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The Asymptotic Stability Of An Epidemiological Model "Covid-19 Variant English"

Khadija CHANNAN*, Khalid HILAL and Ahmed KAJOUNI

ABSTRACT: We have all been injured by corona and its mutations, not just us but the whole world. We have all lost people who died because of corona, this last one has mutations one of it is the English variant, which will be our interest in this article. Therefore, in this work we are interested in the study of the local and global asymptotic stability of a new epidemiological model "covid 19 variant English".

Key Words: Global stability, local stability, equilibrium points , lyapunov function.

Contents

1. Introduction

Coronavirus 2019 (covid 19) is an infectious disease caused by the $SARS\_COV\_2$ virus. Coronaviruses are a crown-shaped family of viruses, microbe muscles that enter living things and make them sick. In December 2019 a new coronavirus appeared in China causing a respiratory disease called Covid 19 [26]. Infectious disease models were first used to understand the temporal dynamics of an epidemic, then to apply a ther apeutic or infectious disease control strategy. Mathematical models are used more and more frequently in medicine, and even in biology in increasingly varied fields of application. Formalizing complex biological phenomena, they make it possible to evaluate hypotheses by providing elements of understanding or prediction [41,42].

At the beginning of its existence, the Covid-19 acquired a capacity that will prove to be crucial in its relationship to humans. The virus detected a seemingly minimal change in the genetic code that gave us the English variant mutation.

As we have seen, the world has been negatively affected by the emergence of Corona in recent years, which is why we decided to work on this infectious disease. The sudden and dazzling appearance of the Covid-19 pandemic first in the town of Wuham (East China's Hubei province) before expanding to the rest of the planet, posed the recurring problem of identifying the pathogen and diagnosing of its propagation dynamics. If the first observation relates exclusively to epidemiologists, the second on the

* Corresponding author

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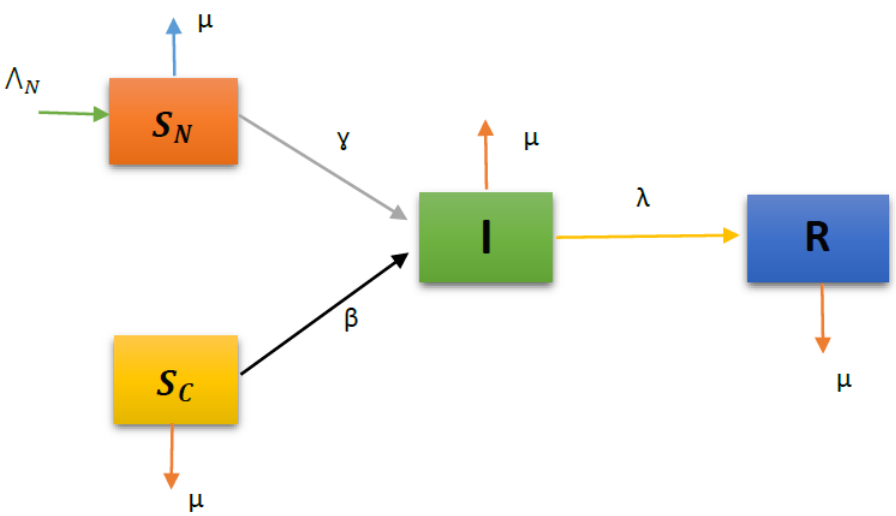
other hand allowed epi demiology to open up to other scientific disciplines whose core is the mathematical modeling of the propagation of a epidemic. This approach is then referred to as mathematical epidemiology. Mathematical modeling of an infectious disease can reveal non-obvious aspects at the origin of the sequential progression of an epidemic and participate in health management by providing insight into the impacts that could result.

Mathematical modeling in epidemiology is not recent in itself since historically, more or less reliable models relating to epidemics are reported in the epidemiologi cal literature. In the case of Covid-19, perhaps due to the emergency of the situation, considerable efforts have been made in the development of the models. going from the simplest model (the SIR model for example) to the most complicated includ ing diversified epidemiological parameters and a sometimes complex mathematical formulation, modeling resulted in proposing patterns of spread of an epidemic rela tively reliable [1].

Mathematical Infectious Disease Modeling is a tool to study how diseases spread, predict the future trajectory of an outbreak, help guide public health planning and infectious disease control. This is what we apply in our work, we bring reality to life in a mathematical model to study the stability of the disease. First, we use the SIR model, on compartment S (Susceptible) we divide it into two parts S_N (those susceptible who have not had Covid 19) and S_C (those susceptible who have already had Covid 19) more compartment I (individuals infected with the English variant) and finally compartment R (recovered).

2. Diagram transmission of british variant Covid-19 between humans

Some of the emergence of Corona disease and the infection of many people in the whole world with it and for a short time, then a mutated appearance of this disease called 'British Variant'. Moreover, the new idea in our article is to divide the people who are exposed to the disease into two categories, a category that has previously contracted the normal corona virus, and the other type has not been sick with corona.



Description of biological parameters:

- S_C : The susceptible individuals who already had the covid-19.
- S_N : The susceptible individuals who not already had the covid-19.

- I : Infected individuals by the british variant covid-19.
- R : The individuals withdrawn (healed or dead).
- β The rate of individuals who become infected by the british variant covid-19 who had already contacted covid-19.
- γ : The rate of individuals who become infected by the british variant covid-19.
- λ : Recovery rate.
- μ : Natural mortality rate .
- Λ_N : Birth rate.

This diagram can translated mathematically by the following system of differential equations:

$$(1)\begin{cases} \dfrac{dS_N(t)}{dt} = \Lambda_N - \gamma S_N(t)I(t) - \mu S_N(t) \\ \dfrac{dS_C(t)}{dt} = -\beta S_C(t)I(t) - \mu S_C(t) \\ \dfrac{dI(t)}{dt} = \gamma S_N(t)I(t) + \beta S_C(t)I(t) - \lambda I(t) - \mu I(t) \\ \dfrac{dR(t)}{dt} = \lambda I(t) - \mu R(t) \end{cases}$$

The system (1) is provided with the initial conditions:

$$S_N(0) = S_{N_0} > 0,\ \ S_C(0) = S_{C_0} > 0,,\ \ I(0) = I_0 > 0,,\ \ R(0) = R_0 > 0.$$

And,

$$N = S_{N_0} + S_{C_0} + I_0 + R_0$$

3. Global existence, positivity and limitation of the solution

Proposition 3.1 *Given* $(S_{N_0}, S_{C_0}, I_0, R_0) \in \mathbb{R}^4$, *there is a unique solution to the problem* (1) *defined on* $[0, +\infty)$ *and this solution rest non négative and bounded* $\forall t \geq 0$.

Proof:

We put,

$$X(t) = \begin{pmatrix} S_N(t) \\ S_C(t) \\ I(t) \\ R(t) \end{pmatrix}$$

and,

$$F : \mathbb{R}^4 \longrightarrow \mathbb{R}^4$$

$$F\begin{pmatrix} S_N \\ S_C \\ I \\ R \end{pmatrix} = \begin{pmatrix} \Lambda_N - \gamma S_N I - \mu S_N \\ -\beta S_C I - \mu S_C \\ \gamma S_N I + \beta S_C I - \lambda I - \mu I \\ \lambda I - \mu R \end{pmatrix}$$

The system is in the following form:

$$X'(t) = F(X(t)),\ \forall t \geq 0$$

with,

$$X(0) = X_0 = \begin{pmatrix} S_{N_0} \\ S_{C_0} \\ I_0 \\ R_0 \end{pmatrix}$$

We observe that F is a vector polynomial function. Then, it is class C^∞. So, it locally lipschitzian. We deduce that there is a unique local solution defined on $[0, T_{max})$, where T_{max} is the maximum existence time.

Now, we show the positivity of the solution, we have:

$$\begin{aligned} &\frac{dS_N(t)}{dt}|_{S_N=0} = \Lambda_N \geq 0 \\ &\frac{dS_C(t)}{dt}|_{S_C=0} = 0 \geq 0 \\ &\frac{dI(t)}{dt}|_{I=0} = 0 \geq 0 \\ &\frac{dR(t)}{dt}|_{R=0} = \lambda I \geq 0 \end{aligned}$$

and since the initials conditions are positives, then we deduce the positivity of the local solution.

Finally, we establish the boundary of the solution.

the set

$$\Omega = \{(S_N,\, S_C,\, I,\, R) \in \mathbb{R}^4,\ S_N + S_C + I + R \leq \frac{\Lambda_N}{\mu}\}$$

is compact and positively invariant by the system (1).

Proof :

Let $(S_{N_0}, S_{C_0}, I_0, R_0) \in \Omega$ and let $(S_N, S_C, I, R) \in \mathbb{R}^4_+$.

Then the differential equation of the total population is given by:

$$\frac{dN(t)}{dt} = \frac{d}{dt}\left(S_N(t), S_C(t), I(t), R(t)\right) = \Lambda_N - \mu N(t).$$

Using the formula for the variation of the constant, the solution of the equation is given by

$$N(t) = \exp(-\mu t)(N_0 - \frac{\Lambda_N}{\mu}) + \frac{\Lambda_N}{\mu},\ \ \forall t \in [0, T_{max}]$$

With,

$$N_0 = N(0) = S_{N_0} + S_{C_0} + I_0 + R_0 \leq \frac{\Lambda_N}{\mu}.$$

Consequently, $N(t) \leq \frac{\Lambda_N}{\mu}$, that is to say, $S_N(t) + S_C(t) + I(t) + R(t) \leq \frac{\Lambda_N}{\mu}$.

Hence, Ω is positively invariant.

Mereover, $S_N(t), S_C(t), I(t), R(t) \in [0, \frac{\Lambda_N}{\mu}]$, $\forall t \in [0, T_{max}]$.

We conclude that $T_{max} = +\infty$

4. Equilibrium points

4.1. Disease free equilibrium (DFE)

We search $\overline{S_N} \geq 0$, $\overline{S_C} \geq 0$ et $\overline{R} \geq 0$ satisfying:

$$\begin{cases} 0 &= \Lambda_N - \gamma \overline{S_N} I - \mu \overline{S_N} \\ 0 &= -\beta \overline{S_C} \overline{I} - \mu \overline{S_C} \\ 0 &= \gamma \overline{S_N} \overline{I} + \beta \overline{S_C} \overline{I} - \lambda \overline{I} - \mu \overline{I} \\ 0 &= \lambda \overline{I} - \mu \overline{R} \end{cases}$$

With, $\overline{I} = 0$ We obtain: $\overline{S_N} = \frac{\Lambda_N}{\mu}$, $\overline{S_C} = 0$ et $\overline{R} = 0$.

Therefore,

$$E_0 = (\frac{\Lambda_N}{\mu}, 0, 0, 0)$$

4.2. Calcul of R_0: (Method of van den Driessche watmough)

We denote by:

- $\mathcal{F}_j(S_N, S_C, I, R)$ the rate of newly infected in the compartment j.
- $\mathcal{V}_j(S_N, S_C, I, R)$ the transfer rate of an individual from one compartment to another everywhere average.

The matrices $\mathcal{F}$ and $\mathcal{V}$ are represented by:

$$\mathcal{F} = \begin{pmatrix} 0 \\ 0 \\ \gamma S_N I + \beta S_C I \\ 0 \end{pmatrix}$$

And,

$$\mathcal{V} = \begin{pmatrix} \Lambda_N - \gamma S_N I - \mu S_N \\ -\beta S_C I - \mu S_C \\ -(\lambda + \mu) I \\ \lambda I - \mu R \end{pmatrix}$$

The calculation of their resprctive Jacobian at the disease free equilibrium

point $E_0 = (\frac{\Lambda_N}{\mu}, 0, 0, 0)$ given:

$$\mathcal{F}(E_0) = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{\gamma \Lambda_N}{\mu} & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$$\mathcal{V}(E_0) = \begin{pmatrix} -\mu & 0 & -\frac{\gamma\Lambda_N}{\mu} & 0 \\ 0 & -\mu & 0 & 0 \\ 0 & 0 & -(\lambda+\mu) & 0 \\ 0 & 0 & \lambda & -\mu \end{pmatrix}$$

Consider F and V the matrices given by:

$$F = \begin{pmatrix} \frac{\gamma\Lambda_N}{\mu} & 0 \\ 0 & 0 \end{pmatrix} \quad and \quad V = \begin{pmatrix} -(\lambda+\mu) & 0 \\ \lambda & -\mu \end{pmatrix}$$

The basic reproduction rate is the spectral radius of the matrix $-FV^{-1}$ the calculation given:

$$R_0 = \frac{\gamma\Lambda_N}{\mu(\lambda+\mu)}$$

4.3. Endemic equilibrium (EE)

For $\overline{I} > 0$. Using the second equation of the system we get:

$$\overline{S_C} = 0$$

By considering the third equation of the system we obtain:

$$\overline{S_N} = \frac{\lambda+\mu}{\gamma}$$

Using the first equation of the system we get:

$$\overline{I} = \frac{\mu}{\gamma}\left(\frac{\gamma\Lambda_N}{\mu(\lambda+\mu)} - 1\right)$$

According to the fourth equations we obtain:

$$\overline{R} = \frac{\lambda}{\gamma}\left(\frac{\gamma\Lambda_N}{\mu(\lambda+\mu)} - 1\right)$$

Therefore, the endemic equilibrium point given by:

$$E = \left(\frac{\lambda+\mu}{\gamma}, 0, \frac{\mu}{\gamma}(R_0-1), \frac{\lambda}{\gamma}(R_0-1)\right)$$

5. Local stability of the disease free equilibrium

Consider the Jacobian matrix in $E_0 = (\frac{\Lambda_N}{\mu}, 0, 0, 0)$

In other words,

$$J(E_0) = \begin{pmatrix} -\mu & 0 & -\frac{\gamma\Lambda_N}{\mu} & 0 \\ 0 & -\mu & 0 & 0 \\ 0 & 0 & \frac{\gamma\Lambda_N}{\mu} - (\lambda+\mu) & 0 \\ 0 & 0 & \lambda & -\mu \end{pmatrix}$$

We observe that the polynomial characteristic of $J(E_0)$ is

$$\begin{aligned} P_{J(E_0)}(X) &= det(XI - J(E_0)) \\ &= (X+\mu)^3(X - \tfrac{\gamma\Lambda_N}{\mu} + (\lambda+\mu)) \\ &= (X+\mu)^3(X - (\lambda+\mu)(R_0-1)) \end{aligned}$$

Consequently the spectrum of the matrix $J(E_0)$

$$\sigma(J(E_0) = \{-\mu, (\lambda+\mu))(R_0-1)\}$$

All the eigen values are strictly negative since $R_0 < 1$.

Hence, E_0 is locally asymptotically stable.

6. Global stability of the disease free equilibrium

As the composant $R(t)$ does not appear in the first three equations of (1). We can restrict ourselves to the system (2)

$$\begin{cases} \dfrac{dS_N(t)}{dt} = \Lambda_N - \gamma S_N(t)I(t) - \mu S_N(t) \\ \dfrac{dS_C(t)}{dt} = -\beta S_C(t)I(t) - \mu S_C(t) \\ \dfrac{dI(t)}{dt} = \gamma S_N(t)I(t) + \beta S_C(t)I(t) - \lambda I(t) - \mu I(t) \end{cases}$$

Theorem 1 :
Suppose that $R_0 < 1$. In this case the disease free equilibrium is globally asymptotically stable.

Case $R_0 = 1$.

Theorem 2 :
Suppose that $R_0 = 1$. In this case the disease free equilibrium is globally asymptotically stable.

The central theorem of Alexander Liapunov says that a point of equilibrium E_0 is stable (in the sense of Liapunov) for a dynamic system (described by a differential equation of the type $X'(t) = F(X(t))$ if and only if there exists a function satisfying certain precise conditions and related to the function F of the differential equation and to E_0.
The problem of stability therefore comes down to looking for such a function (called Liapunov's function) and which satisfies the conditions of a Liapunov function of the dynamic problem. So, to show the overall stability of our disease-free equilibrium point we have to construct a new lyapunov function which has appeared in the proves.

Proof :

We consider the following Lyapunov function:

$$V(S_N, S_C, I) = S_N - S_{NE_0} \ln\left(\frac{S_N}{S_{NE_0}}\right) + I + S_C.$$

We have,

$$\begin{aligned} \frac{dV(S_N,S_C,I)}{dt} &= S'_N - S_{NE_0}\frac{S'_N}{S_N} + I' + S'_C \\ &= \Lambda_N - \mu S_N - S_{NE_0}\left[\frac{\Lambda_N}{S_N} - \mu\right] + \frac{\gamma\Lambda_N}{\mu}I - (\lambda+\mu))I - \mu S_C - \mu S_{CE_0} \\ &\qquad \left(And,\ \ R_0 = \frac{\gamma\Lambda_N}{\mu(\lambda+\mu)} = 1 \ \ we\, obtain \ \ \frac{\gamma\Lambda_N}{\mu}I = (\lambda+\mu)I\right) \\ &= \frac{\Lambda_N S_N - \mu S_N^2 - S_{NE_0}\Lambda_N + \mu S_{NE_0}S_N}{S_N} - \mu(S_C - S_{CE_0}) \\ &= \frac{-\mu}{S_N}(S_N - S_{CE_0})^2\mu(S_C - S_{CE_0}) < 0. \end{aligned}$$

Furthermore,

$$\frac{dV(S_N, S_C, I)}{dt} = 0 \text{ if } (S_N, S_C, I) = (S_{NE_0}, S_{CE_0}, I_{E_0})$$

Let M the largest invariant set content in

$$E = \{(S_N, S_C, I) \in \Omega / \frac{dV(S_N, S_C, I)}{dt} = 0\}$$

We then have, $M \subset E = \{S_{NE_0}, S_{CE_0}, I_{E_0}\}$. According to LaSalle's generalized invariance principle, the DFE is globally asymptotically stable.

7. Global stability of the endemic equilibrium (EE)

Theorem 3 :
If $R_0 > 1$. The endemic equilibrium point is globally asymptotically stable.

Proof :

To study the global asymptotic stability of the endemic equilibrium, we constructed another lyapunov function which is written as a function of the compartments S_N, S_C, I.

Consider the following Lyapunov function:

$$V(S_N, S_C, I) = S_N - S_{NE} \ln\left(\frac{S_N}{S_{NE}}\right) + I - I_E \ln\left(\frac{I}{I_E}\right) + S_C$$

$$\begin{aligned}
\frac{dV(S_N, S_C, I)}{dt} &= S'_N - S_{NE}\frac{S'_N}{S_N} + I' - I_E\frac{I'}{I} + S'_C \\
&= (S_N - S_{NE})\frac{S'_N}{S_N} + (I - I_E)\frac{I'}{I} - \beta S_C I - \mu S_C \\
&= (S_N - S_{NE})\left[\frac{\Lambda_N}{S_N} - \mu\right] - \gamma I(S_N - S_{NE}) + \gamma S_N I \\
&-(\lambda + \mu))I - \gamma S_N I_E - \beta S_C I_E + (\lambda + \mu))I_E - \mu S_C \\
&= \frac{-\mu R_0}{S_N}(S_N - S_{NE})^2 - \beta I_E(S_C - S_{CE}) - \mu(S_C - S_{CE}) < 0
\end{aligned}$$

$\frac{dV(S_N, S_C, I)}{dt} < 0$, if $S_N, S_C, I > 0$ and $\frac{dV(S_N, S_C, I)}{dt} = 0$ only at the endemic equilibrium point.

Therefore according to Lyapunov's theorem, the endemic equilibrium point is globally asymptotically stable.

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Khadija CHANNAN,
Khalid HILAL,
Ahmed KAJOUNI,
Laboratory LMACS,
FST of Beni Mellal, Sultan Moulay Slimane University
Morocco.
E-mail address: channankhadija@gmail.com
E-mail address: hilalkhalid2005@yahoo.fr
E-mail address: kajjouni@gmail.com