On the Estimation of Some Relevant Parameters in the COVID-19 Pandemic

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Abstract. This paper gives simple rules to calculate the transmission rate and some other parameters in COVID-19 from recorded data on the infection, recovery and death through several SIR-based epidemic models. In particular, it is emphasized how the transmission rate is highly dependent on the quarantine or confinement interventions. The proposed rules estimate the relevant time-derivative of some of the subpopulations of the model by using the standard known discretization rules.

1. Introduction

This paper relies on the study of an infective disease evolution which recorded data which are used to estimate the relevant parameters such as the transmission rate, the recovery rate and the disease-related mortality. The basic models are of continuous SIR (susceptible-infectious-recovered)-type either without or with demography and the most relevant equation is that of the time-evolution of the infectious. The needed time derivatives are calculated through known typical evaluation methods from the recorded daily discrete data. Such a model is positive by nature in the sense that the state-trajectory solution is non-negative under any given finite non-negative initial conditions. Epidemic models and other kinds of biological systems have been exhaustively studied through mathematical models based on differential, difference or differential-difference mixed equations. The biological and epidemic models have to be positive by nature. In particular, results on positivity and passivity of dynamic systems have been given in [1][2][3][4][5], in [6][7][8][9], and also in [10][11][12] and in some related references therein. Specific results for epidemic systems and for biological systems being based on the known Beverton-Holt equation were supplied in [13][14][15]. The subsequent sections give and discuss some continuous-time SIR epidemic models (either without demography or with demography) from the point of view of estimating some of its defining parameters, mainly, the transmission rate (but also the recovery rate and the mortality rate) from discrete recorded data related to COVID-19.

2. The basic infection differential equation

In this section, the infectious subpopulation is assumed to be subject to the following dynamics:

\[ \dot{I}(t) = (\beta S(t) - \gamma) I(t) ; \quad I(0) = I_0 \]  

(1)

where \( I(t) \) and \( S(t) \) are the susceptible and infectious subpopulations, respectively, and \( \beta \) and \( \gamma \) are the transmission rate (or disease transmission coefficient) and the recovery rate, respectively. Eqn. 1 is a part of the system of first-order differential equations which describe the simplest SIR (susceptible-infectious-recovered) epidemic models. The solution of (1) is:
\[ I(t) = e^{-\left[\gamma_{0} - \beta_{0}S(t)\right] \mu_{0} I(t)} I_{0} \]  

(2)

It is assumed in the following that the recovery rate is known from medical data. In the case that data of the disease have been registered, obviously with a discretization map, different techniques with distinct degrees of complexity can be used to estimate the transmission rate, which is the main objective of this study, depending on the more or less involved considerations about dynamic couplings of the infectious with other subpopulations and the way of estimating the derivative with respect to time of the infectious subpopulation. The transmission rate is considered time-varying through the estimation processes so that quarantine or confinement interventions could be evaluated in its average value along certain periods of times where the intervention authorities decrees apply.

Some simple potential estimation techniques are discussed in the sequel.

2.1 Neglecting the dynamics of the susceptible subpopulation

The basic assumptions of this subsection are the following ones:

Assumptions 1. The discretized infection function is registered, \( \gamma \) is known, while \( \beta \) is unknown, and the susceptible subpopulation is constant and equalizes the constant total population \( N \).

The situation where these assumptions can work is that of a very small percentage of infectious subpopulation related to the total population which is assumed constant. Typically, it can be reasonable at the beginning of the infective period of a new virus when almost the total population is susceptible with very small amounts of infectious and practically zero levels of immunity. That means that the level of natural mortality of the species is not considered to be relevant according to the length of the period of time under study and to the amount of total population of the environment under study and that, as a result, the mortality of the disease might also be neglected.

One gets from (1) and Assumptions 1 that:

\[ \beta(t) = \frac{1}{N} \left( \frac{I(t)}{I(t)} + \gamma \right) \]  

(3)

Now, assume that the registered infection data are supplied once per day so that the period is \( T = 1 \) day. The value of \( \dot{I}(kT) = \dot{I}_{k} \) is estimated accordingly to some of the subsequent rules:

Rule 1: Forward difference approximation
\[ \dot{I}_{k} \rightarrow \dot{I}_{k+1} - \dot{I}_{k} \]  

(4)

Since the period between consecutive data is 1(day). Then, one has from (3), that a point-to-point estimation of the transmission rate is under Assumptions 1 (so that \( S(t) = N \)):

\[ \beta_{f} = \frac{1}{N} \left( \frac{I_{k+1} - I_{k}}{I_{k}} + \gamma \right) \]  

(5)

Rule 2: Backward difference approximation
In this case, \( \dot{I}_{k} \rightarrow \dot{I}_{k} - \dot{I}_{k-1} \) so that

\[ \beta_{b} = \frac{1}{N} \left( \frac{I_{k} - I_{k-1}}{I_{k}} + \gamma \right) \]  

(6)

Rule 3: Three-point difference approximation formula (central difference)
In this case, one has that \( \dot{I}_{k} \rightarrow (\dot{I}_{k+1} - \dot{I}_{k})/2 \) so that

\[ \beta_{c} = \frac{1}{N} \left( \frac{I_{k+1} - I_{k-1}}{2I_{k}} + \gamma \right) \]  

(7)

Rule 4: Five-point difference approximation formula
In this case,
The SIR model with no demography and no mortality is as follows:

\[
I_k \rightarrow I_{k-2} - 8I_{k-1} + 8I_{k+1} - I_{k+2}
\]

so that

\[
\beta_{kfp} = \frac{1}{N} \left( \frac{I_{k-2} - 8I_{k-1} + 8I_{k+1} - I_{k+2}}{2I_k} + \gamma \right)
\]

Assume that the Intervention Phase \( p \) of the quarantine or confinement intervention lasts \( \ell_p \) days from the day \( k_p \) to the day \( k_{p+1} = k_p + \ell_p \) (excluded), so along the time interval \([k_p, k_p + \ell_p - 1] = [k_p, k_p + \ell_p)\). Then, the respective average values of the above estimations become on such a time interval:

\[
\beta_f(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+1} - I_k}{I_k} \right) \right)
\]

\[
\beta_b(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+1} - I_k}{I_k} \right) \right)
\]

\[
\beta_c(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+1} - I_k}{I_k} \right) \right)
\]

\[
\beta_{fp}(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+2} - 8I_{k+1} + 8I_{k+2} - I_{k+1}}{12I_k} \right) \right)
\]

2.2 The variation of the susceptible subpopulation is accounted for

Assume that \( R(t) \) is the recovered subpopulation which is evaluated from available data while no consideration about its dynamics is made and Assumptions 1 are s replaced with Assumptions 2 below.

Assumptions 2. Both the discretized infection and recovered sequences are registered, \( \gamma \) is known, \( S(t) = N - I(t) - R(t) \), with the total population \( N \) being constant, and \( \beta \) is unknown.

By using the same approximations as in the above section, it turns out that the average estimations of (10)-(13) on \([k_p, k_p + \ell_p)\) become increased as follows:

\[
\beta_f(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+1} - I_k}{I_k} \right) \right)
\]

\[
\beta_b(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+1} - I_k}{I_k} \right) \right)
\]

\[
\beta_c(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+1} - I_k}{I_k} \right) \right)
\]

\[
\beta_{fp}(k_p) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \beta_{kfp} \right) = \frac{1}{\ell_p} \left( \sum_{k=k_p}^{k_{p+\ell_p-1}} \frac{1}{N_k - I_k - R_k} \left( \frac{I_{k+2} - 8I_{k+1} + 8I_{k+2} - I_{k+1}}{12I_k} \right) \right)
\]

Remark 1. An estimation variant is the estimation of the above formulas (14)-(17) without using the recorder sequence of the recovered and to consider their values as a previous value of the infectious being closer to the foreseen recovery time period. For instance, it could be taken \( R_k = I_{k-q} \) with \( q \in \left[ \gamma^{-1} - \varepsilon , \gamma^{-1} + \varepsilon \right] \).

2.3 SIR model without demography and without mortality

The SIR model with no demography and no mortality is as follows:
\[ S(t) = -\beta S(t) I(t) ; \quad S(0) = S_0 \]  
\[ I(t) = (\beta S(t) - \gamma) I(t) ; \quad I(0) = I_0 \]  
\[ R(t) = \gamma I(t) ; \quad R(0) = R_0 \] 

The solution of (11) is:

\[ S(t) = e^{-\beta_0 t} I(t) e^{\beta_0 d^2} S_0 \] 

which can be approximately rewritten in a sampled one-step-ahead version with re-updated initial conditions for a period of \( T = 1 \text{ day} \) from \( t_0 = kT \) to \( t_1 = (k+1)T \) as:

\[ S_{k+1} = e^{-\beta k} I_k S_k = \prod_{j=0}^{k} \left[ e^{-\beta j} I_j \right] S_0 = \prod_{j=0}^{k} \left[ e^{-\beta j} I_j \right] S_t \] 

Thus, the explicit assumptions for this subsection are as follows:

**Assumptions 3.** The discretized infection sequence is registered, \( \gamma \) is known, while \( \beta \) is unknown, and the day-to-day sampled susceptible are evaluated from (10)-(13) subject to \( S_0 = N \).

Thus, one has from (5), (6), (7) and (9) with the change \( N \rightarrow S_k \) , (10)-(13) and \( S_0 = N \) that the following set of implicit equations have to be solved to calculate the transmission rate sequence:

\[ \beta_{kf} e^{-\beta f_l I_k} = \frac{1}{S_{k-1}} \left( I_{k+1} I_k + \gamma \right) = \frac{1}{\prod_{j=0}^{k-1} \left[ e^{-\beta j} I_j \right] S_{t_k}} \left( I_{k+1} I_k + \gamma \right) \] 
\[ \beta_{kb} e^{-\beta b_l I_k} = \frac{1}{\prod_{j=0}^{k-1} \left[ e^{-\beta j} I_j \right] S_{t_k}} \left( I_{k+1} I_k - \gamma \right) \] 
\[ \beta_{kc} e^{-\beta c_l I_k} = \frac{1}{\prod_{j=0}^{k-1} \left[ e^{-\beta j} I_j \right] S_{t_k}} \left( I_{k+1} I_k + \gamma \right) \] 
\[ \beta_{kfp} e^{-\beta f_p I_k} = \frac{1}{\prod_{j=0}^{k-1} \left[ e^{-\beta j} I_j \right] S_{t_k}} \left( I_{k+1} I_k + \gamma \right) \]

where \( \{\ell k \}_{k=0}^{\infty} \) is any non-decreasing sequence of non-negative integers subject to \( 0 = \ell_0 \leq \ell_k < k \) which is defined for initialization of the calculation of the current value of \( S_k \) at the \( k \)-th sampling instant from a previous stored pre-calculated value. Then, the resulting average values for each Intervention Phase \( p \) are got from the solutions of (23) to (26) into their corresponding general average formulas:

\[ \beta f (p) = \frac{1}{\ell_p} \left( \sum_{k=\ell_0}^{p} S_{k-1} \beta_{kf} \right) \]
\[ \beta b (p) = \frac{1}{\ell_p} \left( \sum_{k=\ell_0}^{p} S_{k-1} \beta_{kb} \right) \]
\[ \beta c (p) = \frac{1}{\ell_p} \left( \sum_{k=\ell_0}^{p} S_{k-1} \beta_{kc} \right) \]
\[ \beta f p (p) = \frac{1}{\ell_p} \left( \sum_{k=\ell_0}^{p} S_{k-1} \beta_{kfp} \right) \]

A more sophisticated variant consists in estimating the recovery rate from a recorded sequence of data and to combine that estimation with the above one of the transmission rate under the subsequent assumptions.
Assumptions 4. Both the discretized infection and recovered sequences are registered, and are unknown and the day-to-day sampled susceptible are evaluated from (10)-(13) subject to $S_0 = N$.

First, note that one has to compute from (20) the derivative with respect to time at the sampling time instants of the recovered subpopulation. The same methods as used previously for the infectious subpopulation can be used, namely, the one-step forward one, the one-step backward one, the centred one or the five-point. In parallel, the discretization of the recovered has to be combined with that of the infectious in order to jointly estimate the recovery rate and the transmission rate by following up the following computational steps:

Step 1: Calculate the recovered rate sequence by one of the subsequent discretization methods in (20) using the recorder recovered sequence:

$$
\gamma_{kf} = \frac{R_{k+1} - R_k}{I_k} ; \quad \gamma_{kb} = \frac{R_k - R_{k-1}}{I_k}
$$

$$
\gamma_{kc} = \frac{R_{k+1} - R_{k-1}}{2I_k} ; \quad \gamma_{kfp} = \frac{R_{k-2} - 8R_{k-1} + 8R_{k+1} - R_{k+2}}{12I_k}
$$

Step 2: Calculate the transmission rate from the corresponding implicit equation (23)-(26) to the chosen discretization method in Step 1 by replacing $\gamma \to \gamma(k)$ (with $k = f, b, c$ or $fp$).

Step 3: Calculate the Intervention Phase average values for each Intervention Phase $p$ of the corresponding transmission rate via the corresponding formula of (27)-(30) and the corresponding similar expression for the average recovery rate.

Remark 2. Note that the solution to (20) is $R(t) = e^{\int_0^t \gamma(s)ds} R_0$ which leads to the following one-step-ahead discretized sequence for a period of one day $R_{k+1} = e^{\gamma I_k} R_k$ which suggest an estimation of a sequence of recovered rates from the recorded recovered data given by:

$$
\gamma_k = \frac{1}{I_k} \ln \frac{R_{k+1}}{R_k}
$$

which is an alternative estimation to those in the above mentioned Step 1 to be potentially used instead of any of the methods in (31)-(32).

3. An SIR epidemic model with demography and natural and disease-related mortality

Now consider the following model:

$$
\dot{S}(t) = \nu - (\beta I(t) + \mu)S(t) ; \quad S(0) = S_0
$$

$$
\dot{I}(t) = (\beta S(t) - \gamma - \mu)I(t) ; \quad I(0) = I_0
$$

$$
\dot{R}(t) = (1 - \rho)I(t) - \mu R(t) ; \quad R(0) = R_0
$$

where $\mu$ and $\rho \in [0,1]$ are, respectively, the natural and disease-related mortality rates and $\nu(\geq \mu)$ is the population recruitment $\mu$ and $\nu$ are known from the life expectation and demographic registers of a certain country or region under study. Note that the total population $N(t) = S(t) + I(t) + R(t)$ obeys the following differential equation:

$$
\dot{N}(t) = \nu - \mu N(t) - \rho I(t)
$$

We first introduce the next assumptions which replace Assumptions 2:

Assumptions 5. The discretized infection and disease-related mortality sequences are registered and $\gamma$, $\nu$ and $\mu$ are known while $\beta$ and $\rho$ are unknown.

Note that $\dot{S}(t) = N(t) - I(t) - R(t)$. In view of (35), the Intervention Phase $p$ averaged equations are:
\[ \beta_{kf}(k_p) = \frac{1}{\ell_p} \left[ \sum_{k=k_p}^{k_p+\ell_p-1} \frac{1}{N_k - I_k - R_k} \left( \gamma + \mu + I_{k+1} - I_k \right) \right] \]  
\[ \beta_{kh}(k_p) = \frac{1}{\ell_p} \left[ \sum_{k=k_p}^{k_p+\ell_p-1} \frac{1}{N_k - I_k - R_k} \left( \gamma + \mu + I_k - I_{k-1} \right) \right] \]  
\[ \beta_{kc}(k_p) = \frac{1}{\ell_p} \left[ \sum_{k=k_p}^{k_p+\ell_p-1} \frac{1}{N_k - I_k - R_k} \left( \gamma + \mu + I_{k+1} - I_{k-1} \right) \right] \]  
\[ \beta_{fc}(k_p) = \frac{1}{12\ell_p} \left[ \sum_{k=k_p}^{k_p+\ell_p-1} \frac{1}{N_k - I_k - R_k} \left( \gamma + \mu + I_{k-2} - 8I_{k-1} + 8I_{k+1} - I_{k+2} \right) \right] \]  

The disease-related mortality is calculated from the associated sequence to the dead mortality differential equation \( \dot{D}(t) = \rho_f(t) \). Then, one gets in a similar way to (38)-(41) for the various discretization rules that the Intervention Phase-dependent average disease-related mortality rate is:

\[ \rho_f(k_p) = \frac{1}{\gamma_p} \left( \sum_{k=k_p}^{k_p+\ell_p-1} \frac{D_{k+1} - D_k}{I_k D_k} \right) \]  
\[ \rho_h(k_p) = \frac{1}{\gamma_p} \left( \sum_{k=k_p}^{k_p+\ell_p-1} \frac{D_k - D_{k-1}}{I_k D_k} \right) \]  
\[ \rho_c(k_p) = \frac{1}{2\gamma_p} \left( \sum_{k=k_p}^{k_p+\ell_p-1} \frac{D_{k+1} - D_k}{I_k D_k} \right) \]  
\[ \rho_{fc}(k_p) = \frac{1}{12\gamma_p} \left( \sum_{k=k_p}^{k_p+\ell_p-1} \frac{D_{k-2} - 8D_{k-1} + 8D_{k+1} - D_{k+2}}{I_k D_k} \right) \]

If the recovery sequence is known then, the average recovery rate can also be calculated and used in (38)-(41). In particular, let us introduce the next assumptions:

**Assumptions 6.** The discretized infection, recovery, and disease-related mortality sequences are registered and \( \nu \) and \( \mu \) are known while \( \beta, \gamma \) and \( \rho \) are unknown.

It is possible to estimate the average values of \( \beta, \gamma \) and \( \rho \) as follows. First, we examine the forward discretization method in (34)-(37) with the replacements \( I(t) \rightarrow I_{k+1} - I_k \), \( R(t) \rightarrow R_{k+1} - R_k \), \( N(t) \rightarrow N_{k+1} - N_k \). In particular, one gets from (37) and (36) that:

\[ (\rho\gamma)_{kf} = \frac{\nu + (1 - \mu)N_k - N_{k+1}}{l_k}; \quad ((1 - \rho)\gamma)_{hf} = \frac{(\nu - 1)R_k + R_{k+1}}{l_k} \]  

and summing up the two above equations yields the following sequences of estimated parameters:

\[ \gamma_{kf} = \frac{\nu + (1 - \mu)N_k - N_{k+1} + (\mu - 1)R_k + R_{k+1}}{l_k} \]  

which replaced into the first equation of (46) yields:

\[ \rho_{kf} = \frac{\nu + (1 - \mu)N_k - N_{k+1}}{\nu + (1 - \mu)N_k - N_{k+1} + (\mu - 1)R_k + R_{k+1}} \]  

Then,

\[ \beta_{kf} = \frac{1}{N_k - I_k - R_k} \left( \mu + \frac{\nu + (1 - \mu)N_k - N_{k+1} + (\mu - 1)R_k + R_{k+1} + l_k}{l_k} \right) \]  

Their average values for the Intervention Phase \( p \) on the interval of samples \([k_p, k_p + \ell_p - 1]\) can be calculated as in the former cases. Similarly, we have for the backward estimation of derivatives from samples:
\[\gamma_{kb} = \frac{v - \mu N_k + N_{k-1} - N_k + (\mu + 1)R_k - R_{k-1}}{I_k}\]

(50)

\[\rho_{kb} = \frac{v - (\mu + 1)N_k + N_{k-1}}{v - (\mu + 1)N_k + N_{k-1} + (\mu + 1)R_k - R_{k-1}}\]

(51)

\[\beta_{kb} = \frac{1}{N_k - I_k - R_k} \left( \mu + \frac{v - (1 + \mu)N_k + N_{k-1} + (\mu + 1)R_k - R_{k-1} + I_k - I_{k-1}}{I_k} \right)\]

(52)

For the three-point discretization method, one gets:

\[\gamma_{kc} = \frac{v - \mu N_k + N_{k+1} - N_k + \mu R_k + R_{k+1} - R_{k-1}}{2I_k}\]

(53)

\[\rho_{kc} = \frac{v - \mu N_k - N_{k+1} + N_{k-1}}{v - \mu N_k - N_{k+1} + N_{k-1} + \mu R_k + R_{k+1} - R_k}\]

(54)

\[\beta_{kc} = \frac{1}{N_k - I_k - R_k} \left( \mu + \frac{v - \mu N_k - N_{k-1} + N_{k+1} + \mu R_k + R_{k+1} - R_{k-1} + I_{k+1} - I_{k-1}}{2I_k} \right)\]

(55)

and one can proceed in a similar way with the five-point corresponding discretization method and then to get the calculations of their averaged values for each Intervention Phase.

4. Some simple tests

The following tests have been performed with some provided official data of the COVID-19 evolution. The simpler model of Section 2.1 under Assumptions 1, it has been taken \( \gamma = 1/18.8\) days\(^{-1}\) [16]. The infection recorded data have been used. Between March 17 and April 3, 2020, along 17 days, the pandemic was growing to a fast rate along the first days of confinement which started by March 15. The confinement was very general for the population except for Basic Services and Industry (from March 15 to 31). Also, the first two weeks of April, the Industry was almost completely closed for production except some basic tasks and services. The discretization Rule 1 (two-point discrete forward approximation of the infectious time-derivative) has given a transmission rate \( \beta_f \approx 0.2002 \) which is very close to related data obtained from Japan in [16]. There is a discrepancy with the value got from Rule 2 (two-point discrete backward approximation) from March 10 to March 17 which gives a transmission rate \( \beta_b \approx 0.1603 \). In this period, the first five days, it was no confinement decree. However, it is known that the infection is clearly viewable after two or three months after the first contagion. The discrepancy can be caused by the fact that the per day increment of the infection grows very fast when the infection is exploding without control so that the increment used in the backward approach is small related to the increment used in the forward approximation. The forward method gives a larger transmission rate value along a six-day period from March 17 to March 23 of \( \beta_f \approx 0.5532 \). The interpretation is that new cases were being detected in large amounts along the first days of confinement probably coming from contagions which had taken place days before. From March 11 to March 17, the data corresponding to the backward method give a value \( \beta_f \approx 0.1532 \). The three-point approach of Rule 3 (three-point approximation) gives \( \beta_f \approx 0.3532 \) along the period March 11 to March 23. If we repeat the last results by taking into account that the susceptible are less than the total population, we estimate also the death (very doubtful official data by that time) and recovery levels in an extended Assumption 2 which lead by March 23 to a global amount of 89520 after increasing the data by a factor 10 since at that time they were no abundant tests performed and it is foreseen that the real data of infective and recovered have to be multiplied by such a factor to consider the asymptomatic individuals and the non-serious ill individuals which are not under hospital evaluation. This yields that the susceptible by that time were about 99.8% of the population. The above transmission rates become changed to \( \beta_f \approx 0.5543 \), \( \beta_b \approx 0.1535 \) and \( \beta_f \approx 0.3539 \) which is a very slight variation related to the case of considering all the population to be susceptible. However, as the susceptible subpopulation percentage increases the variations of these values would become more significant.

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