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# SEIR Mathematical Model of COVID-19 Epidemic Transmission in France

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## Abstract

The COVID-19 pandemic, first identified in Wuhan, China, in December 2019, rapidly spread across the globe, necessitating mathematical models to understand its transmission dynamics. This study presents a susceptible-exposed-infected-removed (SEIR) model to analyze the spread of COVID-19 in France. The model incorporates key epidemiological parameters, including the transmission rate ($\alpha$) and social interaction factor ($\kappa$), which influence disease spread. To solve the system of differential equations, we employ the fourth-order Runge-Kutta (RK4) method. A parametric study is conducted to validate the model, and the basic reproduction number ($R_0$) is derived to assess disease stability. The results align with real-world data, confirming the model's effectiveness in describing the outbreak. Our findings highlight the critical role of social distancing, recovery rates, and transmission reduction measures in mitigating the spread of COVID-19.

**Keywords:** COVID-19, SEIR Model, RK4, Reproduction number, Stability

## 1 | Introduction

COVID-19 is a widespread, epidemic disease, brought about by a virus attacking the higher part of the breathing apparatus, marked by fever and a great loss of power in muscles. The disease was first disclosed in 2019 in Wuhan, a well-populated commercial city, located in the Hubei Province of China, and spread worldwide [1].
The consequences of this disease are not the same for all individuals which vary from person to person. It is difficult to establish some relationship between the severity of this virus and the ethnicity or gender of the individuals, but the severity of consequences mainly depends on the immune system of the people. In the majority of cases, patients face mild symptoms and endure it easily; however, there are also a reasonable number of instances when the affected persons are subjected to severe issues such as acute respiratory illness, clotting of blood, failure of the organs, etc.
COVID-19 is a zoonotic type virus means that it can transfer between animals and humans. The major source of virus spread is close contact with the affected person from which this virus may transmit via tiny droplets

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mainly through coughing and sneezing of the affected person. These droplets may directly transmit the virus during close contact, or these may retain on the surfaces and transfer later upon contact with those surfaces. No evidence is available about the traveling of the virus through the air over long distances. The degree of contagiousness is significantly high during the initial few days after the outbreak of symptoms. However, the transmission of the virus is possible even from those affected persons having no symptoms[2].
To control the spread of this infection, it is recommended to wash your hands frequently, maintain a safe physical distance from others, not touch your face with unwashed hands, and cover the cough and sneeze. Suspected individuals are recommended to cover their faces with a proper covering to prevent the spread of this infectious disease. Research work has resulted in a number of effective Covid vaccines however due to rapid mutations for this virus but so far, no success has been achieved to produce any vaccine for COVID-19. The best solution is to take necessary precautionary measures to avoid the spread.
The most familiar/typical symptoms of this disease consist of cough with fever and fatigue accompanied by hotness of breath. Loss of taste and smell were also noted as symptoms of COVID-19, but these are not very common. It is also possible that no symptoms would appear in the COVID-19 carrier. Generally, the incubation period of this virus is five days which may vary between two to fourteen days. The COVID-19 Patient and Number of deaths per day show that the individuals seem to be susceptible to this virus [3].
Recently, the epidemic of Coronavirus (COVID-19) is growing and the cases of infected individuals have been fastly growing. The safety measure for COVID-19 the government of different countries take some actions (such as lock-down) closing all businesses, all educational institutes, suspending public transport, and all national and international affairs and public gatherings to relieve the effect of the epidemic.
The mathematical model assumes a significant function to acclimatize the cycle of transmission of infection and gives various measures to control its multiplication. Mathematicians present different models to discuss this infectious disease like SIR, SEIR, and SEIHR models. In this work, a novel differential model (SEIR (Susceptible, Exposed, Infectious, Removed (Recovered or Death)) for COVID-19 is presented. The Runge Kutta of order 4 is acknowledged as a differential operator in the model [4].
The Runge-Kutta method gives the relative value of y for a given point x. The fourth order Runge-Kutta order yields: $y_{m+1} = y_m + \frac{1}{6}(m_1 + 2m_2 + 2m_3 + m_4)$
Where
$m_1 = hf(t_m, y_m)$
$m_2 = hf(t_m + \frac{h}{2}, y_m + \frac{m_1}{2})$
$m_3 = hf(t_m + \frac{h}{2}, y_m + \frac{m_2}{2})$
$m_4 = hf(t_m + h, y_m + m_3)$
Here, $m_1, m_2, m_3$, and $m_4$ denotes the slopes and $h$ is the time step.

## 2 | Preliminaries

In this category, we will present some significant definitions of ordinary differential equations, their key properties, and notations used in this article.

### 2.1 | Model Formulation

In this model, the Susceptible-Exposed-Infected-Removed (SEIR) system is presented and it will be used to portray the ongoing outbreak of COVID-19 in France. We consider a basic SEIR model to model the virus spread. People were each chosen to one of the accompanying malady states i.e. (S, E, I, R) the number of Susceptible cases (S), Exposed cases (E), Infectious cases (I), Removed cases (R) with a total population (N) and which wants to individuals not yet infected and sickness free, people that are encountering incubation period, the confirmed cases, removed people, respectively. The following is a detailed description of the state variables [5, 6].
**Susceptible (denoted by $S$):** The individuals who are at the possibility of contracting a disease.
**Exposed (denoted by $E$):** A individual who is infected by the disease but has not transmitted it to others.
**Infectious (denoted by $I$):** A person which can transfer the disease to another person.
**Removed (denoted by $R$):** A person who are removed(recovered/death) from this disease.

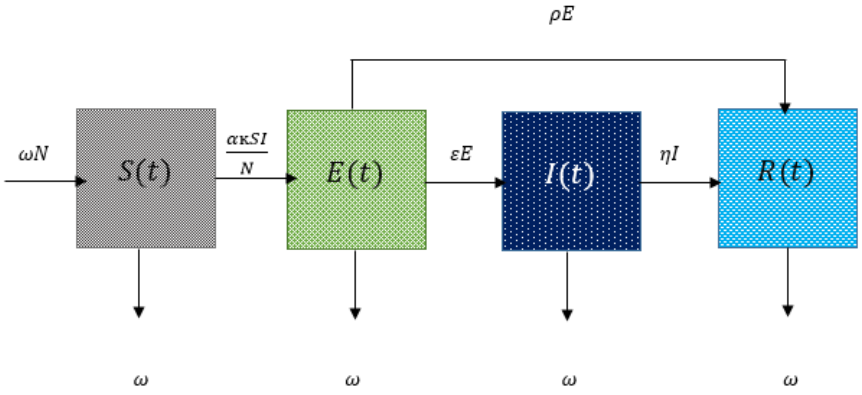


FIGURE 1. Flow diagram of the COVID-19 SEIR model

The corresponding model is given below:

$$\frac{dS(t)}{dt} = \omega N - \frac{\alpha\kappa SI}{N} - \omega S, \tag{1}$$

$$\frac{dE(t)}{dt} = \frac{\alpha\kappa SI}{N} - \rho E - \varepsilon E - \omega E, \tag{2}$$

$$\frac{dI(t)}{dt} = \varepsilon E - \eta I - \omega I, \tag{3}$$

$$\frac{dR(t)}{dt} = \eta I + \rho E - \omega R. \tag{4}$$

Here $S(0) = \vartheta_1, E(0) = \vartheta_2, I(0) = \vartheta_3, R(0) = \vartheta_4$. In this model, $\alpha$ represents the transmission rate, $\eta$ represents the rate of recovery, $\varepsilon$ denotes the exposure rate of the infected, $\rho$ indicates the proportion of exposed people who potentially become infected, $\omega$ is the rate of individuals that leave the compartment, and $\kappa$ is the social factors of contracting COVID-19 [7].
$S(t) + E(t) + I(t) + R(t) = N$
then,
$\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = \frac{dN}{dt}$
$\Rightarrow \frac{dN}{dt} = \omega N - \frac{\alpha\kappa SI}{N} - \omega S + \frac{\alpha\kappa SI}{N} - \rho E - \varepsilon E - \omega E + \varepsilon E - \eta I - \omega I + \eta I + \rho E - \omega R$
By canceling the terms, we get,
$\Rightarrow \frac{dN}{dt} = \omega N - \omega S - \omega E - \omega I - \omega R$
$\Rightarrow \frac{dN}{dt} = \omega(N - S - E - I - R)$
$\Rightarrow \frac{dN}{dt} = \omega(N - N)$
$\Rightarrow \frac{dN}{dt} = 0$
Many numerical methods, including the Runge-Kutta method and the Euler method, can be used to solve this model. The RK4 approach is employed in this study to solve the differential equations model [2, 7, 8].

| Parameters for SEIR COVID-19 Model | | |
|---|---|---|
| **Parameters** | **Definition** | **Parametric Values** |
| $\alpha$ | transmission rate | 0.27926 |
| $\eta$ | recovery rate | 0.005 |
| $\varepsilon$ | exposure or infection risk rate | 0.3165682 |
| $\rho$ | rate of individuals who are exposed and potentially become infected | 0.039661667 |
| $\kappa$ | the social factors of contracting COVID-19 disease | $0 < \kappa < 1$ |
| $\omega$ | rate of individuals that leave the compartment | 0.0023977 |
| $R(t)$ | the susceptible Individuals | |
| $E(t)$ | the exposed Individuals | |
| $I(t)$ | the infected Individuals | |
| $R(t)$ | the removed Individuals | |

## 2.2 | Equilibrium Points

The system of equations (1)-(4) is solved below by substituting $S(t) \to x_1$, $E(t) \to x_2$, $I(t) \to x_3$, and $R(t) \to x_4$:

$$\frac{dx_1}{dt} = \omega - x_1(\alpha\kappa x_3 + \omega) \tag{5}$$

$$\frac{dx_2}{dt} = \alpha\kappa x_1 x_3 - x_2(\varepsilon + \omega + \rho) \tag{6}$$

$$\frac{dx_3}{dt} = \varepsilon x_2 - x_3(\eta + \omega) \tag{7}$$

$$\frac{dx_4}{dt} = \eta x_3 + \rho x_2 - \omega x_4 \tag{8}$$

For the equilibrium points
$\frac{dx_1}{dt} = \frac{dx_2}{dt} = \frac{dx_3}{dt} = \frac{dx_4}{dt} = 0$
then equation (5)-(8) becomes:

$$\omega - x_1(\alpha\kappa x_3 + \omega) = 0 \tag{9}$$

$$\alpha\kappa x_1 x_3 - x_2(\varepsilon + \omega + \rho) = 0 \tag{10}$$

$$\varepsilon x_2 - x_3(\eta + \omega) = 0 \tag{11}$$

$$\eta x_3 + \rho x_2 - \omega x_4 = 0 \tag{12}$$

The point $P_1 = (1, 0, 0, 0)$ is trivial/negligible, everyone of a people is sound and stay-good healthy for constantly means they are disease-free [9].
Now for finding the second equilibrium point, we deal with (9)-(12).
Add (9) and (10)
$\omega - x_1(\alpha\kappa x_3 + \omega) + \alpha\kappa x_1 x_3 - x_2\varepsilon - x_2\omega - x_2\rho = 0$
$\Rightarrow \omega - \alpha\kappa x_1 x_3 - x_1\omega + \alpha\kappa x_1 x_3 - x_2\varepsilon - x_2\omega - x_2\rho = 0$
$\Rightarrow \omega(1 - x_1 - x_2) - x_2\varepsilon - x_2\rho = 0$
$\Rightarrow \omega(1 - x_1 - x_2) - x_2(\varepsilon + \rho) = 0$
or
$x_1(1 - \omega) - x_2(\varepsilon - \omega - \rho) = 0$
$\Rightarrow x_1(1 - \omega) = x_2(\varepsilon - \omega - \rho)$

$$x_1 = \frac{x_2(\varepsilon - \omega - \rho)}{(1 - \omega)} \tag{13}$$

From (11)
$\varepsilon x_2 - x_3(\eta + \omega) = 0$
$\Rightarrow \varepsilon x_2 = x_3(\eta + \omega)$

$$x_2 = \frac{x_3(\eta + \omega)}{\varepsilon} \tag{14}$$

Put the value of $x_2$ in (12)
$\Rightarrow \eta x_3 + \rho(\frac{x_3(\eta+\omega)}{\eta}) - \omega x_4 = 0$

$\Rightarrow \eta x_3 + \rho\frac{(\eta+\omega)}{\eta}x_3 - \omega x_4 = 0$
$\Rightarrow \frac{\varepsilon\eta+\rho\eta+\rho\omega}{\eta}x_3 = \omega x_4$

$$x_4 = \frac{\varepsilon\eta + \rho\eta + \rho\omega}{\eta\omega}x_3 \tag{15}$$

Put the value of $x_1$ and $x_2$ in (10)
$\Rightarrow \alpha\kappa(\frac{x_2(\varepsilon+\omega+\rho)}{1-\omega})x_3 - (x_3\frac{(\eta+\omega)}{\varepsilon})(\varepsilon+\omega+\rho) = 0$
$\Rightarrow \alpha\kappa(\frac{x_3(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon(1-\omega)})x_3 - (\frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon})x_3 = 0$
$\Rightarrow x_3^2(\frac{\alpha\kappa(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon(1-\omega)}) - (\frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon})x_3 = 0$
$\Rightarrow x_3[(x_3\frac{\alpha\kappa(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon(1-\omega)}) - (\frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon})] = 0$
$\Rightarrow x_3(\frac{\alpha\kappa(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon(1-\omega)}) - (\frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon}) = 0$
$\Rightarrow x_3(\frac{\alpha\kappa(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon(1-\omega)}) = (\frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\varepsilon})$
$\Rrightarrow x_3(\frac{\alpha\kappa}{1-\omega}) = 1$

$$x_3 = \frac{1-\omega}{\alpha\kappa} \tag{16}$$

Put the value of $x_3$ in (14), we get,

$$x_2 = \frac{(1-\omega)(\eta+\omega)}{\alpha\kappa\varepsilon} \tag{17}$$

Put the value of $x_2$ in (13),
$x_1 = \frac{(1-\omega)(\eta+\omega)(\varepsilon+\omega+\rho)}{\alpha\kappa\varepsilon(1-\omega)}$

$$x_1 = \frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\alpha\kappa\varepsilon} \tag{18}$$

Now put the value of $x_3$ in (15), we get

$$x_4 = \frac{(1-\omega)(\varepsilon\eta+\rho\eta+\rho\omega)}{\alpha\kappa\varepsilon\omega} \tag{19}$$

The point $P_2 = (x_{10}, x_{20}, x_{30}, x_{40})$ that coincides with an endemic case i.e. the Coronavirus disease prevails in two populations.
The determined values of $x_{10}, x_{20}, x_{30}, x_{40}$ are:
$x_{10} = \frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\alpha\kappa\varepsilon}$,
$x_{20} = \frac{(1-\omega)(\eta+\omega)}{\alpha\kappa\varepsilon}$,
$x_{30} = \frac{1-\omega}{\alpha\kappa}$,
$x_{40} = \frac{(1-\omega)(\varepsilon\eta+\rho\eta+\rho\omega)}{\alpha\kappa\varepsilon\omega}$.
Hence it is proved that system (1)-(4) have two equilibrium points $P_1(1,0,0,0)$ and $P_2(x_{10}, x_{20}, x_{30}, x_{40})$.

## 2.3 | Stability Analysis

For Simplicity [10], we let:
$\frac{(\eta+\omega)(\varepsilon+\omega+\rho)}{\alpha\kappa\varepsilon} = \gamma$, $\frac{(1-\omega)(\eta+\omega)}{\alpha\kappa\varepsilon} = \beta$, $\frac{1-\omega}{\alpha\kappa} = \psi$, and $\frac{(1-\omega)(\varepsilon\eta+\rho\eta+\rho\omega)}{\alpha\kappa\varepsilon\omega} = \theta$.
Then we have,
$x_{10} = \gamma, x_{20} = \beta, x_{30} = \psi, x_{40} = \theta$.
For obtaining the variational matrix, we utilize the model equation (5)-(8) at the first equilibrium point $P_1$ we get,

$$J = \begin{pmatrix} -\omega & 0 & -\alpha\kappa & 0 \\ 0 & -(\varepsilon+\omega+\rho) & \alpha\kappa & 0 \\ 0 & \varepsilon & -(\eta+\omega) & 0 \\ 0 & \rho & \eta & -\omega \end{pmatrix}$$

Now let $\mu_1 = \varepsilon + \omega + \rho$ and $\mu_2 = \eta + \omega$ then the matrix becomes,

$$J(1,0,0,0) = \begin{pmatrix} -\omega & 0 & -\alpha\kappa & 0 \\ 0 & -\mu_1 & \alpha\kappa & 0 \\ 0 & \varepsilon & -\mu_2 & 0 \\ 0 & \rho & \eta & -\omega \end{pmatrix}$$

the eigenvalue of the Jacobian matrix is,

$$J - \lambda I_4 = \begin{pmatrix} -\omega - \lambda & 0 & -\alpha\kappa & 0 \\ 0 & -\mu_1 - \lambda & \alpha\kappa & 0 \\ 0 & \varepsilon & -\mu_2 - \lambda & 0 \\ 0 & \rho & \eta & -\omega - \lambda \end{pmatrix}$$

$$\Rightarrow \lambda_1 = -\omega, \tag{20}$$

$$\Rightarrow \lambda_2 = -\omega, \tag{21}$$

$\lambda_1$ and $\lambda_2$ are real values. The other two eigenvalues are calculated from 2x2 sub-matrix $A - \lambda I$

$$A - \lambda I = \begin{pmatrix} -\mu_1 - \lambda & \alpha\kappa \\ \varepsilon & -\mu_2 - \lambda \end{pmatrix} = 0$$

$\Rightarrow (\mu_1 - \lambda)(-\mu_2 - \lambda) - (\varepsilon)(\alpha\kappa) = 0$
$\Rightarrow \mu_1\mu_2 + \mu_1\lambda + \mu_2\lambda + \lambda^2 - \alpha\varepsilon\kappa = 0$
$\Rightarrow \mu_1\mu_2 + (\mu_1 + \mu_2)\lambda + \lambda^2 - \alpha\varepsilon\kappa = 0$
$\Rightarrow \lambda^2 + (\mu_1 + \mu_2)\lambda + \mu_1\mu_2 - \alpha\varepsilon\kappa = 0$
the roots of the equations are:

$$\lambda_3 = -\frac{1}{2}[\mu_1 + \mu_2 - \sqrt{(\mu_1 + \mu_2)^2 + 4\alpha\varepsilon\kappa - 4\mu_1\mu_2}] \tag{22}$$

$$\lambda_4 = -\frac{1}{2}[\mu_1 + \mu_2 + \sqrt{(\mu_1 + \mu_2)^2 + 4\alpha\varepsilon\kappa - 4\mu_1\mu_2}] \tag{23}$$

## 3 | Reproduction number

In the discipline of epidemiology, the reproduction proportion ($R0$) is crucial. It is described as "the typical number of secondary infections that result from introducing one infected individual into a population where everyone is susceptible". It is highly practical because it helps determine whether the infection spread among people [11].

Mathematical modeling can play a vital role in measuring conceivable illness control procedures by focusing on the crucial parts of a disease, determining verge quantities for disease survival, and assessing the impact of specific management systems. A very basic verge quantity is the Reproductive number. The epidemiological definition of $R_0$ is the average number of secondary infection cases formed by one infected person is known into a population of susceptible.

In 9152 George Macdonald used the first application of $R_0$ in epidemiology for constructed population models of the spread of malaria.

When the $R_0$ value is less than 1 ($R_0 < 1$) the infection will die out and the human individuals will stay good. But for the value of ($R_0 > 1$) the sickness will spread to people, making it difficult to control the epidemic.

Let **R** represent the rate of infections in the person acquired by the change from a susceptible individual to an infected individual or from an infected individual to a removed individual. **V** denotes the rate of transmission of individuals into or out of the infected [12].

$$R = \begin{pmatrix} \alpha\kappa x_1 x_3 \\ 0 \end{pmatrix}$$

$$V = \begin{pmatrix} x_2(\varepsilon + \omega + \rho) \\ -\varepsilon x_2 + x_3(\eta + \omega) \end{pmatrix}$$

$$R = \begin{pmatrix} \frac{\partial R_1}{\partial x_2} & \frac{\partial R_1}{\partial x_3} \\ \frac{\partial R_2}{\partial x_2} & \frac{\partial R_2}{\partial x_3} \end{pmatrix} = \begin{pmatrix} 0 & \alpha\kappa \\ 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} \frac{\partial V_1}{\partial x_2} & \frac{\partial V_1}{\partial x_3} \\ \frac{\partial V_2}{\partial x_2} & \frac{\partial V_2}{\partial x_3} \end{pmatrix} = \begin{pmatrix} \varepsilon+\omega+\rho & 0 \\ -\varepsilon & \eta+\omega \end{pmatrix}$$

then,

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

and

$$RV^{-1} = \frac{1}{(\varepsilon+\omega+\rho)(\eta+\omega)} \begin{pmatrix} \alpha\kappa\varepsilon & \alpha\kappa(\varepsilon+\omega+\rho) \\ 0 & 0 \end{pmatrix}$$

Here $RV^1$ have a eigenvalue 0 and basic reproduction number

$$R_0 = \frac{\alpha\kappa\varepsilon}{(\varepsilon+\omega+\rho)(\eta+\omega)}$$

As we let $\mu_1 = \varepsilon+\omega+\rho$ and $\mu_2 = \eta+\omega$ then

$$R_0 = \frac{\alpha\kappa\varepsilon}{\mu_1\mu_2}$$

and $\Rightarrow R_0\mu_1\mu_2 = \alpha\kappa\varepsilon$
Put the value of $\alpha\kappa\varepsilon$ in (22) and (23) we get,
$\lambda_3 = -\frac{1}{2}[\mu_1+\mu_2-\sqrt{(\mu_1-\mu_2)^2+4R_0\mu_1\mu_2}]$
$\lambda_4 = -\frac{1}{2}[\mu_1+\mu_2+\sqrt{(\mu_1-\mu_2)^2+4R_0\mu_1\mu_2}]$
For equilibrium point $P_2$, the variational matrix is

$$J_1 = \begin{pmatrix} -(\alpha\kappa\psi+\omega) & 0 & -\alpha\kappa\gamma & 0 \\ \alpha\kappa\psi & -\mu_1 & \alpha\kappa\gamma & 0 \\ 0 & \varepsilon & -\mu_2 & 0 \\ 0 & \rho & \eta & -\omega \end{pmatrix}$$

$$J_1 - \lambda I = \begin{pmatrix} -(\alpha\kappa\psi+\omega)-\lambda & 0 & -\alpha\kappa\gamma & 0 \\ \alpha\kappa\psi & -\mu_1-\lambda & \alpha\kappa\gamma & 0 \\ 0 & \varepsilon & -\mu_2-\lambda & 0 \\ 0 & \rho & \eta & -\omega-\lambda \end{pmatrix}$$

then,

$$\lambda_1 = -(\alpha\kappa\psi+\omega)$$
$$\lambda_2 = -\omega$$

the other two eigenvalues are

$$A - \lambda I = \begin{pmatrix} -\mu_1-\lambda & \alpha\kappa\gamma \\ \varepsilon & -\mu_2-\lambda \end{pmatrix} = 0$$

$\Rightarrow (-\mu_1-\lambda)(-\mu_2-\lambda) - \varepsilon(\alpha\kappa\gamma) = 0$
$\Rightarrow \mu_1\mu_2 + (\mu_1+\mu_2)\lambda + \lambda^2 - \varepsilon\alpha\kappa\gamma = 0$
$\Rightarrow \lambda^2 + (\mu_1+\mu_2)\lambda + \mu_1\mu_2 - \varepsilon\alpha\kappa\gamma = 0$
the roots of the equations are

$$\lambda_3 = -\frac{1}{2}[\mu_1+\mu_2-\sqrt{(\mu_1-\mu_2)^2+4\alpha\kappa\gamma\varepsilon-4\mu_1\mu_2}]$$
$$\lambda_4 = -\frac{1}{2}[\mu_1+\mu_2+\sqrt{(\mu_1-\mu_2)^2+4\alpha\kappa\gamma\varepsilon-4\mu_1\mu_2}]$$

then, the following situations are given below:

$$R_0 > 1 \rightarrow \lambda_3 > 0, \lambda_4 < 0$$

$$R_0 = 1 \rightarrow \lambda_3 = 0, \lambda_4 < 0$$
$$R_0 < 1 \rightarrow \lambda_3 < 0, \lambda_4 < 0$$

## 3.1 | Disease Endemic Equilibrium

$J_1(S_o, E_o, I_o, R_o)$ is disease endemic equilibrium with positive favourable components
i.e. $(S, E, I, R) \neq (0, 0, 0, 0)$

$$\omega - \alpha\kappa x_1 x_3 - \omega x_1 = 0 \tag{24}$$
$$\alpha\kappa x_1 x_3 - x_2\mu_1 = 0 \tag{25}$$
$$\varepsilon x_2 - x_3\mu_2 = 0 \tag{26}$$
$$\eta x_3 + \rho x_2 - \omega x_4 = 0 \tag{27}$$

Equation (26) $\Rightarrow$

$$\Rightarrow x_2^* = \frac{x_3^*\mu_2}{\varepsilon} \tag{28}$$

Put the value of $x_2^*$ in (25)
(25) $\Rightarrow \alpha\kappa x_1^* x_3^* - \frac{x_3^*\mu_1\mu_2}{\varepsilon} = 0$

$$\Rightarrow x_1^* = \frac{\mu_1\mu_2}{\alpha\kappa\varepsilon} = \frac{1}{R_0} \tag{29}$$

put the value of $x_1^*$ in (24)
$\Rightarrow \omega - \alpha\kappa\frac{1}{R_0}x_3^* - \omega\frac{1}{R_0} = 0$
$\Rightarrow \omega - \omega\frac{1}{R_0} = \alpha\kappa\frac{1}{R_0}x_3^*$
then

$$x_3^* = \frac{\omega}{\alpha\kappa}(R_0 - 1) \tag{30}$$

Now using (28) and (30) we get $x_2^*$,

$$x_2^* = \frac{\omega\mu_2(R_0 - 1)}{\alpha\kappa\varepsilon} \tag{31}$$

Substituting (29) and (30) in (27) we get $x_3^*$

$$x_3^* = \frac{(R_0 - 1)(\eta\varepsilon + \rho\mu_2)}{\alpha\kappa\varepsilon} \tag{32}$$

If $R_0 < 1$, the infection should reduced, while if $R_0 > 1$, the infection should settle itself [13].

## 3.2 | Positivity of Solution

The covid model will be essential epidemiological if the model system's solution has a non-negative I.C(initial condition) that will stay positive for all $t > 0$ [14].
**Theorem:**
$\forall\ t > 0$ and I.Cs (initial conditions) $P(0) \geq 0$ where $P(t) = (x_1, x_2, x_3, x_4)$ the solution of the model equations are positive for all $t > 0$.
**Proof:**
Consider the system's initial equation,

$$\frac{dx_1}{dt} = \omega N - \frac{\alpha\kappa x_1 x_3}{N} - \omega x_1$$
$$\frac{dx_1}{dt} = -\frac{\alpha\kappa x_1 x_3}{N} - \omega x_1 + \omega N$$

Now letting $\lambda_1(t) = \frac{\alpha\kappa x_3}{N}$ and $\lambda_2(t) = \omega N$, the equation becomes,

$$\frac{dx_1}{dt} = -\lambda_1(t)x_1 - \omega x_1 + \lambda_2(t)$$
$$\frac{dx_1}{dt} = \lambda_2(t) - (\lambda_1(t) + \omega)x_1$$

When we use integration to solve the aforementioned problem on both sides, it yields

$$\frac{d}{dt}[x_1(t)exp\{dt + \int_0^t \lambda_2(x_1)\,dx_1\}] = \lambda_2(t)exp\{\omega t + \int_0^t \lambda_1(x_1)\,dx_1\}$$

Hence,

$$[x_1(t_1)exp\{dt + \int_0^{t_1} \lambda_2(x_1)\,dx_1\} - x_1(0)] = \int_0^{t_1} \lambda_2 exp\{\omega x_1 + \int_0^{x_1} \lambda_1(x_1)\,dx_1\}dx_1$$

Thus, the solution of the above equation is
$x_1(t_1) = x_1(0)exp\{-(d(t_1) + \int_0^{t_1} \lambda_2(x_1)\,dx_1)\} + exp\{-(d(t_1) + \int_0^{t_1} \lambda_2(x_1)\,dx_1)\} * \int_0^{t_1} \lambda_2(t)exp\{\omega x_1 + \int_0^{x_1} \lambda_1(x_1)\,dx_1\}dx_1 > 0$
Similarly it can be shown that the equation $(x_2, x_3, x_4)$ are positive for $P > 0$ and $\forall\ t > 0$

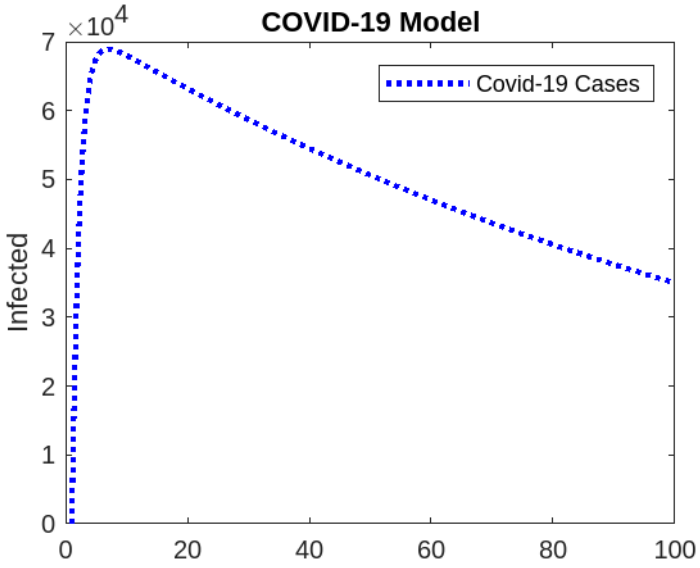


FIGURE 2. COVID-19 cases

## 4 | Numerical estimation of Parameters

The estimated values of the parameters are calculated in this model to aid with predictions. We used the World Health Organization (WHO) to make our approximations for COVID-19 modeling. Our model focuses on France country as shown in figure 2. All the estimated parametric values are listed in the table [15].

### 4.1 | Estimation of $\alpha$

$\alpha \approx 0.27926$ according to the WHO (World Health Organization) 27926 out of 100,000 people have been infected in France with COVID-19.

### 4.2 | Estimation of $\eta$

$\eta \approx 0.005$ is calculated by using WHO (World Health Organization) and some resources statistics that in serious cases, to recover from COVID-19 disease it takes fourteen to forty-two days. But, each person's risk of death from the covid virus will vary relying on their age, even if they have a basic health condition and even if they are vaccinated. whilst individuals who are vaccinated can still get infected, these "breakthrough" instances are unique, and vaccines badly lessen intense contamination and loss of life.

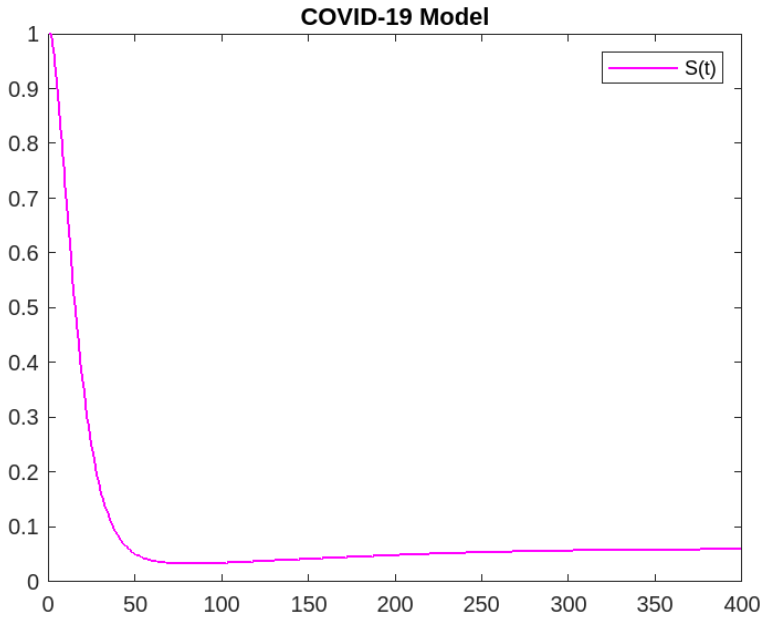


FIGURE 3. Susceptibility of COVID-19

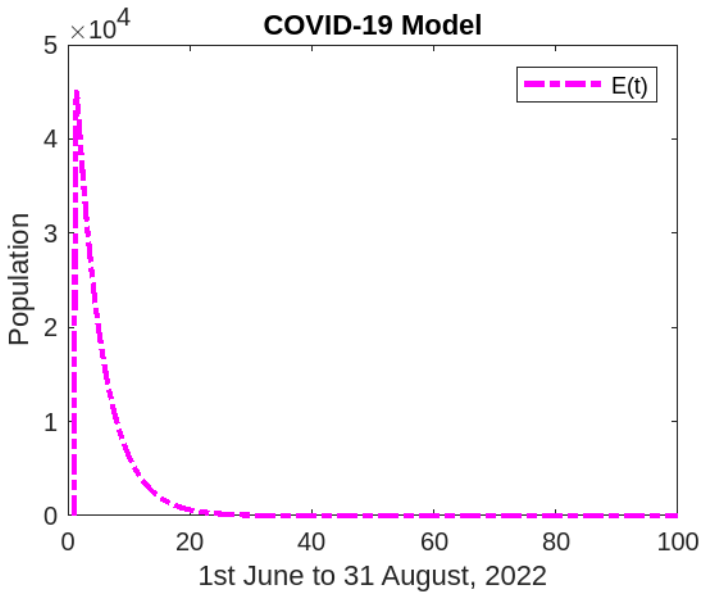


FIGURE 4. Exposed class of COVID-19

## 4.3 | Estimation of $\varepsilon$

$\varepsilon \approx 0.3165682$ is calculated by using the probable cases statistic of WHO (World Health Organization) and some other resources. For a monthly rate, divide the 37,988,187 cases per 100,000,000 by 12.

## 4.4 | Estimation of $\rho$

$\rho \approx 0.039661667$ is estimated by using the statistic of WHO (World Health Organization) and some other resources. We will split the projected number of suspected cases in France by the estimated number of known infected cases in France before multiplying it by 100,000. This was also divided by 12 to get the rate per month.

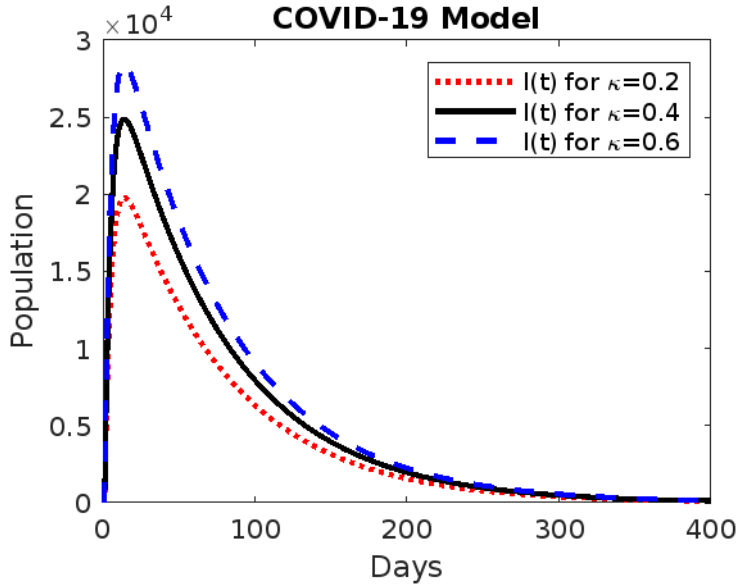


FIGURE 5. I(t) with different Social factors of COVID-19

### 4.5 | Estimation of $\kappa$

$\kappa$ is the estimation between 0 to 1. It is recommended by WHO (World Health Organization) center not to stay close to individuals who are suffering from COVID-19 disease excluding those individuals who are fully immunized or who have had COVID-19 illness during the past three months. Figure 5 illustrates the significant difference that societal factors have on the spread of the COVID-19 disease. We use $\kappa = 0.2$, $\kappa = 0.4$, and $\kappa = 0.6$ to see the difference in the transmission of COVID-19 disease.

### 4.6 | Estimation of $\omega$

$\omega$ is calculated by using the natural death statistic of WHO (World Health Organization) in France (157,364) divided by the population of France (65.6 million). This gave us a natural death rate [16].

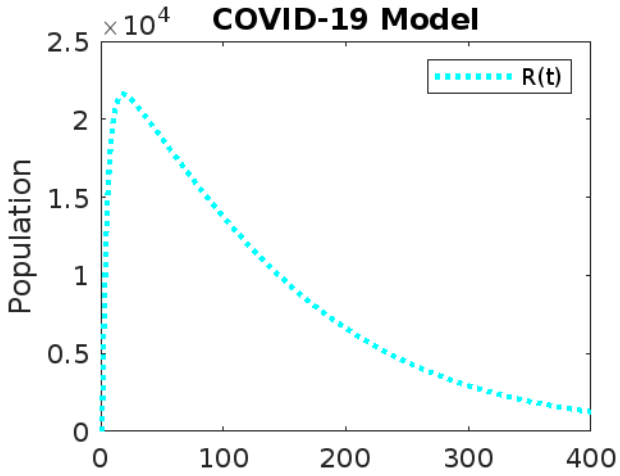


FIGURE 6. Removed class of COVID-19

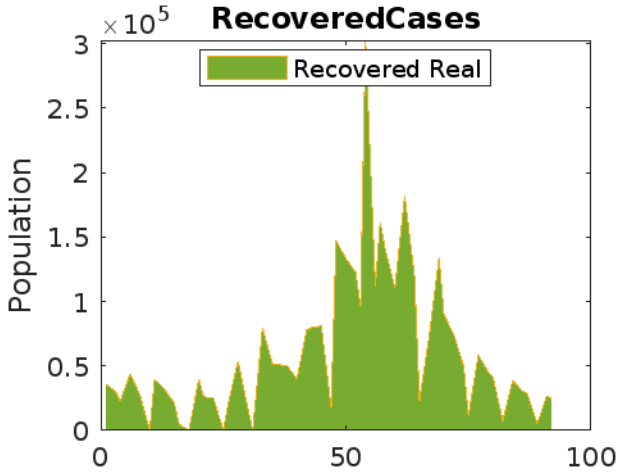


FIGURE 7. Recovered Real Data Graph for COVID-19

## 5 | Discussion

The perfect state of affairs is to maintain contamination of COVID-19 disease to a minimum and to try this we have to begin applying the following protocols [17].

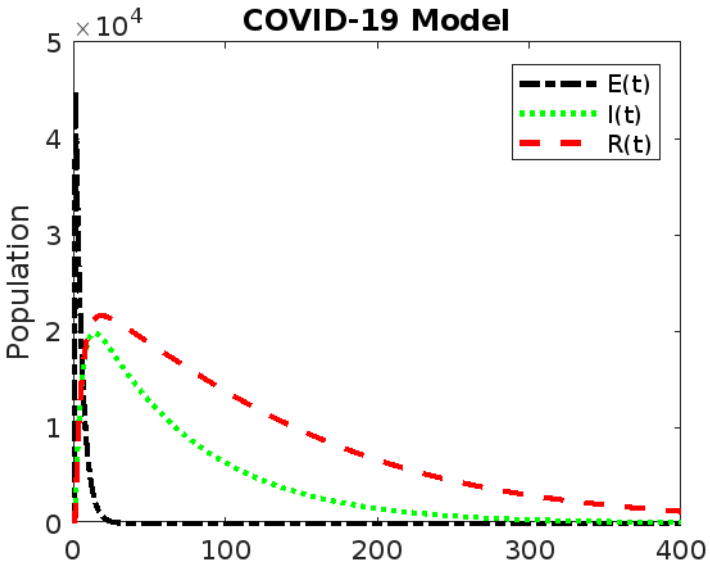


FIGURE 8. Exposed Infected Recovery of COVID-19

- Reduce the transmission rate ($\alpha < 0.27926$ ) from the susceptible individuals to the individuals that are exposed.
- Reduce the transmission rate of the exposed individuals ($\varepsilon < 0.3165682$) of the susceptible individuals. This will be achieved by way of making sure that infected individuals stay apart for a prolonged time from other individuals and remain in at-ease zones.
- Minimize the exposure to COVID-19 disease from the susceptible individuals over societal factors ($\kappa$).
- Raise useful resources for checking out COVID-19 disease to possibly ($\rho$) infectives to lower exposure rate of unknown touch with COVID-19.

- Raise transmission rate of recovery ($\eta$). This approach entails actual obligations and visits to clinical experts for a proper prognosis.

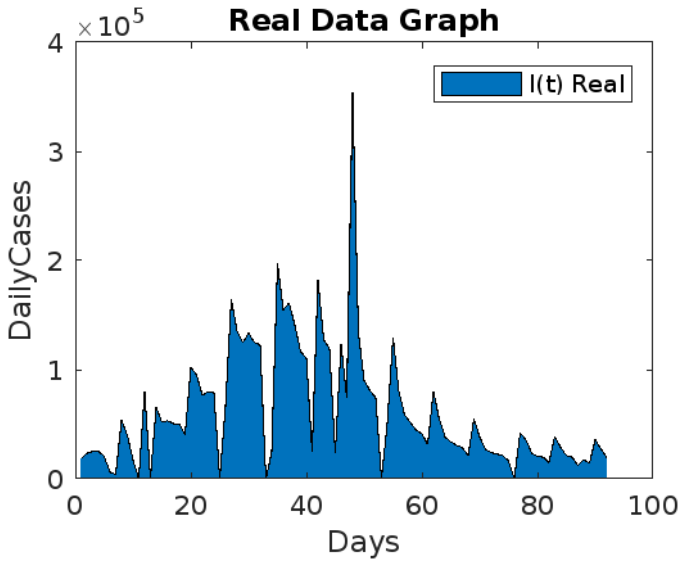


FIGURE 9. Infected Real Data Graph for COVID-19

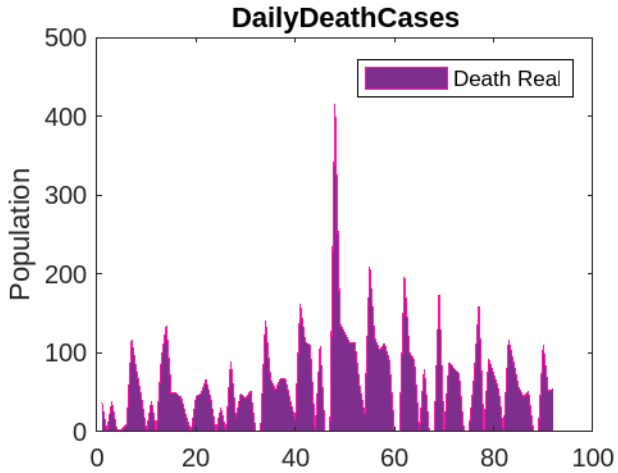


FIGURE 10. Death Real Data Graph for COVID-19

## 6 | Conclusion

The main task of this study was to understand, evaluate, analyze, and find the results of the epidemiological models. In this research study, the differential model of COVID-19 was constructed.
The stability analysis was done by applying the linearizing method and the positivity of the solution was proved. The model equations were solved numerically. The Runge-Kutta (RK4) method was employed to acquire the numerical solutions.
Moreover, the parametric study of coronavirus cases was performed. Coronavirus broadly depends on the infected individuals which have the ability to infect healthy populations immediately. Moreover, synchronization between the simulated outcomes/results and the real-time data of coronavirus cases verified the exactness of the model formulation. These findings support the assertion that the SEIR differential model can be utilized to study the spread of coronavirus disease. [18].
The Runge-Kutta (RK4) technique was practiced to obtain numerical results. The model is solved by applying

ode45 (Runge-Kutta of order four) in MATLAB. It is concluded from the results that The COVID-19 Pandemic's spread can be assessed using the differential order SEIR model.
This research study is an effort to bring aspects of infectious harmful diseases, particularly COVID-19, and try to enhance human health. Differential models are important to analyze the communication of diseases. The models play a vital role in studying the aspects to detach communicable diseases like COVID-19.
Valuable observation has been reaped through the evaluation of main aspects which include the simple reproductive number $R_0$, which suggests under which conditions a deadly disease of infection will appear in the population at threat. When $R_0 < 1$, The model system is designated as the disease-free state of equilibrium because it is locally asymptotically stable. Our analysis of $R_0$ reveals that the parameter $\kappa$, which measures an individual's rate of socializing, holds the key to reducing infection. The number of COVID-19-infected cases in France will decline when these parameters are reduced in rate.[19].

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## Data Availability

The datasets generated during and/or analyzed during the current study are not publicly available due to the privacy-preserving nature of the data but are available from the corresponding author upon reasonable request.

## Conflicts of Interest

The authors declare that there is no conflict of interest in the research.

## Ethical Approval

This article does not contain any studies with human participants or animals performed by any of the authors.

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