Mathematical study for the phase-based transmissibility of a novel COVID-19 Coronavirus

Miled EL HAJJI
ENIT-LAMSIN, BP. 37, 1002 Tunis-Belv`ed`ere, Tunis El Manar University, Tunisia & Higher Institute of Applied Science and Technology of Sousse, Sousse University, Cit`e Taffala, 4003 Sousse, Tunisia
https://orcid.org/0000-0002-4718-4463

Sayed SAYARI
Carthage University, Isteub, 2 Rue de l'Artisanat Chuguia 2, 2035 Tunis, Tunisia

Abdelhamid ZAGHDANI (hamido20042002@yahoo.fr)
University of Tunis, Boulevard du 9 Avril 1939 Tunis. Department of Mathematics, Ensit, Taha Hussein Avenue, Montfleury. Tunis, Tunisia.

Research Article

Keywords: COVID-19, Coronavirus, SEIRW Model, Local and Global Stability, Direct Lyapunov Method, Lasalle's Invariance Principle

Posted Date: May 4th, 2020

DOI: https://doi.org/10.21203/rs.3.rs-26318/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License
Mathematical study for the phase-based transmissibility of a novel COVID-19 Coronavirus

Miled EL HAJJI *1, Sayed SAYARI †2, and Abdelhamid ZAGHDANI ‡3

1ENIT-LAMSIN, BP. 37, 1002 Tunis-Belvédère, Tunis El Manar University, Tunisia
2Higher Institute of Applied Science and Technology of Sousse, Sousse University, Cité Taffila, 4003 Sousse, Tunisia
3Carthage University, Isteub, 2 Rue de l’Artisanat Charguia 2, 2035 Tunis, Tunisia
4University of Tunis, Boulevard du 9 Avril 1939 Tunis. Department of Mathematics, Ensit, Taha Hussein Avenue, Montfleury. Tunis, Tunisia.

April 2020

Abstract

In this paper, a mathematical dynamical system modeling a SEIRW model of infectious disease trans-
mission for a transmissibility of a novel COVID-19 Coronavirus is studied. A qualitative analysis such
as the local and global stability of equilibrium points is carried out. It is proved that if $R_0 \leq 1$, then
the disease-free equilibrium is globally asymptotically stable and if $R_0 > 1$, then the disease-persistence
equilibrium is globally asymptotically stable.

Keywords: COVID-19, Coronavirus, SEIRW Model, Local and Global Stability, Direct Lyapunov
Method, Lasalle’s Invariance Principle.

Mathematics Subject Classification: 34D23, 35N25, 37B25, 49K40, 60H10, 65C30, 91B70.

1 Introduction

On December 31, 2019, the World Health Organization (WHO) alerted several cases of pneumonia of un-
known origin in the city of Wuhan (Hubei Province of China). But this virus was unlike any known virus.
On January 7, 2020, the Chinese authorities confirmed that it was indeed a new virus from the coronavirus
family. At first it was temporarily baptized “2019-nCoV” then definitively COVID-19 or SARS-CoV-2.
Since then, human cases have been reported from almost all countries and COVID-19 has been class-
ified as a pandemic by the World Health Organization (WHO). As the epidemic of pneumonia due to
the new coronavirus 2019-nCoV spreads around the world, Chinese researchers had in recent months,
on several occasions, alerted the international scientific community to the risk of seeing soon emerge a
human infection by a coronavirus from bats in China. The seafood market in Wuhan, central China’s
Hubei province, may be the source of the new coronavirus (2019-nCoV) epidemic, according to Chinese

* miled.elhajji@enit.rnu.tn
† Sayari.sayed@gmail.com
‡ hamido20042002@yahoo.fr; Corresponding author
This epidemic obliges us to propose models allowing to estimate the transmissibility and dynamic of the transmission of the virus. There were several researches focusing on mathematical modelling [6, 7, 8]. However, the transmission route form the seafood market to people were not considered in the published models. Since public concerns were focusing on the transmission from Huanan Seafood Wholesale Market (reservoir) to people, we proposed a simplified model as a Reservoir-People (RP) transmission network model.

This paper is organized as follows. In section 2, a mathematical dynamical system involving “SEIRW” epidemic model is considered. The basic reproduction number \( R \) was calculated using the next generation matrix method to assess the transmissibility of the SARS-CoV-2. A profound qualitative analysis is given. The analysis of the local and global stability of equilibrium points is carried out in sections 3 and 4, respectively. It is proved that if the reproduction number \( R > 1 \), then the disease-persistence (endemic) equilibrium is globally asymptotically stable. However, if \( R \leq 1 \), then the disease-free equilibrium is globally asymptotically stable. Finally, in section 5, some numerical tests are done in order to validate the obtained results.

2 Mathematical model and some properties

\( W \) denotes the SARS-CoV-2 in reservoir (the seafood market). The individuals were divided into four compartments: susceptible individuals \( S \), exposed individuals \( E \), infected individuals \( I \) including symptomatic and asymptomatic infected individuals, and removed individuals \( R \) including recovered and death individuals. The rate of individuals traveling out from the city was defined as \( m \). \( n/m \) denotes the total number of individuals traveling into the city. The incubation period and latent period of human infection are assumed to be equal and defined as \( 1/\omega \). The infectious period of compartment \( I \) was defined as \( 1/\gamma \). The compartment \( S \) will be infected through sufficient contact with compartment \( I \) and compartment \( W \), and the transmission rates were defined as \( b_1 \) and \( b_2 \), respectively.

![Flowchart of the Reservoir-People transmission network model (SEIRW).](image)

Figure 1: Flowchart of the Reservoir-People transmission network model (SEIRW).
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$m$</td>
<td>Rate of individuals traveling out from Wuhan City</td>
</tr>
<tr>
<td>$n/m$</td>
<td>Individuals traveling into Wuhan City</td>
</tr>
<tr>
<td>$1/\omega$</td>
<td>Incubation period of individuals= latent period of individuals</td>
</tr>
<tr>
<td>$1/\gamma$</td>
<td>Infectious period</td>
</tr>
<tr>
<td>$b_1$</td>
<td>Transmission rate from $I$ to $S$</td>
</tr>
<tr>
<td>$b_2$</td>
<td>Transmission rate from $W$ to $S$</td>
</tr>
<tr>
<td>$1/\varepsilon$</td>
<td>Lifetime of the virus in $W$</td>
</tr>
</tbody>
</table>

During the disease outbreak period, birth and death rates are neglected with respect to the rate of individuals traveling into and out from Wuhan City due to the Chinese New Year holiday.

In the proposed model, individuals and viruses have different dimensions. Based on previous researches [1, 2, 3], a normalized Reservoir-People (RP) transmission network model is given as follows:

\[
\begin{aligned}
\dot{S} &= n - mS - b_1SI - b_2SW \\
\dot{E} &= b_1SI + b_2SW - (\omega + m)E \\
\dot{I} &= \omega E - (\gamma + m)I \\
\dot{R} &= \gamma I - mR \\
\dot{W} &= \varepsilon (I - W)
\end{aligned}
\]

For every given initial condition $(S(0), E(0), I(0), R(0), W(0))$ in $\mathbb{R}^5$, system (1) admits a bounded solution with positive components defined for all $t > 0$.

The set $\Omega_1 = \{(S, E, I, R, W) \in \mathbb{R}^5 \mid S + E + I + R + W \leq \frac{n}{m}\}$ is a positively invariant attractor for system (1) where $\bar{m} = \min(m - \varepsilon, \varepsilon)$.

Note that symptomatic and asymptomatic infected people are merged into one compartment $I$ as infected people. The closed non-negative cone in $\mathbb{R}^5$, is positively invariant by the system (1). More precisely, Proposition 1.

1. For every given initial condition $(S(0), E(0), I(0), R(0), W(0))$ in $\mathbb{R}^5$, system (1) admits a bounded solution with positive components defined for all $t > 0$.

2. The set $\Omega_1 = \{(S, E, I, R, W) \in \mathbb{R}^5 \mid S + E + I + R + W \leq \frac{n}{m}\}$ is a positively invariant attractor for system (1) where $\bar{m} = \min(m - \varepsilon, \varepsilon)$.

Proof. The solution is positive due to the fact that:

Since $S = 0$ then $\dot{S} = n > 0$, if $E = 0$ then $\dot{E} = b_1SI + b_2SW > 0$, once $I = 0$ then $\dot{I} = \omega E > 0$, if $R = 0$ then $\dot{R} = \gamma I > 0$, and if $W = 0$ then $\dot{W} = \varepsilon I > 0$.

The boundedness of solutions of system (1) can be proved by adding all equations of system (1), and then one obtains, for $T = S + E + I + R + W - \frac{n}{m}$, the following equation for the total individuals:

\[
\begin{aligned}
\dot{T} &= \dot{S} + \dot{E} + \dot{I} + \dot{R} + \dot{W} \\
&= n - mS - mE - (m - \varepsilon)I - mR - \varepsilon W \\
&\leq \bar{m}\left(\frac{n}{m} - S - E - I - R - W\right) \\
&= -\bar{m}T.
\end{aligned}
\]

Then

\[
S + E + I + R + W \leq \frac{n}{m} + \left(S_0 + E_0 + I_0 + R_0 + W_0 - \frac{n}{m}\right) e^{-\bar{m}t}.
\]

Then the boundedness of the solution of system (1) holds since all compartments of $T$ are positive.

One can easily deduce from equality (2) that the set $\Omega_1$ is positively invariant attractor for system (1).
Define $\hat{Q} = (\frac{n}{m}, 0, 0, 0, 0)$ as the disease free equilibrium point and $Q^* = (S^*, E^*, I^*, R^*, W^*)$ as the endemic equilibrium point of system (1) where $S^*, E^*, I^*, R^* > 0$ and $W^* > 0$ satisfying

$$
\left\{
\begin{array}{l}
n = mS^* + b_1S^*I^* + b_2S^*W^*, \\
b_1S^*I^* + b_2S^*W^* = (\omega + m)E^*, \\
\omega E^* = (\gamma + m)I^*, \\
\gamma I^* = mR^*, \\
I^* = W^*.
\end{array}
\right.
$$

(3)

Diekmann, et al. [4] proposed a method to calculate the basic reproduction number $R$ for complex compartmental models by using the next generation matrix method. This method elaborated later by van den Driessche and Watmough [5]. Let $x = (x_1, x_2, \cdots, x_N)^T$ be the number of individuals in each compartment, where the first $M < N$ compartments contain infected individuals. Consider these equations written in the form $\frac{dX_i}{dt} = F_i(x) - \gamma_i(x)$ for $i = 1, 2, \cdots, M$. In this splitting, $F_i(x)$ is the rate of appearance of new infections in compartment $i$, and $\gamma_i(x)$ is the rate of other transitions between compartment $i$ and other infected compartments. It is assumed that $\gamma_i$ and $\gamma_i \in C^2$, and $F_i = 0$ if $i \in [M + 1, N]$. Let $x_0$ to be the disease free equilibrium and define $F = \left[\frac{\partial F_i(x_0)}{\partial x_j}\right]$ and $V = \left[\frac{\partial \gamma_i(x_0)}{\partial x_j}\right]$ for $1 \leq i, j \leq M, F$ is entrywise non-negative and $V$ is a non-singular M-matrix [4, 5]. Then $FV^{-1}$ is the next generation matrix and

$$R = \rho(FV^{-1}),$$

where $\rho$ is the spectral radius. In our case $F = \begin{pmatrix} 0 & \frac{b_1n}{m} & \frac{b_2n}{m} \\ 0 & 0 & m \\ 0 & 0 & 0 \end{pmatrix}$ and $V = \begin{pmatrix} \omega + m & 0 & 0 \\ -\omega & \gamma + m & 0 \\ 0 & -\varepsilon & \varepsilon \end{pmatrix}$.

The determinant of $V$ is given by $\det(V) = \varepsilon(\omega + m)(\gamma + m) > 0$ and therefore

$$V^{-1} = \begin{pmatrix} \frac{1}{\omega + m} & 0 & 0 \\ \frac{1}{\omega + m}(\gamma + m) & \frac{1}{\omega} & 0 \\ \frac{1}{\omega + m}(\gamma + m) & \frac{1}{\gamma + m} & \frac{1}{\varepsilon} \end{pmatrix}$$

and $FV^{-1} = \begin{pmatrix} \frac{(b_1 + b_2)n}{m(\omega + m)(\gamma + m)} & \frac{(b_1 + b_2)n}{m(\gamma + m)} & \frac{b_2n}{m\varepsilon} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$.

Then the basic reproduction number for model (1) is given by

$$R = \frac{(b_1 + b_2)n}{m(\omega + m)(\gamma + m)} = R_1 + R_2$$

with $R_1 = \frac{b_1\omega n}{m(\omega + m)(\gamma + m)}$ and $R_2 = \frac{b_2\omega n}{m(\omega + m)(\gamma + m)}$.

## 3 Local Analysis

**Theorem 1.**

- If $R < 1$, then the disease-free equilibrium $\hat{Q}$ is locally asymptotically stable.
- If $R > 1$, then the disease-free equilibrium $\hat{Q}$ is unstable.
Proof. The matrix \( \bar{J} \) is evaluated at \( \bar{Q} = \left( \frac{n}{m}, 0, 0, 0 \right) \) is given by:

\[
\bar{J} = \begin{pmatrix}
-m & 0 & -\frac{b_1 n}{m} & 0 & -\frac{b_2 n}{m} \\
0 & -(\omega + m) & \frac{b_1 n}{m} & 0 & \frac{b_2 n}{m} \\
0 & \omega & -(\gamma + m) & 0 & 0 \\
0 & 0 & \gamma & -m & 0 \\
0 & 0 & \varepsilon & 0 & -\varepsilon
\end{pmatrix}
\]

The characteristic equation is

\[
P(\lambda) = (\lambda + m)^2 \left( - (\omega + m + \lambda)(\gamma + m + \lambda)(\varepsilon + \lambda) + \omega \left( \frac{b_1 n}{m}(\varepsilon + \lambda) + \frac{b_2 n}{m} \varepsilon \right) \right)
\]

\[
= (\lambda + m)^2 \left( -\lambda^3 - \lambda^2 \left( \omega + \gamma + \varepsilon + 2m \right) - \lambda \left( (\omega + m)(\gamma + m) + \varepsilon(\gamma + m) + \varepsilon(\omega + m) - \frac{b_1 \omega n}{m} \right) \right)
\]

\[-\varepsilon(\omega + m)(\gamma + m) + (b_1 + b_2) \frac{\omega n \varepsilon}{m}\]

Let \( P(\lambda) = -(\lambda + m)^2 P_3(\lambda) \), with \( P_3(\lambda) = \lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 \), where

\[
a_1 = (\omega + \gamma + \varepsilon + 2m) > 0
\]

\[
a_2 = (\omega + m)(\gamma + m) + \varepsilon(\gamma + m) + \varepsilon(\omega + m) - \frac{b_1 \omega n}{m}
\]

\[
a_3 = \varepsilon(\omega + m)(\gamma + m) - (b_1 + b_2) \frac{\omega n \varepsilon}{m} = \varepsilon(\omega + m)(\gamma + m)(1 - \mathbf{R}).
\]

Therefore

\[
a_1 a_2 - a_3 = (\omega + \gamma + \varepsilon + 2m) \left( (\omega + m)(\gamma + m) + \varepsilon(\gamma + m) + \varepsilon(\omega + m) - \frac{b_1 \omega n}{m} \right)
\]

\[-\varepsilon(\omega + m)(\gamma + m) + (b_1 + b_2) \frac{\omega n \varepsilon}{m}
\]

\[
= \left( \omega + \gamma + \varepsilon + 2m \right) \left( (\omega + m)(\gamma + m) + \varepsilon(\gamma + m) + \varepsilon(\omega + m) - \frac{b_1 \omega n}{m} \right)
\]

\[-\varepsilon(\omega + m)(\gamma + m)(1 - \mathbf{R})
\]

\[
> \left( \omega + \gamma + \varepsilon + 2m \right) \left( (\omega + m)(\gamma + m) + \varepsilon(\omega + m)(1 - \mathbf{R}) \right)
\]

\[-\varepsilon(\omega + m)(\gamma + m)(1 - \mathbf{R})
\]

\[
= \left( \omega + \gamma + \varepsilon + 2m \right) \left( \varepsilon(\gamma + m) + \varepsilon(\omega + m)(1 - \mathbf{R}) + \varepsilon^2(\gamma + m) + \varepsilon^2(\omega + m) \right)
\]

\[
> \left( \omega + \gamma + \varepsilon + 2m \right) \left( \varepsilon(\gamma + m) + \varepsilon(\omega + m)(1 - \mathbf{R}) \right)
\]

Then if \( \mathbf{R} < 1 \), then \( a_1 > 0 \), \( a_3 > 0 \) and \( a_1 a_2 - a_3 > 0 \), and if \( \mathbf{R} > 1 \), then \( a_1 > 0 \) and \( a_3 < 0 \) and thus using Routh-Hurwitz criterion, all eigenvalues have negative real parts if \( \mathbf{R} < 1 \). This completes the proof. \( \square \)

Theorem 2. If \( \mathbf{R} > 1 \), then the disease-persistence equilibrium \( Q^* = (S^*, E^*, I^*, R^*, W^*) \) is locally asymptotically stable.
**Proof.** The matrix $J^*$ is evaluated at $E^* = (S^*, E^*, I^*, R^*, W^*)$ is given by:

$$
J^* = \begin{pmatrix}
-a_1 + b_1I^* + b_2W^* & 0 & -b_1S^* & 0 & -b_2S^* \\
b_1I^* + b_2W^* & -(\omega + m) & b_1S^* & 0 & b_2S^* \\
0 & \omega & -(\gamma + m) & 0 & 0 \\
0 & 0 & \gamma & -m & 0 \\
0 & 0 & \varepsilon & 0 & -\varepsilon \\
\end{pmatrix}
$$

Using the fact that $-m - b_1I^* - b_2W^* = -mR$ and $b_1I^* + b_2W^* = m(R - 1)$

The characteristic equation is given by \( P'(\lambda) = -(\lambda + m)P_4(\lambda) \) with

$$
P_4(\lambda) = \lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4,
$$

where

\[
\begin{align*}
a_1 &= mR + \omega + m + \gamma + m + \varepsilon > 0, \\
a_2 &= mR(\omega + m + \gamma + m + \varepsilon) + \varepsilon(\omega + m + \gamma + m) + (\omega + m)(\gamma + m)(1 - \frac{R_1}{R}), \\
a_3 &= \varepsilon mR(\omega + m + \gamma + m) + mR(\omega + m)(\gamma + m)(1 - \frac{R_1}{R^2}), \\
a_4 &= \varepsilon m(\omega + m)(\gamma + m)(R - 1).
\end{align*}
\]

Therefore, after calculations we get

$$
a_1a_2 - a_3 \geq (\omega + \gamma + 2m + \varepsilon) \left( m^2R^2 + mR(\omega + m + \varepsilon) + \varepsilon(\omega + \gamma + 2m) \right) + mR(\omega + m)(\omega + m + \varepsilon)
$$

$$
\geq 0
$$

and

$$
a_1(a_2a_3 - a_3a_4) - a_2^2 = (mR + \omega + m + \gamma + m)
\left[ \varepsilon^2mR(\omega + \gamma + 2m) + \varepsilon^2m(1 - \frac{R_1}{R})(\omega + m)(\gamma + m) \\
+ \varepsilon mR(\omega + m + \gamma + m)(\omega + m)(\gamma + m)(1 - \frac{R_1}{R}) \\
+ mR(\omega + m)^2(\gamma + m)^2(1 - \frac{R_1}{R})(1 - \frac{R_1}{R}) + \varepsilon^2mR(\omega + \gamma + 2m)(\omega + \gamma + m) \\
+ \varepsilon m(1 - \frac{R_1}{R})(mR + \omega + m + \gamma + m)(\gamma + m) + \varepsilon^2m(\omega + m)(\gamma + m) \\
+ \varepsilon^2mR(\omega + m + \gamma + m)(\omega + m)(\gamma + m)(1 - \frac{R_1}{R}) \\
+ \varepsilon^2mR(\omega + m)^2(\gamma + m)^2(1 - \frac{R_1}{R}^2)(1 - \frac{R_1}{R}) \\
+ \varepsilon^3m(\omega + m)(\gamma + m) + mR^3 + \varepsilon m^2R^3(\omega + m + \gamma + m)^2 \\
+ m^2R^2(\omega + m)^2(\gamma + m)^2(1 - \frac{R_1}{R^2})(1 - \frac{R_1}{R}) \\
+ m^2R^2((\omega + m)^2 + (\gamma + m)^2)(\omega + m)(\gamma + m)(1 - \frac{R_1}{R}) \\
+ \varepsilon m^2R^2(\omega + m + \gamma + m)(\omega + m)(\gamma + m)(1 + \frac{R_1}{R^2}) \\
+ \varepsilon m^2R^2(\omega + m + \gamma + m)((\omega + m)^2 + (\gamma + m)^2).
\right]
$$
Since $1 - \frac{R_1}{R} > 0$ and $1 - \frac{R_2}{R} > 0$ for $R > 1$ we get $a_1(a_2a_3 - a_1a_4) - a_3^2 > 0$ and by the Routh Hurwitz criteria we end the proof.

4 Global Analysis

Lemma 1. $\Omega_2 = \{(S, E, I, R, W) \in \mathbb{R}^5_+ / S + E + I + R + W \leq \frac{n}{m}; S \leq \frac{n}{m}, W \leq I\}$ is a positively invariant attractor set for system (1) where $m = \min(m - \epsilon, \epsilon)$.

Proof. It is proved in Proposition 1 that $\Omega_1$ is a positive invariant attractor set of all solution of system (1). Now, since $\dot{S}(t) < 0$ for $S(t) > \frac{n}{m}$ then $\liminf S(t) \leq \frac{n}{m}$. Similarly, since $W(t) < 0$ for $W(t) > I(t)$ then $\liminf W(t) \leq I(t)$. This completes the proof.

Theorem 3. If $R \leq 1$, then the disease-free equilibrium $\bar{Q}$ is globally asymptotically stable.

Proof. Consider the following Lyapunov function:

$$\mathcal{V}(t) = \omega E + (\omega + m)I$$

with Lyapunov derivative,

$$\dot{\mathcal{V}}(t) = \omega \left[b_1 S I + b_2 S W - (\omega + m)E\right] + (\omega + m)\left[\omega E - (\gamma + m)I\right]$$

$$\leq \omega \frac{m}{n} (b_1 + b_2)I - (\omega + m)(\gamma + m)I$$

$$\leq (\omega + m)(\gamma + m)\left(R - 1\right)I, \forall (S, E, I, R, W) \in \Omega_2.$$

Since all parameters are non-negative, it follows that $\dot{\mathcal{V}}(t) \leq 0$ for $R \leq 1$ with $\dot{\mathcal{V}}(t) = 0$ only if $I = 0$. Hence, $\mathcal{V}$ is a Lyapunov function on $\Omega_2$. Further, by Lemma 1 $\Omega_2$ is a compact, absorbing subset of $\mathbb{R}^5_+$, and the largest compact invariant set in $\{(S, E, I, R, W) \in \Omega_2 : \mathcal{V}(t) = 0\}$ is $\bar{Q}$. Therefore, by the Lasalle’s invariance principle (see, for instance, [15] Theorem 3.1 and [7, 8, 9, 10, 11, 12, 13, 14] for other applications), every solution of system (1) with initial conditions in $\mathbb{R}^5_+$ converges to $\bar{Q}$ as $t \to +\infty$.

The global stability of the disease-persistence (endemic) equilibrium $Q^\ast$ is given in the following theorem.

Theorem 4. If $R > 1$, then the disease-persistence equilibrium $Q^\ast = (S^\ast, E^\ast, I^\ast, R^\ast, W^\ast)$ is globally asymptotically stable.

Proof. Consider the following Lyapunov function:

$$\mathcal{V}_2 = (S - S^\ast \ln\frac{S}{S^\ast}) + (E - E^\ast \ln\frac{E}{E^\ast}) + \frac{\omega + m}{\omega}(I - I^\ast \ln\frac{I}{I^\ast}) + \frac{b_2}{\epsilon}S^\ast(W - W^\ast \ln\frac{W}{W^\ast}).$$

The equilibrium $Q^\ast$ is the only internal stationary point of system (1). The function $\mathcal{V}_2(t)$ admits its minimum value $\mathcal{V}_{2min} = S^\ast + E^\ast + \frac{\omega + m}{\omega}I^\ast + \frac{b_2}{\epsilon}S^\ast W^\ast$ when $S = S^\ast, E = E^\ast, I = I^\ast, W = W^\ast$, and $\mathcal{V}_2(t) \to +\infty$ at the boundary of the positive quadrant. Consequently, $Q^\ast$ is the global minimum point,
and the function is bounded from below.

The derivative, of \( \gamma_2(t) \), along solutions of system (1) is given by

\[
\gamma_2' = \left( 1 - \frac{S^*}{S} \right) \dot{S} + \left( 1 - \frac{E^*}{E} \right) \dot{E} + \frac{\omega + m}{\omega} \left( 1 - \frac{I^*}{I} \right) \dot{I} + \frac{b_2^*}{W^*} \left( 1 - \frac{W^*}{W} \right) \dot{W}
\]

Using the fact that \((S^*, E^*, I^*, R^*, W^*)\) is solution of system (3) then \( n = mS^* + b_1S^*I^* + b_2S^*W^* \), \((\omega + m)E^* = b_1S^*I^* + b_2S^*W^* + \frac{(\omega + m)(\gamma + m)}{\omega} I^* = b_1S^*I^* + b_2S^*W^* \). Therefore the expression of \( \gamma_2' \) reduces to

\[
\gamma_2' = mS^* + b_1S^*I^* + b_2S^*W^* - mS - mS^*S^* - \frac{b_1S^*I^*N^*}{S} - \frac{b_2S^*W^*S^*}{S} + mS^* + b_1S^*I^* + b_2S^*W^* - b_1SI^*E^* - b_2SW^*E^* - (b_1S^*I^* + b_2S^*W^*) I^* + (b_1S^*I^* + b_2S^*W^*) I^*
\]

More simply,

\[
\gamma_2' = mS^* \left( 2 - \frac{S^*}{S} \right) S^* + b_1S^*I^* \left( 3 - \frac{S^*}{S} - \frac{S^*E^*}{S^*E^* - E^*I^*} + b_2S^*W^* \left( 4 - \frac{S^*}{S} - \frac{S^*E^*}{S^*E^* - E^*I^*} \right) \right).
\]

Note that

\[
\frac{S^*}{S^*} = 1, \quad \frac{S^*E^*}{S^*E^* - E^*I^*} = 1,
\]

and

\[
\frac{S^*E^*}{S^*E^* - E^*I^*} \frac{S^*W^*E^*}{S^*W^*E^* - E^*I^*} = 1.
\]

We recall also the following inequality:

\[
x_1 + x_2 + x_3 + \cdots + x_n \geq n \sqrt[3]{x_1x_2x_3 \cdots x_n}, \quad x_1, x_2, x_3, \cdots, x_n \geq 0
\]

(4)

Since arithmetical mean of nonnegative real numbers is greater than the geometrical one, we have the following inequalities

\[
2 - \frac{S^*}{S^*} - \frac{S^*E^*}{S^*E^* - E^*I^*} \leq 0,
\]

\[
3 - \frac{S^*}{S^*} - \frac{S^*E^*}{S^*E^* - E^*I^*} \leq 0,
\]

\[
4 - \frac{S^*}{S^*} - \frac{S^*E^*}{S^*E^* - E^*I^*} \leq 0.
\]

Therefore $\dot{V}_2 \leq 0$. Thank’s to the stability Lyapunov theorem, one deduces that $Q^* = (S^*, E^*, I^*, R^*, W^*)$ is stable.

It remains to show that $Q^* = (S^*, E^*, I^*, R^*, W^*)$ is asymptotically stable using the Lasalle invariance principle (see, for instance, [15, Theorem 3.1] and [12, 13, 14] for other applications).

Define

\[
A = 2 - \frac{S^*}{S} - \frac{S}{S^*} - \frac{S^* S}{S^* E}, \quad B = 3 - \frac{S^* S}{S^* I^* E} - \frac{S^* I^* E}{E^* I} \quad \text{and} \quad C = 4 - \frac{S^*}{S} - \frac{S W^* E}{S^* W^* E} - \frac{S^* W^* E}{E^* I} - \frac{I}{W}.
\]

Then one has

\[
\dot{V}_2 (S, E, I, R, W) = 0 \iff A = B = C = 0.
\]

Using to the above relations, one obtains the following implications.

\[
A = 0 \Rightarrow S = S^*, \quad (S = S^*, B = 0) \Rightarrow IE^* = I^* E, \quad (S = S^*, IE^* = I^* E, C = 0) \Rightarrow WE^* = W^* E.
\]

Finally, we obtain

\[
\dot{V}_2 (S, E, I, R, W) = 0 \iff (S = S^*, IE^* = I^* E, WE^* = W^* E).
\]  \hspace{1cm} (5)

Let $r = \frac{E}{E^*} = \frac{I}{I^*} = \frac{W}{W^*}$, then $E = rE^*$ and $I = W = rI^* = rW^*$. Replacing $S$, $I$ and $W$ in the first equation of system (3) yields

\[
n = mS^* + rb_1 S^* I^* + rb_2 S^* W^* = mS^* + b_1 S^* I^* + b_2 S^* W^*.
\]

Then we obtain $r = 1$ and therefore $I = W = I^* = W^*$ and $E = E^*$. Finally

\[
\dot{V}_2 (S, E, I, R, W) = 0 \iff (S = S^*, E = E^*, I = I^*, R = R^*, W = W^*).
\]

Thus, the largest invariant set contained in \{(S, E, I, R, W) | $\dot{V}_2 = 0$\} is \{Q^* = (S^*, E^*, I^*, R^*, W^*)\}. Then the global stability of the disease-persistence equilibrium $Q^* = (S^*, E^*, I^*, R^*, W^*)$ follows according to the Lasalle invariance principle [16] (see [12, 13, 14] for an application).

5 Numerical Simulations

We validate numerical simulations for system (1). Four cases were considered; two of them (Figure 2) confirming the global stability of the disease-free equilibrium $Q$ when $R \leq 1$. The other two tests (Figure 3) confirm the global stability of the disease-persistence equilibrium $Q^*$ when $R > 1$.  

9
Figure 2: \((S(t), E(t), I(t), R(t), W(t))\) behaviours for (left) \(n = 1000, m = 10, b_1 = 1.5, b_2 = 1, \omega = 1, \gamma = 30, \epsilon = 1, R = 0.568 \leq 1\) and for (right) \(n = 10000, m = 10, b_1 = 1.5, b_2 = 1, \omega = 0.1, \gamma = 30, \epsilon = 1, R = 0.619 \leq 1\).

We remark that the solution of system (1) converge asymptotically to \(\bar{Q}\). Only Susceptible compartment persist, the other compartments vanish.

Figure 3: \((S(t), E(t), I(t), R(t), W(t))\) behaviours for (left) \(n = 1000, m = 10, b_1 = 1.5, b_2 = 1, \omega = 10, \gamma = 30, \epsilon = 1, R = 3.125 > 1\) and for (right) \(n = 10000, m = 10, b_1 = 1.5, b_2 = 1, \omega = 1, \gamma = 30, \epsilon = 1, R = 5.682 > 1\).

In this case, the solution of system (1) converge asymptotically to \(Q^*\) and all compartments persist.

6 Conclusion

A mathematical 5D dynamical system modelling an SEIRW model of transmissibility of the SARS-CoV-2 is studied. A profound qualitative analysis is given. The analysis of the local and global stability of equilibrium points is carried out. It is proved that if \(R > 1\) then the disease-persistence equilibrium is globally asymptotically stable. However, if \(R \leq 1\), then the disease-free equilibrium is globally asymptotically stable.
References


Declarations
Competing interests: The authors declare no competing interests.
Funding: The authors received no external funding for this research.
Figures

Figure 1

Flowchart of the Reservoir-People transmission network model (SEIRW).

Figure 2

(S(t),E(t), I(t),R(t),W(t)) behaviours for (left) n = 1000, m = 10, b1 = 1.5, b2 = 1, w = 1, g = 30, e = 1, R = 0.568 ≈ 1 and for (right) n = 10000, m = 10, b1 = 1.5, b2 = 1, w = 0.1, g = 30, e = 1, R = 0.619 ≈ 1.
Figure 3

$(S(t), E(t), I(t), R(t), W(t))$ behaviours for (left) $n = 1000, m = 10, b_1 = 1.5, b_2 = 1, w = 10, g = 30, e = 1, R = 3.125 > 1$ and for (right) $n = 10000, m = 10, b_1 = 1.5, b_2 = 1, w = 1, g = 30, e = 1, R = 5.682 > 1$. 