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A TRANSMISSION MODEL OF COVID-19 WITH QUARANTINE, TREATMENT AND VACCINATION

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Abstract

A precise characterization of a Sars-Cov 2 dynamics transmission model with vaccination is presented. All the equilibria of the model as well as their stabilities have been described by use of algebraic geometry approach. The model analysis shows that the combined use of the quarantine and treatment strategy with a vaccination strategy may lead to the effective disease control or elimination.

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0. Introduction

The novel corona virus pandemic (Covid-19), which appeared in December 2019 in the Chinese province of Wuhan and has since spread throughout the world, still remains a source of concern for all the countries [2]. The socio-economic impacts of containment strategies make their scope very limited in time since vaccines against Covid-19 are available, even if the side effects are not yet fully known for some of them. The purpose of the current study is to assess the combined use of quarantine, treatment and vaccine strategies. The use of algebraic geometry and computer algebra approaches can allow the characterization of all the equilibria as well as their stability analysis [8, 10]. The model presented has 3 equilibria. Note that the basic reproduction number denoted by R_0 can be calculated using the van den Driessche and Watmough method [11]. The disease free equilibrium is stable if $R_0 < 1$ and unstable if $R_0 > 1$: If there are only two equilibria, then the second one is endemic. When there are more than two equilibria, the basic reproduction number does not allow to control exactly the stability of endemic equilibria.

We present in this paper a compartmental model, with three equilibria of Covid-19 in an assumed constant population. Part of this population is under quarantine or treatment and another part is under vaccination. We show how exact methods of algebraic geometry and computer algebra can be used to understand the behavior of the disease.

We start with the presentation of the model in Section 1. In Section 2, we determine and characterize the equilibria of the model algebraically using Gröebner's basis. In Section 3, we study the stability of equilibria of the model by the methods of algebraic geometry and in particular for disease-free equilibrium, we calculate the basic reproduction number for a verification of algebraic characterizations. The study of the bifurcations between equilibria is made in Section 4. Section 5 is devoted to global stability of disease-free equilibrium.

1. Mathematical Model

We present a model to study the spread of Covid-19 in a constant population of which a portion is under treatment, quarantine or vaccination. The population is divided into six classes. Those who are not carrying Covid-19 and who are not in quarantine or not vaccinated are in class *S*. The undiagnosed infectious of Covid-19 are in class I_1. The diagnosed infectious (who are under treatment) are in class I_2. Those who are in quarantine are in class *Q*. The vaccinated people are in class *V*. Those who are vaccinated and under quarantine are in class V_Q. The model transfer diagram is given in Figure 1. The model is represented by the following system of ordinary differential equations:

$$\begin{cases} \dot{S} = \mu(1-\tau) + \omega V - \mu S - (\beta S I_1 + \beta S I_2)(1-e) + r(I_1 + I_2) + (1-\gamma)Q \\ \dot{I}_1 = (1-e)\beta S I_1 - \beta I_1 I_2 (1-e) - (\gamma + \mu + r) I_1 \\ \dot{Q} = \omega V_Q + (1-e)\beta(S + I_1) I_2 - (1+\mu) Q \\ \dot{I}_2 = \gamma(I_1 + Q) - (\mu + r) I_2 \\ \dot{V} = \mu\tau + (1-\omega) V_Q - (1-e)\beta V I_1 - (\omega + \mu) V \\ \dot{V}_Q = (1-e)\beta V I_1 - (1+\mu) V_Q, \end{cases} \tag{1}$$

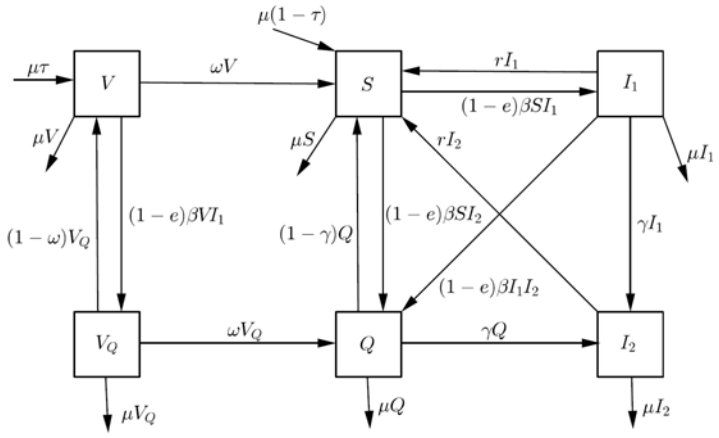

Figure 1. Model transfer diagram.

where

β: contact rate,

e: rate of compliance with instructions,

r: cure rate,

γ: coverage rate,

τ: vaccination rate,

μ: birth rate = death rate,

ω: loss of immunity rate.

Given a differentiable vector field $f : \mathbb{R}^n \to \mathbb{R}^n$, we recall that $\mathbb{R}^n_+$ is positively invariant under f if and only if for each $i \in [1, n]$ and $x \in \mathbb{R}^n_+$ such that $x_i = 0$, we have $f_i(x) \geq 0$ [12]. Applying this property, it makes easy to verify that $\mathbb{R}^n_+$ is positively invariant under the field of vectors associated with the system (1). On the other hand, we can easily verify that

$$0 = \dot{S} + \dot{I}_1 + \dot{Q} + \dot{I}_2 + \dot{V} + \dot{V}_Q = \mu(1 - S - I_1 - Q - I_2 - V - V_Q),$$

and further $S + I_1 + Q + I_2 + V + V_Q = 1$ for any solution of the system (1).

So $\Omega = \{S, I_1, Q, I_2, V, V_Q \geq 0 | S + I_1 + Q + I_2 + V + V_Q = 1\}$ is positively invariant and the system (1) is mathematically and epidemiologically well defined.

2. Model Equilibria

If we write the system (1) in the form $\dot{x} = f(x, u)$, where $u = (\beta, e, r, \gamma, \tau, \mu, \omega)$ is the list of parameters and $x = (S, I_1, Q, I_2, V, V_Q)$ is the list of state variables, an important characteristic of the model common to a large class of epidemiological models, [5, 9] is that the components of the vector

field f are polynomials in variables u and x. So we can use the powerful tools of the computer algebra such as Gröebner bases [1, 4, 7] to determine the equilibria of the model, which are the solutions in Ω of the system of algebraic equations $f(u, x) = 0$, that is

$$\begin{cases} \mu(1-\tau) + \omega V - \mu S - (\beta S I_1 + \beta S I_2)(1-e) + r(I_1 + I_2) + (1-\gamma)Q = 0 \\ (1-e)\beta S I_1 - \beta I_1 I_2 (1-e) - (\gamma + \mu + r) I_1 = 0 \\ \omega V_Q + (1-e)\beta(S + I_1) I_2 - (1+\mu) Q = 0 \\ \gamma(I_1 + Q) - (\mu + r) I_2 = 0 \\ \mu\tau + (1-\omega) V_Q - (1-e)\beta V I_1 - (\omega + \mu) V = 0 \\ (1-e)\beta V I_1 - (1+\mu) V_Q = 0. \end{cases} \tag{2}$$

The computation of the Gröebner base [1] of the system f_1, f_2, f_3, f_4, f_5, f_6 according to the lexicographic order $S \prec I_1 \prec Q \prec I_2 \prec V \prec V_Q$ allows us to have a triangular system (a). The first element of the computed Gröebner base is a polynomial of degree 3 in S whose roots are

$$s_0 = \frac{\mu + \omega - \mu\tau}{\mu + \omega}, \quad s_1 = \frac{(1+\mu)(\mu + r)}{(1-e)\gamma\beta},$$

and

$$s_2 = \frac{a_1 + ((\gamma + \mu + r)^2 + (\mu + 1)(\mu + r))(\mu + \omega)}{\beta(\mu + \omega)(1-e)(2\gamma + \mu + r)},$$

where

$$a_1 = \gamma\beta(\mu + \omega - \mu\tau)(1-e) - (1+\mu)(\mu + r)(\omega + \mu).$$

Replacing S by s_0 in the system (a) and by substituting in the other equations, we get a single equilibrium, noted E_0, whose coordinates are

$$\left(s_0,\ 0,\ 0,\ 0,\ \frac{\mu\tau}{\omega + \mu},\ 0\right).$$

It is the disease-free equilibrium of the model and exists for all parameter values.

Replacing S by s_1 in the system (a) and by substituting in the other equations, we get a second equilibrium, noted E_1, whose coordinates are

$$s_1 = \frac{(\mu+1)(\mu+r)}{(1-e)\gamma\beta},$$

$$i_{11} = 0,$$

$$q_1 = \frac{(\mu+r)a_1}{(1-e)\gamma\beta(\omega+\mu)(\gamma+\mu+r)},$$

$$i_{21} = \frac{a_1}{(1-e)\beta(\omega+\mu)(\gamma+\mu+r)},$$

$$v_1 = \frac{\mu\tau}{\omega+\mu},$$

$$v_{Q_1} = 0.$$

This equilibrium corresponds to the absence of undiagnosed infectious of Covid-19 and it exists if and only if $a_1 \geq 0$.

Finally, by replacing S by s_2 in the system (a) and by substituting in the other equations, we get a third equilibrium, noted E_2, whose coordinates are

$$s_2 = \frac{a_1 + ((\gamma+\mu+r)^2 + (\mu+1)(\mu+r))(\omega+\mu)}{(1-e)\beta(\omega+\mu)(2\gamma+\mu+r)},$$

$$i_{12} = 0,$$

$$q_2 = \frac{a_2(\mu+r)}{(1-e)\beta(2\gamma+\mu+r)(\omega+\mu)},$$

$$i_{22} = \frac{\gamma a_2}{(1-e)\beta(\omega+\mu)(2\gamma+\mu+r)},$$

$$v_2 = \frac{a_4}{(1-e)\beta\omega(\omega+\mu)^2(2\gamma+\mu+r)^2},$$

$$v_{Q_2} = \frac{-a_2 a_3}{(1-e)\beta\omega(\omega+\mu)^2(2\gamma+\mu+r)^2}, \tag{3}$$

where

$$a_2 = (1-e)\beta(\omega+\mu-\mu\tau) - (\omega+\mu)(\gamma+\mu+r),$$

$$a_3 = \gamma^2(1-e)\beta(\omega+\mu-\mu\tau) + (\omega+\mu)(\gamma((\gamma+\mu+r)^2 - 2(\mu+1)(\mu+r)) - (1+\mu)(\mu+r)^2)$$

and

$$a_4 = a_2 a_3 + (1-e)\beta\omega\mu\tau(2\gamma+\mu+r)^2(\omega+\mu).$$

This equilibrium corresponds to the presence of Covid-19 carriers in observation or in Quarantine and it exists if and only if $a_3 \leq 0$, $a_1 \geq 0$, $a_2 \geq 0$ and $a_4 \geq 0$.

3. Stability of Equilibria

We are interested in this part in the local stability of the three equilibria of the model. We use the classical linearization method and the Lienard-Chipart criterion [3] or Lyapunov function when the equilibrium is not hyperbolic. In other words, we calculate the characteristic polynomial of the Jacobian of the system at each equilibrium and we analyze its roots. Moreover, for the disease-free equilibrium, we calculate the basic reproduction number of the model. We will write the characteristic polynomials without the non-intervening factors in the stability analysis. We start with disease-free equilibrium.

3.1. Equilibrium E_0 stability

For the disease-free equilibrium E_0, the characteristic polynomial χ_0 of the Jacobian matrix $\partial_x f(u, E_0)$ is factorizable [6]:

$$\chi_0 = (Z+\mu)(Z+\omega+\mu)(Z+\mu+1)((\mu+\omega)Z - a_2)((\mu+\omega)Z^2 + (2\mu+1)(\mu+\omega)Z - a_1).$$

Thus, the equilibrium E_0 is hyperbolic and locally asymptotically stable if and only if $a_1 < 0$ and $a_2 < 0$ [3].

Basic reproduction number

From the variations of the infectious compartments:

$$\dot{I}_1 = (1-e)\beta I_1 S - (1-e)\beta I_1 I_2 - (\gamma+\mu+r)I_1,$$

$$\dot{I}_2 = \gamma(I_1+Q) - (r+\mu)I_2$$

and by setting $w = (I_1, I_2)$ and $\mathcal{F}(w) = \begin{pmatrix} (1-e)\beta I_1 S \\ \gamma(I_1+Q) \end{pmatrix}$ the column matrix of the rates of appearance of new cases of infection by infectious compartment and $\mathcal{V}(w) = \begin{pmatrix} (1-e)\beta I_1 I_2 + (\gamma+\mu+r)I_1 \\ (r+\mu)I_2 \end{pmatrix}$ the column matrix of the differences between the rates of transfer of individuals leaving and those arriving by infectious compartment, we determine the matrices

$$F = \partial_w \mathcal{F}(w)(E_0) = \begin{pmatrix} (1-e)\beta s_0 & 0 \\ \gamma & 0 \end{pmatrix}$$

and

$$V = \partial_w \mathcal{V}(w)(E_0) = \begin{pmatrix} r+\mu+\gamma & 0 \\ 0 & r+\mu \end{pmatrix}.$$

The basic reproduction number of the disease-free equilibrium is the spectral radius of the matrix $F \cdot V^{-1}$.

We have

$$V^{-1} = \begin{pmatrix} \frac{1}{r+\mu+\gamma} & 0 \\ 0 & \frac{1}{r+\mu} \end{pmatrix} \text{ and } F \cdot V^{-1} = \begin{pmatrix} \frac{(1-e)\beta s_0}{r+\mu+\gamma} & 0 \\ \frac{\gamma}{r+\mu+\gamma} & 0 \end{pmatrix}.$$

The determinant $|F \cdot V^{-1}|$ is equal to 0, thus 0 is an eigenvalue of $F \cdot V^{-1}$ and the second eigenvalue is the trace: $\frac{(1-e)\beta s_0}{r+\mu+\gamma}$. The basic reproduction number R_0 of the model is therefore the strictly positive eigenvalue of the matrix $F \cdot V^{-1}$, that is

$$R_0 = \frac{(1-e)\beta s_0}{\gamma+\mu+r} = \frac{(1-e)\beta(\mu(1-\tau)+\omega)}{(\mu+\omega)(\gamma+\mu+r)}.$$

The following result is a consequence of Theorem 2 of [11].

Theorem 1. *The disease-free equilibrium E_0 of the model is locally-asymptotically stable if $R_0 < 1$ (that is if $a_2 < 0$) and unstable if $R_0 > 1$.*

Note that the inequality $R_0 < 1$ reflects exactly the condition $a_2 < 0$.

3.2. Stability of equilibria E_1 and E_2

Theorem 2. *With the previous notations, the equilibrium E_1 exists and is hyperbolic and locally asymptotically stable if and only if $a_1 > 0$ and $a_3 > 0$.*

Proof. The characteristic polynomial of the Jacobian matrix $\partial_x f(u, E_1)$ does not factorize completely (in first degree factor product), but can be factorized [6] under the form

$$\chi_1 = (Z+\mu)(Z+\omega+\mu)(Z+\mu+1)(\gamma(\omega+\mu)(\gamma+\mu+r)Z + a_3)P_1(Z),$$

where

$$P_1(Z) = ((\omega+\mu)(\gamma+\mu+r)Z^2 + (a_1 + (2\mu+r+1)(\omega+\mu)(\gamma+\mu+r))Z + (\gamma+\mu+r)a_1.$$

The equilibrium E_1 is therefore hyperbolic and locally asymptotically stable if and only if $a_1 > 0$ and $a_3 > 0$. □

Theorem 3. *The equilibrium* E_2 *exists and is stable asymptotically if and only if* $a_1 > 0$, $a_2 > 0$ *and* $a_3 < 0$.

Proof. The characteristic polynomial of the Jacobian matrix $\partial_x f(u, E_2)$ does not factorize completely. We can notice that the non-specialized characteristic polynomial is factorized [6] in the form

$$\chi_2 = (Z + \mu)(Z + \omega + \mu)(Z + \mu + 1)ZP_2(Z)$$

with

$$P_2(Z) = (\omega + \mu)(2\gamma + \mu + r)Z^2 + (a_1 + p_2(\omega + \mu))Z$$
$$- a_3 + \gamma(\gamma + \mu + r)a_2,$$

where

$$p_2 = -\gamma^2 + 3\gamma\mu + \gamma r + 3\mu^2 + 4\mu r + r^2 + 2(\gamma + \mu + r).$$

For the stability of E_2, we apply the Liénard-Chipart theorem [3] to polynomial P_2. All non-zero eigenvalues have a negative real part. As E_2 is not hyperbolic, we use a Lyapunov function to decide its stability. Let the Lyapunov function $L : \mathbb{R}_+^6 \to \mathbb{R}_+$ be such that $L(x) = (\mu\tau - (\omega + \mu)(V + V_Q))^2$ (with $x = (S, I_1, Q, I_2, V, V_Q)$).

On Ω, $L'(x) = -2(\omega + \mu)(\mu\tau - (\omega + \mu)(V + V_Q))^2 = -2(\omega + \mu)L(x) \leq 0$. Hence, E_2 exists and is stable if and only if $a_1 > 0$, $a_2 > 0$, $a_3 < 0$ and $a_4 > 0$. □

4. Bifurcations

Let $U \subseteq \mathbb{R}^n$ and $V \subseteq \mathbb{R}^n$ be two open subsets and $f(v, x) : V \times U \to \mathbb{R}^n$ be differentiable. We say that $f(v, x)$ is a differentiable family of vector fields. We designate by $\phi(t, v, x)$ the flow family generated by *f*.

When we vary the parameters v, the family $\phi(t, v, x)$ generally undergoes qualitative changes. For example, equilibria may appear or disappear, just as they may change stability. Other phenomena more complex may appear. Studying these qualitative changes constitute the bifurcation theory.

4.1. Stability exchange between E_0 and E_1

Let e_1 be the value of β that cancels a_1. If $a_1 > 0$, then E_0 is stable and E_1 does not exist. If $a_1 = 0$, then E_0 and E_1 coincide and the corresponding characteristic polynomial has a single null eigenvalue and the others are negative:

$$\frac{P_0}{\gamma}(H + 2\mu + r + 1)(H\gamma + \gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1)),$$

where

$$P_0 = H(H + \mu)(H + \omega + \mu)(H + \mu + 1).$$

Let us prove that

$$\gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) > 0 \text{ if } a_1 = 0.$$

We have

$$\begin{aligned} a_2 < 0 &\Leftrightarrow (1 - e)\beta(\omega + \mu - \mu\tau) - (\omega + \mu)(\gamma + \mu + r) < 0 \\ &\Leftrightarrow (1 - e)\beta(\omega + \mu - \mu\tau) < (\omega + \mu)(\gamma + \mu + r) \\ &\Leftrightarrow \frac{\gamma}{\mu + \omega}(1 - e)\beta(\omega + \mu - \mu\tau) < \gamma(\gamma + \mu + r) \\ &\Leftrightarrow \gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) > \frac{a_1}{\omega + \mu} \\ &\Leftrightarrow \gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) > 0 \text{ if } a_1 = 0. \end{aligned}$$

If $a_1 > 0$, then E_0 is unstable and E_1 appears stable. So E_0 lost stability at profit of E_1 when a_1 went through 0. Hence, we have the existence of a transcritical bifurcation when $a_1 = 0$, that is to say when $\beta = e_1$.

4.2. Stability exchange between E_0 and E_2

Let e_1 be the value of β that cancels a_2. If $a_2 < 0$, then E_0 is stable and E_2 does not exist. If $a_2 = 0$, then E_0 and E_2 coincide and the corresponding characteristic polynomial has as in the previous case a single null eigenvalue and the others are negative:

$$P_0(H^2 + (2\mu + r + 1)H - \gamma(\gamma + \mu + r) + (\mu + r)(\mu + 1)).$$

Let us prove that $\gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) < 0$ if $a_2 = 0$.

We have

$$\begin{aligned} a_1 > 0 &\Leftrightarrow \gamma\beta(\mu + \omega - \mu\tau)(1 - e) - (1 + \mu)(\mu + r)(\omega + \mu) > 0 \\ &\Leftrightarrow \gamma\beta(\mu + \omega - \mu\tau)(1 - e) > (1 + \mu)(\mu + r)(\omega + \mu) \\ &\Leftrightarrow \frac{\gamma}{\omega + \mu}\beta(\mu + \omega - \mu\tau)(1 - e) > (1 + \mu)(\mu + r) \\ &\Leftrightarrow \gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) < -\frac{\gamma}{\omega + \mu}a_2 \\ &\Leftrightarrow \gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) < 0 \text{ if } a_2 = 0. \end{aligned}$$

If $a_2 > 0$, then E_0 is unstable and E_2 appears stable. So E_0 lost stability at profit of E_2 when a_2 has passed through 0. Hence, there exists a transcritical bifurcation when $a_2 = 0$, that is to say when $\beta = e_2$.

4.3. Stability exchange between E_1 and E_2

Let e_3 be the value of β that cancels a_3. If $a_3 > 0$, then E_1 is stable and E_2 does not exist. If $a_3 = 0$, then E_1 and E_2 coincide and the corresponding characteristic polynomial has a single null eigenvalue and the others are negative:

$$\begin{aligned} P_0(\gamma H^2 &+ (\gamma(1 + \mu - \gamma) + (\mu + r)(\mu + 1))H \\ &+ ((\mu + r)(\mu + 1) - \gamma(\gamma + \mu + r))(\gamma + \mu + r)). \end{aligned}$$

Let us prove that $\gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) < 0$ if $a_2 > 0$.

We have

$$a_1 > 0 \Leftrightarrow \gamma\beta(\mu + \omega - \mu\tau)(1-e) - (1+\mu)(\mu + r)(\omega + \mu) > 0$$

$$\Leftrightarrow \gamma\beta(\mu + \omega - \mu\tau)(1-e) > (1+\mu)(\mu + r)(\omega + \mu)$$

$$\Leftrightarrow \frac{\gamma}{\omega + \mu}\beta(\mu + \omega - \mu\tau)(1-e) > (1+\mu)(\mu + r)$$

$$\Leftrightarrow \gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) < -\frac{\gamma}{\omega + \mu}a_2$$

$$\Leftrightarrow \gamma(\gamma + \mu + r) - (\mu + r)(\mu + 1) < 0 \text{ if } a_2 > 0.$$

So E_1 lost stability at profit of E_2 when a_3 has passed through 0. Hence, we have the existence of a transcritical bifurcation when $a_3 = 0$, that is to say when $\beta = e_3$.

Finally, to summarize, we have the following results:

Theorem 4. *The model represented by the system* (1) *has*:

• *A disease-free equilibrium* E_0 *which exists at all times and is locally asymptotically stable if* $a_1 < 0$ *and* $a_2 < 0$ (*if* $R_0 < 1$), *with*

$$a_1 = \gamma\beta(\mu + \omega - \mu\tau)(1-e) - (1+\mu)(\mu + r)(\omega + \mu) \text{ and}$$

$$a_2 = (1-e)\beta(\omega + \mu - \mu\tau) - (\omega + \mu)(\gamma + \mu + r).$$

• *An equilibrium* E_1 *with the existence of patients under treatment or possibly among people in quarantine or observation, locally asymptotically stable if* $a_1 > 0$ *and* $a_3 > 0$ *with*

$$a_3 = \gamma^2(1-e)\beta(\omega + \mu - \mu\tau) + (\omega + \mu)(\gamma((\gamma + \mu + r)^2$$

$$- 2(\mu + 1)(\mu + r)) - (1+\mu)(\mu + r)^2).$$

• *An endemic equilibrium* E_2 *is locally asymptotically stable if* $a_1 > 0$, $a_2 > 0$, $a_3 < 0$ *and* $a_4 > 0$ (*if* $R_0 > 1$).

5. Global Stability of the Disease-free Equilibrium

The domain Ω is positively invariant when the trajectory of any solution of the system (1) which begins in Ω stays in Ω, for all positive *t*. With the previous notations, we have:

Lemma 1. *The domain* $\Omega_1 = \{(S, I_1, Q, I_2, V, V_Q) \in \mathbb{R}_+^6 : S \leq s_0\}$ *is positively invariant under* $\dot{x} = f(x(t), u)$.

Proof. Let $(S, I_1, Q, I_2, V, V_Q) \in \mathbb{R}_+^6$ with positive initial conditions. Then we show that

$$\limsup_{t \to +\infty}(S(t)) \leq s_0.$$

Let us pose $X = S + I_1 + Q + I_2$. Then by taking the derivative with respect to the time of X following the trajectories of the system solution $\dot{x} = f(x(t), u)$, we have: $\dot{X} = \mu + \omega - \mu\tau - (\mu + \omega)X$. This gives us a differential equation whose solution is $X = s_0 + (X(0) - s_0)e^{-(\mu+\omega)t}$.

Indeed as $S \leq X$, we obtain $\limsup_{t \to +\infty}(S(t)) \leq s_0$.

Thus, when $t \to +\infty$, $0 \leq S \leq s_0$. Indeed, all possible solutions of the system start and remain in the domain

$$\Omega_1 = \{(S, I_1, Q, I_2, V, V_Q) \in \mathbb{R}_+^6 : S \leq s_0\},$$

so Ω_1 is positively invariant. □

Theorem 5. *If* $R_0 < 1$, *then the disease-free equilibrium* $E_0 = (s_0, 0, 0, 0, v_0, 0)$ *is globally asymptotically stable*.

Proof. Consider Lyapunov's function $L : \mathbb{R}_+^6 \to \mathbb{R}_+$ such that $L(x) = I_1$: We have

$$\frac{dL(x(t))}{dt} = (1 - e)\beta I_1 S - (1 - e)\beta I_1 I_2 - (\gamma + \mu + r)I_1.$$

Then

$$\frac{dL(x(t))}{dt} \leq (1-e)\beta I_1 S - (\gamma + \mu + r) I_1$$
$$\leq I_1((1-e)\beta S - \gamma - \mu - r)$$
$$\leq I_1((1-e)\beta s_0 - \gamma - \mu - r)$$
$$\leq \frac{I_1 a_2}{\mu + \omega}.$$

So E_0 is globally asymptotically stable in Ω_1 if $a_2 < 0$. Hence, $R_0 < 1$. □

6. Numerical Simulations

In the following simulations, we fix μ, γ, β, ω and r.

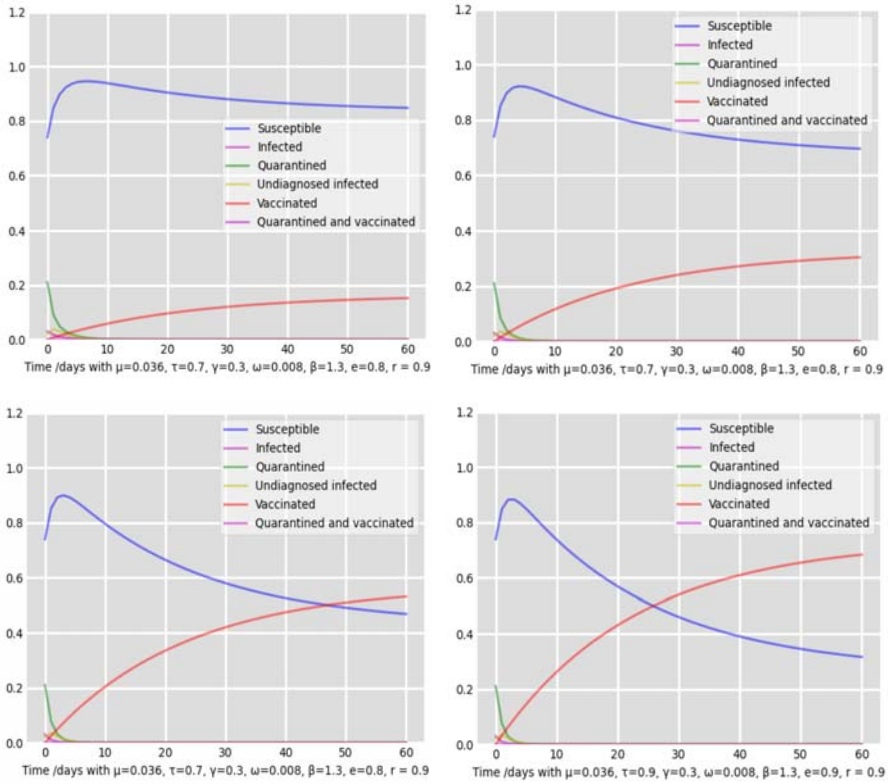

Figure 2. Model simulation.

Note that, we have seen in Section 2, at the disease-free equilibrium all the compartments are zero except for S and V. Figure 2 clearly shows that for a very high vaccination rate and increasing values of e, the number of infections decreases rapidly.

7. Conclusion

For our Covid-19 transmission model, all the equilibria, their stabilities and the sets of bifurcation are exactly characterized by the use of algebraic geometry and computer algebra methods. The disease-free equilibrium is globally asymptotically stable, that is to say that all trajectories tend asymptotically towards disease-free equilibrium. For very high rates of vaccination and adherence to instructions, the number of infections decreases very rapidly. Vaccination is therefore one of the best disease control tools.

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