Vaccination Strategies based on a Mathematical Model of Epidemics Considering the Age Structure of the Population

MACIEJ URBAN[1], JULIA JODŁOWSKA[2], JOANNA BALBUS[3], KRYSTIAN KUBICA[2]
[1]Student's Scientific Group BioModel Department of Biomedical Engineering,
Wroclaw University of Science and Technology,
POLAND

[2]Department of Biomedical Engineering,
Wroclaw University of Science and Technology,
POLAND

[3]Department of Pure and Applied Mathematics,
Wroclaw University of Science and Technology,
POLAND

Abstract: - During the COVID-19 pandemic, it is important to promote the skills needed for analyzing the disease course, including determining the relevance of vaccinations, especially among people who are unfamiliar with computer programming. This paper describes the basic epidemiological model (SIR), its extensions that allow vaccinations, and the emergence of renewed waves of disease growth. It also discusses a literature model, extended SEIRD, which includes a more detailed division of the population into susceptible, latent, symptomatic, and asymptomatic infected, recovered, and dead in eight age groups. Modifying the SEIRD model as shown on the basic SIR model, we analyzed five vaccination strategies, considering the limited vaccine supply, the number of vaccinations performed per day, and their effectiveness. The analysis was performed for a group of one million people, using the parameters of the model characteristic of the COVID-19 pandemic and Sweden's generational structure. We analyzed in terms of reducing both the number of deaths and the incidence of symptomatic infections, which represent the main burden of healthcare.

Key-Words: - SIR, SEIRD, epidemiology, vaccinations, vaccination effectiveness, mathematical model, social contact matrix, COVID-19.

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1 Introduction

The goal of this study is to popularize scientific research on the course of the pandemic. There are various methods for studying the course of the pandemic, including deterministic models such as those based on ordinary differential equations, [1], stochastic models, [2] and statistical models, [3]. We chose to employ the system of ordinary differential equations (ODE). However, it is challenging to solve the majority of mathematical models analytically without making additional assumptions, [4]. Nevertheless, they can be solved numerically. Since this work is dedicated to everyone interested in the subject of pandemic analysis, including those who cannot program on their own, we created and made available a ready-to-use program for this purpose. Instructions for using the program are available at:

https://github.com/BlankTiger/SEIRD_model/releases/download/v1.0.3-rust/Instructions.docx

The basic model of the epidemic (SIR)

The basic model used to study the course of the epidemic is the Kermack–McKendrick model, which is often referred to as the SIR model, [5]. The SIR model contains simplifications that do not allow effective prognosis of disease development in the case of many diseases, but it enables to the creation of more complex models. This model describes the disease development in a closed population of N people divided into groups as susceptible to infection (S), infected (I), and recovered (R). If we want to include deaths due to the studied disease, the number of fatal cases should be added to the group of recovered because they are no longer transmitting the disease. The SIR model generates a system of three ordinary differential equations that describe the

kinetics of changes in the S, I, and R groups. This model is based on the following assumptions:

- The probability of direct contact is the same for each pair of individuals.
- The decrease in the number of susceptible cases (S) depends on their number, the number of infected (I), and the coefficient describing the infection rate (here β).
- The change in the number of infected people (I) depends on two terms: the one describing increasing I, which is proportional to S, I, and β; and the one describing decreasing I, which is proportional to I and coefficient recovery rate (here γ).
- The increase in recovered (R) and dead due to infection is proportional to the number of infected I and coefficient γ.
- The incubation period is negligibly short, so immediately after the infection the susceptible person becomes infected and can infect others, which makes it difficult to realistically assess the disease variability over time.

In line with these assumptions, the SIR model can be written as Equations 1–3:

$$S/dt=-\beta SI \quad (1)$$

$$dI/dt=\beta SI-\gamma I \quad (2)$$

$$dR/dt=\gamma I \quad (3)$$

To solve these equations, we have to assume the initial conditions. Most often, they meet the condition S + I = N, which means that there are no people in the R group at the beginning. Since this model should be able to predict the development of the disease, it is worth assuming that at the initial moment t0 the given population already had a small group of infected people, I(t0) > 0. Since the SIR model cannot be solved analytically (although the modified SIR model is analytically solvable), [4], it can be easily solved numerically, yielding time dependencies in the S, I, and R groups.

To solve the SIR equations, it is also necessary to assign values to parameters β and γ. If we consider one day as the unit of time, then parameter γ, which is the rate of healing, can be defined as the reciprocal of the recovery time for an individual patient's infection. According to Equation 3, the values of γ are expressed in day^{-1} units. On the other hand, the value of parameter β will be expressed in units day^{-1} * number of $people^{-1}$ (based on Equation 1). The appropriate value of β can be found by considering the changes in the number of infected, as described by Equation 2. If the number of infected people does not change, i.e. dI/dt = 0, then, based on Equation 2, the product βS = γ. If we take the initial value of S = S (t0), then a comparison of the product of βS(t0) with γ will allow assessing whether the infection will develop or be inhibited. If βS(t0) > γ, the epidemic will continue to develop; otherwise, it will be inhibited. From the equality βS(t0) = γ, the limit value of β can be determined for a given S(t0) and γ. The basic reproduction number R0 is also used to assess the development or inhibition of the infection, which for the SIR model is defined by β, γ, and S values: R0 == βS(t0)/γ. R0 specifies the number of people who are secondarily infected in the susceptible group S by one person who was initially infected at time t0. If R0 > 1, the epidemic will continue to develop; otherwise, it will be inhibited.

2 Problem Formulation

2.1 Extension of the SIR Model to Include Vaccinations

The mathematical models allowing the exploration of the significance of vaccinations in preventive measures that reduce the risk of epidemic development have been described in [1]. In this work, they demonstrate how to determine the vaccination threshold for the population to curb infections. The analysis also examines the importance of the loss of immunity acquired through vaccinations, the variability of infectious factors, and the limited capacity for daily vaccinations. A simple method for modeling the significance of vaccinations is described in [6], in which the group of recoverers (R) resulting from natural immunity is separated from the group acquiring immunity through vaccination. However, this model specifically pertains to preventive vaccination conducted in newborn groups.

The basic SIR model does not explicitly consider the presence of a subset of the population (S) exhibiting natural immunity. However, in cases where the epidemic under consideration does not result in fatalities, the parameter γ, representing the recovery rate, can also be interpreted as indicative of natural immunity. This is because it is through this parameter that we observe the decline and eventual extinction of the epidemic. However, epidemics can be effectively controlled through vaccination campaigns, which contribute to an increase in the number of individuals resistant to infection and/or experiencing mild symptoms. In this work, we have demonstrated how to easily modify the SIR model to analyze the importance of vaccinations, considering their effectiveness and the limited number of

vaccinations performed each day. Assuming permanent immunity obtained through vaccination, vaccinated people should be transferred from group S to group R, taking into account the effectiveness of vaccination and the speed of vaccination of the population. For this purpose, we have modified Equations 1 and 3. Since in the case of COVID-19 vaccines, the effectiveness ranges from 70.4% to 95%, [7], in the example shown in Figure 1, we assumed a vaccination effectiveness (ef) of 90%. Moreover, we had to assume the number of vaccinations performed each day (vac), and select the day of the epidemic when vaccination started. To study the importance of the timing of vaccination initiation and completion, Heaviside function (Hev) (Appendix) can be beneficial. If t1 is the day of vaccination initiation and t2 is the day of vaccination completion, then Equation 1 should be supplemented with the expression: –ef * vac * Hev(t, t1) * (1 – Hev(t, t2)). The same expression should be added to Equation 3. So the SIR model including vaccination would take the form of Equations 4–6:

$$dS/dt=-\beta SI-ef\ vac\ Hev(t,t_1)(1-Hev(t,t_2)) \quad (4)$$

$$dI/dt=\beta SI-\gamma I \quad (5)$$

$$dR/dt=\gamma I+ef\ vac\ Hev(t,t_1)(1-Hev(t,t_2)) \quad (6)$$

Since the number of people in each group must be positive, we must select the number of vaccinations performed per day and the duration of vaccination accordingly.

2.2 Modeling an Epidemic with Multiple Incidence Waves

As a result of temporally limited immunity, whether acquired naturally or through vaccination, there are recurring waves of increasing numbers of individuals falling ill. This can be observed firsthand and is also the subject of modeling studies, [8], [9]. Building upon the basic SIR model, it is also possible to illustrate recurring waves of increased infections.

The consequence of temporally limited immunity, whether acquired naturally or through vaccination, is the recurrence of waves with increased numbers of infected individuals. Currently, every person can observe this phenomenon, which is also the subject of modeling studies, [8], [9]. Additionally, based on the basic SIR model, it is possible to illustrate these recurring waves of disease increases.

To analyze the epidemic development with multiple waves of increase in the number of infected based on the SIR model, the following assumptions should be made:

1. No one dies due to the infection, i.e. there are only recovered in group R.
2. Recovered individuals lose immunity after t_x days with a certain probability a.

This problem can be solved based on the SIR model by gluing the solutions after each time unit, e.g. after each day. After the SIR equations are solved, the number of recovered $R(t_i)$ should be noted after each day t_i. Then, the initial conditions for the next solution (for the next day) should be changed. Thus, for $t_i \leq t_x$, the equations are solved with the initial conditions: $S(t_0)$, $I(t_0)$, and $R(t_0)$, while for $t_i > t_x$ the initial conditions for the following step t_i are $S(t_0) = S(t_i) + a * R(t_i - t_x)$, $I(t_0) = I(ti)$, and $R(t_0) = R(t_i) - a * R(t_i - t_x)$.

2.3 An Epidemiological Model with the Age Structure of the Population and Intergenerational Contacts (SEIRD)

The SIR model includes many simplifications, including grouping recovered and deceased individuals in the same group. In addition, it is not always true that people who become ill acquire permanent immunity after their recovery and that the incubation time is short enough to be skipped. To make the basic SIR model more appropriate for analyzing the current state of the COVID-19 pandemic, [10], it is necessary to extend it by including additional groups, i.e. those in the latent phase E, and divide the infected group into symptomatic (I_s) and asymptomatic (I_a). Furthermore, it is important to clearly distinguish convalescents (R) and individuals who died due to infection (D). For the inclusion of an additional latent (E) group, we must take into account an additional coefficient of transition from this group to the infected group I. Since the course of the disease and mortality significantly differ by age groups, the age structure of the population under study should also be introduced, due to the need for differentiation of susceptibility to infection and mortality. When dividing the population under consideration into age groups, we also consider the differences in contacts within a given age group and between groups. The application of such a model for the analysis of the course of the COVID-19 pandemic has already been demonstrated in [10]. The analyzed model is a system of six differential equations (Equations 7–12), for age groups 0–9, 10–19, 20–29, 30–39, 40–49, 50–59, 60–69, and 70+ years, for n = 1, 2, 3, 4, 5, 6, 7, and 8, respectively.

$$\frac{dS_n}{dt} = -\beta \sigma_n S_n \left(\sum_m k_{n,m} I_m\right), \quad (7)$$

$$\frac{dE_n}{dt} = \beta \sigma_n S_n \left(\sum_m k_{n,m} I_m\right) - \varepsilon E_n, \quad (8)$$

$$\frac{dI_{s,n}}{dt} = \varepsilon f_s E_n - (\gamma_s + \delta_n) I_{s,n}, \quad (9)$$

$$\frac{dI_{a,n}}{dt} = \varepsilon (1 - f_s) E_n - \gamma_a I_{a,n}, \quad (10)$$

$$\frac{dR_n}{dt} = \gamma_a I_{a,n} + \gamma_s I_{s,n}, \quad (11)$$

$$\frac{dD_n}{dt} = \delta_n I_{s,n}, \quad (12)$$

where:
n—index denotes age groups 1–8,
S_n—susceptible,
E_n—latent,
$I_{s,n}$—symptomatic cases among age group n,
$I_{a,n}$—asymptomatic cases among age group n,
R_n—recovered,
D_n—dead,
σ_n—susceptibility of age group n,
β—transmission coefficient,
$k_{n,m}$—an element of the contact matrix between age group n and m,
ε—progression rate from latent to infectious,
f_s—symptomatic cases,
γ—recovery rate, and
δ_n—mortality rate in age groups.

To determine the values of the $k_{n,m}$ parameter (matrix of contacts of various age groups), data collected in studies conducted in 152 countries were used, [11].

As mentioned above, the basic reproduction number R_0 is an important factor in the emergence of the epidemic. For the discussed SEIRD model, the value of this parameter for each age group can be calculated based on Equation 13 (Appendix):

$$R_{n0} = \frac{\beta \sigma_n s_n \sum_m k_{nm} (f_s \gamma_a + (1 - f_s)(\delta_n + \gamma_s))}{\gamma_a (\gamma_s + \delta_n)} \quad (13)$$

If R_{0n} is >1 within a given age group *n*, then an epidemic will develop. Thus, for the established values of parameters f_s, γ_a, γ_s, and δ_n, size of the $S_n(t_0)$ age of susceptible groups, and social contact matrix, epidemic development will depend on the product $\beta\text{Б}_n$.

3 Problem Solution

3.1 SIR model with Vaccination

For the proposed extension of the SIR model, it was assumed that the vaccinated subjects achieve sustained immunity. The modified SIR model can be used to analyze the impact of vaccination rate and the time of vaccination commencement on epidemic extinction.

Figure 1 shows two examples of vaccination with 90% effectiveness, started on day 50 of the pandemic for parameters $S(t_0) = 1000{,}000$; $I(t_0) = 1$; $R(t_0) = 0$; $\beta = 4 \times 10^{-7}$; days of recovery = 5; $R_0 = 2$:

a) 20,000 vaccinations/day; duration of vaccination = 21 days; number of vaccinated = 420,000 (solid lines); and
b) 10,000 vaccinations/day; duration of vaccination = 42 days; number of vaccinated = 420,000 (dotted lines).

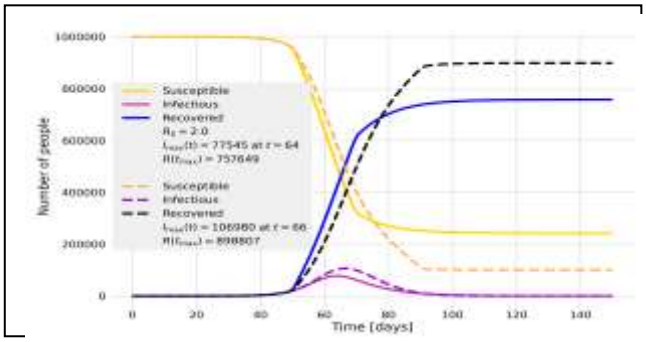

Fig. 1: Vaccination effect as measured by the SIR model. $S(t_0) = 1000{,}000$; $I(t_0) = 1$; $R(t_0) = 0$; $\beta = 4 \times 10^{-7}$; days of recovery = 5; $R_0 = 2$; start of vaccination = 50 days of the epidemic:
a) 20,000 vaccinations/day; duration of vaccination = 21 days; number of vaccinated = 420,000 (solid lines); $I_{max} = 77545$ on the64th day; and
b) 10,000 vaccinations/day; duration of vaccination = 42 days; number of vaccinated = 420,000 (dashed lines); $I_{max} = 106980$ on the 66th day.

Doubling the vaccination period combined with twice fewer vaccinations per day results in an increase in the number of I and R and a decrease in the number of S, while the maximum number of infected people appears two days later.

3.2 The SIR Model with Multiple Incidence Waves

Figure 2 shows an example for the initial conditions $S(t_0) = 1000{,}000$, $I(t_0) = 1$, $R(t_0) = 0$, for two cases of loss of immunity with the same probability $a = 0.01$, after 30 and 60 days.

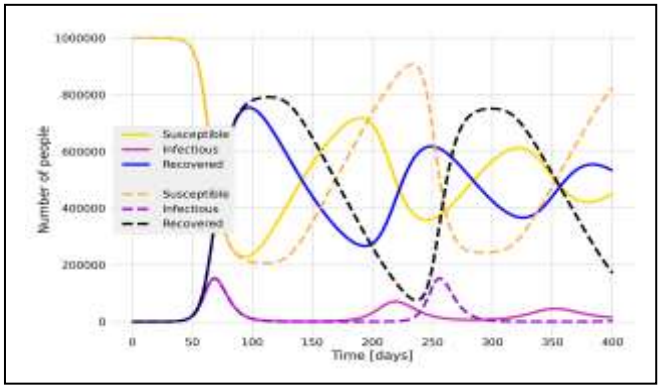

Fig. 2: Impact of the loss of immunity to the solutions of the SIR model.
$S(t_0) = 1000{,}000$; $I(t_0) = 1$; $R(t_0) = 0$; $\beta = 4 \times 10^{-7}$; days of recovery = 5; $\gamma = 0.2$; $R_0 = 2$;
a) duration of immunity = 30 days with probability 0.99 (solid line); and
b) duration of immunity = 60 days with probability 0.99 (dashed line).

For a longer period of natural immunity, there are greater variations in the number of S, R, and I in the next wave of the epidemic. If immunity resulting from vaccination is of similar duration, then similar changes in numbers in groups S, I, and R should be expected.

3.3 Analysis of Selected Vaccination Strategies based on the SEIRD Model

Based on epidemiological data related to the COVID-19 pandemic, we simulated selected vaccination strategies in a closed population of 106 people. To start the simulation, we had to give values to the parameters of the SEIRD model. According to the World Health Organization (WHO), [12], the average incubation time of a virus in an infected organism is 5–6 days, but it may even extend up to 14 days. We assumed that the time of transition from latent group E to infected group I is 5.5 days; therefore, coefficient $\varepsilon = 1/5.5$ [day^{-1}]. As asymptomatic cases may even account for 40–45% of all infection cases, [13], we assumed that coefficient fs, which determines symptomatic cases, can range from 0.55 to 0.6. The original guidelines of the WHO indicated that an infected person should be quarantined for 14 days. Thus, it can be assumed that 14 days is the duration of infection in a patient. Consequently, we estimated that the value of the recovery rate coefficient in symptomatically affected individuals (γ_s) is 1/14. However, asymptomatic people who are infected can infect others for longer than 14 days, [13]. Therefore, we assumed that the recovery time for this group is 16 days. Accordingly, the estimated value of the recovery rate coefficient of asymptomatic patients (γ_a) is 1/16. The COVID-19 mortality rate δ was determined for each age group based on the data from Sweden, [14]. According to Equation 7, epidemic development is mainly determined by the product of β and σ_n; therefore, to differentiate age groups based on susceptibility to disease development, different values of σ_n can be adopted while maintaining β value constant for all n.

During the first wave of the Covid-19 pandemic, Sweden, compared to other countries, adopted the least drastic measures to prevent the spread of the disease, [15]. However, the number of deaths per 1 million inhabitants in 2020 in Sweden was lower than in Germany, France, or Spain. It is, therefore, worth conducting a simulation of selected vaccination strategies based on detailed data for the Swedish population, [16]. To evaluate various vaccination strategies and analyze potential observed effects, it's necessary to adjust the model parameters to reflect the characteristics of the Swedish population accurately. This adjustment aims to achieve a good fit with the known pandemic trajectory in Sweden in 2020, a period when vaccines were not yet available. The parameters ε, fs, γs, γa take the values 0.18, 0.6, 0.07, and 0.06, respectively, [11], [12], [13], [14], [15], [16]. The parameter $\beta = 6 \times 10^{-6}$ was selected to align with the literature data, [15], aiming to observe the highest number of daily fatal cases approximately 60 days after the appearance of the first infected person (12 cases per 1 million). The parameter responsible for mortality in individual age groups was estimated based on the relationship between crude case-fatality rates (CFR), mortality rate δ_n, and recovery rate γ_s: $CFR = \delta_n/(\delta_n+\gamma_s)$, [10], and the values of CFR were extracted from [14]. However, the values of this parameter calculated in this manner resulted in ten times the overall total number of fatal cases during the first pandemic wave in 2020. A tenfold decrease in its value for all age groups leads to a mortality rate similar to reality. Finally, the parameter δ_n takes values of [2.8×10^{-7}, 2×10^{-6}, 5×10^{-6}, 8.58×10^{-6}, 2.22×10^{-5}, 7.58×10^{-5}, 3.4×10^{-4}, 18.7×10^{-4}] for individual age groups n. The parameter σ_n was also modified. Setting the same value for all age groups leads to an overestimation of mortality cases in the oldest age groups 7 and 8. The best reproduction of the pandemic course in Sweden in 2020 was achieved by adopting the following values for this parameter for subsequent age groups: σ_n = [1, 1, 1, 1, 1, 1, 0.1, 0.01]. To perform simulations, the initial values for the Swedish population, [16], should also be adopted:

$S_n(0)$ = [119000, 110000, 130000, 128000, 127000, 128000, 109000,148000]
$E_n(0)$ = [0, 0, 0, 0, 0, 0, 0, 0]
$I_{sn}(0)$ = [0, 0, 0, 1, 0, 0, 0, 0]
$I_{an}(0)$ = [0, 0, 0, 0, 0, 0, 0, 0]
$R_n(0)$ = [0, 0, 0, 0, 0, 0, 0, 0]
$D_n(0)$ = [0, 0, 0, 0, 0, 0, 0, 0].

The Swedish social contact matrix is provided in the Appendix.

We assumed that in a group of a million people, the pandemic begins with a single person in the age group 4 (I_{s4}) who is symptomatically infected. For such assumptions, we solved the system of equations of the SEIR model using our application https://github.com/BlankTiger/SEIRD_model/releases/download/v1.0.3-rust/SEIRD_model.exe.These solutions are shown in Figure 3.

After 12 days, there is a significant decline in the number of susceptible cases (S_n) in age groups 1-6 for about 8 days. This decrease is accompanied by a significant increase in group E for about 6 days in age groups 1-6, followed by a decrease in the next 14 days. With a slight delay—i.e., starting from 12 days after the first appearance of I_{s4}—I_s begins to increase until day 22 in age groups 1-6, and then decreases within 50 days. Similar changes are observed in the I_a group (1-6).

In the oldest age groups 7 and 8, the growth of I_s begins later, specifically after 17 and 20 days, and lasts longer, extending to 35 and 45 days, respectively. Similarly, I_a changes in these age groups.

From days 15 and 20 of the pandemic for age groups 7 and 8 respectively, the number of recoveries also begins to increase, reaching asymptotic values after about 80 days. Fatalities begin to occur between days 15 and 20 of the pandemic.

The eighth age group has the highest mortality rate of about 0.4%, whereas in groups 1-7, the mortality rate is significantly lower. The value of the R_0 parameter for age groups 1–7 is >1 and for group8 is <1.The results of the simulation are presented in Table 1, where the R_0 parameter was given for each age group, the maximum number of I_{sn}, asymptomatic $I_{an,}$ and the number of fatal cases, D_a. The analysis of the results collected in Table 1 indicates the highest mortality in the 8, 7, and 6 age groups.

Based on the presented analysis of pandemic development (Figure 3 and Table 1), we compared five vaccination strategies, assuming the following: we have 150000 doses of vaccines and can vaccinate 10000 people per day, and the effectiveness of the vaccine is 90%. Vaccinations will be performed from days 1 to 15 (from the moment the first case of a symptomatically infected person is noted). Since the previous analysis revealed the highest mortality in age groups 8, 7, and 6, it is worth examining the potential effects of vaccinating these age groups first.

Given the constraints imposed (limited availability of vaccinations per day), it is valuable to compare the outcomes with other vaccination strategies. These strategies may include limiting vaccinations to only two groups of the oldest people (8 and 7), vaccinating only group 8, administering vaccines evenly across all age groups (1 to 8), and comparing results with vaccinations targeted at age groups highly active in the labor market and those maintaining frequent intergenerational contacts, specifically groups 4 and 5. In summary, we will compare the results of the following vaccination strategies:

a) Vaccination of 3333 people per day in age groups 8, 7, and 6
b) Vaccination of 5000 people per day in age groups 8 and 7
c) Vaccination of 10000 people per day in age group 8
d) Vaccination of 1250 people per day in all age groups
e) Vaccination of 5000 people per day in age groups 4 and 5.

Because mortality and the number of symptomatically ill people are the most important social parameters, the numbers of symptomatic patients and the number of fatal cases in each age group are presented in Table 2, Table 3, Table 4, Table 5 and Table 6. The bold values are lower than the number of cases in the absence of vaccinations. The percentage change from the predicted number of unvaccinated cases is shown in parentheses. From Table 2, Table 3, Table 4, Table 5 and Table 6, it can be understood that the greatest total decrease in deaths (i.e. about 53%) can be achieved by vaccinating only people in age group 8. However, this results from a 91.8% decrease in mortality in this group. A similar high decrease in the number of symptomatically infected cases can be seen in group 8. By evenly vaccinating age groups 8, 7, and 6 and 8, 7, the total number of deaths can be reduced by approximately 38.8% (Table 2) and 49.6% (Table 3), respectively. However, by extending the vaccination campaign to all age groups, a more than 19% decrease in mortality and a decrease in the number of symptomatic patients from 13% to 23% in various age groups (Table 5).

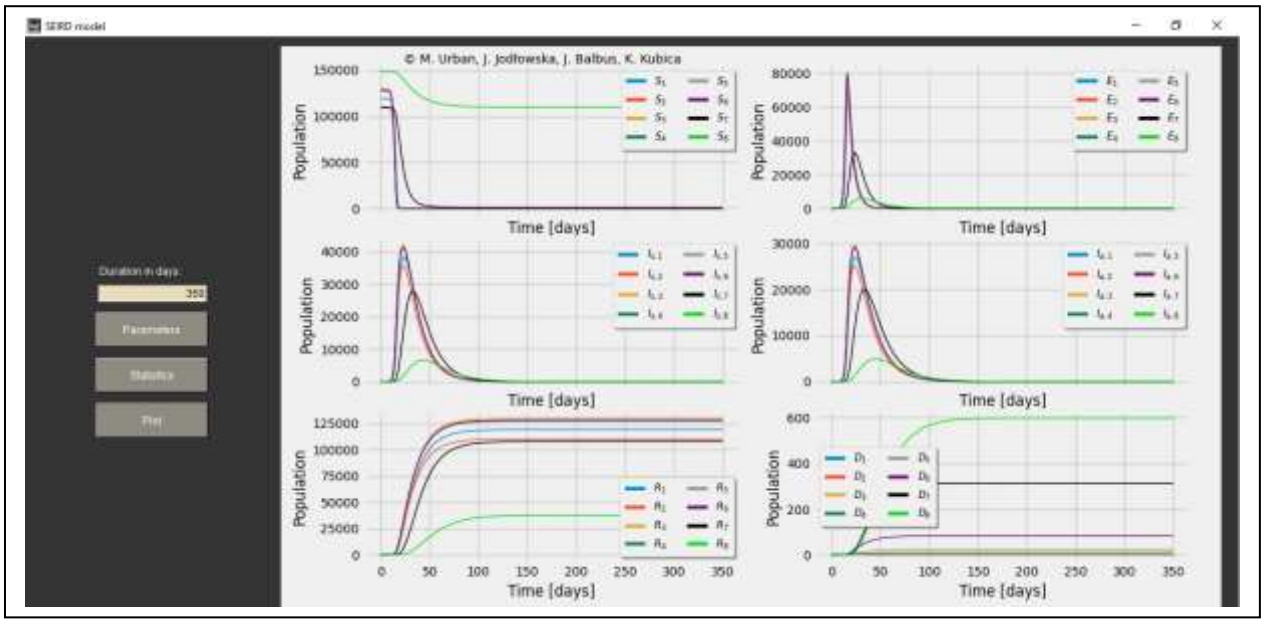

Fig. 3: Solutions of SEIRD model for Swedish

Considering the global decline in the number of symptomatic patients (who constitute the greatest burden for medical services), simultaneous vaccination of all age groups can reduce the total number of symptomatic cases by 14.7% (Table 5), which is 12.5% (Table 4) higher compared to the decline achieved with vaccination of only age group 8. For strategies b (Table 3) and a (Table 2), the number of symptomatic cases decreases by 7.6 and 10.7%, respectively. When limiting vaccinations to groups 4 and 5, the most significant reduction in the number of symptomatic patients (17.4%) is observed, alleviating the burden on the health service the most. However, this approach leads to the lowest decrease in mortality (11.5%) for the entire population.

Table 1. Summary of the results of the non-vaccination seird model

Number of age group	R_{0n}	Maximum of I_{sn}	Maximum of I_{an}	Number of D_n
1	57.9	38385	27022	0
2	78.1	35581	25039	1
3	90.2	42053	29593	5
4	92.3	41405	29137	9
5	87.4	41072	28906	24
6	84.4	41371	29126	83
7	4.4	27778	19981	313
8	0.42	6606	4931	598
Total		274251	193735	1033

Table 2. Summary of the results of the SEIRD model solutions taking into account vaccinations of age groups 8, 7, and 6 (3333 vaccinations per day in each group with 90% efficiency).

Number of age group	Maximum of I_{sn}	Number of D_n
1	38366	0
2	35569	1
3	42031	5
4	41382	9
5	41047	24
6	**26769 (–35)**	**53 (–36)**
7	**15667 (–43.5)**	**182 (–42)**
8	**4012 (–39)**	**358 (–40)**
Total	**244843 (–10.7)**	**632 (–38.8)**

Table 3. Summary of the results of the SEIRD model solutions taking into account vaccinations of age groups 8 and 7 (5000 vaccinations per day in each group with 90% efficiency).

Number of age group	Maximum of I_{sn}	Number of D_n
1	38384	0
2	35581	1
3	42053	5
4	41404	9
5	41071	24
6	41370	83
7	**10265 (–63)**	**118 (–62)**
8	**3199 (–51.6)**	**280 (–53)**
Total	**253327 (–7.6)**	**520 (–49.6)**

Table 4. Summary of the results of the SEIRD model solutions taking into account vaccinations of only age group 8 (10000 vaccinations per day with 90% efficiency)

Number of age group	Maximum of I_{sn}	Number of D_n
1	38385	0
2	35581	1
3	42053	5
4	41405	9
5	41072	24
6	41371	83
7	27746	312
8	**564 (–91.5)**	**49 (–91.8)**
Total	**268177 (–2.2)**	**483 (–53.2)**

Table 5. Summary of the results of the SEIRD model solutions taking into account vaccinations of all age groups (1250 vaccinations per day in each group with 90% efficiency)

Number of age group	Maximum of I_{sn}	Number of D_n
1	**32824 (–14.5)**	**0**
2	**30033 (–15.6)**	1
3	**36495 (–13)**	**4**
4	**35848 (–13.4)**	**8**
5	**35515 (–13.5)**	**20 (-16.6)**
6	**35814 (–13.4)**	**72 (-13.2)**
7	**22355 (–19.5)**	**262 (-16,3)**
8	**5050 (–23.5)**	**461 (-23)**
Total	**233934 (14.7)**	**828 (–19.8)**

Table 6. Summary of the results of the seird model solutions taking into account vaccinations of age groups 4 and 5 (5000 vaccinations per day in each group with 90% efficiency)

Number of age group	Maximum of I_{sn}	Number of D_n
1	38199	0
2	35477	1
3	41890	5
4	**19404 (-53.1)**	**4 (-55.5)**
5	**19080 (-53.5)**	**11 (-54)**
6	41179	83
7	**25772 (–7.2)**	309
8	**5383 (–18.5)**	**501 (-16.2)**
Total	**226384 (–17.4)**	**914 (–11.5)**

4 Conclusion

The expected vaccination results can be assessed from the point of view of reducing mortality rates across various age groups, and/or reduction in the number of infected in individual groups of a given population. Considering the availability of vaccines, their effectiveness, and restrictions on the number of vaccinations per day, articulating an optimal vaccination strategy becomes challenging, requiring consideration of ethical, financial, and social criteria. The COVID-19 pandemic was declared by the WHO, [17], on 11th March 2020, and the first vaccines were only available at the end of 2020. Therefore, during the period without vaccines, significant emphasis was placed on isolating infected individuals from the healthy population. Due to financial and/or organizational constraints, different quantities of diagnostic tests were conducted by healthcare services in various countries. These tests were intended to form the basis for the mandatory isolation of infected individuals and the identification of a group of healthy but susceptible individuals, who would be vaccinated, [18]. In many countries, individuals were qualified for vaccination based on a medical interview, which did not allow for the identification of individuals from the latent group or those infected asymptomatically. This led to significant variations in individual responses to vaccinations, including post-vaccination symptoms, [19]. Analyzing the solutions of the SEIRD model excluding vaccinations, it becomes apparent that individuals in groups E (who had already come into contact with the infecting factor) and I_a appear almost simultaneously with group Is. Thus, without specialized tests, people from groups S, E, and I_a will be eligible for vaccination. This suggests that extensive testing is required to detect groups E and I_a, for whom vaccination is not advisable.

Analyzing the values of the R_0 reproduction number for all age groups, it should be noted that only for the oldest age group 8 is its value less than 1 – thus, the expected effect should be the absence of pandemic development in this group. It should also be noted that intergenerational contact matrices were published over 17 years ago during a pandemic-free period. During this time, there have also been socio-cultural changes in many countries around the world, which likely result in changes to the estimated values of contact matrices.

Since the appearance of vaccines on the market, it was necessary to establish rules for their global distribution and carry out widespread awareness campaigns about the importance of vaccination. Unfortunately, in various countries, anti-vaccination movements also developed, leading to the underutilization of purchased vaccine doses. In the quest for an optimal vaccination strategy, considering the limited vaccine supply, the organization of vaccination campaigns (the possible number of vaccinations per day) should also take into account the organizational efficiency of the healthcare system in a given country. This includes

the speed of establishing temporary hospitals, the capacity for medical transport, monitoring the isolation of infected individuals, and ensuring the effectiveness of protecting healthcare workers as a top priority. Prioritizing vaccinations for groups with the highest mortality rate (given limited vaccine supply) results in a smaller decline in the total number of symptomatically infected individuals compared to vaccinations carried out initially in groups with the highest professional and familial engagement (groups 4 and 5). This may lead to limited access to medical services unrelated to COVID-19, ultimately resulting in an increase in mortality compared to the pre-pandemic period.

In the future, comprehensive literature studies in search of reliable epidemiological data on COVID-19 in different countries will allow for the comparison of outcomes from selected vaccination strategies, taking into account cultural customs, social relations, and the level of national income. According to the data presented in the publication, [20], the number of COVID-19 vaccine doses varies from 0 to 120 per 100 people in different countries and is not correlated with the gross domestic product (GDP) per capita. Understanding the current values of the SEIRD model parameters, which vary with successive waves of epidemic growth caused by other variants of the SARS-CoV-2 virus, will enable the analysis of the pandemic's progression with multiple recurrent waves.

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APPENDIX

Heaviside function
The Heaviside function is defined as:

$$H_\tau(t) = \begin{cases} 0 & for \quad t < \tau \\ 1 & for \quad t \geq \tau \end{cases}$$

Using this function, it is possible to control the course of vaccinations, starting on t_1 and ending on t_2, with vaccination rate and effectiveness *ef*: *ef* * *vac* * Hev(t, t_1) * (1 – Hev(t, t_2)).

SEIRD model
Denote R_{n0} (n=1,2,…,8) as the basic reproduction number for each age group.
To calculate R_{n0} we use the method described in [21].
The models SIR and SEIRD are the ODEs of the following type

$$\frac{dy}{dt} = g(y) \qquad (1)$$

where $y = (y_1, \dots, y_n)$ and $g = (g_1, \dots, g_n)$.
Let y_j be $j = 1, \dots, m$ infected population groups of $j = 1, \dots, n$ compartments in y.
Let $\mathcal{F}_i(y)$ be the rate of appearance of new infections in the *i*-th compartment, and let $\wp_i(y)$ be the rate of the transition rates in the *i*-th compartment.

Then, Equation (1) takes a form:

$$\frac{dy_i}{dt} = \mathcal{F}_i(y) - \wp_i(y)$$

Define $F = \left[\frac{\partial \mathcal{F}_i(y^*)}{\partial y_j}\right]$ and $V = \left[\frac{\partial \wp_i(y^*)}{\partial y_j}\right]$
for $i, j = 1, \dots, m$, where $y^* = (y_1^*, \dots, y_n^*)$ is the disease-free equilibrium.

Then, $R_0 = \rho(F \cdot V^{-1})$, where $\rho(F \cdot V^{-1})$ is the spectral radius of the matrix $F \cdot V^{-1}$.
(the spectral radius of the matrix can be defined as the largest eigenvalue of the matrix).

The model SIR can be written as:

$$\frac{d}{dt}\begin{bmatrix} S \\ I \\ R \end{bmatrix} = \begin{bmatrix} 0 \\ \beta SI \\ 0 \end{bmatrix} - \begin{bmatrix} \beta SI \\ \gamma I \\ \gamma \end{bmatrix}$$

Define $(S_0, 0, 0)$ as disease-free equilibrium.
Then, $F = \beta S_0$ and $V = \gamma$. Hence
$R_0 = F \cdot V^{-1} = \frac{\beta S_0}{\gamma}$.

The SEIRD model we rewrite as

$$\frac{d}{dt}\begin{bmatrix} S_n \\ E_n \\ I_{sn} \\ I_{an} \\ R_n \\ D_n \end{bmatrix} = \begin{bmatrix} -\beta\sigma_n S_n(\sum_m k_{nm}(I_{sn}+I_{an})) \\ \beta\sigma_n S_n(\sum_m k_{nm}(I_{sn}+I_{an})) \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ \epsilon E_n \\ -\epsilon f_s E_n + (\gamma_s+\delta_n)I_{sn} \\ -\epsilon(1-f_s)E_n + \gamma_a I_{an} \\ -\gamma_a I_{an} - \gamma_s I_{sn} \\ -\delta_n I_{sn} \end{bmatrix}$$

for n=1,2,…,8

Let $(S_0, 0,0,0,0,0)$ be a disease-free equilibrium.

Then,

$$F_n = \begin{bmatrix} 0 & \beta\sigma_n S_{0n}\sum_m k_{nm} & \beta\sigma_n S_{0n}\sum_m k_{nm} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

(n=1,….,8)

and

$$V_n = \begin{bmatrix} \epsilon & 0 & 0 \\ -\epsilon f_s & \gamma_s+\delta_n & 0 \\ -\epsilon(1-f_s) & 0 & \gamma_a \end{bmatrix}$$

(n=1,…,8)

Therefore

$$R_{n0} = \frac{\beta\sigma_n S_n \sum_m k_{nm}(f_s\gamma_a + (1-f_s)(\delta_n+\gamma_s))}{\gamma_a(\gamma_s+\delta_n)}$$

(n=1,…,8)

Matrices of contacts between age groups (social contact matrix)

Table IA presents social contact matrices for Sweden—based on the literature data, [11].

n is the number of age groups (each 10-year). The values of $k_{n,m}$ are average values calculated based on the contact matrix for the population divided into 5-year groups (data from publication, [11], —16 × 16 matrices), e.g. the value $k_{1,1}$ = 2.583 for contacts of people from the n = 1 group with people of the same age group is the mean value calculated based on 16 × 16 matrix: $(k_{1,1} + k_{1,2} + k_{2,1} + k_{2,2})/4$.

Table IA. Swedish Social Contact matrix

n	1	2	3	4	5	6	7	8
1	2.583	0.450	0.399	0.986	0.459	0.217	0.169	0.061
2	0.496	4.615	0.690	0.644	0.912	0.279	0.092	0.046
3	0.292	0.933	2.895	1.443	1.160	0.721	0.104	0.043
4	0.811	0.655	1.267	2.523	1.582	0.780	0.210	0.061
5	0.448	1.091	1.058	1.624	2.175	0.884	0.174	0.076
6	0.479	0.893	1.082	1.289	1.531	1.526	0.322	0.092
7	0.393	0.349	0.448	0.716	0.579	0.587	1.108	0.253
8	0.231	0.353	0.192	0.346	0.474	0.365	0.579	0.606

Contribution of Individual Authors to the Creation of a Scientific Article (Ghostwriting Policy)

- Maciej Urban has implemented the SEIRD algorithm in Python,
- Julia Jodłowska carried out the simulation,
- Joanna Balbus provided mathematical oversight and derived the formula for the basic reproduction number for each age group,
- Krystian Kubica conceived and designed research approved final version of the manuscript.

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Conflict of Interest

The authors have no conflicts of interest to declare.