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Stochastic Generalization of the Epidemiological SIR Model

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In this paper we propose stochastic modification of well-known in epidemiology CIR model. This modification allows us to simulate various scenarios of infection and can be used for the risk management.

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1. Introduction

Nowadays, there are a fairly large number of models used in epidemiology to describe the process of the spread of the disease. Usually, the main task of the models used is to describe the trends in the spread of the disease and to estimate some average state of the population in the future. For this purpose models of various types can be used, e.g. deterministic, statistical, time-series [1–5].

In a number of cases, models demonstrates good predictive properties, but it is difficult to use them to estimate the values of functionals from a random process. For example, often deterministic models doesn't allow to estimate the possible variance, and for statistical models the availability of statistical data is necessary to construct such estimates. One of the approaches that could be used to estimate the values of functionals can be a transition to stochastic processes, which are built on the basis of a formal description of the investigated processes.

In this paper we propose stochastic modification of the SIR model, which is well-known in epidemiology. It should be noted that we deliberately do not modify more modern and multifactorial modifications of modern models in epidemiology, since our goal is to assess the impact of the appearance of a stochastic component, for example, in the deterministic equation We need to remind, that in SIR model $S \equiv S(t)$ denotes a number of susceptible individuals at time t, $I \equiv I(t)$ – infectious and $R \equiv R(t)$ – recovered.

The origin of the model is the early 20th century, with important works being that of Ross in 1916 [6], Ross and Hudson in 1917 [7, 8], Kermack and McKendrick in 1927 [9] and Kendall in 1956 [10]. In this model the extension of an epidemics formalized in the form of the following differential equations:

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta IS}{N}, \\ \frac{dI}{dt} &= \frac{\beta IS}{N} - \gamma I, \\ \frac{dR}{dt} &= \gamma I \end{aligned}$$

where N is population size, β is the average number of contacts per person per time, probability of an infectious individual recovering in interval dt is γdt. In the model we suppose,

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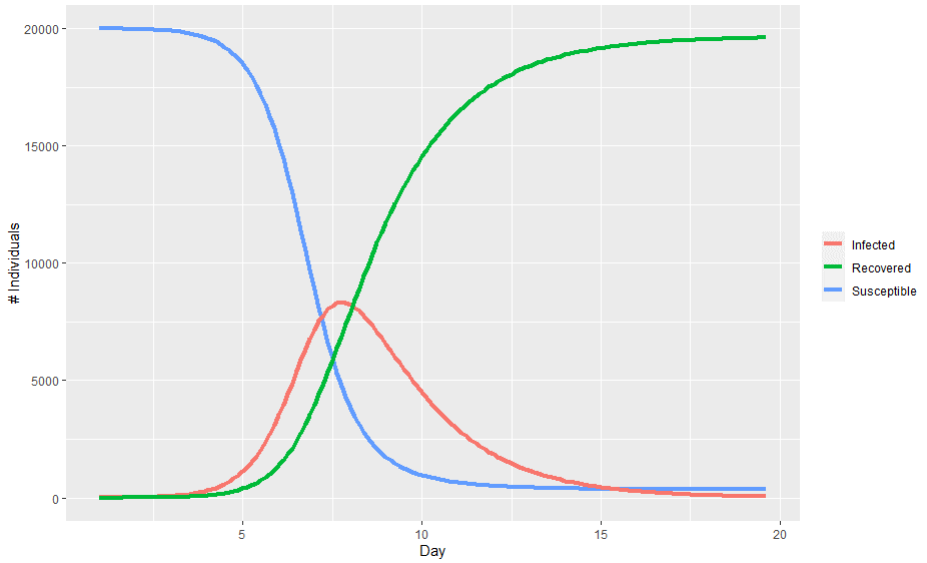

FIG. 1: (color online) A typical solution of SIR model [13].

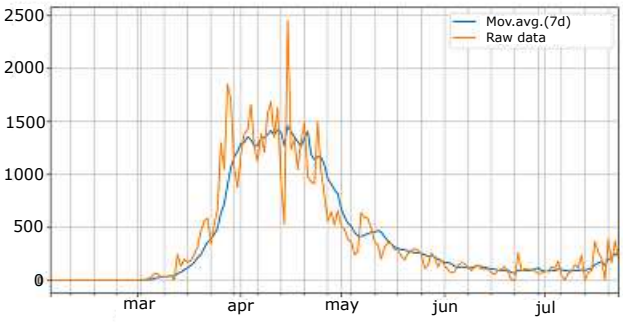

FIG. 2. (color online) Dynamic of COVID-19 for Belgian, 2020 (Src: https://coronavirus.jhu.edu/).

that

$$\frac{dS}{dt}+\frac{dI}{dt}+\frac{dR}{dt}=0, \quad S(t)+I(t)+R(t)=N=\ \text{const}.$$

A solution of the SIR model was found by Miller in the following form (see [11, 12]):

$$\begin{aligned} S(t) &= S(0)\mathrm{e}^{-\zeta(t)}, \\ I(t) &= N-S(t)-R(t), \\ R(t) &= R(0)+\rho\zeta(t) \end{aligned}$$

where

$$\zeta(t)=\frac{\beta}{N}\int_0^t I(\tau)d\tau, \quad \rho=\frac{\gamma N}{\beta}.$$

Currently, the SIR model and its modifications are used for the description of COVID-19 dynamics (see fig. 1).

As shown at Figure 2 (the data provided by Johns Hopkins University & Medicine), the deterministic SIR model can somehow be used to describe some averaged dynamics of the number of infected, but it absolutely does not take into account the random nature of the observed process. The solution of the model somehow coincides with the moving average shown in the plot, but if the constructed solution is used as a forecast, then in a significant number of cases we will not be ready for the increased number of the infected. To overcome such a drawback we propose the stochastic modification of the model.

2. Stochastic SIR model

Since the SIR model does not provide an opportunity to estimate fluctuations in the

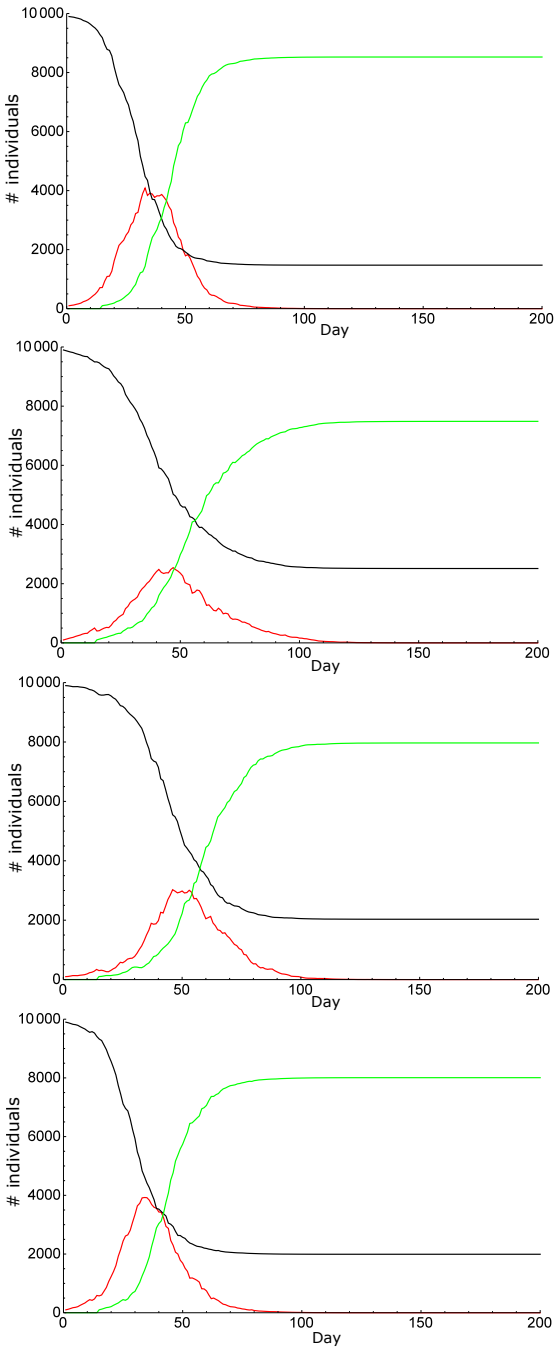

FIG. 3. (color online) Realizations of decease dynamics. Red, green, and black curves are numbers of infected, recovered, and susceptible individuals, respectively.

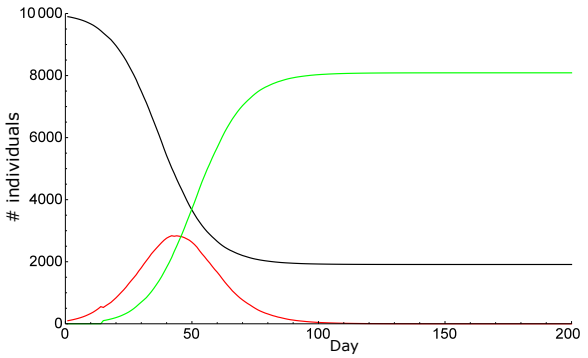

FIG. 4. (color online) Mean values for proposed model. Red, green, and black curves are numbers of infected, recovered, and susceptible individuals, respectively.

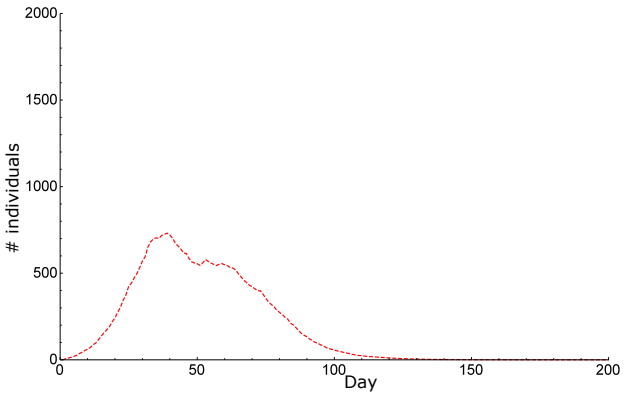

FIG. 5: Standard deviation for infected individuals.

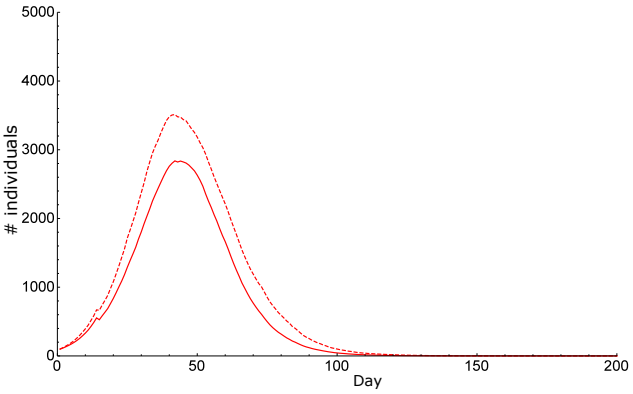

FIG. 6. (color online) Mean with standard deviation for infected individuals. Solid line is the mean of infected individuals, dashed line is sum of mean and standard deviation of infected ones.

Table 1: Probabilistic rule.

	infected	not infected
p	$\beta I_n/N$	$1-\beta I_n/N$

number of infected, it is difficult to use this model for assessing the required amount of resources in the case when an infection developing according to a scenario worse than the predicted value. This means, that if we assume that the distribution of the number of infected is symmetric or close to symmetric, then the estimate based on the above solution will be correct for approximately 50% of all possible scenarios, that is unacceptable.

In our modification of the SIR model we suppose, that the time is discrete $n = 0, 1, 2, \ldots$. Also we add the following parameters:

- ξ is a random infection rate,
- $\mathcal{L}$ is the duration of illness,

and the additional equation for variable DI_n, which denotes the increase of the number of infected persons at time n.

then, the proposed model has the following form:

$$\begin{aligned} DI_n &= S_{n-1} I_{n-1} \xi, \\ I_n &= I_{n-1} + DI_n - DI_{n-\mathcal{L}}, \\ S_n &= S_{n-1} - DI_n, \\ R_n &= R_{n-1} + DI_{n-\mathcal{L}}. \end{aligned} \tag{1}$$

Here we have uses an additional condition $DI_j = I_j = S_j = R_j = 0$ for $j < 0$. For a large number of samples and assumptions on the independence of the trajectories, according to the central limit theorem, we can assume that ξ is a random variable with a normal distribution. Let us define the distribution of the random infection rate ξ. According to the SIR model the chance of infection p at time n is defined by the rule presented in Table 1.

Since this scheme actually calculates the number of cases based on the number of infected at a previous step I_{n-1}, i.e. constants under the conditions of step n, the randomness of the choice of ξ depends on the factor β/N. In this case, according to the central limit theorem, ξ has a normal distribution, the parameters of which are not depended on the step and the mean $\mathbb{E}\xi = \beta/N$. The open question is how a value of a variance of ξ can be estimated. For example, the variance can be calibrated based on experimental data.

3. Numeric experiment

During numeric experiment we use the following parameters. Population size is $N = 10000$, the durability of illness is $\mathcal{L} = 14$, where the parameters $\beta = 2/\mathcal{L}$, $\xi = \mathcal{N}(\frac{\beta}{N}, \frac{\beta}{2N})$ is the normal distribution with the mean value β/N and standard deviation $\beta/(2N)$. Here we suppose that the initial number of infected is $I(0) = 0.01N$. For the experiment, the Monte-Carlo method is used with a total number of the simulated trajectories equals to 1000. It should be noted again that the same initial conditions were used for different simulations.

The fig. 3 shows us various scenarios of decease. Here black curve is for the number of susceptible persons, red curve is for the number of infectious and green one is for the number of recovered. The proposed model demonstrates us various trajectories during a course of the epidemic (see. fig. 3). For determined population size we have a quite "good" disease course, when the number of infected person is above 2000 of infected, and a "bad" scenario, where the number of infected is more than 4000.

Figure 4 shows the dynamics of the means of the proposed stochastic model. It should be noted that the behavior of the mean of the proposed

model coincides with the behavior of the mean of the original one (see fig. 1,4).

The standard SIR model allows us to predict a certain average scenario for the development of the epidemic. The proposed model allows also to take into account the random nature of the infection process. Fig. 5 demonstrates the standard deviation for the infected individuals. Moreover, usually risk assessment requires the determination of some upper level of the amount of infected individuals, which can be reached in the worst case of the decease course, and the model (1) allows us to estimate such a level. For example, as one can see from the Fig. 6, the appearance of a trajectory is possible, in which the number of infected significantly exceeds the mean value. Such a behavior cannot be described in terms of the deterministic models.

4. Conclusion

An important aspect of the modeling and subsequent forecasting is the presence of simplifications and inaccuracies in the description of a process, but also we need to create models that allow evaluating the values of functionals from the obtained solutions, which, we believe, is confirmed by researches (see, e.g. [14, 15]).

The proposed modification of the SIR model into a stochastic one allows us to predict the dynamics of the epidemic as well as to calculate the parameters of a possible random course of the disease, expressed in the form of functionals along trajectories, which can be used in risk management.

In this paper, we have shown that the random nature of the process under study can lead to significant fluctuations so that deviation of a specific value of the number of infected people relative to the predicted one can be very significant (see. Fig. 4–6).

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