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Article

Deciphering the complexity of COVID-19 transmission: Unveiling precision through robust vaccination policies and advanced predictive modeling with random forest regression

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Abstract: In the realm of COVID-19 transmission data, scientists are scrutinizing policies to identify the ideal vaccination rate for halting the virus. This study aimed to pinpoint the minimal vaccinated percentage needed to break the virus cycle within communities. The underlying motivation stems from the urgent need to contain COVID-19's spread and reduce the strain on healthcare systems worldwide. With fluctuating infection rates and the emergence of new variants, understanding the optimal vaccination rate has become a cornerstone in public health planning and pandemic response. Using diverse machine learning methods, this study analyzed infection peaks and hospitalization rates during vaccination campaigns across countries. The goal was to find the vaccination threshold necessary to prevent virus resurgence, even with new variants. This critical milestone is crucial for health systems to combat the pandemic effectively. The study's analysis revealed the correlation between vaccination rates and hospitalizations, highlighting immunization's pivotal role. Employing Random Forest regression, the study successfully predicted new cases and hospitalization rates, offering valuable insights into pandemic management strategies. For future research, we recommend exploring the impact of vaccination on the evolution of virus variants and the potential influence of socio-economic factors on vaccination uptake. Moreover, a broader analysis across different geographical regions can further validate the study's findings and enhance global pandemic preparedness.

Keywords: COVID-19; vaccine; random forest regression; chain of infection; public health policies

1. Introduction

The novel coronavirus, COVID-19, first identified in December 2019, is attributed to the SARS-CoV-2 virus (Hu et al., 2021; Krammer, 2020; Ludwig and Zarbock, 2020). Its rapid global dissemination led to a pandemic, with over 777 million reported cases and 6.9 million deaths worldwide (WHO Coronavirus (COVID-19) https://data.who.int/dashboards/covid19/cases). Throughout the COVID-19 pandemic, numerous governments endeavored to curb virus transmission through non-pharmaceutical interventions (Liu et al., 2021). These encompassed measures such as social distancing, contact tracing, closure of public gathering spaces like schools and restaurants, and the implementation of societal measures such as home quarantine, isolation, lockdowns, and border closures (Kasting et al., 2020; Putra and Drajati, 2023).

These non-pharmaceutical policies were designed to interrupt the chain of virus transmission, affording scientists the time needed to develop vaccines (Cevik et al., 2020). However, their impact on reducing hospitalization and mortality rates was comparatively modest when contrasted with the efficacy of vaccination (Bian et al., 2021). Notably, certain non-pharmaceutical interventions proved successful in reducing hospitalization and death rates in specific countries (e.g., Korea, Taiwan, Japan, China, New Zealand, and the Czech Republic) (Kandikattu et al., 2021). Yet, with the emergence of new virus variants, subsequent peaks in hospitalization and death rates were observed (Arvind et al., 2023).

Vaccination emerges as a pivotal strategy in mitigating the hospitalization rate and facilitating a gradual reopening of society (Malik et al., 2022). The primary challenge associated with the implementation of non-pharmaceutical rules and regulations was the societal discomfort stemming from the closure of various facets of public life (Ryan, 2023; Ryan and Nanda, 2023).

Amidst the vast pool of information on COVID-19 transmission, government policies, vaccinations, and the proliferation of various virus variants, contemporary scientists possess the capability to meticulously analyze data for enhanced policy formulation (Campos et al., 2020; Cevik et al., 2021). Today, armed with abundant data, scientists can assess the effectiveness of specific rules and policies enacted by diverse governing bodies in distinct areas and populations.

A central question arises: What is the optimal vaccination rate required to swiftly interrupt the cycle and chain of transmission within society and the broader population? Thus, the focal point of this research paper is to identify the most effective vaccination rate capable of not only mitigating but also controlling virus transmission, ultimately breaking the chain of infection.

This study delves into unraveling the intricate relationships between the number of vaccinated individuals, including those fully vaccinated, and the occurrence of new cases, encompassing new deaths, in Southeast Asian countries. The investigation sought to determine the minimum threshold of vaccinated and fully vaccinated individuals necessary to halt the rise in new cases and new deaths within each country. Importantly, the identified rates varied among Southeast Asian countries due to disparities in immunity, ethnicity, and races. The rest of the research paper is organized into the following sections: Data Collection and Methodology, including Data Sources; Results and Discussion, with separate subsections for each; and finally, the Conclusion, which addresses Limitations and offers Recommendations for future work.

2. Data collection and methods

2.1. Methodology

Forest regression, epitomized by the Random Forest algorithm, offers several distinctive advantages in the realm of machine learning. Chief among these is its remarkable resilience against overfitting. By harnessing the power of ensemble learning, Random Forest combines multiple decision trees, each constructed from a random subset of both data points and features. This technique inherently injects diversity into the model, thereby reducing the risk of overfitting while promoting greater generalization across unseen data. Furthermore, this approach is well-suited to capturing complex, nonlinear relationships without the need for extensive feature engineering, a common hurdle for traditional linear models. The ability to seamlessly adapt to intricate patterns in the data is a testament to the robustness of forest-based methods (Fawagreh et al., 2014).

Additionally, the Random Forest algorithm provides invaluable insights into the relative importance of different features within a dataset. This built-in feature importance metric not only aids in refining the model by focusing on the most impactful variables but also contributes to greater model transparency and interpretability. The flexibility of forest regression extends to its ability to handle missing data with minimal impact on performance, while also accommodating high-dimensional datasets with aplomb. This scalability, coupled with the capacity for parallelization, ensures that Random Forest can manage large datasets efficiently. Ultimately, its resilience to noisy data and the reduced need for intensive parameter tuning make forest regression a compelling choice for our research compare to a wide array of machine learning applications.

In our research, Random Forest for regression is an ensemble learning technique often used to predict continuous outcomes, such as the rate of vaccination based on changes in the rate of hospitalizations. The process starts with data collection, focusing on gathering historical data that links hospitalizations with vaccination rates. Preprocessing is crucial to ensure the data is clean, consistent, and ready for modeling. In the Random Forest regression, the algorithm creates multiple decision trees, each trained on a random subset of the training data, both in terms of samples and features. This method introduces a high level of diversity, which reduces the risk of overfitting and improves model reliability. During the prediction stage, the ensemble of trees generates individual predictions, which are then aggregated, typically by taking the average. This approach enables the model to account for variations in the data and produce robust predictions, allowing researchers to estimate how changes in hospitalization rates might correspond to vaccination rates, providing valuable insights for public health planning and policy decisions.

2.2. Data sources

Data acquisition and computational processes were conducted utilizing information extracted from https://coronavirus.jhu.edu/data/variant-data. The countries within South East Asia, namely Brunei, Singapore, Indonesia, Myanmar, Cambodia, Malaysia, Thailand, Philippines, Vietnam, Laos, and Timor, were specifically targeted for data collection. The pertinent attributes under consideration encompassed new cases per million, new deaths per million, people vaccinated per hundred, and people fully vaccinated per hundred, spanning from January 2020 to December 2021.

The primary objective of this data collection initiative was to discern the intricate relationships between vaccination metrics and the occurrence of new cases. Leveraging machine learning methodologies and the Python programming language, a comprehensive analysis of the collected data was undertaken. The utilization of these advanced analytical tools aimed to unravel patterns and correlations within the dataset, shedding light on the dynamic interplay between vaccination efforts and the incidence of new cases across the specified time frame and geographic region.

3. Results and discussion

3.1. Results

Examination of the data gleaned from eleven Southeast Asian countries has unveiled a consistent pattern amid the COVID-19 pandemic. The presentation of three distinct zones is predicated on crucial attributes, namely new cases and the metrics related to vaccination and full vaccination. These zones can be delineated based on various variants of the COVID virus, with significant attention given to widely spreading variants such as alpha, beta, delta, and gamma, initially identified in the UK, South Africa, India, and Brazil. It is noteworthy that the graph also facilitates the tracking of other virus variants, contributing to a comprehensive understanding of the dynamic landscape of COVID-19 across the region.

The data depicted in **Figure 1** pertains specifically to Brunei, serving as a focal point for analysis. The graph's initiation aligns with the onset of the vaccination reporting period. Preceding this phase, governmental policies demonstrated efficacy in controlling transmission rates; however, they fell short in curtailing or halting infections. The commencement of vaccination coincided with the circulation of different virus variants, specifically alpha and beta.

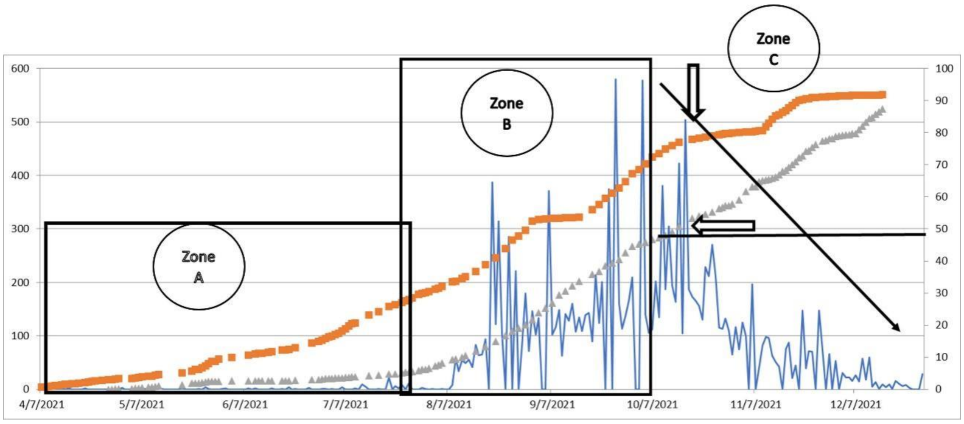

Figure 1. The graph presented Brunei data of covid-19 the new cases in blue, fully vaccinated in gray and vaccinated in orange. The highest peak indicated with an arrow.

Zone A of the graph illustrates a notable correlation: An increase in vaccination rates successfully correlated with the control of transmission for these pivotal virus variants. Remarkably, even with less than 10 percent of Brunei's total population vaccinated, the region achieved zero new cases on many days. However, this positive trend encountered a setback with the emergence of the delta variant, which exhibited a significantly faster transmission rate, abruptly impacting the growth of new cases.

Zone B represents the onset of a new cases outbreak, necessitating a strategic response involving an escalation in the number of vaccinated individuals. To effectively mitigate the escalating new cases rate and exert control over the gamma variant of the virus, a critical juncture was identified. This juncture entailed reaching a specific threshold, notably 80 percent of the population vaccinated and 49 percent fully vaccinated—where "fully vaccinated" denotes having received three doses of the vaccine. Notably, at this stage in Brunei, approximately 49 percent of the population had achieved full vaccination status, translating to one person out of every two.

It is crucial to highlight that the observed trend, as described, manifested across all eleven scrutinized countries, albeit with distinct points and dates of significance. Notably, the attainment of the identified point varied among these nations; for instance, Brunei achieved this milestone at 49 percent full vaccination, while Indonesia reached it at 39 percent, and Singapore at 80 percent full vaccination (**Figure 2**). The disparities in these critical thresholds can be attributed to a range of factors including population density, vaccine type, cultural nuances, ethnicity, and diverse governmental policies such as isolation measures, lockdowns, and border closures. Additionally, the efficiency of the healthcare system played a significant role in shaping these outcomes (Araújo et al., 2020).

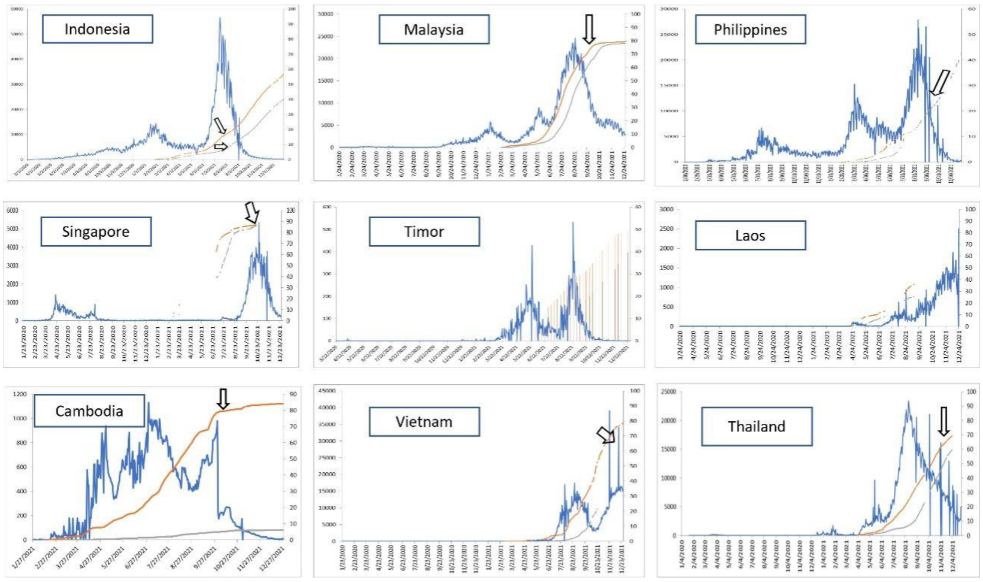

Figure 2. The graph presented data of COVID-19 in different southeast Asian countries, the new cases in blue, fully vaccinated in gray and vaccinated in orange.

It is pertinent to note that, based on the insights derived from the presented data, we posit the concept of "population immunity" against not only the coronavirus but also other pathogens. This term denotes a specific threshold within the population, unique to each country and even distinct local communities, wherein rapid vaccination becomes imperative to impede the transmission and proliferation of new pathogens, particularly viruses. Recognizing and understanding this population-specific immunity point is crucial for devising targeted and effective public health strategies tailored to the distinctive characteristics of each region.

Table 1 provides a comprehensive overview of the correlation between new cases and the metrics of total vaccination and full vaccination. The data reveals a robust negative correlation between the incidence of new cases and the specified vaccination attributes. In delving deeper into this aspect of the analysis, establishing a regression model between these attributes proves instrumental. Such regression analysis serves as a valuable tool for authorities, offering a precise quantification of the specific relationship between new cases and vaccination metrics. By uncovering the nuances of this relationship, policymakers can make informed decisions and implement targeted strategies to effectively manage and mitigate the impact of the ongoing public health challenges.

Table 1. Correlation between the attributes: new cases vs total vaccination (%) and new cases and fully vaccinated (%).

Correlation	New cases vs total vaccinated	New cases vs fully vaccinated
Brunei	−0.71443	−0.7132
Cambodia	−0.93485	−0.86682
Indonesia	−0.71162	−0.64712
Malaysia	−0.97736	−0.97556
Philippines	−0.95899	−0.79605
Singapore	−0.86115	−0.79371
Thailand	−0.57629	−0.5849
Timor	−0.68985	−0.68865

The outcomes indicate the absence of a linear relationship between vaccination metrics, encompassing both the percentage of vaccinated people and fully vaccinated individuals per hundred, and the occurrence of new cases. Consequently, to discern more nuanced patterns and unveil predictive insights, advanced machine learning approaches were employed. These methodologies aim to forecast new cases based on the intricate interplay of vaccination attributes, offering a more sophisticated understanding of the relationship between these variables. By leveraging machine learning, we strive to uncover non-linear dependencies and capture the complexities inherent in the dynamics of new cases and vaccination metrics, ultimately enhancing our ability to anticipate and manage the course of the ongoing public health challenges.

Random forest machine learning:

In this study, the employed machine learning methodology was Random Forest Regression. Initially, we utilized the Random Forest Regression approach, focusing on the percentage of fully vaccinated people per hundred, to predict the incidence of new cases. The outcomes of this analysis are illustrated in **Figure 3A**. The evaluation of the machine learning model's performance, assessed through the mean absolute error (MAE), yielded a value of 27.395, indicating an acceptable level of accuracy in predicting new cases based on the chosen attributes.

In the subsequent phase of the analysis, the machine learning model extended its scope to encompass vaccinated people, as a percentage, rather than solely focusing on fully vaccinated individuals. The predictive outcomes for new cases across all countries are illustrated in **Figure 3B**. The evaluation of this model's performance, expressed through the mean absolute error (MAE), yielded a value of 28.476. Notably, both models generated using the Random Forest method exhibited comparable performance, with MEAs falling within an acceptable range. The consistent pattern discerned from these results underscores a noteworthy trend: An increase in vaccination correlates with a decrease in new cases across the studied countries.

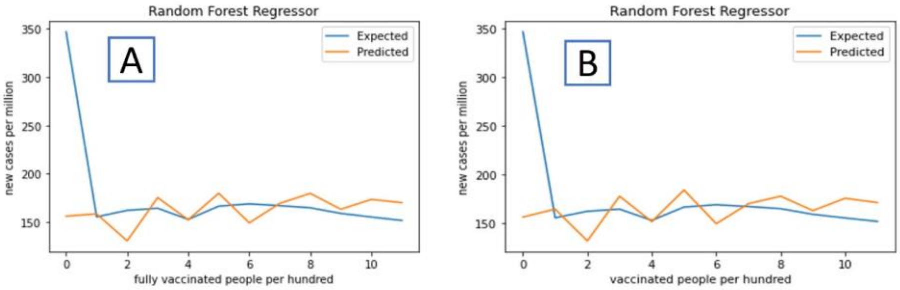

Figure 3. Results from random forest regressor predicted new cases from fully vaccinated people (A) and vaccinated people (B).

In summary, the collective findings from the preceding sections suggest that, on a broad scale, both fully vaccinated and partially vaccinated populations demonstrate an ability to arrest the escalation of new cases. It is crucial to note, however, that the duration for which countries experience a decline in new cases varies significantly. The heterogeneity in the timelines for the reduction of new cases underscores the complex interplay of factors influencing the effectiveness of vaccination strategies across different regions and populations. This nuanced understanding is vital for tailoring public health interventions to the specific dynamics and challenges encountered by each country in their efforts to manage and mitigate the impact of the ongoing health crisis.

3.2. Discussion

The ability to predict the different stages and situation of the infected population have great impact on society (Jones et al., 2021; Wang et al., 2020). This prediction can shape the quality of life and therefore is very important for making decision individually and policy makers and leaders for the society (Ahamad et al., 2020). Infection disease transfection models can help generally to answer the questions which help the society to reduce human suffering (Buitrago-Garcia et al., 2020). The modeling of the infection disease can even provide some idea and prospective of the future impact of the disease and therefore can be useful in society management (Coro, 2020). The models usually should answer the future case counts increase after the specific period of time. Thus, can be very useful on providing the enough healthcare facilities (Jones et al., 2021). Furthermore, they can be useful to estimate the effective reproductive number of the specific pathogen at specific time (Saha et al., 2021). In the case of the COVID-19 with very severe infection the data available can provide the huge impact on prediction of the case count, reproductive number and non-pharmaceutical and vaccination on the pathogen situation.

Stages of infection in the individual from exposure to infection and transmission between individual from timing to magnitude should be investigated in details with huge data available in COVID-19 pandemic. Exposure the individual to the pathogen whether from another person, vector, injection or even respiratory route commonly usual route of infections. Scientific consensus affirms that certain conditions, referred to as the chain of infection, must be fulfilled for the spread of infectious diseases to occur (Purssell and Gould, 2023). The chain of infection is a process comprising six essential segments: organism (in this case, the virus), reservoir (animal bat), mode of escape (infection in the human respiratory tract), mode of transfer (airborne), mode of entry (inhalation in the respiratory tract), and susceptible host (humans) (Haque et al., 2020). This sequence completes a cycle, as illustrated in **Figure 4**, where the virus serves as the agent, and humans are both the susceptible host and the mode of escape, creating a continuous loop. The basic of infection disease transmission models and different models such as mechanistic (Perelson and Ke, 2021; Rian et al., 2021) and statistical (Wang et al., 2020), ensemble (Chasapis et al., 2023; Evensen et al., 2021) and agent-based modeling (Luong et al., 2023) approach including their strength and weakness should be discuss in different paper (Reme et al., 2023; Ruffieux et al., 2023). It is important to note that specific aspects of each section in the chain of infection warrant more detailed investigation. In the context of COVID-19, non-pharmaceutical policies have played a pivotal role in addressing the mode of transfer. These policies effectively work to separate individuals from one another, disrupting the transmission route and mitigating the spread of the virus. The understanding and management of each link in the chain of infection provide valuable insights for developing targeted interventions and public health strategies to control infectious diseases.

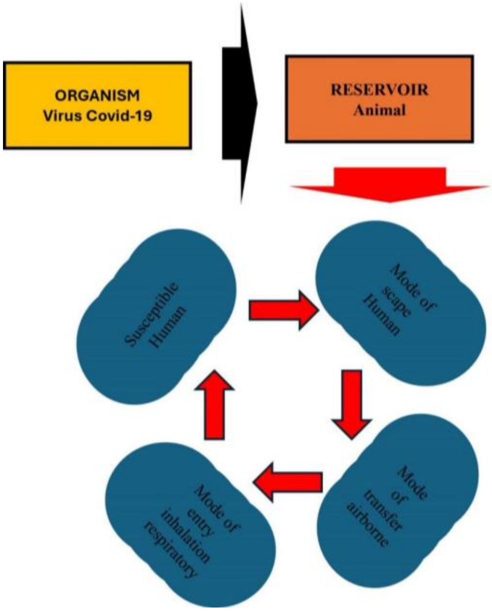

Figure 4. The chain of infection for COVID-19.

Vaccines stand out as one of the most impactful medical interventions, contributing significantly to global health and well-being. Various vaccines have played a crucial role in immunizing populations worldwide, offering protection against a range of diseases (Shulman, 2023). These immunization efforts, integrated into medical and public health administrations across different countries, have notably contributed to the eradication or substantial reduction of infections such as smallpox, polio, measles, and rubella in various regions of the world (Waheed et al., 2023). The widespread implementation of vaccines has led to substantial gains in disease prevention, with estimates suggesting the prevention of over 14 million cases of diseases like hepatitis B and polio in recent years (Argirova and Zlatareva, 2023). Beyond the evident health benefits, vaccines also yield significant economic advantages. Notably, data indicates savings exceeding $9.9 billion through vaccination efforts (Ryan, 2023).

Moreover, the positive impact of vaccines extends to other diseases, including pneumococcal conjugate, rotavirus, and hepatitis A, demonstrating remarkable effectiveness in reducing illness and hospitalization rates (Karadimas, 2023). The cumulative effect of vaccination emerges as a cornerstone in public health, showcasing the substantial strides made in disease prevention and overall healthcare outcomes globally. The effectiveness of COVID-19 vaccination represents a significant triumph in the global battle against a highly transmissible virus, marking the onset of a new era in medicine facilitated by vaccination. The pivotal aspect of mass vaccination lies in its ability to disrupt the chain of infection. In this research, the Random Forest approach was employed to predict new COVID-19 cases in Southeast Asia, revealing a consistent and substantial reduction in new cases through vaccination. Importantly, this reduction varied among countries within the same region.

The COVID-19 pandemic has underscored a complex interplay between the virus and the environment, illuminating several critical aspects that reflect both the direct and indirect impacts of the outbreak on environmental health (Malki et al., 2020). During the initial stages of global lockdowns, air quality saw a marked improvement due to decreased industrial activity and reduced vehicular traffic, leading to lower concentrations of pollutants like nitrogen dioxide (NO_2) and particulate matter (PM2.5) in urban areas (Poole, 2020). This temporary reduction in air pollution not only highlighted the environmental benefits of decreased human activity but also suggested that long-term exposure to polluted air might exacerbate COVID-19 severity, given its established links to respiratory and cardiovascular conditions (Yang et al., 2021). Additionally, the pandemic's suspected zoonotic origins drew attention to the risks of wildlife trade and human encroachment into natural habitats, emphasizing the need for protecting biodiversity to prevent future zoonotic spillovers (Ye et al., 2020). On the behavioral front, the reduced travel prompted by lockdowns led to a surge in local and sustainable activities such as cycling, gardening, and supporting local agriculture, suggesting a possible shift towards more environmentally conscious lifestyles (Choi et al., 2021). However, the pandemic also brought challenges, notably in waste management, due to a significant increase in single-use plastics and medical waste, posing further risks to environmental sustainability (Merow and Urban, 2020). This nuanced relationship between COVID-19 and the environment reveals the broader implications for public health, biodiversity, and the urgent need for sustainable practices in a post-pandemic world.

An accurate prediction of outbreak timing could significantly mitigate the impact of COVID-19, enabling governments to adjust their preventive strategies and proactively plan protective measures (Adetunji et al., 2022; Lalmuanawma et al., 2020). COVID-19 spread modeling is crucial for understanding potential future effects (Sultana et al., 2022). Artificial intelligence (AI) methods surpass traditional statistical modeling techniques in creating high-quality predictive models (Ballı, 2021). AI-based models can identify key parameters that influence variations in COVID-19 spread across different regions or populations, integrate multiple intervention strategies (Ardabili et al., 2020), and simulate "what-if" scenarios by incorporating data from diseases with similar trends to COVID-19 (Hussein and Abdulazeez, 2021).

To improve decision-making in predicting the development of COVID-19 infections, several studies have been conducted (Abduljabbar and Alhayani 2023; Kwekha-Rashid et al., 2021; Rahman et al., 2021; Shinde et al., 2020). Fong et al. (2020) applied the GROOMS methodology alongside the Composite Monte-Carlo simulator (CMC) to enhance a deep learning network and fuzzy rule induction for predicting the progression of COVID-19 cases. Similarly, Xiang et al. (2021) reviewed the models to forecast the growth of COVID-19 infections in respect to public health. Qiang et al. (2020) used three encoding algorithms to screen spike protein features, enabling them to assess the risk of infection and track the evolution of the COVID-19 virus. Additionally, Poole (2020) advocated the use of machine learning to create predictive models that leverage big data to monitor the spread of both COVID-19. It has been suggested that there is a correlation between climatological temperatures, latitude, and the spread of COVID-19. Furthermore, Bai et al. (2020) employed deep learning and multivariate logistic regression to compare patients' data at the admission stage and during hospital stays to predict the progression of COVID-19.

For public health considerations, we introduce the concept of "population immunity" as a novel predictor. This encompasses factors such as age, ethnicity, race, poverty index, and intra-community mobility. Our findings underscore that a significant reduction in new cases can lead to a proportional decrease in hospitalization and mortality rates. Nevertheless, these reduction rates exhibit variability across different countries.

4. Conclusion

In conclusion, the rapid vaccination efforts against COVID-19 have achieved significant milestones. However, there is a wealth of knowledge to be gleaned from the data and the scientific insights derived from observing vaccination rates and their impact on new cases across diverse countries. Beyond the crucial aspects of vaccine production and delivery, the formulation of transparent population immunity programs within the framework of social and political rules and regulations is paramount. These programs are essential for maintaining the well-being of populations and meeting the unique needs of communities in the face of a formidable viral infection. Furthermore, the integration of machine learning approaches emerges as a valuable tool in shaping effective population immunity programs. Leveraging advanced analytics can contribute significantly to understanding the nuanced dynamics of vaccination, new cases, and the intricate interplay of factors influencing population health. As we move forward, a comprehensive and data-driven approach, encompassing both scientific understanding and technological innovations, will be instrumental in navigating the complexities of infectious disease management on a global scale.

5. Limitations

The study has some limitations, including the absence of province-level analysis, which could provide a more granular understanding of hotspot rates in smaller communities. Despite these limitations, our results offer valuable insights for decision and policy makers in public health. The information presented can guide the implementation of tailored guidelines and regulations, considering the minimum vaccination rates for local areas. Timely vaccine distribution based on our guidelines stands to yield substantial benefits. Moreover, this approach aids in preventing new cases through the correct vaccination of communities, contributing to the disruption of the infection chain by integrating policies and regulations with other non-pharmaceutical measures.

6. Recommendations

For future research, we recommend exploring the impact of vaccination on the evolution of virus variants and the potential influence of socio-economic factors on vaccination uptake. Moreover, a broader analysis across different geographical regions can further validate the study's findings and enhance global pandemic preparedness.

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References

Adetunji, C. O., Olaniyan, O. P., Adeyomoye, O., et al. (2022). Machine learning approaches for COVID-19 pandemic. In: Assessing COVID-19 and Other Pandemics and Epidemics using Computational Modelling and Data Analysis. Springer.

Ahamad, Md. M., Aktar, S., Rashed-Al-Mahfuz, Md., et al. (2020). A machine learning model to identify early stage symptoms of SARS-Cov-2 infected patients. Expert Systems with Applications, 160, 113661. https://doi.org/10.1016/j.eswa.2020.113661

Araújo, J. L. de, Oliveira, K. K. D. de, & Freitas, R. J. M. de. (2020). In defense of the Unified Health System in the context of SARS-CoV-2 pandemic. Revista Brasileira de Enfermagem, 73(suppl 2). https://doi.org/10.1590/0034-7167-2020-0247

Ardabili, S., Mosavi, A., Ghamisi, P., et al. (2020). COVID-19 Outbreak Prediction with Machine Learning. Algorithms, 13(10), 249. https://doi.org/10.3390/a13100249

Argirova, R., & Zlatareva, A. (2023). Lifelong vaccination model: for a better quality of life. Biotechnology & Biotechnological Equipment, 37(1), 24–33. https://doi.org/10.1080/13102818.2022.2151379

Arvind, K. S., Vanitha, S., & Suganya, K. S. (2023). Pandemic Management Using Internet of Things and Big Data – A Security and Privacy Perspective. IoT and Big Data Analytics for Smart Cities, 159–173. https://doi.org/10.1201/9781003217404-8

Bai, X., Fang, C., Zhou, Y., et al. (2020). Predicting COVID-19 Malignant Progression with AI Techniques. SSRN Electronic Journal. https://doi.org/10.2139/ssrn.3557984

Ballı, S. (2021). Data analysis of Covid-19 pandemic and short-term cumulative case forecasting using machine learning time series methods. Chaos, Solitons & Fractals, 142, 110512. https://doi.org/10.1016/j.chaos.2020.110512

Bian, L., Gao, F., Zhang, J., et al. (2021). Effects of SARS-CoV-2 variants on vaccine efficacy and response strategies. Expert Review of Vaccines, 20(4), 365–373. https://doi.org/10.1080/14760584.2021.1903879

Buitrago-Garcia, D., Egli-Gany, D., Counotte, M. J., et al. (2020). Occurrence and transmission potential of asymptomatic and presymptomatic SARS-CoV-2 infections: A living systematic review and meta-analysis. PLOS Medicine, 17(9), e1003346. https://doi.org/10.1371/journal.pmed.1003346

Campos, D. M. de O., Fulco, U. L., de Oliveira, C. B. S., et al. (2020). SARS-CoV-2 virus infection: Targets and antiviral pharmacological strategies. Journal of Evidence-Based Medicine, 13(4), 255–260. Portico. https://doi.org/10.1111/jebm.12414

Cevik, M., Kuppalli, K., Kindrachuk, J., et al. (2020). Virology, transmission, and pathogenesis of SARS-CoV-2. BMJ, m3862. https://doi.org/10.1136/bmj.m3862

Cevik, M., Marcus, J. L., Buckee, C., et al. (2021). Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)

Transmission Dynamics Should Inform Policy. Clinical Infectious Diseases, 73(Supplement_2), S170–S176. https://doi.org/10.1093/cid/ciaa1442

Chasapis, C. T., Perlepes, S. P., Bjørklund, G., et al. (2023). Structural modeling of protein ensembles between E3 RING ligases and SARS-CoV-2: The role of zinc binding domains. Journal of Trace Elements in Medicine and Biology, 75, 127089. https://doi.org/10.1016/j.jtemb.2022.127089

Choi, Y., Tuel, A., & Eltahir, E. A. B. (2021). On the Environmental Determinants of COVID-19 Seasonality. GeoHealth, 5(6). Portico. https://doi.org/10.1029/2021gh000413

Coro, G. (2020). A global-scale ecological niche model to predict SARS-CoV-2 coronavirus infection rate. Ecological Modelling, 431, 109187. https://doi.org/10.1016/j.ecolmodel.2020.109187

Evensen, G., Amezcua, J., Bocquet, M., et al. (2021). An international initiative of predicting the SARS-CoV-2 pandemic using ensemble data assimilation. Foundations of Data Science, 3(3), 413. https://doi.org/10.3934/fods.2021001

Fawagreh, K., Gaber, M. M., & Elyan, E. (2014). Random forests: from early developments to recent advancements. Systems Science & Control Engineering, 2(1), 602–609. https://doi.org/10.1080/21642583.2014.956265

Fong, S. J., Li, G., Dey, N., et al. (2020). Composite Monte Carlo decision making under high uncertainty of novel coronavirus epidemic using hybridized deep learning and fuzzy rule induction. Applied Soft Computing, 93, 106282. https://doi.org/10.1016/j.asoc.2020.106282

Haque, S. M., Ashwaq, O., Sarief, A., et al. (2020). A comprehensive review about SARS-CoV-2. Future Virology, 15(9), 625–648. https://doi.org/10.2217/fvl-2020-0124

Hu, B., Guo, H., Zhou, P., et al. (2021). Characteristics of SARS-CoV-2 and COVID-19. Nature Reviews Microbiology, 19(3), 141–154. https://doi.org/10.1038/s41579-020-00459-7

Hussein, H. A., Abdulazeez, A. M. (2021). COVID-19 pandemic datasets based on machine learning clustering algorithms: a review. PalArch’s Journal of Archaeology of Egypt/Egyptology, 18, 2672–700.

Jones, T. C., Biele, G., Mühlemann, B., et al. (2021). Estimating infectiousness throughout SARS-CoV-2 infection course. Science, 373(6551). https://doi.org/10.1126/science.abi5273

Kandikattu, H. K., Manohar, M., Verma, A. K., et al. (2021). Macrophages-induced IL-18–mediated eosinophilia promotes characteristics of pancreatic malignancy. Life Science Alliance, 4(8), e202000979. https://doi.org/10.26508/lsa.202000979

Karadimas, P. (2023). Public Choice Theory: An Explanation of the Pandemic Policy Responses. In: The Covid-19 Pandemic: A Public Choice View. Springer.

Kasting, M. L., Head, K. J., Hartsock, J. A., et al. (2020). Public perceptions of the effectiveness of recommended non-pharmaceutical intervention behaviors to mitigate the spread of SARS-CoV-2. PLOS ONE, 15(11), e0241662. https://doi.org/10.1371/journal.pone.0241662

Krammer, F. (2020). SARS-CoV-2 vaccines in development. Nature, 586(7830), 516–527. https://doi.org/10.1038/s41586-020-2798-3

Kwekha-Rashid, A. S., Abduljabbar, H. N., & Alhayani, B. (2021). Coronavirus disease (COVID-19) cases analysis using machine-learning applications. Applied Nanoscience, 13(3), 2013–2025. https://doi.org/10.1007/s13204-021-01868-7

Lalmuanawma, S., Hussain, J., & Chhakchhuak, L. (2020). Applications of machine learning and artificial intelligence for Covid-19 (SARS-CoV-2) pandemic: A review. Chaos, Solitons & Fractals, 139, 110059. https://doi.org/10.1016/j.chaos.2020.110059

Liu, Y., Morgenstern, C., Kelly, J., et al. (2021). The impact of non-pharmaceutical interventions on SARS-CoV-2 transmission across 130 countries and territories. BMC Medicine, 19(1). https://doi.org/10.1186/s12916-020-01872-8

Loey, M., Manogaran, G., Taha, M. H. N., et al. (2021). A hybrid deep transfer learning model with machine learning methods for face mask detection in the era of the COVID-19 pandemic. Measurement, 167, 108288. https://doi.org/10.1016/j.measurement.2020.108288

Ludwig, S., & Zarbock, A. (2020). Coronaviruses and SARS-CoV-2: A Brief Overview. Anesthesia & Analgesia, 131(1), 93–96. https://doi.org/10.1213/ane.0000000000004845

Luong, N.-D. M., Guillier, L., Federighi, M., et al. (2023). An agent-based model to simulate SARS-CoV-2 contamination of surfaces and meat cuts in processing plants. International Journal of Food Microbiology, 404, 110321. https://doi.org/10.1016/j.ijfoodmicro.2023.110321

Malik, J. A., Ahmed, S., Mir, A., et al. (2022). The SARS-CoV-2 mutations versus vaccine effectiveness: New opportunities to new challenges. Journal of Infection and Public Health, 15(2), 228–240. https://doi.org/10.1016/j.jiph.2021.12.014

Malki, Z., Atlam, E.-S., Hassanien, A. E., et al. (2020). Association between weather data and COVID-19 pandemic predicting mortality rate: Machine learning approaches. Chaos, Solitons & Fractals, 138, 110137. https://doi.org/10.1016/j.chaos.2020.110137

Merow, C., & Urban, M. C. (2020). Seasonality and uncertainty in global COVID-19 growth rates. Proceedings of the National Academy of Sciences, 117(44), 27456–27464. https://doi.org/10.1073/pnas.2008590117

Perelson, A. S., & Ke, R. (2021). Mechanistic Modeling of SARS-CoV-2 and Other Infectious Diseases and the Effects of Therapeutics. Clinical Pharmacology & Therapeutics, 109(4), 829–840. Portico. https://doi.org/10.1002/cpt.2160

Poole, L. (2020). Seasonal Influences On The Spread Of SARS-CoV-2 (COVID19), Causality, and Forecastabililty (3-15-2020). SSRN Electronic Journal. https://doi.org/10.2139/ssrn.3554746

Purssell, E., and Gould, D. (2023). Infection Prevention and Control in Healthcare Settings. John Wiley & Sons.

Putra, K. A., & Drajati, N. A. (2023). Moving ahead: Challenges and opportunities for teachers in post-pandemic pedagogy. Teacher Education and Teacher Professional Development in the COVID-19 Turn, 3–8. https://doi.org/10.1201/9781003347798-1

Qiang, X.-L., Xu, P., Fang, G., et al. (2020). Using the spike protein feature to predict infection risk and monitor the evolutionary dynamic of coronavirus. Infectious Diseases of Poverty, 9(1). https://doi.org/10.1186/s40249-020-00649-8

Rahman, M. M., Islam, Md. M., Manik, Md. M. H., et al. (2021). Machine Learning Approaches for Tackling Novel Coronavirus (COVID-19) Pandemic. SN Computer Science, 2(5). https://doi.org/10.1007/s42979-021-00774-7

Reme, B.-A., Gjesvik, J., & Magnusson, K. (2023). Predictors of the post-COVID condition following mild SARS-CoV-2 infection. Nature Communications, 14(1). https://doi.org/10.1038/s41467-023-41541-x

Rian, K., Esteban-Medina, M., Hidalgo, M. R., et al. (2021). Mechanistic modeling of the SARS-CoV-2 disease map. BioData Mining, 14(1). https://doi.org/10.1186/s13040-021-00234-1

Ruffieux, H., Hanson, A. L., Lodge, S., et al. (2023). A patient-centric modeling framework captures recovery from SARS-CoV-2 infection. Nature Immunology, 24(2), 349–358. https://doi.org/10.1038/s41590-022-01380-2

Ryan, J. M. (2023). COVID-19: Surviving a Pandemic. Routledge. https://doi.org/10.4324/9781003302698

Ryan, J. M., & Nanda, S. (2023). Pandemic Politics and the Politics of the Pandemic1. COVID-19: Individual Rights and Community Responsibilities, 105–123. https://doi.org/10.4324/9781003302643-7

Saha, I., Ghosh, N., Maity, D., et al. (2021). COVID-DeepPredictor: Recurrent Neural Network to Predict SARS-CoV-2 and Other Pathogenic Viruses. Frontiers in Genetics, 12. https://doi.org/10.3389/fgene.2021.569120

Shinde, G. R., Kalamkar, A. B., Mahalle, P. N., et al. (2020). Forecasting Models for Coronavirus Disease (COVID-19): A Survey of the State-of-the-Art. SN Computer Science, 1(4). https://doi.org/10.1007/s42979-020-00209-9

Shulman, L. M. (2023). Infectious Diseases. In: Encyclopedia of Sustainability Science and Technology Series. Springer. https://doi.org/10.1007/978-1-0716-2463-0

Sultana, J., Kumar Singha, A., Tabrez Siddiqui, S., et al. (2022). COVID-19 Pandemic Prediction and Forecasting Using Machine Learning Classifiers. Intelligent Automation & Soft Computing, 32(2), 1007–1024. https://doi.org/10.32604/iasc.2022.021507

Waheed, Y., Sah, R., & Muhammad, K. (2023). Recent Developments in Vaccines for Viral Diseases. Vaccines, 11(2), 198. https://doi.org/10.3390/vaccines11020198

Wang, S., Pan, Y., Wang, Q., et al. (2020). Modeling the viral dynamics of SARS-CoV-2 infection. Mathematical Biosciences, 328, 108438. https://doi.org/10.1016/j.mbs.2020.108438

Xiang, Y., Jia, Y., Chen, L., et al. (2021). COVID-19 epidemic prediction and the impact of public health interventions: A review of COVID-19 epidemic models. Infectious Disease Modelling, 6, 324–342. https://doi.org/10.1016/j.idm.2021.01.001

Yang, X.-D., Li, H.-L., & Cao, Y.-E. (2021). Influence of Meteorological Factors on the COVID-19 Transmission with Season and Geographic Location. International Journal of Environmental Research and Public Health, 18(2), 484. https://doi.org/10.3390/ijerph18020484

Ye, Z.-W., Yuan, S., Yuen, K. S., et al. (2020). Zoonotic origins of human coronaviruses. International journal of biological sciences, 16, 1686.