Chapter 16
Modelling and Sensitivity Analysis of COVID-19 Under the Influence of Environmental Pollution

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Abstract The ongoing COVID-19 pandemic emerged as one of the biggest challenges of recent times. Efforts have been made from different corners of the research community to understand different dimensions of the disease. Some theoretical works have reported that disease becomes severe in the presence of environmental pollution. In this work, we propose a nonlinear mathematical model to study the influence of air pollution on the dynamics of the disease. The basic reproduction number plays a vital role in predicting the future of an epidemic. Therefore, we obtain the expression of the basic reproduction number and performed a detailed sensitivity and uncertainty analysis. The values of partial rank correlation coefficients (PRCC) have been calculated corresponding to six critical parameters. The positive values of PRCC for pollution-related parameters depicts that pollution enhances the chances of a rapid spread of COVID-19.

Keywords COVID-19 · Environmental pollution · Mathematical model · The basic reproduction number · Sensitivity analysis

Introduction

The ongoing pandemic of COVID-19 was originated in Wuhan (China). Since then, it has invaded almost every country across the globe and created unprecedented stress on medical facilities and infrastructure. Due to its severity, the World Health Organization (WHO) first declared a Public Health Emergency of International Concern

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on 30 January 2020, and subsequently a pandemic on 11 March 2020 [1]. Coronaviruses, responsible for COVID-19, belong to the Coronaviridae family in the Nidovirales order [2]. Due to the presence of crown-like spikes on its outer surface, it is known as coronavirus. The coronaviruses diameter ranges between 65–125 nm and contain a single-stranded RNA as a nucleic material. The coronaviruses family has four subgroups namely; alpha (α), beta (β), gamma (γ) and delta (δ) [2]. Before 2002, it was believed that coronaviruses infect only animals. The 2002 outbreak (in Guangdong, China) of severe acute respiratory syndrome (SARS) was the first event caused by SARS-CoV [3]. After 2002, the SARS outbreak, the world faced an outbreak of Middle East respiratory syndrome coronavirus (MERS-CoV) caused by the coronaviruses family [4].

The coronavirus (responsible for COVID-19) initially transmitted to humans from the Wuhan seafood market [5, 6]. Later, it was established that the disease can also spread through human to human transmission mode. As per scientific and clinical research, the transmission of the coronavirus from infected individuals to healthy individuals spreads due to physical contacts and droplets in the air due to sneezing and coughing of an infected person [7]. The primary symptoms of COVID-19 are approximately 95% similar to SARS coronavirus and include dry cough, abnormality in body temperature, breathing difficulty and bilateral lung infiltration [7, 8]. Moreover, the role of environmental pollution on the spread of waterborne diseases has also been studied [9–11]. The correlation between exposure to air pollution and COVID-19 mortality poses a serious question in front of the research community. Owning to this, attempts have been made to identify the possible impact of environmental pollution on the spread of COVID-19 and COVID-19 mortalities. In particular, the study carried out by Conticini et al. [12] explored the correlation between air pollution and COVID-19 mortality. They further observed that the regions with a high level of pollution (Lombardy and Emilia Romagna) are also registered the maximum number of deaths due to COVID-19. Further, based on the data, the study concludes that people living in areas with high pollutants concentration may easily fall prey to respiratory disease. The work carried out by Zoran et al. [13] investigates the correlation between high transmissibility and lethality COVID-19 and the surface air pollution in the Milan metropolitan area, Lombardy region, Italy. To achieve this goal, authors collected daily data (from 1 January to 30 April 2020) of average concentrations of $PM_{2.5}$ and PM_{10} and maxima PM_{10} ground-level atmospheric pollutants and air quality and climate variables (e.g., daily average temperature, wind speed, relative humidity, atmospheric pressure field, etc.). The study demonstrates the strong influence of daily averaged ground levels of particulate matter concentrations on COVID-19 cases outbreaks in Milan. The study, further, concludes that chronic or short-term exposure to particulate matter $PM_{2.5}$ or PM_{10} carrying different viruses or bacteria has a major negative impact on the human immune system and thus makes people vulnerable towards COVID-19.

Mathematical modelling of infectious disease provides critical information about its transmission mechanism. The results obtained on the long-term dynamics of an epidemic through the analysis of the mathematical model are crucial in the planning intervention programs [14]. In case of COVID-19, many mathematical models have been deployed to study the difference dimensions of the disease (see [15–22, 22–26] and references cited therein).

In [21], the authors proposed a mathematical model to make short-term predictions about the future of COVID-19 in India, Argentina, Mexico and South Africa. Moreover, they also explore the conditions under which the proposed model exhibits backward bifurcation. In [23], a mathematical model is proposed to study the role of different nonpharmaceutical intervention policies (e.g. contact tracing, quarantine, social distancing, isolation, the use of face masks, etc.) in controlling the disease. With the help of the data of COVID-19 for USA (US), the authors demonstrate that these intervention strategies are successful in controlling the ongoing pandemic. In [24], the authors investigate the importance of the lockdown in controlling the wave of COVID-19 with the help of a mathematical model and simulating the same over the real data available for Florida, Arizona, New York and for the entire country. The study also underscores the importance of the identification of pre-symptomatic and asymptomatic patients. Further, authors also observe that control of COVID-19 will be significantly achieved if the implementation of lockdown is complemented by the use of face masks. In [17], the authors used a simple SIR epidemic model to study the COVID-19 scenario in France, China and Italy. Through the simulation of the model on the available data for the three countries, the authors identify that the recovery rate is the same for all the three countries. On the other hand, a very high variability has been observed among the three countries in terms of disease-induced death and disease transmission rate. In [22], authors extended the generic SEIR epidemic model by including a separate compartment for the super spreader, hospitalized and fatality class. The analysis of the model reveals the role of the super spreader in the dynamics of COVID-19 in Wuhan (China). In [20], authors proposed a mathematical model by including the bat population. Further, the authors extended the model to a fractional mathematical model to study the role of bats and the seafood market on the spread of COVID-19. In [26], authors proposed a mathematical model by incorporating some time dependent parameters to investigate the COVID-19 outbreak in Wuhan. Through the calculation of the effective daily reproduction ratio, authors demonstrate that delay in providing medical facilities play a key role in the increase in the size of the epidemic. In [18], authors formulated an eight stages SIDARTHE epidemic model to investigate the COVID-19 scenario in Italy. The model subsequently analysed to identify effective control strategies. The authors conclude that collective implementation of restrictive social distancing along with widespread testing and contact tracing may end the ongoing COVID-19 wave in Italy. In [19], a stochastic epidemic model has been used to study the COVID-19 pandemic in China. The model further used to estimate the reproduction number and gauge the success of implemented control measures. The authors also investigate the effect of the work timing on the disease dynamics. In [16], authors apply Monte–Carlo simulation on a stochastic SEIR compartmental model and predict the future of COVID-19 using the initial data of the reported cases in India. In [22], authors used a compartmental model to investigate the spread of the COVID-19 in Wuhan. Subsequently, the authors proposed a detailed dynamical study of the model and obtained the necessary conditions for the stability of the equilibrium solutions.

Sensitivity analysis also carried out to gauge the impact of the individual parameters on the dynamics of the disease. In [25], authors demonstrate the success of the SIR epidemic model over the SEIR epidemic model (in terms of the representation of confirmed cases) using the Akaike Information Criterion (AIC) in the term. In [15], authors used a SLIAR epidemic model to study the future of COVID-19 using the initial data of the disease. They demonstrate that during the initial phase of the infection simple models are more helpful and provides significant information about the disease.

From the above discussion, it can be concluded that mathematical models are vastly used to study different dimensions of the COVID-19. Moreover, the model also employed to identify robust control measures to reduce the size of the epidemic.

During the formulation of a disease model, one has to make different assumptions helping in representing the transmission mechanism of disease in the language of mathematics. But, the assumptions lead to the formulation of an epidemic model often introduce uncertainties in the estimation of parameters involved in the model. In many cases, this seriously affects the accuracy of the results obtained through the analysis of the model. The information obtained through the sensitivity analysis will provide key information about the impact of different parameters on the dynamics of the disease. Due to this, sensitivity and uncertainty analysis of epidemic models is an important area of research, and many researchers are performing sensitivity analysis of epidemic models [27–29]. A nice review of the methods and techniques of sensitivity analysis can be found in [30].

Recently, a number of studies are found an active role of the environmental pollution in the spread of a number of infections [31–35]. Some studies observed that regular exposure to environmental pollution results in diminishing of immunity [31, 36, 37]. This enhances the susceptibility of an individual towards an infection. In particular, Lafferty et al. [32] give a nice illustration of the impact of environmental stress on the dynamics of an infectious disease. The work carried out in [38] proposed an SIS type epidemic model by including a separate compartment of stressed individuals (those having regular exposure to environmental pollution) demonstrate the positive impact of environmental pollution on the spread of the disease. Despite this, to the best of our knowledge, no mathematical model available to study the correlation between environmental pollution and COVID-19. To fill this gap, in this work, we propose a new mathematical model to investigate the possible impact of environmental pollution on the spread of COVID-19. We obtain the expression of the basic reproduction number for the proposed model and then perform a rigorous sensitivity analysis of the same. The sensitivity analysis helps us to identify the impact of a particular parameter on the dynamics of the system. In particular, the current work demonstrates that environmental pollution may play a significant role and should be considered as one of the factors in the study of COVID-19.

Mathematical Model

In this section, we present the mathematical model considered during the work. In the modelling process, we divide the total human population $N(t)$ at a particular time t into seven mutually exclusive compartments; namely susceptible $S_1(t)$, stressed (those with weaken immune system due to regular or frequent exposure to environmental pollution) $S_2(t)$, exposed $E(t)$, quarantine $Q(t)$, infected $I(t)$, hospitalized $H(t)$ and recovered $R(t)$.

$$
\begin{aligned}
\frac{\mathrm{d}S_1}{\mathrm{d}t} &= \Lambda - \frac{\delta S_1(I+\delta_0 E)}{N} - dS_1 - \gamma S_1\\
\frac{\mathrm{d}S_2}{\mathrm{d}t} &= \gamma S_1 - \frac{\delta(1+\epsilon\delta^{'})S_2(I+\delta_0 E)}{N} - dS_2\\
\frac{\mathrm{d}E}{\mathrm{d}t} &= \frac{\delta S(I+\delta_0 E)}{N} + \frac{\delta(1+\epsilon\delta^{'})S_2(I+\delta_0 E)}{N} - (d+\theta)E\\
\frac{\mathrm{d}Q}{\mathrm{d}t} &= \theta(1-p)E - (d+\alpha)Q - \phi Q - \phi_0 Q\\
\frac{\mathrm{d}I}{\mathrm{d}t} &= \theta p E - (d+\alpha+r)I - \psi I\\
\frac{\mathrm{d}H}{\mathrm{d}t} &= \psi I - (d+\alpha\alpha^{'})H - \xi H + \phi_0 Q\\
\frac{\mathrm{d}R}{\mathrm{d}t} &= \xi H + \phi Q - dR + rI
\end{aligned}
\tag{16.1}
$$

In the model system, Λ is the constant recruitment rate. δ is the disease transmission rate for the individuals of S_1 class from the infected individuals. It is assumed that disease transmission rate from exposed individuals to susceptible individuals is less than δ and to incorporate the same we introduce δ_0 as the reduction factor. Next, using the approach of Lafferty et al. [32], we modify the disease transmission rate for stressed individuals (S_2) as $\delta(1+\epsilon\delta^{'})$, where ϵ measures the impact of environmental pollution on the transmission rate and the effect of pollution δ is represented by $\delta^{'}$. The model also considers the natural death rate of d. θ is the rate at which exposed individuals leave the exposed class and join the infected class, out of which one fraction p joins the infected class while the remaining $1-p$ joins the quarantine class. Parameter α represents the disease-induced death rate. It is also assumed that the disease-induced death rate for hospitalized individuals is less (due to availability of medical treatment) than that of infected individuals and to incorporate this we introduce $\alpha^{'}$ as the reduction factor. ψ is the rate at which infected individuals admitted to hospitals. The hospitalized individuals after initial treatment/checkup are allowed to move in self-quarantine at the rate ϕ_0. Parameters ϕ, ξ and r represent the recovery rates for individuals of quarantine, hospitalized and infected class, respectively.

The Basic Reproduction Number

It is trivial to observe that proposed model system possesses a unique disease free equilibrium point $E_0 = \left(S_1^0, S_2^0, 0, 0, 0, 0, 0\right)$, where $S_1^0 = \frac{\Lambda}{(\gamma+d)}$ and $S_2^0 = \frac{\gamma\Lambda}{d(\gamma+d)}$. Next, to calculate the basic reproduction number for the proposed model system 16.1, we use the popular next generation matrix method [39]. Now, the matrix F and V can be obtained as

$$\mathscr{F} = \begin{bmatrix} \frac{\delta S(I+\delta_0 E)}{N} + \frac{\delta(1+\epsilon\delta^{'})S_2(I+\delta_0 E)}{N} \\ 0 \\ 0 \end{bmatrix}, \quad \mathscr{V} = \begin{bmatrix} (\theta+d)E \\ -\theta(1-p)E + (\alpha+d+\phi+\phi_0)Q \\ -p\theta E + (\alpha+d+r+\psi)I \end{bmatrix}$$

Subsequently, we can obtained the Jacobians F and V of $\mathscr{F}$ and $\mathscr{V}$, respectively, at the disease free equilibrium point E_0 as

$$F = \begin{bmatrix} \frac{\delta\delta_0 S_1^0 + \delta\delta_0(1+\epsilon\delta^{'})S_2^0}{N} & \frac{\delta S_1^0 + \delta(1+\epsilon\delta^{'})S_2^0}{N} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Similarly,

$$V = \begin{bmatrix} (\theta+d) & 0 & 0 \\ -\theta(1-p) & 0 & (\alpha+d+\phi+\phi_0) \\ -p\theta & (\alpha+d+r+\psi) & 0 \end{bmatrix}$$

Now, the spectral radius of the matrix FV^{-1} will provide us the expression of the basic reproduction number (R_0) as

$$R_0 = \frac{\delta\delta_0 d + \delta\delta_0(1+\epsilon\delta^{'})\gamma}{(\gamma+d)(\theta+d)} + \frac{p\theta\delta d + \delta(1+\epsilon\delta^{'})}{(\theta+d)(\gamma+d)(\alpha+d+r+\psi)} \tag{16.2}$$

Sensitivity Analysis

Mathematical models pertaining to infectious disease are considered as an exciting field of research. The availability of a variety of mathematical models helps agencies to reduce the burden of a number of infectious diseases. In the study of disease dynamics using mathematical models, basic reproduction plays a very important role as it provides the threshold for the disease elimination and persistence. The mathematical epidemiological model may acquire a complex structure depending upon the complexity involved in the transmission mechanism of a particular infection. Therefore, in many cases, it will be difficult to identify the impact of an individual parameter on the dynamics of the disease. Sensitivity analysis of the epidemic model plays an important role to overcome this problem. The sensitivity analysis corresponding to some key parameters of an epidemic model provides crucial information that helps the authorities to frame some robust policies to combat infectious disease.

In this section, the sensitivity analysis of R_0 using two sampling schemes (namely random and Latin hypercube) to investigate how sensitive R_0 to an input parameter involved in the mathematical model. Sensitivity analysis generally constitutes a series of tests involving different sets of input parameters. This helps us to observe how a change in the predictor parameter values changes the dynamical behaviour of the system. It also provides information on how closely input parameters are related to a particular predictor parameter. The results obtained through sensitivity analysis helps in determining the level of change necessary for an input parameter to obtain the desired value of a predictor parameter.

In the study of disease models, sensitivity analysis is used to identify the key parameters, among the parameters involved in the model, which have a significant impact on the outcome of R_0 depending on the uncertainty involved in their estimation. Partial rank correlation coefficients (PRCCs) are a popular technique used to determine the statistical influence of any parameter on the R_0. In the present work, we first performed uncertainty analysis for R_0, subsequently, we obtain partial rank correlation coefficients corresponding to all uncertain parameters.

There are 11 parameters involved in the model system (16.1) and the estimated values of the same have been given in Table 16.1. Out of 11 parameters, δ, θ, p, r, ϵ and $\delta^{'}$ have been identified to conduct uncertainty analysis due to uncertainties involved in their estimation. To carry out the uncertainty analysis, we consider each of these parameters as a random variable with an appropriate probability density function. The remaining five parameters are kept fix and their values have been taken from the literature (given in Table 16.1).

Following are the distributions selected for six parameters

1. Four parameters consider to follow uniform distribution as discussed in [15]
    (a) δ with minimum $5 \times (10)^{-5}$ and maximum $3 \times (10)^{-4}$.
    (b) θ with minimum 1 and maximum 14.
    (c) p with minimum 0 and maximum 1.
    (d) r with minimum 2 and maximum 14.
2. ϵ follows Weibull distribution with parameters 0.6386 (scale) and 12.766 (shape).
3. $\delta^{'}$ follows exponential distribution with rate 1.

Two sampling methods random sampling (RS) and Latin hypercube sampling (LHS) have been considered to generate the values of these six uncertain parameters. A set of 1000 parameter values have been sampled using RS and LHS for six parameters from different types of parameter distribution. Histograms of the parameters considered for the study are given in Figs. 16.1 and 16.2. Histograms and box plots for the distributions of R_0 are shown in Fig. 16.5. These histograms and box plots have been generated from Eq. 16.2 using RS and LHS.

Table 16.1 Model parameters with interpretation and values/distribution

Parameter	Description	Value/distribution	References
δ	Disease transmission rate from infected to susceptible individuals	Uniform	[15]
δ_0	Reduction in disease transmission for exposed individuals	0.2	[40]
d	Natural death rate	0.00003961	[41]
θ	Rate at which exposed individuals leaving exposed class to infected class	$\frac{1}{5.1}$	[16]
p	Fraction of exposed class joining infected class	Uniform	–
α	Disease related death rate	0.0175	[40]
$\alpha^{'}$	Reduction factor and lies between 0 and 1	0.1	Assumed
r	Recovery rate for infected class	Uniform	[15]
ψ	Rate at which infected individuals admitted to hospitals	0.2174	[42]
ρ	Recovery rate of hospitalized individuals	$\frac{1}{14}$	[40]
ϕ	Recovery rate of quarantine individuals	0.1162	[40]
ϵ	Amount by which environmental pollution affects the transmission rate	Weibull	[43]
$\delta^{'}$	Effect of pollution on δ	Exponential	[32]
γ	Rate at which individuals of S_1 class join S_2 class	0.004	Assumed

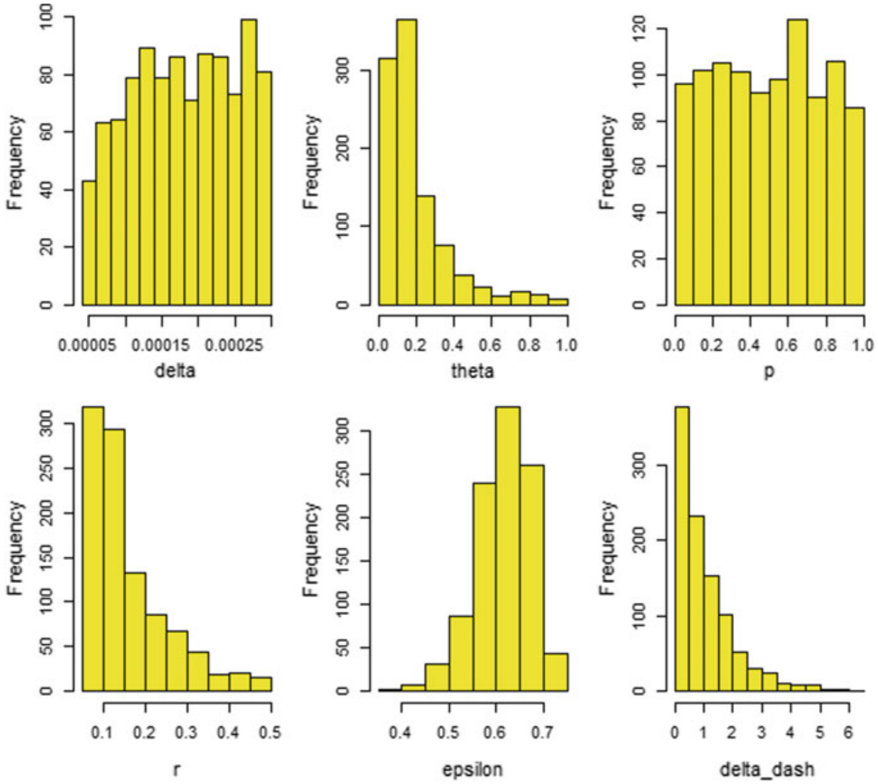

Fig. 16.1 Histograms of the values obtained through random sampling with a sample size of 1000 (*Source* own)

Results and Discussion

The partial rank correlation coefficients (PRCC) indicate the degree of effect of a particular parameter on the outcome. Scatter plots comparing the basic reproduction number for each of the parameters; δ, θ, p, r, ϵ and $\delta^{'}$ are shown in Figs. 16.3 and 16.4 for RS and LHS, respectively. These scatter plots clearly show the linear relationships between input parameters and R_0.

The sign of the PRCC depicts the qualitative relationship between the input parameter and the related output variable. The positive sign of the PRCC of the variables corresponds to the situation that an increase in the value of the input parameter, the value of R_0 also increases. On the other hand, the negative sign of the PRCC signifies that any increase in the corresponding parameter results in the decrease of the basic reproduction number, and hence such parameters have the potential to reduce the size of the epidemic.

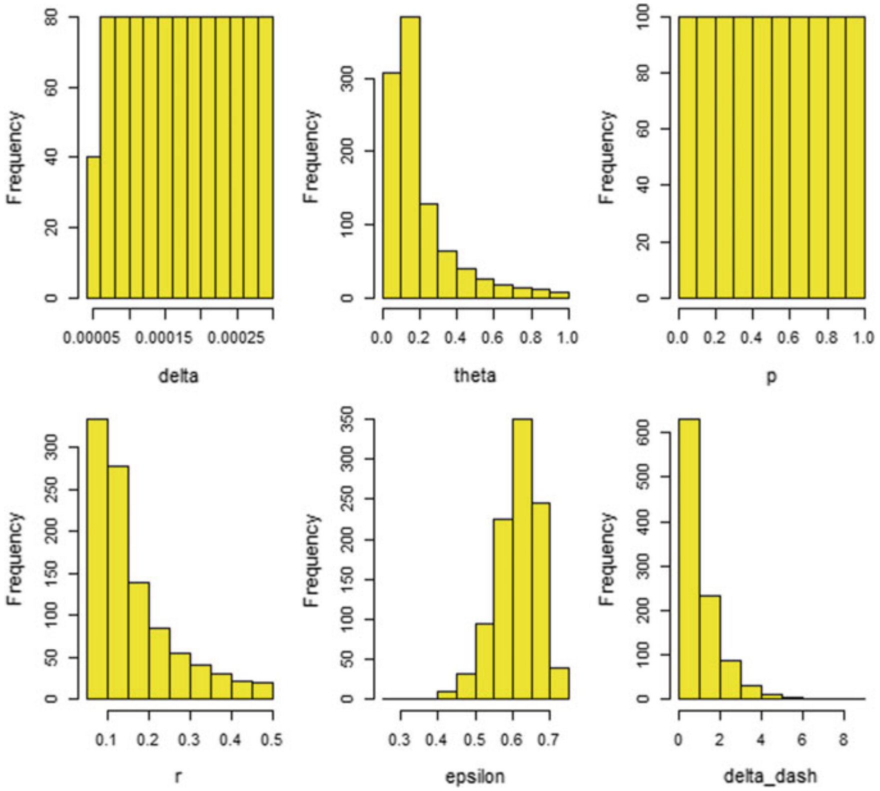

Fig. 16.2 Histograms of the values obtained through Latin hypercube sampling with a sample size of 1000 (*Source*: own)

The results obtained through sensitivity analysis are given in Table 16.2. On the basis of random sampling, we can conclude that parameters θ, δ and $\delta^{'}$ have higher degree of relationship with R_0 with PRCC values 0.9077, 0.8591 and 0.749, respectively. From the values of the parameters, it is easy to observe that δ and $\delta^{'}$ have positive association while the parameter θ has a negative association. Further, the other pollution-related parameters ϵ also recorded the positive value of PRCC.

Similar results have been obtained for the Latin hypercube sampling as θ emerged as the most sensitive parameter with the highest value (-0.924458593) of PRCC. δ and $\delta^{'}$ are observed as the next two most sensitive parameters with PRCC values 0.879221188 and 0.763274350, respectively. The PRCC value for ϵ is 0.096838976, which clearly reflects the positive association of the pollution on the spread of the disease.

The positive values of PRCC clearly depict that pollution plays a supportive role in the spread of the disease and can increase the size of the epidemics. Since pollution is a global problem and many developing countries are suffering severely with the menace

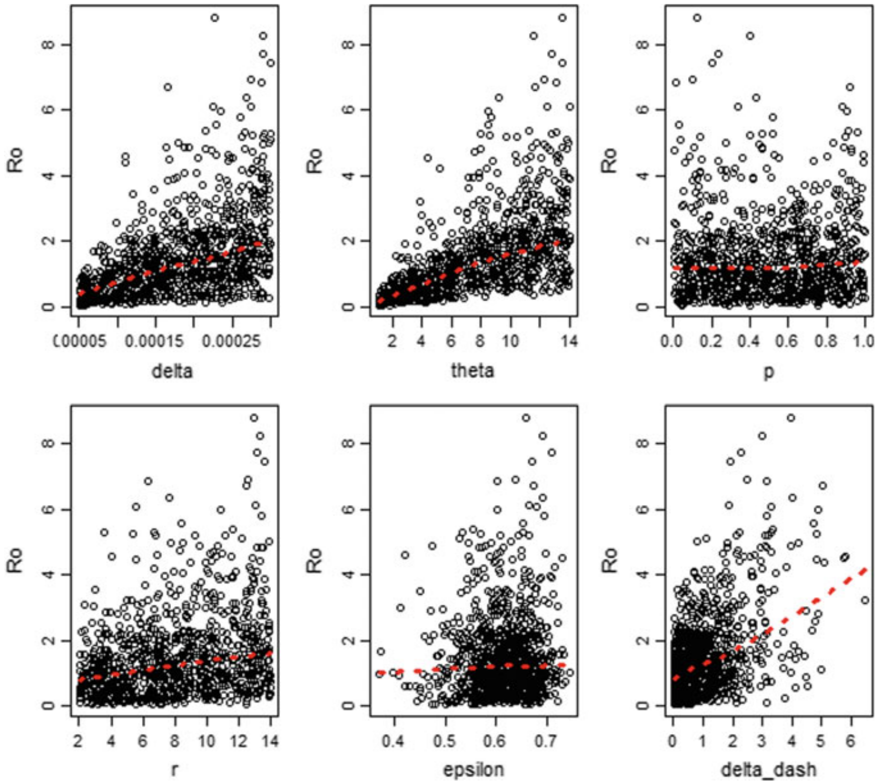

Fig. 16.3 Scatter plots for R_0 obtained from random sampling (*Source*: own)

of pollution. These countries also lack a robust medical infrastructure. Therefore, the results obtained in this work clearly highlights the need for some appropriate steps from the different research community in order to control the ongoing COVID-19 pandemic.

In short, the following points can be concluded from the current study

1. θ is the most sensitive parameter followed by δ and $\delta^{'}$.
2. The positive values of PRCC for pollution-related parameters ($\delta^{'}$ and ϵ) are positive. This clearly reflects the positive association of pollution on the spread of the disease.
3. The PRCC value for $\delta^{'}$ is significantly high, which shows that disease spread more rapidly in the presence of pollution.
4. Disease eradication needs more effort in the presence of pollution.

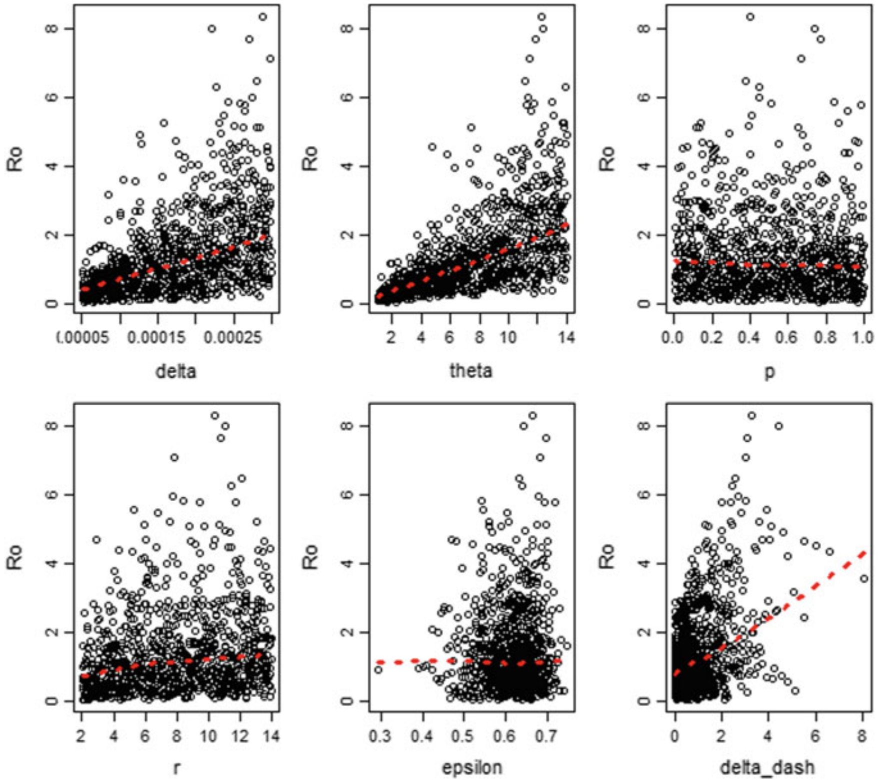

Fig. 16.4 Scatter plots for R_0 obtained from Latin hypercube sampling (*Source*: own)

Table 16.2 PRCC values for the basic reproduction number R_0

Parameter	Sampling	PRCCs
δ	RS	0.85912837
	LHS	0.879221188
θ	RS	−0.90773120
	LHS	−0.924458593
p	RS	0.02250202
	LHS	0.009476424
r	RS	−0.57183391
	LHS	−0.617232256
ϵ	RS	0.07814241
	LHS	0.096838976
$\delta^{'}$	RS	0.74904911
	LHS	0.763274350

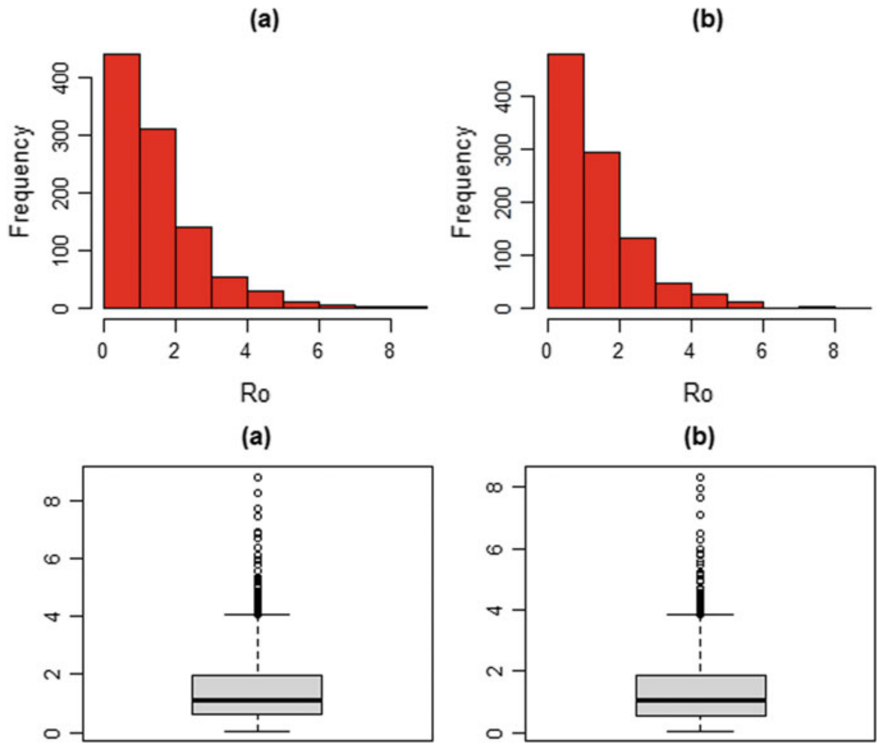

Fig. 16.5 Histogram and box plot of the basic reproduction number, **a** obtained from random sampling and **b** obtained from Latin hypercube sampling (*Source*: own)

Accounts to the rapid growth in the industry and automobiles, the level of pollution will rise significantly in the near future. And there is a high chance that many new chemical pollutants will come into existence. Therefore, the current study can be extended, in the future, by incorporating more variables or parameters as per the available field data.

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