

Development of a MATLAB application for simulating the SEIQRD pandemic spread model

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Abstract—This paper details the development of a MATLAB application simulating the SEIQRD model for the spread of pandemic diseases. Using App Designer and differential equations, we demonstrate the usefulness of the model for modeling pandemics by replicating Slovakia's COVID-19 pandemic data. The study analyzes how various factors affect infection waves and assesses public health interventions. The SEIQRD model expands on SEIR, including categories for exposed, symptomatic, asymptomatic, quarantined, recovered, and deceased individuals.

Index Terms—epidemic, SEIQRD model, pandemic, Matlab

I. INTRODUCTION

Epidemiological models are essential tools for predicting the spread of infectious diseases and guiding public health interventions [1]. Emerging pandemics require rapid and accurate modeling to forecast the impact of various non-pharmaceutical interventions, such as quarantines, lockdowns, and mask-wearing. [2] This study presents the development of a Matlab-based application for simulating the SEIQRD (Susceptible, Exposed, Infected, Quarantined, Recovered, Deceased) model to track the spread of pandemic diseases.

Pandemic modeling plays a pivotal role in understanding disease dynamics and guiding public health policies. Building upon classical compartmental models like SIR, newer frameworks like SEIR and SEIQRD provide enhanced insights. For instance, studies [3] [4] demonstrated the necessity of quarantine measures and their direct effect on the reproduction number R_0 , underscoring the vital role of early intervention. Furthermore, advancements in fractional-order models have proven useful [5] for analyzing the long-term memory effects and uncertainties in disease transmission.

The SEIQRD model is an extension of traditional epidemiological models, designed to account for specific behaviors observed during a pandemic, including the impact of asymptomatic carriers and quarantining infected individuals. In this paper, we demonstrate the implemented model by using real-world data from Slovakia's COVID-19 epidemic¹ as an

example of infectious disease. The model was used to simulate the progression of the pandemic and assess the effectiveness of interventions.

Our goal was to create a user-friendly Matlab application that allowed policymakers and researchers to visualize the impact of parameter changes in real-time, enabling dynamic adjustments based on emerging data. The application was designed with flexibility, allowing for adaptation to future waves of COVID-19 or other infectious diseases with similar transmission dynamics.

II. RELATED WORK

The field of mathematical modeling of disease spread has witnessed significant advancements in recent years, driven by the recent emergence of infectious diseases, in particular, the COVID-19 pandemic.

A number of studies have explored the spread of COVID-19 pandemic. For instance, Iboi [6] has created a mathematical model of pandemic spread in Nigeria and has analyzed the continuum of disease-free equilibria. Riyapan [7] has created a mathematical model for the spread of the pandemic in Thailand using a next-generation matrix approach for calculating the basic reproduction number of the model. These works have provided valuable insights into mathematical modeling.

Our work builds upon these previous efforts by modeling the pandemic spread in Slovakia. Unlike previous works [6] [7], our approach focuses on creating a software implementation of the mathematical model with adjustable parameters. This approach allows the model to be used in modeling various infectious diseases, as well as focusing on certain periods of the disease spread.

III. SEIQRD MODEL OVERVIEW

The SEIQRD model is a compartmental model in epidemiology, extending the classical SEIR model [8] by incorporating quarantined individuals and differentiating between symptomatic and asymptomatic infections. Recent studies [5] have extended this model by incorporating fractional derivatives to improve accuracy in representing memory effects in epidemic transmission. It is formulated as a set of ordinary

¹[Slovak] Koronavírus na Slovensku v číslach. [English] Coronavirus in Slovakia in numbers. Available: <https://web.archive.org/web/20220303113735/https://korona.gov.sk/koronavirus-na-slovensku-v-cislach/> [Accessed: Dec. 04, 2024]

differential equations that describe the transitions between six compartments [9]:

- Susceptible (S): Individuals who are not yet infected but are at risk of contracting the disease,
- Exposed (E): Individuals who have been exposed to the virus but are not yet infectious. This stage captures the latency period,
- Infected (I): The model splits infected individuals into:
 - Symptomatic (I_s): Individuals who exhibit symptoms,
 - Asymptomatic (I_a): Infected individuals who do not show symptoms but can still transmit the virus,
- Quarantined (Q): Infected individuals who have been isolated to prevent the further spread of the virus,
- Recovered (R): Individuals who have recovered from the infection and are assumed to have immunity,
- Deceased (D): Individuals who succumbed to the disease.

The system of ordinary differential equations for SEIQRD is written as:

$$\begin{aligned}\frac{dS}{dt} &= \rho - \beta_s (1 - \psi\xi) SI_s - \beta_a (1 - \psi\xi) SI_a - \mu S, \\ \frac{dE}{dt} &= \beta_s (1 - \psi\xi) SI_s + \beta_a (1 - \psi\xi) SI_a - (\varphi + \mu) E, \\ \frac{dI_s}{dt} &= (1 - \theta) \varphi E - (\alpha_s + \delta_s + \lambda_s + \mu) I_s, \\ \frac{dI_a}{dt} &= \theta \varphi E - (\alpha_a + \lambda_a + \mu) I_a, \\ \frac{dQ}{dt} &= \alpha_s I_s + \alpha_a I_a - (\lambda_q + \delta_q + \mu) Q, \\ \frac{dR}{dt} &= \lambda_s I_s + \lambda_a I_a + \lambda_q Q - \mu R, \\ \frac{dD}{dt} &= \delta_s I_s + \delta_q Q.\end{aligned}$$

Where β_s and β_a are the transmission rates for symptomatic and asymptomatic individuals, respectively, ϕ is the rate at which exposed individuals become infectious, θ is the proportion of infected individuals who are asymptomatic, α_a and α_s represent the rates at which symptomatic and asymptomatic individuals are quarantined, λ_a , λ_s and λ_q represent recovery rates for symptomatic, asymptomatic, and quarantined individuals, δ_q and δ_s are the death rates for symptomatic and quarantined individuals, μ represents the natural death rate, while ρ represents the birth rate or population growth.

These equations capture the time-dependent dynamics of each compartment, driven by the spread of the infection and the impact of interventions as illustrated by schematics Fig. 1.

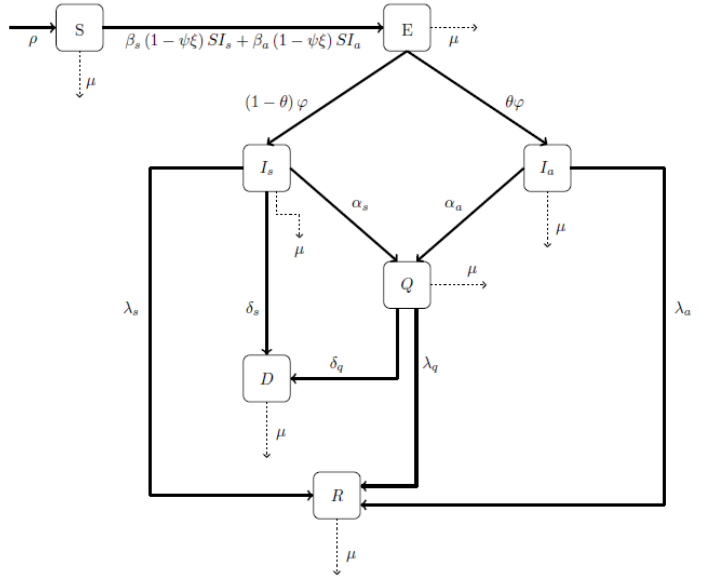


Fig. 1. SEIQRD schematics

A key feature of the SEIQRD model is the inclusion of asymptomatic individuals (I_a) and the quarantined compartment (Q) [10]. In the context of COVID-19, asymptomatic carriers played a crucial role in the disease's rapid transmission, making it necessary to account for them in the model. Quarantine, another critical factor, was an essential intervention adopted by governments to isolate infected individuals and prevent further spread.

IV. DESIGN AND DEVELOPMENT OF THE MATLAB APPLICATION

The SEIQRD model was implemented using Matlab and Matlab's App Designer to develop a graphical user interface (GUI) as shown on Fig. 2 that made the model accessible to users without deep coding expertise.

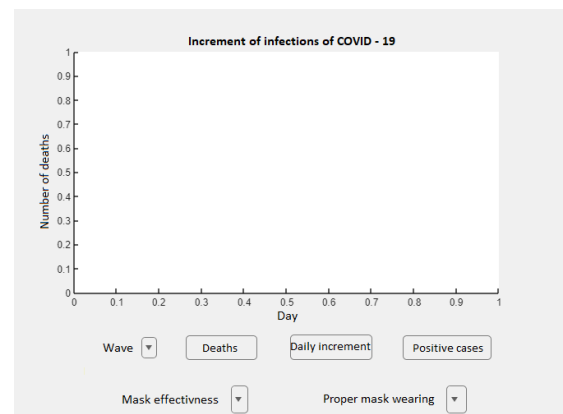


Fig. 2. GUI design of Matlab app

A. Features of the Matlab application

The Matlab application was designed with user flexibility in mind, allowing users to explore different scenarios by

adjusting model parameters in real-time. The key features of the application include:

- **Interactive Graphs:** The primary output of the application is a series of graphs that show the progression of the pandemic over time. Users can select which compartment (e.g., Susceptible, Infected, Recovered) to display and can toggle between daily and cumulative data,
- **Parameter Controls:** The application allows users to adjust parameters such as infection rate (β_s, β_a), quarantine rate (α_s, α_a), and mask effectiveness (ξ). Each parameter is controlled via a slider, which instantly updates the simulation when adjusted.
- **Time Frame Selection:** Users can simulate different phases of the pandemic by selecting the time period they are interested in. The application includes pre-set options for the first, second, and third waves of COVID-19 in Slovakia, based on real data from official sources.
- **Real-Time Data Integration:** The application incorporates actual COVID-19 data from Slovakia, stored in an Excel file. This data is used to compare the model's predictions with real outcomes, providing users with a visual assessment of the model's accuracy. As highlighted in studies [11] [12], algorithms that prioritize data segments based on importance can significantly reduce processing delays. This approach allows for immediate visualization of critical segments while the rest of the data is processed in the background, ensuring an uninterrupted user experience even when working with substantial datasets.

V. SIMULATION OF COVID-19 WAVES

In the case of COVID-19 pandemic, 4 distinct waves of infection were recorded in Slovakia. In this study we focused on the first three waves. To accurately test the model, each wave was simulated individually.

A. First wave: March 2020 – June 2020

The first wave of COVID-19 in Slovakia began in early March 2020², shortly after the global pandemic was declared. The SEIQRD model was initialized using population data from Slovakia and the early reported cases of COVID-19. During this period, strict lockdown measures were implemented³ and public health authorities mandated mask-wearing and social distancing.

In the Matlab application, the parameters for the first wave were estimated based on real-world interventions. The initial infection rate (β_s) was set relatively low, reflecting the impact of early intervention measures, while the quarantine rate

(α_s) was set high to simulate the isolation of symptomatic individuals.

Despite the effective interventions, the model demonstrated high sensitivity to the mask compliance rate (ξ). Small changes in mask compliance resulted in significant differences in the infection curves. This highlighted the importance of widespread mask adoption during the early stages of the pandemic.

B. Second Wave: August 2020 – June 2021

The second wave was significantly more severe than the first, driven by a combination of relaxed public health measures and increased public mobility. Slovakia experienced a sharp rise in cases beginning in late August 2020. The SEIQRD model in this period was adjusted to account for these changes, with increased infection rates and lower quarantine compliance as restrictions were lifted.

The model was adjusted to reflect the characteristics of the second wave of the pandemic. Specifically, the infection rates were increased to account for the higher transmission of the virus, the mask compliance rate was lowered to reflect declining public adherence to mask-wearing, and the proportion of symptomatic individuals was increased to align with reports of a higher proportion of symptomatic cases compared to the first wave. These adjustments allowed the model to better capture the unique dynamics of the second wave and provide more accurate predictions and insights.

The application accurately captured the steep rise in infections during the second wave but overestimated the mortality rate initially as shown on Fig. 3. This discrepancy was later addressed by refining the quarantine rates (α_s) and death rates (δ_s) based on feedback from public health data.

Graphs generated by the Matlab application shown on Fig. 4 showed that, while the model predicted a rapid increase in infections, the actual data exhibited a more gradual rise. This discrepancy was attributed to public health interventions, such as localized lockdowns and mass testing campaigns, which were not immediately reflected in the model parameters.

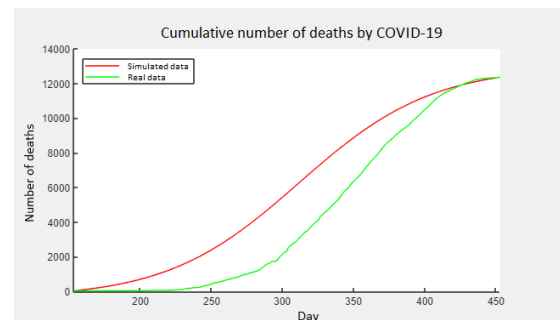


Fig. 3. Cumulative number of deaths by COVID-19 wave 2

²[Slovak] Slovensko zaznamenalo prvý potvrdený prípad ochorenia COVID-19. [English] First confirmed case of COVID-19 recorded in Slovakia. Available: https://web.archive.org/web/20220302020145/https://www.uvzsr.sk/index.php?option=com_content&view=article&id=4061:slovensko-zaznamenalo-prvy-potvrdeny-pripad-ochorenia-covid-19&catid=250:koronavirus-2019-ncov&Itemid=153 [Accessed: Dec. 04, 2024]

³[Slovak] COVID-19: Krízový štáb zavádza prísne opatrenia, zatvárajú sa školy, letiská. [English] The crisis team is implementing strict measures, schools and airports are closing. Available: <https://www.health.gov.sk/Clanok?koronavirus-opatrenia-sprisnene> [Accessed: Dec. 04, 2024]

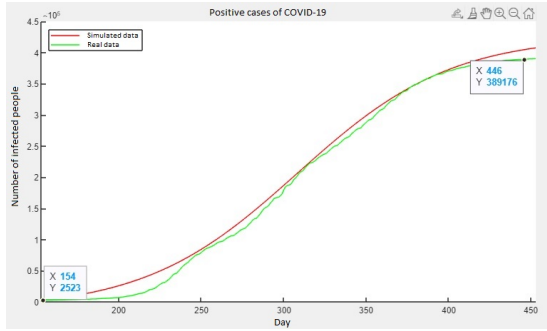


Fig. 4. Positive cases of COVID-19 wave 2

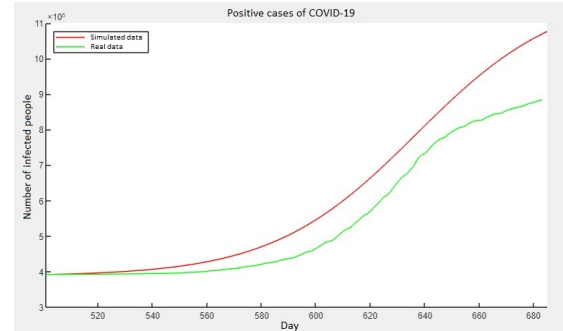


Fig. 5. Positive cases of COVID-19 wave 3

C. Third wave: July 2021 – January 2022

The third wave of COVID-19 in Slovakia was driven by the emergence of the Delta variant ⁴, which was more transmissible than previous strains. This variant's higher transmissibility was captured in the SEIQRD model by increasing the transmission rates (β_s and β_a) even further.

One significant challenge during the third wave was modeling the interaction between vaccination and the spread of the Delta variant. While the SEIQRD model does not explicitly account for vaccination, adjustments were made to the recovery rates (λ_s and λ_a) to reflect the protective effect of vaccines. Additionally, the proportion of symptomatic individuals ($1 - \theta$) was decreased, as vaccinated individuals who contracted COVID-19 were more likely to be asymptomatic.

The model captured the rapid rise in cases but struggled to accurately simulate the decline in cases following the peak as pictured on Fig. 5. This was due to the introduction of new public health measures, such as the implementation of the "OTP" ⁵ (vaccinated, tested, recovered) system, which restricted access to public spaces based on individuals' health status.

⁴[Slovak] Na Slovensku sa už začala tretia vlna pandémie, delta variant zvýšil reprodukčné číslo nad kritickú hodnotu. [English] The third wave of the pandemic has already begun in Slovakia, the delta variant has increased the reproduction number above the critical value. Available: <https://sita.sk/vzdravotnictve/lengvarskeho-ministerstvo-potvrdilo-spravu-ktorej-sa-obava-mnogo-ludi-na-slovensku-zacala-tretia-vlna-pandemie/> [Accessed: Dec. 04, 2024]

⁵[Slovak] Slovensko prechádza na nový režim a najviac to pocítia nezačkovaní. [English] Slovakia is transitioning to a new regime, and the unvaccinated will feel it the most. Available: <https://tvnoviny.sk/koronavirus/clanok/136686-slovensko-prechadza-na-novy-rezim-a-najviac-to-pocitia-nezaockovani> [Accessed: Dec. 04, 2024]

D. Model visualization and comparison with real data

Throughout all three waves, the Matlab application provided visualizations of the pandemic's progression. Users could compare simulated infection, recovery, and death curves with actual COVID-19 data from Slovakia. In each case, the model captured the general trend of rising and falling case numbers, though some discrepancies were noted due to changing public health policies and behavioral factors that were not directly modeled.

VI. MODEL CALIBRATION AND PARAMETER ADJUSTMENT

Calibrating the SEIQRD model involved adjusting a large number of parameters, including transmission rates, quarantine rates, recovery rates, and mask compliance rates. The initial parameter values were based on literature estimates and real-world data from Slovakia. However, manual tuning was required to improve the fit between the simulated and actual data.

The parameter tuning process in the SEIQRD model involves systematically adjusting the values of model parameters to achieve a closer fit between simulated outputs and real-world data. Parameters such as transmission rates (β_s , β_a) quarantine rates (α_s , α_a) and mask compliance (ξ) are modified iteratively. This ensures that the model reflects changing dynamics, such as shifts in public behavior or the introduction of public health measures.

Manual tuning was carried out by adjusting parameters individually and observing the model's outputs compared to real-world data. Below in Table I is an example of parameter adjustments made for different COVID-19 waves in Slovakia:

TABLE I
PARAMETER TUNING FOR DIFFERENT WAVES OF COVID-19 INFECTION

Parameter	Wave 1 Value	Wave 2 Value	Wave 3 Value
β_s	0.1 (low due to lockdown)	0.25 (higher due to mobility)	0.3 (Delta variant transmission)
α_s	0.7 (high quarantine rate)	0.5 (relaxed compliance)	0.6 (improved isolation efforts)
ξ	0.9 (strict mask usage)	0.6 (reduced adherence)	0.7 (partial improvement)

For instance, during the second wave, a decrease in ξ from 0.9 to 0.6 simulated the public's lower adherence to mask-wearing, leading to a sharper increase in cases. These adjustments were repeated iteratively for each parameter until the simulated curves aligned closely with the observed data.

Transmission rates (β_s, β_a) were adjusted for each wave to reflect changes in public health measures and the emergence of new variants. Quarantine rates (α_s, α_a) were adjusted based on the effectiveness of isolation measures during different phases of the pandemic. Mask compliance (ξ) was one of the most sensitive parameters, and small changes in this value had a large impact on the model's predictions.

A sensitivity analysis was conducted to assess how changes in each parameter impacted the model's predictions. The analysis revealed that the model was most sensitive to changes in the transmission rates (β_s, β_a) and mask compliance (ξ). Small increases in these parameters resulted in disproportionately large increases in infection numbers, especially during the second and third waves.

Conversely, the model was less sensitive to changes in the recovery rates (λ_s, λ_a), as these rates primarily impacted the tail end of the infection curves.

VII. RESULTS AND DISCUSSION

The SEIQRD model, as implemented in the Matlab application, was able to approximate the spread of COVID-19 in Slovakia with reasonable accuracy. The model performed particularly well in capturing the early stages of each wave, where the infection numbers were relatively small, and public health measures were uniformly applied.

In the later stages of each wave, however, the model's accuracy diminished. This was due to several factors:

The model's limitations include its inability to dynamically adjust for the introduction of new public health measures, such as lockdowns or mass testing campaigns. These interventions had a significant impact on the course of the pandemic but were challenging to model in real-time.

Additionally, the model did not account for changes in public behavior, such as increased mobility during holiday periods or fluctuations in mask compliance. While the model did not explicitly include vaccination, adjustments to the recovery rates were made to approximate its impact. These factors highlight the need for further refinement and development of epidemiological models to accurately capture the complex dynamics of infectious diseases.

A. Visualization of pandemic waves

The application provided clear visualizations of the pandemic waves, allowing users to compare the progression of the pandemic under different parameter assumptions. For each wave, the application generated graphs that showed:

- Daily new infections: The number of new infections reported each day.
- Cumulative infections: The total number of infections over time.

- Recoveries and deaths: The number of recoveries and deaths as a function of time.

These visualizations were particularly useful for exploring "what-if" scenarios. For example, users could adjust the mask compliance rate (ξ) to see how more widespread mask-wearing could have reduced infection numbers during the second wave. Similarly, users could increase the quarantine rate (α_s) to explore how stricter isolation measures might have mitigated the spread of the Delta variant during the third wave.

B. Comparison with real-world data

Throughout the pandemic, real-world data from Slovakia's COVID-19 dashboard was used to validate the model's predictions. In general, the model's predictions aligned closely with the actual data during the early stages of each wave, though some discrepancies were noted during the later stages.

For example, during the second wave, the model overestimated the mortality rate, predicting a higher number of deaths than was observed. This was later corrected by adjusting the death rates (δ_s, δ_a) based on updated public health data.

In the third wave, the model underestimated the speed of the Delta variant's spread, likely due to the emergence of new public health interventions that were not fully accounted for in the model.

C. Limitations

The proposed model is not without its limitations. The model cannot dynamically incorporate sudden policy changes like lockdowns or mass testing campaigns, which significantly impact the pandemic's course.

Some behavioral factors were also not accounted for. Variations in human behavior, such as increased mobility during holidays or changes in mask-wearing compliance, are challenging to simulate.

Moreover, the vaccination poses an issue to model's accuracy. While adjustments to recovery rates (λ_s, λ_a) were made to approximate vaccination effects, the model lacks explicit compartments for vaccinated individuals and could be expanded in this way in the future.

The model also struggles when the cases decline rapidly. As seen during the third wave, the model struggled to simulate the rapid decline in cases driven by new interventions like the OTP system.

Lastly, the manual tuning process is labor-intensive and relies on iterative comparisons, limiting real-time applicability and could have had significant impact on its accuracy.

VIII. CONCLUSION

The development of the Matlab-based SEIQRD model application has demonstrated the value of mathematical modeling in understanding and responding to infectious disease outbreaks. The application provided a flexible and user-friendly platform for simulating the spread of COVID-19, allowing users to explore the impact of different interventions and visualize the progression of the pandemic.

While the model required manual calibration, the results were promising, and the application proved to be a useful tool for visualizing the effects of public health measures. Future improvements to the application could include the automation of parameter estimation, the integration of vaccination data, and the addition of real-time updates to account for changing public health policies.

The SEIQRD model, as implemented in Matlab, offers a framework for future pandemic preparedness, providing valuable insights into the dynamics of disease spread and the effectiveness of interventions. As new variants of COVID-19 and other diseases emerge, the ability to model and predict their spread will remain a critical component of public health planning.

REFERENCES

- [1] B. Jahn et al., "On the role of data, statistics and decisions in a pandemic," *Advances in statistical analysis*, vol. 106, 2022, pp. 349-382.
- [2] S.E. Eikenberry et al., "To mask or not to mask: Modeling the potential for face mask use by the general public to curtail the COVID-19 pandemic," *Infectious Disease Modelling*, vol. 5, 2020, pp. 293-308.
- [3] I. Darti et al., "A SEIQRD epidemic model to study dynamics of COVID-19 disease," *Communications in Mathematical Biology and Neuroscience*, 2023.
- [4] M. Aakash, C. Gunasundari, S. Sabarinathan, S. M.Boulaaras and A. Himadan, "Mathematical insights into the SEIQRD model with Allee and fear dynamics in the context of COVID-19," *Partial Differential Equations in Applied Mathematics*, vol. 11, 2024.
- [5] S. Paul et al., "Fractional order SEIQRD epidemic model of COVID-19: A case study of Italy," *PLOS ONE*, vol. 18, 2023.
- [6] E. A. Iboi, O. O. Sharomi, C. Ngonghala, A. B. Gumel, "Mathematical Modeling and Analysis of COVID-19 pandemic in Nigeria," *Mathematical Biosciences and Engineering*, vol. 17, 2020, pp. 7192-7220.
- [7] P. Riyapan, S. E. Shuaib and A. Intarasit, "A Mathematical Model of COVID-19 Pandemic: A Case Study of Bangkok, Thailand," *Computational and Mathematical Methods in Medicine*, 2021.
- [8] P.E. Parham and E. Michael, "Outbreak properties of epidemic models: The roles of temporal forcing and stochasticity on pathogen invasion dynamics," *Journal of Theoretical Biology*, vol. 271, 2011, pp. 1-9.
- [9] R. Pakwan, E.S. Sherif and I. Irthit, "A Mathematical Model of COVID-19 Pandemic: A Case Study of Bangkok, Thailand," *Computational and Mathematical Methods in Medicine*, 2021. [Online]. Available: <https://www.hindawi.com/journals/cmmm/2021/6664483/>
- [10] E. A. Iboi, O. O. Sharomi, C. N. Ngonghala, and A. B. Gumel, "Mathematical modeling and analysis of COVID-19 pandemic in Nigeria," *Mathematical Biosciences and Engineering*, vol.17, 2020.
- [11] B. Mados and N. Adam, "Reading volume datasets from storage - using segmentation metadata, for an enhanced user experience," *Acta Polytechnica Hungarica*, vol. 18, 2021, pp. 187-205.
- [12] B. Mados, A. Balaz, N. Adam, J. Hurtuk and Z. Bilanova, "Algorithm design for user experience enhancement of volume dataset reading from storage using 3D binary image as the metadata" 2019 IEEE 17th World Symposium on Applied Machine Intelligence and Informatics (SAMI 2019), 2019, pp. 269-273.