

AI – Based Mathematical Model for Predicting the spread of Infectious Diseases

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ABSTRACT:

The accelerated dissemination of infectious illnesses creates substantial difficulties for public health systems and demands exact mathematical and computational strategies for timely prediction and regulation. This study proposes an **AI-Based Mathematical Model for Predicting the Spread of Infectious Diseases** by integrating classical epidemic models with Artificial Intelligence (AI) techniques. The proposed framework extends compartmental models such as **SIR (Susceptible–Infected–Recovered)** and **SEIR (Susceptible–Exposed–Infected–Recovered)** by incorporating AI-based learning mechanisms to estimate dynamic epidemiological parameters, including transmission rate, recovery rate, and disease progression. Historical and real-time epidemiological data can be used to train machine-learning algorithms for identifying nonlinear relationships and temporal patterns that may not be adequately captured by conventional mathematical models. The predicted parameters are subsequently incorporated into the mathematical model to generate short- and medium-term forecasts of infection trends. The proposed hybrid approach aims to improve prediction accuracy, support early identification of epidemic growth, and provide quantitative insights for evaluating intervention strategies such as vaccination, isolation, social distancing, and other preventive measures. The study demonstrates the potential of combining mathematical epidemiology with AI to develop a flexible and data-driven framework for infectious disease forecasting and public-health decision support.

Keywords: Artificial Intelligence, Mathematical Modeling, Infectious Diseases, SIR Model, SEIR Model, Machine Learning, Disease Prediction, Epidemic Forecasting, Epidemiological Parameters.

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INTRODUCTION

Infectious diseases remain a major challenge to global public health because of their ability to spread rapidly within populations and across geographical boundaries. Outbreaks of diseases such as influenza, COVID-19, dengue, malaria, and other communicable diseases can place considerable

pressure on healthcare systems, affect economic activities, and cause substantial social disruption. Therefore, the ability to understand, predict, and control the transmission of infectious diseases is an important research problem. Mathematical modelling provides a systematic framework for describing

disease transmission and analysing the effects of different epidemiological and intervention parameters.

Classical mathematical epidemic models have played an important role in understanding the dynamics of infectious diseases. One of the most widely used approaches is the **Susceptible–Infected–Recovered (SIR) model**, in which a population is divided into susceptible, infected, and recovered compartments. The **Susceptible–Exposed–Infected–Recovered (SEIR) model** further introduces an exposed compartment to represent individuals who have been infected but are not yet infectious. These models are generally formulated using systems of differential equations and provide valuable information about important quantities such as the number of infected individuals, recovery patterns, epidemic peaks, and basic reproduction characteristics. However, conventional models often rely on assumptions involving fixed or predetermined parameters, whereas disease transmission in real-world populations can be highly nonlinear and time-dependent.

The availability of large-scale epidemiological and demographic datasets has created new opportunities for applying **Artificial Intelligence (AI)** and machine-learning techniques to infectious disease prediction. AI algorithms can identify complex relationships and temporal patterns from historical and real-time data. Variables such as population density, mobility, climate conditions, vaccination coverage, healthcare capacity, and reported infection cases can potentially be incorporated into predictive models. Machine-learning methods can therefore complement traditional mathematical models by estimating parameters that vary over time and by improving the ability to capture nonlinear disease dynamics.

The integration of mathematical epidemiology and AI provides a **hybrid modelling framework** in which the strengths of both approaches can be utilized. Mathematical models offer interpretability and a theoretical representation of disease transmission, while AI techniques provide data-driven learning and parameter estimation capabilities. In the proposed framework, epidemiological data are used to train an AI model to estimate relevant parameters, such as the transmission rate and recovery rate. These estimated parameters are then incorporated into a compartmental epidemic model to predict the future evolution of the disease. Such an approach can provide a more adaptive representation of disease transmission than a model based solely on fixed parameters.

Another important aspect of infectious disease prediction is the identification of the timing and magnitude of epidemic peaks. Early prediction of increasing infection trends can assist public-health authorities in planning healthcare resources and evaluating possible intervention strategies. AI-based forecasting can provide estimates of future infection levels, while the underlying mathematical model can be used to investigate how changes in transmission, recovery, vaccination, or other intervention parameters affect epidemic behaviour. Thus, the combination of prediction and mathematical analysis can provide both forecasting capability and epidemiological interpretation.

The present study proposes an **AI-Based Mathematical Model for Predicting the Spread of Infectious Diseases**. The main objective is to develop a hybrid framework that combines a compartmental mathematical model with AI-based parameter estimation and prediction. The proposed model is intended to analyse the nonlinear and time-dependent nature of infectious disease transmission and to improve the accuracy of epidemic forecasting. The study also aims to examine the influence of important epidemiological parameters and evaluate the effectiveness of the proposed framework using appropriate statistical and predictive performance measures.

The significance of this research lies in establishing a bridge between **traditional mathematical epidemiology and modern AI-based data analytics**. Rather than replacing mathematical models with purely data-driven methods, the proposed approach seeks to integrate both methodologies to obtain a model that is predictive, adaptable, and mathematically interpretable. Such a framework can contribute to the development of effective forecasting systems and may support evidence-based planning for infectious disease prevention, monitoring, and control.

Objectives of the Study

The major objectives of the proposed research are:

1. To formulate a mathematical model for describing the spread of an infectious disease using a suitable compartmental framework.
2. To develop an AI-based mechanism for estimating time-dependent epidemiological parameters.
3. To integrate the AI predictions with the mathematical epidemic model.

4. To predict the future number of susceptible, exposed, infected, and recovered individuals.
5. To analyse epidemic growth, peak infection levels, and disease progression.
6. To evaluate the predictive performance of the proposed hybrid model using suitable error and accuracy measures.
7. To investigate the potential effects of intervention parameters on disease transmission.

1. LITERATURE REVIEW

The prediction and control of infectious diseases have traditionally relied on mathematical and statistical models that describe the mechanisms of disease transmission. With the rapid growth of epidemiological databases, computational power, and artificial intelligence (AI), recent research has increasingly combined mathematical epidemiology with machine learning and deep learning. This section reviews the major developments relevant to the proposed study, “AI-Based Mathematical Model for Predicting the Spread of Infectious Diseases.”

2.1 Mathematical Modeling of Infectious Diseases

Mathematical modeling provides a quantitative framework for describing the transmission and progression of infectious diseases. Classical compartmental models divide a population into epidemiological groups such as Susceptible (S), Infected (I), and Recovered (R). The SIR model and its extensions, including the SEIR, SIS, SIRS, SEIAR and SEIHR models, have been extensively used to analyze epidemic dynamics.

These models are generally formulated using systems of differential equations, with parameters representing epidemiological quantities such as transmission rate, recovery rate, incubation period, and mortality rate. Mathematical models can be used not only to estimate the evolution of an epidemic but also to investigate the effects of vaccination, isolation, quarantine, and other interventions.

A recent review published in 2026 highlights the continuing importance of deterministic and stochastic mathematical models, including compartmental and network-based models, for understanding transmission mechanisms and evaluating epidemic-control strategies. The review also identifies AI and data-driven approaches as increasingly important extensions of traditional epidemic modeling.

2.2 Data-Driven Epidemic Modeling

Although mechanistic mathematical models provide interpretable representations of disease transmission, their performance can depend strongly on assumptions about epidemiological parameters. In real-world situations, parameters such as the

transmission rate may vary with time because of changes in human behavior, population mobility, environmental conditions, vaccination, public-health interventions, and pathogen characteristics.

Demongeot and Magal (2024) reviewed 260 articles concerning data-driven mathematical modeling of COVID-19. Their review covered epidemic waves, time-dependent parameters, social and environmental changes, multi-compartment models, and parameter identification. Their findings demonstrate the importance of allowing epidemic models to adapt to changing transmission conditions rather than relying exclusively on fixed parameters.

This development is particularly relevant to an AI-based mathematical framework because machine-learning techniques can be employed to estimate or update parameters from observed epidemiological data.

2.3 Machine Learning in Infectious Disease Prediction

Machine learning has emerged as an important tool for infectious-disease forecasting because of its ability to identify nonlinear relationships and patterns within large datasets. Algorithms such as Random Forest (RF), Support Vector Machine (SVM), Gradient Boosting, Artificial Neural Networks (ANN), and other supervised-learning methods have been applied to disease incidence and risk prediction.

A systematic review covering 237 studies published between 2001 and 2021 examined machine-learning and deep-learning applications for infectious-disease prediction. The review found that tree-based machine-learning methods and feed-forward neural networks were frequently used, with temporal incidence, disease risk, and spatial movement among the major prediction tasks. However, fewer than 10% of the reviewed studies addressed important operational issues such as uncertainty quantification, computational efficiency, and missing-data handling. These findings indicate that predictive accuracy alone is insufficient for practical epidemic forecasting; reliability, uncertainty, data quality, and operational applicability must also be considered.

2.4 Deep Learning for Epidemic Forecasting

Deep-learning techniques have expanded the capabilities of infectious-disease prediction, particularly when large time-series and spatial datasets are available. Long Short-Term Memory (LSTM) networks are especially relevant because they can learn temporal dependencies in sequential data. Other approaches include convolutional neural networks, graph neural networks, transformers, and hybrid deep-learning architectures.

Recent literature indicates that advanced AI methods are increasingly being used to analyse heterogeneous data sources, including epidemiological surveillance, human mobility, environmental variables, pathogen

genomic information, and other health-related data. A 2026 review reports applications of Random Forest, Gradient Boosting, LSTM, Transformer, and Graph Neural Network approaches in infectious-disease prediction and outbreak forecasting.

However, deep-learning models may require large quantities of high-quality data and can be difficult to interpret. Consequently, there is increasing interest in combining deep-learning methods with epidemiological knowledge rather than relying exclusively on black-box prediction.

2.5 Integration of AI with Mechanistic Epidemiological Models

One of the most important recent developments is the integration of AI with mechanistic mathematical models. Mechanistic models incorporate prior knowledge about disease transmission, while AI provides data-driven learning capabilities. This combination can potentially overcome some limitations of both approaches.

Ye et al. (2025) conducted a scoping review of the integration of AI with mechanistic epidemiological modeling. The review identified 245 eligible studies from 15,460 records and found that integrated approaches have been applied to disease forecasting, model parameterization, and model calibration. The authors also identified continuing research gaps involving decision-making, diverse datasets, and biological and socio-behavioral mechanisms.

The integration can be represented conceptually as:

Epidemiological Data

→ AI Model

→ Parameter Estimation

→ Mathematical Epidemic Model

→ Disease Forecast

2. METHODOLOGY

The proposed methodology for the **AI-Based Mathematical Model for Predicting the Spread of Infectious Diseases** integrates a classical compartmental epidemiological model with Artificial Intelligence (AI) techniques. The objective is to develop a predictive framework capable of estimating disease transmission patterns and identifying important epidemiological parameters.

Data Collection and Pre-processing

Historical epidemiological data are collected from reliable sources such as health departments, public-health databases, hospitals, and international disease surveillance systems. The dataset may include:

- Number of susceptible individuals
- Number of infected individuals
- Number of recovered individuals

- Daily new cases
- Deaths and hospitalizations
- Population size
- Vaccination rates
- Environmental and demographic factors
- Mobility and contact-related information

The collected data are cleaned to remove missing, duplicated, and inconsistent observations. Data normalization and transformation are then performed to make the dataset suitable for AI-based analysis.

3. Mathematical Epidemiological Model

A **Susceptible–Infected–Recovered (SIR)** model is initially considered. Let

$S(t)$, $I(t)$ & $R(t)$

represent the numbers of susceptible, infected, and recovered individuals at time t , respectively.

The basic SIR model is given by

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \quad \& \quad \frac{dR}{dt} = \gamma I$$

Where

$N = S + I + R$ is the total population,

- β is the transmission rate,
- γ is the recovery rate.

The basic reproduction number is calculated as

$$R_0 = \frac{\beta}{\gamma}$$

When $R_0 > 1$ transmission can increase under the model assumptions, whereas $R_0 < 1$ corresponds to declining transmission.

For diseases requiring greater epidemiological detail, the model can be extended to an **SEIR model** by introducing an exposed compartment $E(t)$:

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dI}{dt} = \gamma I$$

where σ represents the rate at which exposed individuals become infectious.

AI-Based Prediction

An AI model is then trained using the epidemiological and mathematical-model outputs. Machine-learning algorithms such as **Artificial Neural Networks (ANN)**, **Random Forest**, **Support Vector Regression (SVR)**, **Long Short-Term Memory (LSTM)**, or hybrid deep-learning models can be considered.

For time-series prediction, an LSTM model can learn temporal relationships in the number of infected cases. The input variables may include:

$$X_t = [I_t R_t, \beta_t, \gamma_t, V_t, M_t, \dots]$$

where V_t represents vaccination-related information and M_t represents mobility or other relevant variables.

The AI model produces a predicted number of infections:

$$I_{t+l} = f(X_t; W)$$

where f represents the trained AI model and W denotes its learned parameters.

Hybrid Mathematical–AI Model:

The central component of the proposed methodology is the integration of the mathematical and AI models. The mathematical model provides epidemiological structure, while the AI model learns complex nonlinear patterns that may not be adequately represented by fixed parameters.

4. Conclusion

The present study proposes an **AI-Based Mathematical Model for Predicting the Spread of Infectious Diseases** by integrating mathematical

epidemiological models with Artificial Intelligence techniques. The mathematical component, based on compartmental models such as the SIR or SEIR framework, provides a systematic representation of the interactions among susceptible, exposed, infected, and recovered populations. At the same time, the AI component enables the model to identify complex nonlinear patterns and temporal relationships present in epidemiological data.

The proposed hybrid approach can incorporate important factors such as transmission rate, recovery rate, vaccination coverage, population mobility, and intervention measures. By allowing epidemiological parameters to vary with changing conditions, the model can provide more flexible predictions than a conventional mathematical model with fixed parameters.

The methodology also supports sensitivity and scenario analysis, which can be used to examine how changes in transmission, vaccination, and preventive interventions may influence disease dynamics. Thus, the proposed framework provides both **predictive capability and mathematical interpretability**, making it useful for studying epidemic trends and supporting evidence-based public-health planning.

Future work can extend the proposed model by incorporating real-time epidemiological data, spatial and demographic factors, climate variables, mobility patterns, vaccination effectiveness, and emerging disease variants. Advanced deep-learning architectures and uncertainty-quantification techniques can also be incorporated to improve forecasting reliability. Further validation using multiple diseases and datasets from different geographical regions would strengthen the generalizability of the proposed framework.

Overall, the integration of **mathematical epidemiology and Artificial Intelligence** provides a promising computational framework for understanding and forecasting infectious-disease dynamics and for evaluating potential intervention scenarios.

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