Journal homepage: https://itce.com.ua/en

Information Technologies and Computer Engineering **Vol. 22, No. 2. 2025**

Article's History: Received: 31.03.2025 Revised: 08.07.2025 Accepted: 28.08.2025

UDC 519.876:614.4 DOI: 10.31649/vitce/2.2025.118

Modelling the impact of adaptive quarantine restrictions on the dynamics of the epidemic process

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Abstract. The relevance of the study arises from the need to develop effective strategies for epidemic management under conditions of limited resources. This study aimed to assess the effectiveness of adaptive quarantine restrictions in curbing the spread of COVID-19 and in shaping approaches to managing epidemic processes. To achieve the aim, mathematical modelling was employed to simulate the epidemic dynamics under different scenarios of quarantine measures. The study analysed the impact of the adaptive quarantine introduced in Ukraine, which divided regions into four zones – green, yellow, orange, and red – depending on the epidemiological situation, ranging from minimal restrictions to the complete suspension of public institutions. The modelling results demonstrated that adaptive quarantine measures can reduce overall morbidity by 35%-50%, shorten the duration of peak phases by 20%-30%, and decrease the burden on the healthcare system. The territorial segmentation by epidemiological risk level contributed to optimising the socio-economic consequences of quarantine measures, allowing economic activity to be maintained in regions with more favourable epidemiological conditions. The study confirmed that adaptive quarantine is an effective tool for controlling the spread of infection, ensuring a balance between public health needs and the minimisation of economic losses. This approach is recommended for adoption in other countries facing similar challenges, as it enables effective epidemic management under resource constraints while reducing adverse impacts on society and the economy. The findings thus have practical significance for shaping health policy during epidemic periods. Mathematical modelling can serve as a basis for forecasting the development of morbidity and for making prompt decisions on the tightening or relaxation of quarantine restrictions. The use of an adaptive approach makes it possible to account for regional features of the epidemic process, thereby enhancing the flexibility and effectiveness of management. This renders adaptive quarantine a universal instrument capable of reducing both medical and socio-economic losses during epidemics

Keywords: SARS-CoV-2 virus; communication system; socio-economic impact of restrictions; infection dynamics; isolation of infected individuals; COVID-19 transmission dynamics; SIRV model

Introduction

The COVID-19 pandemic, caused by the SARS-CoV-2 virus, became a global crisis that profoundly affected all spheres of life – economy, social relations, healthcare, education, and even political processes. The pandemic compelled governments worldwide to adapt rapidly to new challenges, particularly through the introduction of quarantine measures. One of the key strategies for managing the epidemic process was the implementation of adaptive quarantine restrictions, which allowed for the consideration of local conditions and more effective containment of the virus. Mathematical modelling of epidemic dynamics played a significant role in shaping strategies to counter the pandemic.

M.S. Aronna *et al.* (2021) developed a model to describe the spread of SARS-CoV-2 within a susceptible population. Their model incorporated several characteristics of the pathogen and its transmission among susceptible groups. It enabled in-depth analysis of the course of the SARS-CoV-2 epidemic, assessment of the effectiveness of different interventions (such as quarantine, social distancing, and mobility restrictions), forecasting of outcomes resulting from changes in population

Suggested Citation:
Havrylchyk, L. (2025). Modelling the impact of adaptive quarantine restrictions on the dynamics of the epidemic process. *Information Technologies and Computer Engineering*, 22(2), 118-131. doi: 10.31649/vitce/2.2025.118

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behaviour or in the nature of viral transmission, identification of critical thresholds for the introduction or reinforcement of restrictions, evaluation of the potential impact of vaccination, and scenario-based modelling to support decision-making in healthcare policy.

The adaptive approach became an important instrument in combating the pandemic, as it enabled a balance to be maintained between the need to protect public health and to mitigate the socio-economic impact of restrictions. L. Horstmeyer *et al.* (2022), M. Gosak *et al.* (2021), and A.D. Susanto *et al*. (2021) examined the relative importance of two key measures for controlling the spread of the epidemic: endogenous social self-distancing and exogenous imposed quarantine. Endogenous social self-distancing arises as a behavioural response of the population to an increase in the number of infections, while exogenous imposed quarantine results from external administrative decisions. Modelling demonstrated that the combination of both measures is critical for effective epidemic control, as it reduces peak burdens on the healthcare system and ensures a more sustainable decline in infection rates.

D. Azis *et al.* (2023) and A. Moujahid & F. Vadillo (2021) employed the SIRV (Susceptible-Infected-Recovered-Vaccinated) model to analyse the spread of COVID-19. Their findings indicated that the introduction of vaccination substantially decreases the number of susceptible individuals, which in turn slows the transmission of infection within the population. The model identified two equilibrium points: a disease-free state, where no new infections occur, and an endemic state, where infection levels stabilise despite the continued presence of the virus. Stability analysis revealed that vaccination contributes to maintaining infection at a low level, provided that vaccination coverage is sufficiently high. The accuracy of the model, validated against real-world data with a mean absolute relative error of 2.8%, confirmed its effectiveness in forecasting epidemic dynamics and underscored the significance of vaccination as a powerful instrument for controlling the spread of COVID-19. The use of adaptive network structures, moment closure, and ordinary differential equations was necessary to overcome the limitations of classical Susceptible-Infected-Recovered (SIR) models, which assume a fixed contact structure between individuals.

Incorporating changes in social behaviour and the dynamics of human interactions into epidemiological models is crucial for developing effective strategies to respond to a pandemic. Based on such approaches, and in view of the rapid spread of infection, the Ukrainian government introduced strict nationwide restrictions during the early stages of the pandemic to reduce social contacts and curb morbidity. These measures included border closures, suspension of international and domestic air travel, restrictions on public transport, closure of educational institutions, and the transition to remote learning. However, these measures had a considerable negative impact on the economy, which necessitated a revision of the pandemic response strategy. O. Canuto (2020) examined the impact of the infection on the global economy and likewise highlighted its substantial adverse effects on all spheres of life. The author analysed how the COVID-19 pandemic triggered a severe global economic shock comparable to the Great Depression. It was found that the primary losses were driven not only by the direct effects of the virus but also by disruptions to global supply chains, declines in consumer demand, and reduced investment, all of which call for long-term structural adaptation of economic policy.

In June 2020, an adaptive quarantine was introduced, based on a differentiated approach to regions according to the epidemiological situation. This system comprised four levels of restrictions – green, yellow, orange, and red – each determined by a set of criteria such as incidence rate, hospital occupancy, testing volume, and the percentage of positive results. Adaptive quarantine enabled the government to respond promptly to changes in the epidemiological situation while minimising negative effects on the economy. For example, regions with low incidence rates were subject to less stringent restrictions, whereas areas with high morbidity faced stricter measures. This approach provided flexibility and allowed for more effective control of viral spread. At the same time, the implementation of adaptive quarantine was accompanied by numerous challenges, including insufficient testing capacity, low vaccination coverage, and an inadequate communication system between authorities and the population (Ministry of Health of Ukraine, 2021).

This research aimed to analyse a mathematical model describing the impact of adaptive quarantine restrictions on the dynamics of infectious disease transmission, particularly COVID-19, taking into account epidemiological parameters, socio-economic factors, and population mobility. The objectives of the study included examining different scenarios of quarantine measures through mathematical modelling, assessing their effects on morbidity, pressure on the healthcare system, and socio-economic outcomes. The key challenge lay in identifying the optimal balance between the severity of quarantine measures and their economic and social consequences, while also considering regional specificities of the epidemic process.

Materials and Methods

In the course of the study, mathematical modelling was carried out to examine the impact of adaptive quarantine measures on the dynamics of COVID-19 transmission in Rivne Region. The SIR model was adopted as the basis, as it has proven to be an effective tool for modelling the dynamics of infectious diseases. The model divides the population into three main groups: susceptible (S), infected (I), and recovered or otherwise removed from the epidemic process (R). Susceptible individuals were at risk of infection through contact with infected individuals, while infected persons transmitted the virus until recovery or death. The model was described by a system of differential equations that allowed changes in the number of individuals in each group to be tracked over time. The main parameters were the infection rate (β) and the recovery rate (γ), and the dynamics were based on the assumption that the total population size remained constant.

The basic model equation takes the form:

$$N = S(t) + I_{wait}(t) + I(t) + R(t) + Q(t), \tag{1}$$

where N is the total population; $S(t)$ is the number of susceptible individuals; $I_{wait}(t)$ is the number of infected individuals in the delay period; $I(t)$ is the number of infected individuals; $R(t)$ is the number of recovered individuals; and $Q(t)$ is the number of individuals in quarantine.

The dynamics of disease spread are described by the system of differential equations (2-6):

$$\frac{dS}{dt} = -\beta \frac{S(I+I_{wait})}{N}; \tag{2}$$

$$\frac{dI_{wait}}{dt} = \beta \frac{S(I+I_{wait})}{N} - \frac{I_{wait}}{d} - \gamma I_{wait}; \tag{3}$$

$$\frac{dI}{dt} = \frac{I_{wait}}{d} - \gamma I - \alpha(t)(1-\rho)I; \tag{4}$$

$$\frac{dQ}{dt} = \alpha(t)(1-\rho)I - \gamma Q; \tag{5}$$

$$\frac{dR}{dt} = \gamma(I_{wait} + I + Q); \tag{6}$$

where β is the transmission rate; γ is the recovery rate; d is the quarantine delay duration; ρ is the proportion of asymptomatic cases; and $\alpha(t)$ is the quarantine coefficient.

A distinctive feature of this model is the introduction of an additional group, I_{wait}, which at first glance appears similar to the E (exposed) group found in the SEIR model. However, these groups differ fundamentally in their interpretation and function. In the SEIR model, the E group represents individuals in the latent stage of the disease who are already infected but not yet capable of transmitting the infection further. By contrast, I_{wait} describes infected individuals who are already spreading the infection but have not yet moved to the I (infected) group due to delays in isolation.

The key distinction lies in the fact that individuals in the E group cannot transmit the infection, whereas those in I_{wait} actively participate in its spread. Moreover, the transition from $E \rightarrow I$ is determined by biological factors, such as the incubation period, while the transition from $I_{wait} \rightarrow I$ is influenced by organisational factors – namely, the delay before isolation due to the absence of symptoms. For the modelling itself, a modified SIR-type epidemiological model was used, which accounted for regional epidemiological conditions, levels of social contact, and the effectiveness of quarantine measures (Fig. 1).

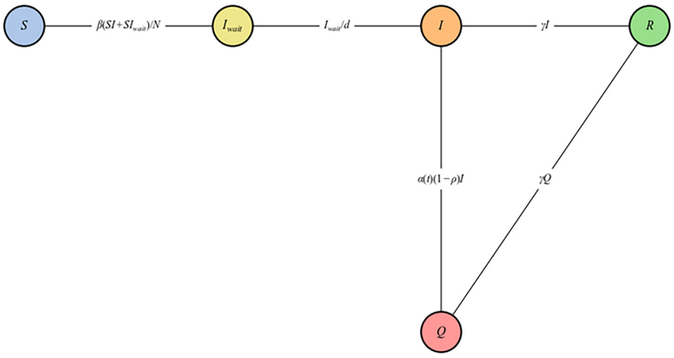

Figure 1. General scheme of the modified SIR model

Source: compiled by the author

The quarantine coefficient $\alpha(t)$ varies depending on the introduction of quarantine measures:

$$\alpha(t) = \begin{cases} 0, t < t_{start} \\ \alpha_i, t \geq t_{start} \end{cases}, \tag{7}$$

where t_{start} is the time when quarantine restrictions are introduced, and α_i denotes the intensity of quarantine measures.

The initial conditions for the model are defined as follows:

$$S(0) = S_0 > 0, I_{wait}(0) = I_{wait_0} > 0, I(0) = I_0 > 0, R(0) = 0, Q(0) = 0. \tag{8}$$

This system of equations allows for the modelling of the impact of adaptive quarantine measures of varying intensity on the dynamics of the epidemic process and enables assessment of their effectiveness. The model parameters have clear epidemiological and social interpretations. The infection transmission coefficient β reflects the rate of disease spread and is defined as the product of the probability of infection per contact and the average number of contacts (in this case, 0.02 and 10, respectively). The recovery rate is calculated as the reciprocal of the average duration of illness, which is assumed to be 10 days, giving $\gamma = 0.1$. Particular attention should be paid to the quarantine coefficient $\alpha(t)$, which reflects the effectiveness of restrictive measures. Its theoretical value may range from 0, corresponding to the complete absence of restrictions, to 1, indicating full isolation. However, under real-world conditions, owing to the practical impossibility of absolute isolation, the maximum values of $\alpha(t)$ rarely exceed 0.7-0.8. The proportion of asymptomatic cases, ρ, was set at 0.2 on the basis of epidemiological observations, consistent with global statistics.

When interpreting the modelling results, it is necessary to take into account certain limitations of the proposed approach. The model treats the population as a homogeneous group, disregarding age and social differences that may significantly influence the dynamics of infection spread. It also does not consider the possibility of reinfection, which may become an important factor during a prolonged epidemic. Another major simplification is the assumption that quarantine measures have the same effect on the entire population, although in reality their effectiveness can vary considerably across social groups. Furthermore, the model does not account for the spatial spread of infection between regions or the seasonality of the disease, both of which may be particularly relevant for long-term forecasting. Despite these limitations, the model remains an effective tool for analysing the impact of quarantine measures on epidemic dynamics and for assessing their effectiveness.

The model was visualised using graphs illustrating the dynamics of the "susceptible – infected – recovered" groups over time. This was implemented in the Python programming language with the matplotlib library. Models were constructed for three main scenarios of quarantine measures: minimal, moderate, and maximum restrictions. For each scenario, the impact of measures on key epidemiological parameters was assessed, including morbidity rate, epidemic peak, pressure on the healthcare system (number of infected individuals requiring hospitalisation), and the number of individuals in isolation.

In addition, results from the adaptive model were compared with two other scenarios – permanent maximum restrictions and historical data. Comparison with real statistical indicators enabled verification of the model at the early stages of the epidemic and the evaluation of discrepancies in forecasts during later phases. The analysis was conducted by superimposing the modelled graphs onto official data for the corresponding periods, which made it possible to establish the degree of consistency and the limits of the model's accuracy. This, in turn, allowed the potential effectiveness of adaptive strategies to be determined in comparison with alternative approaches to quarantine regulation.

The modelling incorporated the average incubation period of the virus, estimated at 6.2 days, with symptoms manifesting in 95% of cases within 12.5 days. The mean duration of infectiousness was set at 10 days, consistent with the recommended quarantine period. The probability of transmission per contact was estimated at 2%, corresponding to a basic reproduction number (R_0) of 1.4-3.9 under normal conditions. Accurate data on the number of individuals in isolation is unavailable, as it is difficult to distinguish between those who remained at home voluntarily and those under official quarantine supervision. For the modelling, official data from the Ministry of Health of Ukraine (n.d.) and archival materials published by Minfin were used. At the onset of the epidemic, Rivne Region had a population of 1,152,400, among whom 11 cases of infection and 1 death were recorded. The absence of precise data on the number of individuals in isolation complicated the assessment of quarantine effectiveness. The modelling was based on the average number of daily contacts per person, which was 13.4 in European countries. In Ukraine, specifically in Rivne Region, this figure was estimated at approximately 10 contacts per day. Vaccination data were also considered, showing a rate of only 0.1% at the time of the study. Hospitalisation was required in 11.2% of cases, while the probability of intensive care was approximately 4.7%. The study also accounted for asymptomatic carriers of the virus, estimated at 20%-40% of all infected individuals.

Results

Mathematical modelling of epidemic dynamics makes it possible to reproduce various scenarios of the pandemic depending on the level of intervention. This section examines how variations in the intensity of quarantine measures – from minimal to strict – affect the number of infected, isolated, and susceptible individuals, as well as the overall trajectory of disease spread. The modelling results highlight the critical role of the timely implementation of restrictions and an effective system for detecting and isolating infected individuals in stabilising the epidemic situation (Fig. 2).

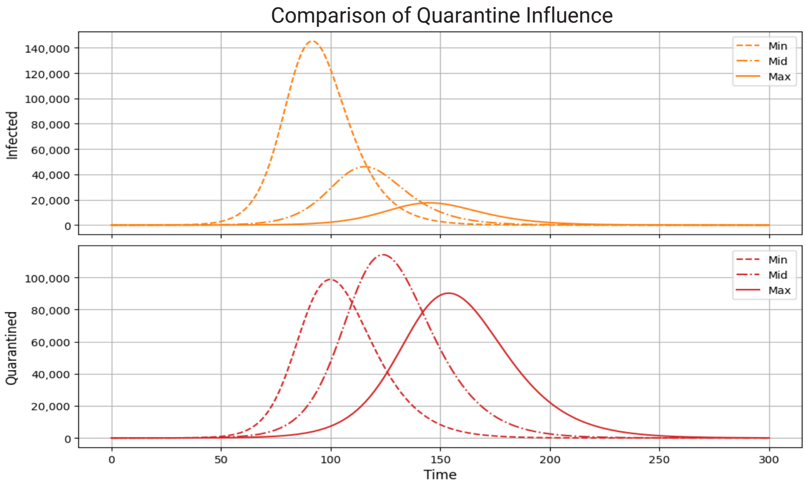

Figure 2. Impact of maximum, moderate, and minimal restrictions on model outcomes

Source: compiled by the author

Analysis of the figure indicates that under a scenario of continuous maximum restrictions, the epidemic develops more slowly but in a more stable manner. The number of susceptible individuals gradually decreases from an initial level of 1.15 million to approximately 450,000, with the most pronounced decline occurring between days 100 and 200. The number of infected individuals remains relatively low throughout the modelling period, peaking at around 20,000 on day 160. The number of recovered individuals rises to about 650,000, while those in quarantine reach a peak of approximately 100,000 on day 175. Monitoring these changes over time allows trends and disease dynamics to be tracked, which is critical for the development of active disease control strategies.

In the case of minimal restrictions – which involved only partial closure of public catering establishments, recommendations for social distancing without strict enforcement, and the absence of mass testing or mandatory isolation of contacts – a sharp increase in the number of infected individuals was observed, peaking at around 140,000 on day 100 of the epidemic. This occurred because these measures were largely ineffective at limiting contacts between groups of potentially infected individuals. Moderate restrictions – which included limits on mass gatherings, partial closure of educational institutions, flexible working arrangements for businesses, enhanced enforcement of social distancing, mandatory mask-wearing in public spaces, and isolation of confirmed cases – helped delay the epidemic peak by approximately 20-25 days (Mossong *et al.,* 2008). In the study, the proportion of individuals in isolation substantially exceeded the number of infected individuals, reaching peak values of over 100,000, while the number of infected individuals reached approximately 45,000. This indicates that measures to isolate infected individuals were significantly more effective than the scenario with minimal restrictions. Under maximum restrictions, the most favourable epidemic containment dynamics were observed. The peak number of infections fell to 15,000 and was delayed by 50 days, allowing the healthcare system more time to prepare. The modelling of the epidemic under a scenario of sustained maximum restrictions is presented in Figure 3.

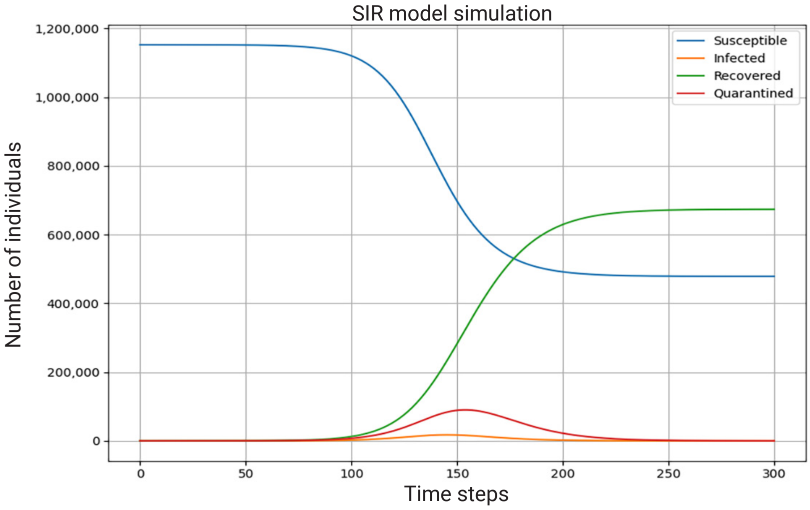

Figure 3. Modelling the impact of strict restrictions on epidemic progression
Source: compiled by the author compiled by the author compiled by the author

Modelling the scenario with strict restrictions involved developing mathematical models that accounted for constraints that were either constant or very stringent. Various factors were considered during the modelling process, including technical, economic, and environmental limitations. In addition, safety regulations defining acceptable boundaries to protect public health were incorporated. Such models are used to inform decision-making, enabling the efficient allocation of available resources while maintaining a balance between economic benefits and adherence to strict public health requirements. The implementation of strict quarantine measures provides a high level of control over the epidemic situation; however, it has a substantial negative impact on the socioeconomic environment. Under these conditions, there arose a need for an alternative model of quarantine restrictions that could achieve an effective balance between controlling the spread of infection and maintaining the functioning of the country's economy. This search led to the adoption of a strategy based on adaptive restrictions (Brinks & Hoyer, 2024). Overall, the dynamics of quarantine measures in Rivne Region were characterised by periodic tightening and easing of restrictions depending on the epidemiological situation and decisions made by central and local authorities. Accordingly, the quarantine coefficient varied in response to the local situation and the measures implemented, as shown in Table 1.

Based on the information above, numerical experiments with the model yielded data reflecting the quarantine aspects of the epidemic. In the illustrated dataset, conditional time points $t = 20$ and $t = 60$, as well as the initial and final simulation times, are presented to demonstrate changes in the model's input data at each time step. Analysis of changes in these indicators over time makes it possible to track the progression of the disease, which is critically important for developing active disease control strategies (Table 2).

Table 1. Dynamics of quarantine measures

Modelling step, day	Quarantine coefficient, *α*
1	0.70
60	0.60
90	0.50
180	0.70
300	0.50

Source: compiled by the author

Table 2. Example of changes in input data in the SIR model

t	S	I	R	Q	β	γ	α
1.00	1,152,400.00	11.00	1.00	0.00	0.2000	0.1000	0.7000
…	…	…	…	…	…	…	…
20.00	1,152,346.32	4.61	24.38	15.25	0.2000	0.1000	0.7000
21.00	1,152,341.11	4.99	26.44	16.35	0.2000	0.1000	0.7000
22.00	1,152,335.47	5.40	28.65	17.57	0.2000	0.1000	0.7000
23.00	1,152,329.38	5.84	31.03	18.89	0.2000	0.1000	0.7000
24.00	1,152,322.78	6.31	33.60	20.33	0.2000	0.1000	0.7000
…	…	…	…	…	…	…	…
60.00	1,150,940.09	106.11	561.50	333.31	0.2000	0.1000	0.6000
61.00	1,150,819.63	121.50	607.21	353.73	0.2000	0.1000	0.6000
62.00	1,150,688.08	135.34	656.65	378.81	0.2000	0.1000	0.6000
63.00	1,150,544.80	148.84	710.16	407.71	0.2000	0.1000	0.6000
64.00	1,150,388.93	162.69	768.09	440.10	0.2000	0.1000	0.6000
…	…	…	…	…	…	…	…
300.00	416,516.82	0.66	735,877.33	13.85	0.2000	0.1000	0.5000

Note: t – time; S – susceptible; I – infected; R – recovered; Q – quarantine; β – transmission rate; γ – recovery rate; α – quarantine coefficient
Source: compiled by the author

Based on the data presented in Table 2, changes in the key indicators within the SIR model were tracked. In particular, the number of susceptible individuals (S) gradually decreased from 1,152,400 at the start to approximately 416,516 by day 300. The number of infected individuals (I) initially rose from 11 to peak values of over 160 between days 60 and 64, before declining sharply to fewer than one individual. The number of recovered individuals (R) increased as expected within the model, reaching 735,877 by the end of the period. The adaptive coefficient α also changed, decreasing from 0.7 to 0.5, indicating the implementation of effective containment measures. This confirms the effectiveness of the adaptive scenario in curbing the epidemic. Figure 4 illustrates the results of modelling the epidemic dynamics under the adaptive scenario.

As shown, in the initial stage (up to day 100), the situation remains relatively stable, with a gradual reduction in the number of susceptible individuals from the initial level of 1.15 million. This corresponds to the period when quarantine measures had not yet reached full effectiveness but had begun to influence the infection dynamics. The most intense phase of the epidemic occurs between days 100 and 200, during which the number of susceptible individuals declines sharply while the number of recovered individuals rises. The peak number of infected individuals is observed around day 150, reaching approximately 40,000. The maximum number of individuals in quarantine is reached on day 160, amounting to approximately 100,000, reflecting the effective functioning of the system for detecting and isolating infected individuals. After day 200, the dynamics enter a stabilisation phase.

The number of susceptible individuals stabilises at around 400,000, while the number of recovered individuals reaches approximately 750,000. The numbers of infected individuals and those in quarantine gradually decline to minimal levels. Modelling indicates that applying an adaptive approach can reduce the overall infection rate by 35%-50% and lower the epidemic peak by 20%-30%, thereby significantly alleviating the burden on the healthcare system.

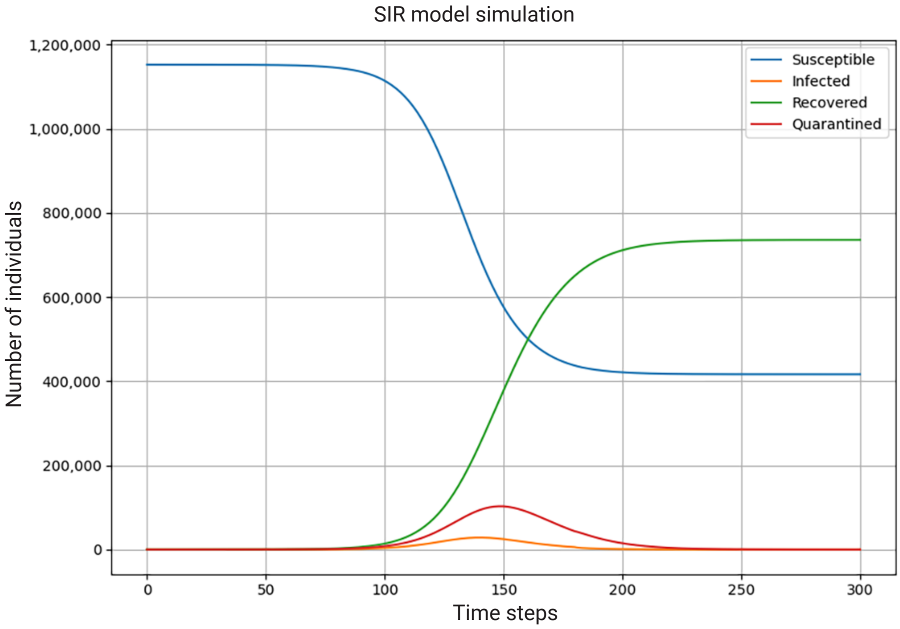

Figure 4. Modelling the impact of adaptive restrictions on epidemic progression

Source: compiled by the author

Overall, the trends observed in the graphs demonstrate the satisfactory effectiveness of the adaptive quarantine approach, which achieves a balance between controlling the epidemic and maintaining socio-economic activity. Compared with sustained strict restrictions, the adaptive approach produces a smoother epidemic trajectory while retaining control over the spread of infection. Compared with more flexible adaptive restrictions – where measures are adjusted according to the current situation – the strict scenario produces a more stable but slower decline in the number of infected individuals. The adaptive approach allows for more responsive adjustments to changing conditions, reducing the negative impact on the economy and social activity. However, it may result in a more uneven distribution of the burden on both the healthcare system and society. In conclusion, it can be stated that strict restrictions provide more stable control over an epidemic; however, their implementation may have significant economic and social consequences compared with adaptive scenarios. The choice between these approaches depends on the priorities in balancing public health with socio-economic activity.

In this context, the approach to selecting and interpreting statistical data in epidemiological modelling is crucial. Specifically, C.N. Ngonghala *et al.* (2021), S. Bekesiene *et al.* (2022), and D. Svoboda *et al.* (2025) emphasised that misinterpreted indicators can create misleading impressions of the situation. They highlighted the importance of a critical approach to analysing statistical data and the need to consider context in their interpretation. For example, they noted that comparing COVID-19 mortality with that of other diseases without accounting for the specific characteristics of each disease can lead to erroneous conclusions. They also stressed that using absolute numbers without relative measures, such as deaths per 100,000 population, can distort the true picture. Furthermore, the authors indicated that changes in data collection methodology or diagnostic criteria can affect statistics, necessitating caution when interpreting such data. Under an adaptive quarantine, where regions transitioned between levels of epidemiological risk based on statistical indicators – such as cases per 100,000 population or hospital occupancy rates – distortions or misinterpretation of data could result in untimely easing or tightening of restrictions. Thus, the critical approach to statistical analysis emphasised by the authors was particularly important for making well-founded decisions within the adaptive quarantine model described in this study, where data accuracy directly affected the effectiveness of epidemic management.

An essential aspect of forecasting the course of the COVID-19 epidemic was assessing the dynamics of population infection. To this end, simulations were conducted for two scenarios – under strict restrictive measures and with the implementation of adaptive quarantine. For model verification, the forecast data were compared with real historical data. Figure 5 presents the dynamics of the number of infected individuals under adaptive quarantine restrictions overlaid on historical data for the number of infections in Rivne Region.

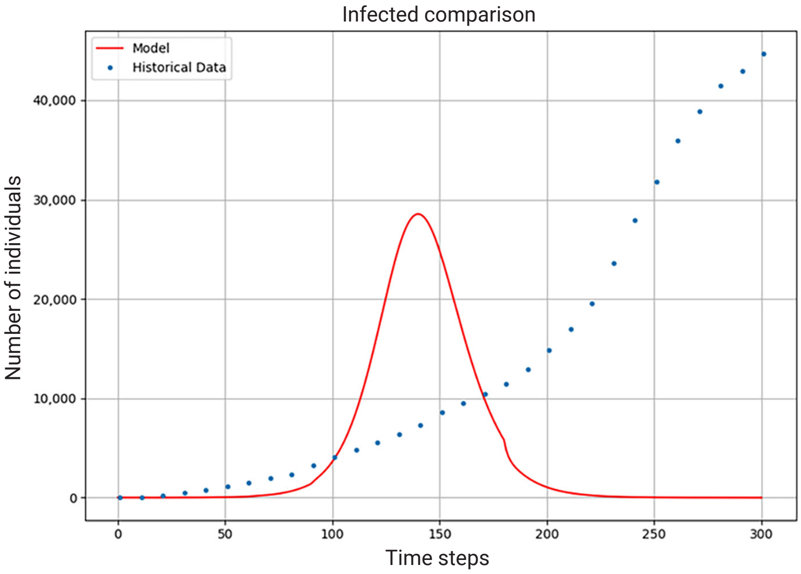

Figure 5. Comparison of population infection dynamics according to the adaptive restriction model and historical data
Source: compiled by the author

As shown in the figure, at the early stages of the epidemic, up to approximately day 100, the model closely reproduces historical data. This is evidenced by the similarity in the growth dynamics of the modelled curve with actual data, indicating the adequacy of the initial model parameters and the correctness of the description of the early epidemic phases. However, after day 100, significant discrepancies emerge between the model forecasts and the real data. According to the model, the epidemic peak was expected around day 150, with a maximum of approximately 28,000 infected individuals, followed by a sharp decline in infection rates. In contrast, real data indicate a continued rise in the number of infected individuals, which exceeded 40,000 by the end of the observation period. This discrepancy may have been caused by several factors, such as changes in public behaviour, the level of compliance with quarantine measures, seasonal influences on infection dynamics, or the model's insufficient consideration of important parameters.

Similar results, when compared with historical data, were observed in the model constructed under the scenario of strict quarantine measures (Fig. 6). It is also noteworthy to compare the dynamics of the graphs from both models. The second model demonstrates that, under constant strict restrictions, both the infection dynamics and the number of infected individuals is substantially lower compared with the adaptive quarantine scenario.

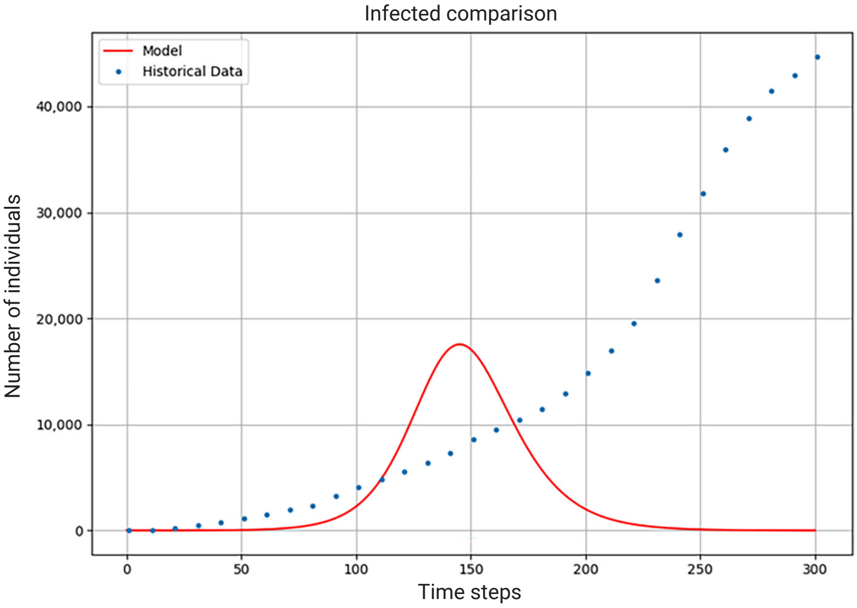

Figure 6. Comparison of population infection dynamics according to the maximum-restriction model and historical data
Source: compiled by the author

As illustrated in Figure 6, the graph reflects the discrepancies between the model forecasts and real data. Compared with the adaptive restriction scenario, the model with maximum restrictions shows a lower epidemic peak but also greater deviations from real data in the latter half of the observation period. The comparison of both models' results indicates that under strict restrictions, the number of infected individuals increased much more slowly and steadily, reflecting effective epidemic control. However, it does not always capture real-world conditions, where numerous variables influence the infection rate. At the same time, the comparison between modelling results and historical data, despite the discrepancies, allows an assessment of the effectiveness of adaptive restrictions – specifically, the extent to which they slowed or reduced the epidemic peak. The historical data on the graph show a more gradual increase in the number of infected individuals than the model predicts. This indicates that the implementation of adaptive measures was beneficial, helping to prevent a complete collapse of the healthcare system. The next aspect of the analysis was a comparison of the number of recovered individuals. Figure 7 presents a comparison between the modelled results and historical data. The graph reveals a significant mismatch between the model forecasts and the official statistics.

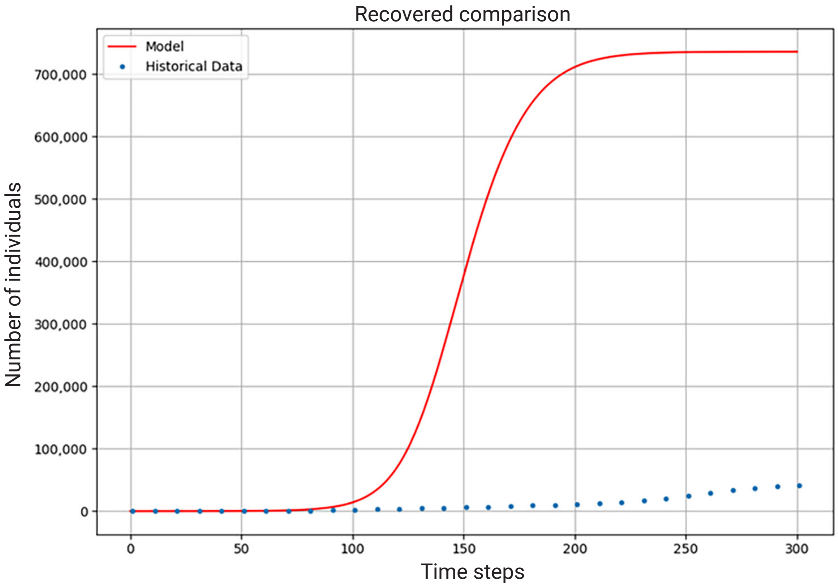

Figure 7. Comparison of population recovery dynamics between the adaptive-restriction model and historical data
Source: compiled by the author

As shown in Figure 7, up to day 100, the modelled results align well with real data, indicating the adequacy of the initial parameters. However, after this point, the discrepancies become substantial. According to the model, the number of recovered individuals reaches approximately 700,000 by day 190 of the observation period, whereas official statistics report around 50,000 recoveries by day 300. This gap may be attributed not only to the model's limitations but also to methodological differences in the collection of statistical data. Official statistics accounted only for laboratory-confirmed cases recorded in the healthcare system, that is, only those instances where patients sought medical attention. At the same time, the actual number of people who contracted and recovered from the disease may have been significantly higher due to factors such as a considerable proportion of asymptomatic cases (up to 20%); mild illness that did not require medical consultation; limited testing capacity, particularly during the early stages of the epidemic; reluctance of some individuals to seek medical care; and difficulties in tracking recoveries due to an overburdened healthcare system. These factors affect the forecasting of recovery numbers, as the system no longer behaves in a stable or linear manner. Under unstable conditions, including changes in the infection rate or the introduction of new quarantine measures, the number of recoveries could either rise sharply or fall abruptly, complicating modelling and necessitating more adaptive and non-standard approaches (Piasecki *et al.,* 2020; Toomey *et al.,* 2021). Thus, the study demonstrates that epidemic dynamics can be highly sensitive to parameter changes, and conventional linear models are unable to capture this variability. This highlights the need for a comprehensive approach to evaluating the epidemic situation, incorporating not only official statistics but also the results of modelling and serological studies.

Comparing the dynamics of infection and recovery in the population between modelled results and historical data was an essential step in assessing the accuracy of the model. Such an analysis allowed not only an assessment of how accurately the model reflected the real situation but also the identification of potential errors in the model's parameters or limitations inherent in the model itself. This made it possible to detect deviations between predicted and actual data, which could indicate insufficient adherence to restrictions, changes in population behaviour, or the influence of unplanned external factors (for example, outbreaks in closed communities). The findings highlight the need for further refinement of the model, incorporating additional factors that affect the epidemic process, in order to improve the accuracy of long-term epidemic forecasts.

Discussion

Modelling the impact of adaptive quarantine measures on the dynamics of an epidemic is an important tool for predicting disease progression and evaluating the effectiveness of control measures. In the context of complex social interactions and variable population behaviour, adaptive models allow for consideration not only of the biological characteristics of infection spread but also of social, behavioural, and network-related factors. Several studies examining different approaches to modelling quarantine strategies and their impact on epidemic dynamics are outlined below.

M. Mancastroppa *et al.* (2020) investigated the effect of two types of quarantine – active and inactive – on epidemic spread within adaptive networks, where individual behaviour changes according to infection status. The researchers found that both strategies share the same epidemic threshold, yet they differ significantly in the dynamics of the active phase: active quarantine is less effective in mitigating the impact of the epidemic compared to inactive quarantine, and within an SIR model, late implementation of measures requires an inactive quarantine to achieve containment. However, unlike the study by M. Mancastroppa *et al.*, this research emphasises the evaluation of quarantine effectiveness within real, unscaled networks without a clear division into active or inactive quarantine. Nonetheless, both approaches converge in their conclusions regarding the critical role of the timing and scale of quarantine implementation, which is a decisive factor in shaping epidemic dynamics.

Similar conclusions were reached by A. Wiraya *et al.* (2024), who examined the dynamics of COVID-19 spread using a mathematical model incorporating catastrophic phenomena and strange attractors via Hopf bifurcations. In contrast, the present model relies on more conventional approaches and focuses on evaluating the impact of various restrictions without accounting for complex nonlinear effects. While this reduces its sensitivity to abrupt changes, it provides stable longterm forecasts relevant for socio-economic planning. Accordingly, the model by A. Wiraya *et al.* is better suited for identifying potential critical points, whereas the model in this study is designed to assess epidemic progression under more stable conditions.

The results of the numerical simulations indicated that the rapid implementation of strict social distancing measures and large-scale testing had a significant effect on containing the spread of COVID-19. The detection and isolation of asymptomatic carriers proved to be particularly critical, as these individuals, unaware of their infection, could serve as sources of new transmissions (Adu *et al.,* 2025). According to the simulations, testing was effective only when conducted regularly and on a large scale, with infected individuals immediately placed into isolation. M.S. Aronna *et al.* (2021) and L. Horstmeyer *et al.* (2022) recommended reducing social activity among high-risk groups for an extended period and emphasised the necessity of maintaining effective restrictive measures until the epidemiological situation stabilised, even if partial relaxation of quarantine measures was possible for other population groups. The findings of this study support these conclusions. In particular, the simulations highlighted that the timely implementation of restrictions, especially when combined with large-scale testing and isolation of asymptomatic carriers, is critical for controlling the epidemic. The scenarios demonstrating the greatest effectiveness were those in which vulnerable population groups remained under prolonged or partial isolation. As in the studies by J. Song *et al*. (2020), the results emphasise that not only the presence of quarantine measures matters, but also their duration, coverage, and specific targeting of the most vulnerable groups.

The impact of the distribution of latent and infectious periods on epidemic dynamics was also investigated in SEIR models that incorporate quarantine and isolation measures. Z. Feng (2007) conducted a detailed analysis of two SEIR model modifications, which differed in the distribution of the durations of the latent (incubation) and infectious periods: one model employed an exponential distribution, while the other used a gamma distribution. The results demonstrated that the gammadistribution model provided more accurate predictions, particularly in situations with significant variability in incubation and infectious periods. This approach allowed for a more realistic representation of the time individuals spent in each epidemiological state. The findings highlighted a complex interplay between the choice of distribution and the effectiveness of epidemic control measures. In cases of low isolation effectiveness – when symptomatic infected individuals were insufficiently isolated – the gamma-distribution model exhibited a higher overall level of infection. For example, when quarantine measures were weak (i.e., only a small proportion of latent carriers were subjected to restrictions), the exponential-distribution model produced a higher peak of infection, as more individuals quickly progressed to the infectious phase, triggering a sharp outbreak. Conversely, under conditions of low isolation effectiveness (i.e., symptomatic infected individuals were not adequately isolated), the gamma-distribution model resulted in a higher total incidence. S. Yang *et al.* (2020) clearly demonstrated that the choice of the mathematical structure of the model significantly affects the assessment of the effectiveness of control measures. The results of this study support these findings, demonstrating that changes in the distribution of latent and infectious periods indeed affect disease dynamics.

H. Kang *et al.* (2017), Z. Du *et al.* (2020), and C. Chen *et al.* (2024) investigated the impact of structural characteristics of scale-free networks on the spread of infectious diseases. The authors developed a mathematical model combining epidemic dynamics with quarantine effectiveness within the context of real social networks. In scale-free social networks, where "hubs" with a high number of social contacts play a central role, transitions between states (susceptible, infected, recovered) can occur more rapidly. The study found that implementing quarantine measures targeting the isolation of the most highly connected individuals can substantially reduce the rate of disease transmission. The results of the present study are fully consistent with these conclusions.

A system for detecting and isolating infected individuals relies on regular large-scale testing to rapidly identify infected persons, including those without apparent symptoms, and on effective contact tracing to determine individuals who may have been exposed. Z. Du *et al.* (2020) concluded that transmission of the virus can occur before the appearance of symptoms in an infected individual. Identified infected individuals are immediately isolated, which may involve quarantine or hospitalisation, to prevent further spread. Continuous monitoring of infected persons and verification of the effectiveness of isolation measures enable timely responses to new cases. The proportion of isolated individuals, which peaks on day 160, indicates the successful implementation of this system, effectively limiting the spread of infection among the population. P. Lehohla (2020) highlights the challenges inherent in all statistical assessments of the pandemic, noting that traditional statistical models – such as regression approaches, time series models, and extrapolation methods – proved insufficient for accurately predicting pandemic development. The continually evolving nature of the virus, incomplete data, and differences in testing approaches between countries complicated the creation of reliable models.

M. Xue *et al.* (2022) proposed a new model for monitoring, analysing, and forecasting official COVID-19 statistics, which demonstrated its effectiveness compared with other models in Romania, Moldova, and the Campania region of Italy. This model combined mathematical methods with machine learning to predict the epidemiological situation accurately. Following initial training, the model underwent further optimisation using stochastic coordinate descent, allowing parameters to be refined for each specific region. The findings of this study align closely with those presented here, as both employ complex models for precise forecasting and analysis of epidemiological or medical situations.

Modelling epidemiological processes remains a crucial tool for understanding the dynamics of infection spread and for developing effective containment strategies. The study demonstrated that even minor changes in parameters – such as the duration of the latent and infectious periods, the structure of social contacts, or the timing of quarantine measures – can significantly influence the course of an epidemic. Such models not only allow for the forecasting of epidemic dynamics under variable conditions but also provide a scientific basis for public health decision-making, which is particularly relevant in the context of growing global threats.

Conclusions

During the research, a modified SIR-type epidemiological model was developed and tested, enabling both qualitative and quantitative assessment of the effectiveness of adaptive quarantine measures on the dynamics of the COVID-19 epidemic in the Rivne Region. Analysis of different scenarios showed that, under minimal restrictions, the number of infected individuals could reach 140,000, whereas the implementation of moderate restrictions reduced this figure to 45,000, and maximum restrictions limited it to 15,000, while simultaneously delaying the epidemic peak by 50 days. Adaptive restrictions proved to be an effective compromise: while maintaining economic activity, the peak number of cases remained around 40,000, allowing for a manageable epidemic situation. Model verification against real-world data showed satisfactory alignment during the first 100 days of the epidemic. Subsequent discrepancies were attributable to factors not accounted for in the model, such as seasonal variations in disease incidence, changes in population behavioural patterns, the possibility of reinfection, and the absence of mitigating factors. The substantial discrepancy between the modelled and recorded numbers of recovered individuals (700,000 versus 50,000) indicated underreporting in official statistics, particularly among asymptomatic cases and those with mild forms of the disease.

It was established that the implementation of an adaptive quarantine reduced infection rates by 35%-50%, delayed the epidemic peak by 20%-30%, and eased the burden on the healthcare system while maintaining socio-economic activity. The adaptive restriction scenario, in which the peak number of infections reached approximately 40,000, proved more effective than minimal measures (up to 140,000 cases) and simultaneously less disruptive than continuous strict restrictions. Model verification against historical data demonstrated good alignment during the early phase of the epidemic; however, discrepancies grew over time due to factors not accounted for in the modelling – specifically, seasonality, changes in population behaviour, and the limitations of testing and official reporting. The model exhibited particular sensitivity to changes in the quarantine coefficient and confirmed the effectiveness of the timely isolation of infected individuals and widespread testing. The results demonstrated that an adaptive approach can achieve a balance between epidemiological effectiveness and economic feasibility and may be recommended for application in similar epidemic situations.

Key directions for future research include: accounting for the impact of vaccination, studying population behavioural patterns, refining the role of social networks in disease transmission, and improving the collection and analysis of statistical data. Limitations of the study include restricted access to accurate data, imperfect testing, variability in quarantine regimes, and the impossibility of fully capturing all social, behavioural, and medical factors within a single model.

Acknowledgements

None.

Funding

The study was not funded.

Conflict of Interest

None.

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Моделювання впливу адаптивних карантинних обмежень на динаміку епідемічного процесу

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Анотація. Актуальність дослідження зумовлена необхідністю розробки ефективних стратегій управління епідеміями в умовах обмежених ресурсів. Метою роботи було оцінити ефективність адаптивних карантинних обмежень у стримуванні поширення COVID-19 та підходів до управління епідемічними процесами. Для досягнення цієї мети використано математичне моделювання динаміки епідемії залежно від різних сценаріїв карантинних заходів. У дослідженні проаналізовано вплив адаптивного карантину, запровадженого в Україні, який передбачав поділ регіонів на чотири зони: зелену, жовту, помаранчеву та червону, залежно від епідеміологічної ситуації, від мінімальних до повної заборони функціонування громадських закладів – залежно від епідеміологічної ситуації. Результати моделювання показали, що адаптивний карантин дозволяє зменшити загальну захворюваність на 35–50 %, скоротити тривалість пікових фаз на 20–30 % та знизити навантаження на систему охорони здоров'я. Сегментація територій за рівнем епідемічного ризику сприяла оптимізації соціально-економічних наслідків карантинних заходів, дозволяючи зберігати економічну активність у регіонах із кращою епідеміологічною ситуацією. Дослідження підтвердило, що адаптивний карантин є ефективним інструментом контролю над поширенням інфекції, забезпечуючи баланс між потребами охорони здоров'я та мінімізацією економічних втрат. Такий підхід рекомендується для використання в інших країнах, що стикаються з подібними викликами, оскільки він дозволяє ефективно управляти епідемією в умовах обмежених ресурсів та мінімізувати негативні наслідки для суспільства та економіки. Таким чином, отримані результати мають прикладне значення для формування політики охорони здоров'я в періоди епідемій. Математичне моделювання може стати основою для прогнозування розвитку захворюваності та прийняття оперативних рішень щодо посилення або пом'якшення карантинних обмежень. Застосування адаптивного підходу дозволяє враховувати регіональні особливості епідемічного процесу, підвищуючи гнучкість та ефективність управління. Це робить адаптивний карантин універсальним інструментом, здатним зменшити як медичні, так і соціально-економічні втрати під час епідемій

Ключові слова: вірус SARS-CoV-2; система комунікації; соціально-економічний вплив обмежень; динаміка інфекції; ізоляція інфікованих; динаміка поширення COVID-19; модель SIR