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### Simulation of the behaviour of covid-19 with the stochastic SIRD model: case of Peru

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#### Abstract

*In this work, we simulate the dynamics of COVID-19 pandemic using a deterministic SIRD model and its stochastic SIRD model version. The model is used under a closed population of 32 625 984 from the peruvian country, where the coefficient of the transmission rate, the recovery rate, the dead rate and the initial condition are given for the data taken from the initial days reported by the first disease people in Perú.*

**Keywords** . COVID-19 pandemic, deterministic and stochastic model, SIRD model, simulation.

**1. Introduction.** In recent years, the world has suffered a tremendous pandemic named Covid-19, which is a respiratory disease that generally transmits through direct contact with an infected person, but it also can spread by indirect contact with a virus infected environment. This changed the lifestyle at all the human beings, in schools, workplaces, etc. Mathematical models are tools for modeling and studying disease transmission.

The COVID-19 is focused to developed in Perú and the parameters of the model are determined with the data of peruvian stations, the reports of infected, deceased and recovered people provided are used. As a result, we obtained the configuration of the infected, susceptible and removed populations.

There are many studies that have adopted mathematic approaches to model the transmission of COVID-19. For example, in [1], the authors used the classical deterministic SIR epidemic model to formulate a model for the transmission of COVID-19 in Perú and for differents peruvian regions [2].

El Koufi [3], presents a stochastic model of the COVID-19 epidemic for a population with five compartments.

Jianhai Bao et al. [4], using a variation-of-constants formula for a class of SDEs with jumps, they provide an explicit solution for one-dimensional competitive Lotka–Volterra population dynamics with jumps, and investigate the sample Lyapunov exponent for each component and the extinction to n-dimensional model.

Gao and Wang [5] have studied a stochastic mutualism model integrating the Lévy and Markov processes. This article presents a stochastic model of the Covid-19 epidemic for a population with five compartments.

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The present work shows a deterministic model and a stochastic model of the COVID-19 epidemic for the peruvian population using a basic SIRD model. A numerical study is made of the both proposed deterministic and stochastic models. Also, the results of each model are compared.

**2. Deterministic model.** When in a certain population  $N$  there is someone people infected with a virus, it is divided into the group of infected ( $I$ ), group of susceptible ( $S$ ), the group of recovered ( $R$ ) and the group of dead ( $D$ ), and that over time evolve according to the scheme of the figure 2.1.

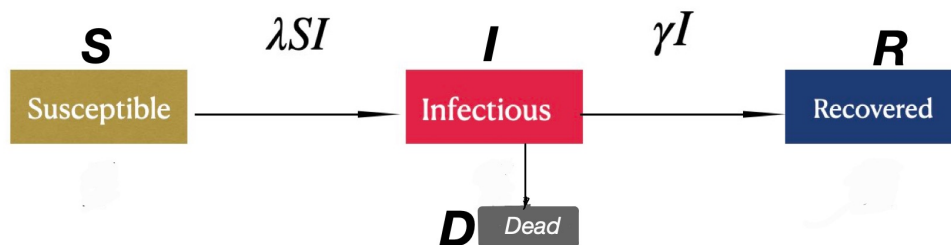


Figure 2.1: Dynamic of the pandemic population

Which is expressed at a modification of the mathematical model( proposed in 1927 by Kermack & McKendrick [6]) by the system of four equations:

$$\begin{cases} \frac{dS(t)}{dt} = -\lambda S(t)I(t), \\ \frac{dI(t)}{dt} = \lambda S(t)I(t) - \gamma I(t) - \mu I(t), \\ \frac{dR(t)}{dt} = \gamma I(t), \\ \frac{dD(t)}{dt} = \mu I(t). \end{cases} \tag{2.1}$$

It is called the model SIRD, where the variables and parameters are described in Table 2.1

Variables	Meaning
$S(t)$	Susceptible population to be infected at time $t$ ,
$I(t)$	Infected population at time $t$ ,
$R(t)$	Recovered population at time $t$ ,
$D(t)$	Dead population at time $t$ ,
$t$	The time expressed at days.
$\lambda$	The trasmission rate through exposure of the disease,
$\gamma$	The rate of recovering,
$\mu$	Mortality rate.

Table 2.1: Variables and parameters for the system (2.1).

All the variables must be satisfy the compatibility condition  $N = S(t) + I(t) + R(t) + D(t)$ , that is, the total population remain unchanged.

**2.1. Population data of Perú.** According to the national census of October 22, 2017, the Peruvian population reaches 31 million 237 thousand 385 people, and based on forecasts as of June 30 of each year [7], from the estimate of this Institucion indicates that the aproximate population is  $N = 32625948$ .

Therefore, for this work, we assume that data of global population is the estimate  $N = 32625948$ .

**2.2. Data COVID-19 of Perú (March-September 2020).** To use the system of equations (2.1) in the calculation of the parameters we need the values of  $S(t)$ ,  $I(t)$ ,  $R(t)$  and  $D(t)$ , which have been obtained from the official reports of MINSA (Ministry of Health) [2] from March 5 to September 30, 2020. For example, the Table 2.2, shows only some days.

Day t	Date	Susceptible S(t)	Infected I(t)	Recovered R(t)	Deceased D(t)
0	mar-05	32 625 948	0	0	0
1	mar-06	32 625 947	1	0	0
12	mar-17	32 625 831	116	0	1
26	mar-31	32 624 883	630	394	41
27	apr-01	32 624 625	829	447	47
33	apr-07	32 622 994	1 734	1 100	120
40	apr-14	32 615 645	7 204	2869	230
47	apr-21	32 608 111	10 371	6 982	484
56	apr-30	32 588 972	25 520	10 405	1 051
57	may-01	32 585 489	28 206	11 129	1 124
71	may-15	32 541 453	54 956	27 147	2 392
87	Jun-01	32 455 909	96 898	68 507	4 634
117	Jul-01	32 337 471	100 372	178 245	9 860
148	Aug-01	32 203 765	111 940	290 835	19 408
179	Set-01	31 962 511	154 001	480 177	29 259
208	Set-30	31 807 651	95 234	690 528	32 535

Table 2.2: Data related to COVID-19 in Perú (Mar. 05 to Set. 30, 2020).

**2.3. Estimate of parameters  $\lambda$ ,  $\gamma$  and  $\mu$ .** The equations of the former model for COVID-19 implies the determination of parameters  $\lambda$ ,  $\gamma$  and  $\mu$  based on the evolution of the official data of the effects of COVID-19 (see Table 2.2) reported by the respective Regional Health Managements[2], which satisfy the system of equations (2.1).

In order to calculate the parameters we use the approximation of the derivative by central difference  $f'(t) \approx \frac{f(t+h)-f(t-h)}{2h}$ , implies that for each day of the sample data  $t = 1, 2, \dots, 208 = T$  we calculate the parameters  $\lambda_t$ ,  $\gamma_t$  y  $\mu_t$ , which give us a sequence of data. Then we calculate the simple average of such values to have the final parameters which we can see at table 2.3 .

$$\lambda = \frac{\sum_{t=1}^T \lambda_t}{T}, \quad \text{where } \lambda_t = \frac{S(t+1) - S(t-1)}{2S(t)I(t)}, \quad (2.2)$$

$$\gamma = \frac{\sum_{t=1}^T \gamma_t}{T}, \quad \text{where } \gamma_t = \frac{R(t+1) - R(t-1)}{2I(t)}, \quad (2.3)$$

$$\mu = \frac{\sum_{t=1}^T \mu_t}{T}, \quad \text{where } \mu_t = \frac{D(t+1) - D(t-1)}{2I(t)}. \quad (2.4)$$

Country	t=0	S(0)	I(0)	R(0)	D(0)	$\lambda$	$\gamma$	$\mu$
Perú	march 17	32 525 831	116	0	1	2.53195E-09	0.0457600061	0.0019902810

Table 2.3: Parameters of model SIR for Covid-19 in Perú (Mar. 17 to Set. 30, 2020).

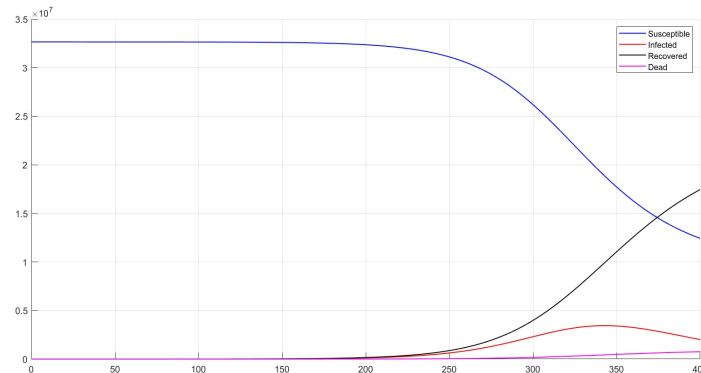
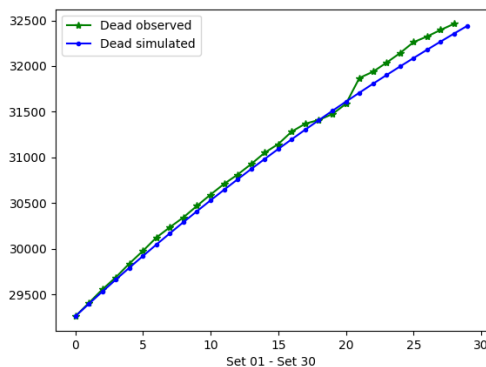


Figure 2.2: Deterministic results with Data: from Mar. 17 to Set. 30 of 2020.

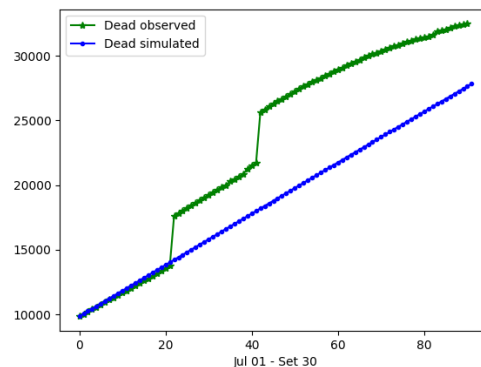
**2.4. Deterministic simulation results.** Now, we solve the equation system (2.1), using de initial values and parameters of Table 2.3 and we get the results shown in Fig. 2.2

In the projection to May 2021 we can see that the period of greatest infection is from February 09 - March 30, the day of greatest infection is March 11, which reaches 2,708,144 infected.

The code is tested with observed data and we see that the simulated data behaves very well for short periods of time, as see the period 01 september to 30 of september, see the subfigure 2.3a, but for longer periods such as July 1 to September 30, there are some separation at the final part, see subfigure 2.3b



(a) Comparison September 1 to September 30



(b) Comparison July 1 to September 30

Figure 2.3: Two periods of comparison of deaths .

**3. Stochastic model.** Note that in the deterministic model all parameters are assumed to be deterministic, regardless of environmental fluctuations. From a biological point of view, this hypothesis imposes some limitations on the mathematical modeling of ecological systems, as we can see in the behavior of the deceased variable, in figure 3.1, the behaviour of the observed data and the simulated data, from march 19 to may 16; population dynamics in the real world are inevitably affected by environmental noise.

from the environment affects the spread of covid 19 and considering that we are still not sure that we have the completely accurate data. we consider that the stochastic aspect could be interesting. In addition,

in the case of infected people who do not develop the disease and disperse it (for example, the case of some children) But we can also mention the case of asymptomatic patients who are not monitored, but are the cause of transmission in the community.

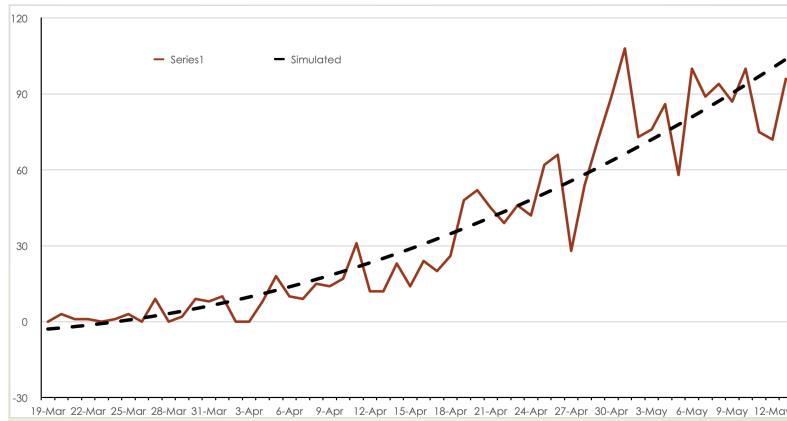


Figure 3.1: Dead in Perú, Mar. 19 to May. 16, 2020 (simulated vs observed data).

There is other possibility, of touching an infected object could be generate transmission of the disease, this is a variety of possibilities of transmission consequently we can assume that there are two ways considered in the literature for modelling the influence of environmental fluctuations in population dynamics[4]. One is to consider random perturbations of each of the variables and their not very well known influence between the susceptible ones in the infected and the recovered ones by a white noise. Similar to Jiang et al. [8] it is proposed a stochastic system of the form:

$$\begin{cases} dS(t) = -\lambda S(t)I(t)dt + \sigma_1 S(t)dW_1(t), & S(0) = s_0, \\ dI(t) = (\lambda S(t)I(t)dt - \gamma I(t))dt + \sigma_2 I(t)dW_2(t), & I(0) = i_0, \\ dR(t) = \gamma I(t)dt + \sigma_3 R(t)dW_3(t), & R(0) = r_0, \\ dD(t) = \mu I(t)dt + \sigma_4 D(t)dW_4(t), & D(0) = d_0. \end{cases} \quad (3.1)$$

Here,  $s_0, i_0, r_0, d_0 \geq 0$  with  $s_0 + i_0 + r_0 + d_0 = 1$ ;  $W_i(t)$  are independent standard Brownian motions and  $\sigma_i^2 \geq 0$  represent the intensities of  $W_i(t), i = 1, 2, 3, 4$ .

In addition to the above, the unpredictability of growth can be considered, this implies the existence of a stochastic disturbance of the growth rate  $\lambda(t)$  due to white noise, therefore, the growth rate has the following transformation:

$$\lambda \rightarrow \lambda + \sigma_5(t)\dot{W}(t),$$

leading to the next system, similar to one at [9]:

$$\begin{cases} dS(t) = -\lambda S(t)I(t)dt + \sigma_1 S(t)dW_1(t) - \sigma_5 S(t)I(t)dW_5(t), \\ dI(t) = (\lambda S(t)I(t) - \gamma I(t) - \mu I(t))dt + \sigma_2 I(t)dW_2(t) + \sigma_5 S(t)I(t)dW_5(t), \\ dR(t) = \gamma I(t)dt + \sigma_3 R(t)dW_3(t), \\ dD(t) = \mu I(t)dt + \sigma_4 D(t)dW_4(t). \end{cases} \quad (3.2)$$

where  $W_5(t)$  is the classic Brownian motion,  $\sigma_5$  is the intensity of the environmental white noise.

The entire system is defined on a complete probability space  $(\Omega, \mathcal{F}, \mathbb{P})$  with a filtration  $\mathcal{F}_{t \geq 0}$  satisfying the usual conditions (i.e., it is right continuous and increasing, while  $\mathcal{F}_0$  contains all the null sets on  $\mathbb{P}$ ).

On the existence and uniqueness of the solution of the system (3.2), the coefficients of the system do not satisfy the Lipschitz condition and linear growth, as required in [10], only satisfy a local continuous Lipschitz . However, under certain conditions, Zhou et al.[11] proved the existence of the unique global solution of the system (3.2).

**3.1. Numerical simulation: Milstein method.** Before the discretization of model (3.2), we will normalize the system; as the population considered has a constant size  $N = 32625948$ , and we used this constant to normalized the variables in order to have  $N = 1$ , therefore we have  $S(t) + I(t) + R(t) + D(t) = 1$  for all  $t \geq 0$ . The initial conditions of system (3.2) is given as follows:

$$\begin{cases} S(0) = \frac{32645831}{N}, \\ I(0) = \frac{116}{N}, \\ R(0) = \frac{0}{N}, \\ D(0) = \frac{1}{N}. \end{cases} \quad (3.3)$$

For obtain a approximate solution of the system (3.2), we take  $dw_l \sim \Delta W_l = \zeta_l \sqrt{dt}$  where  $\zeta_l$  is the standard Gaussian random variable whit mean 0 and variance 1.

Then we have to do the discretization of the system, for this we use the finite difference method called, the Milstein's Higher Order Method given in [12], we get the discretization equation:

$$\begin{cases} S_{i+1} = S_i - \lambda S_i I_i \Delta t + S_i [\sigma_1 \zeta_{1,i} \sqrt{\Delta t} + \frac{1}{2} \sigma_1^2 (\zeta_{1,i}^2 - 1) \Delta t] \\ \quad - S_i I_i [\sigma_5 \zeta_{5,i} \sqrt{\Delta t} + \frac{1}{2} \sigma_5^2 (\zeta_{5,i}^2 - 1) \Delta t], \\ I_{i+1} = I_i + (\lambda S_i I_i - \gamma I_i - \mu I_i) \Delta t + I_i [\sigma_2 \zeta_{2,i} \sqrt{\Delta t} + \frac{1}{2} \sigma_2^2 (\zeta_{2,i}^2 - 1) \Delta t] + \\ \quad + S_i I_i [\sigma_5 \zeta_{5,i} \sqrt{\Delta t} + \frac{1}{2} \sigma_5^2 (\zeta_{5,i}^2 - 1) \Delta t], \\ R_{i+1} = R_i + \gamma I_i \Delta t + R_i [\sigma_3 \zeta_{3,i} \sqrt{\Delta t} + \frac{1}{2} \sigma_3^2 (\zeta_{3,i}^2 - 1) \Delta t], \\ D_{i+1} = D_i + \mu I_i \Delta t + D_i [\sigma_4 \zeta_{4,i} \sqrt{\Delta t} + \frac{1}{2} \sigma_4^2 (\zeta_{4,i}^2 - 1) \Delta t], \end{cases} \quad (3.4)$$

**3.1.1. Results.** The discrete equations (3.4) is solved explicitly by a code written in octave, whose results we present.

At the following we proceed to present some results obtained by the Milstein method. For this we use the following data: the interval step  $dt = 0.01$  days, the parameters given by the table 2.3, that is  $\lambda = 0.00000000253195$ ,  $\gamma = 0.047600061$ ,  $\mu = 0.0019902810$  and the initial point  $S(0) = \frac{32625831}{N}$ ,  $I(0) = \frac{116}{N}$ ,  $R(0) = \frac{0}{N}$ ,  $D(0) = \frac{1}{N}$ . For numerical simulations of discrete stochastic system (3.4) is used with the noise parameters  $\sigma_1 = \sigma_2 = \sigma_3 = \sigma_4 = \sigma_5 = 0.03$ .

The figure 3.2 present the stochastic simulations of discretized trajectories over the interval  $[0, 360]$ , with a sample of  $n = 100$  paths, for each separate variables, Susceptibles, Infected, Recovered and Dead populations, with  $\sigma_1 = 0$  and  $\sigma_2 = \sigma_3 = \sigma_4 = \sigma_5 = 0.03$ .

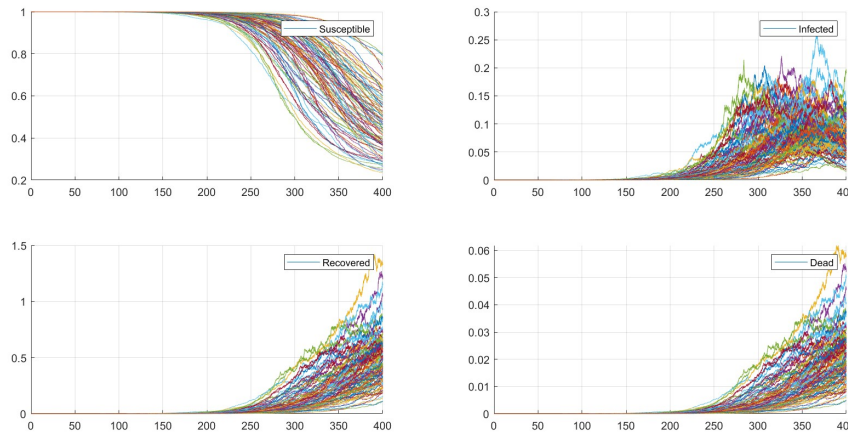


Figure 3.2: Susceptible, infected, recovered and dead: ensemble of 100 sample paths.

In figure 3.3, we present a comparison between the sample mean of stochastic solutions given in (3.2) with blue lines and the solutions of deterministic system (2.1) with red lines;

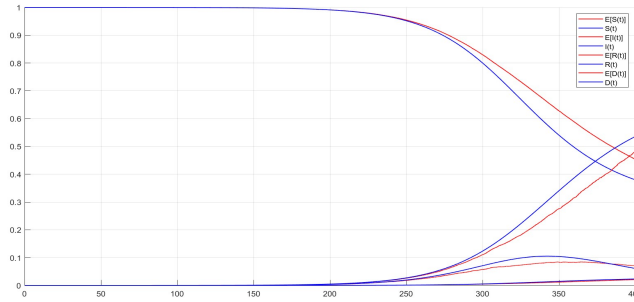


Figure 3.3: Deterministic solution (red) and sample mean stochastic solution (blue) with  $\sigma_i = 0.03, i=1:5$ .

At the following we present a sequence of results of the adimensionalized variables, for different parameter values  $\sigma_1, \sigma_2, \sigma_3, \sigma_4, \sigma_5$ , compared with the deterministic case ( $\sigma_i = 0, i = 1, \dots, 5$ ), in order to understand their role on the dynamics:

In the figure 3.4a for the susceptible variable, we see the comparison between the stochastic paths generated by stochastic system (3.2) for different noise values and the deterministic path given by the equation system (2.1);

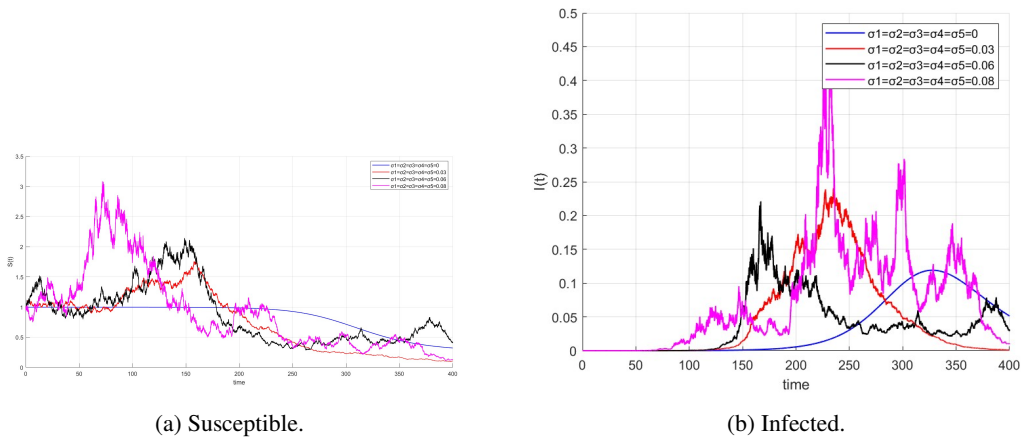


Figure 3.4: Dynamics of susceptible and infected variables.

Figure 3.4b shows the dynamics of the infected variable, we see the comparison between the paths of the stochastic system (3.2) for different noise values and the deterministic path given by the system (2.1).

In the figures 3.5a the Recovered variable and 3.5b the Dead variable, also are presented with some paths of stochastic system (3.2) for different noise values and the path of the deterministic system (2.1) respectively.

When intensities of white noise increasing, the maximums of  $I(t)$  and  $R(t)$  decrease, moreover the duration of the disease increases, the curves of system (3.2) always fluctuate around the curves of deterministic system (2.1).

Finally, we present some results where we can see that the presence of the random fluctuation of the variables as well as the random variation of the transmission rate allows us to improve the approximation of the simulated data to the observed data.

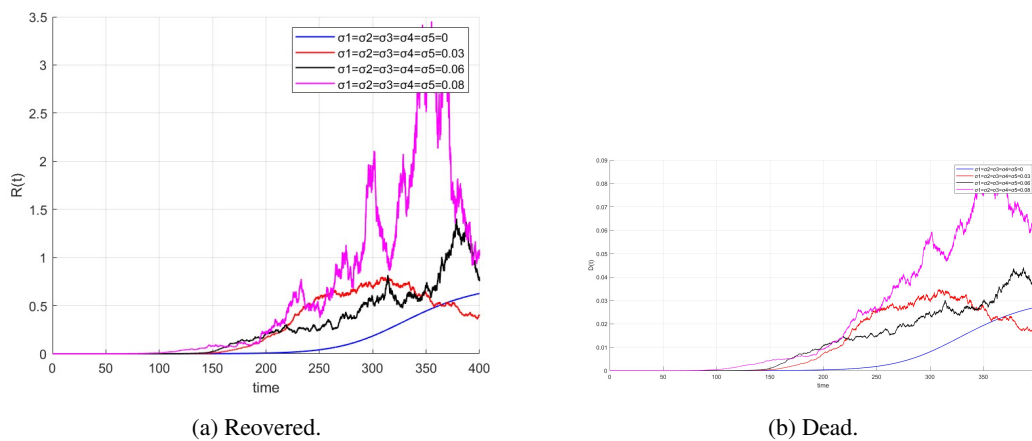


Figure 3.5: Dynamics of recovered and death variables.

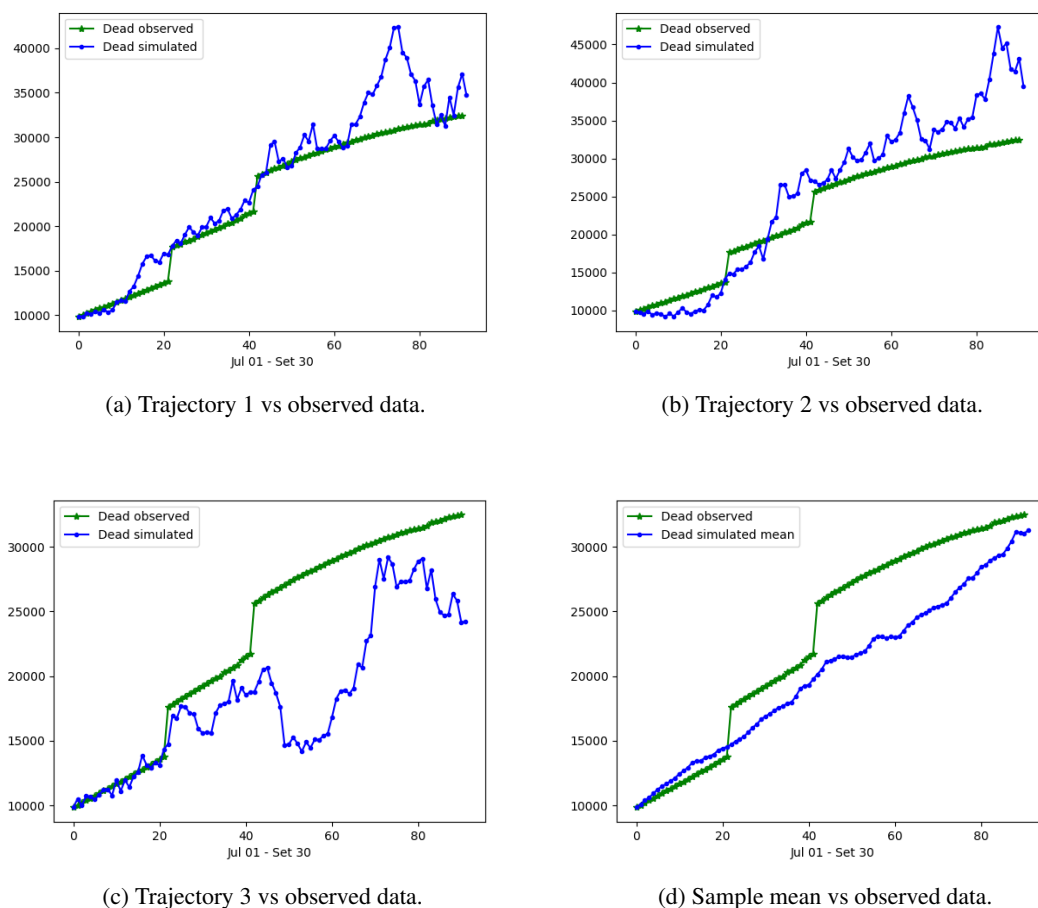


Figure 3.6: Comparison data observed vs data simulated stochastic case: July 01 to september 30 of 2020.

Unlike the deterministic case, presented in the figure 2.3, where we can see that after day 92 the difference between the observed and simulated data is 4020 units. In stochastic case presented in the figure 3.6, we can see that: three random paths at subfigures (a)(b)(c) compared with the observed data, moreover in the subfigure 3.6d we present the sample mean of 100 paths compared with the observed data, we see that at day 92 the difference between the simulated data and observed one of 950 units, with which the stochastic prediction could be more reliable than in the deterministic dynamic, with which we can conclude that



stochasticity incorporates improves at the simulation.

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