Harnessing AI for Accurate Detection and Prediction of Ebola Virus Epidemics

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Abstract

In this review paper, the authors discuss the development and application of methods for modeling and control and comparison of viral spreading in society with fractional-order and ML techniques for data analysis. Some of the most well-known epidemiological models are based on traditional approaches to describing disease diffusion and often need to be more sufficient when mapping the realistic disease distribution. However, fractional-order models give more flexibility and accuracy due to the memory incorporated and interaction factors. Moreover, the amalgamation of ML and artificial intelligence allows the analysis of considerable and heterogeneous amounts of data, enabling real-time prediction and favorable outbreak response measures. This paper outlines some benefits of integrating these sophisticated techniques while discussing issues such as the quality of inputs, problems in the methods deployed, and issues of visibility of the methods deployed. Finally, it proposes better epidemic preparedness and response through interdisciplinary approaches that emphasize the role of these technologies in a society that is more vulnerable to epidemic diseases.

Keywords: Epidemiological modeling; fractional Order models; Artificial intelligence; Viral outbreaks; Public health and predictive modeling

1. Introduction

Seasonal epidemic and sporadic disease outbreaks, including Ebola, Marburg and COVID-19, have presented significant scientific, medical, social, and economic challenges in understanding how they start, their incidence, and prevention. SIR and SEIR models have been the standard epidemiological models adopted to explain disease transmission and predict epidemic trends. However, it is also true that emerging cases involve a more significant number of people and show a high level of diversity, indicating that better methods must be applied to solve these problems. Given the dynamic nature of viruses and the emergence of different variants in different socio-ecological settings, innovative models must be used to capture infectious disease transmission dynamics [1].

One of them is the development of the so-called fractional-order models. Compared with the integer-order models, the FOIs contain memory effects and long-range interactions, which make them more appropriate for describing epidemic processes. The advantage of these models is that they allow the simulation of processes that do not follow an exponential course, which improves the fit of these models to actual epidemiological data. For example, initial studies have indicated that employing fractional-order SEIR models of the recent Ebola scenario offers far more realistic assessments of the virus spread and management than its integer counterpart. Such improvements are critical for determining the best intervention strategies, making these models valuable tools for future epidemic events [2].

Another significant advancement in epidemic modeling is the application of machine learning (ML) and artificial intelligence (AI) techniques. Unlike fixed models based on a specific set of equations, ML models can observe and predict trends in data. This approach has been instrumental in epidemic forecasting, often requiring rapid changes. For example, machine learning models have predicted the evolution of COVID-19, potential waves, and the role of non-pharmacological measures (NPI) within these waves. This is possible because AI can process large

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amounts of data related to a patient's clinical status, the environment, and the disease population structure, such as social networks [3].

The upsurge of machine learning in fisheries modeling has also been facilitated by the availability of more sophisticated tools, with neural networks, decision trees and support vector machines (SVMs) being some of them. Such tools can process high-dimensional and complex data and analyze and predict events, which is impossible using conventional tools. In one example, ANNs have been used to monitor and assess the spread of outbreaks such as Ebola and dengue fever, allowing health experts to trace the epidemiological model and implement appropriate control measures. Moreover, advanced deep learning approaches were applied to look for significant predictors of how transmission dynamics operated within the study area, thereby increasing the chances of effectively containing the outbreaks [4].

AI techniques and predictive analytics have proven to be instrumental in enhancing disease surveillance and early warning systems. For instance, these techniques can detect new pathogens or variations of existing viruses through machine-learning algorithms that process clinical and genetic information. This is particularly crucial in the context of zoonotic diseases, which can cross species boundaries and lead to disease outbreaks or public health crises. For example, the use of AI for genomics has empowered epidemiologists to actively monitor and analyze genetic changes in viruses such as SARS-CoV-2. These advancements underscore that AI is about managing outbreaks and effectively addressing the challenges posed by such outbreaks [5].

The merger of fractional order models with machine learning has recorded much progress, though certain aspects remain a work in progress. For example, these models have limitations due to reliance on data; the data definition may differ from region to region and over diseases. On the other hand, AI use for epidemics modeling raised suspicions over data privacy and algorithm or machine learning models and the likelihood of bias in the deliberations. It is consequently clear that while such technologies may be helpful, there is a need for solid strategies that will protect data and be ethical because healthy disparities exist that should be represented in the data [6], [7].

A comprehensive overview of epidemic modeling is presented in this article with a focus on how it has developed over time, covering both old and new methods. It states the benefits of using fractional order models instead of classical ones and looks at how AI could improve the prevention and management of epidemics. This paper aims to understand how lessons learned from outbreaks of ailments such as Ebola, Marburg, and COVID-19, among others, can be translated into valuable strategies for averting any future outbreaks of infectious diseases. Advanced modeling techniques and AI will change how epidemics are predicted, detected, and controlled for the better, leading to more robust and more agile global health systems.

2. Literature Review

The historical experience of the epidemiological catastrophe 2014, which claimed many thousands of lives, demonstrated the importance of developing sophisticated epidemiological models to predict and curb the spread of viral diseases. Subsequent works have sought to use numerous mathematical and computational models of viral transmission involving Susceptible-Infected-Recovered (SIR), Susceptible-Exposed-Infected-Recovered (SEIR), and fractional-order models. It also enables the calculation of other parameters that help design the various simulation models of disease spread and outbreak type. Furthermore, improved machine learning has made it possible to create accurate outbreak prediction models from various data patterns. This literature shows many techniques ranging from mathematics modeling techniques to artificial intelligence techniques that can be used in fighting viral outbreaks such as Ebola, Marburg, and coronavirus.

As pointed out in [8], the Ebola of 2014 saw infections increase with many deaths; hence, several models, including SIR, SIS, and SEIR, were used to analyze the virus spread. This paper used the modeling approach to show that fractional-order models could better capture the dynamics of an epidemic compared to integer-order models. This research extended the analysis to consider a fractional order Ebola model where the nonnegative solutions and essential reproduction were discussed in addition to the stability of equilibrium points. Conventional numerical approximations commonly fail to map experimental data well; therefore, using the Gorenflo–Mainardi–Moretti–Paradisi scheme (GMMP), the study obtained numerical solutions of the system of Ebola fractional order SEIR. Furthermore, the modified grid approximation method (MGAM) was used to compute the system parameters of the proposed model. The study also gave a convergence analysis for the GMMP method regarding some possible numerical solutions that may be absurd. When fractional orders were refined and basic parameters were fine-tuned, the SEIR model showed a better fit to actual data than other models. Moreover, the research incorporated Caputo derivatives to establish fractional order Ebola systems of different orders and improve accurate data modeling through the MGAM algorithm to estimate unique parameters and applicable orders.

The paper [9] described that the 2014 and 2018 Ebola outbreaks were analyzed to explain the roots and dissemination process. The outbreak of 2014, declared by WHO on March 23, began in a rural village in southeastern Guinea in the forest. Three methodologies were employed to determine the outbreak's source: The

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Topological Weighted Centroid method located the origin at Longitude −10.5337, Latitude: 8.1517, about 64 kilometers from Guekedou, Guinea. Furthermore, a Dynamic Naive Bayesian/Dynamic Networks Block Algorithm points out Kissidougou as the ground zero, approximately 69 km from Guekedou, reconfirming the outbreak location in southeast Guinea. An ANN programmed as Selfie was employed to approximately predict the diffusion patterns of the outbreak. The current one, which started in 2018 in DR Congo, is relatively confined to the Health zones of Bikoro, Iboko and Wangata. The ANN algorithm predicted the outbreak's origin at Longitude 18.3046, Longitude 15.1897, and Latitude −0.6865, about 20 km northwest of Bikoro. The tracking and prediction of the outbreak show that it was targeted.

In the research presented in [10], Ebola Virus Disease (EVD) is highlighted as one of the most lethal viral infections, with mortality rates ranging from 50% to 90% during outbreaks. Since its initial identification in 1976 near the Ebola River in the present-day Democratic Republic of Congo, EVD has caused sporadic but devastating outbreaks. The study focuses on the recent West African epidemic, underscoring the urgent need for robust healthcare systems and enhanced international cooperation in managing disease outbreaks. The analysis centered on Guinea, Sierra Leone, and Liberia, the nations most affected by the epidemic due to their fragile healthcare infrastructures. By examining the dynamics of the outbreak and the response strategies employed, the study seeks to provide insights into strengthening healthcare systems and shaping effective policies for managing EVD and other global health emergencies.

As described in the paper [11], Ebola Virus Disease (EVD) is a severe, often fatal illness in humans with an average mortality rate of around 50% that can reach 90% in cases of an outbreak. EVD was first identified in 1976 near the Ebola River in the Democratic Republic of Congo; since then, it has occurred in twelve sporadic but large outbreaks. The worst of these happened recently in West Africa, most affecting Guinea, Sierra Leone and Liberia because these countries have weak health facilities. This evil has brought out the urgent need for a better global health system and multilateral cooperation in managing these diseases. The research focuses on the patterns of the spread and concern measures in these countries to identify the lessons learned for bettering the control of EVD and similar threatening public health hazards in the future.

The publication described as [12], stressed the importance of the host response when infection occurs in Ebola (EVD). However, the gene expression programs associated with patient outcomes must be better understood. The study employs mice to understand strain-associated variation in EVD working through various outcomes, including tolerance and fatal toxicosis. Using this approach, researchers find important clinical, virologic, and transcriptomic variables distinguishing between tolerant and lethal outcomes in ten CC lines. Tolerance is described in a well-controlled immune and inflammatory response early after infection with decreased inflammatory macrophages and increased numbers of antigen-presenting cells, B1 cells, and T cells.

On the other hand, lethal disease is characterized by early limited gene manifestation, reduced lymphocytes, and uncontrollable inflammation signaling that ultimately causes death. The study then utilizes signal processing, analyzing transcriptomic profiles to predict outcomes with 99% accuracy in mice. This predictive signature also possesses clinical implications as it was formulated to predict outcomes in a West African cohort of EVD patients with a good accuracy of 75 percent.

As stated by Frieden [13], new diseases like Ebola can be a threat to global health, but effective treatments are scarce. To this end, the present work formulates an epidemic model for the dynamics and control measures of the Ebola virus employing a mathematical novel described by the Mittag–Leffler kernel. The research focuses on fractal analysis that explores the regularity characteristic across different scales linked to complex biological systems. Several local Lipschitz conditions are tested for statistical determination on a time scale, and the existence, boundedness and uniqueness of positive solutions follow the Leray Schauder theorem. Furthermore, chaos control techniques bring the system to several equilibrium points, and the fractional order maintains the solutions within the feasible domain. Stability results in terms of Ulam–Hyers for solutions are considered under the constant or increasing functions and extend the qualitative analysis. The model confirms stable solutions within a practicable interval and reveals how various measures and infection rates affect the occurrence of Ebola. This fractional-order model benefits the understanding of transmission dynamics and gives a concrete model for predicting outbreaks and applying effective control measures. Thus, it has an excellent potential for epidemiological analysis of actual data.

According to the work highlighted above [14], the Marburg virus is now posing a significant threat to public health since it kills both humans and animals and is fatal. The number of Marburg virus incidents has recently risen, especially in areas with low health facilities, which makes new a threat to health leaders. This rising incidence may be owed to inadequate swift intercessions, an area of interest to public health and scientific society since, for the most part, there is no known cure or vaccination for this disease. To understand the transmission dynamics of the Marburg virus, this study proposes two transmission chains: human-human transmission and bat-human transmission. It adopts quarantine measures as a control factor and public health awareness as a factor within the control framework, which looks at the efficacy of awareness about controls. The properties of the model

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established through mathematical analysis give a firm foundation for infection control, proved by the positivity and boundedness of solutions under some initial conditions. Stability analysis is performed near the disease-free equilibrium points to identify the primary reproduction number for managing the disease. When incorporated with the PRCC and a surface plot, Monte Carlo simulation and analysis elucidate the effects of transmission rates, awareness efficacy, and quarantine rates underlying the dynamics of the disease. Further, a Deep Neural Network is designed, and hyper-parameters are fine-tuned by the grid search method to build the numerical model simulating the designed model while cross-validation to check the model performance. The findings from this topology of the neural network are then benchmarked with the LSODA numerical approach, which proves that the DNN identifies important parameters governing disease transmission, which aids in determining preventions and cures for diseases.

As established in the research by [15] investigating Virus-Borne Diseases (VBDs), annual outbreaks of the diseases in different areas have been reported, which is evidence of continuing transmission. Arboviruses are some of the most widespread globally, with the emerging issue of causing more viral fevers. The current work suggests the implementation of the Enhanced Back Propagation with Artificial Neural Network algorithm (EBP-ANN) to enhance the viral prediction's effectiveness and efficiency. The research starts by gathering the preprocessed virus data set by applying the Z-score normalization. The feature extraction task uses a dynamic angle projection pattern, and the genetic algorithm is used for feature selection. The usefulness of the proposed EBP-ANN can be proved by its better prediction accuracy, as shown in the above algorithm. The system is compared to the existing techniques in terms of prediction accuracy, the time used to make the predictions, precision, and recall. In conclusion, it is inferred that the proposed method is superior in improving the virus-borne diseases' predictability efficiency and has allowed early diagnosis and intervention.

The analysis made in the work from [16] reveals that the threats of new IEs are considerable globally as the uncontrolled virus affects large populations, and the prevention of viruses' spread and minimization of the adverse outcomes of their effects on societies and economies are complicated. Students and academicians may not appreciate that institutions are often in deaf-and-blind situations concerning real-time decisions on the optimum measures to be adopted to contain an epidemic. This paper proposes a framework for an online decision support tool serving policymakers by incorporating a reinforcement learning module to choose the directions of governmental actions at each time step of an epidemic. The above framework is flexible since its application depends on the changes in the epidemic pattern concerning modern disease control and prevention approaches. These mitigation measures are customized to fit the government's local objectives. To evaluate the applicability of the proposed model, data on COVID-19 cases from New York State, USA, has been used in this study to support its possible efficacy regarding boosting the flexible and selective relevance of concepts in public health response to new ID threats.

As was explained in [17], the fact is that viruses can mutate very quickly and are challenging to track. It is possible to lose thousands of lives within a short period before the immune system produces the necessary inhibitory antibodies. The new coronavirus virus, which is COVID-19, is an example of this problem, which has caused massive infections and deaths around the world. Concerning the present investigation, this research centers on the highly demanded process of identifying peptides or antibody sequences that react with the viral epitopes of SARS-CoV-2 expeditiously before saving numerous lives. The potential impact of this research is immense, offering hope in the fight against COVID-19. To screen for the neutralizing antibodies in a high throughput manner, the research uses a range of machine learning (ML) models to select possible synthetic antibodies against SARS-CoV-2. One thousand nine hundred and thirty-three virus-antibody sequences and other clinical patient neutralization response data were used to train the ML model. This work employs graph featurization alongside an array of the most popular ML algorithms, such as XGBoost, the Random Forest classifier, the Multilayered Perceptron classifier, the Support Vector Machine classifier, and the Logistic Regression classifier to filter thousands of hypothetical antibody sequences. From this result, nine stable antibodies were found to have the potential for inhibiting Sars Cov 2. Moreover, the researchers supplemented bioinformatics, structural biology, and molecular dynamics (MD) simulations to confirm the stability of these antibody candidates And devise a multi-faceted approach to fighting the virus.

As mentioned in the research in [18], EVI is a severe health concern, often called Ebola hemorrhagic fever, which occasionally affects different parts of Africa. The Ebola virus epidemiology elicits interest, and research has been conducted. This work uses a simple Susceptible Infected Recovered Deceased and Environment (SIRDP) model to understand the complexity of EVI. The authors used fractional operator concepts to enrich the model's description and include memory effects. The EBOLA disease model is analyzed using the Caputo–Fabrizio arbitrary operator in Caputo sense (CFC). Fixed point theory proves the existence and uniqueness of solutions to fractional systems.

Moreover, averaging fractional conformable and β-conformable derivatives gives more representations of the model. To this end, the study presents a method based on the fractional calculus first theorem for CFC derivatives

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definition and the Adams Mulone numerical scheme for conformable derivatives. In addition, the present theoretical study is complemented with computations, confirming the postulated theory.

In the study described in [19], the Ebola virus (EBOV) is described as a specific but rather fatal disease that has been affecting humanity for more than four decades with the symptoms of severe bleeding and organ dysfunction that, without treatment, are nearly always fatal. The worst is that fruit bats in the Pteropodidae family are considered the natural reservoir of the virus. Even though EBOV is a continuing threat, no vaccine can confer immunity to the virus. Given the current need for an EBOV vaccine, this study aims to develop a multi-epitope subunit vaccine for EBOV using an immunoinformatics approach. The vaccine construct here presents the virus's structural and nonstructural proteins. It expects the Class I and II MHC epitopes to be linked with β defensing and compatible linkers.

Further, B-cell linear epitopes were studied, and the physiological characteristics of the vaccine were measured to determine its compatibility with human use and immunogenicity. Furth numbering of the vaccine further explored the binding interaction between the vaccine and TLR4 receptor by docking, and 20 ns of the simulation yielded a highly interactive binding profile with as much as 18 hydrogen bonds on average. The vaccine construct was cloned in a frame with His-tag with pET28a (+) vector for easier purification. The outcomes suggest that this vaccine construct may help establish immunity against the Ebola virus; however, more experimental and immunological research is required to analyze its potential as a commercial vaccine.

In the publication that was earmarked as [20], it becomes clear that a framework for identification and evaluation of fashioning emerging infectious threats has to be put in place so that available resources can be channeled efficiently in the struggle for preparedness and responsive measures. Organized within the Division of National Infection Service and comprising the National Infection Service EIZS, it is responsible for acquiring epidemic intelligence and prioritizing emerging pathogens that may threaten public health in England and elsewhere in the UK. This is done through day-to-day horizon scanning, which involves identifying incidents of public health concern and sharing appropriately derived findings regarding high-consequence infectious diseases such as EVD with stakeholders in PHE and, more widely, within the government. The EIZ Section regularly screens around 100 publicly accessible sources of daily information, irrespective of the medium, and scientific publications on weekdays. This new epidemic intelligence knowledge is compared to estimate its effects on the contemporary analysis of public health threats linked to the observed mishaps worldwide. For instance, horizon scanning identified media reports of newly confirmed EVD cases in the Democratic Republic of the Congo [DRC] and Guinea on February 7 and 14, 2021. The EIZ Section then actively sought the verification of these reports with the World Health Organization (WHO). The organization in question has produced daily situational updates since February 16, 2021, to support PHE’s Strategic Response Group, which has ramped up the response to both outbreaks. This intelligence was also used to inform UK Risk Assessments to identify predetermined ‘triggers’ that indicated the level of risk posed by these outbreaks to public health in the UK and to reactivate the Returning Worker Scheme (RWS) to safeguard and monitor the health of individuals traveling to EVD-affected regions for work-related purpose.

As presented in [21], an epidemic of infectious diseases is an essential problem of population and economic security worldwide. At the same time, elaborating prevention approaches is still a critical issue because of epidemic processes’ non-linearity and complexity. This work also proposes using DRL to learn prevention strategies without human intervention, particularly in the case of pandemic influenza. The authors created an epidemiological meta-population model with multiple patches to mimic the infection process of pandemic influenza in Great Britain; each patch reflected an administrative district. A high level of model complexity would not be easily manageable while implementing reinforcement learning approaches; hence, complexity was mitigated while ensuring the feasibility aspect of the model. To assess the efficacy of using this approach, the “Proximal Policy Optimization” algorithm was run in one area of a single district with a known accurate solution. Further, the study enlarged the context by testing the method on a grander scale, the cluster of 11 strongly integrated districts with no prior ‘ground truth.’ The results show that DRL can learn and improve the mitigation strategies in more overall states and action space for various epidemiological situations, which indicates that DRL is a potential approach to cope with large-scale infectious disease spread.

In the analysis done in [22], the authors discuss the application of non-pharmaceutical interventions (NPIs), including social distancing, to lower or delay the epidemic curve in areas where drugs and vaccines are unavailable. Although these measures reduce contact ratios and slow epidemic transmission, they are associated with social and economic implications and cannot be sustained in the long term. The work proposes the theoretically best approach for time-limited interventions in a SIR epidemic model that reduces the anion’s maximum occurrence. It also demonstrates that several more accessible methods can achieve nearly the same result as the optimal solution. However, the research highlights a critical issue: it is conceivable that both the first and second best are highly sensitive to those implementation errors; slight disparities in timing would lead to high epidemic peaks. This study

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highlights the specificity, timeliness, and preferably prolonged measures for effective epidemic containment and shows both the advantages and drawbacks of NPIs in combating epidemic threats.

I agree with Lars in paper [23], where authors used machine learning approaches to model the dynamics of the COVID-19 epidemic – an approach critical for identifying possible future trends in this disease and taking appropriate measures. The study works with publicly available data from global sources, including data from India, to estimate the parameters of the pandemic and give ten-day forecasts of the number of COVID-19 cases. The authors selected and employed Prophet, Polynomial Regression, Auto ARIMA, and SVM for the study, which yielded satisfactory results. Furthermore, this paper looks at four different measures of growth: growth factor, growth ratio, rate of growth and second derivative to assess the patterns of Covid-19 transmission in the USA and India. Thus, the formulated and computed parameters offer valuable information about the dynamics of the pandemic. The paper also considers various hypotheses regarding the source and emergence of the coronavirus, and it opens a new chapter in understanding its effect and transmission.

Table 1 provides a detailed overview of the impact of modern modeling and artificial intelligence technologies on the prediction, detection and management of infectious disease outbreaks. The publications examine the threat of numerous ailments, such as Ebola, COVID-19, and Marburg viruses, among others, and the strategies of modeling fractional order systems, employing machine learning and deep reinforcement learning techniques. The evidence suggests that these methods have successfully increased the accuracy of outbreak predictions, improved strategies for mitigation, and bolstered preparedness in health systems. For example, fractional order models have been recommended for modeling the trends of epidemics because they tend to perform better than ordinary models. Moreover, machine learning has made it easy to predict the course of an outbreak and the interventions that would control the outbreak. Furthermore, research incorporating artificial neural networks with immunoinformatics has assisted in developing vaccines and neutralizing antibodies against viruses, indicating the need for a multidisciplinary approach to addressing health issues worldwide.

Table 1: Summary of Literature Review

Study Reference	Disease Focus	Methods/Techniques Used	Key Findings/Outcomes
[8] Pan et al. (2021)	Ebola	Fractional order SEIR model	Fractional models offer a better fit to actual data than integer-order models; stability of equilibrium points analyzed.
[9] Buscema et al. (2020)	Ebola (2014, 2018)	Adaptive Systems, ANN	Topological and Bayesian methods were used to locate outbreak origins; ANN effectively predicted outbreak diffusion.
[10] Smith (2024)	Ebola (West Africa)	Optimization Strategies	She highlighted the need for robust healthcare systems and international cooperation.
[11] Johnson (2024)	Ebola (West Africa)	Optimization Models	Identified lessons for better control strategies through optimization.
[12] Price et al. (2020)	Ebola	Transcriptomic Analysis	Early immune responses distinguished between tolerance and fatal outcomes, with predictive models achieving 99% accuracy in mice.
[13] Ahmad et al. (2024)	Ebola	Fractal Analysis, Hybrid Fractional Models	Stability results showed effectiveness in predicting outbreak dynamics using fractional models.
[14] Mustafa et al. (2024)	Marburg	Deep Learning, Quarantine Models	Proposed DNN to simulate transmission dynamics and control interventions.
[15] Choubey et	Virus-Borne	Enhanced Back Propagation	Improved prediction accuracy,

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al. (2022)	Diseases	ANN	enabling early diagnosis and intervention.
[16] Vereshchaka & Kulkarni (2021)	Epidemics (General)	Reinforcement Learning (RL)	Framework to optimize mitigation strategies; applied to COVID-19 data in New York.
[17] Magar et al. (2021)	COVID-19	Machine Learning, Antibody Screening	Identified nine potential neutralizing antibodies for COVID-19 using ML.
[18] Momani et al. (2021)	Ebola	SIRDP Model, Fractional Calculus	Enhanced model's accuracy by including memory effects; theoretical framework confirmed with computations.
[19] Kadam et al. (2020)	Ebola	Immunoinformatics	We designed a multi-epitope subunit vaccine showing potential for EBOV immunity.
[20] Mahon et al. (2022)	Ebola	Epidemic Intelligence	Framework for tracking public health threats using horizon scanning and real-time analysis.
[21] Libin et al. (2021)	Pandemic Influenza	Deep Reinforcement Learning	She demonstrated DRL's capability to develop adaptive control strategies for epidemic spread.
[22] Morris et al. (2021)	Epidemics (General)	Non-Pharmaceutical Interventions (NPIs)	We studied the timing and effectiveness of NPIs, highlighting challenges with implementation sensitivity.
[23] Tiwari et al. (2022)	COVID-19	Machine Learning (ML)	ML models effectively predicted case trends and provided insights for mitigation measures.

Therefore, continuous epidemiological modeling and machine learning studies provide vivid and useful findings on transmitting and controlling infectious diseases. This has been achieved through different mathematical models such as fractional-order systems, where fine details on epidemic behavior have been realized, and through machine learning algorithms with higher accuracy for prediction. However, the viral behavior in its evolution and wave pattern still poses uncertainties that need further study and more inventions. Proper modeling and early actions remain, which prevent severe epidemics and reduce their influence on population health. Further, improving and enhancing more inclusive datasets, together with real-time analyses, must be the primary direction for future studies on this topic so that efforts can be made to establish enhanced epidemic readiness and response internationally.

3. Conclusion

To wrap up, this assessment has highlighted the influence of AI and fractional order models in detecting and predicting an Ebola virus outbreak. Classic epidemiological frameworks such as SIR and SEIR serve valuable purposes. However, their usefulness tends to be limited under the realistic transmission of a virus or in a situation such as Ebola, which can vary spatially and temporally. Introducing fractional-order models improves such systems by addressing history and growth that is not necessarily exponential, hence more or less fitting with all the figures observed in the respective epidemiological curves. This modification helps strategize the rate at which an outbreak will likely occur, supporting a comprehensive approach to health care provision.

The integration of machine learning with the predictions of epidemic models also enables the inclusion of essential data in epidemic prediction with approaches that go beyond structure and process, thanks to the availability of numerous large databases containing genetic, clinical and other environmental information, among others. The distribution and analysis of advanced techniques such as neural networks, decision trees and support vector

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machines must be iterated across an ocean of data to extract and highlight specific trends or patterns that remain out of reach. This ability to evaluate data swiftly is fundamental in current-day surveillance and intervention strategy design, thereby improving the efficiency of containment measures employed during an outbreak.

Nonetheless, the assessment notes that specific difficulties remain, especially regarding data confidentiality, the risk of bias in the systems designed, and the availability of uniform and quality datasets. Although a more advanced epidemic preparedness framework with the aid of AI and fractional order models can be envisaged, concerns about the ethics in practice and the disparity in data availability by regions need to be resolved to facilitate fair access and dependability. In the coming years, refining such models should be the focal research direction. At the same time, the enhancement of cross-disciplinary efforts and collaborations will be geared toward developing effective and flexible epidemic surveillance and response systems that can be employed worldwide.

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