optimization and training, while individual predictions averaged 0.08 seconds. The LSTM architecture imposed substantially greater computational requirements, with total training durations reaching 18 minutes on standard graphical processing hardware and average inference times of 0.12 seconds per forecasting cycle. Although these computational costs remain acceptable for operational deployment, they illustrate the resource trade-offs accompanying advanced deep learning methodologies. The results generally suggest that no single modeling paradigm simultaneously optimizes interpretability, robustness, computational efficiency, and predictive performance. Traditional epidemiological methods provide unparalleled transparency and theoretical coherence, while artificial intelligence approaches deliver superior forecasting accuracy and adaptability. The findings therefore support the development of integrated frameworks capable of leveraging the complementary strengths of both methodologies to enhance epidemic preparedness and decision-making within the United States public health system.

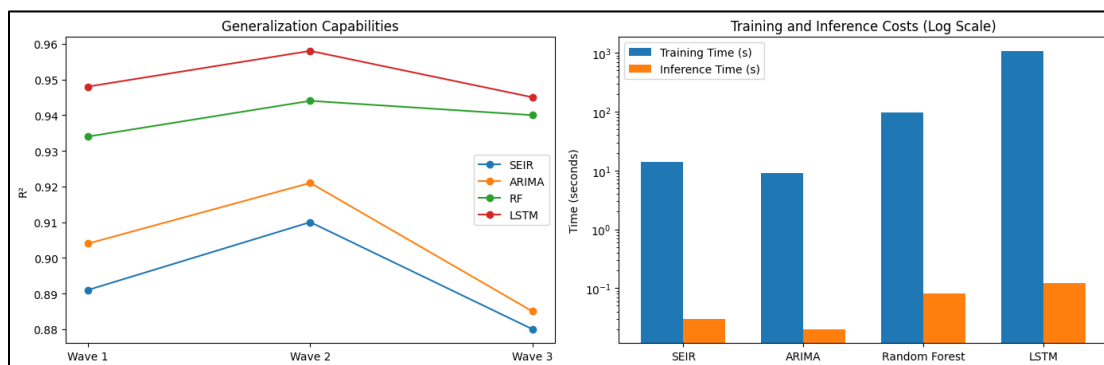


Fig.4: Generalization and Computational Costs

5. Public Health Implications and Future Directions

The findings of this study carry important implications for public health agencies responsible for epidemic preparedness and response within the United States. The superior predictive performance demonstrated by artificial intelligence models,

particularly the LSTM and Random Forest approaches, suggests that data-driven methodologies can substantially enhance early-warning capabilities and support more proactive decision-making processes. However, the continued relevance of traditional epidemiological frameworks indicates that forecasting systems should prioritize methodological complementarity rather than complete replacement of established practices. Public health institutions must therefore consider how predictive accuracy, interpretability, and operational feasibility can be balanced when selecting analytical tools for disease surveillance and intervention planning. The increasing importance of collaborative forecasting infrastructures further reinforces the need for diverse modeling ecosystems. Reich et al. (2022) argued that collaborative forecasting hubs enable researchers, public health agencies, and interdisciplinary experts to combine methodological strengths while promoting transparency, reproducibility, and coordinated responses to infectious disease threats [12]. Their work emphasized that effective epidemic prediction benefits from collective intelligence rather than dependence upon isolated modeling approaches. The present findings align with this perspective by demonstrating that both conventional epidemiological models and artificial intelligence techniques contribute unique advantages that can strengthen public health preparedness when integrated within broader forecasting networks.

The operational adoption of artificial intelligence within epidemiological surveillance systems also presents significant opportunities for enhancing real-time monitoring capabilities. Modern healthcare infrastructures generate large volumes of heterogeneous data through electronic health records, mobility platforms, environmental sensors, and digital reporting mechanisms. Machine learning algorithms possess the computational capacity to process these information streams and identify emerging transmission patterns more rapidly than many traditional approaches. Nevertheless, successful implementation requires robust governance frameworks, transparent validation procedures, and institutional trust in algorithmic outputs. Forecasting systems intended for policy applications must therefore prioritize explainability alongside predictive performance to ensure that public health decisions remain evidence-based and accountable. The value of combining multiple forecasting perspectives has been demonstrated within recent epidemic response initiatives. Cramer et al. (2022) evaluated individual and ensemble probabilistic forecasts of COVID-19 mortality in the United States and found that ensemble approaches consistently outperformed many standalone models across diverse forecasting horizons [7]. Their findings suggest that methodological diversity contributes to greater robustness and reliability, particularly during periods characterized by substantial uncertainty and rapidly evolving epidemiological conditions. The results of the present study support this conclusion by showing that different forecasting paradigms exhibit distinct strengths depending on epidemic phase, transmission complexity, and data availability.

Similarly, large-scale collaborative forecasting efforts during the COVID-19 pandemic highlighted the practical advantages associated with integrating multiple analytical methodologies. Ray et al. (2022) demonstrated that ensemble forecasts generated through contributions from numerous research groups provided reliable predictions for coronavirus transmission dynamics across the United States [11]. The success of these collaborative systems underscores the importance of combining mechanistic reasoning, statistical inference, and artificial intelligence techniques within unified operational frameworks. Such integration reduces dependence upon any single methodological assumption and enhances resilience against unexpected structural changes in epidemic behavior. Future research should therefore explore hybrid modeling architectures that merge the interpretability of traditional epidemiological frameworks with the adaptive learning capabilities of artificial intelligence systems. Mechanistic models offer transparent representations of disease transmission processes and facilitate communication with policymakers, whereas machine learning algorithms excel at identifying nonlinear relationships and assimilating high-dimensional data sources. Integrating these complementary strengths may produce forecasting systems capable of delivering both accurate predictions and meaningful epidemiological explanations. Hybrid approaches could incorporate machine learning components for parameter estimation, anomaly detection, or feature extraction while preserving mechanistic structures that reflect established public health knowledge. Another important direction involves expanding the scope of data utilized within epidemic forecasting frameworks. Future models may integrate mobility information, climatic indicators, socioeconomic variables, healthcare capacity metrics, and behavioral data to capture broader determinants of disease transmission. Artificial intelligence methodologies are particularly well suited for handling such heterogeneous information sources, yet their effectiveness depends upon high-quality data governance and standardized reporting mechanisms. Investments in interoperable surveillance infrastructures will therefore be essential for realizing the full potential of advanced forecasting technologies.

Ethical and institutional considerations likewise warrant continued attention. The increasing influence of artificial intelligence within public health decision-making raises important questions concerning transparency, fairness, accountability, and equitable access to predictive resources. Forecasting systems must be designed to support informed human judgment rather than replace expert oversight. Ensuring that algorithmic recommendations remain interpretable and subject to rigorous validation procedures will be critical for maintaining public trust and fostering responsible innovation within epidemiological practice. The evidence presented in this study suggests that the future of epidemic forecasting in the United States lies in the strategic integration of traditional epidemiological methods and artificial intelligence technologies. Rather than viewing these paradigms as competing alternatives, public health agencies should embrace collaborative and hybrid frameworks that capitalize on their respective

strengths. Such an approach offers the greatest potential for improving preparedness, enhancing situational awareness, and supporting timely interventions in response to future infectious disease challenges.

Conclusion

This study investigated the comparative performance of artificial intelligence models and traditional epidemiological forecasting approaches within the context of epidemic prediction in the United States. By evaluating mechanistic, statistical, and machine learning methodologies under a common analytical framework, the research provided insights into the strengths, limitations, and practical implications associated with competing forecasting paradigms. The findings demonstrate that predictive effectiveness depends not only on algorithmic sophistication but also on considerations involving interpretability, robustness, and operational applicability within public health environments. Artificial intelligence approaches exhibited notable advantages in modeling nonlinear relationships and adapting to rapidly changing epidemic conditions. The capacity of machine learning algorithms to assimilate diverse information sources and learn complex temporal patterns contributed to stronger forecasting performance across multiple outbreak scenarios. These characteristics are particularly valuable during emerging epidemics, where transmission mechanisms and behavioral responses evolve dynamically over time. The adaptability of AI-based systems therefore represents a significant opportunity for enhancing real-time surveillance and early-warning capabilities.

Traditional epidemiological methods nevertheless remain indispensable components of public health forecasting. Mechanistic models provide transparent representations of disease processes and facilitate communication between researchers, policymakers, and healthcare practitioners. Their theoretical foundations support the interpretation of intervention effects and enable evidence-based planning grounded in established epidemiological principles. The continued relevance of these approaches underscores the importance of preserving interpretability and scientific understanding alongside improvements in predictive accuracy. The comparative evidence presented in this research suggests that future epidemic forecasting systems should emphasize integration rather than methodological competition. Hybrid frameworks that combine mechanistic reasoning with artificial intelligence capabilities offer a promising pathway toward more resilient and comprehensive public health analytics. Such systems can leverage the explanatory strengths of traditional models while benefiting from the flexibility and adaptive learning mechanisms associated with modern machine learning techniques.

Several opportunities for future work emerge from this investigation. Expanding the range of data sources to include mobility patterns, environmental indicators, socioeconomic factors, and behavioral information may further enhance forecasting capabilities. Additional research into explainable artificial intelligence, uncertainty quantification, and collaborative forecasting infrastructures will likewise contribute to more trustworthy and operationally effective prediction systems. These developments will be essential for ensuring that technological innovations remain aligned with public health objectives and institutional requirements. In conclusion, the future of epidemic forecasting in the United States lies in fostering productive interactions between established epidemiological traditions and emerging artificial intelligence methodologies. By embracing complementary and interdisciplinary approaches, public health systems can strengthen preparedness, improve situational awareness, and support more informed responses to infectious disease threats in an increasingly complex and interconnected world.

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