

Predictive Modelling of Infectious Diseases

Bhupendar Kumawat C¹, Darshan D², Gangadhara B³ and Dr. Bondu Venkateswarlu⁴

¹⁻⁴Dayananda Sagar University, Harohalli, India

Email: Bhupendar.1822@gmail.com, {darshandivakar3, gangagangadhara38}@gmail.com bonduvenkat-cse@dsu.edu.in

Abstract—Epidemics and Pandemics are occurring more often and spreading faster and further than ever. Epidemics demand urgent responses, Planning and preparing for prevention and control are essential. (WHO, 2023). Epidemic modelling is essential for predicting disease dynamics and planning public health interventions. Allocating just the right number of resources is Essential. With limited resources and potentially dangerous diseases, accuracy in epidemic models is crucial, as inaccurate forecasts can lead to either over-preparation, which strains resources, or under-preparation, which leaves health systems vulnerable. In addition to guiding interventions, epidemic models inform healthcare providers and policy makers about the expected number of cases, peak infection times, and duration of an epidemic. This is significant for making decisions on where to deploy healthcare workers. This paper reviews some recently published papers on various methods that are used to predict epidemics. We also propose the use of Monte-Carlo methods to iterate over the hyperparameters dynamically. Moreover, models must account for social behaviours, demographics, and geography, as these factors strongly influence disease dynamics. Epidemic modelling is not a complete tool; rather, it must adapt to the disease at hand, the resources available and the specific characteristics of the affected population.

Index Terms—SEIR, Demographics, Monte-Carlo Simulations in epidemiology.

I. INTRODUCTION

The current socio-economic and political processes, globalization, rising number of conflicts, migration problem, environmental pollution, an increase in infectious diseases and epidemics affect everyday life of individuals significantly and impedes the sustainable development of countries.[3] In today's globalized world, the dynamics of infectious disease outbreaks are increasingly shaped by complex socio-economic, political, and environmental factors.

Epidemic modelling has thus become an essential tool for predicting disease spread, informing public health responses, and supporting effective outbreak management. The World Health Organization (WHO) emphasizes the critical role of epidemic modelling in supporting public health planning, preparedness, and response to infectious disease outbreaks. Epidemiologists use various methods to track infections and plan intervention methods with limited resources. Researchers traditionally used compartmental models—like the SIR and SEIR (Susceptible-Exposed-Infected-Recovered) frameworks.

Compartmental Models (like SIR and SEIR) categorize individuals into compartments based on disease status (susceptible, exposed, infected, and recovered) and assume specific rates of movement between these compartments. For COVID-19, SEIR models were commonly used because they allow for an “exposed” category, capturing the incubation period before an infected individual becomes symptomatic or infectious.

Researchers calibrated these models with real-world data to estimate infection and recovery rates, then used them to predict case counts, peak times, and healthcare demands. Compartmental models, are widely used due to their simplicity and computational efficiency but come with notable limitations like Oversimplification of Population Heterogeneity, Fixed Parameter Values, Lack of Spatial and Network Structure and Limited Interaction Complexity. In addition to compartmental models, researchers applied statistical techniques to fit trends in COVID-19 case data and to forecast future cases. Machine learning models and regression techniques were also used to capture real-time transmission trends and assess the impact of interventions on disease spread. Statistical models, which use data to infer patterns and predict outcomes, also have inherent limitations like Data Dependency, Lack of Mechanistic Insight, Assumption of Stationarity and Overfitting Risks.

Researchers also use Agent-Based Models, these models simulate the interactions of individual agents (representing people) within a virtual environment to capture more granular transmission dynamics. For COVID-19, agent-based models were beneficial in assessing how specific public health interventions (like social distancing, mask-wearing, or lockdowns) impacted transmission on a local scale. Agent-based models are powerful for simulating individual-level.

Epidemic modelling is a powerful tool for understanding and predicting disease spread, particularly in managing large-scale outbreaks and informing public health policy. Models like SEIR and SIR have become indispensable in epidemiology due to their simplicity and ability to simulate disease transmission patterns. However, traditional models typically assume a homogeneous population and fixed transmission rates, which can fail to reflect real-world complexities. In particular, demographic factors—such as age distribution, population density, and varying access to healthcare—affect susceptibility to and recovery from diseases, while environmental factors, such as seasonal climate shifts, can influence transmission rates. Incorporating these variables into the SEIR model may yield more realistic projections of disease spread and improve epidemic control measures. The objective of this study is to develop and evaluate an enhanced SEIR model that incorporates demographic characteristics and seasonal transmission rate adjustments. By doing so, we aim to explore how these additional factors alter disease dynamics, provide insights into their practical implications for epidemic management.

Additionally, Monte Carlo simulations are employed to introduce stochasticity, capturing the uncertainty inherent in epidemic dynamics.

This allows the model to explore a range of possible outcomes, enhancing its predictive robustness. While the model has not yet been fully validated, preliminary simulations demonstrate promising results. The goal is to apply this enhanced model to improve epidemic preparedness and response, especially in contexts with varying demographic and environmental conditions.

II. LITERATURE SURVEY

Upon reading numerous research papers on epidemic modelling, we discovered that the SEIR model is the most popular. The SEIR model classifies individuals into four compartments: Susceptible (S), Exposed (E), Infected (I), and Recovered (R).

$$N = S + I + R. \quad (1)$$

For most infectious diseases, however, there is a latent period between being infected and becoming infectious: the exposed group (E). The new group is capable of spreading disease unknowingly and are sometimes also referred as “Lurkers” Here are the equations for a basic SEIR model:

$$\frac{dS}{dt} = -\frac{\beta_I IS}{N} - \frac{\beta_E ES}{N} \quad (2)$$

$$\frac{dE}{dt} = \frac{\beta_I IS}{N} + \frac{\beta_E ES}{N} - \alpha E \quad (3)$$

$$\frac{dI}{dt} = \alpha E - \gamma I \quad (4)$$

$$\frac{dR}{dt} = \gamma I \quad (5)$$

This SEIR model describes disease transmission dynamics using four compartments: S (susceptible individuals who can contract the disease), E (exposed individuals who are infected but not yet infectious), I (currently infectious individuals), and R (recovered or removed individuals, including those deceased). The total population size (N) remains constant. Disease transmission occurs at rates β_I (from infectious individuals) and β_E (from exposed individuals, if partially infectious). Exposed individuals progress to the infectious stage at rate α (inverse of the incubation period), while infectious individuals recover or are removed at rate γ (inverse of the

infectious period). This framework captures the flow of individuals through disease stages and helps analyse epidemic spread. Another approach towards SEIR model is adding more parameters. In Method and Application of Estimating Epidemiological Parameters (Yuqing Sun, Zhonghua Zhang and Gaochang Zhao, 2024), SAIUHR model is proposed. The SAIUHR model has additional factors with the same base concept of SEIR model. We divide the population into six compartments: susceptible individuals (S), asymptomatic infectious individuals (A), reported symptomatic infectious individuals (I), underreported symptomatic infectious individuals (U), hospitalized individuals (H) and recovered individuals (R).[9].

Even though now, The SEIR model is far very accurate from the basic SEIR with the inclusion of demographic data, there lies another factor that effects the curve significantly. The season factor. One might argue that seasonal changes change transmission rates and might not be much significant. Seasonal changes effect the migration, population behaviour, pathogen behaviour and ecological variability. In the paper "Impact of Seasonal Conditions on Vector-Borne Epidemiological Dynamics" (M. Arquam, Anurag Singh and Hocine Cherifi, 2020) researchers propose a seasonal SIR model. While SEIR model assumes a homogenous population and does not account for climate, Results show that failing to incorporate these features on the model can lead to a poor estimation of the maximum fraction of infected individuals in the host population.[8].

Although the paper is study on mosquitoes and the spread of malaria, the seasonal factors don't only significantly affect malaria spread but also other contagious diseases. For example, the indoor gathering increases when the temperature is cold outside. Gathering without proper ventilation can spread pathogens quicker.

Although SEIR models are the most popular method, relying on only SEIR model is not ideal. SEIR model has major assumptions and also does not account for demographic data, Population data, whether changes, Dynamic nature of pathogens, behaviour of humans, patterns or even the randomness of the disease spread. During recent COVID-19 pandemic researchers (R. Alguliyev, R. Aliguliyev and F. Yusifov, 2021) stated that "There is a need for developing realistic models considering the human behaviour for the purpose of fighting COVID-19 pandemic at global level and preventing future cases of pandemic." [3]. The paper has used a graph-based approach to explain the significance of demographical data that is required in compliment with SEIR model.

The paper "Effect of Population Density on Epidemics"(Ruiqi Li, Peter Richmond, Bertrand M. Roehner) uses KMK (Kermack-McKendrick) model to isolate the effects of population density on number of deaths using an early 20th century dataset. For low-density areas historically (early 20th century Alaska or Australia), disease spread was limited, offering insights into public health policies for managing epidemic outbreaks with appropriate resource allocation in urban and rural settings. The study offers a theoretical basis for why sparsely populated areas may experience less severe epidemics The authors conclude: "we have shown that there is a weak but clearly defined relationship between population density and the death rate of epidemics providing sufficiently large density ranges are considered and background noise is kept under control" [23].

Another such study in the paper "A Novel Epidemic Model Considering Demographics and Intercity Commuting on Complex Dynamical Networks" (Qian Yin et al., 2020) explores a two-city epidemic model that factors in demographics and intercity commuting between populations. Unlike standard models, it considers commuting as a conduit for disease transmission between two urban areas, addressing real-world factors that contribute to epidemics. The paper uses SIR model with varying birth and death rates. A numerical simulation was conducted with 2 cities of different population. The paper emphasises on reproduction number R_0 . Through theoretical analysis, we proved that it is globally asymptotic stable for the endemic equilibrium when $R_0 > 1$, and it is also globally asymptotic stable for the disease free one when $R_0 < 1$. [22] They also conclude that in the demographics of each city, the commuting between the two cities is also an important factor affecting the epidemic size in the proposed model.[22].

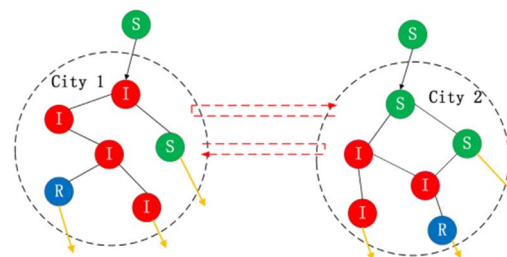


Figure 1. Figure taken from [22] (Q. Yin, Z. Wang and C. Xia et al, 2020) Showing 2 different cities through which the transmission can occur

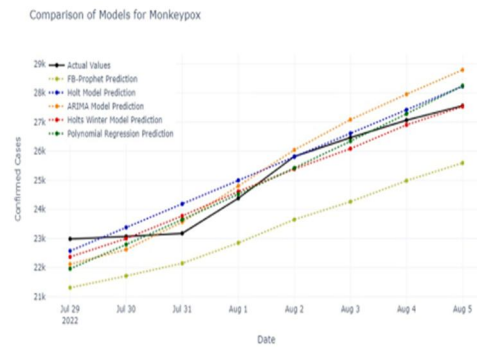


Figure 2. Figure taken from [1] (A. Chhabra et al., 2024), comparing various time-series models with the actual data

Another unique approach from a team of researchers (A. Chhabra et al., 2024) tried using time-series models to predict short term pattern in the dataset to estimate future patterns. The researchers have compared various time-series models like ARIMA, Holt's linear, Holt's winter, Fb- prophet and polynomial regression to estimate on 4 dataset consisting data of monkey pox, HIV, Influenza and COVID. The Arthurs quoted that: We can clearly see that Holt's winter model has the most accurate predictions with the MAPE value of 0.012907 and R2 score of 0.953980 which is performed just better than polynomial regression with MAPE value of 0.016952 and R2 score of 0.917986.[1].

Using time-series models to estimate infection numbers may initially appear unsuitable; however, their application in epidemic studies is both logical and valuable. Time-series models analyse past data patterns to forecast future data points, a method widely adopted for predictive tasks across various domains, including stock market forecasting. Although the stock market is influenced by numerous external factors, time-series models still effectively predict trends, demonstrating their utility even in complex systems. In epidemic modelling, these models provide valuable insights over short-term periods, capturing immediate trends and fluctuations. However, due to their reliance on historical patterns, time-series models may lack practicality for long-term epidemic forecasting, especially in dynamically changing scenarios. Despite these limitations, time-series models remain instrumental in offering small-scale, actionable insights within the broader scope of epidemic analysis.

Another very interesting study uses neural network to predict infections and is conducted in [10]. The models include the GFT regression model (model 1), the weighted GFT regression model (model 2), the GFT + CDC regression model (model 3), the CDC regression model (model 4), and the weighted CDC regression model (model 5). All models were utilized to predict and assess influenza activity across ten regions of the United States.[10].

Here, MAPE (Mean Absolute Percentage Error) measures the accuracy of predictions by calculating the average absolute percentage error between predicted and actual values. A lower MAPE value indicates better model performance. R2 (R-squared) measures how well the model explains the variance in the data. A value closer to 1 means that the model is better at explaining the data. Root Mean Square Error (RMSE) is a standard metric used to measure the difference between observed values and predicted values in statistical and machine learning models. It gives an idea of how well a model's predictions match the actual data and is commonly used for regression analysis. MSE (Mean Squared Error) is a statistical metric used to measure the average squared difference between predicted values and actual values. It is commonly used in regression analysis and machine learning to evaluate the performance of a model.

TABLE I. ACCURACY METRICS FROM [1] (A. CHHABRA ET AL., 2024), AS FROM THE ABOVE GRAPH.

Model	RMSE	MSE	MAPE	R2 Score
FB-Prophet	1794.84	3.221448e+06	0.069247	0.027517
ARIMA	708.32	5.017225e+05	0.025078	0.839970
Holt's	531.171	2.821429e+05	0.017937	0.910007
Holt's Winter	379.84	1.442808e+05	0.012907	0.953980
Polynomial Regression	507.07	2.571288e+05	0.016952	0.917986

Numerous studies have focused on deterministic models of epidemic spread, including the foundational SIR and SEIR frameworks, as well as SEIR models that account for demographic changes and seasonal factors. These models, often with carefully tuned parameters, have shown success in achieving high predictive accuracy under controlled conditions. However, a key limitation of these traditional models is their lack of inherent stochasticity, which is an essential feature of real-world epidemics.

TABLE II. TAKEN FROM [10] (H. XUE ET AL, 2017) FOR THE GRAPH ABOVE ON REGION 10 AS IN THE PAPER

Model	Method	MSE	RMSE	MAPE (%)
Model 1	LS	8.5045e+05	0.5031	60.5858
Model 1	NET	6.2772e+05	0.3299	51.5190
Model 2	LS	4.9017e+05	0.3816	53.0634
Model 2	NET	1.5994e+05	0.0871	26.2857
Model 3	LS	3.8498e+04	0.0319	14.6947
Model 3	NET	7.0350e+04	0.0460	17.6407
Model 4	LS	1.7283e+04	0.0116	8.7504
Model 4	NET	1.3367e+04	0.0083	7.3531
Model 5	LS	1.2219e+04	0.0063	5.8859
Model 5	NET	2.0746e+04	0.0092	7.5220

Epidemic spread is fundamentally influenced by various factors, with randomness playing a particularly critical role. Disease transmission involves multiple uncertain elements, from the heterogeneity in human behaviour to the variability in pathogen interactions. Consequently, parameters such as the transmission rate (β) cannot be treated as fixed values without compromising the model's realism. For example, while a transmission rate might be estimated at $\beta=0.8$, individual transmission varies significantly: certain individuals (e.g., superspreaders) may contribute disproportionately to the spread, while others transmit at lower rates. This randomness is further compounded by social dynamics, such as varying contact rates due to cultural practices or mobility restrictions during an outbreak. Similarly, changes in environmental conditions, like temperature and humidity, can amplify the uncertainty in disease transmission. This variability introduces randomness that persists throughout the epidemic's lifecycle, impacting not only transmission but also recovery rates, immune response, and environmental factors.

III. COMPARATIVE STUDY

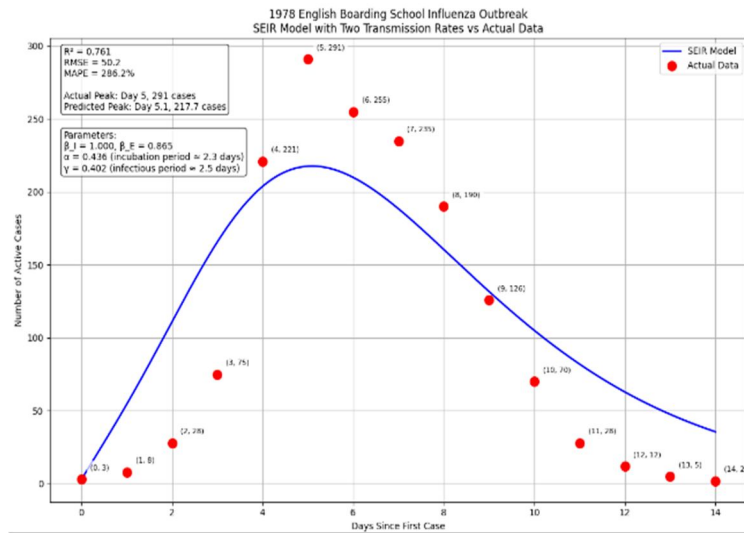


Figure 3. A Basic SEIR model trained on 1978 English Boarding school for Influenza

TABLE III. ACCURACY SCORE OF THE SEIR MODEL FROM THE ABOVE GRAPH

Metric	Value
R ² (Coefficient of Determination)	0.7612
RMSE (Root mean square Error)	50.1735
MAPE (Mean absolute Percentage Error)	286.2485
Actual Peak Day	5
Actual Peak cases	291
Predicted Peak Day	5.0871
Predicted peak Cases	217.7095

After looking through various models and approaches towards the prediction of infectious disease, it is clear that there is no one-size-fits-all model. All the models are tuned differently and have been carefully run to eliminate noise and isolate the parameters as close to actual data as possible. We have structured the approaches as follows:

A. SEIR model

SEIR models are easy to understand and implement; widely used in epidemic modelling. It Provides clear insights into epidemic progression through compartments and acts as a foundational model for more advanced epidemic modelling techniques.

While it provides all these advantages, it Ignores individual variability (e.g., age, location) and assumes uniform population mixing and fixed parameters, which may not hold in real-world scenarios

B. SEIR with Demographics (KMK model)

The kmk model Incorporates population heterogeneity (e.g., age, sex, location), improving realism and prediction accuracy. It Captures region-specific factors like population density and movement, enabling localized interventions and helps design targeted interventions (e.g., strategies for vulnerable age groups).

While these sound good, kmk model Requires detailed demographic and epidemiological data, which may not always be available or reliable. The model also becomes harder to implement and validate compared to SEIR.

C. Time-Series Models.

Time series models Captures trends and seasonality effectively using historical data, without explicit knowledge of disease dynamics. The model can adjust to real-time data and respond quickly to new patterns (e.g., flu cases or Google search trends).

But the model fails with sparse data, Performance drops significantly when there is a lack of reliable or consistent historical data. It also Lacks epidemiological grounding and cannot explain the underlying mechanisms driving observed trends.

D. Neural Networks

Neural networks Excels at capturing complex, non-linear relationships in data, making it ideal for modelling intricate outbreaks and can incorporate multiple data sources (e.g., CDC data, Google Flu Trends) to improve prediction accuracy.

But Neural networks Requires large amounts of labelled data for training, which might not be available for all diseases or regions and Training neural networks requires significant computational resources and expertise in tuning parameters.

IV. PROPOSED WORK

Mapping phenomena characterized by high randomness and ambiguity is inherently challenging, and creating a one-size-fits-all model may be infeasible. However, simulation-based approaches provide a robust alternative for approximating complex systems, such as the spread of infectious diseases. By leveraging simulations that incorporate known parameters and replicate real-world human behaviour, we can generate insights into these dynamic processes. Repeated iterations of these simulations allow for the refinement of results, potentially converging toward values that closely align with real-world observations. This method enables researchers to explore a range of scenarios and account for variability, improving the accuracy and reliability of predictive models. In epidemiology, Monte Carlo simulations can help account for variability in parameters such as transmission rates, recovery rates, contact patterns, and environmental factors. In summary, Monte Carlo simulations could enhance the realism of the model, capturing a broader range of epidemic scenarios that consider seasonal variability, contact network heterogeneity, and uncertain transmission parameters. This approach would make your model's predictions more robust and relevant for public health planning in response to vector-borne diseases. Model parameters like the transmission rate β , recovery rate γ , and death rate μ are often uncertain, varying with time or across different populations. Monte Carlo methods can help account for this uncertainty by generating a range of possible values for these parameters and running multiple simulations. Incorporating stochastic processes into epidemic models introduces randomness into disease transmission and progression, allowing these models to reflect the variability in real-world interactions and outcomes more accurately.

Instead of using fixed rates, stochastic models assign probabilities to transitions—such as infection, recovery, and death—based on probability distributions. For example, the likelihood of a susceptible individual becoming infected may fluctuate based on random interactions modelled by a Poisson distribution, while recovery times might follow a log-normal distribution to capture individual variation. This approach is particularly useful for smaller populations or scenarios with environmental and seasonal influences, where random events significantly affect disease dynamics, making predictions more nuanced and adaptable to real-life conditions.

Monte Carlo simulations run many independent simulations of the SEIR model, each with a randomly chosen set of parameters. After a sufficient number of simulations, you can analyze the output to understand the range of possible epidemic outcomes (e.g., peak infection levels, duration, total number of deaths) and how sensitive they are to various model parameters. Through this approach, incorporating demographic and seasonal factors, simulations, and Monte Carlo methods, our enhanced SEIR model provides a robust tool for understanding epidemic dynamics.

V. CONCLUSION

The future scope of epidemic modelling holds considerable potential for enhancing predictive accuracy, scalability, and usability across diverse health scenarios. Future research could focus on developing hybrid models that combine deterministic and stochastic elements, providing a more robust approach to capturing disease dynamics under various environmental and social factors. Integrating artificial intelligence and machine learning could allow models to learn from real-time data, improving responsiveness to emerging outbreaks. Additionally, advancements in virtual and augmented reality offer new avenues for immersive, visual simulations, aiding public health officials and policymakers in understanding complex disease spread scenarios. With anticipated increases in the frequency and variability of epidemics due to factors like global travel and climate change, there is a pressing need for models that can adapt to new pathogens. Tools like Monte Carlo simulations can make epidemic modelling more accessible, allowing even novice researchers to gain a better understanding of complex dynamics. While no single model can fit all scenarios, continuous advancements in simulation techniques promise more precise and adaptable epidemic models moving forward.

REFERENCES

- [1] Anureet Chhabra, Sunil K. Singh, Sudhakar Kumar, Varsha Arya, Sunil K. Singh, Akash Sharma, Brij B. Gupta, Varsha Arya, Kwok Tai Chui h, Sustainable and intelligent time-series models for epidemic disease forecasting and analysis (2024) 100064.
- [2] Gbenga Adegbite, Sunday Edeki, Itunuoluwa Isewon, Jerry Emmanuel, Titilope Dokunmu, Solomon Rotimi, Jelili Oyelade, Ezekiel Adebisi, Mathematical modeling of malaria transmission dynamics in humans with mobility and control states. KeAi 2023.
- [3] Alguliyev, R., Aliguliyev, R., & Yusifov, F. (2020). Graph modelling for tracking the COVID-19 pandemic spread. *Infectious Disease Modelling*, 6, 112 - 122. <https://doi.org/10.1016/j.idm.2020.12.002>.
- [4] C. Hameni Nkwayep, R. Glé e Kakai, S. Bowong, Prediction and control of cholera outbreak: Study case of Cameroon KeAi 2024
- [5] Mandal, S., Sarkar, R., & Sinha, S. (2011). Mathematical models of malaria - a review. *Malaria Journal*, 10, 202 - 202. <https://doi.org/10.1186/1475-2875-10-202>.
- [6] Lubinda, J., Bi, Y., Hamainza, B., Haque, U., & Moore, A. (2021). Modelling of malaria risk, rates, and trends: A spatiotemporal approach for identifying and targeting sub-national areas of high and low burden. *PLoS Computational Biology*, 17. <https://doi.org/10.1371/journal.pcbi.1008669>.
- [7] Feng, S., & Jin, Z. (2020). Infectious Diseases Spreading on an Adaptive Metapopulation Network. *IEEE Access*, 8, 153425-153435 <https://doi.org/10.1109/ACCESS.2020.3016016>.
- [8] Arquam, M., Singh, A., & Cherifi, H. (2020). Impact of Seasonal Conditions on Vector-Borne Epidemiological Dynamics. *IEEE Access*, 8, 94510-94525. <https://doi.org/10.1109/ACCESS.2020.2995650>.
- [9] YUQING SUN, ZHONGHUA ZHANG, AND GAOCHANG ZHAO, Method and Application of Estimating Epidemiological Parameters Based on Data-Driven Approach, *IEEE Access*, 2023, Digital Object Identifier 10.1109/ACCESS.2023.3342920.
- [10] Xue, H., Bai, Y., Hu, H., & Liang, H. (2018). Influenza Activity Surveillance Based on Multiple Regression Model and Artificial Neural Network. *IEEE Access*, 6, 563-575. <https://doi.org/10.1109/ACCESS.2017.2771798>.
- [11] Olukanmi, S., Nelwamondo, F., & Nwulu, N. (2021). Utilizing Google Search Data With Deep Learning, Machine Learning and Time Series Modeling to Forecast Influenza-Like Illnesses in South Africa. *IEEE Access*, 9, 126822-126836. <https://doi.org/10.1109/ACCESS.2021.3110972>.
- [12] Venna, S., Tavanaei, A., Gottumukkala, R., Raghavan, V., Maida, A., & Nichols, S. (2017). A novel data-driven model for real-time influenza forecasting. *bioRxiv*. <https://doi.org/10.1101/185512>.
- [13] Lazebnik, T., & Blumrosen, G. (2022). Advanced Multi-Mutation With Intervention Policies Pandemic Model. *IEEE Access*, 10, 22769-22781. <https://doi.org/10.1109/ACCESS.2022.3149956>.
- [14] Haochun Wang and Ju Jiang, Epidemic Model and Parameter Estimation, 023 6th International Symposium on Autonomous Systems (ISAS) | 979-8-3503-1615-5/23/\$31.00 ©2023 IEEE | DOI: 10.1109/ISAS59543.2023.10164368.
- [15] Jiao, H., & Shen, Q. (2020). Dynamics Analysis and Vaccination-Based Sliding Mode Control of a More Generalized SEIR Epidemic Model. *IEEE Access*, 8, 174507-174515. <https://doi.org/10.1109/ACCESS.2020.3026089>.

- [16] Kuzdeuov, A., Baimukashev, D., Karabay, A., Ibragimov, B., Mirzakhmetov, A., Nurpeissov, M., Lewis, M., & Varol, H. (2020). A Network-Based Stochastic Epidemic Simulator: Controlling COVID-19 With Region-Specific Policies. *IEEE Journal of Biomedical and Health Informatics*, 24, 2743-2754. <https://doi.org/10.1109/JBHI.2020.3005160>.
- [17] Chen, X. (2020). Infectious Disease Modeling and Epidemic Response Measures Analysis Considering Asymptomatic Infection. *IEEE Access*, 8, 149652-149660. <https://doi.org/10.1109/ACCESS.2020.3016681>.
- [18] Lopes, M., Simoes, F., Esmi, E., & De Barros, L. (2023). The Use of Triangular Norms in Epidemiological Models: A Comparative Study Using COVID-19 Data. *IEEE Transactions on Fuzzy Systems*, 31, 1542-1551. <https://doi.org/10.1109/TFUZZ.2022.3205357>.
- [19] Alaeddini, A., & Klein, D. (2017). Application of a second-order stochastic optimization algorithm for fitting stochastic epidemiological models. 2017 Winter Simulation Conference (WSC), 2194-2206. <https://doi.org/10.1109/WSC.2017.8247951>.
- [20] Guo, X., Xiong, N., Wang, H., & Ren, J. (2021). Design and Analysis of a Prediction System About Influenza-Like Illness From the Latent Temporal and Spatial Information. *IEEE Transactions on Systems, Man, and Cybernetics: Systems*, 52, 66-77. <https://doi.org/10.1109/TSMC.2020.3048946>.
- [21] Blaizot, S., Riche, B., Maman, D., Mukui, I., Kirubi, B., Etard, J., & Écochard, R. (2015). Estimation and Short-Term Prediction of the Course of the HIV Epidemic Using Demographic and Health Survey Methodology-Like Data. *PLoS ONE*, 10. <https://doi.org/10.1371/journal.pone.0130387>.
- [22] R. Li, P. Richmond, B.M. Roehner, Effect of population density on epidemics, *Physica A* (2018), <https://doi.org/10.1016/j.physa.2018.07.025>
- [23] Ottar N. Bjørnstad, Katriona Shea, Martin Krzywinski and Naomi Altman, The SEIRS model for infectious disease dynamics, *Nature Methods* | VOL 17 | June 2020 | 557–558 | www.nature.com/naturemethods