Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
Assessing the impact of vaccination in a COVID-19 compartmental model

Ernesto P. Esteban a, *, Lusmeralis Almodovar-Abreu b

a Physics Department, University of Puerto Rico-Humacao, Puerto Rico
b Chemistry Department, University of Puerto Rico-Humacao, Puerto Rico

ARTICLE INFO

Keywords:
Vaccine
COVID-19
Compartmental model
Coronavirus
Optimal vaccine
Vaccinated reproductive number

ABSTRACT

Background: The aim of this research is to understand the role played by vaccination in the dynamics of a given COVID-19 compartmental model. Most of all, how vaccination modifies the stability, sensitivity, and the reproduction number of a susceptible population.

Methods: The proposed COVID-19 compartmental model (SVEIRD) has seven compartments. Namely, susceptible (S), vaccinated (V), exposed (E, infected but not yet infectious), symptomatic infectious (I s), asymptomatic infectious (I a), recovered (R), and dead by Covid-19 disease (D).

We have developed a computational code to mimic the first wave of the coronavirus pandemic in a state like New York (NYS). First a stability analysis was carried out. Next, a sensitivity analysis showed that the more relevant parameters are birth rate, transmission coefficient, and vaccine failure. We found an alternative procedure to easily calculate the vaccinated reproductive number of the proposed SVEIRD model. Our graphical results allow to make a comparison between unvaccinated (SEIRD) and vaccinated (SVEIRD) populations. In the peak of the first wave, we estimated 21% (2.5%) and 6% (0.8%) of the unvaccinated (vaccinated) susceptible population was symptomatic and asymptomatic, respectively. At 180 days of the NYS pandemic, the model forecast about 25786 deaths by coronavirus. A vaccine with 95% efficacy could reduce the number of deaths from 25786 to 3784.

Conclusion: The proposed compartmental model can be used to mimic different possible scenarios of the pandemic not only in NYS, but in any country or region. Further, for an unvaccinated reproductive number \( R > 1 \), we showed that the vaccine’s efficacy must be greater than the herd immunity to stop the spread of the COVID-19 disease.

1. Introduction

Nowadays several vaccines intended to provide immunity against COVID-19 have been already authorized worldwide for emergency use. Clinical trials have shown that a given vaccine’s efficacy varies from 60% to 95% [1]. Unfortunately, vaccines’ production cannot keep with the world demand, bringing consequently a slow immunization process, i.e., a low coverage rate. Furthermore, in many countries the total number of coronavirus positive cases are increasing due to the emerging of several new coronavirus strains. Because of this fact, coronavirus’ vaccines will need to be boosted, and perhaps the human population will have to be vaccinated periodically. These uncertainties suggest that the coronavirus disease will stay with us for many years to come. Therefore, a better understanding of the role played by a vaccine in the coronavirus epidemic is of great health interest. One step in that direction, it is to consider mathematical compartmental models to capture the key features of the coronavirus pandemic. Many authors already have applied different mathematical models to study the coronavirus pandemic [2–5] but only few have included vaccination [6–8].

In this paper, we have modified a SEIRD compartmental model by adding an extra vaccinated compartment to make a comparison between vaccinated and unvaccinated populations. In particular, we would like to have an answer for several queries related to the coronavirus dynamics. Namely: i) How much an unvaccinated infected population could be reduced by a vaccine? ii) How the reproduction number changes when the susceptible population is vaccinated? iii) For a given country or region what is the optimal vaccine (in terms of efficacy and coverage rate) to stop the spread of the coronavirus disease?

This paper is organized as follows. In section 2, we write seven first order coupled differential equations to describe mathematically our proposed SVEIRD compartmental model (Fig. 1). Disease free and endemic equilibrium points are derived in a closed form in sections 3

---

* Corresponding author.
E-mail address: Ernesto.Esteban@upr.edu (E.P. Esteban).

https://doi.org/10.1016/j.imu.2021.100795

Received 29 July 2021; Received in revised form 7 November 2021; Accepted 15 November 2021
Available online 18 November 2021
2352-9148/© 2021 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license

<http://creativecommons.org/licenses/by-nc-nd/4.0/>
In Section 6, we use an alternative procedure (other than the Next Generation Matrix [9,10]) to obtain an analytical expression of the vaccinated reproduction number ($R_v$). Finally, in Section 7, we applied the proposed SVEIRD compartmental model to study the coronavirus epidemic in a state like New York. Because there are still many uncertainties in the SVEIRD parameters values and in the understanding of the coronavirus disease, we do not claim that our results for NYS should be considered definitive. Although we are aware that NYS had to endure one wave of six months of duration. Moreover, our analytical, graphical, and numerical results could be useful as test-bed calculations of more complex and realistic coronavirus models. Here, we shall mention that Schneider et al. [11] have developed a COVID-19 pandemic simulation tool based on an extension of a SEIR model.

Notice that for Sections 2 to 3.5 all derivations are obtained in a closed form and presented as analytical expressions. This is to benefit any interested reader who could use these results in a country or region besides NYS. Numerical results and related figures for NYS are discussed in Section 4.

Table 1
The SVEIRD model’s parameters of Fig. 1.

| Parameters | Name |
|-----------|------|
| $\Lambda$ | Recruitment |
| $\beta$ | COVID-19 transmission coefficient rate |
| $\gamma_1$ | Natural mortality rate |
| $\gamma_2$ | COVID-19 symptomatic mortality rate |
| $\gamma_3$ | COVID-19 asymptomatic mortality rate |
| $\phi$ | Vaccine failure |
| $\alpha$ | Incubation rate |
| $K$ | Proportion of exposed to the symptomatic population |
| $k_1$ | Proportion of symptomatic to recovered population |
| $k_2$ | Proportion of asymptomatic to symptomatic population |
| $k_3$ | Proportion of asymptomatic to recovered population |
| $k_4$ | Proportion of asymptomatic to death by COVID-19 population |
| $\theta_1$ | Proportion of asymptomatic to death by COVID-19 population |
| $\theta_2$ | Re-infection rate |
| $\omega$ | Neither inherited immunity |

Notice that for Sections 2 to 3.5 all derivations are obtained in a closed form and presented as analytical expressions. This is to benefit any interested reader who could use these results in a country or region besides NYS. Numerical results and related figures for NYS are discussed in Section 4.

2. Methods

In Fig. 1, the proposed biomathematical (SVEIRD) compartmental model assumes vaccination only to the susceptible population, no reinfection, and neither inherited immunity. The seven compartments are: susceptible (S), vaccinated (V), exposed (E, infected but not yet infectious), symptomatic infectious ($I_1$), asymptomatic infectious ($I_0$), recovered (R), and dead by coronavirus (D).

The meaning of the parameters connecting the different compartments is given below in Table 1.

Eqs. (1)–(7) mathematically describe the dynamics among the different compartments showed in Fig. 1. All compartments’ populations of Fig. 1, have been normalized by the total population ($N = S + V + E + I_1 + I_0 + R + D$). The new normalized variables will be still denoted by the same letters as in Fig. 1. Namely, $S \to \overset{\circ}{S}$, $V \to \overset{\circ}{V}$, $E \to \overset{\circ}{E}$, $I_1 \to \overset{\circ}{I_1}$, $I_0 \to \overset{\circ}{I_0}$, $R \to \overset{\circ}{R}$, and $D \to \overset{\circ}{D}$.

$$\frac{dS}{dt} = \Lambda - S(\gamma_1 + \alpha_1 + \beta(I_0 + I_1))$$

(1)

$$\frac{dV}{dt} = S\alpha_1 - V(\gamma_1 + \theta_1 \beta(I_0 + I_1))$$

(2)

$$\frac{dE}{dt} = \beta S(I_0 + I_1) + V \theta I_0 + I_0 - ET_5$$

(3)

$$\frac{dI_1}{dt} = \gamma_1 I_0 + k_3 \gamma V - I_1 T_5$$

(4)

$$\frac{dI_0}{dt} = \gamma_1 I_0 + k_3 \gamma V - I_1 T_5$$

(5)

$$\frac{dR}{dt} = k_3 \alpha_1 I_0 + k_1 \alpha_1 I_1 - \gamma_1 R$$

(6)

$$\frac{dD}{dt} = (1 - k_5) \gamma_2 I_1 + k_4 \gamma V$$

(7)

where

$$T_1 = \frac{\rho}{\gamma_1 + \gamma_1}$$

(8)

$$T_2 = (1 - k_5) \gamma_2 + k_1 \alpha_1 + \gamma_1$$

(9)

$$T_3 = k_5 \rho + k_4 \gamma_3 + k_3 \alpha_2 + \gamma_4$$

(10)
follows Eqn. (12). Using a similar algebraic procedure, we obtain Eqns. – and inserted into Eqn. (4), to obtain Eqn. (13). From there, it easily follows Eqs. (12). Using a similar algebraic procedure, we obtain Eqs. 14–16

\[ E_p = \frac{T_0 T_3 I_p}{\epsilon (1 - k) T_3} \quad (12) \]

\[ I_{sp} = \frac{T_0 I_{sp}}{T_3} \quad (13) \]

\[ S_p = \frac{\Lambda}{I_1 + \alpha_0 (I_{sp} + I_p)} \quad (14) \]

\[ V_p = \frac{\alpha_0 S_p}{I_1 + \theta (I_{sp} + I_p)} \quad (15) \]

\[ R_p = \left( \frac{1}{I_1} \right) \left( \alpha_1 I_{sp} + \alpha_1 I_p \right) \quad (16) \]

where

\[ T_4 = k k_4 T_3 + k k_5 \alpha_2 + k \theta \phi + k \phi' \]

\[ T_5 = k T_3 + (1 - k) k_2 \phi \quad (17) \]

\[ J_{df} = \begin{pmatrix} -\gamma_1 - \beta (I_{sp} + I_p) - \alpha_0 & 0 & 0 & 0 & -\beta S_p & -\beta S_p & -\beta S_p & -\beta S_p \\ \alpha_0 & 0 & 0 & -\gamma_1 - \beta (I_{sp} + I_p) \theta_1 & -\beta_0 V_p & -\beta_0 V_p & -\beta_0 V_p & -\beta_0 V_p \\ 0 & -\gamma_1 & \beta (I_{sp} + I_p) \theta_1 & \beta_0 V_p & \beta_0 V_p & \beta_0 V_p & \beta_0 V_p & \beta_0 V_p \\ 0 & 0 & 0 & k_2 \phi & -T_1 & 0 & k_1 \alpha_2 & k_1 \alpha_2 \\ 0 & 0 & \epsilon - \epsilon \kappa & 0 & -T_1 & 0 & k_1 \alpha_2 & k_1 \alpha_2 \\ 0 & 0 & -\gamma_1 & 0 & 0 & k_1 \alpha_2 & k_1 \alpha_2 & 0 \end{pmatrix} \quad (27) \]

\[ J_{std} = \begin{pmatrix} \gamma_1 \gamma_1 I_{sp} + I_p & 0 & 0 & 0 & 0 & -\beta S_p & -\beta S_p & -\beta S_p & -\beta S_p \\ \alpha_0 & 0 & 0 & -\gamma_1 - \beta (I_{sp} + I_p) \theta_1 & -\beta_0 V_p & -\beta_0 V_p & -\beta_0 V_p & -\beta_0 V_p \\ 0 & -\gamma_1 & \beta (I_{sp} + I_p) \theta_1 & \beta_0 V_p & \beta_0 V_p & \beta_0 V_p & \beta_0 V_p & \beta_0 V_p \\ 0 & 0 & 0 & k_2 \phi & -T_1 & 0 & k_1 \alpha_2 & k_1 \alpha_2 \\ 0 & 0 & \epsilon - \epsilon \kappa & 0 & -T_1 & 0 & k_1 \alpha_2 & k_1 \alpha_2 \\ 0 & 0 & -\gamma_1 & 0 & 0 & k_1 \alpha_2 & k_1 \alpha_2 & 0 \end{pmatrix} \quad (28) \]

\[ T_0 = (1 - k) T_2 \quad (19) \]

Next, we set Eqn. (3) to zero and substitute Eqs. 12–15 to obtain the following cubic equation

\[ C_1 I_{sp}^3 + C_2 I_{sp}^2 + C_3 I_{sp} = 0 \quad (20) \]

where

\[ C_1 = \beta^2 T S_3 (T_3 + T_5) \gamma_1 \theta_1 \quad (21) \]

\[ C_2 = \beta T S_3 (T_5 + T_6) \left( \beta \epsilon (1 - k) (T_5 + T_6) \delta \theta_1 + T_6 T_7 (\gamma_1 + \gamma_1 \theta_1 + \theta_1 \omega_1) \right) \quad (22) \]

\[ C_3 = T_5^2 (\gamma_1 T_7 T_5 (\gamma_1 + \omega_1)) - T_5^2 \left( \beta \epsilon (1 - k) (T_5 + T_6) (\gamma_1 + \omega_1 \theta_1) \right) \quad (23) \]

3.2. Disease free equilibrium points

The trivial solution of Eqn. (20); i.e., \( I_p = 0 \) defines the disease equilibrium point (DFE). Thus, from Eqs. 12–16 the only non-zero solutions are

\[ S^* = \frac{\Lambda}{y_1 + \omega_1} \quad (24) \]

\[ V^* = \frac{\Lambda \omega_1}{y_1 (y_1 + \omega_1)} \quad (25) \]

3.3. Disease endemic equilibrium points

To obtain the disease endemic equilibrium points \( (I_p \neq 0) \) we first must solve from,

Eqs. (20) the quadratic equation. Namely

\[ C_1 I_{sp}^3 + C_2 I_{sp}^2 + C_3 I_{sp} = 0 \quad (26) \]

where \( C_1, C_2 \) and \( C_3 \) are given by Eqs. 21–23. Then \( I_p \) is to be substituted in Eqs. 12–16 to obtain the remaining endemic point values.

3.4. Stability

To study the stability of the disease free and endemic equilibrium points we built the Jacobians \( J_{df} \) and \( J_{std} \) respectively. They are explicitly given bellow in Eqs. (27) and (28).

As is well known, a local stable equilibrium is achieved when all the eigenvalues of matrices \( J_{df} \) and \( J_{std} \) are negative. Otherwise, there is an unstable equilibrium. By setting \( \theta_1 = \omega_1 = 0 \) in Eqs. (27) and (28) we shall obtain the respective Jacobians for the unvaccinated population. Here, we shall point out that the eigenvalues of matrices given by Eqs. 27 and 28 are numerically calculated for NYS in Section 4.

3.5. Alternative procedure to calculate the effective reproductive number

The Basic Reproductive Number \( (R) \) is perhaps one of the most important variables in epidemiology. It is related to the average number of secondary infections and allows to estimate the spread of the disease. In fact, if \( R > 1 \) the disease will persist, and it will die out when \( R < 1 \). Although the majority of the scientists agree with this interpretation of \( R \), there are some caveats that some authors still have [12,13]. Although
Table 2
This Table shows for NYS the positive (L, β, η₁, k₃, ω), and negative sensitivities (γ₁, α₁, α₂, k₂, θ₁, θ₂, φ, TF, Tₛ, W₁).

| Parameter | Sensitivity |
|-----------|-------------|
| L         | 1           |
| β         | 1           |
| η₁        | 0.990774    |
| k₂        | 0.447102    |
| ε         | 0.0016164   |
| θ₃        | -0.0002613  |
| k₄        | -0.0002613  |
| θ₂        | -0.0076717  |
| φ         | -0.0076717  |
| η₁        | -0.087607   |
| γ₂        | -0.0124228  |
| κ         | -0.0829919  |
| θ₂        | -0.196499   |
| α₂        | -0.196499   |
| α₁        | -0.782753   |
| θ₁        | -0.991793   |

Table 3
The SVEIRD parameters values for NYS first wave coronavirus pandemic.

| Parameters | Estimated Values | References |
|------------|------------------|------------|
| L          | 0.3640 × 10⁻⁵(1/day) | www.osc.state.ny.us [20] |
| β          | 0.55/day (first period), 0.09/day (second period) | Estimated |
| η₁         | 0.2328 × 10⁻⁴ (1/day) | https://webbi1.health.ny.gov [22] |
| γ₂         | 0.0949 (1/day) | [23] |
| θ₃         | 0.0500 (1/day) | Estimated |
| α₁         | 0.144 | [23] |
| k          | 0.749 | [23] |
| k₁         | 0.001 | Estimated |
| k₂         | 0.100 | Estimated |
| k₃         | 0.899 | Estimated |
| φ          | 0.200 (1/day) | Estimated |
| α₁         | 0.0504 | [23] |
| α₂         | 0.0583 | [23] |

The Next Generation Matrix method [9,10,14] is widely used to obtain R, there are other methods to make the same calculation [12]. They are: The Survival Function, the Jacobian, Constant Term of the Characteristic Polynomial, The Graph-Theoretic Method, and the Existence of the Endemic Equilibrium. The pro and cons of using these methods to obtain R are discussed by Jing et al. [12].

We argue here, that in the case of an infectious disease with no more than three forces of infection the Existence of the Endemic Equilibrium may be the best method to calculate R. This is because, to obtain R all remaining methods face cumbersome calculations. Also, notice that the standard procedure to obtain R is the Next Generation Matrix method [8,9,12]. This procedure does not provide a clear biological interpretation, and occasionally it gives a wrong result [12].

In this section, we shall use a simpler although not trivial calculation within the framework of the Existence of the Endemic Equilibrium method to calculate R. To fulfill this purpose, we shall solve Eqn. (20) to obtain the equilibrium point Iₒ. Notice, Iₒ > 0 means an infectious population threshold which is maintained at a certain baseline level. As is well known, the quadratic equation solutions of Eqn. (20) can be written as shown in Eqn. (29), where C₁, C₂, and C₃ = C₃ₐ – C₃ₘₐ, are explicitly given by Eqns. (21)–(23), respectively. Thus,

\[ Iₒ = \frac{C₂}{2C₁} \pm \sqrt{\frac{1}{4C₁(C₃ₐ – C₃ₘₐ)} \left( C₂^2 + \frac{4C₁C₃ₐ(C₂C₃ₐ)}{C₃ₐ} \right)} \]

(29)

Notice from Eqns. (21) and (23) that C₁ > 0, and

\[ C₃ₐ = Tₐ^2(T₁T₃T₄(f₁ + α₁)) > 0 \]

(30)

\[ C₃ₘₐ = Tₐ^2(β⁺αk(T₄ + (1 – k))(T₁ + T₄)(f₁ + α₁θ₁)) > 0 \]

(31)

where

\[ T₄ = k₄ + (1 – k)k₂φ \]

(32)

\[ T₃ = (1 – k)T₂ \]

(33)

Now we can easily from Eqn. (29) identify the vaccinated reproduction number as

\[ R_v = \frac{C₂}{2C₁} > 1 \] to satisfy the necessary condition Iₒ > 0. Therefore, from Eqns. 29–31

![Fig. 2. In red and blue, unvaccinated, and vaccinated susceptible populations, respectively. In green, the vaccinated population. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)](image-url)
Of course, we have verified (Appendix 1) that the value of Eqn. (34) agrees with the one obtained using the standard method i.e., the Next Generation Matrix [9,10,14].

The unvaccinated reproductive number \( R_v \) is found by setting \( \omega_1 = \theta_1 = 0 \) in Eqn. (34). Thus

\[
R_v = \frac{(\beta \Lambda e (kT_3 + (1 - \kappa)(T_2 + k_2 \phi))(\gamma_1 + \omega_1 \theta_1))}{\gamma_1 T_1 T_2 T_3 (\gamma_1 + \omega_1)} \tag{34}
\]

Now, from Eqs. 34 and 35 we obtain a relationship between \( R_v \) and \( R \) as follows

\[
R_v = R \frac{T_1 + \omega_1 \theta_1}{\gamma_1 + \omega_1} \tag{36}
\]

Eqn. (36) implies that for any \( 0 < \theta_1 < 1 \), \( R_v < R \). This shows analytically that a vaccine diminishes the spread of the coronavirus disease. Also notice, when \( \gamma_1 << \omega_1 \) Eqn. (36) reduces to Eqn. (37)

\[
R_v = R \theta_1 \tag{37}
\]

Therefore, in Eqn. (37), the vaccine’s efficacy \( (1 - \theta_1) \) will stop the spread of the coronavirus provides the following inequality is satisfied. Namely

Vaccine’s efficacy \( > 1 - \frac{1}{R} \tag{38} \)

Eq. (38) can also be written as follows

Vaccine’s efficacy \( > \) Herd immunity \( \tag{39} \)

Without a vaccine the coronavirus will die out when the population reach herd immunity. However, Eqn. (39) provides an additional interpretation. Namely, to stop the spread of COVID-19 the optimal vaccine’s efficacy must be greater than the herd immunity. In other

\[\text{Fig. 3. The unvaccinated symptomatic (red) population. Vaccination reduces the symptomatic population (blue). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)}\]

\[\text{Fig. 4. The unvaccinated asymptomatic (red) population. Vaccination reduces the asymptomatic population (blue). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)}\]
words, the optimal vaccine will move the endemic disease equilibrium to the disease-free equilibrium. A similar conclusion was discussed by Beckley et al. [15].

Thus, provide $R > 1$, Eqn. (39) allows to choose the optimal vaccine to stop the coronavirus spread in each country or region.

3.6. Sensitivity analysis

For the sensitivity analysis we have used the method: Normalized Forward Sensitivity Index of a Variable [16–18]. The vaccinated reproduction number ($R_v$) as given by Eqn. (34) depends on several parameters. To obtain the most relevant parameters of $R_v$, a sensitivity analysis is carried out. The sensitivity of each parameter $x_n$ is given by $S(x_n)$:

\[ S_v(x_n) = \left( \frac{x_n}{f} \right) \frac{\partial R_v}{\partial x_n} \]  \hspace{1cm} (40)

From Eqn. (36), the relationship between the unvaccinated ($S(x_u)$) and vaccinated ($S_v(x_u)$) sensitivities between is

\[ S_v(x_u) = \frac{S_u(x_u)}{f} + S(x_u) \]  \hspace{1cm} (41)

where $f = \frac{n - \theta_1 x_n}{\gamma_1 + \omega_1}$.

Therefore, for all parameters except $\theta_1$, $\omega_1$, and $\gamma_1$, $S_v(x_u) = S(x_u)$. Also notice that $S_v(x_u)$ does not depend of $\beta$, $\Lambda$, and $\epsilon$. For NYS model’s parameters sensitivities are given in Table 2.

The most sensitive parameters for $R_v$ are $\Lambda$, $\beta$, and $\theta_1$. To diminish (increase) the value of $R_v$ we must diminish (increase) the positive

![Fig. 5. The accumulated unvaccinated (Red) COVID-19 deaths. Vaccination reduces the number of COVID-19 deaths (blue). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)](image1)

![Fig. 6. The unvaccinated (red) and vaccinated (blue) reproductive numbers in function of the transmission coefficient rate ($\beta$) in green.. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)](image2)
Fig. 7. In blue, the vaccinated reproduction number ($R_v$). In green, a plane of value 1. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

Fig. 8. In red, the unvaccinated reproduction number ($R$). In green, a plane of value 1. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)
(negative) sensitivities.

4. Discussion

One of the aims of the proposed model is to understand how vaccination change the dynamics of a SEIRD compartmental models. In Section 1, we have provided analytical expressions to describe the disease free and endemic equilibrium points for SVEIRD and SEIRD compartmental models. These results are needed to study the stability of these solutions and to determine whether the epidemic will persist (i.e., \( R_0 \neq 0 \)). If \( R_0 > 1 \) there is only one biological meaningful solution of Eqn. (29). When \( R_0 < 1 \), there are two real negative or two imaginary solutions. This means that there are not endemic points and therefore the disease died out.

We have also developed a novel procedure to derive \( R_0 \), which is easier to understand and calculate than the standard method, i.e., the Next Generation Matrix \([9, 10]\). We have check that this new alternative procedure to derive analytically \( R_0 \), it is valid for any compartmental model with three or less forces of infection.

To illustrate our theoretical procedure, we have chosen the first wave of the NYS coronavirus pandemic. In the first 65 days we expect a highly contagious environment and we have assumed a value of \( R = 14.6 \). Thus, using Eqn. (35) we obtained a value of \( \beta = 0.55/day \). The next 115 days, social distance, masks, and the lockdown will diminish the value of \( R \) and \( \beta \) to 2.39 and 0.09, respectively. Next, a MATHEMATICA [19] code is developed to plot the numerical solutions of Eqs. (1)-(7). In Table 3 we list the parameters’ values used in the simulations.

Figs. 2-5, summarize for NYS first wave the dynamics of the susceptible, vaccinated, infectious and death populations during a six-month period.

We show in Fig. 2, the evolution on time of the vaccinated (blue) and unvaccinated (red) susceptible populations. After 180 days about 80% of the initial susceptible population will be vaccinated. As can be seen in Figs. (3) and (4), vaccination will diminish the symptomatic (from 0.21 to 0.025) and asymptomatic (from 0.06 to 0.008) population’s proportions in the peak of the first wave. Accumulated covid-deaths are plotted in Fig. (4). The proposed model forecast for the first six months of the NYS pandemic 25785 deaths due to the coronavirus. Vaccination could have reduced the number of deaths from 25785 to 3784. The total NYS coronavirus deaths reported in the web, after six-months is 33139 [24].

For NYS, vaccination reduces the unvaccinated reproductive number from 14.6 to 0.76 (first 65 days), and from 2.39 to 0.12 for the remaining period (65 days–180 days). It is showed that for \( R = 2.39 \), only exist one real positive endemic equilibrium point \( (S_p, E_p, I_p, R_p) \). Thus, without vaccination the Covid-19 disease will persist and converge to the endemic equilibrium point \( (S_p = 0.00362, E_p = 0.00015, I_p = 0.00029, R_p = 0.90782) \). It is expected that all meaningful solutions of Eqs. (1)-(7) will converge to this unique equilibrium point and the disease will become endemic. Regarding the unvaccinated disease-free solutions all of them will converge to the value of \( S^* = \frac{1}{\hat{\beta}} = 1.56 \). Using the respective Jacobians we found that both of these equilibrium points are unstable. For \( R_p = 0.12 \) all solutions of Eqs. (1)-(7) will converge to the disease-free equilibrium points \( (S^* = 0.0036, \; \hat{V}^* = 1.5599) \) and the Covid-19 disease will be died out.

In Eqn. (38), we showed that the optimal vaccine \((1- \theta)\) must be greater than the herd immunity to stop the coronavirus spread in a given country or region. This information may be useful in choosing what Covid-19 vaccine’s must be acquired. Notice that herd immunity values depend on \( R \), and thus, on the mathematical models and parameters obtained for a specific country. For example, in NYS, at the beginning of the pandemic our model estimated an unvaccinated reproduction number of 14.60. Therefore, our SVEIRD proposed model advocates that the optimal vaccine for NYS should have at least 93% efficiency.

Fig. 6 shows in red (without vaccination) that \( \beta \) must be greater than 0.05/day to become endemic. On the other hand, if the population was vaccinated \( \beta \) should be less than 1.1/day to die out. Therefore, after the second period, a second wave was expected.

In Figs. (7)-(8), we plot three-dimensional figures of the \( R_n \) intersecting a plane of value 1. These figures are useful to determine what are the values of the transmission coefficient, vaccine failure, or recruitment rate to stop the coronavirus disease.

4.1 Limitations

There are several limitations in this paper. First, as any compartmental model, it cannot make a perfect forecast. The proposed SVEIRD compartmental model only provides an approximation that is accurate enough for a better understanding of the pandemic’s first wave. Although there is NYS coronavirus data published in different websites [24-26] we cannot make it a direct comparison with our respective results (except for COVID-deaths). This is because the number of symptomatic and asymptomatic patients reported in the literature is based on the number of tests taken daily. There is some reliable data available: the number of COVID-19 cumulative deaths, and the average number for the reproductive number. The compartments’ parameters describing the biology of the disease are perhaps the more reliable because they are based in COVID-19 clinical data. In summary, there is not yet high-quality data for the SVEIRD compartmental model parameters. Regarding the effective reproductive number, its value depends on the compartmental model chosen.

5. Conclusions

In this paper, we focus on how vaccination modifies the dynamics of a coronavirus SEIRD compartmental model. To this purpose a simple but not trivial SVEIRD compartmental model was built. In the first part, we derived in a closed form analytical expressions for the endemic and disease-free equilibrium points and its respective Jacobians. Next, we derive an alternative procedure to obtain the reproductive number. This approach is easier to calculate and understand than the standard method: The Next Generation Matrix. Moreover, we show that the optimal vaccine (in terms of efficacy and coverage rate) for a region or country must be greater than the herd immunity to stop the spread of the Covid-19.

As an application, we developed a MATHEMATICA code to mimic the first wave of the coronavirus pandemic in a state like New York. Two periods (65 days, 65 days-180 days) were considered. We assumed for the first two months a highly infectious (\( R = 14.6 \)) period, which diminish to \( R = 2.39 \) in the subsequent four months.

As expected, Figs. (1)-(4) shows that the vaccine reduces the prevalence of the disease. At the peak of the first wave (Figs. 3–4), the program forecasts that a quarter of the susceptible population will be infectious (symptomatic and asymptomatic). Vaccination (95% efficacy, 1% daily coverage rate) will reduce the number of infectious patients for an approximate factor of 10. Accumulated COVID-19 deaths (25785) after six months of the pandemic have a 22% difference with the reported values (33139) [24]. Vaccination (95% efficacy, 1% daily coverage rate) will reduce the number of deaths from 25785 to 3784.

Finally, to contain the pandemic in NYS, the optimal vaccines should have at least 93% and 60% efficacies for the first and second period, respectively.

Ethics statement

The data and parameters values were collected via public domain, and thus, neither ethical approval nor individual consent is applicable.

Code availability

(MATHEMATICA code used in this research can be requested to Ernesto P. Esteban.)
APPENDIX 1

1. Vaccinated Reproductive Number

The next-generation matrix was introduced by Diekmann, Driessche and Watmough [9] to obtain the basic reproductive number of a given compartmental model. Since then, it has been the standard way to derive an analytical value of the basic reproductive number. Following closely this approach, we shall obtain $R_v$ for our proposed biomathematical compartmental model. First, Eqns. (A3), (A4), (A5), and (A6) in the paper are written in a matrix form as seen below.

$$
\begin{array}{c}
\frac{dE}{dt} \\
\frac{dI_s}{dt} \\
\frac{dI_a}{dt} \\
\frac{dR}{dt}
\end{array}
= F(\vec{x}) - \left[
\begin{array}{c}
V^+ (\vec{x}) \\
V^+ (\vec{x}) \\
V^- (\vec{x}) \\
V^- (\vec{x})
\end{array}
\right]
$$

(A1)

where $F$, $V^+$ and $V^-$ are as follow

$$
F = \begin{pmatrix}
I_b(S + \theta_1 V) + I_a(S + \theta_1 V) \\
0 \\
0 \\
0
\end{pmatrix}
$$

(A2)

$$
V^+ = \begin{pmatrix}
0 \\
\epsilon \kappa E + k_0 k_2 \\
\epsilon (1 - \kappa)E \\
0
\end{pmatrix}
$$

(A3)

$$
V^- = \begin{pmatrix}
T_1 E \\
T_2 I_s \\
T_3 I_a \\
\gamma_1 R
\end{pmatrix}
$$

(A4)

Next, the linearized Jacobian around the disease free equilibrium point is given by matrix $J$

$$
J = \begin{pmatrix}
-T_1 & \beta(S' + \theta_1 V') & \beta(S' + \theta_1 V') & 0 \\
0 & -T_2 & -\phi k_2 & 0 \\
\epsilon (1 - \kappa) & 0 & -T_3 & 0 \\
0 & \alpha_1 k_1 & \alpha_2 k_3 & -\gamma_1
\end{pmatrix}
$$

(A5)

and $S^*$ and $V^*$ are given in the paper by Eqns. (24) and (25), respectively. Following the Next Generation Matrix Method $J = F_1 - G_1$, where $F_1$ and $G_1$ are given by

$$
F_1 = \begin{pmatrix}
0 & \beta(S' + \theta_1 V') & \beta(S' + \theta_1 V') & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0
\end{pmatrix}
$$

(A6)

$$
G_1 = \begin{pmatrix}
T_1 & 0 & 0 & 0 \\
-\epsilon (1 - \kappa) & T_2 & -\phi k_2 & 0 \\
0 & -\alpha_1 k_1 & -\alpha_2 k_3 & -\gamma_1
\end{pmatrix}
$$

(A7)

Finally, the largest eigenvalue value of $F_1 G_1^{-1}$ defines the vaccinated reproductive number ($R_v$). Thus

$$
R_v = \frac{\alpha \epsilon (1 - \kappa)(\omega + T_1) + \alpha T_1 (\gamma_1 + \omega_1 \theta_1)}{\gamma_1 (\gamma_1 + \omega_1) T_1 T_2 T_3}
$$

(A8)
References

[1] CDC, COVID-19 vaccine effectiveness research. https://www.cdc.gov/vaccines/covid-19/effectiveness-research/protocols.html. [Accessed 16 July 2021].

[2] Batistela CM, Correa DPF, Bueno AM, Piqueira JRC. SIRSi compartmental model for COVID-19 pandemic with immunity loss. Chaos, Solit Fractals 2021;142. https://doi.org/10.1016/j.chaos.2020.110388.

[3] Sinha DN, Tan P. Title: mathematical model and simulations of COVID-19 2020 outbreak in New York: predictions and implications for control measures, n.d. https://doi.org/10.1093/pcmedi/pbaa018.

[4] Dashtbali M, Mirzaie M. A compartmental model that predicts the effect of social distancing and vaccination on controlling COVID-19. Sci Rep 2021:11. https://doi.org/10.1038/s41598-021-86873-0.

[5] Wang T, Wu Y, Lau JY-N, Yu Y, Liu L, Li J, Zhang K, Tong W, Jiang B. A four-compartment model for the COVID-19 infection—implications on infection kinetics, control measures, and lockdown exit strategies. Precision Clinical Medicine 2020;3:104–12. https://doi.org/10.1093/pcmedi/pbaa018.

[6] Blackwood JC, Childs LM. An introduction to compartmental modeling for the budding infectious disease modeler. Letters in Biomathematics 2018;5:195–221. https://doi.org/10.1080/23737867.2018.1509026.

[7] Schneider KA, Ngove GA, Schwebm H, Eicher L, Eicher M. The COVID-19 pandemic preparedness simulation tool: CovidSIM. BMC Infect Dis 2020;20. https://doi.org/10.1186/s12879-020-05566-7.

[8] Wolfram, wolfram mathematica. https://www.wolfram.com/mathematica/. [Accessed 16 July 2021].

[9] Office of the New York STATE COMPTROLLER, New York STATE COMPTROLLER. 2021.

[10] Ramezani SB, Amirlatifi A, Rahimi S. A novel compartmental model to capture the nonlinear trend of COVID-19. Comput Biol Med 2021:134. http://doi.org/10.1016/j.compbiomed.2021.104421.

[11] Worldometer, Worldometer coronavirus New York Cases, deaths and recovered. https://www.worldometers.info/coronavirus/usa/new-york/; 2021.

[12] Smith RJ, Li J, Blakeley D. The failure of R0, computational and mathematical methods in medicine. 2011. https://doi.org/10.1155/2011/527610; 2011.

[13] Delamater PL, Street JJ, Leslie TE, Yang YT, Jacobsen KH. Complexity of the basic reproduction number (R0). Emerg Infect Dis 2019;25:1–4. https://doi.org/10.3201/eid2501.171901.

[14] Teles F. A time-dependent SEIR model to analyse the evolution of the SARS-CoV-2 epidemic outbreak in Portugal. http://arxiv.org/abs/2004.04755; 2020.

[15] Beckley R, Weatherspoon C, Alexander M, Chandler M, Johnson A, Bhatt GS. Modeling epidemics with differential equations. 2013.

[16] Beckley R, Weatherspoon C, Alexander M, Chandler M, Johnson A, Bhatt GS. Modeling epidemics with differential equations. 2013.