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Novel numerical methods for solving the SEIRD model

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Резюме

The purpose of the research. *The COVID-19 pandemic has shown that mathematical modeling has become important in the management of infectious diseases. The relevance of the study lies in understanding the dynamics of the spread of COVID-19 using mathematical modeling methods that play a key role in developing control strategies. Infection-specific models make it possible to analyze patterns, predict trajectories, and evaluate the effect of measures, including quarantine, social distancing, and vaccination.*

The purpose of the research is to develop and analyze an improved SEIRD model using a hybrid numerical method designed to improve the accuracy of forecasting the occurrence and development of pandemic waves and assessing the impact of sanitary measures.

Methods. *The research objectives include building a new SEIRD model as an extension of the classic SIR model with the addition of additional categories – "Exposed", "Recovered" and "Dead". To implement the proposed categories, the following methods were applied: explicit Euler method, fourth – order Runge – Kutta and adaptive Runge-Kutta schemes to increase reliability. Methodologically, the SEIRD system is solved using a hybrid numerical scheme combining the advantages of classical and adaptive methods, which made it possible to obtain accurate simulations and assess the impact of interventions.*

Results. *The results showed that the proposed refined SEIRD model provides reliable forecasts of the occurrence and development of pandemic waves.*

Conclusion. *An analysis of the results shows that a 10% increase in the number of infections signals the beginning of a new wave that requires adjustments to the parameters and rapid response of public health services, as well as the implementation of rapid sanitary and epidemiological measures. The SEIRD model with hybrid methods reflects the dynamics of COVID-19, and can also be adapted to model future epidemics.*

Keywords: *SEIRD model; hybrid numerical methods; epidemic modeling; COVID-19 dynamics; predictive epidemiology.*

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Новые численные методы для решения модели SEIRD

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Abstract

Цель исследования. *Пандемия COVID-19 показала, что математическое моделирование приобрело важное значение в управлении инфекционными заболеваниями. Актуальность исследования заключается в понимании динамики распространения COVID-19 с помощью методов математического моделирования, которые играют ключевую роль в разработке стратегий контроля. Специфические для инфекции модели позволяют анализировать закономерности, прогнозировать траектории и оценивать эффект мер, включая карантин, социальное дистанцирование и вакцинацию.*

Цель исследования – разработать и проанализировать усовершенствованную модель SEIRD с использованием гибридного численного метода, предназначенную для повышения точности прогнозирования возникновения и развития пандемических волн и оценки воздействия санитарных мер.

Методы. *Задачи исследований включают построение новой модели SEIRD как расширения классической модели SIR с добавлением дополнительных категорий: «Подверженные» (Exposed), «Выздоровевшие» (Recovered) и «Умершие» (Dead). Для реализации предложенных категорий были примененены методы: явный метод Эйлера, Рунге – Кутта четвёртого порядка и адаптивные схемы Рунге – Кутты для повышения надёжности. Методологически система SEIRD решается с помощью гибридной численной схемы, сочетающей преимущества классических и адаптивных методов, что позволило получить точные симуляции и произвести оценку влияния вмешательств.*

Результаты. *Полученные результаты показали, что предложенная уточнённая модель SEIRD обеспечивает надёжные прогнозы возникновения и развития пандемических волн.*

Заключение. *Анализ полученных результатов свидетельствует о том, что увеличение роста числа инфекций на 10% сигнализирует о начале новой волны, требующей корректировки параметров и оперативного реагирования служб общественного здравоохранения, а также реализации быстрых санитарно-эпидемиологических мер. Модель SEIRD с гибридными методами отражает динамику COVID-19, а также может быть адаптирована для моделирования будущих эпидемий.*

Ключевые слова: *модель SEIRD; гибридные численные методы; эпидемиологическое моделирование; динамика COVID-19; прогностическая эпидемиология.*

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Introduction

The simplest [1] one has its dynamics defined in terms of differential equations, which describe state transitions through how parameters such as the basic reproduction number (R0) determine epidemic dynamics [2], [3]. However, this is also somewhat simplistic; such omissions from models as the incubation period and variations within the population are handled in many different ways, such as including an 'exposed' category in the SEIR model [4]. Mathematical modeling provides an opportunity to evaluate a wide variety of strategies for epidemic control as they allow for a range of relevant simulations for whatever permutations of intervention one wants, such as social distancing and the addition of a seasonal pattern to infectious disease [5]. A simple SIR model can predict that such measures may have as much effect as a reduction of the number of infections by more than 30%, given that rigid timing can be preserved [6].

SIR-like formalism has shown both benefits and limitations; however, it can be successfully modeled through the SEIR framework. It admits asymptomatic transmission of the infection, and it acts to lengthen the incubation period [7]. The COVID-19 pandemic has highlighted the need for extending and, at times, developing accurate mathematical models to understand its dynamics. Nevertheless, building upper echelons of the SIR model aligned with real-time data has allowed researchers to calculate the peak of cyst infection and put forth ways for developing the best control strategies, sometimes showing how minor changes in either public policy or individual behavior can bring remarkable changes in epidemiologic outcomes [8].

The addition of Exposed (E) and Dead (D) compartments to the SEIRD model profoundly enhances the natural ability to simulate infectious disease dynamics, providing a genuinely rich perspective of infection processes and mortality impacts [9]. It fills certain voids left by simpler models through the introduction of an assortment of contextual epidemiological factors of a rigorous description of both natural birth and death rates-that makes it relevant for long-term investigations while also making a better fit with the real-world dynamics of populations [10]. Its applicability in such situations is a tribute to the model's ability to administer different scenarios and evaluate various interventions' effectiveness and significance in epidemiological research [11].

The role of classic numerical methods like Euler's Method and Runge-Kutta is that of their description of dynamics disease dynamics. Implementations have largely deviated from providing traditional information required from infectious disease models since they are simpler, Euler generally assumes that higher-order complex equations could lead to bigger, more significant errors because, under certain conditions, there seem to be nothing more than approximations in the results from simple steepness [12].

On the other hand, the Runge-Kutta methods, especially the fourth order (RK4), are preferred for more complex epidemiological models. These methods provide a higher degree of accuracy in simulating the intricate dynamics of infectious diseases. The RK4 method, despite its greater computational demand, offers enhanced stability and precision, making it better suited for detailed simulations that require a nuanced understanding of disease transmission dynamics [13].

Research comparing these methods often highlights the trade-offs between computational efficiency and accuracy. For instance, while Euler's Method is computationally less intensive, it may not adequately capture the critical thresholds of disease spread, potentially leading to less reliable predictions [14]. This evaluation underscores the importance of selecting a numerical method that aligns with the complexity of the epidemiological model and the specific dynamics of the disease being studied, ensuring that predictions are both accurate and computationally feasible [15].

Materials and methods

In light of the careful arrangement of additional compartments defining infectious diseases such as COVID-19, the classical SEIRD model demonstrates a wider organizational scheme, in which both Exposed compartments and a Dead compartment are furnished to make the model simulate disease progression more realistically than traditional SIR or SEIR models [16]. The presence of the Exposed compartment makes the SEIR model an improvement upon the classical SIR model since it allows for a state of infection without contagiousness. In a way, the SEIRD model could be said to be building upon this by modeling an even more fine-grained approach that distinguishes among individuals by incorporating compartments for recovering individuals who are immune versus those who are dead, thereby enabling a more detailed analysis of disease outcomes.

SIR and SEIRD Model Equations Permission from Your Dissertation Allowed to Present Here.

$$\begin{cases} \dfrac{\mathrm{dS}}{\mathrm{dt}} = \text{-}\beta \mathrm{SI}, \\ \dfrac{dI}{dt} = \beta SI - \alpha I, \\ \dfrac{dR}{dt} = \alpha I. \end{cases} \tag{1}$$

SEIRD Model Equations [17]:

$$\begin{cases} \dfrac{dS}{dt} = -(\beta SI + Sf + Sv) + (\xi R + Nb), \\ \dfrac{dE}{dt} = -(\,Ef + \sigma E) + (\beta SI + \eta R), \\ \dfrac{dI}{dt} = -(If + \alpha[\mu I + (1-\mu)I]) + \sigma E, \\ \dfrac{dR}{dt} = -(Rf + R\xi + \eta R) + (\alpha(1-\mu)I + Sv), \\ \dfrac{dD}{dt} = \alpha(\mu I). \end{cases} \tag{2}$$

The factoring in of natural birth and death rates, vaccination rates informed from real data, and the immunity waning take place in SEIRD model, which makes it a highly relevant prediction tool for long-term studies, able to portray the disease's spread in variable populations realistically [18]. These features position the SEIRD model favorably toward promising applications in predicting the trajectory of the disease and assessing different public health interventions, thereby furnishing vital insights for policymakers and health officials in controlling the spread of COVID-19 and similar diseases.

Parameter estimation is a more complex task. The basic reproductive number R0 can be defined and used for estimation. Typically, mathematical models are used to estimate the value of the basic reproductive number, and thus, the calculated value depends on the chosen model as well as on the values of all other parameters.

Suppose that infected patients, on average, have an effective contact rate β with an average infectious period of α^{-1}. Thus, the basic reproductive number is defined as [19]:

$$R_0 = \beta/\alpha. \tag{3}$$

This leads to.

$$\beta = \alpha \cdot R_0. \tag{4}$$

Usually, the number of diagnosed infected individuals $I(t)$ at time t is known during an epidemic. The epidemic growth K in the early stages follows an exponential pattern, accompanied by a logarithmic growth rate. Usually, the number of diagnosed infected individuals $I(t)$ at time t is known during an epidemic. The epidemic growth K in the early stages follows an exponential pattern, accompanied by a logarithmic growth rate.

$$K = \frac{d ln[I(t)]}{dt}. \tag{5}$$

The second equation in the system of equations can be written as $\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I]$, forming an initial value problem with $I(0) = I_0$, which has an analytical solution.

$$I(t) = I_0 e^{\left(\frac{\beta S_0}{N}-\gamma\right)t}. \tag{6}$$

o find the doubling time T_d, substituting $I(T_d) = 2I_0$ into equation 6, we obtain:

$$2I_0 = I_0 e^{\left(\frac{\beta S_0}{N}-\alpha\right)T_d},$$

$$2 = e^{\left(\frac{\beta S_0}{N}-\alpha\right)T_d}. \tag{7}$$

Assuming $K = \frac{\beta S_0}{N} - \alpha$ and applying the logarithm to both sides, we obtain:

$$K = \frac{ln2}{T_d}. \tag{8}$$

If a patient infects exactly R_0 new people immediately after being infected, then after a certain time α^{-1}, the number of infected patients increases as

$$I(t) = I_0 R_0^{t\alpha},$$

$$\ln[I(t)] = \ln[I_0] + t\alpha \ln[R_0]. \tag{9}$$

The corresponding differential equation is as follows:

$$\frac{dI}{dt} = I(t)\alpha \ln[R_0], \tag{10}$$

or

$$\frac{d ln[I(t)]}{dt} = \ln[R_0]\,\alpha. \tag{11}$$

Substituting equation 5 into equation 11 gives $K = \alpha \ln[R_0]$ or

$$R_0 = e^{\frac{k}{\alpha}}. \tag{12}$$

Key parameters such as transmission rate (β), current population (*N*), vaccination rate (υ), natural mortality (*f*), birth rate (*b*), and mortality rate (μ) were estimated based on real-time data provided by the "Our World in Data" platform. These parameters were refined to reflect the specific dynamics of individual behavior, spatial movement, family interactions, and immunity levels.

Using detailed data from "Our World in Data," the model accounted for fluctuations in disease dynamics, including infection surges during periods of relaxed public measures and the protective effect of mass vaccination. This allowed the model to more accurately reflect the progression of the pandemic, providing a reliable tool for modeling future outbreak scenarios and developing public health measures. The algorithm will begin by calculating the approximate number of individuals in each compartment. Based on these compartment values, the missing parameter values will be computed, serving as the initial values for the model. These parameters will then be optimized using the least squares method with real data for these five compartments.

There is a parameter that calculates the percentage of recovered individuals that move to susceptibles compartment as their immunity wine with time after about 180 days, so if we consider that they all will lose their immunity after 180 days, if a fixed rate is considered to move from *R* to *S* compartment, with name, so

$$\xi = \frac{1}{180}. \tag{13}$$

We can consider the same explanation for the percentage of recovered individuals who can become infected again, as they have recovered and have immunity. Studies have shown that 14% of recovered individuals have immunity, so a fixed percentage of recovered individuals also transition from the recovered category back to the susceptible category.

$$\eta = 0{,}14 \cdot \xi. \tag{14}$$

So, summarizing each period (wave) of the pandemic: if this is the first wave, we can use α as the inverse of the recovery period from the disease, then calculate the doubling time, which is the time required to double the number of infected individuals, then calculate R_0, and then calculate β. Other parameters can be derived from the collected dataset of the governmental statistical organization. If this is the first period (wave), we can use $\alpha = \frac{1}{recovery\ time}$.

If this is not the first period (wave), we can use the following formula to calculate α:

$$case\ fatality\ rate(CER) = \frac{death\ at\ day\ X}{cases\ at\ day(X-T)},$$

$$Recovery\ rate(RR) = \frac{recovery\ at\ day\ (x)}{cases\ at\ day\ (X-T)},$$

$$CER_{av} = \frac{1}{period\ lendth\ (days)} \sum_{first\ day\ in\ period}^{last\ day\ in\ period} CER,$$

$$RR_{av} = \frac{1}{period\ lendth\ (days)} \sum_{first\ day\ in\ period}^{last\ day\ in\ period} RR,$$

$$\alpha = CER_{av} + RR_{av}. \tag{15}$$

Parameters such as the transmission rate (β), natural death rate (f), birth rate (b), and others are estimated using real-time data provided by platforms like Our World in Data.

The SEIRD model offers a general approach to modeling diseases such as COVID-19, which immensely improves on the traditional SIR model by introducing the compartments known as Exposed (E) and Dead (D). This upgrade allows the simulation to include details about the infection process, the period of latency before one is infectious, as well as mortality, and this is vital for an accurate depiction of the complexities and dynamics of the disease. The Dead Compartment is a crucial component in considering models for calculating the death rate and as such, it plays a great deal of utility in planning and intervening in matters to do with public health.

The SEIRD model also accounts for the natural birth and death rates, thus enhancing its validity yet also enabling long-term studies of disease dynamics in fluctuating populations. And with the aforementioned considerations in SEIRD modeling, one can, thus, ascertain any possible pathways of diseases and estimate the effectiveness of different control measures to assist policymakers and health leaders in thinking through efforts in management and mitigation of outbreak situations. The SEIRD model provides an intensive and sophisticated instrument for modeling diseases such as COVID-19, eventually proving to be an adept way to channel through the complex dry flows between the Exposed compartment and the Dead compartment. The model provides a representation of the length of time individuals are infected before they are considered capable of infecting others while at the same time modeling mortality, which enables a realistic model to explore the epidemiological impacts on public health. The SEIRD model, therefore, finds its use in a real-world representation of complex disease dynamics such as the durations between infection and symptom onset, thereby enhancing realism with its long-term modeling since natural birth and death rates are also observed [20].

Most importantly, it combines a Dead compartment to capture fatality rates, which are critical in planning effective healthcare and public health interventions. This model requires the basic reproduction number R_0: so-called because of its role in the epidemiology of the infectious disease, expressed by the basic reproduction number as R_0 = e (k/α), where α is the recovery or death rate, while k is the effective contact rate and useful for understanding and slowing down the transmission process of any diseases. Most importantly, a Dead compartment is included to gauge fatality rates, which are vital for effective health planning and public health interventions. For this model, R0 is selected, describing the basic reproduction number since it is widely used during the epidemiology course of infectious diseases and expressed by R0=e(k/a), where a is the recovery or death rate and k is the effective contact rate, which serves as building blocks for modern models describing the transfer of any disease. This measure estimates the probability of disease delivery from one human to another and plays an integral role in ensuring that control measures keep it from becoming epidemic. All necessary computations are entirely performed in Python/Google Colab, where Python is selected for the need of its robust availability for data analysis presentation and modeling while giving rise to different numerical libraries, and by Google Colab to run computations using an Internet browser. The combination allows the conduct of several simulations and data handling efficiently without missing other important functions needed for testing and developing new numerical methods such as the hybrid method used in this study. In this study, the hybrid method is adaptive and is enhanced by traditional numerical techniques to handle the SEIRD model's complexities with truth, stability, and efficiency of the simulations, as this is critical for the design of public health plans and collective decisions consisting of responses or mitigations during pandemics.

The SSH-(SEIRD specific hybrid) Numerical Method

Traditional numerical methods each come with significant limitations when applied to the SEIRD model. Euler's method is too inaccurate and unstable for epidemic simulations, while RK4, though more accurate, demands excessive computations per step. RK45 improves adaptability but is computationally expensive due to its error control mechanisms. Pretty much between these two sides where implicit methods like Backward Euler would never hesitate in providing stability for stiff systems is simply much too inefficient for large-scale epidemic modeling. Such types of problems require something more desirable, that is, an optimized numerical method that strikes a balance between efficiency and stability. The SSH method is a compilation of numerical techniques for this optimization of large SEIRD simulations. The model thus applies in this moment Explicit Euler S and E, devoting high speed computations, while for the I, Predictor-Corrector scheme increases the accuracy and stability of the predications. For preservation of long-term numerical stability, Semi-Implicit update adopted for R and D is being complemented with Adaptive Time

Stepping to safeguard overall balance and bring on dynamic approach towards step sizes according to infection dynamics vis`-a`-vis efficiency and precision. Differential across the various numerical methods contained in the SEIRD model equations-one quite important-depend on the capacity for partitioning of compartments so that they operate quite differently and require specific treatments to ensure accuracy and efficiency in terms of computations. Time and thus usually much slower progress with S and D can be aptly reduced to a highly well-timed yet simply and accelerated-stylized Explicit Euler; However, the Infected compartment I is extremely sensitive, with quick oscillations that can lead to numerical instabilities; hence, a Predictor-Corrector approach should be applied to ameliorate accuracy and prevent oscillations. Furthermore, Recovered and Deceased compartments accumulate slowly and work quite well with Semi-Implicit updates because they allow a degree of numerical stability over the long term with a modest increase in computations. Also, Adaptive Time-Stepping is used to allow the step size to follow infection dynamics, providing a finer resolution during rapid changes and allowing for computational efficiency when the system stabilizes. The allocation of numerical methods in this way allows the SEIRD model to be run fast, stable, and very accurate in simulating epidemics.

Explicit Euler for Susceptible (S) and Died (D)

$$S_{n+1} = S_n - \Delta t\big(\beta S_{n+1} I_{n+1} + S_{n+1} f + S_{n+1}\nu\big) + \Delta t\big(\xi R_{n+1} + Nb\big), \quad (16)$$

$$D_{n+1} = D_n + \Delta t \alpha\big(\mu I_{n+1}\big). \quad (17)$$

Predictor-Corrector for Infected (I) and Exposed (E)

$$I_{n+1}^{pred} = I_n + \Delta t\big(-\big(I_n f + \alpha I_n\big) + \sigma E_n\big), \quad (18)$$

$$I_{n+1} = I_n + \frac{\Delta t}{2}\big(-\big(I_n f + \alpha I_n\big) + \sigma E_n\big) + \frac{\Delta t}{2}\Big(-\big(I_{n+1}^{pred} f + \alpha I_{n+1}^{pred}\big) + \sigma E_{n+1}\Big), \quad (19)$$

$$E_{n+1}^{pred} = E_n + \Delta t\big[-\big(\, E_n f + \sigma E_n\big) + \big(\beta S_n I_n + \eta R_n\big)\big], \quad (20)$$

$$E_{n+1} = E_n + \frac{\Delta t}{2}\Big(-\big(\, E_n f + \sigma E_n\big) + \big(\beta S_n I_n + \eta R_n\big)\Big) + \quad (21)$$

$$+ \frac{\Delta t}{2}\Big(-\Big(\, E_{n+1}^{pred} f + \sigma E_{n+1}^{pred}\Big) + \big(\beta S_n I_n + \eta R_n\big)\Big).$$

Semi-Implicit Updates for Recovered (R)

$$R_{n+1} = R_n - \Delta t\big(R_n f + R_n \xi + \eta R_n\big) + \Delta t\big(\alpha(1-\mu) I_n + S_n \nu\big)\big). \quad (22)$$

Adaptive Time Stepping Rule

Significant variations in epidemic dynamics over an extended time frame clearly demarcate the inception and development of the SSH-Method through the regulation of the rate of epochs dynamically as a function of the variation in the course of infections.

$$\Delta t_{new} = \Delta t \times \\ \times \max\left(0{,}5, \min\left(1{,}5, \frac{1}{1+\left|\frac{dI}{dt}\right|}\right)\right). \quad (23)$$

The dynamic and active nature of the infection compartment (dI/dt) makes its rate of change the primary variable that underpins adaptive time-stepping.

If $| dI/dt |$ is large, Δt decreases to improve accuracy.

If $| dI/dt |$ is small, Δt increases to speed up computation.

Adaptive Time-Stepping allows for more efficient computation by using small time steps when infections are rapidly changing and more efficient coercive computational effort when the area is stable.

Results and their discussion

The course of infection dynamics throughout the COVID-19 pandemic has gone into a series of waves due to varying government responses, public health strategies, and vaccine introductions. In turn, the case levels jumped almost straight up in the first few days of the pandemic, leading to the implementation of strict lockdown measures in the major cities of Moscow and St. Petersburg. were especially hard hit. After the summer of 2020, improved statistics came as the result of tighter quarantines and increased testing. The second wave during late 2020 spurred a drastic surge in caseloads where the measures imposed by the regional authorities were based on local conditions. The introduction of the Sputnik V vaccine in late December 2020 gradually saw a reduction in the cases that took advantage of extended holiday breaks as well as social distancing.

The rise of the Delta variant by the center of 2021 saw another boom of cases, aggravated by a slow vaccination-willing and with phasing-out of restrictions. Yet, much toward the end of summer, several intensified vaccination drives lumped together with reinstating certain measures brought infection rates down. The other remaining parts of late 2021 into early 2022 saw the emergence of other very dramatic shifts with the spread of the Omicron variant as well as others further challenging ongoing response efforts. However, targeted lockdowns and continued vaccination campaigns effectively managed these surges.

Throughout 2022 and into 2023, Russia faced additional challenges from new variants and waves, managing these through sustained vaccination efforts, including booster shots, and adherence to health guidelines. The country's response has adapted over time, with a continued focus on managing the pandemic's impact through a combination of health measures and vaccination strategies.

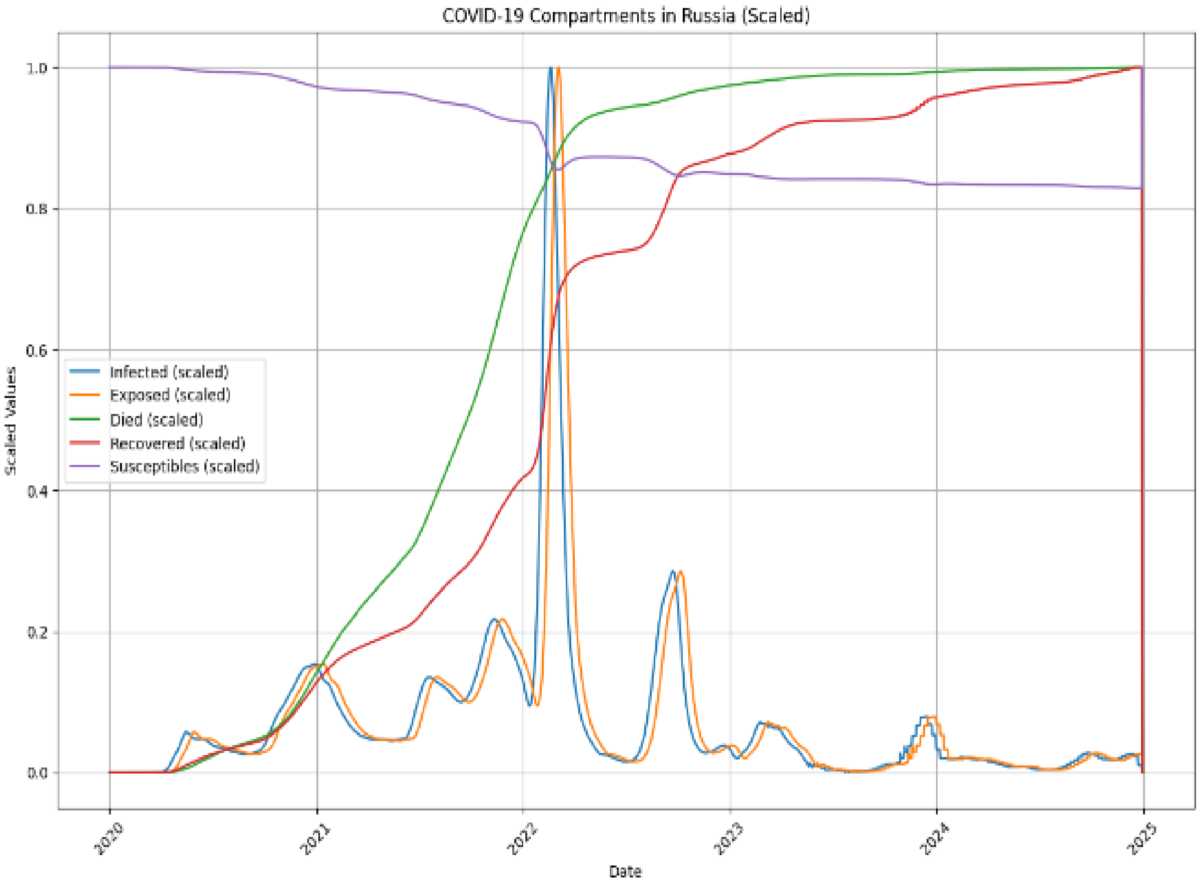


Fig. 1. Real data of SEIRD compartments (would in data site)

We split the pandemic into 8 main waves according to number of infected individuals ,and we calculated alpha and beta for each period, it is indicated in table 1.

Table 1. Values of Alpha and Beta for Eight Time Periods in the Russian Federation

Start of Period	3/12/20	8/30/20	6/5/21	9/16/21	1/12/22	7/18/22	11/15/22	1/11/23
α	2.2708	0.3360	0.5151	0.3384	0.4491	0.6217	0.9053	0.7967
β	2.3860	0.3591	0.5460	0.3608	0.5426	0.6874	0.9199	0.8309

We compared the real time data with the predicted individual used = g тьSEIRD model and the result is shown in figure 2, we used Euler and RK numerical methods.

At last, we used our hybrid novel numerical method SHH versus, Euler, RK4, adaptive RK45, and backward Euler, the result shown in figure 3.

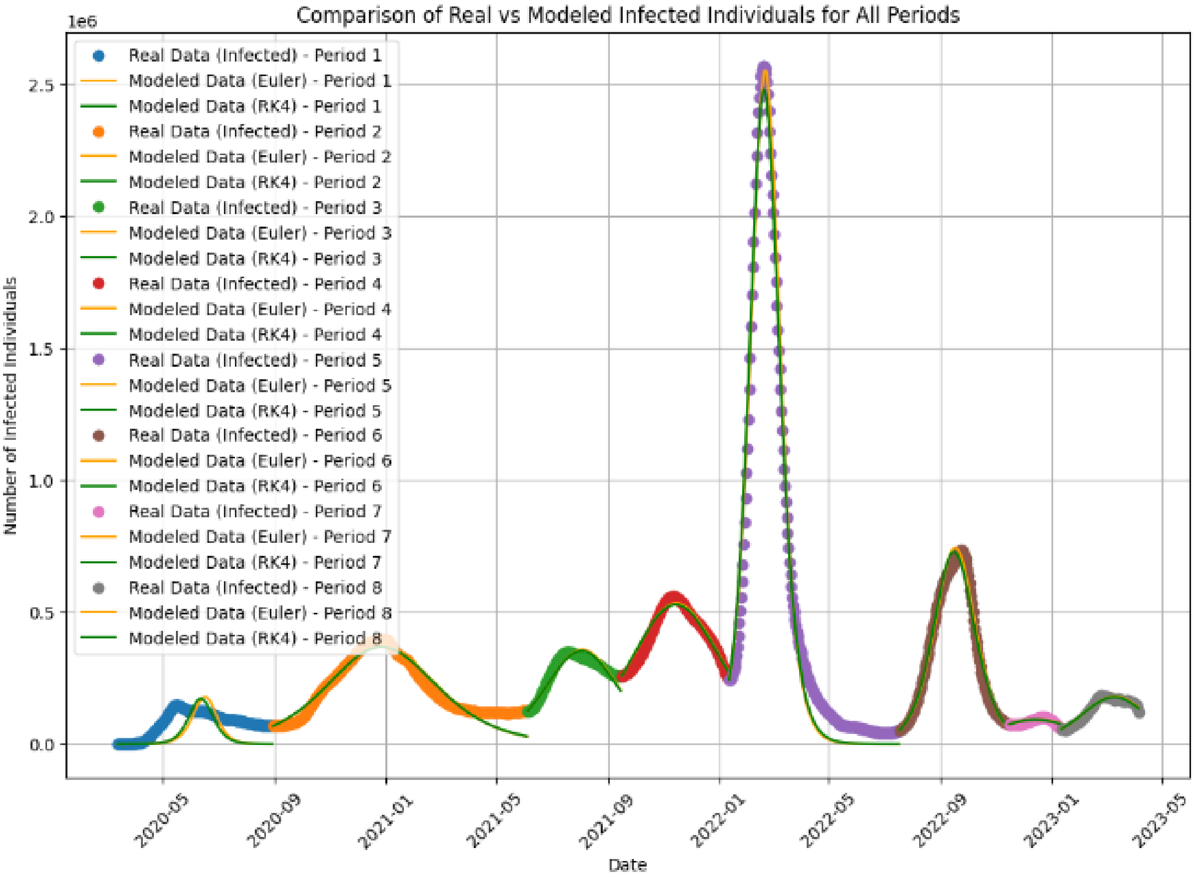
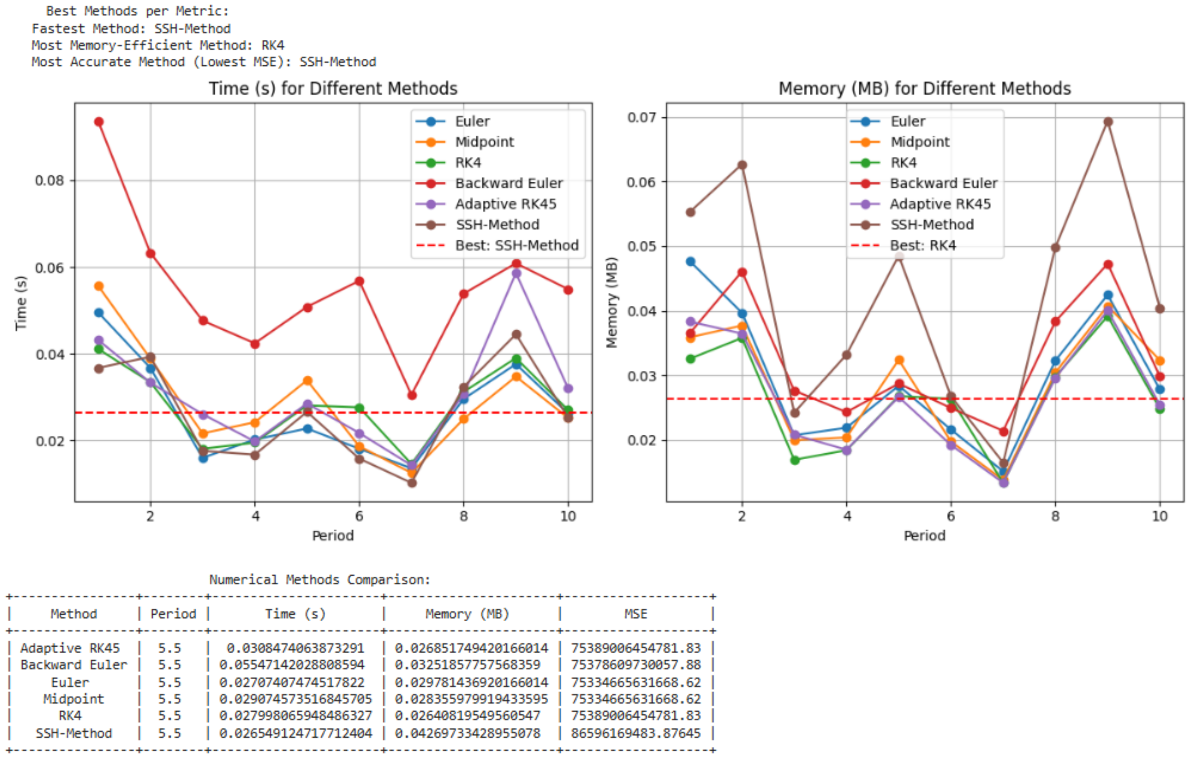


Fig. 2. modeling SEIRD fir compartment for the pandemic periods



```
  Best Methods per Metric:
Fastest Method: SSH-Method
Most Memory-Efficient Method: RK4
Most Accurate Method (Lowest MSE): SSH-Method
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                      Numerical Methods Comparison:
+----------------+--------+---------------------+---------------------+------------------+
|     Method     | Period |      Time (s)       |     Memory (MB)     |       MSE        |
+----------------+--------+---------------------+---------------------+------------------+
|  Adaptive RK45 |  5.5   |  0.0308474063873291 | 0.02685174942016014 | 75389006454781.83 |
| Backward Euler |  5.5   | 0.05547142028808594 | 0.03251857757568359 | 75378609730057.88 |
|     Euler      |  5.5   | 0.02707407474517822 | 0.02978143692016014 | 75334665631668.62 |
|    Midpoint    |  5.5   | 0.029074573516845705 | 0.02835597991943359 | 75334665631668.62 |
|      RK4       |  5.5   | 0.027998065948486327 | 0.02640819549560547 | 75389006454781.83 |
|   SSH-Method   |  5.5   | 0.026549124717712404 | 0.04269733428955078 | 86596169483.87645 |
+----------------+--------+---------------------+---------------------+------------------+
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Fig. 3. A comparison between our proposed numerical method and existing methods

The study utilized the SEIRD model to simulate the spread of the pandemic and applied five numerical methods, including the newly proposed SSH method. The SSH method proved to be the best overall, primarily because it strategically uses different numerical approaches for various components of the SEIRD model. This hybrid approach allows it to more effectively balance speed, accuracy, and memory efficiency compared to traditional methods.

In terms of execution speed, the SSH method significantly outperformed other methods thanks to adaptive time step selection and specific numerical strategies for individual components. With the explicit Euler method used for the Susceptible (S) and Dead (D) compartments, it is the fastest way of solving the problem where large-scale stability is not an issue; meanwhile, using others would enhance stability with a modest computation overhead concerning the classical RK4 higher-order methods for the Infected (I) and the Exposed (E) compartments. In terms of memory efficiency, the RK4 found itself optimally so. It executes an equivalent number of function calls per step, thus allowing direct access to memory in substantial amounts for large computations. Differently from it, the SSH was the most memory-consuming method; this was due to the need for additional memories to store intermediate values and corrections. The predictor-corrector formulation for the Infected (I) introduces additional computational steps, increasing memory usage.

The SSH emerges as the optimum numerical solver for high accuracy, recording the lowest Mean Squared Error (MSE). This can be attributed to its adaptive refinement that avoids gross numerical errors, thus being able to deal with changing periods of infections much more accurately. The predictor-corrector scheme for I, by preventing error accumulation, and semi-implicit updates for R and D, already luggage long-term stability. With this in mind, computed solutions could remain sufficiently close to real data.

The results are clearly showing the SSH method as the high one in the solution, providing a good trade-off between computation efficiency, memory efficiency, and numerical accuracy. The SSH is, however, a blend of various models such that each solution finds one basis at that point, contrary to those models that generally apply the same single numerical scheme. Whereas in memory effectiveness, RK4 surfaces best among the rest, the SSH duly provides the fastest computation time and high accuracy, making it quite practical in numerical modeling for the SEIRD models.

Conclusions

The SEIRD model successfully captured a revealing trend in the disease-spread behavior. The model mimics several epidemiological dynamics. The new numerical techniques unsustainably supported the efficacious solution of the model while engaging other inherent complexities of epidemiological modeling. These methods, particularly the hybrid SSH method, increased both computational speed and accuracy, greatly enhancing the reliability of the model. Overall, this combination of advanced numerical techniques with the SEIRD model holds significant importance for the formulation and planning of a public health response. This study stresses, therefore, the importance of post-school tailor-made and specialized numerical techniques for improvement in the predictive capabilities of the epidemiological models.

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