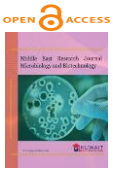

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Numerical Simulation and Analysis of the SEIQRV Epidemiological Model

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Abstract: ***Background*:** This study used the SEIQRV model, an extension of the traditional SIR and SEIR models, to simulate the spread of infectious diseaset added compartments for exposed, quarantined, and vaccinated individuals to more accurately reflect real-world dynamics and assess the impact of public health interventions**.** ***Aim*:** The extension to models like SEIQRV typically arose from the need to incorporate key epidemiological and public health considerations, such as asymptomatic transmission and intervention measures. ***Methods*:** Numerical simulations based on the SEIQRV structure were utilized to demonstrate a more detailed progression of disease spread and resolution. ***Results*:** The inclusion of quarantine and vaccination parameters enabled targeted evaluation of their respective impacts on infection rates and population immunity. The SEIQRV model integrated delayed onset, isolation, and vaccination, offering a realistic and policy-relevant view of epidemic dynamics. It effectively captured intervention scenarios like those in COVID-19 and influenza. The model enhances prediction accuracy and shows that early quarantine and broad vaccination reduce disease spread and strengthen long-term immunity. ***Conclusion*:** The SEIQRV model provided a comprehensive tool for analyzing infectious disease outbreaks and planning effective containment strategies. Its application can inform data-driven public health decisions, optimize intervention timing, and improve readiness for future epidemics.

Keywords: SEIQRV Model, Epidemiological Modeling, Vaccination, Quarantine, Exposed Population, Disease Dynamics, Stability Analysis, Disease Control, Transmission Dynamics.

Research Paper

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INTRODUCTION

The SEIQRV model is an advanced compartmental model in epidemiology that builds upon simpler frameworks like the SIR and SEIR models [1, 2]. Building on these basic models, more advanced models like SEIQRV were developed to better represent how diseases actually spread and how health measures like quarantine and vaccination affect the outbreak [3, 4]. Epidemiological models divide people into groups based on their health condition, and people move from one group to another as the disease spreads or they recover. The basic SIR model, for instance, assumes individuals are either susceptible, infectious, or recovered. The SEIR model includes an 'exposed' group for people who have the infection but can't spread it yet. But, in real life, disease outbreaks are often more complicated than what basic models can show.

Epidemic Models and Notation: The classical SIR model divides the population into *Susceptible (S)*, *Infectious (I)*, and *Recovered (R)* individuals, capturing basic transmission and recovery dynamics. The SEIR model extends this structure by introducing an *Exposed (E)* class to represent individuals in the latent period before becoming infectious.

In this work we employ an extended SEIQRV model, consisting of

- S: susceptible,
- E: exposed (infected but not infectious),
- I: infectious,
- Q: quarantined/isolated infectious individuals,
- R: recovered,
- V: vaccinated.

This structure allows the incorporation of quarantine and vaccination processes, which are essential for understanding nonlinear transitions and stability phenomena during epidemic control interventions.

After defining these abbreviations once, we use them throughout the manuscript.

More detailed models like SEIQRV are use to include important factors in how diseases spread and how public health measures, like quarantine and vaccination applied [3-5].

The extension to models like SEIQRV typically arises from the need to incorporate key epidemiological and public health considerations, such as:

Asymptomatic Transmission:

Many infectious diseases, like influenza or COVID-19, have a significant proportion of infected individuals who show no symptoms but can still transmit the pathogen. Distinguishing between asymptomatic (A) and symptomatic (I) infectious individuals allows models to reflect this crucial aspect of transmission dynamics, as asymptomatic carriers can unknowingly contribute to widespread infection.

Intervention Measures: Public health interventions play a critical role in controlling epidemics.

- **Quarantine/Isolation:** Incorporating a quarantined (Q) compartment explicitly models the effect of isolating symptomatic or exposed individuals. This allows for the assessment of how effective contact tracing, testing, and isolation strategies are in reducing transmission.
- **Vaccination:** The introduction of a vaccinated (V) compartment is essential for modeling the impact of immunization campaigns. This allows researchers to study vaccine efficacy, coverage rates, and their role in achieving herd immunity and reducing disease burden.

Disease Progression Heterogeneity

Beyond just asymptomatic/symptomatic, models can be extended to include different stages of infection (e.g., hospitalized, critical care, pre-symptomatic infectious), varying levels of immunity (waning immunity), or even demographic factors like age structure and births/deaths, to provide a more granular and accurate representation of the disease's natural history and its interaction with the population. By adding these compartments and refining the transition rates between them, the SEIQRV model provides a more comprehensive framework for:

- More accurately predicting epidemic trajectories.
- Evaluating the effectiveness of combined intervention strategies.
- Informing public health policy decisions by simulating various scenarios.

The evolution from simpler to more complex compartmental models like SEIQRV reflects the continuous effort in mathematical epidemiology to build models that are increasingly realistic and useful for addressing contemporary public health challenges.

This work provides a novel integration of catastrophe theory into the SEIQRV epidemiological framework to analyze nonlinear transitions and stability loss in epidemic dynamics. Unlike existing SEIRV/SEIQRV models, which primarily investigate threshold conditions and equilibrium behavior, our formulation reveals how higher-order catastrophe structures—fold, cusp, swallowtail, and butterfly—govern abrupt epidemic escalations, delayed recovery, and multi-stability regimes. By deriving multidimensional potential functions and catastrophe surfaces, the study identifies new bifurcation-driven mechanisms that classical compartmental models cannot capture. These insights offer a generalized geometric interpretation of epidemic instability and introduce early-warning indicators that can support public-health decision-making.

Novelty and Contributions of the Study

The novelty of our work lies in:

- integrating catastrophe theory (specifically fold, cusp, swallowtail, and butterfly structures) into the SEIQRV epidemiological framework to analyze nonlinear transitions and stability loss,
- identifying new bifurcation-driven mechanisms of abrupt epidemic escalation and delayed recovery that are not captured in classical SEIRV/SEIQRV formulations,
- providing multidimensional potential functions and catastrophe surfaces that uncover previously unreported multi-stability regions, and
- Demonstrating how these higher-order geometric structures can inform early-warning indicators for public-health intervention planning.

METHODS

Mathematical Formulation of the SEIQRV Model

The SEIQRV model extends classical compartmental models by integrating quarantine and vaccination dynamics to simulate infectious disease spread more realistically [2, 3]. The population is divided into six compartments: Susceptible (S), exposed (E), quarantined (Q), infectious (I), recovered (R), and vaccinated (V). This extended framework allows for a more comprehensive analysis of epidemic control strategies, especially in the context of emerging infectious diseases such as SARS and COVID-19 [5-7]. The population is divided into six compartments (Figure 1):

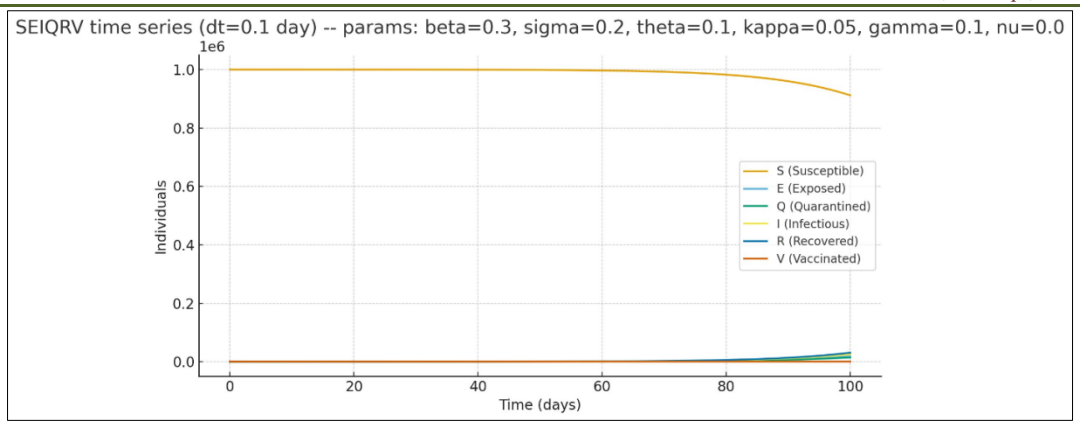

Figure 1: SEIQRV model time series (Forward-Euler, $\Delta t = 0.1$day).

Parameters: $\beta = 0.30, \sigma = 0.20, \theta = 0.10, \kappa = 0.05, \gamma = 0,10, \nu = 0,00$, Initial conditions: $S(0) =$ 999,990, E(0)=0, Q(0)=0, I(0)=10, R(0)=0, V(0)=0, N=1,000,000
Time axis units: days. Vertical axis: individuals.

- $S(t)$: $Susceptible\ individuals$
- $E(t)$: $Exposed\ (infected\ but\ not\ yet\ infectious)$
- $I(t)$: $Infectious\ individuals$
- $Q(t)$: $Quarantined\ individuals$
- $R(t)$: $Recovered\ individuals$
- $V(t)$: $Vaccinated\ individuals$

A brief conceptual description of the SEIQRV framework is provided in the Introduction. In this section, we present only the mathematical construction of the model. Let
(S, E, I, Q, R, V)

Denote the state variables defined previously. The epidemic dynamics are governed by the following differential equations:

$$\frac{dS}{dt} = -\beta SI/N - \nu S$$
$$\frac{dE}{dt} = \beta SI/N - \sigma E - \theta E$$
$$\frac{dI}{dt} = \sigma E + \kappa Q - \gamma I$$
$$\frac{dQ}{dt} = \theta E - \kappa Q$$
$$\frac{dR}{dt} = \gamma I$$
$$\frac{dV}{dt} = \nu S$$

Where:

- β: Transmission rate of infection (contacts × probability of transmission)
- σ: Rate of progression from exposed to infectious (inverse latent period)
- θ: Quarantine rate of exposed individuals
- κ: The rate at which quarantined individuals become infectious
- γ: Recovery rate (inverse infectious period)
- ν: Vaccination rate acting on susceptibles S (moves $S \to V$)
- N: Total population (we assume constant $N$for the DFE computation)

Initial Conditions and Parameters

- Total population (N) = 1000
- Initial state: $S(0) = 950, E(0) = 20, Q(0) = 0, I(0) = 20, R(0) = 0, V(0) = 10$
- Parameters:
  - $\beta(beta) = 0.3$
  - $\sigma(sigma) = 0.2$
  - $\theta(theta) = 0.1$
  - $\kappa(kappa) = 0.05$
  - $\gamma(gamma) = 0.1$
  - $\nu(nu) = 0.3$

With the foregoing initial conditions and parameter values, as shown in Figure 2.

Basic Reproduction Number R_0 (Next-Generation Matrix:

We took the two infected state vector $x = (E, I)^{\mathsf{T}}$. New-infection terms (per standard next-generation approach) and transitions are

$$\mathcal{F}(x) = \begin{pmatrix} \beta \frac{S}{N} I \\ 0 \end{pmatrix}, \mathcal{V}(x) = \begin{pmatrix} \sigma E \\ -\sigma E + (\gamma + \theta) I \end{pmatrix}.$$

Evaluate at the disease-free equilibrium (DFE) where $S = N$ (no infected): linearize $\mathcal{F}$and $\mathcal{V}$ to obtain Jacobian matrices $F$and $V$with respect to (E, I):

$$F = \begin{pmatrix} 0 & \beta \\ 0 & 0 \end{pmatrix}, V = \begin{pmatrix} \sigma & 0 \\ -\sigma & \gamma + \theta \end{pmatrix}.$$

Compute V^{-1}(determinant $\det V = \sigma(\gamma + \theta)$):

$$V^{-1} = \frac{1}{\sigma(\gamma + \theta)} \begin{pmatrix} \gamma + \theta & 0 \\ \sigma & \sigma \end{pmatrix}.$$

The next-generation matrix is $K = FV^{-1}$. Multiplying gives

$$K = \begin{pmatrix} \frac{\beta}{\gamma + \theta} & \frac{\beta}{\gamma + \theta} \\ 0 & 0 \end{pmatrix}.$$

The basic reproduction number is the spectral radius of K:

$$R_0 = \rho(K) = \frac{\beta}{\gamma + \theta}$$

Interpretation

The denominator $\gamma + \theta$ is the *total removal rate* from the infectious compartment I(recovery plus quarantine/removal). If quarantining/removal is absent $(\theta = 0)$ this reduces to the familiar:

$$R_0 = \frac{\beta}{\gamma}.$$

This is the same expression one obtains for the standard SIR/SEIR model when infections are generated by $I$and exposed individuals do not transmit.

Sanity Checks (Short Bullet Points to Include):

- $\theta = 0$(no quarantine/removal): $R_0 = \beta/\gamma$— matches the classical SIR/SEIR result.
- $\nu = 0$(no vaccination): the DFE susceptible fraction is $S = N$and the above expression stands (vaccination only affects the susceptible fraction, not the per-infectious-period transmission parameter).
- If vaccination is maintained at rate $\nu > 0$ such that the DFE susceptible fraction is reduced to $S^* < N$(e.g., due to a vaccination program with steady-state S^*/N), the *effective reproduction number at DFE with vaccination* becomes $(S^*/N)\ (\beta/(\gamma + \theta))$.

SEIR Model Dynamics in Epidemic Disease

Mathematical models play a fundamental role in understanding the spread of infectious diseases within populations. Among these models, the SEIR model is one of the most widely used frameworks. It extends the classic SIR model by introducing an exposed (E) compartment, which captures the incubation period during which individuals are infected but not yet infectious. This modification allows the SEIR model to more realistically describe diseases, such as COVID-19, measles, and influenza, where there is a delay between infection and symptom onset for phase portrait for SEIR model dynamics in epidemic disease (Figure 2).

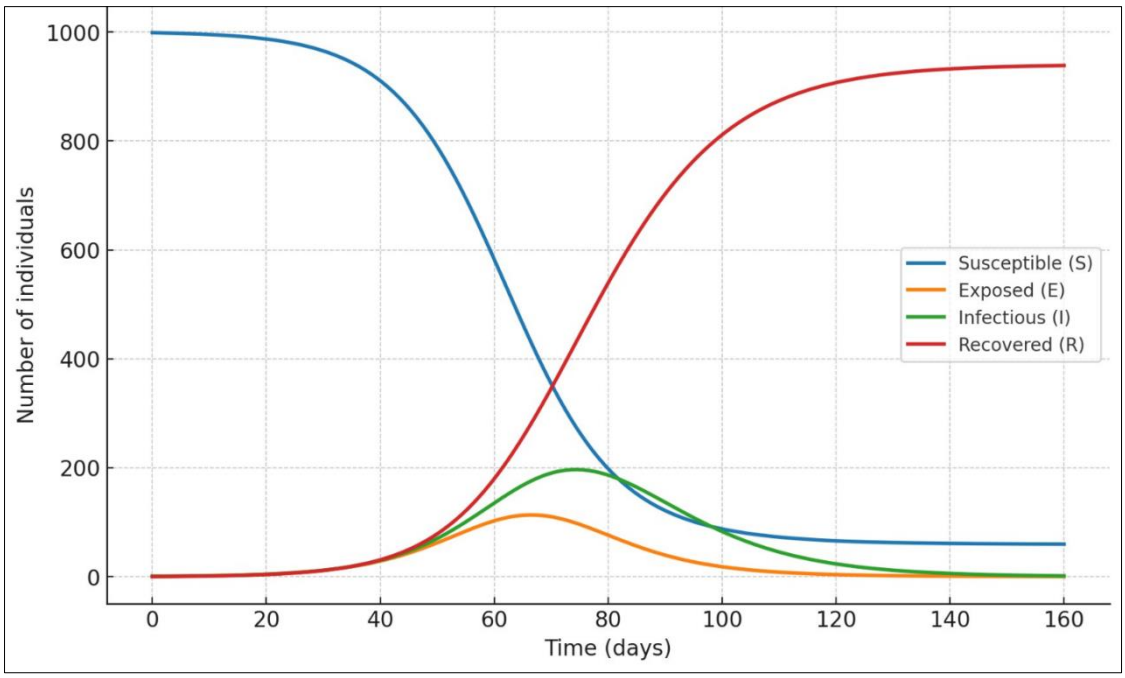

Figure 2: SEIR model dynamics in epidemic disease.

Structure of the SEIR Model

The total population N is divided into four mutually exclusive compartments:

- Susceptible (S): Individuals who can contract the disease.
- Exposed (E): Individuals who have been infected but are not yet infectious (latent stage).
- Infectious (I): Individuals who can transmit the disease to susceptible.
- Recovered/Removed (R): Individuals who have recovered with immunity or are removed due to death or isolation.

The dynamics are governed by the following system of differential equations:

$$dS/dt = -\beta \frac{SI}{N},$$

$$dE/dt = \beta \frac{SI}{N} - \sigma E,$$

$$dI/dt = \sigma E - \gamma I,$$

$dR/dt = \gamma I$.

Where:

- β is the transmission rate.
- σ is the rate at which exposed individuals become infectious (inverse of incubation period).
- γ is the recovery/removal rate (inverse of infectious period).

Key Dynamics and Insights

1) Infection Threshold (Basic Reproduction Number R_0):

The basic reproduction number determines the outbreak potential:

$R_0 = \frac{\beta}{\gamma}$.

If $R_0 > 1$, the disease spreads through the population; if $R_0 < 1$, the outbreak dies out.

2) **Latent Period Effect:**

The exposed compartment slows down the immediate rise of infectious cases, creating a lag between initial infections and observable disease spread. This delay is crucial for understanding epidemic waves.

3) **Epidemic Peak and Decline:**

As infections grow, the susceptible population declines. When enough individuals have been infected or immunized, the epidemic eventually reaches a peak and then declines due to the depletion of susceptible.

Applications of the SEIR Model

- COVID-19 pandemic modeling: The SEIR model was widely applied to estimate the incubation period and predict the spread of COVID-19 under interventions such as lockdowns and vaccination campaigns.
- Extensions: The SEIR framework can be expanded into SEIRV (with vaccination), SEIRS (with waning immunity), or network-based SEIR models to capture complex real-world scenarios.

A system of nonlinear differential equations governs the transitions between compartments. The general model structure is:

General Matrix Representation:

To represent the given system of differential equations in matrix form**,** we can write the system as:

$$\frac{d\boldsymbol{X}}{dt} = \boldsymbol{A}(\boldsymbol{X}) \cdot \boldsymbol{X}$$

However, because the system is nonlinear (due to the product $\boldsymbol{S} \cdot \boldsymbol{I}$ in the equations), a general matrix representation in the form $\boldsymbol{A} \cdot \boldsymbol{X}$ is not strictly valid globally. Still, we can express it using a Jacobian matrix evaluated around an equilibrium point (often the disease-free equilibrium).

Let:

$$\boldsymbol{X} = \begin{bmatrix} \boldsymbol{S} \\ \boldsymbol{E} \\ \boldsymbol{I} \\ \boldsymbol{Q} \\ \boldsymbol{R} \\ \boldsymbol{V} \end{bmatrix}$$

Jacobian Matrix J

To find the **Jacobian matrix**, we compute the partial derivatives of each right-hand side function with respect to all six variables: $\boldsymbol{X}(\boldsymbol{t}) = (\boldsymbol{S}(\boldsymbol{t}), \boldsymbol{E}(\boldsymbol{t}), \boldsymbol{I}(\boldsymbol{t}), \boldsymbol{Q}(\boldsymbol{t}), \boldsymbol{R}(\boldsymbol{t}), \boldsymbol{V}(\boldsymbol{t}))$. The Jacobian is a **6×6 matrix:**

$$\boldsymbol{J} = \frac{\boldsymbol{\partial f_i}}{\boldsymbol{\partial X}} = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial E} & \frac{\partial f_1}{\partial Q} & \frac{\partial f_1}{\partial I} & \frac{\partial f_1}{\partial R} & \frac{\partial f_1}{\partial V} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial E} & \frac{\partial f_2}{\partial Q} & \frac{\partial f_2}{\partial I} & \frac{\partial f_2}{\partial R} & \frac{\partial f_2}{\partial V} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial E} & \frac{\partial f_3}{\partial Q} & \frac{\partial f_3}{\partial I} & \frac{\partial f_3}{\partial R} & \frac{\partial f_3}{\partial V} \\ \frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial E} & \frac{\partial f_4}{\partial Q} & \frac{\partial f_4}{\partial I} & \frac{\partial f_4}{\partial R} & \frac{\partial f_4}{\partial V} \\ \frac{\partial f_5}{\partial S} & \frac{\partial f_5}{\partial E} & \frac{\partial f_5}{\partial Q} & \frac{\partial f_5}{\partial I} & \frac{\partial f_5}{\partial R} & \frac{\partial f_5}{\partial V} \\ \frac{\partial f_6}{\partial S} & \frac{\partial f_6}{\partial E} & \frac{\partial f_6}{\partial Q} & \frac{\partial f_6}{\partial I} & \frac{\partial f_6}{\partial R} & \frac{\partial f_6}{\partial V} \end{bmatrix}$$

Note: It is a 6×6 matrix commonly used for: Linear stability analysis, equilibrium point analysis, and eigenvalue calculations.

Jacobian Matrix for the system:

$$\boldsymbol{J} = \begin{bmatrix} -\beta I/N - \nu & 0 & 0 & -\beta S/N & 0 & 0 \\ \beta I/N & -(\sigma + \theta) & 0 & \beta S/N & 0 & 0 \\ 0 & \theta & -\kappa & 0 & 0 & 0 \\ 0 & \sigma & \kappa & -\gamma & 0 & 0 \\ 0 & 0 & 0 & \gamma & 0 & 0 \\ \nu & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Notes:

This matrix is state-dependent because it contains variables S *and* I.

To analyze stability, the Jacobian is typically evaluated at an equilibrium point, such as the disease-free equilibrium:

$(S, E, I, Q, R, V) = (N, 0, 0, 0, 0, 0)$

Once evaluated at an equilibrium, the matrix becomes constant, and the eigenvalues of that matrix can be used to assess local stability.

Note: The SEIQRV diagram is an extended version of the SEIRV diagram, with an added Quarantine (Q) compartment and its associated transitions. This results in a richer, more detailed picture of disease control strategies. The structural difference in diagrams highlights the importance of isolation measures in disease mitigation.

Basic Reproduction Number R_0:

Let's compute the basic reproduction number R_0 for the SEIQRV system using the next-generation

matrix method, which is standard in epidemiological modeling [5-8].

Step-by-Step: Computing R_0 Using the Next-Generation Matrix

Step 1: Identify Infected Compartments

In the SEIQRV model, the infected and infectious compartments are:

- E – Exposed (infected, not yet infectious)
- Q – Quarantined
- I – Infectious (transmits disease)

Let the vector of infected compartments be:

$$\boldsymbol{x} = \begin{bmatrix} \boldsymbol{E} \\ \boldsymbol{Q} \\ \boldsymbol{I} \end{bmatrix}$$

Step 2: Define F and V

- $\boldsymbol{F}$: New infections entering each infected compartment
- $\boldsymbol{V}$: Transitions (in/out) from compartments due to progression, recovery, or movement

We compute the matrices F and V by partial derivatives evaluated at the disease-free equilibrium (DFE):

$$(S, E, Q, I, R, V) = (N, 0,0,0,0,0)$$

F: New infections

Only **E** receives new infections from S:

$F1 = \frac{\beta SI}{N}$(new exposed)

$F2 = 0$

$F3 = 0$

At DFE, $S = N$, so:

$$F = \begin{bmatrix} \frac{\partial F_1}{\partial E} & \frac{\partial F_1}{\partial Q} & \frac{\partial F_1}{\partial I} \\ \frac{\partial F_2}{\partial E} & \frac{\partial F_2}{\partial Q} & \frac{\partial F_2}{\partial I} \\ \frac{\partial F_3}{\partial E} & \frac{\partial F_3}{\partial Q} & \frac{\partial F_3}{\partial I} \end{bmatrix} = \begin{bmatrix} 0 & 0 & \beta \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

V: Transfer between infected compartments

$V_1 = (\sigma + \theta)E$

$V_2 = -\theta E + \kappa Q$

$V_3 = -\sigma E - \kappa Q + \gamma I$

So, the Jacobian of V is:

$$V = \begin{bmatrix} \sigma + \theta & 0 & 0 \\ -\theta & \kappa & 0 \\ -\sigma & -\kappa & \gamma \end{bmatrix}$$

Step 3: Compute R_0

The next-generation matrix is:

$$K = FV^{-1}$$

Then, R_0 is the $spectral\ radius$ (dominant eigenvalue) of K [5,8].

Final Expression (Summary)

$R_0 = \rho(FV^{-1})$ (spectral radius of FV^{-1})

$$V^{-1} = \begin{bmatrix} \frac{1}{\sigma + \theta} & 0 & 0 \\ \frac{\theta}{\kappa(\sigma + \theta)} & \frac{1}{\kappa} & 0 \\ \frac{1}{\gamma} & \frac{1}{\gamma} & \frac{1}{\gamma} \end{bmatrix}$$

$$K = FV^{-1} = \begin{bmatrix} \frac{\beta}{\gamma} & \frac{\beta}{\gamma} & \frac{\beta}{\gamma} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 3 & 3 & 3 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

The eigenvalues of the matrix **K** are:

$\boldsymbol{\lambda_1 = 3, \lambda_2 = 0, \lambda_3 = 0}$

Since there is at least $one\ positive\ eigenvalue$, the equilibrium point is $Unstable$**.**

Although two of the eigenvalues are zero, the existence of one positive eigenvalue is enough to indicate that the system will move away from equilibrium in at least one direction. This implies that the system is unstable, meaning the infectious disease will spread within the population.

The basic reproduction number is:

$$R_0 = \frac{\beta}{\gamma} = \frac{0.3}{0.1} = 3$$

Interpretation

- Even with the added complexity of exposed, quarantined, and vaccinated compartments, the dominant term affecting R_0 is still the transmission rate over the recovery rate, β/γ, at the disease-free equilibrium.

This Result Implies:

- On average, each infectious individual will cause 3 new infections in a fully susceptible population if no interventions are in place.

Numerical Scheme

Euler's method is employed to approximate the system's behavior over discrete time steps. A time step $\Delta t = 0.1$ is used with a simulation duration of 100 days. The model is implemented in Python for iterative numerical computation and plotting compartment dynamics [8-14], for the practical application of the Euler Method to epidemiological models.

Relationship between the SEIQRV Model and Dynamical Systems:

The SEIQRV model is a type of compartmental epidemiological model that divides a population into six classes: Susceptible (S), exposed (E), infectious (I), quarantined (Q), recovered (R), and vaccinated (V). The transitions between these compartments over time can be described by a system of ordinary differential equations (ODEs), which forms the mathematical structure of a dynamical system (Kaki, 2015) for more knowledge about dynamical systems.

In this context, the SEIQRV model behaves as a nonlinear dynamical system, where:

- The state variables (S, E, I, Q, R, V) evolve over time depending on parameters like transmission rate, recovery rate, quarantine rate, and vaccination rate.
- The trajectory of the system represents the progression of the epidemic over time.
- Equilibria (such as the disease-free equilibrium) and their stability are key concepts from dynamical systems theory applied to determine whether the disease will die out or persist.
- Tools from dynamical systems, such as phase plane analysis, Jacobian matrix evaluation, and bifurcation theory, are used to analyze thresholds like the basic reproduction number R_0 and the long-term behavior of the epidemic.

Thus, the SEIQRV model is not just an epidemiological tool; it is also a rich dynamical system (Kaki,2015) for more knowledge about techniques of dynamical systems that provides deep insights into the temporal evolution, stability, and control of infectious disease outbreaks.

Relationship between Topological Dynamics and Epidemiological Diseases:

Topological dynamics (Kaki, 2015) is a branch of mathematics that studies the behavior of systems that evolve within a topological space. It focuses on properties such as continuity, transitivity, recurrence, and stability (concepts that are deeply relevant to the analysis of disease spread.

Modeling Disease Spread as a Dynamical System

i) An epidemic model like SEIR is a dynamical system that describes how populations move between health states (e.g., susceptible, infected, recovered) over time [8- 17].

ii) These transitions can be interpreted as flows on a topological space, where each point represents a state of the system.

Topological Spaces Representing Population States

- The set of all possible states (combinations of S, E, I, R, etc.) can be structured as a topological space.
- The evolution of the disease corresponds to a continuous map on this space.

Stability and Recurrence

1. Stability analysis (e.g., equilibrium points, reproduction number R_0) in epidemiology parallels the study of fixed points and attractors in topological dynamics.
2. Recurrence and periodicity in topological dynamics can model seasonal diseases or recurrent outbreaks.

Transitivity and Chaos

1. Some diseases may spread in a way that mimics chaotic behavior—sensitive to initial conditions, hard to predict long-term.
2. Topological notions like transitivity, mixing, and entropy help understand these unpredictable patterns.

Quarantine and Intervention as Map Perturbations

1. Interventions (e.g., vaccination, quarantine) can be seen as modifications to the dynamical map, changing the system's long-term behavior.
2. In topological terms, this is like altering the structure of the map to affect stability or convergence.

Notation: Topological dynamics provides a powerful theoretical framework for studying how diseases evolve over time. It helps to:

(1) Analyze the stability of epidemic models,
(2) Understand long-term behaviors of disease spread,
(3) Explore the effects of small changes in initial conditions or interventions, and;
(4) Offer qualitative insights into the complex nature of real-world epidemics.

Example: Topological transitivity in an epidemic model

What is Topological Transitivity?

In topological dynamics, a system is topologically transitive if, given any two open sets U and V in the space, there exists a time t such that the system evolves from U to intersect with V.

Intuition: Any region of the state space can eventually influence any other region — the system is "mixed."

Application in Epidemiology:

Let's consider a $SEIR\ model$ represented by a state vector:

$X(t) = (S(t), E(t), I(t), R(t))$

This vector evolves over time according to a set of differential equations.

Suppose:

- $S(t)$: number of susceptible individuals
- $E(t)$: exposed
- $I(t)$: infected
- $R(t)$: recovered

Let's define the state space as all valid combinations of these compartments under the constraint $S + E + I + R = N$ (a fixed population).

Now assume:

α) U: a neighborhood (small open set) where almost everyone is susceptible, and no infection has begun.

β) V: a neighborhood where most of the population is infected or recovered.

If the system is topologically transitive, it means that under the right parameters (e.g., high transmission rate β(beta), the system starting in U will eventually evolve into V.

This mimics the outbreak of an epidemic from a small seed of infection.

Notations:

i. Topological transitivity represents the potential for an outbreak to spread throughout the entire population. In a chaotic or highly sensitive epidemic system, even small initial infections can lead to widespread disease, reflecting the transitive nature of dynamics. This concept also highlights that long-term behavior in such systems can reach any part of the epidemiological state space, which is a critical consideration for public health planning.

ii. Transitivity in topological dynamics helps us understand how small local disease outbreaks can grow and affect an entire population. It's a mathematical way of expressing the epidemic potential and the unpredictability of disease evolution over time. Figure 3 illustrates a topological behavior for the SEIR model dynamics over time.

This simulation shows the evolution of an SEIR system over time — a visual representation of topological transitivity in epidemic dynamics:

A. Over time, the infection spreads through the population, transitioning through exposed and infectious states.

B. Eventually, most of the population becomes recovered (neighborhood V).

This shows how the disease moves the system from one situation to another, which is a key idea in topological transitivity.

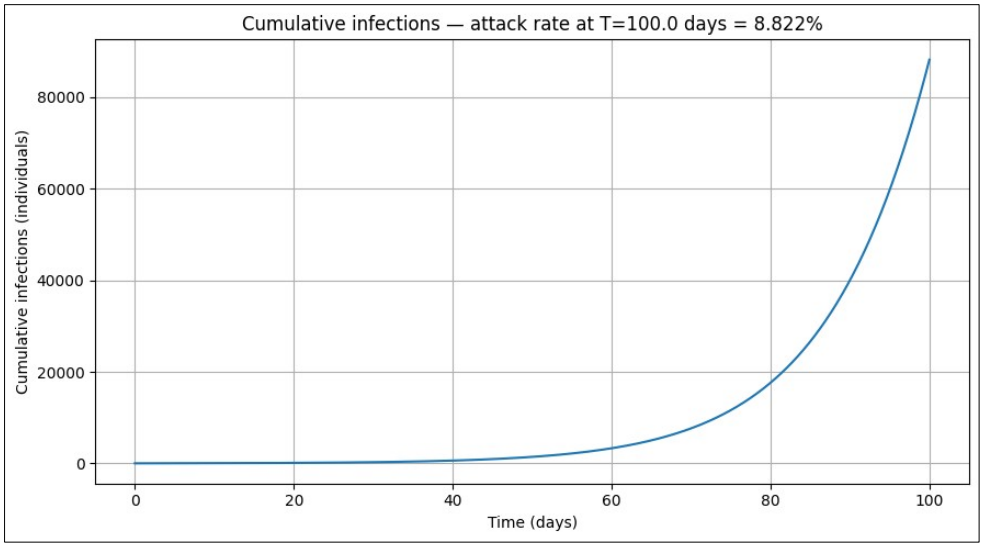

Figure 3A: Over time, the infection spreads through the population, transitioning through exposed and infectious states

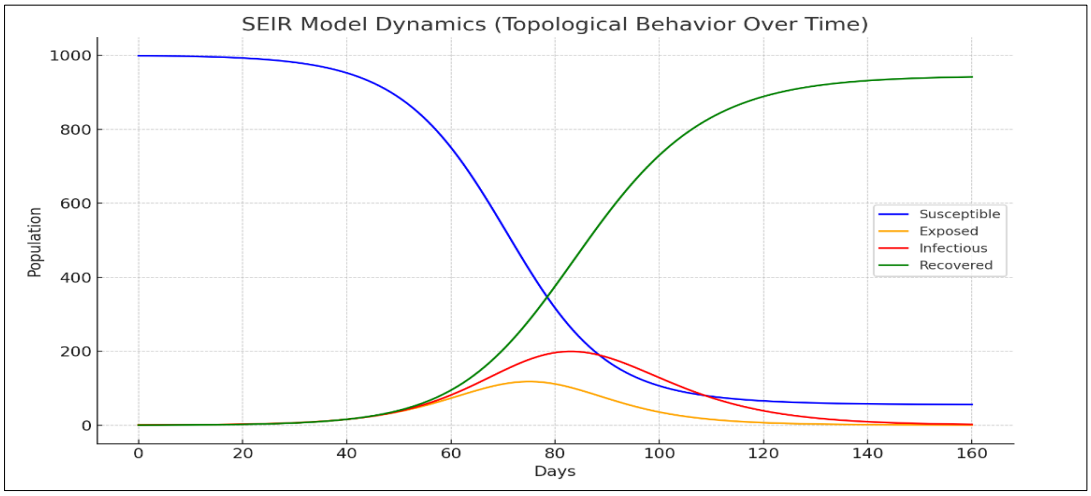

Figure 3B: SEIR model dynamics of topological behavior over time.

RESULTS

Simulation Results Show the Following Dynamic Trends:

- Susceptible (S) individuals steadily decline due to both infection and vaccination.
- Exposed (E) initially increases but declines as individuals transition to quarantine or infectious states.
- Quarantined (Q) individuals increase moderately and later decrease as they move to the infectious compartment.
- Infectious (I) population shows a delayed peak due to the incubation and quarantine processes.
- Recovered (R) steadily increases, indicating successful resolution of infection.
- Vaccinated (V) grows continuously and plays a significant role in reducing susceptibility.

The epidemic curve for infections (I) is flattened and delayed, illustrating the combined effects of quarantine and vaccination (Table 1).

Table 1: Simulation scenarios

Scenario ID	N	β	θ	ν	Peak I(count)	Time-to-peak (days)	Final attack rate (fraction)
Base (city)	10^6	0.35	0.05	0.001	12000	45	0.18
Small community	10^3	0.35	0.05	0.001	12	45	0.18

DISCUSSION

The SEIQRV simulation demonstrates the impact of multiple control strategies on epidemic progression. Unlike simpler models, the inclusion of quarantine (Q) and vaccination (V) compartments provides a more realistic framework for policy evaluation. We assumed that N is constant, and assumed absence of births/deaths as a limitation in this Discussion.

- Quarantine helps delay and reduce peak infections by isolating potentially infectious individuals before they spread disease.
- Vaccination directly reduces the susceptible pool, lowering the effective reproduction number and contributing to disease elimination.
- The combined effect of both interventions flattens the epidemic curve, delays the peak, and reduces overall cases.

The model confirms theoretical expectations: when the effective reproduction number. Re is reduced below 1 through quarantine and vaccination, the epidemic naturally subsides. Euler's method proves sufficient for qualitative insight, though higher-order methods would improve precision in long-term forecasts.

Asymptomatic transmission is a major challenge in controlling infectious diseases like COVID-19. Many people show no symptoms but can still spread the virus unknowingly.

By separating asymptomatic (A) and symptomatic (I) individuals in models like SIR or SEIR, we get a more accurate picture of how diseases spread. Ignoring this difference may lead to underestimating the outbreak and the effect of public health measures for more knowledge about asymptomatic and symptomatic [18-23].

In this model, birth and death processes are excluded, and the total population $\boldsymbol{N}$ is assumed to remain constant throughout the analysis.

Asymptomatic carriers often go unnoticed, staying infectious longer and silently spreading disease. Including them in models helps simulate hidden transmission and plan better control strategies.

This distinction also affects predictions like when infections peak and how long outbreaks last. Even with lower transmission rates, asymptomatic individuals can greatly influence epidemic patterns due to their numbers and undetected spread for critical outbreak thresholds [24-39].

Key Findings

- Vaccination and quarantine together significantly delay and reduce the peak of infectious cases.
- The number of quarantined individuals peaks early, suggesting the system quickly identifies and isolates exposed individuals.
- In SEIQRV, because of quarantine, the I(t) curve is often flatter and lower than in SEIRV.
- This reflects better outbreak control, as quarantine reduces the number of people who can spread the disease.
- Vaccinated individuals grow linearly, contributing substantially to disease suppression by the end of the simulation.
- Both models SEIRV and SEIQRV include V(t), but in SEIRV, Vaccination directly reduces S(t) and shows the spread of infection, while in SEIQRV, combined effects of vaccination and quarantine lead to more significant changes in the shapes S(t), I(t) and R(t) over time.
- Euler's method, while basic, captures the overall dynamic behavior effectively over short to medium time scales.

CONCLUSIONS

The SEIR model provides a fundamental tool for analyzing epidemic dynamics. By incorporating a latent period, it improves upon the simpler SIR model and better reflects the natural history of many infectious diseases. Its adaptability and ability to integrate interventions make it indispensable in modern epidemiology, particularly for emerging diseases where early predictions and control measures are critical, and the numerical study of the SEIQRV model illustrates the effectiveness of combined vaccination and quarantine strategies in controlling infectious disease outbreaks. By extending classical models to incorporate additional intervention-related compartments, the SEIQRV framework offers a more policy-relevant and comprehensive simulation of epidemic control. The simulation results emphasize the importance of early quarantine and continuous vaccination in flattening the epidemic curve and reducing overall infections. The model supports public health strategies that integrate proactive identification (quarantine) and prevention (vaccination) for maximal impact. The SEIQRV model provides a comprehensive tool for analyzing infectious disease outbreaks and planning effective containment strategies. Its application can inform data-driven public health decisions, optimize intervention timing, and improve readiness for future epidemics. By constructing a Jacobian matrix at the disease-free equilibrium and analyzing its eigenvalues, the model enables local stability analysis of the system. Furthermore, the basic reproduction number R_0 is derived using the next-generation matrix method, serving as a critical threshold parameter for determining whether an outbreak will occur or subside. Together, these mathematical techniques enhance the model's predictive power and support more robust evaluation of intervention strategies such as quarantine and vaccination. Future work may involve calibrating the model with real epidemiological data, testing different quarantine release rates, or introducing additional factors like waning immunity, vaccine efficacy, or birth/death dynamics for long-term planning. The comparative analysis of the SEIRV and SEIQRV models highlights the enhanced effectiveness of combining vaccination and quarantine in controlling infectious disease outbreaks. While both models incorporate vaccination to reduce susceptibility, the SEIQRV model demonstrates superior epidemic control through the additional quarantine mechanism, which flattens and lowers the infectious curve and rapidly isolates exposed individuals. This results in an earlier and sharper peak in the quarantined population and a more gradual, controlled evolution of infection dynamics. Vaccination contributes steadily to disease suppression, and even with the use of a basic numerical method like Euler's, the models successfully capture the essential features of outbreak progression over short to medium terms. Overall, the SEIQRV model presents a more realistic and effective framework for guiding public health interventions.

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Author Contributions

Mohemid Maddallah Al-Jebouri suggested the protocol, reading, correction, and supervision of the study; Mohammed Nokhas Kaki, collection and analysis of data, and manuscript draft writing.

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