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SIMULATION OF EPIDEMIC PROCESSES: A REVIEW OF MODERN METHODS, MODELS AND APPROACHES

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Abstract

The paper is devoted to an overview of the current state of research on the modeling of epidemic processes. The classification of mathematical and simulation models of epidemic processes is carried out. The disadvantages of classical models are revealed. Specific characteristics inherent in epidemic processes have been determined, which must be taken into account when constructing mathematical and simulation models. A review of deterministic compartment models is carried out. Various methods and approaches to the construction of statistical models of epidemic processes are considered. The types of problems that are solved using machine learning are analyzed.

Keywords: *epidemics, forecasting, infected organism, infections, mathematical modeling, simulation modeling, susceptible organism.*

INTRODUCTION

Epidemics and pandemics of infectious diseases have accompanied the entire history of mankind. New emergent infections continue to appear, while old infections, which humanity has already learned to fight, return. The spread of the SARS-CoV-2 pathogen, first identified in December 2021, has led to a pandemic that has been going on for almost two years. The current COVID-19 pandemic has affected all aspects of human life and reiterated the importance and need for tools to prevent, prepare, detect and respond to epidemics and pandemics. Therefore, it is necessary to be able to predict epidemics, i.e., to determine the probability of occurrence, scale of development of epidemics and their consequences in order to develop and justify measures to prevent the spread of infectious diseases among the population and eliminate the socio-economic consequences caused by epidemics. An epidemic is a progressive spread of an infectious disease among humans that significantly exceeds the usual incidence rate in the area and can cause an emergency. However, the basis of any epidemic is an epidemic process – the continuous transmission of an infectious disease agent among humans – from the source of the infectious agent through transmission mechanisms to the susceptible organism.

Simulation of the epidemic process is a tool that is used to study the mechanisms of the spread of diseases at the population level, predict a possible increase in the development of an outbreak, and assess the feasibility and rationality of strategies to combat the epidemic.

The aim of the review paper is to classify models of epidemic processes and to analyze current state of researches in field.

1. Classification of epidemic process models

The following types of models of the epidemic process are distinguished:

- a stochastic model is a tool for estimating the probability distributions of potential outcomes by allowing for random variation in one or more inputs over time. Stochastic models depend on random variations in the risk of disease occurrence and spread;
- when working with large populations, deterministic mathematical models are often used. In the deterministic model, individuals in a population are divided into different subgroups, any of which represents a specific stage of the epidemic;

The coefficients of transition from one class to another are mathematically defined by derivatives, and the model is described by the corresponding differential equations. When creating such models, it is assumed that the function of population change is differentiated over time, and the epidemic process is deterministic. In other words,

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population change is calculated using only the background history used to estimate the model parameters.

The simplest definition of epidemic dynamics considers the total population in the system as a fixed one, consisting of N individuals and ignoring any other demographic process (migration, birth, etc.). One of the simplest possible compartments is the SIS model with two possible transitions: the first labeled S → I, occurs when a susceptible individual interacts with an infected individual and becomes infected. The second transition, designated I → S, occurs when an infectious individual recovers from illness and returns to the susceptible pool.

The SIS model suggests that disease is not immune and people can be infected over and over again by undergoing the S → I → S cycle, which under certain conditions can be sustained forever.

Another basic model is the classic three-state SIR model. In the SIR model, the I → S transition of the SIS process is replaced by I → R, which occurs when an infectious individual recovers from an illness and is considered to have acquired permanent immunity or has been removed (e.g., died).

2. Formalization of epidemic processes

Classic epidemic models do not take into account many factors, which reduces the accuracy of modeling and the reliability of the dynamics of the epidemic process under consideration.

Among these factors are the following:

- vertical transmission. In the case of certain diseases, such as HIV infection and hepatitis B, the offspring of the parents may be born infected. This transmission of disease from the ancestor is called vertical transmission. The appearance of additional members in the category of infected can be considered within the framework of the model, including the proportion of newborn members in the infected cell of the environment [1];
- vector transmission. Diseases transmitted from person or animal to person through a vector, that is, the spread of malaria by mosquitoes or Lyme disease through ixodid ticks, are transmitted through a vector. In these cases, the infection is transmitted from person to vector, and the epidemic model should include both, usually requiring much more properties than the direct transmission model [2];
- population heterogeneity;
- age groups of the population;
- variable infectivity. As a result of seasonality or other influencing factors;
- heterogeneity of the environment;
- immunity acquired through vaccination.

To eliminate this disadvantage and take into account the above factors, it is proposed to use an intelligent multi-agent approach to modeling the epidemic process of the population dynamics system. For this, it is necessary to distinguish a class of models of the epidemic process among the models of population dynamics.

The following characteristics are specific of the epidemic process:

- *cyclicity (periodicity)* of the epidemic process is an increase or decrease in the incidence of the population, regularly repeating in long-term dynamics. Most of the manifestations of cyclicality are explained by the infectious-immunological relations of populations. An increase in the susceptible layer due to fertility and migration determines the formation of a pathogen with higher epidemic potential and an increase in morbidity. The activation of the epidemic process, in turn, is accompanied by an increase in the layer of immune cells, which reduces the epidemic potential of the pathogen and determines the decline in the incidence even before the layer of susceptible ones is exhausted. Identification of long-term cyclicality is important for the development of forecasts of morbidity and the development of rational preventive measures;
- *irregular ups* and downs in morbidity in long-term dynamics arise in connection with episodic changes in social and natural factors. These changes contribute to the formation of pathogens with a high epidemic potential, which leads to the development of epidemic outbreaks or epidemics. Epidemics develop in times of war, after natural disasters, with omissions in the conduct of highly effective anti-epidemic measures. Any pronounced migration processes are accompanied by the development of epidemics.

The annual dynamics of the incidence is characterized by regular increases and decreases in the incidence, the so-called seasonal and off-season periods. The interval that includes the first month of a seasonal increase in incidence in one year and the month preceding a new seasonal increase in incidence the next year is called an epidemic year. When considering different epidemic processes, different seasonality stands out. For example, they usually talk about the winter seasonality of aerosol infections and the summer seasonality of intestinal infections, when considering viral marketing on the Internet, autumn-spring seasonality is observed, etc. However, the specific manifestations of seasonality are individual for different forms of the epidemic process, and within individual forms, they are individual for different territories and for separate groups of the population in the same territory. Seasonality is one of the most intelligible manifestations of the phasic nature of the development of the epidemic process. It is here that interepidemic and epidemic periods associated with the phases of reservation of the pathogen and its epidemic spread are easily detected.

In the annual dynamics of morbidity, in addition to periodically recurring seasonal epidemics, epidemics develop that do not have a regular recurrence or are characterized by one or another relatively local manifestation. The limits between these concepts are relative since the seasonal epidemic is accompanied by an increase in the number of affected populations in each of them.

When forecasting, there are three types of forecasts: short-, medium- and long-term. At the same time, experts studying the epidemic process are only interested in forecasting an epidemic outbreak, that is, the period of “epidemic-recession” [3]. This is because the dynamics of the process can change the distribution rules after an outbreak as a result of the anti-epidemic measures taken, as well as the natural extinction of the infected population.

3. Deterministic compartment models

The most popular approach to modeling epidemic processes is deterministic models based on the use of systems of differential equations and the use of compartments that characterize the state of objects in the population. The first such type of models was applied by W. Kermack and A. McKendrick [4–6], who expanded the model of R. Ross and H. Hudson [7], and built a model based on the types S (susceptible), I (infected) and R (recovered) to study the epidemic nature of infectious diseases. The first to study the models of epidemic actions on the terrain of Ukraine and the USSR were L.A. Rvachev and O.V. Baroyan, who used this approach to model the incidence of influenza [8–9].

Compartment models are popular now, and many modern studies are based on their extension [10]. M.B. Trawicki [11] considers the extension of the model, adding the state E (incubation period) and additional transitions between the compartments. The proposed model takes into account the dynamics of life activity with unequal fertility and mortality rates, vaccination of infants and non-newborns, as well as temporary immunity from an infectious disease. In this case, the recovered have only temporary immunity from an infectious disease and can potentially go back to the susceptible class. The study authors [12] add states H (hospitalized) and D (dead). The model explored policies that included large-scale quarantine, tight travel controls, monitoring of suspected cases, and social distancing.

The study [13] considers the possibility of close contact and the latent course of morbidity. The model included four compartments based on COVID-19 incidence data in Wuhan and was supported by data collected from Italy, the United Kingdom, and the United States. The model reflects the effectiveness of various disease containment measures through three changing factors: contact ratio per capita, which can be reduced by social distancing; the likelihood of infection through contact with infectious individuals, which can be reduced by wearing face masks, maintaining personal hygiene, etc.; and populations of infectious individuals in contact with susceptible populations, which can be reduced through quarantine. The model was used to predict the best approach to breaking out of lockdown.

In [14] the classical model is extended by the state Q (quarantine) and V (vaccinated), and the spread of coronavirus disease in Saudi Arabia is investigated. The mathematical analysis illustrates the inalienability, limitation, epidemic equilibrium, the existence and uniqueness of endemic equilibrium, as well as the basic reproduction number of the proposed model. To improve the classical model and find little-known parameters, the authors applied a data assimilation structure based on Kalman filters to estimate state parameters to improve the prediction parameters of the model.

The authors of [15] use step-by-step modeling, taking into account the edges, which eliminates the assumption that all people have the same frequency of contacts, and partnerships are fleeting, having a classical model. The authors derive models of simple ordinary differential equations that reflect social heterogeneity (heterogeneity of contacts) and take into account the effect of the duration of the partnership. The paper also provides a graphical interpretation that makes it easy to derive and communicate the model and apply the technique with different assumptions about how the frequency of contacts is distributed and how long the partnership lasts.

Study [16] proposes a non-linear model of the COVID-19 epidemic that simulates the spread of coronavirus influenced by social distancing caused by government measures to halt the spread of coronavirus. At the same time, the study focuses specifically on the impact of public policies aimed at containing the pandemic. [17] investigated the effect of travel from other US states on common infections in the destination state and found a strong inverse correlation of 0.98 between the index of contagiousness and the compartment of social awareness, that is, people who are no longer susceptible to infection. This study uses a compartmental metapopulation model to represent the correlation between exposure and mobility indices and the likelihood of susceptibility to infection. A wealth of cellular data has made it possible to study many aspects of user mobility, including their travel, contact, and residence patterns.

In [18], a model structure is proposed for predicting new outbreaks of tuberculosis based on compartment models that include properties such as, for example, the immigration of infected people from countries with a high prevalence. In addition, the aspect of trained immunity is taken into account in the model. Using a mathematical approach, a system of ordinary differential equations that can be developed for several points in time, different levels of infection or attack were obtained, which led to different effects of vaccination, depending on the setting of certain parameters and initial values in the vaccine compartments.

[19] examines compartment models of epidemic processes from the point of view of economics. It proposes three distinct areas in which economists could contribute or provide information to the epidemiological literature: modeling the heterogeneity of susceptible populations in different dimensions, taking into account the endogeneity of the parameters governing the spread of disease, and helping to understand the importance of political economy in disease control. Case and death projections based on these models are discussed, which went not so much with the early projections, but how they adapted to the current COVID-19 pandemic.

In [20], the spread of the incidence of COVID-19 in Ukraine is investigated using a compartment model extended by the F (lethal) state, and [21] compares this model with regression methods for the territory of Ukraine before vaccination.

Despite the high popularity of compartment models, they have several disadvantages [22], the main of which are low accuracy and the complexity of introducing changes into the model. In particular, the dynamics of the epidemic process lead to an increase in the virulence of the infection, which changes the behavior of its spread. This requires changes in the model, and in the case of using systems of differential equations, it leads to restructuring and calibration of the model from the very beginning.

To improve the accuracy of models of epidemic action, some studies are trying to combine traditional models with other approaches. For example, the study [23] describes a parametric bootstrap approach for generating simulated dynamic system data for quantifying uncertainty and identifying parameters. The confidence intervals and root-mean-square errors of the distributions of the estimated parameters were calculated to assess the identification of the parameters. To demonstrate this approach, it is applied to a low complexity SEIR model that corresponds to pandemic influenza, Ebola, and Zika virus applications. In [24], deep learning methods were applied as an alternative with less dependence on data to estimate the transmission parameters of an individualized compartment model to model the dynamics of the coronavirus disease epidemic in the United States and predict further development. As a result, a comparative model was built and a multi-stage deep learning methodology was developed to estimate the transmission parameters of the model. Then the estimated transmission parameters are loaded into the model to anticipate the development of the COVID-19 epidemic in the United States for 35 and 42 days.

4. Statistical models

More accurate models of epidemic actions are statistical methods for studying time series [25]. Let's consider some applications of such approaches to real problems.

The most popular statistical method used to model epidemic dynamics is the moving average method and its derivatives. Thus, the simple moving average method is applied to modeling COVID-19 in Iraq [26], USA [27], Pakistan [28], Italy and Spain [29], China [30], etc. Also popular are such derivatives of the method as the exponential moving average [31–33], ARIMA (autoregressive moving average) [34–36], and SARIMA (seasonal autoregressive moving average) models [37–39].

Statistical analysis is also used to quickly study the epidemic process of emerging diseases or new outbreaks of already known diseases [40], which is gaining new relevance with the rapid spread of COVID-19. Examples of such models have been applied to SARS [41–42], H1N1 influenza [43–44], Ebola [45], foot and mouth disease [46], COVID-19 [47–48], etc. The main difference from previous tasks is that outbreak assessments are needed to determine effective control measures. It is impossible to wait for the outbreak to end and to use the definitive data on infectious disease virulence parameters and associated parameters. Instead, it is necessary to conclude early in the outbreak's growth. In addition to less data, this also poses the risk of biased assessments because people infected in the early stages of an outbreak are usually not presented to the community as a whole.

5. Machine learning models

Methods for studying epidemic processes based on machine learning are now most accurate. Among them are the following tasks.

Regression. Regression is a predictive approach for examining the relationship between the dependent and independent variables. Separately, parametric equations can be evaluated taking into account all data. These parameters include morbidity and weather [49], the level of population heterogeneity [50], the mortality rate [51], vaccination [52], restrictive measures [53], etc. Regression analysis models are used to show or anticipate the relationship between a process and what the process might trigger. However, such a correlation does not always show causality, so the interpretation of such correlations is another important task. Linear regression [54], logistic regression [55], polynomial regression [56], Ridge regression [57], Lasso regression [58], and others are used, depending on the types of data and the tasks set.

Classification. The classification task is aimed at separating objects according to predefined classes. In the study of epidemic processes, classification methods are applied to various objects: determination of population groups by behavior [59], determination of Spatio-temporal features of the epidemic process [60], distribution of available information about outbreaks [61], identification of climatic zones affecting morbidity [62], determination of geographic zones depending on various infectious diseases [63], etc.

Clustering. The clustering task is aimed at separating objects in the case when the classes are not predefined, and the clusters must be formed according to the similarity of certain characteristics of the elements. In this case, the number of clusters can be determined by the researcher in advance, or by the model itself. Also, the researcher can determine the features according to which the sample needs to be divided independently, or the model will do it on its own. Investigating epidemic processes, models, and methods of clustering are used to solve such applied problems as the determination of geographic territories based on similar signs of the epidemic process [64], the determination of epidemic outbreaks [65], the determination of groups of carriers of infection [66], the determination of the phylogenetic characteristics of individuals of the population [67], determination of patterns of infection spread [68], etc.

Dimension reduction. This is the reduction of a larger number of features to a smaller one for the convenience of their further use. In epidemiological diagnostics, this is an extremely urgent task, since the data collected by institutions and government centers does not depend on their importance for modeling. Therefore, dimensionality reduction methods help to discard unnecessary data on morbidity [69], reduce computational complexity [70], and identify informative signs [71] and factors influencing the epidemic process [72].

Identification of anomalies. The anomaly detection task is designed to detect abnormal deviations from normal cases. The task is akin to classification, but it has a significant difference: anomalies are a rare phenomenon, so there are either very few samples on which a model can be taught, or there are none at all. Therefore, other methods are used for this. In the study of epidemic processes, such methods are used to process morbidity data in real-time [73], monitor trends in the flow of morbidity data [74], and identify epidemic outbreaks [75].

Forecasting. The forecasting problem is most common in the analysis of epidemic processes. Forecasts are calculated taking into account the social dynamics of the processes [76], the nature of the outbreak [77], geographic features [78], trends in epidemic processes in the early stages of the outbreak development [79], the impact on the population [80], data from social networks (Twitter [81], Facebook [82], etc.), queries from search services [83], data from mobile operators [84], and many other factors.

The main disadvantage of machine learning methods in the study of epidemic processes is the interpretation of the results. It is usually impossible to identify factors influencing the dynamics of morbidity and conduct experiments on the effectiveness of preventive measures.

6. Further development of epidemic processes simulation

To study epidemic processes and assess the influence of factors and the effectiveness of various measures, it is advisable to use agent-based simulation. In this approach, objects of the population, that is, people, act as agents. Each agent is characterized by many states and characteristics. The transition between states occurs through events, which can be interaction with other agents, with the external environment, etc. The interaction between agents and changes in their states affect the overall system, so the introduction of changes into the model and its research is much easier than using other approaches.

The disadvantage of the agent-based approach to modeling epidemic processes is the low accuracy of the model. Therefore, a promising area is the combination of agent-based models and machine learning [85].

CONCLUSIONS

The analysis of models and methods for studying epidemic processes carried out in the article showed that different modeling approaches are used for various tasks. At the same time, the greatest number of shortcomings has the classical deterministic compartment models. The greatest accuracy is shown by machine learning methods, but they do not allow conducting experimental studies with epidemic processes to identify factors influencing the epidemic process. Therefore, the most effective is the combined use of an agent-based approach to simulating epidemic processes with machine learning methods.

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Consent for publication

All authors give their consent to publication.

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References

1. Brauer, F., & Castillo-Chavez, C. (2012). Mathematical Models in Population Biology and Epidemiology. In: *Texts in Applied Mathematics*, Vol. 40. New-York: Springer-Verlag. 508 p.
2. Galvani, A. P., & May R. M. (2005). Epidemiology: dimensions of superspreading. *Nature, 438*(7066), 293–295.
3. Chumachenko, D. I., & Chumachenko, T. O. (2020). Mathematical models and methods of forecasting epidemic processes: a monograph. Kharkiv: Planeta-Print LLC. 180 p. doi: 10.25313/978-617-7751-88-4.
4. Kermack, W., & McKendrick, A. (1991). Contributions to the mathematical theory of epidemics – I. *Bulletin of Mathematical Biology, 53*, 33–55. doi: 10.1007/BF02464423.
5. Kermack, W., & McKendrick, A. (1991). Contributions to the mathematical theory of epidemics – II. The problem of endemicity. *Bulletin of Mathematical Biology, 53,* 57–87. doi: 10.1007/BF02464424.
6. Kermack, W., & McKendrick, A. (1991). Contributions to the mathematical theory of epidemics – III. Further studies of the problem of endemicity. *Bulletin of Mathematical Biology, 53,* 89–118. doi: 10.1007/BF02464425.
7. Ross, R. (1929). On some peculiar pigmented cells found in two mosquitoes fed on Malarial blood. *BMJ, 2,* 1986–1788.
8. Baroyan, O. V., & Rvachev L. A. (1977). Mathematics and Epidemiology. M.: «Znaniye» ["Knowledge"]. 64 p.
9. Baroyan, O. V., & Rvachev L. A. (1967). Deterministic models of epidemics for a territory with a transport network. *Cybernetics, 3,* 55–61. doi: 10.1007/BF01120008.
10. Tolles, J., & Luong, T. (2020). Modeling Epidemics with Compartmental Models. *Journal of American Medical Association, 323*(24), 2515–2516. doi: 10.1001/jama.2020.8420.
11. Trawicki, M. B. (2017). Deterministic SEIRS epidemic model for modeling vital dynamics, vaccinations, and temporary immunity. *Mathematics, 5*(7), 1–19. doi: 10.3390/math5010007.
12. Dashtbali, M., & Mirzaie, M. (2021). A compartmental model that predicts the effect of social distancing and vaccination on controlling COVID-19. *Scientific Reports.* 11. 8191. doi: 10.1038/s41598-021-86873-0.
13. Wang, T., Wu, Y., Yiu-Nam Lau, J., Yu, Y., Liu, L., Li, J., … & Jiang B. (2020). A four-compartment model for the COVID-19 infection – implications on infection kinetics, control measures, and lockdown exit strategies. *Precision Clinical Medicine, 3*(2), 104–112. doi: 10.1093/pcmedi/pbaa018.
14. Ghostine, R. Gharamti, M., Hassrouny, S., & Hoteit, I. (2021). An extended SEIR model with vaccination for forecasting the COVID-19 pandemic in Saudi Arabia using an ensemble Kalman filter. *Mathematics, 9,* 636. doi: 10.3390/math9060636.
15. Miller, J. C., Slim, A. C., & Volz, E. M. (2012). Edge-based compartmental modelling for infectious disease spread. *Journal of Royal Society Interface*, 9, 890–906. doi: 10.1098/rsif.2011.0403.

16. Gounane, S., Barkouch, Y., Atlas, A., Bendahmane, M., Karami, F., & Meskine, D. (2021). An adaptive social distancing SIR model for COVID-19 disease spreading and forecasting. *Epidemiologic Methods, 10*(S1), 20200044. doi: 10.1515/em-2020-0044.

17. Romezani, S. B. Rahimi, S., Amirlatifi, A., Hudnall, M., Pete, J., Parrish, A., … & Qian X. (2021). Empowering compartmental modeling with mobility and Shelter-in-Place analysis. *Frontiers in Future Transportation, 2,* 646751. doi: 10.3389/ffutr.2021.646751.

18. Trebeit, S., Brunner, H., & Ehrhardt, M. (2019). Compartment models for vaccine effectiveness and non-specific effects for Tuberculosis. *Mathematical Biosciences and Engineering, 16*(6). 7250–7298. doi: 10.3934/mbe.2019364.

19. Avey, C., Bossert, W., Clark, A., Ellison, G., & Ellison, A. F. (2020). An Economists's guide to epidemiology models of infectious disease. *The Journal of Economic Perspectives, 34*(4), 79–104.

20. Mohammadi, A., Chumachenko, T., Makhota, L., & Chumachenko, D. (2021). Compartment model of COVID-19 epidemic process in Ukraine. *CEUR Workshop Proceedings, 2824*, 100–109.

21. Mohammadi, A., Meniailov, I., Bazilevych, K., Yakovlev, S., & Chumachenko, D. (2021). Comparative study of linear regression and SIR models of COVID-19 propagation in Ukraine before vaccination. *Radioelectronic and Computer Systems, 99*(3), 5–18. doi: 10.32620/reks.2021.3.01.

22. Roberts, M., Andreasen, V., Lloyd, A., & Pellis, L. (2015). Nine challenges for deterministic epidemic models. *Epidemics, 10,* 49-53. doi: 10.1016/j.epidem.2014.09.006.

23. Roosa, K., & Chowell, G. (2019). Assessing parameter identifiability in compartmental dynamic models using a computational approach: application to infectious disease transmission models. *Theoretical Biology and Medical Modelling, 16*, 1. doi: 10.1186/s12976-018-0097-6.

24. Deng, Q. (2020). Dynamics and development of the COVID-19 epidemic in the United States: a compartmental model enhanced with deep learning techniques. *Journal of Medical Internet Research, 22*(8), e21173. doi: 10.2196/21173.

25. Chumachenko, D. I., & Chumachenko, T. O. (2021). Simulation modeling of epidemic processes: applied aspects: monograph. Kharkiv: Planet Print LLC.

26. Irhaif, N. H., Kareem, Z. I., Kareem Abdul, A. D., & Al-joboori, S. M. (2021). Using the moving average and exponentially weighted moving average with COVID-19. *Periodicals of Engineering and Natural Sciences, 9*(3), 625–631. doi: 10.21533/pen.v9i3.2206.g907.

27. Lynch, C. J., Gore, R. (2021). Application of one-, three-, and seven-day forecasts during early onset on the COVID-19 epidemic dataset using moving average, autoregressive, autoregressive moving average, autoregressive integrated moving average, and naïve forecasting methods. *Data in Brief, 35,* 106759. doi: 10.1016/j.dib.2021.106759.

28. Khan, F., Ali, S., Saeed, A., Kumar, R., & Khan, A. W. (2021). Forecasting daily new infections, deaths and recovery cases due to COVID-19 in Pakistan by using Bayesian Dynamic Linear Models. *PLoS One, 16*(6), e0253367. doi: 10.1371/journal.pone.0253367.

29. Chu, J. (2021). A statistical analysis of the novel coronavirus (COVID-19) in Italy and Spain. *PLoS One, 16*(3), e0249037. doi: 10.1371/journal.pone.0249037.

30. He, Y., Wang, X., He, H., Zhai, J., Wang, B. (2020). Moving average based index for judging the peak of the COVID-19 epidemic. *International Journal of Environmental Research and Public Health, 17*(15), 5288. doi: 10.3390/ijerph17155288.

31. Syaharuddin, Negara H. R. P., Ibrahim, M., Ahmad, Zulfikiri M., Primajati G., … & Septyanun, N. (2021). Modify alpha value of EMA method and brown method: a data forecasting comparison of COVID-19 *AIP Conference Proceedings, 2329*(1), 060016. doi: 10.1063/5.0042120.

32. Buckingham-Jeffery, E., Morbey, R., House, T., Elliot, A. J., Harcourt, S., Smith, G. E. (2017). Correcting for day of the week and public holiday effects: improving a national daily syndromic surveillance service for detecting public health threats. *BMC Public Health*. 17. 477. doi: 10.1186/s12889-017-4372-y.

33. Steiner S.H., Grant K., Coory M., Kelly H.A. Detecting the start of an influenza outbreak using exponentially weighted moving average charts. (2010). *BMC Medical Informatics and Decision Making.* 10. 37. doi: 10.1186/1472-6947-10-37.

34. Dansana D., Kumar R., Adhikari J.D., Mohapatra M., Sharma R., Priyadarshini I., Le D.N. (2020). Global forecasting confirmed and fatal cases of COVID-19 outbreak using autoregressive integrated moving average model. *Frontiers in Public Health.* 8. 580327. doi: 10.3389/fpubh.2020.580327.

35. He Z., Tao H. (2018). Epidemiology and ARIMA model of positive-rate of influenza viruses among children in Wuhan, China: A nine-year retrospective study. *International Journal of Infectious Diseases*. 74. 61-70. doi: 10.1016/j.ijid.2018.07.003.

36. Jerónimo-Martínez L.E. Menéndez-Mora R.E., Bolívar H. (2017). Forecasting acute respiratory infection cases in Southern Bogota: EARS vs. ARIMA and SARIMA. *Congreso Internacional de Innovacion y Tendencias en Ingenieria (CONIITI).* 1-6. doi: 10.1109/CONIITI.2017.8273326.

37. Martinez E.Z., Silva E.A. (2011). Predicting the number of cases of dengue infection in Ribeirão Preto, São Paulo State, Brazil, using a SARIMA model. *Cadernos de Saude Publica.* 27 (9). 1809-18. doi: 10.1590/s0102-311x2011000900014.

38. Lau K., Dorigatti I., Miraldo M., Hauck K. (2021). SARIMA-modelled greater severity and mortality during the 2010/11 post-pandemic influenza season compared to the 2009 H1N1 pandemic in English hospitals. *International Journal of Infectious Diseases.* 105. 161-171. doi: 10.1016/j.ijid.2021.01.070

39. Gao J., Li J., Wang M. (2020). Time series analysis of cumulative incidences of typhoid and paratyphoid fevers in China using both Grey and SARIMA models. *PLoS One.* 15 (10). e0241217. doi: 10.1371/journal.pone.0241217

40. Britton T., Giardina F. (2016). Introduction to statistical inference for infectious diseases. *Journal de la Societe Francaise de Statistique, 157*(1), 53-70.

41. Riley, S., Fraser, C., Donnelly, C. A., Ghani, A. C., Abu-Raddad, L. J., Hedley, A. J., … & Anderson, R. M. (2003). Transmission dynamics if the etiological agent of SARS in Hong Kong: impact of public health interventions. *Science, 300*(5627), 1961–1966. doi: 10.1126/science.1086478.

42. Yu, P. L. H., Chan, J. S. K., & Fung, W. K. (2006). Statistical exploration from SARS. *The American Statistician, 60*(1), 81–91. doi: 10.1198/000313006X91421.

43. Goldstein, E., Cobey, S., Takahashi, S., Miller, J. C., & Lipsitch, M. (2011). Predicting the Epidemic Sizes of Influenza A/H1N1, A/H3N2, and B: A Statistical Method. *PLoS Medicine*, 8(7), e1001051. doi: 10.1371/journal.pmed.1001051.

44. Dawood, F. S., Iuliano, A. D., Reed, C., Meltzer, M. I., Shay, D. K., Cheng, P.-Y., … & Widdowson M.-A. (2012). Estimated global mortality associated with the first 12 months of 2009 pandemic influenza A H1N1 virus circulation: a modelling study. *The Lancet. Infectious Diseases, 12*(9), 687–695. doi: 10.1016/S1473-3099(12)70121-4.

45. Khaleque, A., Sen, P. (2017). An empirical analysis of the Ebola outbreak in West Africa. *Scientific Reports, 7,* 42594. doi: 10.1038/srep42594.

46. Ferguson, N. M., Donnelly, C. A., & Anderson, R. M. (2001). The foot-and-mouth epidemic in Great Britain: pattern of spread and impact of interventions. *Science, 292*(5519), 1155–1160. doi: 10.1126/science.1061020.

47. Boschi, T., Lorio, J. Di., Testa, L., Cremona, M.A., & Chiaromonte, F. (2021). Functional data analysis characterizes the shapes of the first COVID-19 epidemic wave in Italy. *Scientific Reports, 11,* 17054. doi: 10.1038/s41598-021-95866-y.

48. Salg, G. A., Ganten, M. K., Bucher, A. M., Kenngott H. G., Fink M. A., Seibold, C., … & Kleesiek, J. (2021). A reporting and analysis framework for structured evaluation of COVID-19 clinical and imaging data. *npj Digital Medicine, 4,* 69. doi: 10.1038/s41746-021-00439-y.

49. Imai, C., Armstrong, B., Chalabi, Z., Mangtani, P., & Hasizume, M. Time series regression model for infectious disease and weather. (2015). *Environmental Research, 142*, 319–327. doi: 10.1016/j.envres.2015.06.040.

50. Bakuli, A., Klawonn, F., Karch, A., & Mikolajczyk, R. (2017). Effects of pathogen dependency in a multi-pathogen infectious disease system including population level heterogeneity – a simulation study. *Theoretical Biology and Medical Modelling, 14*(26), 1–17 p. doi: 10.1186/s12976-017-0072-7.

51. Daniyal, M., Ogundokun, R. O., Abid, K., Khan, M. D., & Ogundokun, O. E. (2020). Predictive modeling of COVID-19 death cases in Pakistan. *Infectious Disease Modelling, 5,* 897–904. doi: 10.1016/j.idm.2020.10.011.

52. Mokhort, H. (2020). Multiple linear regression model of Meningococcal disease in Ukraine: 1992–2015. *Computational and Mathematical Methods in Medicine*, ID 5105120. doi: 10.1155/2020/5105120.

53. Mohammadi, A., Chumachenko, D., & Chumachenko, T. (2021). Machine Learning Model of COVID-19 Forecasting in Ukraine Based on the Linear Regression. *IEEE 12th International Conference on Electronics and Information Technologies (ELIT),* 149-153. doi: 10.1109/ELIT53502.2021.9501122.

54. Hong, Z. (2020). Prediction of 2019-nCoV epidemic by linear regression. *ISAIMS 2020: Proceedings of the 2020 International Symposium on Artificial Intelligence in Medical Sciences*, 1–5. doi: 10.1145/3429889.3429890.

55. Kartono, A., Wahyudi, S. T., Setiawan, A. A., & Sofian, I. (2021). Predicting of the Coronavirus Disease 2019 (COVID-19) Epidemic Using Estimation of Parameters in the Logistic Growth Model. *Infectious Disease Reports, 13,* 465–485. doi: 10.3390/idr13020046.

56. Kapusta, D., Mohammadi, A., & Chumachenko, D. (2021). Machine learning approach to COVID-19 epidemic process simulation using polynomial regression model. *CEUR Workshop Proceedings, 3003,* 83–91.

57. Saqib, M. (2021). Forecasting COVID-19 outbreak progression using hybrid polynomial-Bayesian ridge regression model. *Applied Intelligence, 51,* 2703–2713. doi: 10.1007/s10489-020-01942-7.

58. Chen, Y., Chu, C. W., Chen, M. I. C., & Cook, A. R. (2018). The utility of LASSO-based models for real time forecasts of endemic infectious diseases: A cross country comparison. *Journal of Biomedical Informatics, 81,* 16–30. doi: 10.1016/j.jbi.2018.02.014

59. Jin, M., Lin, Y. (2021). Classification of asymptotic behavior in a stochastic SEIR epidemic model. *Applied Mathematics Letters, 118,* 107184. doi: 10.1016/j.aml.2021.107184.

60. Polyakov, P., Souty, C., Böelle, P. Y., & Breban, R. (2019). Classification of Spatiotemporal Data for Epidemic Alert Systems: Monitoring Influenza-Like Illness in France. *American Journal of Epidemiology, 188*(4), 724–733. doi: 10.1093/aje/kwy254.

61. Alessa, A., & Faezipour, M. (2019). Preliminary flu outbreak prediction using Twitter posts classification and linear regression with historical Centers for Disease Control and Prevention Reports: prediction framework study *JMIR Public Health and Surveillance.* 5 (2). e12383. doi: 10.2196/12383.

62. Yang, X., Liu, D., He, J., Gou, F., Liu, H., Zheng, Y., … & Liu, X. (2019). Classification and regression tree model study on correlation between influenza epidemic and meteorological factors in different areas of Gansu, 2010 to 2016. *Disease Surveillance*, *34*(5), 440–445. doi: 10.3784/j.issn.1003-9961.2019.05.015.

63. Li, F., Shen, Y., Lv, D., Lin, J., Liu, B., He, F., & Wang, Z. (2020). A Bayesian classification model for discriminating common infectious diseases in Zhejiang province, China. *Medicine*, *99*(8), e19218. doi: 10.1097/MD.0000000000019218.

64. Bazilevych, K. O., Menyaylov, Ye. S., & Chumachenko, D. I. (2021). Isolation of areas of COVID-19 coronavirus prevalence based on cluster analysis methods. *The current state of research and technology in industry*, *1*(15), 5–13. doi: 10.30837/ITSSI.2021.15.005.

65. Jung, S., Moon, J., & Hwang, E. (2020). Cluster-based analysis of infectious disease occurrences using tensor decomposition: a case study of South Korea. *International Journal of Environmental Research and Public Health*, *17*, 4872. doi: 10.3390/ijerph17134872.

66. Hamid, J. S., Meaney, C., Crowcroft, N. S., Granerod, J., & Beyene, J. (2010). Cluster analysis for identifying sub-groups and selecting potential discriminatory variables in human encephalitis. *BMC Infectious Diseases*, *10*, 364. doi: 10.1186/1471-2334-10-364.

67. Mehta, S. R., Little, S. J. (2021). Phylogenetic cluster analysis: persons with undiagnosed infection drive Human Immunodeficiency Virus transmission in a population with high levels of virologic suppression. *Clinical Infectious Diseases*, *72*(12), 2184–2186. doi: 10.1093/cid/ciaa401.

68. Ismayilova, R., Nasirova, E., Hanou, C., Rivard, R. G., & Bautista, C. T. (2014). Patterns of Brucellosis infection symptoms in Azerbaijan: a latent class cluster analysis. *Journal of Tropical Medicine*, 2014, ID 593873. doi: 10.1155/2014/593873.

69. Frasca, M., Rizzo, A., Gallo, L., Fortuna, L., & Porfiri, M. (2015). Dimensionality reduction in epidemic spreading models. *EPL Europhysics Letters*, *111*(6), 68006. doi: 10.1209/0295-5075/111/68006

70. Tu, C., D’Odorico, P., & Suweis, S. (2021). Dimensionality reduction of complex dynamical systems. *iScience*, *24*(1), 101912. doi: 10.1016/j.isci.2020.101912.

71. Abellana, D. P. (2021). Modelling the interdependent relationships among epidemic antecedents using fuzzy multiple attribute decision making approaches. *Open Computer Science*, *11*(1), 305-329. doi: 10.1515/comp-2020-0213.

72. Yao, Z., Peng, Y., Bi, J., Xie, C., Chen, X., Ki, Y., … & Zhou J. (2015). Application of the multifactor dimensionality reduction method in evaluation of the roles of multiple genes/enzymes in multidrug-resistant acquisition in Pseudomonas aeruginosa strains. *Epidemiology and Infection*, *144*(4), 856–863. doi: 10.1017/S0950268815001788.

73. Chumachenko, D., Chumachenko, T., Meniailov, I., Pyrohov, P., Kuzin, I., & Rodyna, R. (2020). On-Line Data Processing, Simulation and Forecasting of the Coronavirus Disease (COVID-19) Propagation in Ukraine Based on Machine Learning Approach. *Communications in Computer and Information Sciences*, *1158*, 372–382. doi: 10.1007/978-3-030-61656-4_25.

74. Jombart, T. (2021). Real-time monitoring of COVID-19 dynamics using automated trend fitting and anomaly detection. *Philosophical Transactions of the Royal Society B*, *376*(1829). 20200266. doi: 10.1098/rstb.2020.0266.

75. Homayouni, H., Ray, I., Ghosh, S., Gondalia, S., & Kahn, M. G. (2021). Anomaly Detection in COVID-19 Time-Series Data. *SN Computer Science*, *2*, 279. doi: 10.1007/s42979-021-00658-w.

76. Chowell, G., Luo, R., Sun, K., Roosa, K., Tariq, A., & Viboud, C. (2020). Real-time forecasting of epidemic trajectories using computational dynamic ensembles. *Epidemics*, *30*, 100379. doi: 10.1016/j.epidem.2019.100379.

77. Marzouk, M., Elshaboury, N., Abdel-Latif, A., & Azab, S. (2021). Deep learning model for forecasting COVID-19 outbreak in Egypt. *Process Safety and Environmental Protection*, *153*, 363–375. doi: 10.1016/j.psep.2021.07.034.

78. Nikparvar, B., Rahman, M. M., Hatami, F., & Thill, J. C. (2021). Spatio-temporal prediction of the COVID-19 pandemic in US counties: modeling with a deep LSTM neural network. *Scientific Reports*, *11*, 21715. doi: 10.1038/s41598-021-01119-3.

79. Alessa, A., & Faezipour, M. (2018). A review of influenza detection and prediction through social networking sites. *Theoretical Biology and Medical Modeling*, *15*, 2. doi: 10.1186/s12976-017-0074-5

80. Wong, A., Cao, J., Lyons, P. G., Dutta, S., Major, V. J., Otles, & E., Singh, K. (2021). Quantification of Sepsis model alerts in 24 US hospitals before and during the COVID-19 pandemic. *JAMA Network Open*, *4*(11), e2135296. doi: 10.1001/jamanetworkopen.2021.35286.

81. Rustam, F., Khalid, M., Aslam, W., Rupapara, V., Mehmood, A., & Choi, G.S. (2021). A performance comparison of supervised machine learning models for Covid-19 tweets sentiment analysis. *PLoS ONE*, *16*(2), e0245909. doi: 10.1371/journal.pone.0245909.

82. Amara, A., Taieb, M. A. H., & Aouicha, M. B. (2021). Multilingual topic modeling for tracking COVID-19 trends based on Facebook data analysis. *Applied Intelligence*, *51*, 3052–3073. doi: 10.1007/s10489-020-02033-3.

83. Prasanth, S., Singh, U., Kumar, A., Tikkiwal, V. A., & Chong, P. H. J. (2021). Forecasting spread of COVID-19 using Google Trends: a hybrid GWO-deep learning approach. *Chaos Solutions Fractals*, *142*, 110336. doi: 10.1016/j.chaos.2020.110336.

84. Bengtsson, L., Gaudart, J., Lu, X., Moore, S., Wetter, E., Sallah, K., … Piarroux, R. (2015). Using Mobile Phone Data to Predict the Spatial Spread of Cholera. *Scientific Reports*, 5, 8923. doi: 10.1038/srep08923

85. Yakovlev, S. (2020). The concept of developing a decision support system for the epidemic morbidity control. *CEUR Workshop Proceedings*, *2753*, 265–274.

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