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Novel Coronavirus disease infection in Tunisia: Mathematical model and the impact of the quarantine strategy

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ABSTRACT

Coronavirus disease (COVID-19) is an extremely serious infection with an extremely high death rate worldwide. In March, the disease was declared a "global pandemic" by the World Health Organization (WHO). Until now, there is no known vaccine or drug, since the unknown things related to the disease are more important than our theoretical and empirical knowledge. However, mathematical modeling and the estimation of the basic number of reproductions can provide clarifications in order to determine the potential and severity of this epidemic and therefore provide essential information to identify the type of measures and interventions to be taken to control the intensity of the spread of the disease. Hence, in this paper, we propose a new deterministic compartmental model based on the clinical progression of the disease, the epidemiological state of the individuals and the intervention for the dynamics of COVID-19 infections. Our approach consists of seven phenotypes: the susceptible humans, exposed humans, infectious humans, the recovered humans, the quarantine population, the newly admitted and the deceased population. We proved first through mathematical approach the positivity, boundedness and existence of a solution to the considered model. We also studied the existence of the disease free equilibrium and corresponding stability. Our work shows, in particular, that the disease will decrease if the number of reproduction $R_0$ was less than one. Moreover, the impact of the quarantine strategies to reduce the spread of this disease is discussed. The theoretical results are validated by some numerical simulations of the system of the epidemic’s differential equations. It should be mentioned that, the error between the considered model and the official data curve is quite small.

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1. Introduction

Since the beginning of the COVID-19 epidemic in Wuhan City on December 2019, the opinions of scientists, researchers and commentators contradict each other every day. On 7 January, the coronavirus disease (COVID-19) which was named as a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by the International Committee on Taxonomy of Viruses on 11 February, 2020, was identified as the causative virus by Chinese authorities [14], and has become a pandemic especially by travelers [13]. This forced the World Health Organization (WHO) to consider the dramatic spread of the infection in March 2020 as a public health emergency of international concern. This epidemic is characterized by its rapid spread and its symptoms do not appear quickly. In particular, according to the WHO, the incubation period is from 2 days to 14 days [14]. In addition, there is no anti-viral treatment or vaccination officially approved for the management or prevention of this epidemic. In order to fight this outbreak, the public health decision and policy makers should decide and follow strategic and health-care management. Since the declaration of the first case of COVID-19 in Tunisia in early March 2020, thousands of screenings have been carried out in Tunisia. Following the first recommendations of the WHO Tunisia, as France, Italy or Spain, first opted for rare and targeted screenings on suspicious people, their entourage and certain sources of contamination; in particular for people arriving from abroad. Next, if a person is positive, the authorities try to trace all the people with whom he has been in contact and they are called to place themselves in self-containment without necessarily being tested. They can only be tested if they themselves have symptoms of COVID-19.

It is clear that the low number of screenings, mainly on "suspect" cases or those presenting significant symptoms, does not give a precise idea of the number of people who could potentially be infected without knowing them. This gap between the day of infection and the day of diagnosis can have serious consequences on the spread of the epidemic. All this shows the complexity of the...
situation since the unknown things related to the epidemic are more important than the things we already know.

These are the daily question that must be answered: how many people exactly recover from COVID-19? How many people are infected from COVID-19? How many people died from COVID-19?

Recently, several mathematical models have been published in order to be able to study the dynamics and the evolution of this pandemic. One can refer to \cite{1,4,6-11,15} and their references. It appears from clinical experiences and recent articles that knowing the data of infected people in the population would be very useful to have better models of when disease will peak and decline, and also when we can begin to let people go back to work. Also, knowing the real number of recovered people also could indicate how easily people can build immunity against the virus.

Motivated by the above discussion our method comprises seven phenotypes; the susceptible humans, exposed humans, infectious humans, the recovered humans, the quarantine population, the recovered-exposed and the dead population in order to improve and adapt the susceptible-infected-recovered (SIR) model. In fact, we noticed that people previously infected and recovered from COVID-19 are generally excluded as susceptible individuals in the modeling, which would have an impact on predicting the number of cases that will occur in the near future. In our approach we chose to integrate them into the model as a recovered-exposed population and which we will note \( E_r \). In addition, at the individual level, if people can find out if they have been or slightly infected and cured, and if they show civility and respect the distancing, they can safely return to work once the general quarantine is off.

Our main contributions in this paper are:
- We gave a model of dynamical behavior of COVID-19 in Tunisia.
- We studied the qualitative properties of our model.
- We established the stability of equilibrium point via \( R_0 \).
- We proved theoretically and by numerical simulations the effect of quarantine strategy.

The reminder of the paper is organized as follows. In Section 2, we present our model. Section 3 is devoted to the mathematical analysis: Boundness, positivity, and the equilibrium point. The dynamics of exposed and infected population are also studied in this section. In Section 4, via Matab, we perform numerical simulations of three types of populations. Section 5 concludes the paper with some recommendations.

2. Mathematical model

The classical susceptible-infected-recovered (SIR) model in epidemiology \cite{5} allows the determination of critical condition of disease development in the population irrespective of the total population size over a short period of time. The SIR is considered from the following simplest ODE system:

\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\lambda_1}{N} SI \\
\frac{dI}{dt} &= \frac{\lambda_1}{N} SI - \beta I \\
\frac{dR}{dt} &= \beta I.
\end{align*}
\]  

(2.1)

For the sizes of the susceptible sub-population \( S \), infected \( I \), and recovered \( R \). The term \( \frac{\lambda_1}{N} SI \) describes the disease transmission rate due to the contacts between susceptible and infected individuals, \( \beta I \) characterizes the rate of recovery of infected people. It is assumed here that the recovered individuals do not return to susceptible class, that is, recovered individuals have immunity against the disease; they cannot become infected again and cannot infect susceptible either.

Day by day, we see that the specifics of this virus require more complex models. Roughly speaking, it is necessary to question the duration of the incubation, or the presence of people who do not have symptoms after their infection, but who nevertheless participate in the spread of the virus and consider compartments for these different cases. In our work, we have used a 7-Phenotype model which takes into account people who are infected, exposed, recovered, those susceptible, the deceased, Quarantine but also recovered-exposed people who are not counted by the government.

The interaction between the above sub-populations can be described by the compartmental diagram in Fig. 2.1. The parameters indicated in Fig. 2.1 are described in Table 1.

So the diagram above (Fig. 2.1) can be expressed as a system of non-linear differential equations (SEIRDQ):

\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\lambda_1}{N} SE - \frac{\lambda_2}{N} SI - \lambda_3 S \\
\frac{dE}{dt} &= \frac{\lambda_1}{N} SE + \frac{\lambda_2}{N} SI - (\alpha_1 + \alpha_2) E \\
\frac{dI}{dt} &= \alpha_1 E - (\beta_1 + \beta_2) I \\
\frac{dE_r}{dt} &= \alpha_2 E \\
\frac{dR}{dt} &= \beta_1 I \\
\frac{dD}{dt} &= \beta_2 I \\
\frac{dQ}{dt} &= \lambda_3 S.
\end{align*}
\]  

(2.2)

where

| Parameters and their description. |
|-----------------------------------|
| \( \lambda_1 \)                   | the contact rate with \( S \) and \( E \) |
| \( \lambda_2 \)                   | the contact rate with \( S \) and \( I \) |
| \( \lambda_3 \)                   | the home quarantine rate of \( S \) |
| \( N \)                           | the total population |
| \( S + E + I + E_r + R + D + Q \) | \( \alpha_1 \)                   | the incubation rate |
| \( \alpha_2 \)                   | the recovered rate of \( E \) |
| \( \beta_1 \)                   | the recovered rate of \( I \) |
| \( \beta_2 \)                   | the death rate |

3. Mathematical analysis

3.1. Basic properties of the model

Obviously, the system (2.2) can be written as follows

\[ X'(t) = AX(t) + f(X), \]

(3.1)

where

\[ X(t) = (S \ E \ I \ E_r \ R \ D \ Q)^T. \]
Proof. Then, we have
\[
A = \begin{pmatrix}
-\lambda_3 & 0 & 0 & 0 & 0 & 0 \\
0 & -(\alpha_1 + \alpha_2) & 0 & 0 & 0 & 0 \\
0 & \alpha_1 & -(\beta_1 + \beta_2) & 0 & 0 & 0 \\
0 & \alpha_2 & 0 & 0 & 0 & 0 \\
0 & 0 & \beta_1 & 0 & 0 & 0 \\
0 & 0 & \beta_2 & 0 & 0 & 0 \\
\lambda_3 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}
\]

\[
f(X) = \left(-\frac{\lambda_1}{N}SE - \frac{\lambda_2}{N}\lambda_1 SE - \frac{\lambda_3}{N}SI0 0 0 0 \right)^T.
\]

with the initial conditions satisfying the following inequalities
\[
0 < S(0), \ 0 \leq E(0), \ 0 \leq I(0), \ 0 \leq R(t), \ 0 \leq Q(t), \ 0 \leq D(0) \text{ and } 0 \leq R(0).
\]

(3.2)

3.1. The boundness and positivity of the solution

**Theorem 3.1.** Given the non-negative initial conditions (3.2), then the solutions \(S(t), E(t), I(t), S(t), R(t), D(t)\) and \(Q(t)\) are non-negative for all \(t \geq 0\) and bounded.

**Proof.** First, let us prove that the solution of the system (3.1) is positive.

1st case:

Suppose that \(\exists t_1 > 0\) such that
\[
S(t_1) < 0, \ S(t) > S(t_1); \forall t < t_1,
\]
\[
I(t), E(t) > 0; \forall t \leq t_1.
\]

Then, we have
\[
0 \geq \frac{dS(t_1)}{dt} = -\frac{\lambda_1}{N}S(t_1)E(t_1) - \frac{\lambda_2}{N}S(t_1)I(t_1) - \lambda_3S(t_1) > 0, \text{ absurd.}
\]

2nd case:

Suppose that \(\exists t_1 > 0\) such that
\[
S(t_1), E(t_1) < 0,
\]
\[
E(t) > E(t_1), S(t) > S(t_1); \forall t < t_1.
\]

Then, we have
\[
0 \geq \frac{dE(t_1)}{dt} + \frac{dS(t_1)}{dt} = -\lambda_3S(t_1) - (\alpha_1 + \alpha_2)E(t_1) > 0, \text{ absurd.}
\]

From the second case; \(S\) and \(E\) are not both negative as the same time.

3rd case:

Suppose that \(\exists t_1 > 0\) such that
\[
I(t_1) < 0,
\]
\[
I(t) > I(t_1); \forall t < t_1,
\]
\[
E(t) > 0; \forall t \leq t_1.
\]

Then, we have
\[
0 \geq \frac{dt_1}{dt} = \alpha_1E(t_1) - (\beta_1 + \beta_2)I(t_1) > 0. \text{ absurd.}
\]

4th case:

Suppose that \(\exists t_1 > 0\) such that
\[
E(t_1) = 0,
\]
\[
E(t) > 0; \forall t < t_1,
\]
\[
S(t), I(t) > 0; \forall t \leq t_1.
\]

We can write \(E\) as the following form
\[
E(t) = e^{-(\alpha_1 + \alpha_2)}E(0)
\]
\[
+ \int_0^t e^{-(\alpha_1 + \alpha_2)}\left(\frac{\lambda_1}{N}S(s)E(s) + \frac{\lambda_2}{N}S(s)I(s)\right)ds. \quad (3.3)
\]

So, we get
\[
0 = E(t_1) = e^{-(\alpha_1 + \alpha_2)}E(0)
\]
\[
+ \int_0^{t_1} e^{-(\alpha_1 + \alpha_2)}\left(\frac{\lambda_1}{N}S(s)E(s) + \frac{\lambda_2}{N}S(s)I(s)\right)ds.
\]

which is impossible.

5th case:

Suppose that \(\exists t_1 > 0\) such that
\[
E(t_1) = I(t_1) = 0,
\]
\[
E(t), I(t) > 0; \forall t < t_1,
\]
\[
S(t) > 0; \forall t \leq t_1.
\]

We can write \(E\) as the following form
\[
E(t) = e^{-(\alpha_1 + \alpha_2)}E(0)
\]
\[
+ \int_0^t e^{-(\alpha_1 + \alpha_2)}\left(\frac{\lambda_1}{N}S(s)E(s) + \frac{\lambda_2}{N}S(s)I(s)\right)ds. \quad (3.4)
\]

So, we get
\[
0 = E(t_1) = e^{-(\alpha_1 + \alpha_2)}E(0)
\]
\[
+ \int_0^{t_1} e^{-(\alpha_1 + \alpha_2)}\left(\frac{\lambda_1}{N}S(s)E(s) + \frac{\lambda_2}{N}S(s)I(s)\right)ds.
\]

which is impossible.

Then, we get \(E, I\) and \(S\) as positive functions. Therefore, we get \(E, R, D\) and \(Q\) as increasing functions. Thus, we have \(E, R, D\) and \(Q\) as positive functions.
Now, we prove that the solution is bounded. From the positivity of the solution, we have the following inequality
\[
\frac{dS}{dt} \leq -\lambda_3 S(t).
\]
\[
\frac{dS}{dt} + \frac{dE}{dt} \leq -m_1 (S + E); \quad \text{where} \quad m_1 = \min\{\lambda_3, \alpha_1 + \alpha_2\}.
\]
Then, by integrating
\[
S(t) \leq S(0)e^{-\lambda_3 t},
\]
\[
E(t) + S(t) \leq (S(0) + E(0))e^{-m_1 t}.
\]
We can deduce that \(S(t) \leq S(0) + E(0)\), for all positive real \(t\).

By the same way, we get
\[
E(t) + S(t) + I(t) \leq (S(0) + E(0))e^{-m_2 t};
\]
where \(m_2 = \min\{\lambda_3, \alpha_2, \beta_2\}\).

Then, \(I(t) \leq S(0) + E(0) + I(0)\) for \(t \geq 0\).

Thus, the disease-free state is stable.

3.2. Disease free equilibrium, reproduction number \(R_0\) and extinction of infected population

At the disease-free state, there is no disease in the human population which implies \(E = I = R = D = Q = S_t = 0\). Thus, the disease-free equilibrium of the model (3.1) is given by
\[
(S^0, E^0, I^0, R^0, D^0, Q^0) = (N, 0, 0, 0, 0, 0, 0).
\]

We can also verify whether or not the state-point is stable. In our case, according the positivity of our model, we have from the first equation of system (2.2)
\[
S(t) \leq S(0)e^{-\lambda_3 t} \to 0 \quad (\neq N).
\]

As a result, the state-point is unstable.

Now, let us calculate the basic reproduction number \(R_0\) which is the average number of secondary infections caused by an infectious individual during his or her entire period of infectiousness (Diekmann et al) [3]. The basic reproduction number is an important non-dimensional quantity in epidemiology as it sets the threshold in the study of a disease both for predicting its outbreak and for evaluating its control strategies. Using the next generation operator approach by van den Driessche and Watmough [12], we have
\[
R_0 = \frac{\lambda_1 (\beta_1 + \beta_2) + \alpha_1 \lambda_2}{(\alpha_1 + \alpha_2)(\beta_1 + \beta_2)}
\]
And we have the corresponding effective control reproduction number defined as in [3]
\[
R_0(t) = \frac{\lambda_1 (\beta_1 + \beta_2) + \alpha_1 \lambda_2}{N(\alpha_1 + \alpha_2)(\beta_1 + \beta_2)} S(t).
\]

Fig. 4.1. Infected population.
This quantity provides us with a clear index to evaluate the control strategy for any time \( t \).

**Theorem 3.3.** If \( R_0 < 1 \), then exposed and infected population will extinct.

**Proof.** Let us define the Lyapunov functional

\[ V(t) = \lambda_2 I(t) + (\beta_1 + \beta_2)E(t) \]

The derivative of \( V \) is given by

\[
V'(t) = \lambda_2 I(t) + (\beta_1 + \beta_2)E(t) \\
= (\alpha_1 \lambda_2 + \lambda_1 (\beta_1 + \beta_2) - (\alpha_1 + \alpha_2)(\beta_1 + \beta_2))E(t) \\
\leq (\alpha_1 \lambda_2 + \lambda_1 (\beta_1 + \beta_2) - (\alpha_1 + \alpha_2)(\beta_1 + \beta_2))V(t).
\]

Thus,

\[
V(t) \leq V(0)\exp\left((\alpha_1 \lambda_2 + \lambda_1 (\beta_1 + \beta_2) - (\alpha_1 + \alpha_2)(\beta_1 + \beta_2))t\right),
\]
where \( V(0) = \lambda_2 I(0) + (\beta_1 + \beta_2) E(0) \). Therefore, for \( R_0 < 1 \) we have
\[
\alpha_1 \lambda_2 + \lambda_1 (\beta_1 + \beta_2) - (\alpha_1 + \alpha_2) (\beta_1 + \beta_2) < 0.
\]
Then, \( V(t) \to 0 \) i.e \( \lim I(t) = 0 = \lim E(t) \).
This shows that the disease will be extinct if \( R_0 < 1 \). □

3.3. The effect of quarantine strategies

As most countries of the world, Tunisia fights vigorously against the spread of the COVID-19 epidemic with some disabilities such as the lack of medical equipment. Therefore, in order to brake the spread of this emerging epidemic the general quarantine is adopted. In addition, since the number of beds in intensive care in the hospital is reduced and insufficient, the infected population is not fully hospitalized except in cases with fairly severe symptoms. Besides, the rest of the population should respect total isolation. The natural question here is: What is the impact of this decision in other words this quarantine strategy?

By equation one in the system (2.2), the susceptible population can be evaluate from the following expression
\[
S(t) = e^{-\lambda_2 S(0)} - e^{-\lambda_2 t} \int_0^t e^{\lambda_2 s} \left( \frac{\lambda_1}{N} S(s) E(s) + \frac{\lambda_2}{N} S(s) I(s) \right) ds.
\]
(3.6)

It is clear that the parameter \( \lambda_3 \) reduces the number of people exposed to infection with the disease. From the evolution of exponential function, we can deduce that when the rate \( \lambda_3 \) is getting bigger, the susceptible population is getting smaller.

When the \( \lambda_3 = 0 \), we have this diagram
and the corresponding non-linear differential equations
\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\lambda_1}{N} SE - \frac{\lambda_2}{N} SI \\
\frac{dE}{dt} &= \frac{\lambda_1}{N} SE + \frac{\lambda_2}{N} SI - (\alpha_1 + \alpha_2) E \\
\frac{dI}{dt} &= \alpha_1 E - (\beta_1 + \beta_2) I \\
\frac{dE_r}{dt} &= \alpha_2 E \\
\frac{dR}{dt} &= \beta_1 I \\
\frac{dD}{dt} &= \beta_2 I.
\end{align*}
\]
(3.7)

where the parameters were defined in the Table 1.
Table 2
SEIRDQ Model parameters.

| parameters | values  |
|------------|---------|
| $\lambda_1$ | 0.8 (day$^{-1}$) |
| $\lambda_2$ | 0.02 (day$^{-1}$) |
| $\lambda_3$ | 0.166 (day$^{-1}$) |
| $N$ | $11 \times 10^6$ persons |
| $\alpha_1$ | 0.0109 (day$^{-1}$) |
| $\alpha_2$ | 0.1 (day$^{-1}$) |
| $\beta_1$ | 0.003 (day$^{-1}$) |
| $\beta_2$ | 0.0037 (day$^{-1}$) |
| $R_0$ | 7.5 |

Table 3
Infected and exposed peak values in Tunisia region.

| Peak infected | Peak exposed |
|---------------|--------------|
| day | Number(%) | day | Number(%) |
| 38 | 648($5.9 \times 10^3$) | 12 | 3405($3.1 \times 10^2$) |

Clearly, by the first equation, one has

$$S(t) = S(0)\exp\left(-\int_0^t \frac{\lambda_1}{N}E(s) + \frac{\lambda_2}{N}I(s)ds\right).$$ (3.8)

Hence,

$$S(t) \leq S(0)\exp\left(-t\left(\frac{\lambda_1}{N}E(0) + \frac{\lambda_2}{N}I(0)\right)\right).$$ (3.9)

So,

$$S(t) \rightarrow_{t \rightarrow +\infty} 0.$$

which implies that the disease almost infected every susceptible person.

This theoretical result which justifies the quarantine strategy will be consolidated by a numerical study in the following paragraph.

4. Numerical stimulations

Using data of Tunisia from March 14th to April 8th 2020, we can estimate the parameters’values. The results can be summarized as follows:

And for stimulation, we chose the following initial condition: $S(0) = N-E(0)-I(0), E(0) = 200, I(0) = 18, E_1(0) = R(0) = D(0) = 0$.

In addition to the population plots in Figs. 4.1 and 4.2, we collected some meaningful quantitative information about the model parameters (Table 2) and the peak values for infected and exposed populations (Table 3). The results can be summarized as follows:

And we have $R_0 > 1$, therefore the disease will spread.

The human body needs around 10 days to get rid of the organism. However, cases where the body needed 21 days to get rid of symptoms are detected. So after the peak, it is logical that the rate of recovered population increases. Then, we can get the following figures.

From Figs. 4.1 and 4.4, if the Tunisian people maintain this pattern. After 50 days, the exposed population is fewer and the infected population surpasses the peak and decreases quickly. So, the government of Tunisia can ease up the measures that it took in connection with the outbreak of the epidemic like the general quarantine.

To make a better illustration of quarantine strategy, we tested different home quarantine rates $\lambda_3$ in Fig. 4.7(a-h).

Now, let’s summarize by giving different cases in one figure in order to compare them.

The change in the $\lambda_3$ parameter generates a consequent variation in the rate of the infected population and the deceased persons (Fig. 4.8a-b).

The most spectacular is the case $\lambda_3 = 0$ which corresponds to $Q = 0$; or in other words, in the absence of a quarantine strategy. We can see that on the 20th day of the epidemic we get 3.75x10$^3$ infected people (Fig. 4.3a). This number is far above the capacity of health structures in Tunisia. Consequently, the choice of containment strategy has significantly reduced the number of deceased and infected persons.

5. Discussion

Based on the COVID-19 cases data collected from March 14th to April 8th, we estimated the basic reproduction number $R_0$ and the prediction of the epidemic’s evolution.

According to the comparison between the official epidemic data based on our model (Fig. 4.3) one can see that the simulation curve model of the number of confirmed infections $I(t)$ and the number of dead people $D(t)$ match the official data curve very well during the period of 30 days.

On the one side, the case of this epidemic in Tunisia is not critical: the peak of infected cases less than 700 which was very comfortable than many Arabian countries (Emirate, Qatar, Morocco, Algeria, ...) and also Western countries (Portugal, France, Spainia...).

On the other side, the number of infected and dead due to this disease remains relatively low in Tunisia compared to what is happening elsewhere in the world. And the most remarkable thing is that this situation is better than our neighbors (Algeria, France, Italy). Health policies are probably there for something but is it enough to have a plausible theory?

Based on the data at the start of the disease in March, we can deduce from the theoretical study and the numerical simulations that the modification of the parameter $\lambda_3$ generates a consequent variation in the rate of the infected population and deceased persons (Fig. 4.8a-b). Naturally, the most spectacular case is the case $\lambda_3 = 0$ which corresponds to $Q=0$. In other words, in the absence of a quarantine strategy, we can see that on the 20th day of the epidemic, we get 3.75x10$^3$ infected people (Fig. 4.3a). This number is much higher than the current capacity of health structures in Tunisia. Consequently, the choice of the containment strategy considerably reduced the number of dead and infected people.

With the absence of drug and vaccination, we found that home quarantine can really limit the spread of the epidemic. However, this strategy cannot last for an infinite time, due to the economic consequences on the country. The indicator of infected cases is not the problem. The exposed cases is the most important indicator. We predicted the initial exposed population to be about 200. And after 50 days in Fig. 4.3, the indicator of infected cases shows less infected people. Accordingly, the government is considering the relaxation of the quarantine strategy.

The proposed model is flexible and we believe it could be easily adapted to monitor various infected are as with different restriction policies.

6. Conclusion

In this article, we presented a new model based on nonlinear differential equations allowing to model this COVID-19 in Tunisia. The aim of our work, at first, is to provide initial ideas and guidelines for a quantitative and qualitative study of our considered model. In particular, the positivity, boundedness and the existence of a solution are established. The impact of the quarantine strategy is also investigated and discussed by two methods. It thus appears that in addition to a rigorous application of quarantine, accurately near-casting the epidemic trend and projecting the peak time require real-time data and the knowledge about the implementation resources in order to construct the adequate policy and effective decisions of major public health interventions. We hope
Fig. 4.7. a-b) Infected population and Dead population with $\lambda_3 = 0.166$ which was our case, c-d) Infected population and Dead population with $\lambda_3 = 0.15$. e-f) Infected population and Dead population with $\lambda_3 = 0.13$. g-h) Infected population and Dead population with $\lambda_3 = 0.1$. 
our work motivates new research to produce more elaborate and precise methods related to this model or to give significant improvements.

Declaration of Competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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