MODIFIED SEIRD MODEL FOR DESCRIBING THE COVID-19 EPIDEMIC

A.I. KLYMENKO, G.B. PODKOLZIN

Abstract. This article is devoted to mathematical models in epidemiology, in particular SIR, SEIR, and SEIRD models. It explores the importance of these models in predicting the spread of infectious diseases and evaluating the effectiveness of control measures. These models allow for assessing important epidemic parameters such as the speed of infection transmission, the number of people infected, and the number of deaths. This data can help in making decisions regarding the imposition and lifting of quarantine restrictions, opening and closing of schools and other institutions, as well as in developing vaccination strategies and other control measures. In summary, mathematical models such as SIR, SEIR, and SEIRD are important tools in the fight against epidemics. They enable epidemiologists and medical professionals to predict and control the spread of diseases, thus preserving the health and lives of people.

Keywords: epidemiology, epidemiological models, modified mathematical models, COVID-19 modeling SEIR, SEIRD model, unvaccinated people, virus, division of the population, new strains.

INTRODUCTION

Modeling is a widely used tool to support the evaluation of various disease interventions. The value of epidemiological models lies in their ability to explore "what if" scenarios and provide decision makers with a priori knowledge of the consequences of disease emergence and the impact of control strategies.

To be useful, models must be fit for purpose and properly validated and verified. The complexity and variability inherent in biological systems should limit the use of models as predictive tools during actual outbreaks. Models will be most useful when used prior to an outbreak, particularly in the areas of retrospective analysis of past outbreaks, contingency planning, resource planning, risk assessment, and training. Models are only one tool for providing scientific advice, and results should be evaluated in conjunction with experimental data, field experience, and scientific knowledge.

SIR, SEIR, SEIRD MODELS

The severity and global reach of the COVID-19 pandemic has spurred research in many areas, including disease dynamics modeling, with the goal of using such models to better understand the impact of intervention strategies on disease control [1]. Several factors are known to influence disease dynamics, including incidence rates, recovery rates, quarantine strategies, and the impact of awareness [2]. In the literature, classical epidemic models of susceptible infectious diseases

© А.І. Klymenko, G.B. Podkolzin, 2023 Системні дослідження та інформаційні технології, 2023, № 1 (SIR, SEIR, SEIRD models) have been widely used to model infectious diseases [3].

The SIR model is based on the number of susceptible (S), infectious (I), and recovered (R) individuals. The classical epidemic model is shown below:

$$\begin{cases} \frac{dS(t)}{dt} = -\beta \frac{S(t)I(t)}{N};\\ \frac{dI(t)}{dt} = \beta \frac{S(t)I(t)}{N} - \gamma I(t);\\ \frac{dR(t)}{dt} = \gamma I(t), \end{cases}$$

where S(t) — the number of people who can be infected; I(t) — the number of infected people; R(t) — the number of people who have been isolated from transmission (died or recovered); β — the transmission rate; γ — the recovery rate.

Each group contains a certain number of people each day. However, this number changes from day to day as people move from one group to another. For example, people in Group S will move to Group I when they become infected. Similarly, infected individuals will move to group R after they recover. It is assumed that the total population in the three groups (S + I + R) always remains the same.

The SIR model assumes that recovered individuals cannot be reinfected [2]. The SEIR model has an additional group for individuals who become infected and contagious after the incubation period (E — Exposed). In other words, the SEIR model includes a latency period.

The SEIR model is described by the following system of equations:

$$\begin{cases} \frac{dS(t)}{dt} = -\beta \frac{S(t)I(t)}{N};\\ \frac{dE(t)}{dt} = \beta \frac{S(t)I(t)}{N} - \alpha E(t)\\ \frac{dI(t)}{dt} = \alpha E(t) - \gamma I(t);\\ \frac{dR(t)}{dt} = \gamma I(t), \end{cases}$$

where α — the rate of transition of the disease from the latent period to the overt stage; β — the rate of infection transmission; γ is the rate of recovery; S(t) — the number of people susceptible to the virus; E(t) — the number of people with the virus in the incubation period; I(t) — the number of people who get sick; R(t) — the number of recovered people who have come into contact with the pathogen and have gained stable immunity.

To describe the COVID-19 epidemic, the most appropriate of the above models is the SEIRD model, in which group D — Death appears, i.e. this model takes into account the dead.

The classical SEIRD model is shown below:

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$$\begin{cases} \frac{dS(t)}{dt} = -\beta \frac{S(t)I(t)}{N}; \\ \frac{dE(t)}{dt} = \beta \frac{S(t)I(t)}{N} - \alpha E(t); \\ \frac{dI(t)}{dt} = \alpha E(t) - (\gamma + \mu)I(t); \\ \frac{dR(t)}{dt} = \gamma I(t); \\ \frac{dD(t)}{dt} = \mu I(t), \end{cases}$$
(1)

where β — the coefficient that can be interpreted as the probability of contracting the disease in case of contact between a susceptible individual and an infected person; μ — the mortality rate; γ — the recovery rate; α — the rate of transition from the latent period to the overt stage; S(t) — the number of people susceptible to the virus; E(t) — the number of people with the virus in the incubation period; I(t) — the number of people who fall ill; R(t) — the number of recovered people who have come into contact with the pathogen and have gained stable immunity.

MODIFIED SEIRD-MODEL

Modified models can take into account more realistic factors such as population mobility, different variants of the disease, carrier effects, vaccination, and other factors. For example, the SIR model typically assumes that people in each group interact with each other, but in some cases there may be groups that interact less frequently or not at all. In this case, modified models can be used to describe more complex scenarios.

In epidemiology, it is very important to have a model that covers all stages of the disease, including incubation, clinical course, recovery, and death. The SIR model does not include a parameter responsible for the incubation period of the disease, and SIR and SEIR cannot be used when the epidemic includes mortality and fertility. For this reason, the SEIRD model has become the most relevant in epidemiology, since it includes all the parameters necessary to study the different stages of the disease and allows more accurate predictions of the spread of the disease and the effectiveness of control measures.

The advantages of the proposed model are related to the fact that the population can be divided into vaccinated and unvaccinated. In addition, the modified SEIRD model takes into account fertility and natural mortality unrelated to disease mortality, which allows for the most accurate reproduction of the situation, bringing it as close as possible to real conditions.

The basic SEIRD model is shown in (1). In the modified model, each component is divided into two parts: vaccinated and unvaccinated members of the population (susceptible, exposed, infectious, recovered). The fertility parameter applies only to unvaccinated susceptibles, because by default, people are born unvaccinated. So, the model is:

$$\begin{aligned} \frac{dS_{unvac}}{dt} &= l - \mu S_{unvac} - \frac{S_{unvac}(\beta_{uu}I_u + \beta_{uv}I_v)}{N}; \\ \frac{dS_{vac}}{dt} &= -\mu S_{vac} - \frac{S_{vac}(\beta_{vu}I_u + \beta_{vv}I_v)}{N}; \\ \frac{dE_{unvac}}{dt} &= \frac{S_{unvac}(\beta_{uu}I_u + \beta_{uv}I_v)}{N} - (\mu + \alpha_{unvac})E_{unvac}; \\ \frac{dE_{vac}}{dt} &= \frac{S_{vac}(\beta_{vu}I_u + \beta_{vv}I_v)}{N} - (\mu + \alpha_{vac})E_{vac}; \\ \frac{dI_{unvac}}{dt} &= \alpha_{unvac}E_{unvac} - (\gamma_{unvac} + \mu + \theta_{unvac})I_{unvac}; \\ \frac{dI_{vac}}{dt} &= \alpha_{vac}E_{vac} - (\gamma_{vac} + \mu + \theta_{vac})I_{vac}; \\ \frac{dR_{unvac}}{dt} &= \gamma_{unvac}I_{unvac} - \mu R_{unvac}; \\ \frac{dR_{vac}}{dt} &= \gamma_{vac}I_{vac} - \mu R_{vac}; \\ \frac{dD}{dt} &= \theta_{vac}I_{vac} + \theta_{unvac}I_{unvac} + \mu \left(\frac{S_{vac} + S_{unvac} + E_{vac} + E_{unvac} + R_{unvac}}{H_{unvac} + R_{unvac}}\right), \end{aligned}$$

where S_{unvac} — susceptible unvaccinated persons who are not infected but can become infected through contact with an infected person (unvaccinated or vaccinated); S_{vac} — susceptible to the virus are vaccinated persons in the population who are not infected but can become infected through contact with an infected person (unvaccinated or vaccinated); E_{unvac} — the number of unvaccinated people with the disease in latent mode (they contacted with an infected person); E_{vac} — the number of vaccinated people with the disease in latent mode (they contacted with an infected person); I_{unvac} — the number of unvaccinated sick people who transmit the virus to unvaccinated and vaccinated susceptible persons; I_{vac} — the number of vaccinated patients who transmit the virus to unvaccinated and vaccinated susceptible persons; R_{unvac} — the number of unvaccinated survivors who are susceptible to reinfection, although the probability is lower; R_{vac} the number of vaccinated survivors who are susceptible to re-infection, although the probability is lower; D — people who died from the virus and other causes; θ_{unvac} — deaths from the virus in infected unvaccinated people; θ_{vac} — deaths from the virus in infected vaccinees; β_{uu} — the probability of transmission of the virus from infected unvaccinated persons to unvaccinated persons; β_{uv} — the probability of transmission of the virus from infected unvaccinated persons to vaccinated persons; β_{vu} — the probability of transmission of the virus from infected vaccinated to unvaccinated persons; β_{vu} — the probability of virus transmission from infected vaccinated to vaccinated persons; α_{unvac} — the probability of the disease transition from the latent phase to the overt phase in unvaccinated persons; α_{vac} — the probability of the disease transition from the latent phase to the overt phase in vaccinated persons; γ_{unvac} — recovery of infected unvaccinated people from the virus; γ_{vac} — recovery of infected vaccinated persons from the virus; μ — mortality not due to infection; l — birth rate.

The main difference between this model and the classical SEIRD model is the division of the population into vaccinated and unvaccinated individuals. Probability of infection of vaccinated persons (S_{vac}) is much lower than that of unvaccinated persons (S_{unvac}). Sick vaccinated persons (I_{vac}) are less contagious and less likely to die than unvaccinated infectious people (I_{unvac}).

IMPLEMENTING THE MODIFIED SEIRD MODEL FOR COVID-19 IN UKRAINE IN 2021

Let's model the situation with COVID-19 in Ukraine. To do this, we need to calculate the appropriate coefficients to substitute them. To do this, we will use information for 2021.

The number of Ukrainians in 2021 (excluding the occupied territories) is 41 million 167 thousand people [4]. The mortality rate for 2021 is 714 263 people, of which COVID-19 accounts for 86 015 cases [5]. The birth rate for 2021 will be 271 984 children [6].

The number of all deaths per day averages $714\ 263/365 = 1\ 956.88$ people. That is, $1\ 956.88/41\ 167\ 300 = 0.0000475349$ of the total population dies per day. This number includes deaths from COVID-19. The death rate from COVID-19 is $(86\ 015/365)/41\ 167\ 300 = 0.0000057244$.

Unfortunately, no mortality statistics for vaccinated and unvaccinated people could be found for Ukraine. However, you can calculate this coefficient yourself if the data mentioned in an interview with Professor Leanne Wen of the School of Public Health [14] are true: that vaccinated people are six times less likely to be infected than unvaccinated people and 11 times less likely to die from coronavirus. In this case, the mortality rate of vaccinated people per day is 0.0000004770, and that of unvaccinated people is 0.0000052474. Accordingly, we have $\Theta_{unvac} = 0.0000052474 \ \Theta_{vac} = 0.0000004770$.

Accordingly, the mortality rate per day not due to COVID-19 is 0.0000475349 - 0.0000057244 = 0.0000418105, i.e. $\mu = 0.0000418105$.

The birth rate per day is $(271\ 984\ /365)/41\ 167\ 300 = 0.0000181008$, so l = 0.0000181008.

Since the modeling requires both vaccinated and unvaccinated populations, we need to provide data on these. In 2021, 15 201,112 people have been vaccinated with two vaccines in Ukraine [7]. That is, 15 201 112/41 167,300 = 0.3692521006. Accordingly, if you want to model a population of only 100 people, and one of each of the vaccinated and unvaccinated gets sick, 36.1867058563 will be the vaccinated who have not yet gotten sick, and 61.8132941437 will be the unvaccinated who have not yet gotten sick.

The incubation period is the number of days between the moment of infection and the moment of symptoms. To calculate the coefficient responsible for the rate of transition of the virus from the latent period to the fully infected state, we use formula:

$$\alpha = \frac{1}{T_{inc}},$$

where α — the rate of transition of the disease from the latent to the overt phase; T_{inc} — the average incubation time of the virus.

Viruses are constantly changing, sometimes resulting in the emergence of new strains. Different strains of COVID-19 may have different incubation periods. On average, symptoms appear in a newly infected person about 5.6 days after exposure [8]. So, $T_{inc} = 5.6$, accordingly, $\alpha = 1/5.6 = 0.17858$. According to studies, the incubation period for vaccinated and unvaccinated individuals is the same number of days [9], i.e. $\alpha_{unvac} = \alpha_{unvac} = 0.17858$.

Some studies have shown that it may take the body 2 weeks to recover from a mild illness, or up to 6 weeks in severe or critical cases [10]. Other sources say [11] that recovery usually takes one to two weeks. So let's use the average recovery time of two weeks.

Let's calculate γ according to the formula for calculating the recovery rate coefficient:

$$\gamma = \frac{1}{T_{rec}},$$

where γ — the recovery rate of infected people from the virus; T_{rec} — average recovery time.

So, $T_{rec} = 14$ days. Accordingly, $\gamma = \gamma_{unvac} = 1/14 = 0.0714$.

When the population is divided into vaccinated and unvaccinated, the recovery time will be different. Different sources report different recovery times: some studies show that the overall recovery time was six to seven days shorter than for unvaccinated people [12]. Another study from the Centers for Disease Control and Prevention found that vaccinated participants spent an average of two to six days less in bed than unvaccinated participants [13]. Let's assume that, on average, the vaccinated are sick six days less, that is $\gamma_{vac} = 1/8 = 0.125$.

Now let's calculate the probability of disease transmission. To calculate the data for vaccinated people, we need statistics on the effectiveness of the vaccine (let's take the Pfizer vaccine). According to [15], Pfizer has 95% protection against mild COVID-19. This means that you are less likely to get sick if you are vaccinated:

$$p_{get infected if you are vaccinated} = 0.05$$
.

It should also be noted that vaccinated people are less likely to transmit the disease, even if they become infected. At a press conference in November, WHO Director-General Tedros Ghebreyesus said that vaccines protect against the spread of the virus by 60 percent before the delta variant emerges [16, 19]. This means:

$p_{transmit the disease if you are vaccinated} = 0.4$.

According to the same study [16, 17], vaccinated people are ten times less likely to be infected [18], and the likelihood of me being infected is half, judging by the above figures.

So, $p_{get infected if you are not vaccinated} = p_{get sick if you are vaccinated} \times 10 = 0.5$.

A $p_{transmit the disease if you are not vaccinated} = 0.4 \times 2 = 0.8$.

Now we can calculate the disease transmission rates.

 $\beta_{uu} = p_{transmit the disease if you are not vaccinated} \times p_{get infected if you are not vaccinated} =$

 $= 0.8 \times 0.5 = 0.4$.

 $\beta_{uv} = p_{transmit the disease if you are not vaccinated} imes p_{get sick if you are vaccinated} =$

 $= 0.8 \times 0.05 = 0.04$.

 $\beta_{vu} = p_{get infected if you are vaccinated} \times p_{get infected if you are not vaccinated} =$

 $= 0.4 \times 0.5 = 0.2$.

 $\beta_{vv} = p_{get infected if you are vaccinated} \times p_{get sick if you are vaccinated} =$

 $= 0.4 \times 0.05 = 0.02$.

Let's simulate the model with these parameters. In Fig. 1 you can see the results for one hundred days:

SEIRD-model with vaccine: Susceptible, Exposed, Infectionus, Recovered, Dead

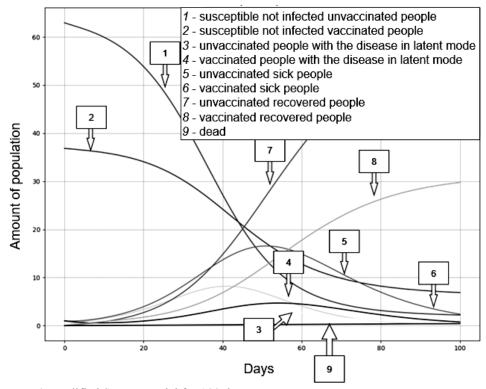
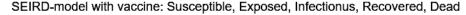


Fig. 1. Modified SEIRD model for 100 days

Fig. 1 shows how the number of people who have not had the disease is decreasing, while the number of people who have had the disease is increasing.

The number of unvaccinated patients is growing faster, which seems logical given the vaccination rate [13]. The number of deaths is growing relatively slowly. The number of uninfected, unvaccinated people is decreasing faster because they are more likely to contract the disease, while vaccinated people are slower to get sick.

If we look at a much longer time period (e.g., 8,000 days), we can see in Fig. 2 how the number of deaths increases and the number of deaths in the rest of the population decreases. The number of people who became ill also decreases because model (2) also takes into account natural mortality, which in this case does not include deaths from COVID-19.



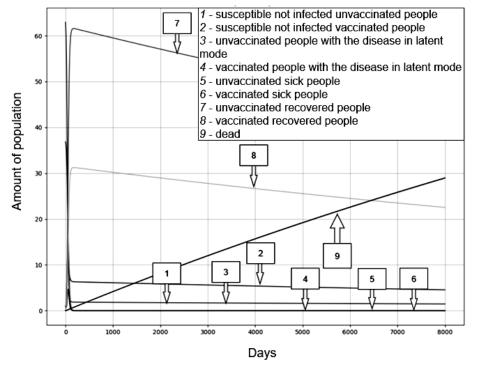
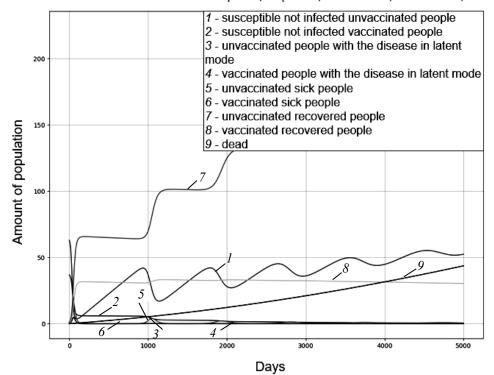


Fig. 2. Modified SEIRD model for 8000 days

This situation with fertility and mortality is due to the fact that in Ukraine the birth rate is lower than the death rate [20]. If we increase the fertility rate so that it exceeds the mortality rate, the situation looks different (fertility l = 0.0500181008) (Fig. 3):

Only the number of unvaccinated people who have not yet become ill increases, because this model does not include vaccination and the corresponding transition from unvaccinated to vaccinated people. The entire birth population is unvaccinated by default. From Fig. 3, you can also see how the disease process progresses over time: on the thousandth and two thousandth day, you can see waves of sick unvaccinated people, and accordingly, the number of unvaccinated people who have not yet become sick decreases over time.



SEIRD-model with vaccine: Susceptible, Exposed, Infectionus, Recovered, Dead

Fig. 3. Modified SEIRD model for 5000 days with a birth rate of 1 = 0.0500181008

CONCLUSIONS

The modified mathematical epidemiological SEIRD model is an important tool for assessing epidemic outbreaks and implementing disease control strategies. It is especially important that this model takes into account vaccination and non-vaccination, as this reflects the real situation with COVID-19 and other diseases for which vaccines exist. This model also allows for the impact of different vaccine variants on the effectiveness of its use.

To effectively combat epidemic outbreaks, it is necessary to know what factors influence the spread of the disease and which control strategies are most effective in specific conditions. The developed modified SEIRD model not only takes into account vaccination and non-vaccination, but also has coefficients responsible for birth and death, and that is why it can reflect a realistic picture. This model can help solve these problems by providing scientists and policymakers with a tool for forecasting, planning, and decision-making to control the epidemic.

Also, for the modified SEIRD model, all parameters were calculated from real statistical data from Ukraine to be able to simulate the situation as close to reality as possible. These data are important for making decisions on the development of medical infrastructure, the provision of medical equipment and medicines, as well as for determining the need for large-scale vaccinations and other epidemic control measures.

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МОДИФІКОВАНА SEIRD-МОДЕЛЬ ОПИСУ ЕПІДЕМІЇ COVID-19 / А.І. Клименко, Г.Б. Подколзін

Анотація. Присвячено математичним моделям в епідеміології, зокрема SIR, SEIR і SEIRD. Досліджено важливість цих моделей у прогнозуванні поширення інфекційних захворювань та оцінювання ефективності контрольних заходів. Ці моделі дають змогу оцінити важливі параметри епідемії, такі як швидкість поширення інфекції, кількість людей, які зазнають захворювання, та померлих від цього захворювання. Ці дані можуть допомогти у прийнятті рішень про введення та зняття карантинних обмежень, відкриття і закриття шкіл та інших установ, а також у розробленні стратегій вакцинації та інших контрольних заходів. Загалом математичні моделі SIR, SEIR і SEIRD є важливим інструментом з боротьби з епідеміями. Вони дозволяють епідеміологам і медичним працівникам прогнозувати та контролювати поширення захворювань, що зберігає здоров'я та життя людей.

Ключові слова: епідеміологія, епідеміологічні моделі, модифіковані математичні моделі, SEIR-моделювання COVID-19, SEIRD-модель, невакциновані люди, вірус, поділ популяції, нові штами.