# Mathematical Model of the COVID-19 Epidemic

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## ABSTRACT

The article deals with the construction of a mathematical model of the epidemic of COVID-19 using data from Hubei Province (China) using the SEIRD-model. SEIRD-model allows you to take into account the ability of infected individuals to contagion others in the latent period of the disease progression, which is very important because it means that the disease spreads covertly. The model curve of SEIRD-model is built with assumptions that do not change its form essentially and do not affect the model. Indexes of SEIRD-model reproduction in latent and active periods differ in size and differ from the index of SIRD-model reproduction in a smaller direction, but these values aren't compatible with known data.

Analyzing the acquired information, it can be concluded that in order to reduce the number of patients and to get out of the epidemic it is necessary to put under restraint the inflow of susceptible individuals into the group; to introduce quarantine measures or artificially immunize susceptible individuums and develop treatment measures to reduce mortality.

***Keywords:*** *mathematical model, epidemiological model COVID-19, SEIRD-model, SIRD-model, differential equation system*

## 1. INTRODUCTION

Deterministic mathematical models of epidemic diseases allow us to study the macroscopic propagation effect of these epidemics spreading in human society. The unequivocal, demonstrativeness and simple nature of these models make them attractive for analysis and provide information for the managing development of the epidemic. H. Bailey remarked that the main significance of these studies is that they are related to the work of public health authorities [1]. The development of such models is facilitated by a number of simplifications: the progression of the epidemic is studied in a homogeneous, continuous and evenly intermixing large group, which makes it possible to consider the general processes of the epidemic in a simplified form.

In 1927, in their work W.O. Kermack and A.G. MacKendrick created and researched a model representing a differential equation system with initial conditions, which is called the classical SIR-model [2]. H. Bailey (Norman T.J. Bailey) researched deterministic models describing simple epidemics, epidemics of a common type, and recurring epidemics [1]. L. Edelstein-Keshet provides insight into the SIR-model (Susceptible, Infected, Recovered) and its SIRS and SIS-modifications [3]. He showed that under certain conditions, the SIRS-model takes the form of SIR-models Kermack and MacKendrick. The development of the SIR-model is also SEIR- (Exposed - latent), MSEIR-models (Maternally derived immunity - endowed congenital immunity) [4]. While studying the COVID-19 disease evoked by SARS-CoV-2 virus, the SIRD-model (Dead - the deceased) and SEIRD-model are proposed for consideration [5, 6]. The SEIRD model which is under consideration in [6] differs in that the parameters characterizing infection and mortality depend on time, but does not take into account the ability of infected individuals to infect susceptible individuals in the latent (incubation) period. The SEIRD model presented in the source [7] to study the Ebola epidemic distinguishes itself by the fact that though it takes into account the presence of individuals in the latent period, it does not take into account the ability of these individuals in the latent period to infect susceptible individuals.

Various deterministic models are an instrument for investigating the population dynamics of individuals in an epidemic environment, in particular, they have been widely used in the study of EHF (Ebola haemorrhagic fever) [7, 8].

## 2. METHODOLOGY

Two deterministic mathematical models of the COVID-19 epidemic are compared: SIRD- and SEIRD-models [9]. The dissimilarity between the SEIRD-model under consideration here and the SIRD-model and other similar deterministic models is that it allows us to take into account the ability of infected individuals to infect susceptible individuals in the latent period [9-10].

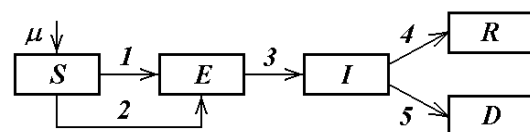Figure 1 shows a block diagram of SEIRD-model processes.

**Figure 1:** Block diagram of SEIRD-models

Parameters of the SEIRD-model under consideration are presented in Table 1.

**Table 1**: Table of SEIRD-model parameters

| p-n | Proceeding | Transition rate |
|---|---|---|
| 1 | $(S, E) \rightarrow (S – 1, E + 1)$ | $\beta_1\,S\,E$ |
| 2 | $(S, I) \rightarrow (S – 1, I + 1)$ | $\beta_2\,S\,I$ |
| 3 | $(E, I) \rightarrow (E – 1, I + 1)$ | $\delta\,E$ |
| 4 | $(I, R) \rightarrow (I – 1, R + 1)$ | $\gamma\,I$ |
| 5 | $(I, D) \rightarrow (I – 1, D +1)$ | $\lambda\,I$ |

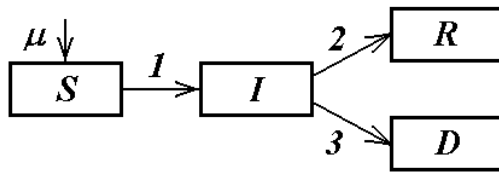Figure 2 shows a block diagram of the SIRD-model processes.



**Figure 2:** Block diagram of SIRD-models

The parameters of the SIRD-model under consideration are presented in Table 2. This model at $\mu = 0$ coincides with the SIRD model considered in the source [5].

**Table 2**: Table of SIRD-model parameters

| p-n | Proceeding | Transition rate |
|---|---|---|
| 1 | $(S, I) \rightarrow (S – 1, I + 1)$ | $\beta\,S\,I$ |
| 2 | $(I, R) \rightarrow (I – 1, R + 1)$ | $\gamma\,I$ |
| 3 | $(I, D) \rightarrow (I – 1, D +1)$ | $\lambda\,I$ |

SEIRD-model (S - susceptible, E - latent, I - infected, R - recovered, D - dead) is reduced to solving the Cauchy problem for a system of five first order ordinary differential equations with unknown *S(t), E(t), I(t), R(t), D(t)* and initial conditions (IC) *S*(0)=n, *E*(0) = a, *I*(0) = 0, *R*(0)=0 and *D*(0)=0.

$$\begin{cases} \dfrac{dS(t)}{dt} = -\beta_1 S(t)E(t) - \beta_2 S(t)I(t) + \mu, \\[2mm] \dfrac{dE(t)}{dt} = \beta_1 S(t)E(t) + \beta_2 S(t)I(t) - \delta E(t), \\[2mm] \dfrac{dI(t)}{dt} = \delta E(t) - \gamma I(t) - \lambda I(t), \\[2mm] \dfrac{dR(t)}{dt} = \gamma I(t), \\[2mm] \dfrac{dD(t)}{dt} = \lambda I(t), \end{cases} \quad (1)$$

The SIRD model (S - susceptible, I - infected, R - recovered, D - dead) comes down to solving the Cauchy problem for a system of four first order ordinary differential equations with the unknown *S(t), I(t), R(t), D(t)* and IC *S*(0) = n, *I*(0) = a, *R*(0) = 0 and *D*(0) = 0.

$$\begin{cases} \dfrac{dS(t)}{dt} = -\beta S(t)I(t) + \mu, \\[2mm] \dfrac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t) - \lambda I(t), \\[2mm] \dfrac{dR(t)}{dt} = \gamma I(t), \\[2mm] \dfrac{dD(t)}{dt} = \lambda I(t). \end{cases} \quad (2)$$

The following coefficients have been implemented: $\beta_1, \beta_2$ and $\beta$- characterize the morbidity in the group in latent, action, and complete periods of the disease respectively; $\delta$ - characterizes the proceeding of individuals from the latent period to the period with the active course of the disease; $\gamma$- characterize the loss of individuals from the group (isolated, recovered and become immune from infection as a result of immunization); $\lambda$- characterize the loss of individuals as a result of death from infection in the group; $\mu$- characterizes the constant influx of susceptible individuals who add to the group.

Coefficient $\beta_1$- the possibility of infection from an infected individual in the latent period will be equal to $\beta_1 = q_1/(T_1 n)$; coefficient $\beta_2$ - the possibility of infection from an individual who is in the active period will be equal to $\beta_2 = q_2/(T_2 n)$; coefficient $\beta$- the possibility of infection from an individual during the whole period of the disease, will be equal to $\beta = \frac{q}{Tn}$. $q_1, q_2$ и $q$ - indices of reproduction in latent, active, and complete periods of the disease consequently, $T_1, T_2$ и $T$- latent, active and complete-time periods of the disease, $n$ - the quantity of the considered group of homogeneously stirring individuals; $q_1 \neq q_2 \neq q$. The coefficient $\delta = 1/T_1$ characterizes the rate of transition from the latent period to the active period. The coefficient $\gamma = 1/T$ - the rate of recovery. The coefficient $\mu$- the number of receptive individuals with whom the group is replenished. The coefficient $\lambda$ can be taken as an established percentage of already infected individuals.

The influx of new susceptible individuals ($\mu$) is not compensated by the death of individuals removed from the population ($\lambda I$), and thus the total population volume does not remain constant, $S(t) + I(t) + R(t) + D(t) + \mu \neq const$ for the SIRD-model and $S(t) + E(t) + I(t) + R(t) + D(t) + \mu \neq const$ for the SEIRD-model.

It is assumed that throughout the development of the epidemic, the coefficients remain constant, i.e., there is a constant influx of susceptible individuals into the group, quarantine measures do not change, the number of deaths remains the same as a percentage of the number of patients, and the virus does not change in terms of infectivity (contagion). Calculations were made with the assumption that the original group has the volume $n = 11$ million susceptible individuals because the eruption occurred largely in Wuhan City of Hubei Province, which has a population of about 10-12 million, and at the time of the collection of statistics, the entire Hubei Province was under strict quarantine measures. Time periods of $T = 30$, $T_1 = 14$and $T_2 = T - T_1$days. Coefficient $\lambda = 0{,}025$, indexes $q =$

8,0, $q_1$ = 2,0 and $q_2$ = 5,5. The maximums of model curves of population dynamics corresponded to the maximum statistical data on Chinese Hubei province [10].

## 3. RESULTS

The solving is performed by the rk function from the Maxima computer algebra system (CAS) «dynamics» library, which solves the Cauchy problem using the Runge-Kutta method of the quartic of accuracy [11].

The time period of the epidemic progression - 200 days. There is no influx of receptive individuals ($\mu$ = 0) because hard quarantine measures are introduced before long [8]. For SEIRD-models $\alpha$- latent, and for SIRD-model $\alpha$- infected individuals, so the second case $\alpha$is taken in 100 times less, initially infected a small group of people. With such IC, the maximum number of infected individuals by SEIRD and SIRD-models is the same numbers since the beginning of the epidemic, according to real values. The number of infected individuals with any obvious symptoms was found to be about 6.7% of the total number of infected individuals; recorded cases would be much lower, at only about 15% of infected individuals with obvious symptoms [9]. Due to the fact that an individual is the virus propagator both in latent and active periods of disease, it is necessary to take into account the dynamics of infected individuals in latent and active periods. In Figure 3, the curve «expos_SEIRD» - dynamics of infected individuals in the latent period of disease according to SEIRD-model, the curve «inf_SEIRD» - dynamics of infected individuals in the active period of disease according to SEIRD-model, the curve «sum_SEIRD» - the total curve of the previous two curves, the curve «inf_SIRD» - dynamics of infected individuals according to SIRD-model. The COVID-19 disease is diagnosed difficult in the latent period, and by decreasing conditionally the influence of «expos_SEIRD» by 50% in «sum_SEIRD» without changing the SEIRD-model parameters, you can get the number of registered cases that are roughly equal for both models.
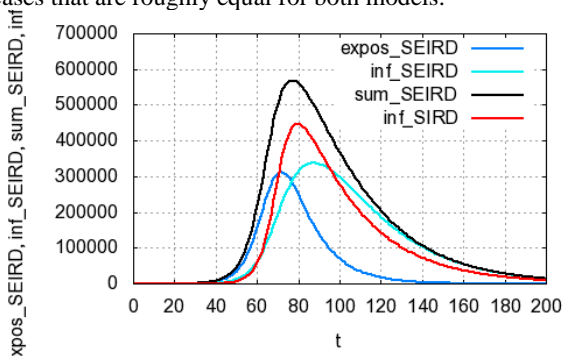


**Figure 3**: Comparison of SIRD- and SEIRD-models

Let there be a sustainable and steady flow of receptive individuals ($\mu$ = 10 000 people). For SEIRD-model IC - $\alpha$ = 1 000, SIRD-model - $\alpha$= 10 people. The time period of 1200 days was examined. The rest of the parameters remain the same. Perceptible the second and third «waves» in the dynamics of the emergence of infected on both models, the amplitude of the «waves» is much smaller than the amplitude of the first «wave», the maximum «waves» are 500 and 900 days from the day when there were $\alpha$ = 1,000 latent individuals on SEIRD-model. A certain number of infected persons are preserved with an established inflow of susceptible individuals. Figure 4 shows the results.
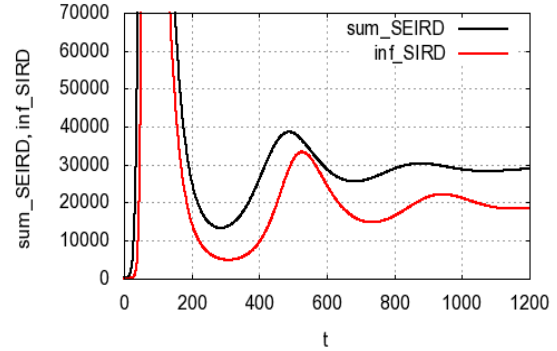


**Figure 4:** "Waves" in the progression of the epidemic

Further the compliance of the models with the statistical data as of April 12, 2020 is considered [10]. There is no influx of receptive individuals ($\mu$ = 0), inasmuch quarantine measures have been introduced. It is thought that the initial mass infection occurred mostly in one place in the first days of December 2019 and amounted to 100 people according to the SEIRD model, who were in the first 14 days of the latent period of disease, were until then relatively infectious to others and were not counted [8]. From the 15th day these 100 people left the latent period, and the first mass infection began on December 20-21, 2019. And although the first hundred continued to actively infect others, the next mass increase in active patients occurred when another 14 days passed, and the next «portion» entered the active phase of the disease, but the first hundred has already contributed to the fuzzification of the picture. Such «discontinuity» in the spread of the disease remained for some time, they were reflected in the statistics on January 28 and February 12, and then there is a «fuzzification» of the growth of registered infections. The amount of growth of registered infected persons is to a large extent «leapfrogging» because the latent state («expos_SEIRD») is poorly visible in the statistics for the first 14 days of the disease, and the total growth of registered persons («sum_SEIRD») is mainly due to infected persons who are in the active disease period («inf_SEIRD»). During the construction of the graph, the latent infections were conditionally counted in «sum_SEIRD» only those that were present on the last day of the previous 14-day period, because they were registered in statistics partially. The computational data have been compared with Hubei province statistics, as shown in Figure 5.
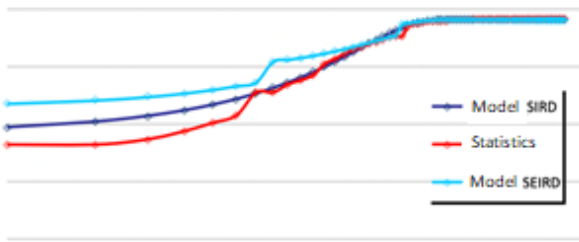
**Figure 5:** Comparison of SIRD- and SEIRD-models with statistics, in the logarithmic axis of reference

Calculation of Fisher's and Student's variance ratio criteria showed that null hypotheses about equality of dispersions and average data sets cannot be rejected, and with 0.95

## 5. CONCLUSION

SEIRD-model allows you to take into account the ability of infected individuals to contagion others in the latent period of the disease progression, which is very important because it means that the disease spreads covertly. The number of infected individuals is much higher than the number of registered cases. In the early epidemic progression stages, no registration was made. During the first days of the accounting period registration is characterized by underreporting of cases, which is especially noticeable on the logarithmic graphs, if we assume that the SIRD- and SEIRD-models appropriately reflects the dynamics of infection. Calculated data show that about 6.7% of infected individuals were probably registered and that the mass spread of the disease began in the early days of December 2019, presumably on December 3-4, 2019. If we take into consideration the hypothesis of the disease spreading through a medical institution, the «zero patient», one or the whole family, arrived on the 15th-21st day of his illness in the active phase in a medical institution, infecting the staff and patients there on December 3-4, 2019. The infection of «zero patient» occurred earlier, 15-21 days earlier, on November 13-20, 2019, with seafood provisions from the Wuhan market or somewhere else.

The curve of validated cases in Hubei Province has the form explained by the peculiarities of disease spread in the latent period. The model curve of SEIRD-model is built with assumptions that do not change its form essentially and do not affect the model.

Indexes of SEIRD-model reproduction in latent and active periods differ in size and differ from the index of SIRD-model reproduction in a smaller direction, but these values aren't compatible with known data.

probability it can be stated that the obtained curves are applicable to describe the morbidity dynamics in Hubei province under accepted assumptions.

## 4. DISCUSSION

Analyzing the information obtained, we can conclude that in order to reduce the number of cases and exit the epidemic it is necessary to limit the influx of susceptible individuals into the group (reduce the coefficient $\mu$ down to zero, which will remove the «waves» and decrease the number of infected after the first peak to zero); introduce quarantine measures or artificially immunize susceptible individuals (reduce the coefficients $\beta_1$, $\beta_2$ and $\beta$); develop treatment measures to reduce mortality (reduce the coefficient $\lambda$).

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