

## Mathematical Modeling and Simulation of SEIRD Model for COVID-19 in Libya

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**Abstract**—This paper is to present an SEIRD epidemic model to describe the progression of COVID-19. Mathematical analysis is used to show the dynamic behavior of the spread of epidemic diseases. The next generation matrix was adopted to calculate the basic reproduction number for the model which plays an important role in determining the stability. Stabilities of disease free and endemic equilibrium are also analyzed. Numerical simulation is provided to confirm the theoretical result

**Keywords:** COVID-19, SEIRD epidemic model, basic reproduction number, next generation matrix, stability, numerical simulation

### INTRODUCTION

COVID-19 is a contagious disease caused by SARS-COV family. the first case of COVID-19 was identified at the end of November 2019 in Wuhan city of China, before it swiftly spread over the world. On March 11<sup>th</sup>, 2020 the world health organization (WHO) had declared COVID-19 as global pandemic. On March 24<sup>th</sup> 2020, Libya reported the first case.

Mathematical models are important tools that can be used to predict the future outbreaks and control infectious diseases. Among all those models, SEIRD is used in this paper to analyze the progression of COVID-19 and predict the epidemic peak of COVID-19. Furthermore, several of mathematical models have been formulated to study the infectious disease and develop helpful strategies for efficient control the infection.

A very important quantity to evaluate the effect of the control strategies is the basic reproduction number.

### THEORETICAL ANALYSIS

#### Mathematical Model Formulation

In this section, we consider the transmission of SARS-COV-2 among people. The total human population can be divided into five compartments of individuals which are: Susceptible S (those are able to contract the disease), the exposed E (those whose their body is a host

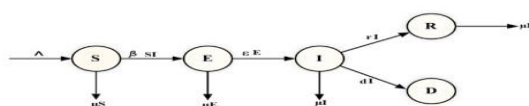


FIG1. Diagram of SEIRD model

for infections but are not yet able to transmit the disease and may not have symptoms), the infected I (those who have the disease and can transmit it), the recovered R (those who have recovered), the dead D (those who have died)

The dynamical process of SEIRD is described by a system of ordinary differential equations

$$\begin{aligned} \dot{E} &= \beta SI - (\mu + \varepsilon)E \\ \dot{I} &= \varepsilon E - (\mu + r + d)I \\ \dot{R} &= rI - \mu R \end{aligned} \quad (1)$$

$$\begin{aligned} \dot{D} &= dI \\ \dot{E} &= \beta SI - (\mu + \varepsilon)E \end{aligned}$$

Parameters	Description
$\Lambda$	recruime rate of population
$\beta$	the contact rate or transmission rate
$\mu$	the natural death rate
$\varepsilon$	the rate of transmission from incubation period individuals to infective
R	the recovery rate of infection individuals
D	the disease-related dead

The dead compartment D does not appear in the first four equations of (1) so the system can be reduced to the following system:

$$\begin{aligned} \dot{S} &= \Lambda - \beta SI - \mu S \\ \dot{E} &= \beta SI - (\mu + \varepsilon)E \\ \dot{I} &= \varepsilon E - (\mu + r + d)I \\ \dot{R} &= rI - \mu R \end{aligned} \quad (2)$$

#### Boundedness

The total population is given by  
 $N(t) = S(t) + E(t) + I(t) + R(t)$ .

Those taking the derivative leads to  $\dot{N} = \dot{S} + \dot{E} + \dot{I} + \dot{R}$

where the initial conditions are non-negative then  $\lim_{t \rightarrow \infty} (S + E + I + R) \leq \frac{\Lambda}{\mu}$ , so the feasible region for the system (2) is

$$\psi = \left\{ (S, E, I, R) : S + E + I + R \leq \frac{\Lambda}{\mu}, S \geq 0, E \geq 0, I \geq 0, R \geq 0 \right\}$$

so, the population is bounded above.

#### The Basic Reproduction Number

The basic reproduction number usually denoted by  $\mathfrak{R}_0$ , which is defined as expected number of secondary infections caused by typical infected individual in a totally susceptible population.  $\mathfrak{R}_0$  can be determined by using the method of Next Generation Matrix.

Apparently, system (2) always has a disease-free equilibrium (DFE) at  $x_0 = \left( \frac{\Lambda}{\mu}, 0, 0, 0 \right)$

Let  $X = (E, I, S, R)^T$  the system can be written as

$$\dot{X} = \mathcal{F}(X) - \mathcal{v}(X) \quad (3)$$

where

$$\mathcal{F}(\mathcal{X}) = \begin{pmatrix} \beta SI \\ 0 \\ 0 \\ 0 \end{pmatrix}, \mathcal{V}(\mathcal{X}) = \begin{pmatrix} (\mu + \varepsilon)E \\ -\varepsilon E + (\mu + r + d)I \\ \Lambda + \beta SI + \mu S \\ -rI + \mu R \end{pmatrix} \quad (4)$$

The infected compartments are only E and I, the matrices  $F$  and  $V$  at DFE  $\mathcal{X}_0$  are:

$$F = \begin{pmatrix} 0 & \frac{\Lambda\beta}{\mu} \\ 0 & 0 \end{pmatrix}, V = \begin{pmatrix} \mu + \varepsilon & 0 \\ -\varepsilon & \mu + r + d \end{pmatrix} \quad (2)$$

The next generation matrix of the system (2)

$$FV^{-1} = \begin{pmatrix} \frac{\Lambda\beta\varepsilon}{\mu(\mu+\varepsilon)(\mu+r+d)} & \frac{\Lambda\beta}{\mu(\mu+r+d)} \\ 0 & 0 \end{pmatrix} \quad (5)$$

The spectral radius of  $FV^{-1}$  is

$$\rho(FV^{-1}) = \frac{\Lambda\beta\varepsilon}{\mu(\mu+\varepsilon)(\mu+r+d)} \quad (6)$$

so, the basic reproduction number of the system is

$$\mathfrak{R}_0 = \frac{\Lambda\beta\varepsilon}{\mu(\mu+\varepsilon)(\mu+r+d)} \quad (7)$$

### Equilibria

the equilibrium points of system (2) can be found by setting the time derivatives of S, E, I, R equal to zero.

It provides two equilibrium points:

1. A disease-free equilibrium point  $\mathcal{X}_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right)$ .
2. an endemic equilibrium point  $\mathcal{X}^* = (S^*, E^*, I^*, R^*)$

where

$$S^* = \frac{\Lambda}{\mu\mathfrak{R}_0} \quad (8)$$

$$E^* = \frac{\mu(\mu+r+d)}{\beta\varepsilon} (\mathfrak{R}_0 - 1) \quad (9)$$

$$I^* = \frac{\mu}{\beta} (\mathfrak{R}_0 - 1) \quad (10)$$

$$R^* = \frac{r}{\beta} (\mathfrak{R}_0 - 1) \quad (11)$$

**Theorem1:** If  $\mathfrak{R}_0 > 1$ , then the system (2) has a disease-free equilibrium point  $\mathcal{X}_0$  and the system also has a unique endemic equilibrium point  $\mathcal{X}^*$

### Local Stability of Equilibria

**Theorem2:** The disease-free equilibrium point  $\mathcal{X}_0$  is locally asymptotically stable If  $\mathfrak{R}_0 < 1$ . The disease-free equilibrium is unstable If  $\mathfrak{R}_0 > 1$ .

To examine the local stability, we find the Jacobian of the system (2)

$$J = \begin{pmatrix} -\beta I - \mu & 0 & -\beta S & 0 \\ \beta I & -(\mu + \varepsilon) & \beta S & 0 \\ 0 & \varepsilon & -(\mu + r + d) & 0 \\ 0 & 0 & r & -\mu \end{pmatrix} \quad (12)$$

Evaluate the Jacobian at  $\mathcal{X}_0$

$$J(\mathcal{X}_0) = \begin{pmatrix} -\mu & 0 & -\beta S & 0 \\ 0 & -(\mu + \varepsilon) & \beta S & 0 \\ 0 & \varepsilon & -(\mu + r + d) & 0 \\ 0 & 0 & r & -\mu \end{pmatrix}$$

By solving the characteristic equation  $|J(\mathcal{X}_0) - \lambda I| = 0$  which has two eigenvalues  $\lambda_1 = \lambda_2 = -\mu$ , and find the remaining eigenvalues by solving the following equation:

$$\begin{vmatrix} -(\mu + \varepsilon + \lambda) & \beta S \\ \varepsilon & -(\mu + r + d + \lambda) \end{vmatrix} = 0 \quad (14)$$

finding the determinant gives:

$$(\mu + r + d)(\mu + \varepsilon + \lambda) - \beta \varepsilon \frac{A}{\mu} = 0 \quad (15)$$

The eigenvalues of previous equation after inserting  $\mathfrak{R}_0$  are given by:

$$\lambda_3 = -\frac{1}{2} \left( N_1 + N_2 - \sqrt{(N_1 - N_2)^2 + 4N_1 N_2 \mathfrak{R}_0} \right) \quad (16)$$

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Where  $N_1 = \mu + \varepsilon$ ,  $N_2 = \mu + r + d$

If  $\mathfrak{R}_0 < 1$ , then the eigenvalues  $\lambda_3, \lambda_4$  are always negative, therefore the DFE  $\mathcal{X}_0$  is locally asymptotically stable, if  $\mathfrak{R}_0 > 1$  then  $\lambda_3 > 0, \lambda_4 < 0$  and the DFE  $\mathcal{X}_0$  is locally asymptotically unstable.

#### Local Stability of Endemic Equilibrium

**Theorem3:** when  $\mathfrak{R}_0 > 1$ , the endemic equilibrium point  $\mathcal{X}^*$  is locally asymptotically stable.

To examine the local stability of the endemic equilibrium  $\mathcal{X}^*$ , we estimate the Jacobian at the endemic equilibrium. we consider the characteristic equation:

$$\begin{vmatrix} -\beta I^* - \mu - \lambda & 0 & -\beta S^* & 0 \\ \beta I^* & -(\mu + \varepsilon + \lambda) & \beta S^* & 0 \\ 0 & \varepsilon & -(\mu + r + d + \lambda) & 0 \\ 0 & 0 & r & -(\mu + \lambda) \end{vmatrix} = 0 \quad (18)$$

It is clear that  $\lambda = -\mu$  an eigenvalue of above characteristic equation. The other eigenvalues can be determined by the following equation:

$$\begin{vmatrix} -\beta I^* - \mu - \lambda & 0 & -\beta S^* \\ \beta I^* & -(\mu + \varepsilon + \lambda) & \beta S^* \\ 0 & \varepsilon & -(\mu + r + d + \lambda) \end{vmatrix} = 0 \quad (19)$$

Expanding the determinant and simplify the equation leads to:

$$(\beta I^* + \mu + \lambda)(\mu + \varepsilon + \lambda)(\mu + r + d + \lambda) = \varepsilon \beta S^* (\gamma)$$

This leads to the following cubic polynomial:

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0 \quad (21)$$

where

$$a_1 = 2\mu + \varepsilon + r + d + \mu\mathfrak{R}_0 \quad (22)$$

$$a_2 = \mu\mathfrak{R}_0(\mu + \varepsilon + r + d) \quad (23)$$

$$a_3 = \mu\mathfrak{R}_0(\mu + \varepsilon)(\mu + r + d) - (\mu + \varepsilon)(\mu + r + d) \quad (24)$$

It is easy to see that  $H_1 = a_1 > 0$ , since  $\mathfrak{R}_0 > 1$  then  $a_3 > 0$ .

$$H_2 = a_1a_2 - a_3 = (2\mu + \varepsilon + r + d + \mu\mathfrak{R}_0)\mu\mathfrak{R}_0(\mu + \varepsilon + r + d) - \mu\mathfrak{R}_0(\mu + \varepsilon)(\mu + r + d) + (\mu + \varepsilon)(\mu + r + d) > 0.$$

From Routh-Herwitz criteria, we conclude that all the eigenvalues of  $J(X^*)$  will be negative, when  $\mathfrak{R}_0 > 0$ .

Hence the endemic equilibrium point  $X^*$  is locally asymptotically stable

#### Global stability of Equilibria

In this section, we analyze the global stability of disease-free equilibrium and the endemic equilibrium for SEIRD model by applying a Lyapunov's theorem.

**Theorem4:** If  $\mathfrak{R}_0 < 1$ , then the disease-free equilibrium is globally asymptotically stable.

It is obvious that if DFE for the SEIRD model of the first three equations is globally asymptotically stable then

$R(t) \rightarrow 0, D(t) \rightarrow 0$  and the DFE for SEIRD model is globally stable.

We construct a Lyapunov function on  $R_+^3$  as follows:

$$L = \mathcal{K} \left( S - S^* - \frac{S^* \ln S}{S^*} \right) + \frac{1}{\mu + \varepsilon} E + \frac{1}{\varepsilon} I \quad (25)$$

where  $\mathcal{K}$  is a positive constant to be determined and  $S^* = \frac{\Lambda}{\mu}$ . It is clear that  $L = 0$  at DFE. To show that

$$L > 0 \text{ for all } (S, E, I) \neq \left( \frac{\Lambda}{\mu}, 0, 0 \right).$$

We can write equation (26) in the following form

$$L = \mathcal{K} S^* \left( \frac{S}{S^*} - 1 - \frac{\ln S}{S^*} \right) + \frac{1}{\mu + \varepsilon} E + \frac{1}{\varepsilon} I. \quad (26)$$

The first term is positive because the function  $h(x) > 0$  for all  $x > 0$  since  $h(x) = x - 1 - \ln x$ , and the remaining terms are also positive, so  $L > 0$ .

differentiating (27) with respect to time t we obtain:

$$\dot{L} = \mathcal{K} \left( 1 - \frac{S^*}{S} \right) \dot{S} + \frac{1}{\mu + \varepsilon} \dot{E} + \frac{1}{\varepsilon} \dot{I}. \quad (27)$$

$$\dot{L} = 2\mathcal{K}\Lambda - \mathcal{K}\beta SI - \mathcal{K}\mu S - \mathcal{K} \frac{\Lambda^2}{\mu S} + \mathcal{K} \frac{\Lambda\beta}{\mu} I + \frac{\beta}{\mu + \varepsilon} SI - \frac{(\mu + r + d)}{\varepsilon} I. \quad (28)$$

If we let  $\mathcal{K} = \frac{1}{\mu + \varepsilon}$  then we have

$$\dot{L} = -\mathcal{K}\Lambda \left[ \frac{\Lambda}{\mu S} + \frac{\mu S}{\Lambda} - 2 \right] + \frac{(\mu + r + d)}{\varepsilon} I [\mathfrak{R}_0 - 1] \quad (29)$$

As long as  $\mathfrak{R}_0 < 1$ , the last term is non-positive. For the first time, suppose  $\omega = \frac{\Lambda}{\mu S}$  then the first term becomes

$$\left[ \omega + \frac{1}{\omega} - 2 \right] = \frac{(\omega-1)^2}{\omega} > 0 \text{ for every } \omega > 0, \omega \neq 1.$$

So  $L > 0$  for all  $(S, E, I) \neq \left( \frac{\Lambda}{\mu}, 0, 0 \right)$ .

Depending on the Lyapunov's theorem, the DFE is globally asymptotically stable.

**Theorem5:** If  $\mathfrak{R}_0 > 1$ , then the endemic equilibrium is globally asymptotically stable.

We consider the following the Lyapunov's function to investigate the global stability of endemic equilibrium, as

$$L = \mathcal{K}_1 \left( S - S^* - \frac{S' \ln S}{S'} \right) + \mathcal{K}_2 \left( E - E^* - \frac{E' \ln E}{E'} \right) + \mathcal{K}_3 \left( I - I^* - \frac{I' \ln I}{I'} \right) \quad (30)$$

where  $\mathcal{K}_1, \mathcal{K}_2, \mathcal{K}_3$  are positive constants to be determined.

Differentiating (31) with respect to time t we get

$$\dot{L} = \mathcal{K}_1 \left( 1 - \frac{S'}{S} \right) S' + \mathcal{K}_2 \left( 1 - \frac{E'}{E} \right) E' + \mathcal{K}_3 \left( 1 - \frac{I'}{I} \right) I' \quad (31)$$

Substituting the expression for  $S', E'$  and  $I'$  from (1) into (32) we get:

$$\begin{aligned} \dot{L} = & \mathcal{K}_1 \left( 1 - \frac{S'}{S} \right) (\Lambda - \beta SI - \mu S) + \\ & \mathcal{K}_2 \left( 1 - \frac{E'}{E} \right) (\beta SI - (\mu + \varepsilon)E) + \mathcal{K}_3 \left( 1 - \frac{I'}{I} \right) (\varepsilon E - (\mu + r + d)I) \end{aligned} \quad (32)$$

Using

$$\Lambda = \beta S^* I^* + \mu S^*.$$

$$\begin{aligned} \dot{L} = & -\mathcal{K}_1 \frac{(S-S^*)^2}{S} + \mathcal{K}_1 \beta S^* I^* - \mathcal{K}_1 \beta SI - \mathcal{K}_1 \beta \frac{S^{*2}}{S} I^* + \mathcal{K}_1 \beta S^* I + \mathcal{K}_2 \beta SI - \mathcal{K}_2 (\mu + \varepsilon)E - \mathcal{K}_2 \beta \frac{E^*}{E} SI + \\ & \mathcal{K}_2 (\mu + \varepsilon)E^* + \mathcal{K}_3 \varepsilon E - \\ & \mathcal{K}_3 (\mu + r + d)I - \mathcal{K}_3 \varepsilon \frac{I^*}{I} E + \mathcal{K}_3 (\mu + r + d)I^*. \end{aligned} \quad (33)$$

If  $\mathcal{K}_1 = \mathcal{K}_2$  and multiply and divide by the equilibrium value then:

$$\begin{aligned} \dot{L} = & -\mathcal{K}_1 \frac{(S-S^*)^2}{S} + \mathcal{K}_1 \beta S^* I^* - \mathcal{K}_1 \beta \frac{S^{*2}}{S} I^* + \mathcal{K}_1 \beta S^* I - \mathcal{K}_2 (\mu + \varepsilon)E - \mathcal{K}_2 \beta S^* I^* \frac{E^* SI}{\beta S^* I^*} + \\ & \mathcal{K}_2 (\mu + \varepsilon)E^* + \mathcal{K}_3 \varepsilon E - \mathcal{K}_3 (\mu + r + d)I - \mathcal{K}_3 \varepsilon E^* \frac{I^* E}{I E^*} + \mathcal{K}_3 (\mu + r + d)I^*. \end{aligned} \quad (34)$$

Since  $\mathcal{K}_1 = \mathcal{K}_2$  we observed that  $\beta S^* I^* = (\mu + \varepsilon)E^*$ .

Let  $\mathcal{K}_3 (\mu + r + d)I^* = \mathcal{K}_2 (\mu + \varepsilon)E^*$ .

Consequently,  $\mathcal{K}_3 = \mathcal{K}_2 \frac{(\mu + \varepsilon)}{\varepsilon}$

$$\dot{L} = -\mathcal{K}_1 \frac{(S-S^*)^2}{S} + \mathcal{K}_1 \beta S^* I^* \left[ 3 - \frac{S'}{S} - \frac{E^* SI}{E S^* I^*} - \frac{I' E}{I E^*} \right] + [\mathcal{K}_1 \beta S^* - \mathcal{K}_3 (\mu + r + d)]I + [\mathcal{K}_3 \frac{E^* SI}{E S^* I^*} - \mathcal{K}_2 (\mu + \varepsilon)]E. \quad (35)$$

$$\dot{L} = -\mathcal{K}_1 \frac{(s-s^*)^2}{s} + \mathcal{K}_1 \beta S^* I^* \left[ 3 - \frac{s^*}{s} - \frac{E^* S I}{E S^* I^*} - \frac{I^* E}{I E^*} \right] \quad (36)$$

It is easy to see the first term is negative unless  $S = S^*$ .

Since the arithmetic mean is larger than the geometric mean. Hence,

$$\frac{s^*}{s} + \frac{E^* S I}{E S^* I^*} + \frac{I^* E}{I E^*} \geq 3.$$

Therefore, the second term is negative, and it is zero if  $(S, E, I) = (S^*, E^*, I^*)$ .

Clearly, the largest invariant set in  $\{(S, E, I) \in \psi: \frac{dL}{dt} = 0\}$  is the singleton  $\{X^* = (S^*, E^*, I^*)\}$ . Using Lasalle's invariance principle,  $X^*$  is globally stable.

### NUMERICAL SIMULATION

In this section, we carry out the numerical simulation to illustrate the theoretical results with MATLAB 2019a. We simulate the model by using the parameters  $\Lambda = 6871292$ ,  $\varepsilon = 0.1923$ ,  $d = 0.032$ ,  $r = 0.0714$ ,  $\mathcal{R}_0 = 2.2$   $\mu$  is assumed to be zero,  $S(0) = 1697$ ,  $E(0) = 1616$ ,  $I(0) = 60$ ,  $R(0) = 18$  and  $D(0) = 3$ .

Figure 2 shows the predictions of spread of pandemic for the next 700 days after May 01, 2020 by using SEIRD model.

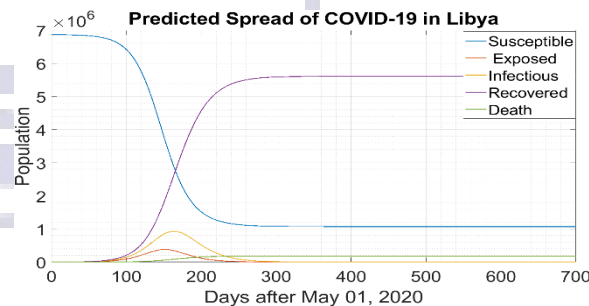


FIG. 2

### CONCLUSION

This paper is concerned with SEIRD epidemic model which can be useful in predicting the future outbreak of disease epidemic in Libya.

the dynamics behavior of disease is determined by the basic reproduction number  $\mathcal{R}_0$ . When  $\mathcal{R}_0 < 1$  the system has a unique DFE  $X_0$  which is locally asymptotically stable and globally stable it means that the disease dies out. When  $\mathcal{R}_0 > 1$  the disease-free equilibrium becomes unstable and the infection always persists but the system has a unique endemic equilibrium  $X^*$  which is locally and globally stable under some conditions.

The SEIRD model results (figure 2) shows that the day of the maximum number of infection cases of COVID-19 in Libya is 163

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