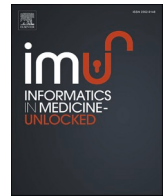Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Assessing the impact of vaccination in a COVID-19 compartmental model

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A B S T R A C T

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*).
Findings: 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
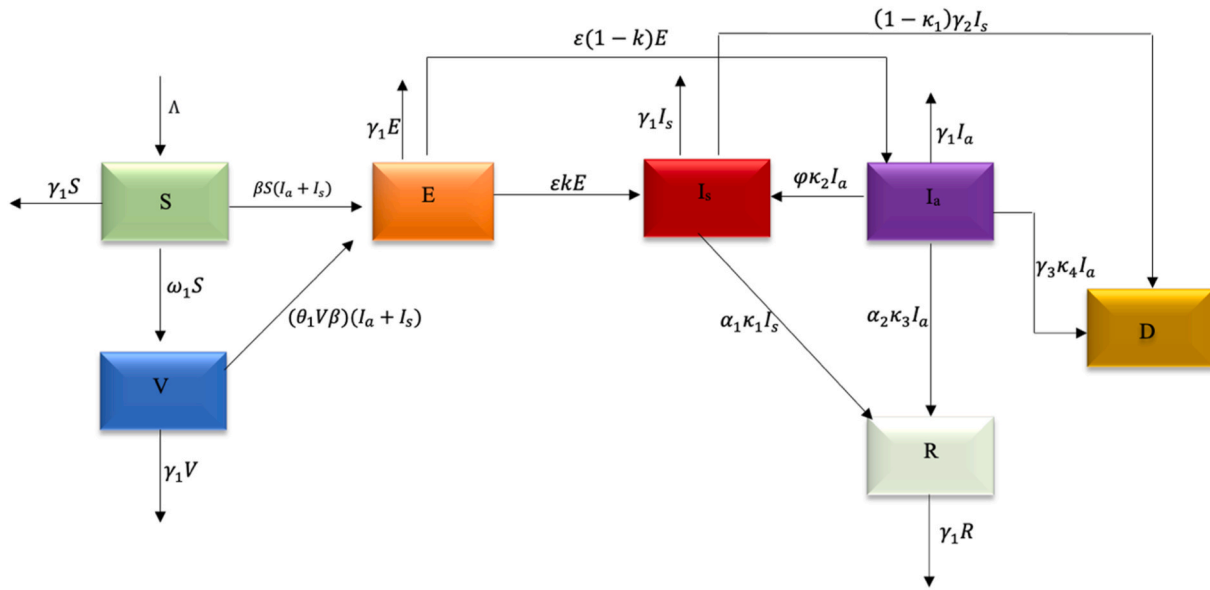
Fig. 1. The SVEIRD compartmental mode.

Table 1
The *SVEIRD* model's parameters of Fig. 1.

Parameters	Name
Λ	Recruitment
B	COVID-19 transmission coefficient rate
γ_1	Natural mortality rate
γ_2	COVID-19 symptomatic mortality rate
γ_3	COVID-19 asymptomatic mortality rate
ω_1	Vaccine coverage rate
θ_1	Vaccine failure
E	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
Φ	Proportion of symptomatic to symptomatic
α_1	Recovery rate of the symptomatic population
α_2	Recovery rate of the asymptomatic population

and 4, respectively. The stability of these equilibrium points is discussed in Sec. 5. 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 corona virus disease, we do not claim that our results for *NYS* should be considered definitive, Although we are aware that *NYS* had to endure two coronavirus waves, in this work we shall attempt only to simulate 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 corona-virus 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.

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_s*), asymptomatic infectious (*I_a*), recovered (*R*), and dead by coronavirus (*D*).

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

Eqns. (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 ($N = S + V + E + I_s + I_a + R + D$). The new normalized variables will be still denoted by the same letters as in Fig. 1. Namely, $\wedge \to \frac{\wedge}{N}$, $S \to \frac{S}{N}$, $V \to \frac{V}{N}$, $E \to \frac{E}{N}$, $I \to \frac{I}{N}$, $R \to \frac{R}{N}$, and $D \to \frac{D}{N}$.

$$\frac{dS}{dt} = \Lambda - S(\gamma_1 + \omega_1 + \beta(I_a + I_s)) \tag{1}$$

$$\frac{dV}{dt} = S\omega_1 - V(\gamma_1 + \theta_1\beta(I_a + I_s)) \tag{2}$$

$$\frac{dE}{dt} = \beta S(I_a + I_s) + V\theta_1\beta(I_a + I_s) - ET_1 \tag{3}$$

$$\frac{dI_s}{dt} = \varepsilon kE + k_2\varphi I_a - I_s T_2 \tag{4}$$

$$\frac{dI_a}{dt} = \varepsilon(1-k)E - I_a T_3 \tag{5}$$

$$\frac{dR}{dt} = k_3\alpha_2 I_a + k_1\alpha_1 I_s - \gamma_1 R \tag{6}$$

$$\frac{dD}{dt} = (1-k_1)\gamma_2 I_s + k_4\gamma_3 I_a \tag{7}$$

where

$$T_1 = \varepsilon + \gamma_1 \tag{8}$$

$$T_2 = (1-k_1)\gamma_2 + k_1\alpha_1 + \gamma_1 \tag{9}$$

$$T_3 = k_2\varphi + k_4\gamma_3 + k_3\alpha_2 + \gamma_1 \tag{10}$$

$$k_4 = 1 - k_2 - k_3 \tag{11}$$

Adding Eqns. (1)–(7) we obtain $\frac{dN}{dt} = \Lambda - \gamma_1 N$. This implies $\frac{dN}{dt} < 0$ when $N > \frac{\Lambda}{\gamma_1}$, and therefore solutions of Eqns. (1)–(7) must be in the following positively invariant subset of R^7: $\{(S,V,E,I_s,I_a,R,D)/ S,V,E,I_s, I_a, R,D \geq 0, \ S + V + E + I_s + I_a + R + D \leq \frac{\Lambda}{\gamma_1}\}$

3. Results

3.1. Equilibrium points

To obtain the equilibrium points $(S_p, E_p, V_p, I_{ap}, I_{sp}, R_p)$ we set Eqns. (1)–(7) to zero. For example, by setting to zero Eqn. (5) we solve it for E_p and inserted into Eqn. (4), to obtain Eqn. (13). From there, it easily follows Eqn. (12). Using a similar algebraic procedure, we obtain Eqns. 14–16

$$E_p = \frac{T_6 T_3 I_{sp}}{\varepsilon (1-k) T_5} \tag{12}$$

$$I_{ap} = \frac{T_6}{T_5} I_{sp} \tag{13}$$

$$S_p = \frac{\Lambda}{\gamma_1 + \omega_1 + \beta (I_{ap} + I_{sp})} \tag{14}$$

$$V_p = \frac{\omega_1 S_p}{\gamma_1 + \theta_1 \beta (I_{ap} + I_{sp})} \tag{15}$$

$$R_p = \left(\frac{1}{\gamma_1}\right)\left(\alpha_2 I_{ap} + \alpha_1 I_{sp}\right) \tag{16}$$

where

$$T_4 = kk_4\gamma_3 + kk_3\alpha_2 + k_2\varphi + k\gamma_1 \tag{17}$$

$$T_5 = k\,T_3 + (1-k)\,k_2\varphi \tag{18}$$

$$J_{df} = \begin{pmatrix} -\gamma_1 - \omega_1 & 0 & 0 & 0 & -\beta S^* & -\beta S^* \\ \omega_1 & 0 & 0 & -\gamma_1 & -\beta\theta_1 V^* & -\beta\theta_1 V^* \\ 0 & 0 & -T_1 & 0 & \beta S^* + \beta\theta_1 V^* & \beta S^* + \beta\theta_1 V^* \\ 0 & 0 & \varepsilon & \kappa & 0 & k_2\varphi & -T_2 \\ 0 & 0 & \varepsilon - \varepsilon & \kappa & 0 & -T_3 & 0 \\ 0 & -\gamma_1 & 0 & 0 & k_3\alpha_2 & k_1\alpha_1 \end{pmatrix} \tag{27}$$

$$J_{end} = \begin{pmatrix} -\gamma_1 - \beta(I_{ap} + I_{sp}) - \omega_1 & 0 & 0 & 0 & -\beta S_p & -\beta S_p \\ \omega_1 & 0 & 0 & -\gamma_1 - \beta(I_{ap} + I_{sp})\theta_1 & -\beta\theta_1 V_p & -\beta\theta_1 V_p \\ \beta(I_{ap} + I_{sp}) & 0 & -T_1 & \beta(I_{ap} + I_{sp})\theta_1 & \beta S_p + \beta\theta_1 V_p & \beta S_p + \beta\theta_1 V_p \\ 0 & 0 & \varepsilon & \kappa & 0 & k_2\varphi & -T_2 \\ 0 & 0 & \varepsilon - \varepsilon\kappa & 0 & -T_3 & 0 \\ 0 & -\gamma_1 & 0 & 0 & k_3\alpha_2 & k_1\alpha_1 \end{pmatrix} \tag{28}$$

$$T_6 = (1-k)T_2 \tag{19}$$

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

$$C_1 I_{sp}^3 + C_2 I_{sp}^2 + C_3 I_{sp} = 0 \tag{20}$$

where

$$C_1 = \beta^2 T_1 T_3 T_6 (T_5 + T_6)^2 \theta_1 \tag{21}$$

$$C_2 = \beta T_5 (T_5 + T_6)\big(\beta\varepsilon(-1+k)(T_5 + T_6)\lambda\theta_1 + T_6 T_1 T_3 (\gamma_1 + \gamma_1\theta_1 + \theta_1\omega_1)\big) \tag{22}$$

$$C_3 = T_5^2(\gamma_1 T_6 T_1 T_3 (\gamma_1 + \omega_1)) - T_5^2(\beta\Lambda\varepsilon(kT_3 + (1-k)(T_5 + T_6))(\gamma_1 + \omega_1\theta_1)) \tag{23}$$

3.2. Disease free equilibrium points

The trivial solution of Eqn. (20); i.e., $I_{sp} = 0$ defines the disease equilibrium point (DFE). Thus, from Eqns. 12–16 the only non-zero solutions are

$$S^* = \frac{\Lambda}{\gamma_1 + \omega_1} \tag{24}$$

$$V^* = \frac{\Lambda\omega_1}{\gamma_1(\gamma_1 + \omega_1)} \tag{25}$$

3.3. Disease endemic equilibrium points

To obtain the disease endemic equilibrium points ($I_{sp} \neq 0$) we first must solve from.

Eqn. (20) the quadratic equation. Namely

$$C_1 I_{sp}^2 + C_2 I_{sp} + C_3 = 0 \tag{26}$$

where C_1, C_2 and C_3 are given by Eqns. 21–23. Then I_{sp} is to be substituted in Eqns. 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_{end}, respectively. They are explicitly given bellow in Eqns. (27) and (28).

As is well known, a local stable equilibrium is achieved when all the eigenvalues of matrices J_{df} and J_{end} are negative. Otherwise, there is an unstable equilibrium. By setting $\theta_1 = \omega_1 = 0$ in Eqns. (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 Eqns 27 and 28 are numerically calculated for *NYS* in Section 4.

3.5. An 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 (Λ, β, θ_1, k_1, ε), and negative sensitivities (γ_1, α_1, α_2, k, k_2, k_3, k_4, φ, γ_2, γ_3, w_1).

Parameter	Sensitivity
Λ	1
B	1
θ_1	0.990774
κ_1	0.447102
ε	0.00016164
γ_3	−0.0002613
κ_4	−0.0002613
κ_2	−0.0076717
Φ	−0.0076717
ω_1	−0.0087607
γ_2	−0.0124228
κ	−0.0829919
κ_3	−0.196499
α_2	−0.196499
α_1	−0.782753
γ_1	−0.991793

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

Parameters	Estimated Values	References
Λ	0.3640 10^{-4} (1/day)	www.osc.state.ny.us [20]
β	0.55/day (first period), 0.09/day (second period)	Estimated
γ_1	0.2328 10^{-4} (1/day)	https://webbi1.health.ny.gov [22]
γ_2	0.0949 (1/day)	[23]
γ_3	0.0697 (1/day)	[23]
ω_1	0.0500 (1/day)	Estimated
θ_1	0.050	Estimated
ε	0.144	[23]
k	0.749	[23]
k_1	0.001	Estimated
k_2	0.100	Estimated
k_3	0.899	Estimated
Φ	0.200 (1/day)	Estimated
α_1	0.0604	[23]
α_2	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_v. To fulfill this purpose, we shall solve Eqn. (20) to obtain the equilibrium point I_{sp}. Notice, $I_{sp} > 0$ 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 showed in Eqn. (29), where C_1, C_2, and $C_3 = C_{3a} - C_{3b}$, are explicitly given by Eqns. (21)–(23), respectively. Thus,

$$I_{sp} = -\frac{C_2}{2C_1} \pm \frac{C_2}{2C_1}\sqrt{1 + \frac{4C_1(C_{3b} - C_{3a})}{C_2^2}} = -\frac{C_2}{2C_1} \pm \frac{C_2}{2C_1}\sqrt{1 + \frac{4C_1 C_{3a}\left(\frac{C_{3b}}{C_{3a}} - 1\right)}{C_2^2}}$$

(29)

Notice from Eqns. (21) and (23) that $C_1 > 0$, and

$$C_{3a} = T_5^2(\gamma_1 T_6 T_1 T_3(\gamma_1 + \omega_1)) > 0$$

(30)

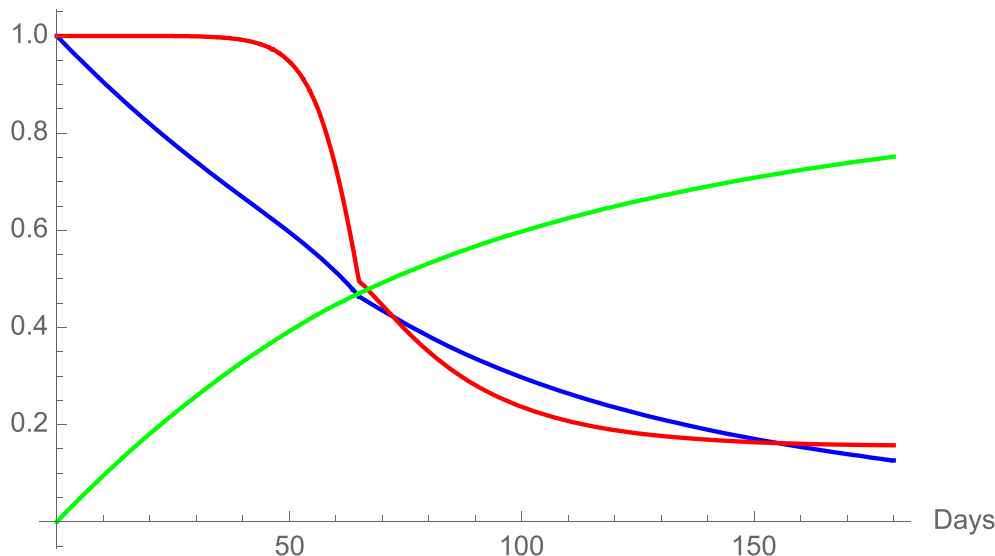$$C_{3b} = T_5^2(\beta \Lambda \varepsilon \, (kT_3 + (1-k)(T_5 + T_6))(\gamma_1 + \omega_1 \theta_1)) > 0$$

(31)

where

$$T_5 = kT_3 + (1-k)k_2\varphi$$

(32)

$$T_6 = (1-k)T_2$$

(33)

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

$R_v = \frac{C_{3b}}{C_{3a}} > 1$ to satisfy the necessary condition $I_p > 0$. 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.)

a
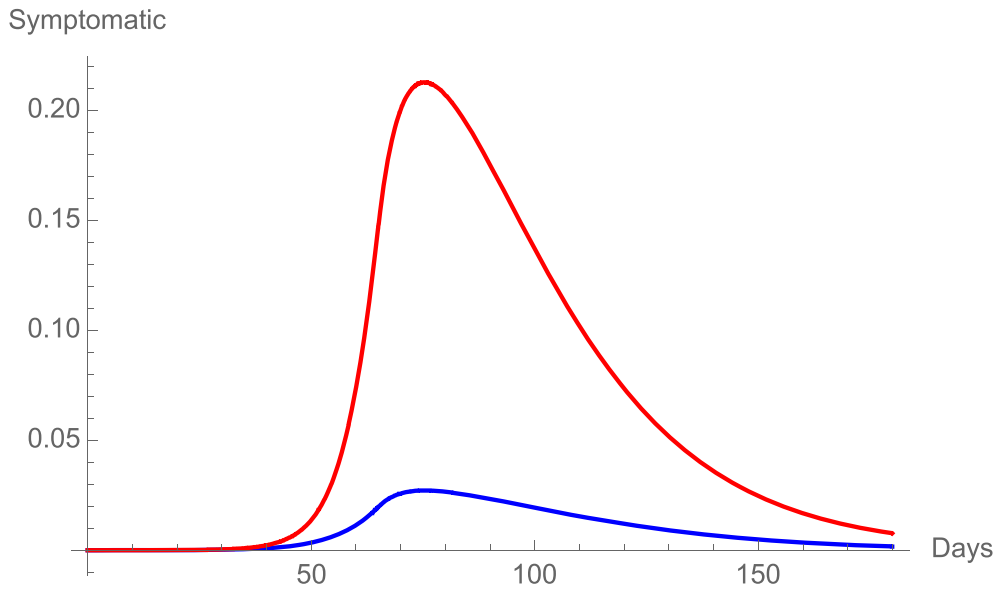
Symptomatic

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.)

Asymptomatic Infected
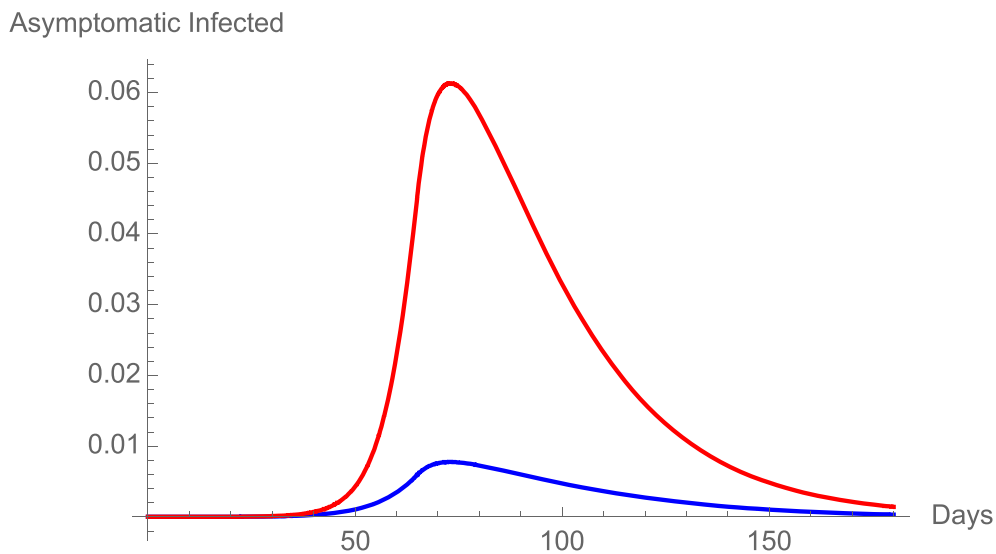
Fig. 4. The unvaccinated asymptomatic (red) population. Vaccination reduces the asymptomatic population (blue). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

$$R_v = \frac{(\beta \Lambda \varepsilon (kT_3 + (1-\kappa)(T_2 + k_2\varphi))(\gamma_1 + \omega_1\theta_1)}{\gamma_1 T_1 T_2 T_3 (\gamma_1 + \omega_1)} \tag{34}$$

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) is found by setting $\omega_1 = \theta_1 = 0$ in Eqn. (34). Thus

$$R = \frac{(\beta \Lambda \varepsilon (kT_3 + (1-\kappa)(T_2 + k_2\varphi))}{\gamma_1 T_1 T_2 T_3} \tag{35}$$

Now, from Eqns. 34 and 35 we obtain a relationship between R_v and R as follows

$$R_v = R \frac{\gamma_1 + \omega_1\theta_1}{\gamma_1 + \omega_1} \tag{36}$$

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

$$\text{Vaccine's efficacy} > 1 - \frac{1}{R} \tag{38}$$

Eq. (38) can also be written as follows

$$\text{Vaccine's efficacy} > \text{Herd immunity} \tag{39}$$

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
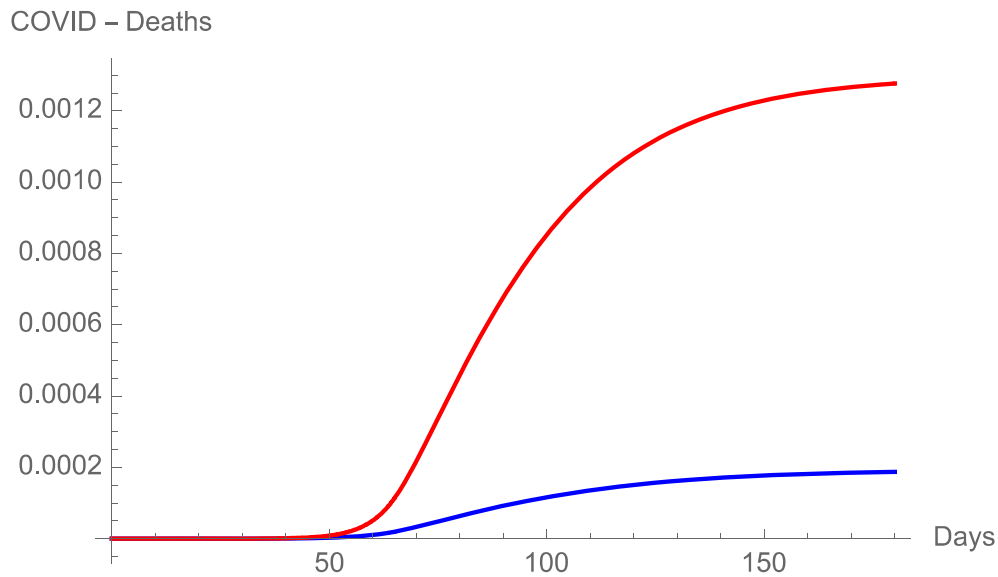
COVID – Deaths

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.)
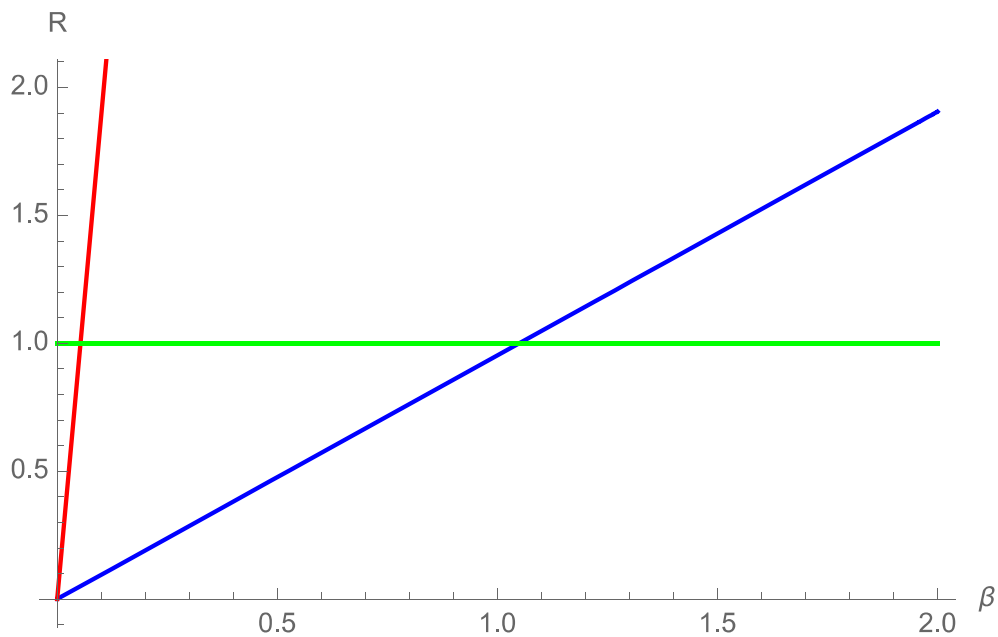

Fig. 6. The unvaccinated (red) and vaccinated (blue) reproductive numbers in function of the transmission coefficient rate (β).In green.. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)$R = 1$.

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 $S(x_n)$

$$S_v(x_n) = \left(\frac{x_n}{R_v}\right)\frac{\partial R_v}{\partial x_n} \tag{40}$$

From Eqn, (36), the relationship between the unvaccinated ($S(x_n)$) and vaccinated ($S_v(x_n)$)sensitives between is

$$S_v(x_n) = \frac{x_n}{f}\frac{\partial f}{\partial x_n} + S(x_n) \tag{41}$$

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

Therefore, for all parameters except θ_1, ω_1, and γ_1, $S_v(x_n) = S(x_n)$.Also notice that $S_v(x_n)$ does not depend of β, Λ, and ε. For *NYS* model's parameters sensitives are given in Table 2.

The most sensitive parameters for R_v are Λ, β and θ_1. To diminish (increase) the value of R_v we must diminish (increase) the positive
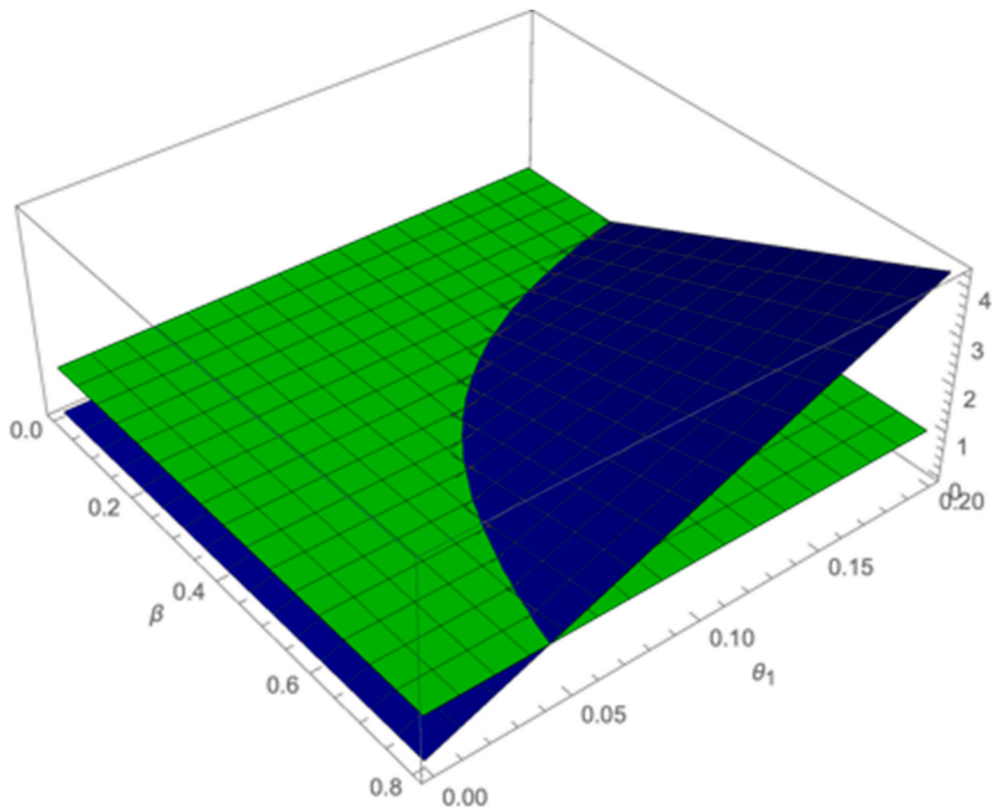
Fig. 7. In blue, the vaccinated reproduction number (R_v). In green, a plane of value 1. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)
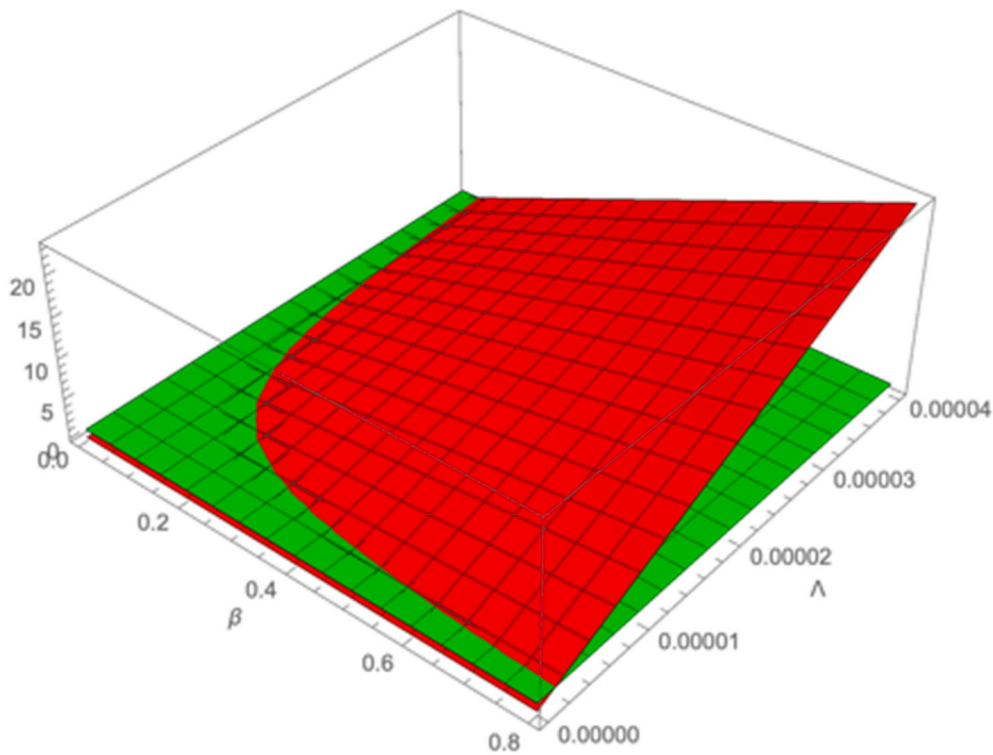
Fig. 8. In red, the unvaccinated reproduction number (R). In green, a plane of value 1. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

(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., $I_p \neq 0$). If $R_v > 1$ there is only one biological meaningful solution of Eqn. (29). When $R_v < 1$, 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_v 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_v, 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* corona-virus 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 β to 2.39 and 0.09, respectively. Next, a MATHEMATICA [19] code is developed to plot the numerical solutions of Eqns. (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 been 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 $(S_p, E_p, I_{sp}, I_{ap}, R_p)$. Thus, without vaccination the Covid-19 disease will persist and converge to the endemic equilibrium point $(S_p = 0.00362, E_p = 0.00015, I_{sp} = 0.00029, I_{ap} = 0.00007, R_p = 0.90782)$. It is expected that all meaningful solutions of Eqns. (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 $S^* = \frac{\Delta}{\gamma_1} = 1.56$. Using the respective Jacobians we found that both of these equilibrium points are unstable. For $R_v = 0.12$ all solutions of Eqns. (1)–(7) will converge to the disease-free equilibrium points $(S^* = 0.0036, V^* = 1.5599)$ and the Covid-19 disease will be died out.

In Eqn. (38), we showed that the optimal vaccine (1- θ_1) 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 β must be greater than

0.05/day to become endemic. On the other hand, if the population was vaccinated β should be less than 1.1/day to died out. Therefore, after the second period, a second wave was expected.

In Figs. (7)-(8), we plot three-dimensional figures of the R_v 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 *SVEIQRD* 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 Erne

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Declaration of competing interest

The authors declare that they have no competing financial interest that has influence in the work reported in this paper.

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 bellow.

$$\begin{pmatrix} \frac{dE}{dt} \\ \frac{dI_s}{dt} \\ \frac{dI_s}{dt} \\ \frac{dR}{dt} \end{pmatrix} = F(\vec{x}) - \left(V^-(\vec{x}) - V^+(\vec{x}) \right) \tag{A1}$$

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

$$F = \begin{pmatrix} I_s\beta(S+\theta_1 V) + I_a\beta(S+\theta_1 V) \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{A2}$$

$$V^+ = \begin{pmatrix} 0 \\ \varepsilon\kappa E + k\varphi I_a \\ \varepsilon(1-\kappa)E \\ \alpha_1 k_1 I_s + \alpha_2 k_3 I_a \end{pmatrix} \tag{A3}$$

$$V^- = \begin{pmatrix} T_1 E \\ T_2 I_s \\ T_3 I_a \\ \gamma_1 R \end{pmatrix} \tag{A4}$$

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

$$J = \begin{pmatrix} -T_1 & \beta(S^*+\theta_1 V^*) & \beta(S^*+\theta_1 V^*) & 0 \\ \varepsilon\kappa & -T_2 & \varphi k_2 & 0 \\ \varepsilon(1-\kappa) & 0 & -T_3 & 0 \\ 0 & \alpha_1 k_1 & \alpha_2 k_3 & -\gamma_1 \end{pmatrix} \tag{A5}$$

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

$$F_1 = \begin{pmatrix} 0 & \beta(S^*+\theta_1 V^*) & \beta(S^*+\theta_1 V^*) & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{A6}$$

$$G_1 = \begin{pmatrix} T_1 & 0 & 0 & 0 \\ -\varepsilon\kappa & T_2 & -\varphi k_2 & 0 \\ -\varepsilon(1-\kappa) & 0 & T_3 & 0 \\ 0 & -\alpha_1 k_1 & -\alpha_2 k_3 & \gamma_1 \end{pmatrix} \tag{A7}$$

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

$$R_v = \frac{\Lambda\beta\varepsilon((1-\kappa)(\varphi+T_2)+\kappa T_3)(\gamma_1+\omega_1\theta_1)}{\gamma_1(\gamma_1+\omega_1)T_1 T_2 T_3} \tag{A8}$$

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