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# Modelling a Compartmental Mathematical Approach for Analysing the Transmission of Covid-19

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**Abstract**
This study presents a mathematical pattern comprising eight interconnected compartments that incorporate immunization and serve as a key component in investigating the transmission characteristics of respiratory disease. This work thoroughly examine the pattern's inherent properties, encompassing solution-contaminated values and bounded ranges, and analyze stability without disorder equilibrium, considering the basic reproduction count using real data with Susceptible Exposed Quarantined Recovered Vaccinated (SEQR-V). Our SEQR-V based study involves estimating ten significant parameters and computing India's basic reproduction count using the suggestedpattern and fitting it to the countriesdaily and cumulative respiratory disease diagnoses. A robustness analysis is performed concerning the reproduction count at equilibrium to identify the essential parameters that significantly influence the pervasive transmission of the disorder. This work expand the pattern into an optimization problem with controls incorporating fourfold control functions representing non-pharmaceutical and pharmaceutical intervention strategies. Our numerical simulations demonstrate that implementing four control strategies significantly reduces respiratory disease transmission dynamics compared to using three, two, or a single control strategy.

*Keywords*- SEQR-V Model, COVID-19, Mathematical Modelling, Vaccination, reproduction count, Quarantine, Susceptible, Patterns.

## 1. Introduction

The respiratory disease pandemic has spread globally, with most countries experiencing significant counts of infections and fatalities. As of August 16, 2023, the global respiratory disease pandemic hasoutputted 769,806,130 reported cases of illness and 6,955,497 demises [1].India was among the countries worst affected by the respiratory disease pandemic, with a substantial count of cases and demises reported nationwide.India's respiratory disease statistics revealed 44,996,599 cases and 531,925 demises, placing it third among countries most affected by the pandemic [2]. In response to the emergence of various respiratory disease variants, scientists, biologists, and healthcare experts are tirelessly researchingshot development and treatments to reduce the spread of the virus [3].A comprehensive review of existing literature reveals a diverse range of research articles and studies that offer various perspectives on reducing the spread of respiratory disease. Mathematical patterns provide a valuable resource for understanding the dissemination of communicable disorders and assessing the consequences of control measures' strategies on disorder prevalence [4].Multiple studies have employed mathematical patterning to determine the effectiveness of immunization strategies in mitigating the pandemic. The author in [5] employed pattern recognition techniques to quantify the impact of the respiratory disease epidemic in Wuhan, particularly emphasizing the role of direct transmission between humans.According to their outputs, controlling the spread of the disorder requires preventative measures that can stop over 60% of transmissions. The author in [6] study highlights the significance of social distancing as a key strategy for mitigating the effects of respiratory disease. The authorformulated a deterministic patternto analyze the transmission patterns of respiratory disease,focusing on super-spreaders role in spreading the disorder. The author formulated a statistical framework that includes a segregation division and administrative actions to curb the dissemination of respiratory disease.

The author in [7] developed a mathematical pattern to investigate the impact of segregated, hospitalized, and undiagnosed compartmentpersons on the transmission patterns of respiratory disease.The author study examines the effectiveness of interventions, including face masks, social distancing, and case detection,in mitigating the

spread of respiratory disease.The author study investigated the impact of face coverings, inpatient care, and segregation measures on mitigating respiratory disease transmission in India. The author in [8] study introduced a nine-stage pattern of infection, revealing that a combination of combination of pharmaceutical and non-pharmaceutical preventive measures is more effective than either approach alone relying on a single approach. The study created a mathematical patternto analyze the effectiveness of social media advertising in driving website traffic and conversions, controlling the respiratory diseasesurge in India through community mitigation strategies. A research built a platform mathematical framework using optimal control theory with mixed constraintsand optimal immunization strategies.The outputs indicate that shots value the immune response gene, and the duration of immunity and reinfection periods play a crucial role in respiratory disease mitigation [9].

The author developed a multi-chamberedpattern to assess the benefits of vaccination for respiratory disease prevention transmission, using immunization as a control measure. Studies have shown that combining therapeutic and shot-based approaches can minimize respiratory disease transmission and improve patient outcomes.Ankama Rao and Venkatesh's research designed a 9-compartment mathematical model to optimize resource allocationpatterns that incorporatean infectious disease protocol, medical facility admission, and protected individual populations, with a focus on NPI strategies to control respiratory disease.The study by [10]presented a multi-strain disease transmission model with 16 compartments, incorporating pharmaceutical interventions to decrease respiratory disease transmission and promote healing. The study developed by [11] an epidemic pattern that includes practical and ineffective immunization strategies to study the spread of respiratory disease. Additionally, a control framework was established to examine the impact of immunization and the benefits of combining vaccination and treatment measures in mitigating disease outbreaks and respiratorydisease transmission. The authordeveloped an analytical mathematical solutionpatternthat encompasses age-related transmission dynamics to evaluate and assess the efficacy of shots and treatments in reducing respiratory disease morbidity.Drawing inspiration from existing studies, our team developed a novel deterministic compartmental model, including hospitalized, vaccinated, and segregated persons, to simulate disease transmission compartments [12]. This research aims to investigate the effects of combining behavioral and pharmacological strategies for disease management interventions, including awareness initiatives, immunization, and treatment, on controlling the spread of respiratory disease. The major research contributions are listed below:

1) An improved Susceptible Exposed Quarantined Recovered Vaccinated (SEQR-V)-based mathematical model was proposed by including compartments for quarantined patients, infected people and unidentified infection, vaccinated and death patients and so on.

2) The outcomes based on SEQR-V transmission model to simulate the dynamic COVID-19 transmission. The proposed mathematical model was developed by considering certain special features of the pandemic in India using real data. The research presentsthe structureof the paper as follows:

Section 2 presents provides the wider analysis on various prevailing approaches. The mathematical pattern analysis with SEQR-V and the comprehensive evaluation with outputs are provided in section 3. The work summary is explained in section 4.

## 2. Related works

Countries are concentrating on determining optimal courses of actionand strategies to combat the respiratory disease pandemic.The government has implemented key measures to fight respiratory disease. Social distancing, regular handwashing, hand hygiene with soap or hand sanitizer, and wearing face masks are essential for public health [13]. The standard preventive measures adopted are surveillance, outbreak investigation, and transmission control. These measures help reduce transmission risk and minimize airborne transmission. The government's proactive approach has impacted effective respiratory disease management. By combining these measures, India aims to control the spread of the virus and protect public health. Indian citizens, residents, and visitors who voluntarily repatriate must undergo a mandatory 14-day segregation at specified locations, as required for all travelers from high-risk areas [14].The respiratory disease measures are regularly reviewed and updated to reflect the current disorder and the prevalence and transmission dynamics of illnesses in a population. In response to the respiratory disease pandemic, various vaccines have been developed by countries and health organizations to help enhance public health strategies and slow the spread of the disease [15].The development and distribution of respiratory diseaseshots have provided a clear pathway to safely and effectively combat the pandemic, protecting against severe illness. Nations with limited economic resources in sub-Saharan Africa have struggled with low respiratory diseaseimmunizationvalues, hindering efforts to curb the transmission of the disorder [16].

On March 17, 2022, the global immunizationvalue stood at 63.8%, with at least one dose administered to nearly two-thirds of the population. As of the latest available data, the United Arab Emirates held the top spot for immunizationvalues, with 98.99% of its population having been administered at least one dose of the respiratory shot [17]. As of the reported date, Africa's respiratory diseaseimmunizationvalues stood at 19.76% partially vaccinated, 14.99% fully vaccinated, and 1.16% without vaccination having received a supplementary dose. By March 17, 2022, India had achieved a notable immunizationvalue, with 66.37% of its population protected against respiratory disease, comprising 58.81% fully vaccinated and 7.56% partially vaccinated [18].Mathematical patterning and simulation are essential for understanding and combating disorders in both human and animal populations. These patterns can forecast potential future trends, describe the progression of infections within populations and persons, and offer insights into the effectiveness of various interventions [19]. Various studies have employed mathematical patterning to describe the dynamics of respiratory disease evolution, utilizing general-purpose patterns like SIR and SEIR to understand the spread of the disorder. A key step in developing an analyticalpattern for respiratory disease is to incorporatethe established characteristics of thisdisorder [20].In their research, the author introduced three phenomenological patterns with broad applications to disorder outbreaks, extending beyond respiratory disease. The study presented variations of SEIR patterns, some of which included stochastic components to account for randomness. Several studies have employed mathematical patterning to understand the respiratory disease pandemic, with many concentrating on its spread and movement within China [21]. The author developed and analyzed an extended mathematical pattern, incorporating vulnerable, exposed, secluded, and symptom-free, not admitted, and admitted compartments, understanding the dynamics of respiratory disease transmission in Ethiopia. Their analysis revealed a basic reproduction count ($R0$) of 1.0029, and they recommended reducing the transmission values of contaminated and asymptomatic persons, as these factors were found to increase $R0$, while also increasing segregation and treatment values to bring $R0$ below 1 [22].The author in [23] – [25] provided an overview of the respiratory disease situation in Eastern Africa, specifically Kenya, Burundi, South Sudan, Ethiopia, Tanzania, and Uganda. They reported basic reproduction counts ($R0$) of 1.32, 8.52 for Kenya, 2.84 for Burundi, 2.57 for Tanzania, and 2.34 for Uganda.The findings were developed using outbreak data and simplified SIR and SEIR patterns, which may not have fully accounted for the complex dynamics of respiratory disease and the effects of government interventions within these states [26].Furthermore, under-reporting in some countries might have impacted the validity of findingsand may have introduced bias into the $R0$ outputs, which should be considered when interpreting the findings [27] – [28]. To better understand and manage respiratory disease, patterns should be developed to analyze the disorder's key epidemiological indicators and government regulatory actions to combat the disease.

This paper outlines the development of a respiratory disease transmission pattern designed to capture the unique dynamics of the disorder.The pattern's framework can be applied to other contexts with similar control measures, making it relevant for the domain [29]. We developed an expanded SEIR framework pattern that includes additional compartments for segregating persons, undetected infections,persons receiving care at home, hospitalized cases, demises, and vaccinated populations [30]. This led to the establishment of a Susceptible Exposed Quarantined Recovered Vaccinated (SEQR-V) transmission dynamics framework, which includes a dynamic model of respiratory disease transmission, incorporating multiple compartments: Vulnerable, Exposed, Segregation, Infectious (with detected, undetected, and home-based care sub-compartments), hospitalized, vaccinated, healed, and Dead. The mathematical pattern was developed considering unique respiratory disease surveillance and monitoring.

## 3. Mathematical pattern

Complex patterns modeling with nonlinear differential mathematical relationships was developed by applying a compartmental structure pattern illustrated in Fig 1. The stability of the pattern was analyzed by computing equilibrium points and using the mathematical modeling of infectious diseases approach to calculate a key indicator of a disease's infectiousness ($R0$). The pattern least squares fitting was employed to determine parameter values.The classical logistic formula served as the basis for our predictions.

### 3.1. Data source

The Worldometer page for India’s COVID-19 statistics provides a comprehensive overview of the pandemic's impact in the country.As of the last update on April 13, 2024, the data includes: https://www.worldometers.info/coronavirus/country/india/. Here, Total Cases: 45,035,393 confirmed cases, Total Deaths: 533,570, Recovered: Not specified, Closed Cases: 45,034,776 and Recovered/Discharged: 44,501,206 (99%) and Deaths: 533,570 (1%). It's important to note that as of April 13, 2024, Worldometer ceased updating its COVID-19 tracker due to the discontinuation of regular reporting by many countries, making it challenging to provide statistically valid global totals.However, historical data remains accessible for

reference. The page also features various graphs and charts illustrating: 1) Total and daily new cases; 2) Total and daily new deaths and 3) Outcomes of cases (recovery or death). These visual tools offer insights into the trends and progression of the pandemic in India over time.

### 3.2. Compartment based analysis

The compartments of the SEQR-Vpattern include Vulnerable ($S$), which refers to persons who are not contaminated with the disorder but are vulnerable to infection. Exposed ($E$) refers to personswho have been contaminated with the disorder pathogen and are in the incubation period but have not yet developed typical symptoms. Persons in this compartment have a slightly lower probability of infecting vulnerable people than those capable of spreading the disease. Following the time between exposure and symptom onset, personswithin this population transition to the subset of persons who can transmit the disease. The transmissible compartment includes those who have contracted the virus, are highly infectious, and are not under segregation. The following are three distinct scenarios. Infectious but undetected ($Iu$) refers to a portion of contagious persons who will not be identified or reported. Persons in this compartment either recover and transition to the healed compartment or die from the disease. Infectious patients receiving home-based medical care ($Ih$) refers to personsdiagnosed with the virus who are being monitored with care from a medical team and may recover spontaneously incident requiring hospitalization or direct medical care.In the event of complications, persons in this category will be referred to the nearest healthcare facility for further treatment.

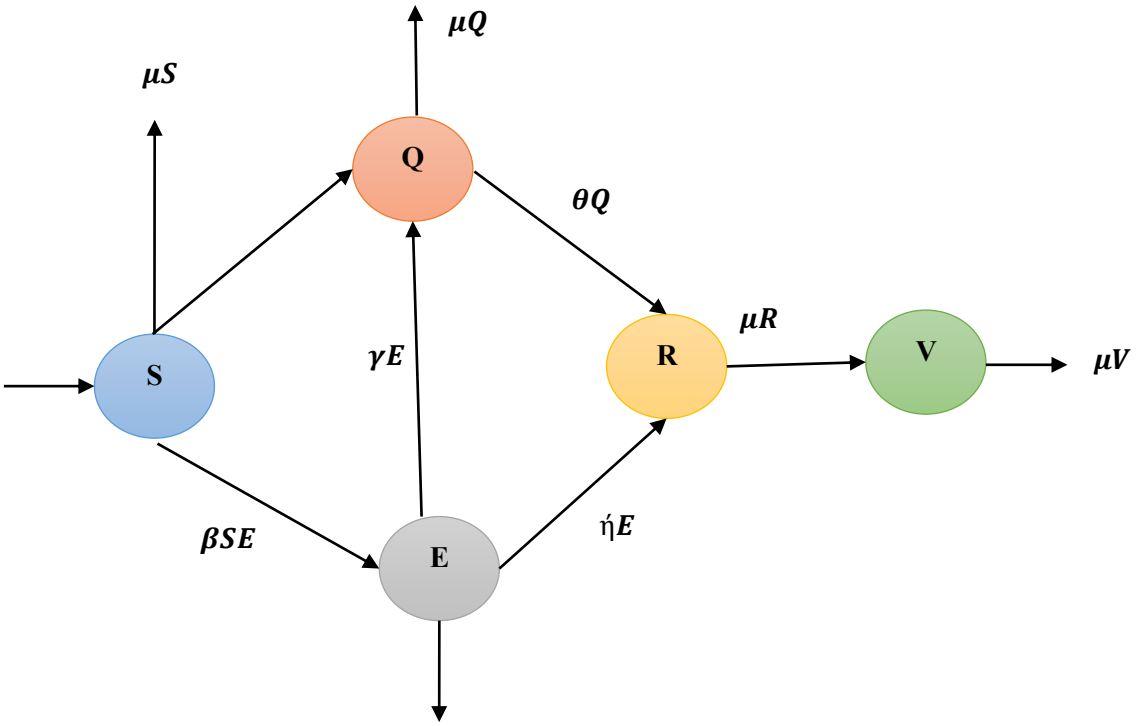



**Fig 1.** Schematic diagram of SEQR-V model

**1. Hospitalized ($H$):** refers to infectious persons admitted to a hospital or isolated and can transmit the infection to others, particularly healthcare workers. Upon completion of treatment, persons in this category may either recover from the disorder or succumb to it.

**2. Quarantine ($Q$):**Persons who are vulnerable and suspected or confirmed to have been near contaminated persons through contact tracing will probably be required to undergo mandatory isolation, either at home or in designated segregation facilities.Additionally, all persons, including persons returning from international destinations, must undergo segregation.Following the segregationinterval, persons who test uncontaminated are released to resume their everyday life at home, while those who test contaminated are admitted to a hospital or isolated.

**3. Healed ($R$):**Personswho were previously identified as communicablehealed from the disorderusing medical therapy or natural immunity and are now immune to the virus, no longer posing a risk of infection to others.

**4. Dead ($D$):**People who lost their lives to respiratory disease.

**5. Immunized persons($V$):**The level of resistance to the disease for those who have received the shot varies based on the effectiveness of the shot. This study considered vaccinated persons to have received multiple doses (more than two).

$$N(t) = Q(t) + H(t) + R(t) + D(t) + V(t) \quad (1)$$

Let $(t)$ represent the total count of persons at time $t$. The subsequent ordinary differential equation pattern represents the respiratory disease dynamics:

$$\frac{dH}{dt} = (1 - \tau_1 - \tau_2)\omega_1 I + (1 - \theta)\omega_3 I_h - \omega_4 H \quad (2)$$

$$\frac{dQ}{dt} = \Lambda + \varepsilon S - (\delta + \sigma)Q \quad (3)$$

$$\frac{dR}{dt} = (1 - \gamma)\omega_2 I_u + \acute{\eta}\omega_4 H + \theta\omega_3 I_h - D_R R \quad (4)$$

$$\frac{dD}{dt} = \gamma\omega_2 I_u + (1 - \acute{\eta})\omega_4 H \quad (5)$$

$$\frac{dV}{dt} = \gamma\omega_2 I_u + (1 - \acute{\eta})\omega_4 H \quad (6)$$

The pattern's initial conditions are set as follows:$Q(0) = 1, H(0) = 1, R(0) = 0, D(0) = 0, and\ V(0) = 0$, with patterncoefficients specified in the subsequent section: Suppose that persons enter the vulnerable compartment at a value of $\lambda$.The value at which persons enter the segregation compartment is $\Lambda$.The transmissibility value parameters are represented by $\beta_E, \beta_{I_u}, \beta_I, \beta_{I_h}, and\ \beta_H$, corresponding to exposed, asymptomatic contaminated, symptomatic contaminated, home-based care recipients, and hospitalized cases, correspondingly. Fig1 showsthe rate of infection, given by $\frac{\beta_E E + \beta_{I_u} I_u + \beta_I I + \beta_{I_h} I_h + \beta_H H}{N}$, which is the value of transition from vulnerable to contaminated.

- ✓ The parameter $\varepsilon$corresponds to the value at which vulnerablepersons are moved into segregation.
- ✓ The parameter $\sigma$corresponds to the value at which segregatedpersons remain noncontaminated.
- ✓ The parameter $\delta$corresponds to the value at which segregatedpersons become contaminated.
- ✓ Suppose that the average latent period is $1/\alpha$ days, implying that $\alpha$is the value at which exposed individuals become infectious to others.
- ✓ Suppose that the average durations of infection are $1/\theta$ days for persons in $H, 1/\gamma$ days for those in $I_h$, and 1 day for those in $I_u$.
- ✓ The transition values from compartments $I_u$, $I_h$, and $H$ are represented by $\omega_1, \omega_2, \omega_3, and\ \omega_4$, correspondingly, measured in days.
- ✓ Shots are introduced gradually, with a daily fraction of $D_S$vulnerablepersons, and $D_R$healedpersons being vaccinated and the shot has an efficacy of $\mu$.

| Symbol | Representation |
|---|---|
| $d_H$ | Mean duration of $H$ |
| $d_Q$ | Mean duration of $Q$ |
| $d_R$ | Mean duration of $R$ |
| $d_D$ | Mean duration of $D$ |
| $d_V$ | Mean duration of $V$ |

### 3.3. Theoretical analysis

**Lemma 1:**The solutions to the pattern with initial conditions are consistently contaminated throughout the domain in $H$.

**Proof:**The optimism of pattern solutions is confirmed via a distinct method outlined. To establish the optimism of pattern, we examine any outcome originating from the non-contaminateddomain and remaining contaminated

for all $t > 0$. To achieve this, we show that the mathematical field on each surface is confined within the non-contaminateddomainusing SEQR-V.

$$\frac{dH}{dt} = K_i I + K_q Q \geq 0 \tag{7}$$

$$\frac{dQ}{dt} = \Lambda \geq 0 \tag{8}$$

$$\frac{dR}{dt} = (\gamma_a A) + (\gamma_q Q) + (\gamma_h H) \geq 0 \tag{9}$$

$$\frac{dD}{dt} = \pi_a A + \pi_i I \geq 0 \tag{10}$$

$$\frac{dV}{dt} = \alpha S \geq 0 \tag{11}$$

From the mathematical relationships of the pattern, we derive that on the boundary surfaces defined by $V = 0, Q = 0, D = 0, H = 0, and\ R = 0$ in the non-contaminateddomain all values are non-contaminated.Therefore, it is evident that the infection will be sustained in all solutions of the pattern for $t > 0$, provided that the initial values correspond to a contaminated scenario.

**Lemma 2:**The solutions of the pattern with initial conditions are confined within a bounded domain within the domain$\Phi$, defined as the set of all points $(D, V, Q, H, R)$ such that $D + V + Q + H, +R \leq \Lambda/\delta$.

**Proof:** Define $N = D + V + Q + H + R$. By summing all mathematical relationships in pattern, we get,

$$\frac{dN}{dt} = \Lambda - (\delta_a A + \delta_d D + \delta_v V + \delta_q Q + \delta_h H + \delta_r R) - \delta N \leq \Lambda - \delta N \tag{12}$$

$$\frac{dN}{dt} + \delta N \leq \Lambda \tag{13}$$

$$N(t) \leq \frac{\Lambda}{\delta} + \left(N(0) - \frac{\Lambda}{\delta}\right) e^{-\delta t} \tag{14}$$

$$\lim_{n \to \infty} sup N(t) \leq \frac{\Lambda}{\delta} \tag{15}$$

Here, infinity yields $t \to \infty$.Therefore, we have $N(t) \leq \Lambda/\delta$, which implies that $D + V + Q + H + R \leq \Lambda/\delta$. Consequently, all solution trajectories $(D, V, Q, H, R)$ of the pattern with initial conditions are contained within the domain$\Phi$.

### 3.2. Qualitative analysis

To analyze the pattern's qualitative behavior, we need to assess the stability of the critical point by calculating the reproduction count of an infectious disease, $R_0 = \rho(FV^{-1})$ which corresponds to the dominant eigenvalue of the next-generation operator, where $F\ and\ V$ represent the Jacobian matrices of infection and transmission progression at the disorder-free equilibrium. A basic reproduction count, $R_0$ of less than 1 suggests respiratory disease will not be sustained, whereas a value greater than 1 implies the disorder will persist in the population. Our pattern calculations yield a basic reproduction count, $R_0$.

### 3.3. Parameter analysis

The unknown parameters in this pattern were estimated using the least squares estimation technique. The objective function was formulated to minimize the variations between reported and actual data-related mortality and morbidity ($CC_r\ and\ CD_r$) and the pattern's estimated cumulative cases and demises ($CC^{\varphi}\ and\ CD^{\varphi}$) for a given set of parameter values $\varphi$. To estimate the pattern parameters, we used an approximate population in 2020 as $N = 13{,}210{,}137$ and assumed a shot efficacy of $\mu = 0.85$. We utilized the daily reported cumulative counts of contaminated cases ($CC_r$) and demises ($CD_r$) from the Ministry of Health (MoH) for the period spanning March 2020, to February 2022.This work calculated the cumulative countevery week, covering

approximately 2 years. The patterndata modeling comparing the total count of contaminated cases and deaths reported, while estimated model parameters are listed. The dynamics of various segments of the populationare illustrated in Figs 1. Table 1 presents the estimated values of the parametersand indicates that the disorder contact values $\beta_D, \beta_V, \beta_Q, \beta_H, and\ \beta_R$ collectively impact 10.21% ofdisorder transmission. A significant proportion of contaminatedpersons (65%) remained undetected, potentially serving as a substantial source of respiratory disease transmission within the Indian population. Approximately 35% of personscontaminated with the disorder receive treatment at home.The outputs indicate that 0.05% of undiagnosed personscontaminated with respiratory disease succumbed to the disorder.A notable finding from the analysis revealed that approximately 95% were suspected to have been affectedby respiratory disease and subsequently segregated.

A significant majority (roughly 97%) of persons in segregation received uncontaminated test outputs, while about 3% tested positive for respiratory disease.The estimated incubation period for respiratory disease is approximately 5 days, which is the time it takes for symptoms to develop and for an individual to transition transmission from exposed individuals to the infectious group. The recovery value for hospitalized patients is 99.5%, whereas 93.21% of persons treated at home recover from the infection. Around 98% of infections can probably be attributed to either hospitalized persons or those with undetected respiratory disease. The probability of demise from respiratory disease for undiagnosed persons is estimated to be 95%, and the probability of recovery for hospitalized patients is approximately 91%. The study findings indicate that approximately 10% who are not contaminated with respiratory disease are vaccinated daily. Personshealed from respiratory disease develop immunity, and vaccinating them requires a certain amount of time. Consequently, the daily count of healedpersons receiving their immunization is relatively low, estimated at 0.086%.The study revealed that an average of 347 persons were segregated daily, with 66 of them being vulnerable to respiratory disease.

Table 1 compares the reported cases of respiratory disease infection, demises, and immunizations and the counts predicted by the mathematical pattern. Here, 133,229 persons contracted respiratory disease in Indiaamid the outbreak. Approximately 85,000 undetected infectious patients and 48,000 patients under home-based care were reported.Hospitalizations for respiratory disease peaked at approximately 108,000 patients. Fig1illustratesthe rise in contaminated, undetected, and home-care individual cases.A portion of these persons are hospitalized, while others either die or recover. As anoutput, the curves representing contaminated($I$), undetected contaminated($I_u$), and hospitalized ($I_h$) persons decline. Respiratory diseasedemises rose to 1358, while the count of exposed persons dropped to 100. Approximately 5.3 million persons were segregated due to rigorous contact efforts to track and manage the return of citizens during the outbreak.However, as these activities were scaled back, the count of segregatedpersons decreased. As India has implemented its immunization program, the count of vaccinated persons rose to approximately 8.7 million. As persons transitioned from the vulnerable group to other categories, the total count of vulnerablepersons representing the India population decreased. The count of healedpersons rose from 0 to approximately 2.9 million, largely due to improvements in healthcare services. The observed count of healedpersons surpassed the cumulative total of cases reported by real dataset, including those detected in both cases encompassing hospitalized, home-based, and undetected patients' recoveries ($I_u$ group).

### 3.4. Prediction

Initially, we examined whether the equation fulfilled the conditions of the derivative Eq. (16):

$$\frac{dFM(t)}{dt} = \rho(t)\left(FM(t) - \frac{[FM(t)]^2}{FM_f}\right) \tag{16}$$

Where,$FM(t)$corresponds to the cumulative count of reported cases of an epidemic viral disease at a particular moment$t$, $\rho(t)$ is a time-dependent variable, and $FM_f$ is a constant parameter. The values of $(t)$ and $FM_f$ are influenced by the fundamental characteristics of breathing difficulties and lung function impairment. The time-dependent nature of $(t)$ captures various factors that change over time, including the impact of the Indian government's control measures which vary with time $t$. The solution to the non-linear Eq. (17) outputs in the well-known logistic formula:

$$FM(t) = \frac{FM_f}{1 + ae^{-\tau}};\ \tau = \int \rho(t)dt \tag{17}$$

Pattern calibration prediction involves examining a specific scenario where $(t)$ is held constant at $b$, outputting in a modified version of Eq. (18):

$$FM(t) = \frac{FM_f}{1 + ae^{-bt}} \tag{18}$$

Once the constants $FM_f, a, and\ b$ are determined from observed data, Eq. (18) can accurately predict respiratory disease progression. This work utilize the built-in Matlab R2018a function to calculate these constants which gene values a non-linear correlation by modeling the relationship. Table 1 provides the pertinent parameters that define the sigmoid functionfor various categoriesincluding quarantined individuals $(Q)$, hospitalized patients $(H)$, vaccinated persons$(V)$, and fatalities $(D)$ and $R$.

**Table 1.** Parameter evaluation

| | | **Estimate** | **SE** | **Stat** | **P-value** |
|---|---|---|---|---|---|
| $Q$ | $FM_f$ | $1.5 * 10^5$ | 3865 | 34 | $2.7 * 10^2$ |
| | $a$ | 1130 | 350 | 3.3 | 0.0019 |
| | $b$ | 0.08 | 0.005 | 19 | $1.6 * 10^{-3}$ |
| $H$ | $FM_f$ | $0.04 * 10^5$ | 1.05 | 0.036 | 0.98 |
| | $a$ | -0.9 | 0.010 | -108.5 | $7.3 * 10^2$ |
| | $b$ | 0.0001 | 0.006 | 0.036 | 0.9 |
| $R$ | $FM_f$ | $2.5 * 10^9$ | 1633 | 17 | $3.4 * 10^{-3}$ |
| | $a$ | 48780 | 2.6 | $1.9 * 10^8$ | 0 |
| | $b$ | 10.8 | 2.5 | 4.5 | $1.2 * 10^{-5}$ |
| $D$ | $FM_f$ | $1.02 * 10^5$ | 909 | 17 | $2.8 * 10^{-3}$ |
| | $a$ | 2571 | 10 | $5.5 * 10^8$ | 0 |
| | $b$ | 0.11 | 2.3 | 4.6 | $3.6 * 10^{-3}$ |
| $V$ | $FM_f$ | $9 * 10^6$ | 9.6 | 2.2 | $4.6 * 10^{-3}$ |
| | $a$ | 4.8 | 32.9 | 19.6 | $3.1 * 10^{-3}$ |
| | $b$ | 0.30 | 1.7 | 15.2 | $2.2 * 10^{-3}$ |

**Table 2.** Sensitivity analysis

| **Parameter** | **Sensitivity analysis** |
|---|---|
| $\Lambda$ | 1 |
| $\sigma$ | 0.3 |
| $\varphi$ | 0.2 |
| $\propto$ | -0.7 |
| $\acute{\eta}$ | 0.5 |
| $\zeta$ | 0.7 |
| $\rho$ | 0.5 |
| $\beta$ | 1 |
| $\pi_a$ | -0.1 |
| $\pi_i$ | -0.5 |
| $\gamma_Q$ | - |
| $\gamma_H$ | -0.3 |
| $\gamma_R$ | -0.08 |
| $\gamma_D$ | - |
| $\gamma_V$ | - |
| $\delta_Q$ | -0.03 |
| $\delta_H$ | -0.0014 |
| $\delta_R$ | - |
| $\delta_D$ | - |
| $\delta_V$ | -0.14 |

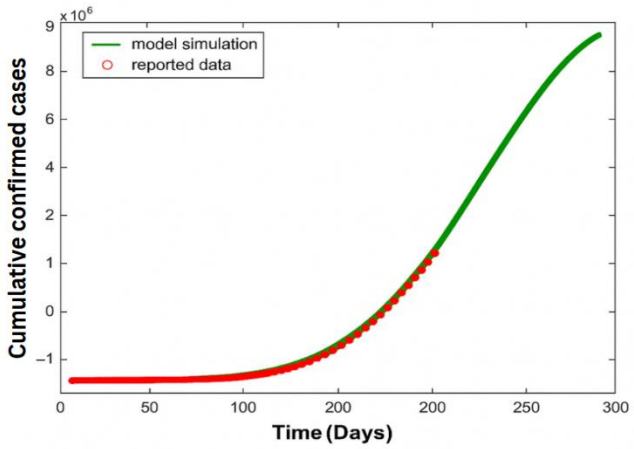



**Fig 2.** Cumulative confirmed cases

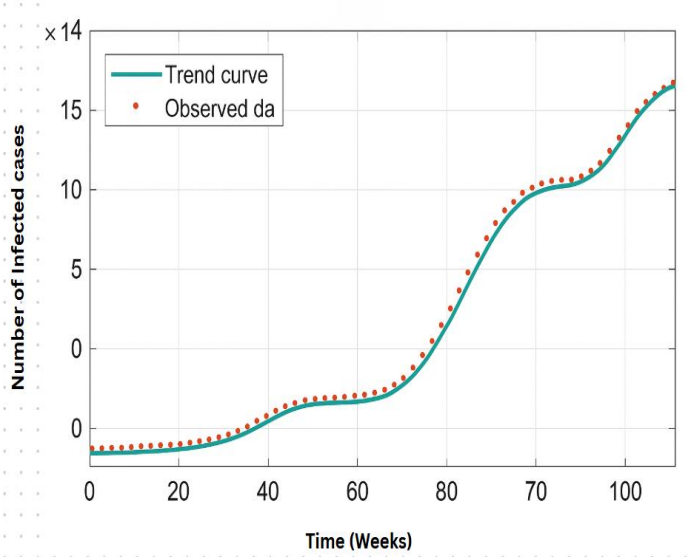



**Fig 3.** Simulation outcomes of No. of infected cases

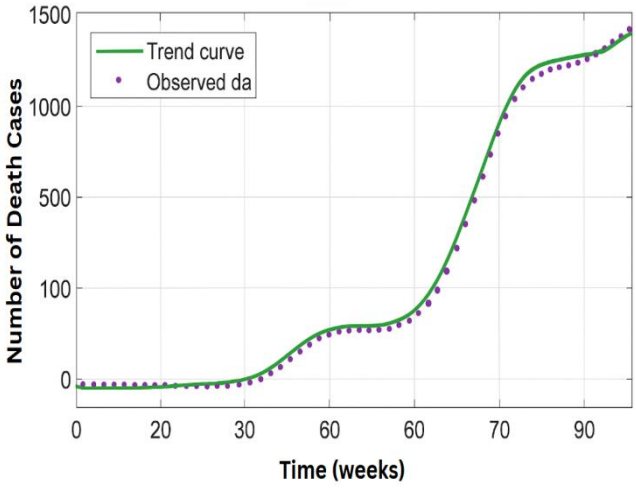



**Fig 4.** Simulation outcomes of No. of death cases

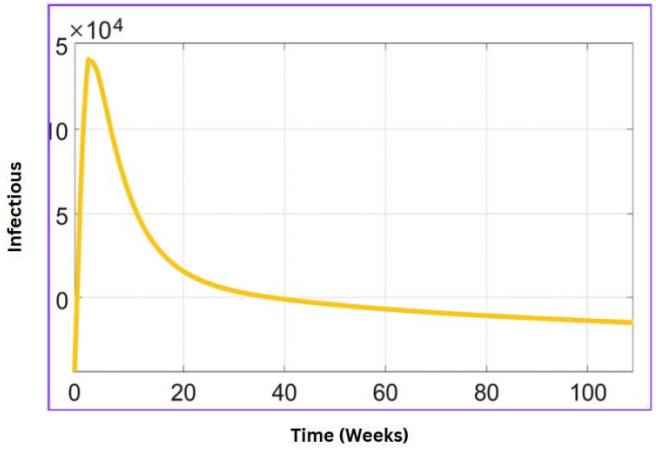



**Fig 5.** Simulation outcomes of Infectious cases vs. time

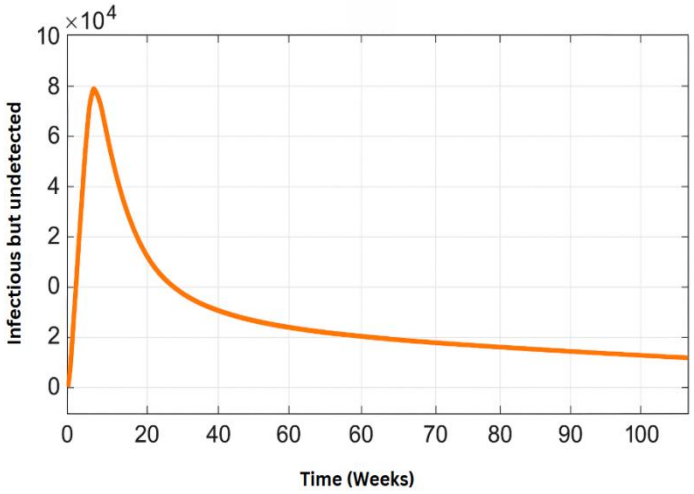



**Fig 6.**Simulation outcomes of Infectious but undetected cases

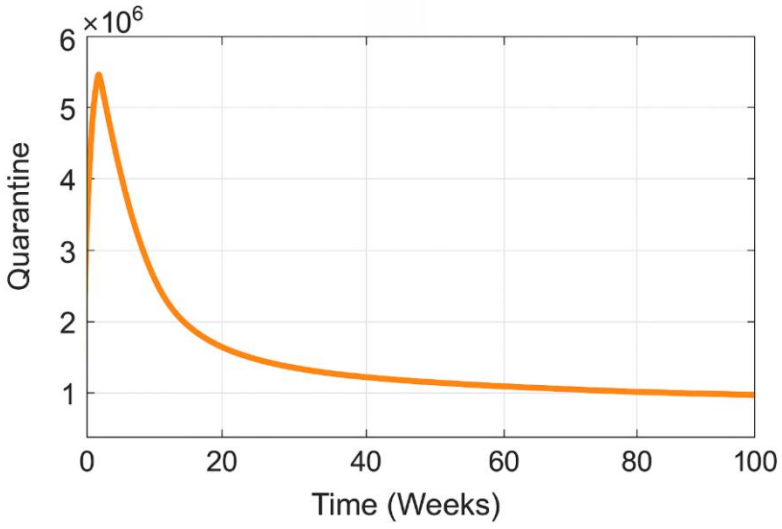



**Fig 7.** Simulation outcomes of Quarantine vs. time

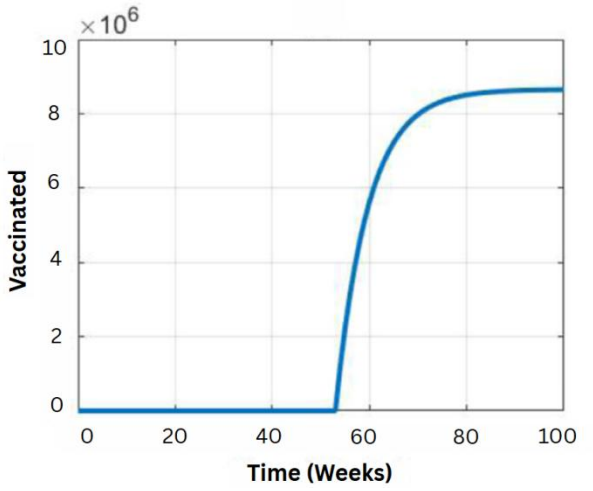



**Fig 8.** Simulation outcomes of Vaccinated vs. Time

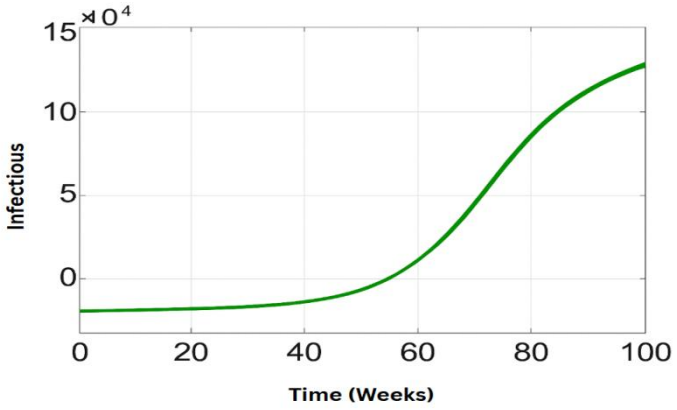



**Fig 9.** Cumulative outcomes of Infectious vs. Time

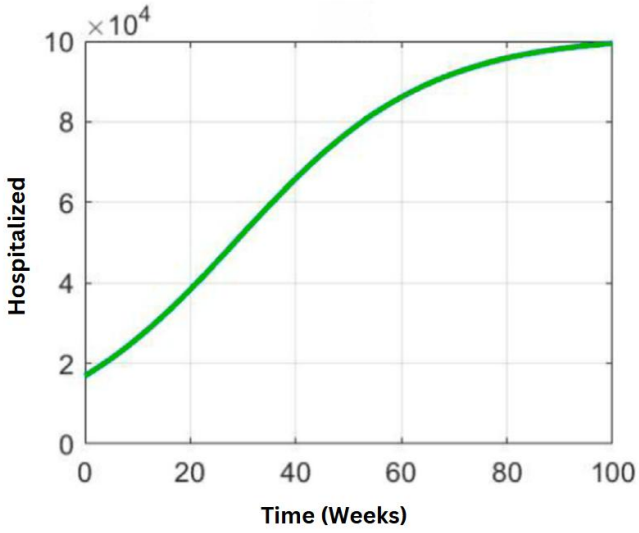



**Fig 10.** Cumulative outcomes of Hospitalized vs. Time

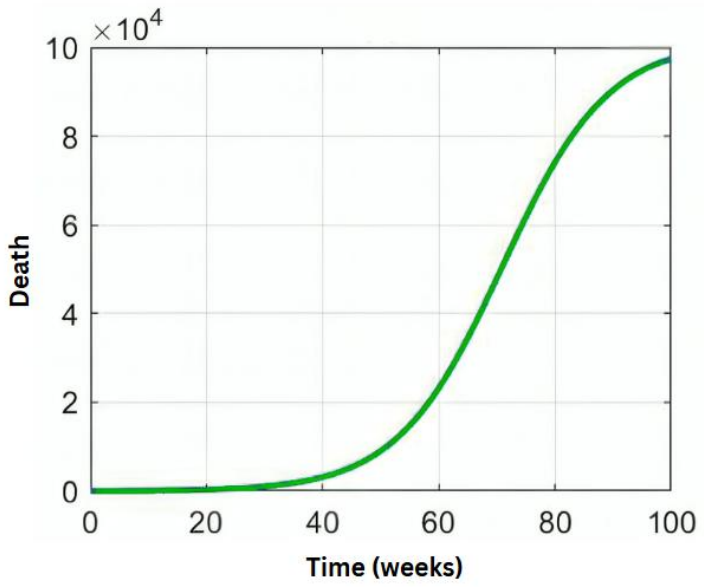



**Fig 11.** Cumulative outcomes of Death vs. Time

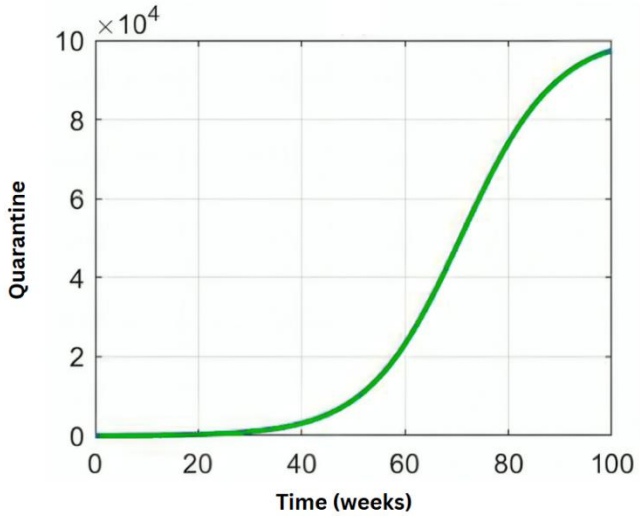



**Fig 12.** Cumulative outcomes of Quarantine vs. Time

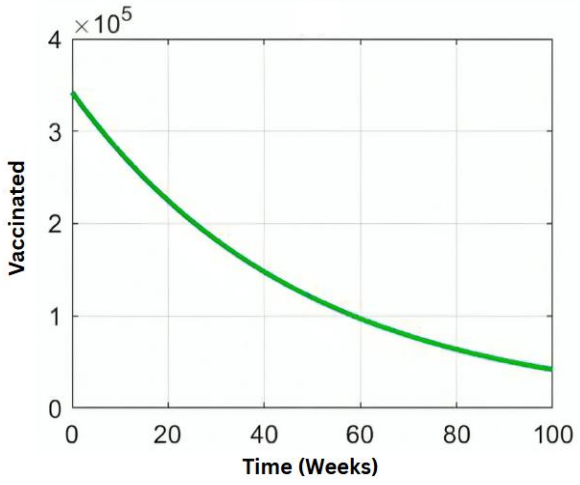



**Fig 13.** Cumulative Vaccinated vs. Time

The predicted counts of contaminated persons, unreported cases, individuals in home-based care, and hospitalized patients over 6 months were approximately 1,200, 28,000, 16,000, and 440,000, respectively.Over the 6 months, India had roughly 89,200 personscontaminated with respiratory disease. The count of demises is expected to rise in tandem with the growing count of contaminatedpersons. As shown in Fig 9 to Fig 13, the count of exposed persons is likely to decrease because those during the asymptomatic phase typically become symptomatic within 5 days and become capable of transmission. The count of segregatedpersons is expected to decline to zero, while Fig 12 projects that at least 9,000,000 people will be vaccinated over the 6 months.

## 4. Conclusion

The compartmental Susceptible Exposed Quarantined Recovered Vaccinated (SEQR-V) transmission network pattern is developed to explore the interactions withinrespiratory disease spread. Parameters connect the different compartments in the pattern. A dynamical systemsmathematical relationships pattern has been developed to pattern the dynamics of persons across various compartments. The pattern was subjected to qualitative analysis to examine its behavior and properties. The pattern parameters were determined through a mix of estimation fitting a model using least squares with observed data points and adoption of values from prior research. The outputs indicate that further transmissions occurfrom the exposed population by various sources, including those without symptoms, symptomatic individuals, unidentified cases, patients in-home care, and hospitalized patients, all impacting the basic reproduction count ($R_0$). The patterndemonstrates a good fit to the respiratory disease data, making it suitable for predictive modeling, as the differences between reported and predicted values for total cases, mortality, andimmunizations are not statistically significant. With the calculated $R_0$ value of 2.16, the Government of India should strengthen mitigation efforts to lower $R_0$.

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