# Regression-Based Sensitivity Characterization of the SIR Model

Banen Kadhim Jawad and Ali Hussein Shuaa Al-Taie
*Department of Mathematics, College of Education for Pure Sciences, Wasit University, 52001 Al-Kut, Iraq*
*std.2024205.b.jawad@uowasit.edu.iq, alishuaa@uowasit.edu.iq*

Keywords: COVID-19, Iraq, Regression, Sensitivity Analysis, SIR.

Abstract: This work presents a statistical regression-based sensitivity analysis to extract interpretable analytical relationships between epidemiological parameters. Unlike previous studies that relied on numerical simulation of the SIR model, this provides a streamlined predictive framework for decision making and rapid evaluation. Mathematical models help us to study the transmission of infectious diseases and evaluate the effectiveness of public health strategies. Here, we emphasize the sensitivity of the Susceptible–Infected–Recovered (SIR) model. A linear regression equation is introduced to facilitate an analysis of the transmission of COVID-19 in Iraq. The model is modified with 2020 data provided by the Iraqi Ministry of Health, which corresponds to the first wave of the pandemic. The estimated value of the basic reproduction number ($R_0$) is about 2.5 which explains the fast exponential rise in infection numbers at this period. There is an inverse linear connection between the rate of recovery ($\gamma$) and the duration of the epidemic ($\hat{t}_d$) given by $\hat{t}_d = -432.87\gamma + 259.75$. The findings show that improved recovery processes also reduce the epidemic period. Furthermore, increasing the transmission coefficient ($\beta$) results in an infection peak more quickly, as indicated by $\hat{T}_{peak} = -163.36\beta + 93.54$. These results are important for improving epidemiological modeling and helping decision makers make important decisions about future disease outbreaks.

## 1 INTRODUCTION

COVID-19 is one of the most serious viral diseases of the modern period, caused by the SARS-CoV-2 virus [1]. It originally appeared in Wuhan, Hubei Province, China, in December 2019 and quickly spread throughout the world. The World Health Organization (WHO) declared COVID-19 a pandemic on March 11, 2020. This disease is transmitted through droplets and direct contact. This has led to millions of infections worldwide. Despite their inherent limitations, mathematical models have played a vital role in supporting health-related decision-making during the crisis by guiding preventive and therapeutic strategies [2]. Mathematical modeling can be used to estimate the basic reproduction number, which can be useful in assessing the likelihood and severity of an epidemic as well as in selecting the type and intensity of disease interventions [3],[4].

Beyond epidemiological modeling, related research has examined the spread of viruses through international trade [5]-[7], the clinical and biological characteristics of SARS-CoV-2 and its associated illness [8]-[10], the estimation of effective reproduction numbers [11], [12], and the environmental determinants of transmission, including the link between climatic conditions and virus spread [13].

Various sensitivity analysis approaches, including local and global methods, have been widely applied to investigate the influence of model parameters and initial conditions in epidemiological models such as SIR and SEIR. These methods aim to identify key factors affecting the basic reproduction number ($R_0$) and to support effective decision-making in the prevention and control of infectious diseases such as COVID-19 [14], [15]. In this paper, we applied linear regression to the mathematical model to study the effect of the underlying parameters, including the transmission rate ($\beta$), recovery rate ($\gamma$), and time ($t$). The year 2020 witnessed the rapid spread of the COVID-19 pandemic in Iraq and worldwide, leading to serious health crises and a public health emergency. The relationship between these variables can be tested using several regression methods that exist today. Among the available regression methods, a straight-line relationship is the most straightforward [16]. The model is applied to Iraqi data from the first

wave of the pandemic in 2020, gathered from the Iraqi Ministry of Health reports.

## 2 SIR MODEL FOR COVID-19

This model, one of the most important epidemiological models, was developed by Kermack and McKendrick in 1927. It has been applied to many serious infectious diseases such as avian influenza, cholera, plague, and others. This model played a key role in the COVID-19 pandemic, as it divided the population into three groups [17]:

- $S(t)$ represents the susceptible population, their number is directly linked to the rate of transmission. When they contact infected people, they become infected and leave this group, reducing the number of susceptible;
- $I(t)$ indicates the population that is sick, including those who have the potential to spread the illness. The spread of epidemics is mostly caused by this class. Its size grows as a result of new infections and shrinks as afflicted people heal;
- $R(t)$ represents the removed population, which includes those who have recovered with permanent immunity, those who have been permanently segregated, and those who have died from the illness. In all of these circumstances, these individuals no longer contribute to the infection's spread.

For the SIR model, the three variables $S(t)$, $I(t)$ and $R(t)$ are governed by the following differential equation:

$$\frac{dS(t)}{dt} = \frac{-\beta\, S(t)\, I(t)}{N} \quad (1)$$

$$\frac{dI(t)}{dt} = \frac{\beta\, S(t)\, I(t)}{N} - \gamma I(t) \quad (2)$$

$$\frac{dR(t)}{dt} = \gamma I(t) \quad (3)$$

where, $\beta$: The rate of transmission, which represents the rate of contact between susceptible and infected individuals, that leads to infection. $\gamma$: recovery rate, describes the speed at which infected individuals recover and move into the recovered category, $t$: time variable representing the progression of the epidemic (measured in days), $N$: total population size.

$S(t)$, $I(t)$, and $R(t)$ are functions of time, while $\beta$ and $\gamma$ are assumed to be constant throughout the epidemic period. During the period of disease transmission, population dynamics such as birth, death, and migration are neglected. Consequently, the total population within the epidemic region is assumed to remain constant, such that $N = S(t) + I(t) + R(t)$.

## 3 ALGORITHMS FOR SIR SIMULATION AND REGRESSION ANALYSIS

The overall computational workflow used for the SIR simulation, sensitivity analysis, and regression modeling is summarized in the following algorithmic procedure:

1) Collect official COVID-19 data for Iraq during the first wave of 2020 from the Iraqi Ministry of Health.
2) Determine the total population $N$ and specify the initial conditions $S(0)$, $I(0)$, and $R(0)$ from the reported data.
3) Formulate the classical SIR model using the system of differential equations governing the susceptible, infected, and recovered populations.
4) Assign baseline epidemiological parameters for the transmission rate $\beta$ and recovery rate $\gamma$.
5) Solve the SIR system numerically in MATLAB using the ODE45 solver over the selected simulation period.
6) Compute the basic reproduction number $R_0 = \frac{\beta}{\gamma}$ using the estimated baseline parameters.
7) Perform sensitivity analysis by varying the recovery rate $\gamma$ while keeping the transmission rate $\beta$ fixed and record the corresponding epidemic duration.
8) Apply linear regression to evaluate the relationship between the recovery rate $\gamma$ and the epidemic duration $t_d$.
9) Vary the transmission rate $\beta$ while keeping the recovery rate $\gamma$ fixed, and determine the corresponding time required to reach the epidemic peak $T_{peak}$.
10) Apply linear regression to examine the relationship between the transmission rate $\beta$ and the peak time $T_{peak}$.
11) Interpret the regression equations and simulation results to describe how changes in key epidemiological parameters affect the duration and peak timing of the epidemic.

12) Comparing the relationships obtained with epidemiological behavior in Iraq, in addition to discussing their importance for public health forecasting and planning.

# 4 MODEL APPLICATION TO IRAQI COVID-19 DATA

The year 2020 was marked by the rapid global spread of COVID-19, including in Iraq, which triggered significant health crises and widespread public health concerns. Serious health crises and a public health emergency in Iraq and throughout the world. To study the epidemic's behavior, the SIR model is applied using 2020 COVID-19 infection data in Iraq. The COVID-19 data used in this study were obtained from official reports issued by the Iraqi Ministry of Health during the first wave of the pandemic in 2020, as shown in Table 1. The dataset comprises daily reported instances of confirmed infected and recovered cases which were compiled to initialize and calibrate the parameters of the SIR model. This section aims to provide a description and an overview of the pattern of COVID-19 disease in Iraq. The purpose of using the 2020 Iraq data is not to present a new epidemiological dataset, but rather to provide a representative case study to validate the proposed regression-based sensitivity framework and demonstrate its practical applicability.

Table 1: Initial conditions of the SIR model using 2020 COVID-19 data for Iraq (Iraqi Ministry of Health).

| Compartment | Initial value |
|---|---|
| Susceptible $S(0)$ | 39,004,055 |
| Infected $I(0)$ | 595,291 |
| Recovered $R(0)$ | 550,654 |
| Total population $(N)$ | 40,150,000 |

A simulation of the COVID-19 model was conducted for the first wave in Iraq. The transmission rate was set to $\beta = 0.1785$ for the baseline simulation. This value was estimated by fitting the exponential growth rate of confirmed cases during the early phase of the outbreak to the standard relation $\beta \approx r + \gamma$, where r is the observed daily growth rate of infections reported in the Iraqi Ministry of Health data. The recovery rate was fixed at $\gamma = 0.0714$ day$^{-1}$ based on an average recovery period of 14 days. Over 200 days, the temporal dynamics of the susceptible, infected, and recovered groups are presented in Figure 1. At the beginning of the outbreak, infections grow rapidly until a maximum level is reached, followed by a steady decrease. Meanwhile, the recovered population shows a continuous upward trend. Such behavior represents the typical evolution of an epidemic within the SIR framework. (using MATLAB). The rates extracted from the data of the Iraqi Ministry of Health ($\beta = 0.1785, \gamma = 0.0714$) constitute the focal point of Section 4.2, where sensitivity analysis was conducted based on them and then regression equations were extracted into experimental standard.

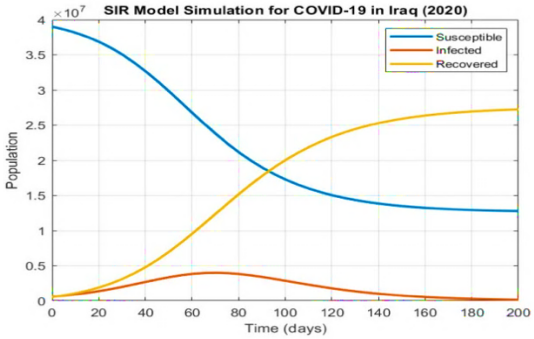


Figure 1: SIR Model Simulation for COVID-19 in Iraq (2020).

## 4.1 Estimating the Basic Reproduction Number ($R_0$)

The basic reproduction number is a key parameter in epidemiology, representing the average number of people who can be infected from a single infected person within a susceptible population. Based on the equations of the SIR (1)-(3) model, the basic reproduction number is calculated according to the following relationship [18]:

$$R_0 = \frac{\beta}{\gamma} \tag{4}$$

Using the previously defined parameter values ($\beta = 0.1785$ and $\gamma = 0.0714$), the basic reproduction number is calculated as:

$$R_0 = \frac{0.1785}{0.0714} \approx 2.5 \tag{5}$$

Since the extracted $R_0$ value ($R_0 > 1$) is greater than one, This value indicates that each infected person transmitted the infection to two or three people until it reached the peak of the disease and then gradually decreased. This explains the rapid exponential spread during the first wave of the epidemic in Iraq.

## 4.2 Sensitivity Analysis and Statistical Regression of SIR Parameters

In this section, regression analysis was employed to investigate the sensitivity of the SIR model to variations in the transmission and recovery rates. Numerical simulations were performed in MATLAB using the ODE45 solver. The sensitivity of SIR model outcomes to variations in transmission and recovery parameters aligns with recent stochastic extensions of the model [19]. To examine the effect of the recovery rate on epidemic duration, selected values of $\gamma$ were associated with the corresponding epidemic duration values. Intermediate points were generated using piecewise cubic interpolation (PCHIP) to provide a smoother representation of the trend. A linear regression model was then applied to the interpolated data using MATLAB's fitlm function. For each selected parameter value, the corresponding epidemic metric (such as duration or peak time) was extracted from the simulation results, forming paired data points (parameter, response), which were then used as input for the regression model.

Table 2: Simulated values of epidemic duration ($t_d$) for different recovery rates ($\gamma$) using the SIR model.

| Recovery rate ($\gamma$) | Number of sick days ($t_d$) |
|---|---|
| 0.0500 | 251.00 |
| 0.0556 | 239.14 |
| 0.0611 | 228.81 |
| 0.0667 | 222.23 |
| 0.0722 | 221.00 |
| 0.0778 | 221.05 |
| 0.0833 | 221.26 |
| 0.0889 | 221.75 |
| 0.0944 | 222.62 |
| 0.1000 | 224.00 |

Table 2 and Figure 2 demonstrate a clear negative linear relationship between the recovery rate ($\gamma$) and the epidemic duration. As $\gamma$ increases, the duration of the epidemic decreases, indicating that improved recovery processes and healthcare interventions can significantly shorten the outbreak period. It should be noted that this negative trend is monotonic only for γ below approximately 0.072; for higher recovery rates the simulated duration stabilizes and rises marginally (Table 2), which is attributable to the fixed case-count threshold used to define "epidemic duration" interacting with the faster depletion of the infected compartment. Consequently, the linear regression below should be interpreted as a local approximation valid over the tested range of γ rather than a globally monotonic law. This relationship is captured by the regression model:

$$\hat{t}_d = -432.87\gamma + 259.75 \quad (6)$$

The values are obtained from numerical simulations of the SIR model.

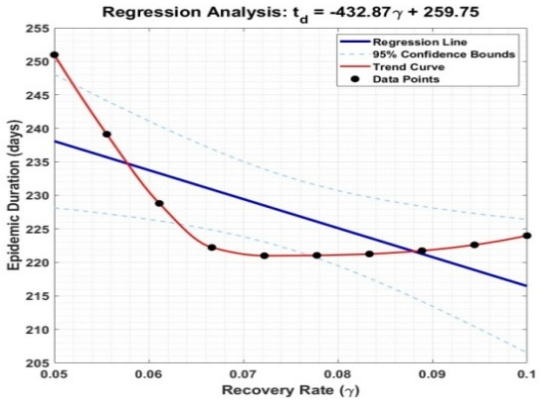


Figure 2: Numerical simulation results showing the effect of changing the recovery rate on the duration of the epidemic with a constant transmission rate $\beta$ = 0.17 (using MATLAB) .

Table 3 and Figure 3 illustrate a strong inverse relationship between the transmission rate ($\beta$) and the time required to reach the epidemic peak. Increasing $\beta$ leads to a faster spread of infection and an earlier peak, which highlights the importance of controlling transmission to delay and manage healthcare system pressure. This behavior is described by the regression model:

$$\hat{T}_{peak} = -163.36\beta + 93.54 \quad (7)$$

The near-perfect linear fit reflects the structural regularity of the SIR model under systematic parameter variation, consistent with the model's deterministic nature. This provides a robust analytical benchmark for sensitivity characterization.

Table 3: The relationship between transmission rate ($\beta$) and time to peak ($T_{peak}$) at $\gamma$ = 0.07.

| Transmission rate ($\beta$) | Peak time ($T_{peak}$) (days) |
|---|---|
| 0.15 | 69.04 |
| 0.20 | 60.87 |
| 0.25 | 52.70 |
| 0.30 | 44.53 |
| 0.35 | 36.36 |
| 0.40 | 28.19 |
| 0.45 | 20.02 |
| 0.50 | 11.85 |

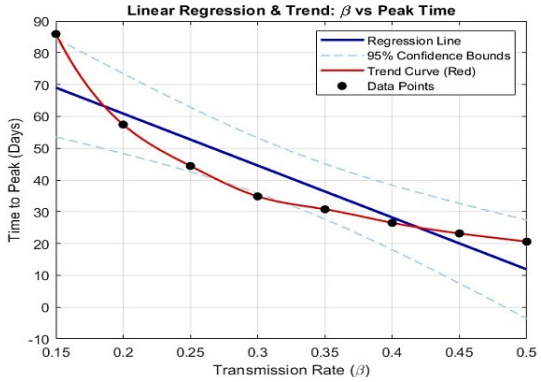


Figure 3: Numerical simulation results showing the impact of varying transmission rate ($\beta$) on the epidemic peak time ($T_{peak}$) for a fixed recovery rate $\gamma$ = 0.07 (using MATLAB).

Slope: $m = -163.36$ means for every 0.1 increase of transmission rate, the peak of the infection wave is accelerated by about 16.3 days.

To assess the reliability of the regression results, statistical validation was performed using confidence interval analysis. The fitted linear models were accompanied by 95% confidence bounds. The confidence intervals shown in Figures 2 and 3 indicate the reliability of the regression models. These bounds provide an estimate of the uncertainty associated with the regression predictions. Despite this limitation, the regression results are useful for capturing the overall trend and sensitivity of the epidemic dynamics with respect to changes in key parameters such as the transmission rate ($\beta$) and recovery rate ($\gamma$).

## 4.3 Error Analysis

To evaluate the regression models, Root Mean Square Error (RMSE) was computed as the criterion of the evaluation. It provides the difference between numerical simulation estimates and estimated values that are calculated from the regression equations. The absolute and squared errors between the simulated and predicted peak time values for the transmission rates are summarized in Table 4. Also, the RMSE produced points to a strong convergence between regression and the numerical numbers for the model.

$$RMSE = \sqrt{\frac{1}{8}\sum_{i=1}^{8}\left(T_{peak,i} - \hat{T}_{peak,i}\right)^2}$$

$$= \sqrt{\frac{0.00024}{8}} = \sqrt{0.00003} \approx 0.0055$$

Table 4: Error analysis for the regression model relating transmission rate ($\beta$) to peak time ($T_{peak}$)

| $\beta$ | $T_{peak}$ | $\hat{T}_{peak}$ | Error | Error² |
|---|---|---|---|---|
| 0.15 | 69.04 | 69.036 | 0.004 | 0.000016 |
| 0.20 | 60.87 | 60.868 | 0.002 | 0.000004 |
| 0.25 | 52.70 | 52.700 | 0.000 | 0.000000 |
| 0.30 | 44.53 | 44.532 | -.002 | 0.000004 |
| 0.35 | 36.36 | 36.364 | -.004 | 0.000016 |
| 0.40 | 28.19 | 28.196 | -.006 | 0.000036 |
| 0.45 | 20.02 | 20.028 | -.008 | 0.000064 |
| 0.50 | 11.85 | 11.860 | -.010 | 0.000100 |

The RMSE is small (≈0.0055 days), implying that the regression model and the simulated data agreed remarkably well. This points towards the linear regressor model predicting the transmission rate versus peak period properly with respect to the time. A comparable operation was conducted for the recovery rate. Error analysis of the relationship between the recovery rate and the epidemic duration is summarized in Table 5. A higher RMSE compared with Table 4 means that the linear model is less applicable to this relationship.

Table 5: Error analysis for the regression model relating recovery rate ($\gamma$) to epidemic duration ($t_d$).

| $\gamma$ | $t_d$ | $\hat{t}_d$ | Error | Error² |
|---|---|---|---|---|
| 0.0500 | 251.00 | 238.1065 | 12.8935 | 166.2423 |
| 0.0556 | 239.14 | 235.6828 | 3.4572 | 11.9522 |
| 0.0611 | 228.81 | 233.3024 | -4.4924 | 20.1817 |
| 0.0667 | 222.23 | 230.8786 | -8.6486 | 74.7983 |
| 0.0722 | 221.00 | 228.4980 | -7.4980 | 56.2198 |
| 0.0778 | 221.05 | 226.0741 | -5.0241 | 25.2416 |
| 0.0833 | 221.26 | 223.6937 | -2.4337 | 5.9230 |
| 0.0889 | 221.75 | 221.2699 | 0.4801 | 0.2305 |
| 0.0944 | 222.62 | 218.8893 | 3.7307 | 13.9181 |
| 0.1000 | 224.00 | 216.4630 | 7.5370 | 56.8064 |

$$RMSE = \sqrt{\frac{1}{10}\sum_{i=1}^{8}\left(t_{d,i} - \hat{t}_{d,i}\right)^2}$$

$$= \sqrt{\frac{431.514}{10}} = \sqrt{43.1514} \approx 6.5686$$

An RMSE value of about 6.57 days is obtained for the regression model describing the relationship between recovery rate and epidemic duration. This result suggests that the model represents the general pattern of the data, although the fit is less precise than that observed for transmission rate and

peak time. Such a discrepancy indicates that the relationship is not strictly linear.

# 5 DISCUSSION

The results clearly show that for the key parameters of the SIR framework, relationships are obvious. It should not be taken that linear tendencies associated with the epidemic duration at that time, and between β and peak timing, are necessarily given from the $\gamma$ model, because, even though the model is nonlinear, it is an approximation to a locally distributed feature at certain parameter ranges. In addition, the high determination coefficient ($R_0 \approx 1$), consistent with findings from recent SIR forecasting studies [20]. does not also reflect strong real-world validity. Mostly it concerns the deterministic configuration of the simulations which does not consider randomness or data uncertainty.

Therefore, the results serve as conceptual explanations for parameter sensitivity, not accurate predictions. These results are also consistent with previous studies of the SIR model, as epidemic dynamics are highly sensitive to infection and recovery rates [14]. However, important considerations of the real world, including demographic variability and behavioral responses, are not within this model. Consequently, such omissions could compromise the reliability of the relationships with respect to actual epidemic cases.

# 6 CONCLUSIONS

This study used statistical linear regression to characterize the relationship of COVID-19 dynamics with official data of the first wave in Iraq, with the classical SIR mathematical model as a basic framework. The analyses identified essential mathematical associations between epidemiological variables, namely transmission rate ($\beta$) and recovery rate ($\gamma$), and their direct effects in predicting pandemic peak and duration. The conclusion is that the duration during pandemic is inversely proportional to recovery rate, denoted as the regression model $t$ = -432.87γ + 259.75; the negative slope implies that increasing the recovery rate of infected individuals (due to enhanced medical measures and treatment) decreases the duration of disease and consequently end of the pandemic. Moreover, the analysis implied that the speed of transmission rate corresponded to the shorter time to the peak as indicated in the regression equation ($T_{\text{peak}}$ = -163.36$\beta$ + 93.54) and the negative slope suggested that the epidemiological curve peaks earlier when the transmission rate rises.

Such results provide important forecasting parameters for health authorities to make effective public health policy interventions and allocate healthcare resources during outbreak episodes or to improve treatment and control curfews for future outbreaks. Future studies could broaden to incorporate vaccination effects, viral mutations, and spatial modeling to better track areas with different disease prevalence. Hybrid approaches combining SIR models with machine learning techniques have shown promise in improving parameter estimation accuracy [21].

# REFERENCES


[1] X. Li et al., "Evolutionary history, potential intermediate animal host, and cross-species analyses of SARS-CoV-2," J. Med. Virol., vol. 92, no. 6, pp. 602-611, Jun. 2020, [Online]. Available: https://doi.org/10.1002/jmv.25731.

[2] A. Msmali, M. Zico, I. Mechai, and A. Ahmadini, "Modeling and simulation: A study on predicting the outbreak of COVID-19 in Saudi Arabia," Discrete Dyn. Nat. Soc., vol. 2021, no. 1, Art. no. 5522928, 2021, [Online]. Available: https://doi.org/10.1155/2021/5522928.

[3] B. Tang et al., "Estimation of the transmission risk of the 2019-nCoV and its implication for public health interventions," J. Clin. Med., vol. 9, no. 2, Art. no. 462, Feb. 2020, [Online]. Available: https://doi.org/10.3390/jcm9020462.

[4] S. Misra, "Mathematical modeling of infectious disease spread using the SIR model," Biomed. Res., Nov. 2024, [Online]. Available: https://biomedres.us/fulltexts/BJSTR.MS.ID.009302.php.

[5] E. Bontempi and M. Coccia, "International trade as critical parameter of COVID-19 spread that outclasses demographic, economic, environmental, and pollution factors," Environ. Res., vol. 201, Art. no. 111514, Sep. 2021, [Online]. Available: https://doi.org/10.1016/j.envres.2021.111514.

[6] E. Bontempi, "Commercial exchanges instead of air pollution as possible origin of COVID-19 initial diffusion phase in Italy: More efforts are necessary to address interdisciplinary research," Environ. Res., vol. 188, Art. no. 109775, Oct. 2020, [Online]. Available: https://doi.org/10.1016/j.envres.2020.109775.

[7] E. Bontempi, M. Coccia, S. Vergalli, and A. Zanoletti, "Can commercial trade represent the main indicator of the COVID-19 diffusion due to human-to-human interactions? A comparative analysis between Italy, France, and Spain," Environ. Res., vol. 201, Art. no. 111529, 2021, [Online]. Available: https://doi.org/10.1016/j.envres.2021.111529.

[8] U. Anand et al., "Novel coronavirus disease 2019 (COVID-19) pandemic: From transmission to control with an interdisciplinary vision," Environ. Res., vol. 197, Art. no. 111126, 2021, [Online]. Available: https://doi.org/10.1016/j.envres.2021.111126.

[9] E. Bontempi, S. Vergalli, and F. Squazzoni, "Understanding COVID-19 diffusion requires an interdisciplinary, multi-dimensional approach," Environ. Res., vol. 188, Art. no. 109814, 2020, [Online]. Available: https://doi.org/10.1016/j.envres.2020.109814.

[10] K. Al Huraimel, M. Alhosani, S. Kunhabdulla, and M. H. Stietiya, "SARS-CoV-2 in the environment: Modes of transmission, early detection and potential role of pollutions," Sci. Total Environ., vol. 744, Art. no. 140946, 2020, [Online]. Available: https://doi.org/10.1016/j.scitotenv.2020.140946.

[11] J. Yuan, M. Li, G. Lv, and Z. K. Lu, "Monitoring transmissibility and mortality of COVID-19 in Europe," Int. J. Infect. Dis., vol. 95, pp. 311-315, 2020, [Online]. Available: https://doi.org/10.1016/j.ijid.2020.03.050.

[12] Y. Liu, A. A. Gayle, A. Wilder-Smith, and J. Rocklöv, "The reproductive number of COVID-19 is higher compared to SARS coronavirus," J. Travel Med., vol. 27, no. 2, pp. 1-4, Mar. 2020, [Online]. Available: https://doi.org/10.1093/jtm/taaa021.

[13] D. K. Rosario, Y. S. Mutz, P. C. Bernardes, and C. A. Conte Junior, "Relationship between COVID-19 and weather: Case study in a tropical country," Int. J. Hyg. Environ. Health, vol. 229, Art. no. 113587, 2020, [Online]. Available: https://doi.org/10.1016/j.ijheh.2020.113587.

[14] C. Ma et al., "Understanding dynamics of pandemic models to support predictions of COVID-19 transmission: Parameter sensitivity analysis of SIR type models," IEEE J. Biomed. Health Inform., vol. 26, no. 6, pp. 2458-2468, Jun. 2022, [Online]. Available: https://doi.org/10.1109/JBHI.2022.3168825.

[15] A. Lawan, A. Salihu, I. Ahmad, J. Abdullahi, and U. Abdullahi, "Qualitative and sensitivity analysis on simple epidemic model (SIR-model): Ensuring well-posedness and stability," J. Stat. Sci. Comput. Intell., vol. 1, no. 4, pp. 312-320, 2025, [Online]. Available: https://doi.org/10.64497/jssci.49.

[16] S. Abolmaali and S. Shirzaei, "A comparative study of SIR model, linear regression, logistic function, and ARIMA model for forecasting COVID-19 cases," AIMS Public Health, vol. 8, no. 4, p. 598, 2021, [Online]. Available: https://doi.org/10.3934/publichealth.2021048.

[17] H. H. Weiss, "The SIR model and the foundations of public health," Mater. Mat., no. 3, pp. 1-17, 2013.

[18] B. Palmieri and M. Vadala, "Oral THC: CBD cannabis extract in main symptoms of Alzheimer disease: Agitation and weight loss," Clin. Ter., vol. 174, no. 1, pp. 53-60, 2023, [Online]. Available: https://doi.org/10.7417/CT.2023.2497.

[19] C. Gouriéroux and Y. Lu, "Susceptible-infected-recovered model with stochastic transmission," Can. J. Stat., vol. 53, no. 2, p. e11835, 2025, [Online]. Available: https://doi.org/10.1002/cjs.11835.

[20] T. Sudhakar, A. Bhansali, J. Walkington, and D. Puelz, "The disutility of compartmental model forecasts during the COVID-19 pandemic," Front. Epidemiol., vol. 4, Art. no. 1389617, 2024, [Online]. Available: https://doi.org/10.3389/fepid.2024.1389617.

[21] S. Rana, "Bridging mechanistic and data-driven models: A novel framework for epidemic forecasting," J. Appl. Stat.: Environ. Stat. Data Sci., vol. 1, no. 1-4, pp. 5-18, 2025, [Online]. Available: https://doi.org/10.1080/29984688.2025.2511594.