Mathematical COVID-19-models including stochastics

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Abstract

The management of the actual COVID-19 pandemic is a great challenge for scientists of quite different research areas. In addition to virology research, mathematical models and simulations can be a valuable contribution to the understanding of the dynamics of the pandemic and can give recommendations to physicians and politicians. In this paper mathematical models of epidemics will be described, developed and applied to yield a contribution to the control and management of the pandemic. Most of the treatment of the current COVID-19 pandemic with SIR-type models was a deterministic description of the epidemic regime. In reality there are some uncertainties like incomplete data, big estimated number of unknown cases and for example mismatched PCR-tests. One possibility to describe this situation is given with the consideration of stochastic processes in the models. In this paper an extension of SIR-type models to stochastic differential equations will be presented exemplarily. The random disturbances of data will be described by addends consisting of random variables and Wiener processes. As a base for this investigations the German data of the beginning of the pandemic of 2020 was used. It could be shown that the developed models with stochastic differential equations are able to describe random influences on the pandemic by comparing the results with those of the deterministic ones.

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1 Introduction

Because of the absence or scarcity of vaccines against the COVID-19 virus it is a great demand of mathematical models to describe the pandemic and to control non-pharmaceutical interventions to decrease number of infected people and to avoid the propagation of the virus.

With the SIR-model (see [1]) it is possible to describe pandemics like the spanish fly ([2]) or the COVID-19 pandemic. The aim of this model consists in tracing the dynamics of sub-populations of susceptible (S), infected (I), and recovered (R) people in a certain region. Classic SIR-type models are deterministic. These are simple but effective for describing the progression of the pandemic. They are able to fit the description of the average infection dynamics in macroscopic sub-populations. SIR-type models were successful used to gave the politicians important recommendations for actions and measures for the fight against the COV-Sars-2 virus (see for example [3], [4], [5], [6], [7], [8], [9], [10], [11], [12]).

Random influences can not fitted by the standard models. But there are some uncertainties which cannot embraced by the model parameters. And this is reason to extent the deterministic models to stochastic ones.

This will be done exemplarily for the classic SIR-model but it is also applicable to other deterministic models like the $SEIR$- or the $SIR-X$-model [4].

2 The Mathematical SIR Model

First, I emphasize one important presupposition for the model. I suppose that the distribution of the included sub-populations is equal, i.e., the density is approximately constant. This is a very strict supposition, but this is acceptable, for example, for cities and congested urban areas like New York or the Ruhr area in Germany. At the beginning of the pandemic, exponential growth of the number of infected people is supposed.

In the so-called SIR model of Kermack and McKendrick [1], I denotes the infected people, S denotes the susceptible people, and R denotes the recovered people. It is a deterministic model. I constrain the investigations to the species I, S, and R only. There are also more complex deterministic models that include sub-populations other than S, I, and R (see [3, 4]), but the basic behavior of SIR-type models can be described by the following simple one. The dynamics of infections and recoveries can be approximated by the following system of ordinary differential equations:

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta \frac{S}{N} I && (1)\\
\frac{dI}{dt} &= \beta \frac{S}{N} I - \gamma I && (2)\\
\frac{dR}{dt} &= \gamma I \, . && (3)
\end{aligned}
$$

β represents the number of others that one infected person encounters per unit time (per day). γ is the reciprocal value of the typical time from infection to recovery. N is the total number of people involved in the epidemic disease, and $N = S + I + R$.

The currently available empirical data suggest that the coronavirus infection typically lasts for some 14 days. This means that $\gamma = 1/14 \approx 0{,}7$.

The choice of β is more complicated. Based on the daily data of infected people in Germany ([13], [14]) at the very beginning of the pandemic in [5] was found $\beta \approx 0{,}21$.

By the division of the compartement I of the infected people into the compartement E of infected people who exposed and not infectious and the compartement I of infected people who are infectious also, the so called $SEIR$-model was introduced (see for example [7]):

$$\begin{aligned}
\frac{dS}{dt} &= -\beta\frac{S}{N}I \\
\frac{dE}{dt} &= \beta\frac{S}{N}I - \alpha E \\
\frac{dI}{dt} &= \alpha E - \gamma I \\
\frac{dR}{dt} &= \gamma I\ .
\end{aligned}$$

α is the reciprocal of the latency period ($\alpha = \frac{1}{4}$ assumed).

3 Stochastic framework

Stochastics pioneers like Norbert Wiener and Kiyoshi Itó (see [15]) introduced the mathematical basics of stochastic analysis and stochastic processes. Key concepts like Brownian motion (Wiener process) or the Ito-integral innovated the theory of stochastic differential equations.

Because of the fact that a Wiener process W_t is not differentiable, an equation like

$$\frac{dX_t}{dt} = f(X_t) + g(X_t)\frac{dW_t}{dt}$$

don't stack up, where X_t is a random variable and W_t is a Wiener process. That's the reason for the integral formulation

$$dX_t = f(X_t)dt + g(X_t)dW_t\ . \tag{4}$$

Equations (4) are called "stochastic differential equations" (sde, see for example [16]). A formal solution of (4) for a given initial state X_0 is of the form

$$X_t = X_0 + \int_0^t f(X_t)dt + \int_0^t g(X_t)dW_t\ . \tag{5}$$

The first integral of (5) is a classic Riemann-integral, but the second integral

$$\int_0^t g(X_t)dW_t \tag{6}$$

is not covered by the classic integration because of the mad properties of the Wiener process W_t. Itó introduced for integrals like (6) the concept of the "Itó integral" and thus he showed a way to solve stochastic differential equations with the formula (5). The stochastic process X_t from equation (5) is called an **Itó-process**.

Now we can augment the deterministic model equation system to the stochastic differential equation system

$$
\begin{aligned}
dS_t &= -\beta \frac{S_t}{N} I_t \, dt - \nu I_t dW_t && (7)\\
dI_t &= (\beta \frac{S_t}{N} I_t - \gamma I_t) \, dt + \nu I_t dW_t && (8)\\
dR_t &= \gamma I_t \, dt \, . && (9)
\end{aligned}
$$

The index t does not mean a time-derivative. I_t, S_t and R_t denote stochastic processes and W_t is a Wiener process with its main characteristic $W_t - W_s \sim N(0, \sqrt{t-s})$, $t > s$ and the independence of W_t and W_s for $t \neq s$. With the addend $\nu I_t dW_t$ we try to describe the random fluctuation of infected people, for instance unrecognized or over/under-estimated infected people. The scope of such random effects can be controlled by the parameter ν.

Together with initial data S_0, I_0 and R_0 a stochastic SIR-model is defined.

4 Numerical Solution methods for the classic deterministic SIR-model and the stochastic SIR-model

I disclaim qualitative mathematical considerations like existence and uniqueness of solutions of the dynamical system of (1)–(3) and concentrate my interest on practical application and numerical experiments. It should be mentioned that both the deterministic SIR-ode-system and the stochastic SIR-sde-system with certain initial values are solvable with unique solutions.

The numerical solution of the ordinary differential equation system of the SIR model was done with a Runge–Kutta integration method of the fourth order. The independence of the time discretization of the solution method was tested by a systematic time-grid refinement. At the end, I found that time-steps of a day or half a day could be used.

For the solution of the stochastic SIR-model I used both the Euler-Maruyama method (order 1) and the Milstein method (order 1,5). An overview on the numerics of sde's is given in [17]. As time-steps I could use a day or half a day also.

5 Numerical Computations for Germany based on SIR-type models

With the choice of a β-value of $0{,}215$ –which is evaluated on the basis of the real data from the ECDC– and $\gamma = 0{,}07$, one gets the progress of the pandemic's dynamics, pictured in Figure 1b ($I0$ denotes the initial value of the I species, that is, 31 January 2020. The total number N for Germany is guessed to be 70 million). R_0 is the basis reproduction number of persons infected by the transmission of a pathogen from an infected person during the infectious time ($R_0 = \beta/\gamma$), shown in the following figures[1]. Because of the delay in development and production of vaccines it was looking for non-pharmaceutical control strategies for the pandemic. In [5] suitable points in time are discussed to start a lockdown by the reduction of people

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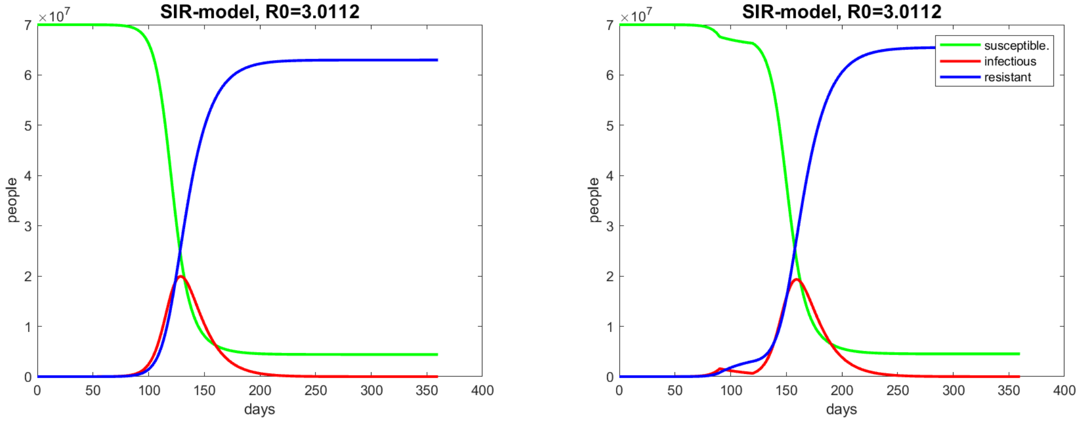
[1] The values of R_0 in all of the following figures are applied to the β-value of the beginning of the pandemic.

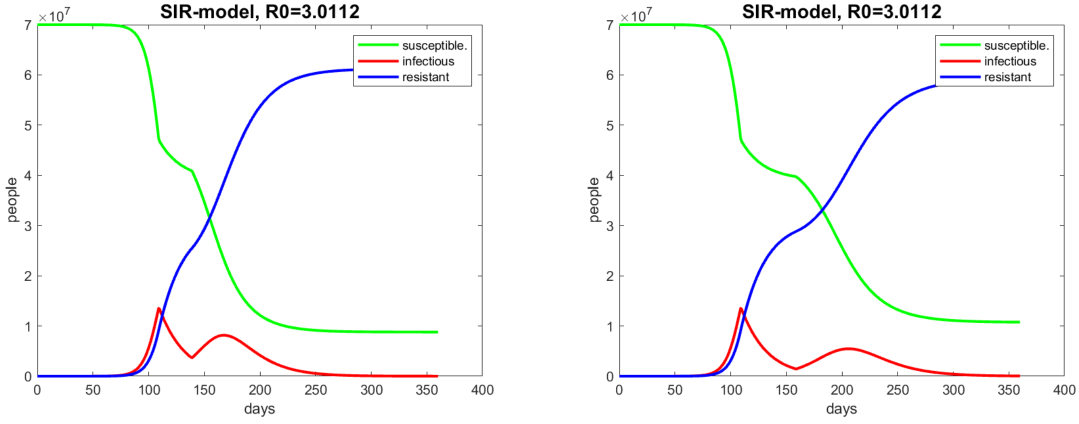
contacts by some measures related to the social life. It could be shown that very early lockdowns move the pandemic behavior by the duration of the lockdown (see Figure 1b).



(a) (b)

Figure 1: (**a**) Typical undisturbed one-year pandemic regime in Germany; (**b**) The pandemic regime as a result of an early 30-days lockdown.

Only starting points of lockdown behind the time (it was called ”dynamical lockdown”) when the curve of infected people changes his behavior from convex to concave are successful for flattening the curve. The Figures 2a and 2b show the effect of dynamical lockdowns.

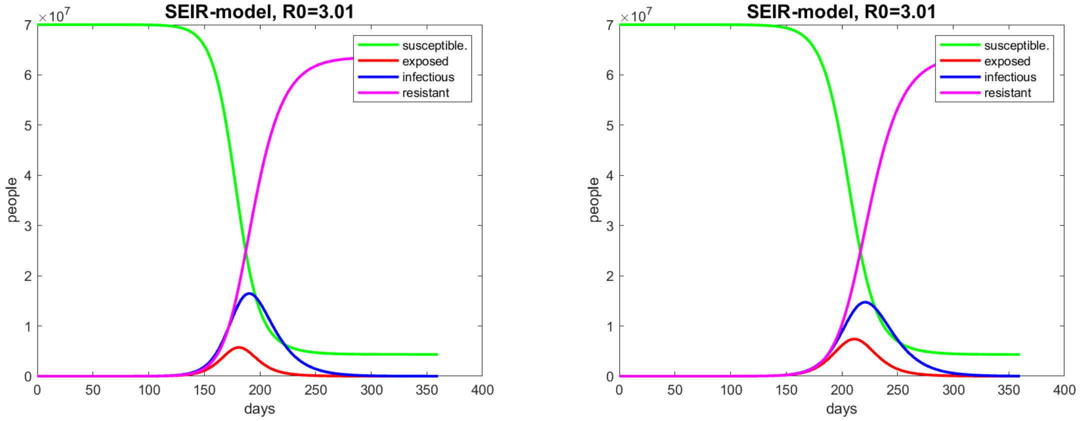


(a) (b)

Figure 2: (**a**) The one-year pandemic behavior for a 30-days dynamical lockdown; (**b**) The one-year pandemic behavior for a 50-days dynamical lockdown.

Other non-pharmaceutical interventions based on SIR-models are discussed for example in [3] or [9].

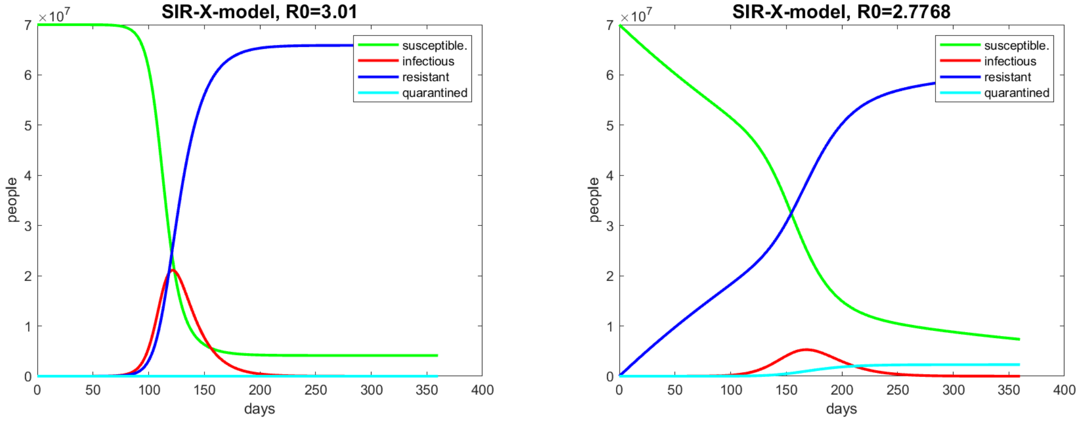
The $SEIR$-model allows more granular investigations of the pandemic propagation. The results of simulations based on the $SEIR$-model are pictured in Figures 3a and 3b.



(a) (b)

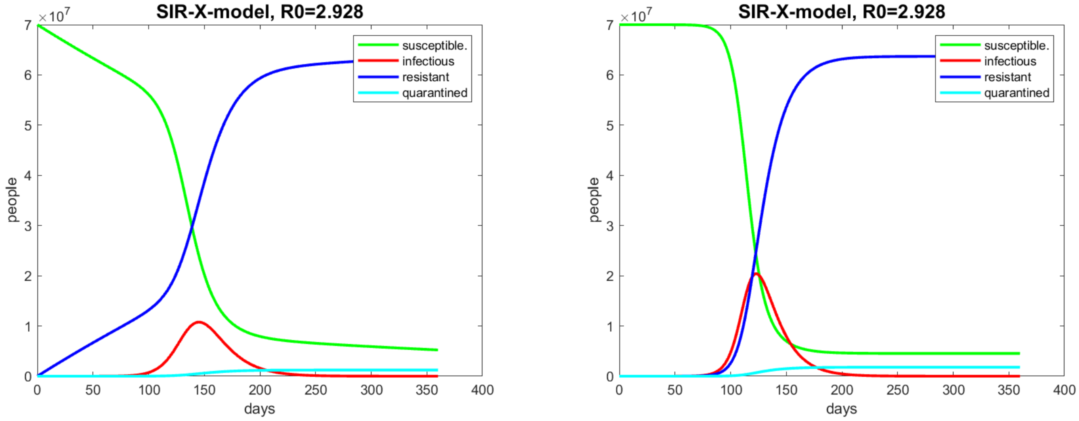
Figure 3: (**a**) The one-year pandemic behavior described with the $SEIR$-model, $\alpha = 1/4$; (**b**) The one-year pandemic behavior described with the $SEIR$-model, $\alpha = 1/6$.

The Figures 4a, 4b, 5a und 5b show the results of the $SIR-X$-simulation for Germany.



(a) (b)

Figure 4: (**a**) The one-year pandemic behavior described with the $SIR-X$-model, $\eta_0 = 0$, $\eta = 0$; (**b**) The one-year pandemic behavior described with the $SIR-X$-model, $\eta_0 = 0\ 003$, $\eta = 0\ 003$.

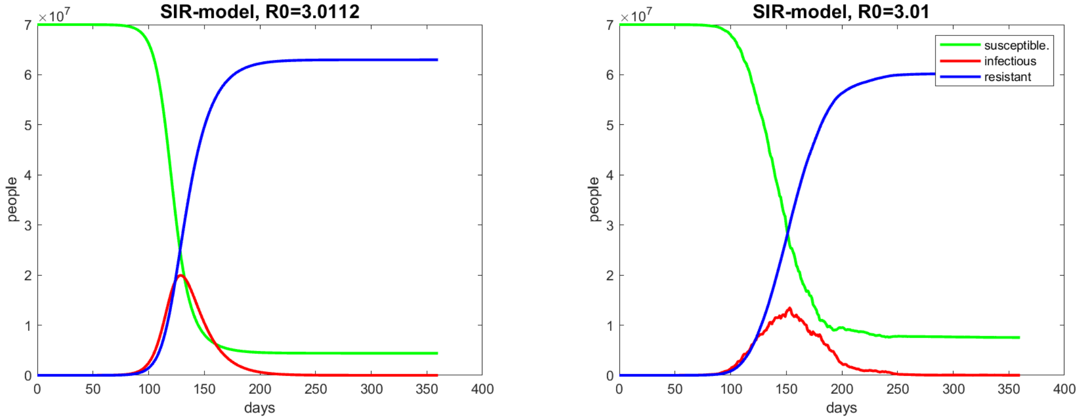


(a) (b)

Figure 5: (**a**) The one-year pandemic behavior described with the $SIR - X$-model, $\eta_0 = 0{,}002$, $\eta = 0$; (**b**) The one-year pandemic behavior described with the $SIR - X$-model, $\eta_0 = 0$, $\eta = 0\ 002$.

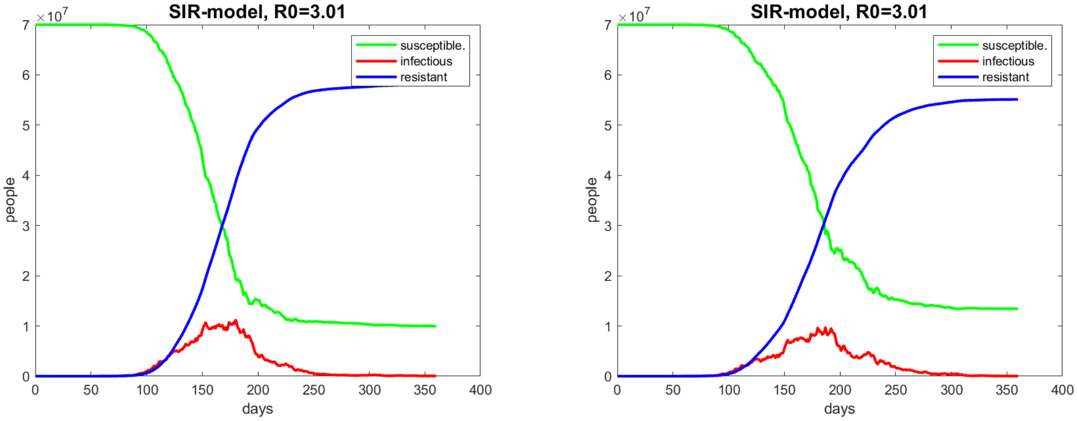
6 Numerical Computations for Germany based on stochastic SIR-models

In all countries concerned by the COVID-19 pandemic, there are random influences on the infection run which can not be covered by deterministic SIR-type models. With the addend $\nu I_t dW_t$ in the sde-system we describe the extend of eventuality of the information about the parameters β and γ based on the real data capture. It means a certain percentage of the infected people is unknown or miscount. In the following we demonstrate the effects caused by the consideration of random disturbances. In Figures 6 and 7 the results of numerical solution of the sde-system (7)-(9) are compared to the deterministic ones. As a solution we understand the mean of 50 paths of the Itó-processes generated by the Euler-Maruyama method of solving the sde-system.



(a) (b)

Figure 6: (**a**) Deterministic simulation of the one-year pandemic regime in Germany; lockdown; (**b**) Stochastic simulation of the one-year pandemic regime in Germany, $\nu = 0{,}2$.



(a)

(b)

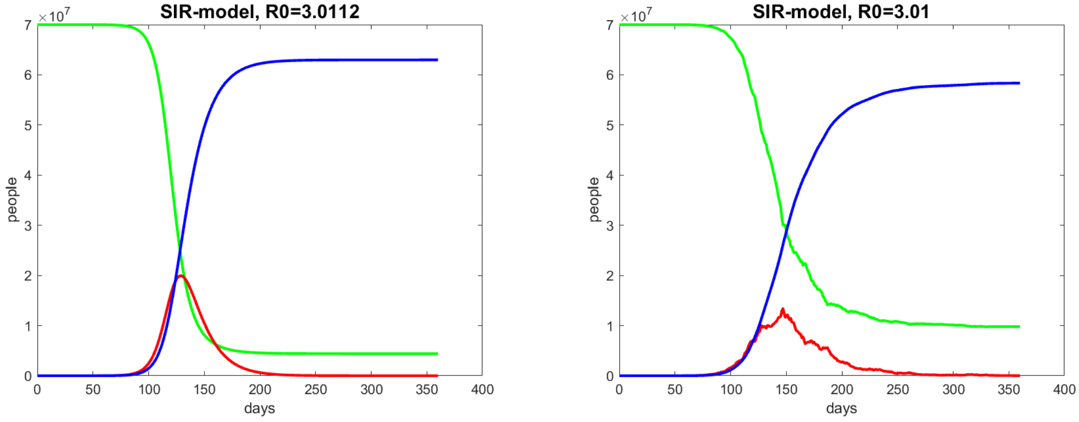
Figure 7: (**a**) Stochastic simulation of the one-year pandemic regime in Germany, $\nu = 0{,}25$; lockdown; (**b**) Stochastic simulation of the one-year pandemic regime in Germany, $\nu = 0{,}3$.

The simulations show that the maximum of infected people is in inverse proportion to the magnitude of ν (which determines the extend of uncertainty about the pandemic data.

The Wiener process W_t follows a Gaussian distribution ($\sim N(0,\sqrt{t})$). Instead of W_t I consider a stochastic process Y_t which is uniform distributed with values in $[-1{,}1]$. Now we analyze the sde-system

$$\begin{aligned} dS_t &= -\beta\frac{S_t}{N}I_t\,dt - \nu I_t dY_t && (10)\\ dI_t &= (\beta\frac{S_t}{N}I_t - \gamma I_t)\,dt + \nu I_t dY_t && (11)\\ dR_t &= \gamma I_t\,dt\;. && (12)\end{aligned}$$

With Y_t and the addend $\nu I_t dY_t$ it is now possible to fix an uncertainty interval $[-\nu,\nu]$. The result of the numerical analysis of the sde-system (10)-(12) compared to the deterministic solution is pictured in Figure 8



(a)

(b)

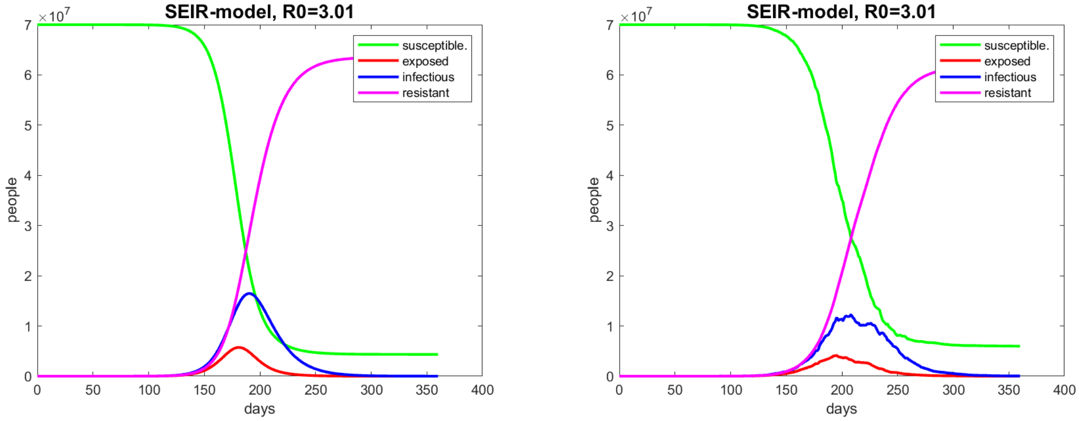
Figure 8: (**a**) Deterministic simulation of the one-year pandemic regime in Germany; lockdown; (**b**) Stochastic simulation of the one-year pandemic regime in Germany, $\nu = 0{,}4$ (solution of (10)-(12).

This result confirms the simulations with the Gaussian distributed Wiener process W_t.

The inclusion of random effects into the $SEIR$-model follows the proceeding with the SIR model in the section above with the result

$$
\begin{aligned}
dS_t &= -\beta\frac{S_t}{N}I_t dt - \nu(E_t + I_t)\, dW_t && (13)\\
dE_t &= (\beta\frac{S_t}{N}I_t - \alpha E_t)dt + \nu E_t\, dW_t && (14)\\
dI_t &= (\alpha E\_\gamma I_t)dt + \nu I_t\, dW_t && (15)\\
dR_t &= \gamma I_t dt\ . && (16)
\end{aligned}
$$

In Figures 9a - 9b the results of the deterministic and stochastic $SEIR$-simulations are pictured.



(a)

(b)

Figure 9: (**a**) Deterministic simulation of the one-year pandemic regime in Germany with the $SEIR$-model; lockdown; (**b**) Stochastic simulation of the one-year pandemic regime in Germany, $\nu = 0{,}125$ (solution of (13)-(16)).

7 Discussion and Conclusions

With the extensions to a $SEIR$- and a $SIR-X$-model a more granular resolution of the pandemic development could achieved. In this paper I gave an overview on different SIR-type models as a base for the development of stochastic extensions of the deterministic SIR-type models. For the appropriate choice of the parameters ν, η_0 and η are further analyses of actual data necessary. But the given simulation results let expect an improvement of the pandemic modeling.

It could be shown that the results of the deterministic simulations over-estimate the height of the infected curve. The stochastic simulations results in a decreased maximum of infected people.

As shown in an earlier paper ([5]) there are two possibilities for the rise of of infected people to be inverted and the medical burden to be reduced. Firstly the reduction of the stock of the species S. This can be obtained by immunization or vaccination. Another possibility is the isolation of high-risk people (70 years and older) as it wa shown with the $SIR-X$-model. Positive tests for antibodies reduce the stock of susceptible persons. The second possibility is the reduction of the infection rate β. This can be achieved by strict lockdowns, social distancing at appropriate times, or rigid sanitarian moves.

In conclusion, it must be said that the results of the simulations show that stochastic extensions of the SIR-model are easy to realize and they are able to describe the pandemic propagation more realistic. Thus the extended stochastic models could be a valuable contribution for the description and control of the actual pandemic.

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