

Data-Driven Comparative Analysis of SI, SIS, and SIR Models for Infectious Disease Transmission Dynamics

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Abstract: *This paper presents a comparative study of three classical epidemic compartmental models SI (Susceptible–Infected), SIS (Susceptible–Infected–Susceptible), and SIRS (Susceptible–Infected–Recovered–Susceptible) augmented with a data-driven framework for adaptive parameter estimation. The central argument is that traditional epidemic models, which assume fixed transmission and recovery rates, are inadequate for capturing real-world disease dynamics, and that incorporating data-driven based dynamic parameter estimation yields smoother, more realistic epidemic forecasting. The study covers mathematical formulation, analytical solutions, and numerical simulation using Euler's method, equilibrium/stability analysis, and graphical comparison of classical and data-driven variants of each mod. Comparative analysis demonstrates that data-driven approaches support outbreak forecasting, parameter estimation, and epidemic transmission analysis.*

Keywords: Transmission Dynamics, Infectious Diseases, Data-Driven Prediction and Epidemic Models

1. Introduction

The transmission dynamics of infectious diseases such as COVID-19, influenza, SARS, and Ebola are continuously influenced by environmental conditions, vaccination campaigns, healthcare interventions, and population behaviour. Mathematical epidemiology plays a significant role in analysing disease spread, predicting outbreak behaviour, and supporting public health decision-making [1–6]. Classical epidemic models such as the SI (Susceptible–Infected), SIS (Susceptible–Infected–Susceptible), and SIRS (Susceptible–Infected–Recovered–Susceptible) models are widely used to study infectious disease transmission dynamics. These compartmental models divide the population into epidemiological classes and describe disease transmission behaviour using systems of differential equations. The SI model explains continuous infection spread without recovery, whereas the SIS model incorporates recovery and reinfection dynamics. The SIRS model further includes temporary immunity loss and reinfection mechanisms, making it suitable for analysing recurring infectious diseases. The mathematical foundations of epidemic modelling were established through the pioneering work of Kermack and McKendrick, who introduced compartmental epidemic models for studying infectious disease transmission dynamics [1]. Anderson and May later expanded the theoretical and practical applications of epidemic models in public health analysis and disease forecasting [2]. Subsequently, numerous studies investigated numerical simulation, stability analysis, and epidemic prediction using compartmental modelling approaches [3–6]. Although classical epidemic models provide important insights into disease transmission behaviour, they generally assume fixed transmission, recovery, and immunity-loss rates, which may not accurately represent real-world epidemic situations. In practice, disease dynamics vary due to

environmental conditions, healthcare interventions, vaccination strategies, behavioural changes, and population mobility.

Recent studies have highlighted the importance of data-driven approaches in epidemic modelling and forecasting [7–17]. Epidemic data can be used to estimate transmission, recovery, and immunity-loss parameters, thereby improving the representation of disease dynamics. Data-driven parameter estimation techniques enable mathematical models to incorporate observed epidemic trends and provide more realistic forecasting results. The integration of classical epidemic models with data-driven methods offers a useful framework for analysing infectious disease transmission and enhancing epidemic prediction. The main objective of this study is to perform a data-driven comparative analysis of SI, SIS, and SIRS epidemic models for infectious disease transmission dynamics. The study investigates the epidemic behaviour of classical and data-driven epidemic models through mathematical formulation, numerical simulation, graphical interpretation, and comparative epidemic analysis. Furthermore, the role of data-driven parameter estimation in improving epidemic prediction and forecasting capability is examined.

2. Literature Review

Mathematical epidemic modelling has been extensively studied for understanding infectious disease transmission dynamics and epidemic forecasting. The pioneering epidemic model proposed by Kermack and McKendrick established the theoretical foundation of compartmental epidemic modelling and significantly contributed to modern mathematical epidemiology [1]. Their work introduced the concept of dividing populations into epidemiological compartments and analysing disease spread using differential equations.

Anderson and May further developed epidemic modelling theory and explored the practical applications of infectious disease models in epidemic control and public health systems [2]. Their studies demonstrated the importance of transmission parameters, recovery dynamics, and epidemic thresholds in disease prediction. Later, Diekmann and Heesterbeek provided comprehensive mathematical approaches for analysing infectious disease dynamics, stability behaviour, and epidemic forecasting [3]. Several researchers have investigated SI, SIS, and SIRS epidemic models for analysing infectious disease transmission behaviour [4–6]. The SI model has been widely used for studying irreversible infection spread, whereas the SIS model has been applied to diseases involving reinfection dynamics. The SIRS model has been considered more realistic for recurring infectious diseases due to the inclusion of temporary immunity loss and reinfection mechanisms.

Recent studies have emphasized the importance of data-driven approaches in epidemic prediction and disease forecasting [7–17]. Infection data have been used to estimate transmission and recovery parameters, analyse epidemic trends, and improve forecasting performance. Data-driven parameter estimation techniques provide a practical framework for incorporating observed epidemic data into mathematical models and enhancing their predictive capability. Although numerous studies have been conducted on mathematical epidemiology and data-driven epidemic forecasting, comparative analyses of SI, SIS, and SIRS models under both classical and data-driven frameworks remain limited. The present study addresses this gap by providing a systematic comparative analysis of SI, SIS, and SIRS epidemic models and demonstrating the role of data-driven parameter estimation in epidemic modelling and forecasting.

3. Mathematical Form of Basic Epidemic Models

Mathematical models play an important role in understanding the transmission dynamics of infectious diseases. In this study, we consider basic epidemic models for infectious diseases such as influenza, COVID-19, dengue, malaria, HIV, and various bacterial infections. These models help describe the spread of disease within a population and provide insights into epidemic behaviour. Many researchers have extended and analyzed epidemic models in numerous ways to better understand disease transmission and control strategies. In this article, we focus on the classical SI, SIS, and SIRS epidemic models. The primary objective of these models is to understand the mechanisms of disease transmission, predict the spread of infection, analyze epidemic dynamics, and support the development of effective disease control and prevention strategies.

3.1 SI Epidemic Model

The SI (Susceptible–Infected) epidemic model is the simplest epidemic framework, describing irreversible infection spread with no recovery mechanism.

3.1.1 Mathematical Formulation and Numerical Analysis of the SI Model

In SI epidemic model the population divided into two groups: susceptible persons (S), infected persons (I). Such as

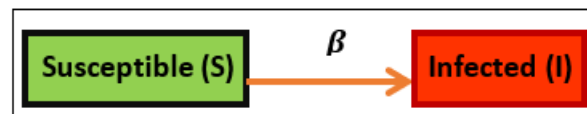


Figure 1: SI Model

SI epidemic model governing ordinary differential equations as

$$\left[\begin{array}{l} \frac{dS}{dt} = -\beta SI \\ \frac{dI}{dt} = \beta SI \end{array} \right] \quad (1)$$

Where S represents the susceptible population, I represents the infected population, and β denotes the disease transmission rate and the initial conditions are $S(0) = n, I(0) = 1$ then the total population is $n + 1$.

$$\frac{dS}{dt} + \frac{dI}{dt} = 0 \quad \text{and} \quad S(t) + I(t) = \text{Constant}$$

Applying initial conditions, now

$$S(t) + I(t) = n + 1 \quad (2)$$

From (1) & (2) the analytical solutions are

$$S(t) = \frac{(n+1)n}{n + e^{(n+1)\beta t}} \quad \text{and} \quad I(t) = \frac{(n+1)}{1 + n e^{-(n+1)\beta t}}$$

As $t \rightarrow \infty$ (be large) then $I(t) = n + 1$ and $S(t) = 0$

The numerical results shows that the as time t increases, all susceptible individuals eventually become infected.

3.1.2 Graphical Representation of the SI Model

The numerical solution of the SI epidemic model is obtained using the Euler numerical method. Euler's method is a simple and efficient numerical technique used for solving systems of ordinary differential equations associated with epidemic transmission dynamics. Using Euler's Approximation method for numerical simulation, the initial conditions and parameters values are considered as $S(0) = 2000, I(0) = 1, \beta = .001$, and $h = 0.1$. The Euler numerical method is applied iteratively to generate the epidemic transmission data and graphical representation of the SI model. The graphical representation of the SI epidemic model describes the transmission dynamics between susceptible and infected populations over time. In the SI epidemic framework, susceptible individuals continuously move into the infected class due to disease transmission, while no recovery mechanism is considered. Therefore, the infected population gradually increases with time, whereas the susceptible population continuously decreases. The graphical analysis helps in understanding outbreak growth, epidemic transmission behaviour, and infection dynamics within the population. Furthermore, the graphical representation provides a useful framework for comparing classical epidemic models with Data-driven epidemic prediction systems.

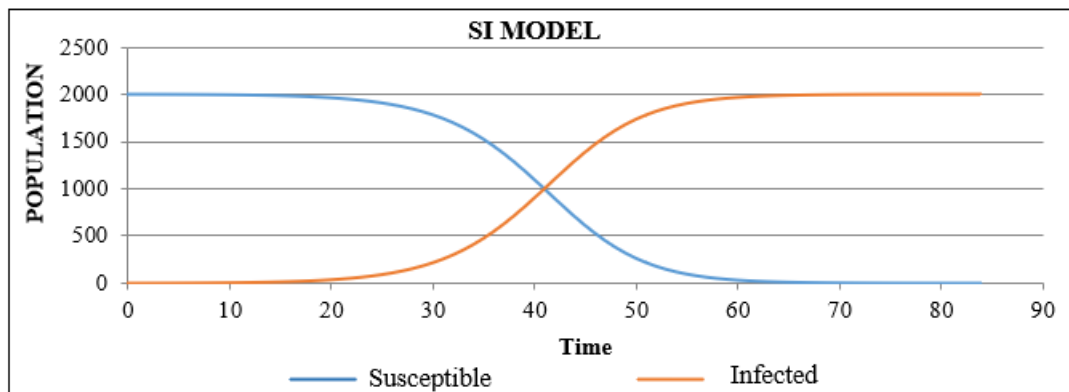


Figure 2: Graphical representation of the SI epidemic model

3.1.3 Comparative Analysis between Classical and Data-Driven SI Models

The classical SI epidemic model assumes that the disease transmission rate remains constant throughout the epidemic process. However, in real-world situations, the transmission dynamics of infectious diseases are influenced by several changing factors such as environmental conditions, population movement, social interaction, and seasonal variations. Therefore, fixed transmission assumptions may not accurately represent practical epidemic behaviour. To improve epidemic prediction and transmission analysis, data-driven parameter estimation techniques can be incorporated into the SI model. In the data-driven framework, the transmission parameter is estimated using historical epidemic data and trend-based analysis. This approach helps in identifying transmission trends and improving the estimation of epidemic parameters.

In the classical SI model, the infected population increases continuously with a fixed epidemic growth pattern. In contrast, the data-driven SI model incorporates transmission rate estimates obtained from infection data, providing a representation that is more closely aligned with observed epidemic trends. Therefore, the comparative analysis indicates that the data-driven SI model enhances epidemic analysis and provides improved forecasting capability compared to the classical SI model.

Classical SI Model

In the classical SI model, the disease transmission rate remains constant throughout the epidemic process. The infected population increases continuously with time, while the susceptible population gradually decreases to zero. Such as $\beta = \text{constant}$

Data-Driven SI Model

In the data-driven SI model, the transmission rate is estimated from epidemic data and may vary according to observed infection trends. Such as $\beta = \beta(t)$

Comparison Table:

Classical SI Model	Data-Driven SI Model
Fixed transmission rate	Data-driven transmission rate estimation
Static epidemic behaviour	Trend- responsive epidemic behaviour
Simple prediction	Involved forecasting capability
Less realistic forecasting	More realistic forecasting
No data-driven parameter estimation	Data-driven parameter estimation capability

3.1.4 Graphical Interpretation of the Data-Driven SI Model

The graphical comparison between the classical SI model and the data-driven SI model highlights the importance of data-driven parameter estimation in epidemic prediction and transmission analysis. In the classical SI model, the infected population increases rapidly due to the assumption of a fixed transmission rate. In contrast, the data-driven SI model incorporates transmission rate estimates obtained from infection data, resulting in a representation that is more closely aligned with observed epidemic trends. The comparative analysis indicates that the data-driven approach improves the interpretation of disease transmission dynamics and provides enhanced forecasting capability compared to the classical SI model.

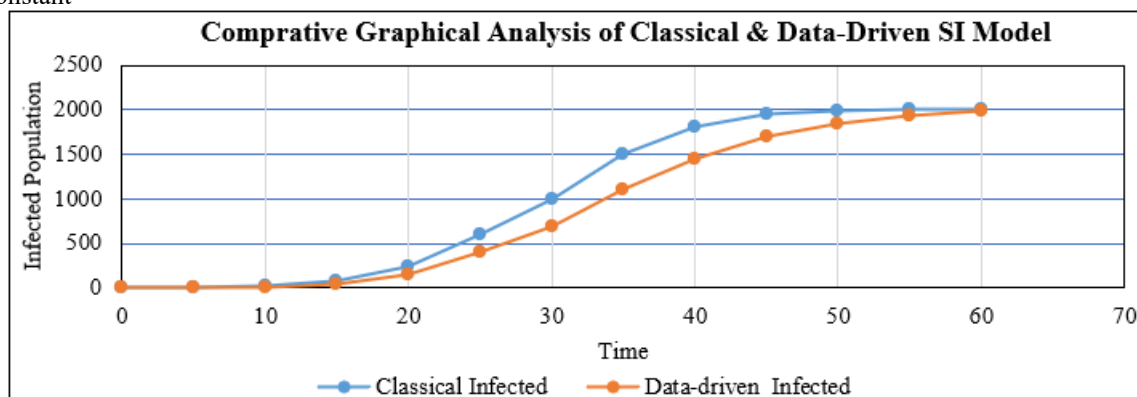


Figure 3: Comparative graphical analysis of classical & Data-driven SI model

4. SIS Epidemic Model

The SIS (Susceptible–Infected–Susceptible) epidemic model extends SI by adding a recovery term, modelling diseases where recovered individuals gain no permanent immunity and return to the susceptible class.

4.1 Mathematical Formulation and Analysis of the SIS Model

SIS model is suitable for analysing diseases involving repeated infection and reinfection dynamics. To accomplish this, the population is divided into two groups: susceptible individuals $S(t)$ and infected individuals $I(t)$. Susceptible individuals become infected through contact with infected individuals, while infected individuals recover and return to the susceptible class due to the absence of permanent immunity. Such as

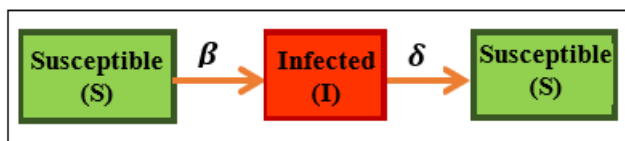


Figure 4: SIS Epidemic Model

The mathematical formulation of the model in the form of ordinary differential equations

$$\left. \begin{aligned} \frac{dS}{dt} &= -\beta SI + \delta I \\ \frac{dI}{dt} &= \beta SI - \delta I \end{aligned} \right\} \quad (3)$$

Where β represent the disease transmission rate of infection and δ represent the recovery rate. Now susceptible persons get infected at the rate βSI , infectious persons recover at the rate δI .

Basic Reproduction Number(R_0):

Basic Reproduction Number (R_0) is the average number of new infections caused by one infected individual in a completely susceptible population. Here $\beta, \delta > 0$ and Initial conditions are $S(0) = n, I(0) = 1$ then the total population $n + 1$

$$R_0 = \frac{\beta}{\delta}(n + 1)$$

- If $R_0 < 1$ the infection cannot sustain itself in the population and gradually disappears over time.
- If $R_0 > 1$ the disease persists in the population since each infected individual produces more than one new infection on average
- If $R_0 = 1$ the disease is at the threshold level where each infected individual generates exactly one secondary infection on average. This represents the critical point between disease eradication and disease persistence.

From Initial condition

$$S(t) + I(t) = n + 1 \quad (4)$$

Now from (3) & (4)

$$\frac{dI}{dt} = \beta S[(n + 1) - I] - \delta I$$

Now

$$I(t) = \frac{(n+1) - \frac{\delta}{\beta}}{1 + [(n+1) - \frac{\delta}{\beta} - 1]e^{-[(n+1)\beta - \delta]t}} \quad (5)$$

Now from (4) & (5) the analytical solutions are

$$I(t) = (n + 1) - \frac{\delta}{\beta} \quad \text{and} \quad S(t) = \frac{\delta}{\beta}$$

The analytical equilibrium at $t \rightarrow \infty$ yields

$I(\infty) = (n + 1) - \frac{\delta}{\beta}$ and $S(\infty) = \frac{\delta}{\beta}$ implying a persistent endemic state when $\beta > \frac{\delta}{n+1}$

For the equilibrium points $\frac{dS}{dt} = 0, \frac{dI}{dt} = 0$

From equations (3) & (4)

- Disease free Equilibrium point (DFE) $E_0(S_0, I_0) = (n + 1, 0)$
- Endemic Equilibrium point (EEP) $E^*(S^*, I^*) = \left(\frac{\delta}{\beta}, (n + 1) - \frac{\delta}{\beta}\right)$

4.1.2 Stability analysis at endemic equilibrium point $E^*(S^*, I^*)$ through jacobian matrix

Lemma1. The endemic equilibrium point $E^*(S^*, I^*) = \left(\frac{\delta}{\beta}, (n + 1) - \frac{\delta}{\beta}\right)$ is locally asymptotical stable if all the Eigen values of the jacobian matrix are negative.

Proof: Jacobian matrix for the epidemic SIR model (6) is represented as

$$J = \begin{bmatrix} -\beta I & -\beta S + \delta \\ \beta I & \beta S + \delta \end{bmatrix}$$

At the endemic equilibrium point $E^*(S^*, I^*) = \left(\frac{\delta}{\beta}, (n + 1) - \frac{\delta}{\beta}\right)$

$$J = \begin{bmatrix} -\beta I^* & 0 \\ \beta I^* & 0 \end{bmatrix}$$

Characteristic equation of jacobian matrix

$$|J - \lambda I| = 0$$

$$\begin{vmatrix} -\beta I^* - \lambda & 0 \\ \beta I^* & -\lambda \end{vmatrix} = 0$$

$$\lambda(\beta I^* + \lambda) = 0$$

Now the eigen value $\lambda = 0$ and $\lambda = -\beta I^*$

Since $I^* > 0$, when $R_0 = \frac{\beta}{\delta}(n + 1) > 1$, the nonzero eigenvalue satisfies $\lambda = -\beta I^* < 0$

From the above analysis, one eigenvalue is zero and the other is negative for $R_0 > 1$. The endemic equilibrium exists in the biologically feasible region and the system approaches this equilibrium, indicating local asymptotic stability of $E^*(S^*, I^*)$.

4.1.3 Numerical Analysis and Graphical Representation of the SIS Model:

To investigate the dynamic behavior of the SIS epidemic model, Euler's numerical method was employed with initial conditions are $S(0) = n, I(0) = 1$ and $\beta, \delta > 0$ then the total population

$$S(t) + I(t) = n + 1 \quad (4)$$

$$\frac{dI}{dt} = \beta SI - \delta I$$

$$S(0) = n = 2000 \quad \beta = .001, \delta = 0.4$$

$$S(t) = \frac{0.4}{.001} = 400 \quad I(t) = 2001 - 400 = 1601$$

The numerical solution of the SIS epidemic model is obtained using the Euler numerical method. Euler's method is a simple and efficient numerical technique used for solving systems of

ordinary differential equations associated with epidemic transmission dynamics. Using Euler's Approximation method for numerical simulation, the initial conditions and parameters values are considered as $S(0) = 2000, I(0) = 1, \beta = .001$, and $h = 0.1$. The Euler numerical method is applied iteratively to generate the epidemic transmission data and graphical representation of the SIS model. The graphical representation of the SIS epidemic model describes the transmission dynamics between susceptible and infected populations over time. The graph demonstrates that, with increasing time t , the susceptible population continuously decreases to nearly 400, whereas the infected population gradually increases to approximately 1601 due to disease transmission dynamics. These results confirm the existence and stability of the endemic equilibrium of the SIS model. The graphical analysis helps in understanding outbreak growth, epidemic transmission behaviour and infection dynamics within the population.

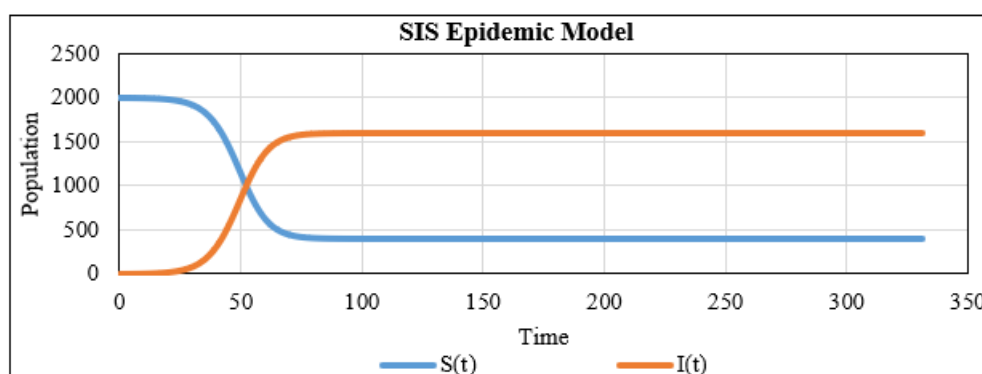


Figure 5: Graphical representation of the SIS epidemic model

4.1.4 Comparative Epidemic Behaviour of Classical and Data-Driven SIS Model

The classical SIS epidemic model assumes fixed transmission and recovery rates throughout the epidemic process. However, real-world infectious disease transmission and recovery dynamics may vary due to environmental conditions, healthcare interventions, population movement, and behavioural changes. To improve epidemic prediction and transmission analysis, data-driven parameter estimation techniques can be incorporated into the SIS framework. In the data-driven SIS model, the transmission and recovery parameters are estimated using epidemic data and trend-based analysis. Unlike the classical SIS model, the data-driven framework provides a representation that is more closely aligned with observed epidemic trends. The data-driven approach assists in parameter estimation, epidemic trend analysis, and forecasting of disease transmission dynamics. Therefore, the incorporation of data-driven parameter estimation enhances epidemic analysis and improves the understanding of infectious disease transmission behaviour.

Classical SIS Model:

In the classical SIS epidemic model, the transmission and recovery parameters remain constant throughout the epidemic process. Such as β & $\delta = \text{constant}$

Data-Driven SIS Model:

In the data-driven SIS epidemic model, the transmission and recovery parameters are estimated from epidemic data and

may vary according to observed infection trends Such as $\beta = \beta(t)$ & $\delta = \delta(t)$

Comparison Table:

Classical SIS Model	Data-Driven SIS Model
Fixed transmission rate	Data-driven transmission rate estimation
Fixed recovery rate	Data based recovery rate estimation
Static epidemic behaviour	Trend- responsive epidemic behaviour
Simple prediction	Involved forecasting capability
Less realistic forecasting	More realistic forecasting
No data-driven parameter estimation	Data-driven parameter estimation capability

4.1.5 Graphical Interpretation

The graphical comparison between the classical SIS model and the data-driven SIS model highlights the importance of data-driven parameter estimation in epidemic prediction and transmission analysis. In the classical SIS model, the infected population approaches epidemic equilibrium based on fixed transmission and recovery rates. In contrast, the data-driven SIS model incorporates parameter estimates obtained from infection data, resulting in a representation that is more closely aligned with observed epidemic trends. The data-driven model provides improved insight into disease transmission behaviour and enhances forecasting capability through data-based parameter estimation. Therefore, the comparative analysis indicates that the data-driven approach

improves the realism and predictive performance of the SIS epidemic model.

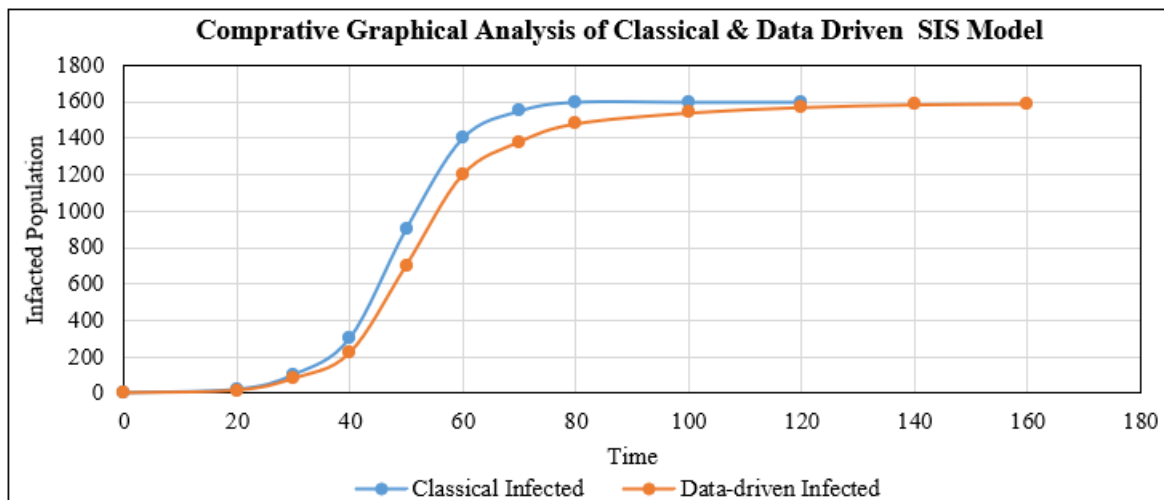


Figure 6: Comparative Graphical Analysis of Classical & Data-driven SIS Model

4.1.6 Exponential Trend-Based Parameter Estimation:

To demonstrate the application of data-driven parameter estimation in epidemic modelling, a sample infection dataset was considered. The dataset consists of time points and the corresponding number of infected individuals. The infection cases increase over time, representing the spread of an infectious disease within a population. An exponential trend fitting approach was employed to estimate the infection growth rate from the epidemic data. The purpose of this analysis is to illustrate how infection data can be utilized to estimate transmission dynamics through curve-fitting techniques. The dataset used for exponential trend fitting is presented in Table 4.1.

Table 4.1: Estimated dataset infected population

Time (t)	Infected Population I(t)
1	1
5	10
10	50
15	100
20	200
25	500
30	800
35	1000
40	1300
45	1500
50	1800

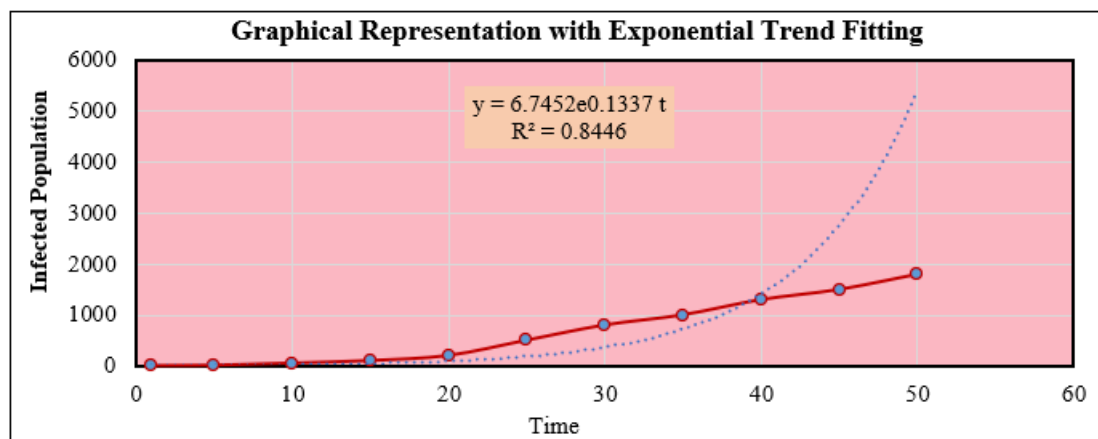


Figure 7: Graphical representation with exponential trend fitting

A sample infection dataset was analyzed using an exponential trend fitting approach in Microsoft excel. The fitted exponential model was obtained as

$$I(t) = Ae^{rt} = 6.7452 e^{0.1337t}$$

with coefficient of determination $R^2 = 0.8446$. The estimated growth rate was $r = 0.1337$. using the SIS model relation $r = \beta N - \delta$ the transmission rate was estimated as $\beta \approx 0.000267$ for $N = 2001$ and $\delta = 0.4$. The corresponding basic reproduction number was calculated as $R_0 \approx 1.33$, indicating disease persistence in the population.

Since ($R_0 > 1$), the results indicate that the disease persists in the population and approaches an endemic state. The exponential trend fitting approach provides a data-driven framework for estimating epidemiological parameters and supports the integration of computational techniques with classical epidemic models.

5. SIRS Epidemic Model

The SIRS (Susceptible–Infected–Recovered– Susceptible) epidemic model is an important compartmental epidemic

framework used to study infectious diseases involving temporary immunity and reinfection dynamics. In this model, recovered individuals lose immunity after a certain period and return to the susceptible class.

5.1.1 Mathematical Formulation and Analysis of the SIRS Model:

In SIRS epidemic model, population divided into three groups: susceptible persons, infected persons, and recovered persons such as

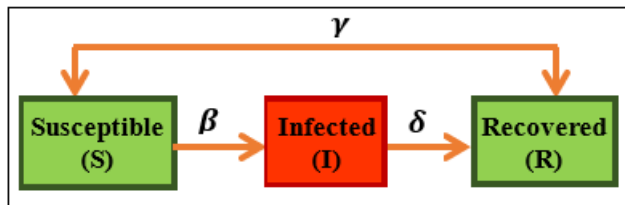


Figure 8: SIRS Model

The mathematical formulation of the model in the form of ordinary differential equations

$$\begin{cases} \frac{dS}{dt} = -\beta SI + \gamma R \\ \frac{dI}{dt} = \beta SI - \delta I \\ \frac{dR}{dt} = \delta I - \gamma R \end{cases} \quad (6)$$

Where β represent the disease transmission rate of infection, which define how effectively the disease spreads from infected persons to susceptible persons and δ represent the removal rate (rate at which infected persons recover), and γ indicates the rate at which recovered individuals lose immunity and return to the susceptible class. Now Susceptible persons get infected at the rate βSI , infectious persons recover at the rate δI , and recovered persons lose immunity and return to susceptible at the rate γR . Initial conditions are $S(0) = n, I(0) = 1, R(0) = 0$ then the total population is $n + 1$.

$$dS/dt + dI/dt + dR/dt = 0 \quad \& \quad S(t) + I(t) + R(t) = \text{Constant}$$

Applying initial condition, now

$$S(t) + I(t) + R(t) = n + 1 \quad (7)$$

Basic Reproduction Number (R_0):

It is observed that the basic reproduction number for the SIRS model has the same form as that of the SIS model, since the infection and recovery terms remain unchanged. Consequently,

$$R_0 = \frac{\beta}{\delta} (n + 1)$$

- If $R_0 < 1$ disease dies out
- If $R_0 > 1$ endemic equilibrium exists and stable

For the equilibrium points

$$\frac{dS}{dt} = 0, \quad \frac{dI}{dt} = 0, \quad \frac{dR}{dt} = 0$$

From equations (6) & (7)

- Disease free Equilibrium point (DFE) $E_0(S_0, I_0, R_0) = \left(\frac{\delta}{\beta}, 0, 0\right)$
- Endemic Equilibrium point (EEP) $E^*(S^*, I^*, R^*) = \left(\frac{\delta}{\beta}, \frac{(n+1)-\frac{\delta}{\beta}}{1+\frac{\delta}{\gamma}}, \frac{\delta}{\beta} \left(\frac{(n+1)-\frac{\delta}{\beta}}{1+\frac{\delta}{\gamma}}\right)\right)$

5.1.2 Stability Analysis at Endemic Equilibrium Point E^* through Jacobian Matrix

Lemma1. The endemic equilibrium point $E^*(S^*, I^*, R^*)$ is locally asymptotical stable if all the eigen values of the jacobian matrix are negative.

Proof: Jacobian matrix for the epidemic SIR model (6) is represented as

$$J = \begin{bmatrix} -\beta I^* & -\beta S^* & \gamma \\ \beta I^* & \beta S^* - \delta & 0 \\ 0 & 0 & -\gamma \end{bmatrix}$$

At the endemic equilibrium point $E^*(S^*, I^*, R^*) =$

$$E^* \left(\frac{\delta}{\beta}, \frac{(n+1)-\frac{\delta}{\beta}}{1+\frac{\delta}{\gamma}}, \frac{\delta}{\beta} \left(\frac{(n+1)-\frac{\delta}{\beta}}{1+\frac{\delta}{\gamma}} \right) \right)$$

$$J = \begin{bmatrix} -\beta I^* & -\delta & \gamma \\ \beta I^* & 0 & 0 \\ 0 & 0 & -\gamma \end{bmatrix}$$

Characteristic equation of jacobian matrix

$$|J - \lambda I| = 0$$

$$\begin{vmatrix} -\beta I^* - \lambda & -\delta & \gamma \\ \beta I^* & -\lambda & 0 \\ 0 & 0 & -\gamma - \lambda \end{vmatrix} = 0$$

Now eigen value $\lambda = -\gamma$ and $\lambda = \frac{-\beta I^* \pm$

$$\sqrt{\frac{(\beta I^*)^2 + 4 \delta \beta I^*}{2}}$$

Where $I^* = \frac{(n+1)-\frac{\delta}{\beta}}{1+\frac{\delta}{\gamma}}$ for all the parameter eigen values are negative.

From the above matrix it is clear that the all Eigen values are negative for the parameters (δ, γ, β) . If all eigenvalues are negative, then the endemic equilibrium point is stable, it shows that the endemic equilibrium point $E^*(S^*, I^*, R^*)$ exist and become locally asymptotically stable.

5.1.3 Numerical Analysis and Graphical Representation of the SIRS Model:

To investigate the transmission dynamics of the SIRS epidemic model, numerical simulations were performed using Euler's approximation method. The numerical analysis was carried out with appropriate initial conditions and parameter values for the susceptible, infected, and recovered populations. Using Euler's Approximation method for numerical simulation, the initial conditions and parameters values are considered as $S(0) = 2000, I(0) = 1, R(0) = 0, \beta = .001, \delta = .004, \gamma = .01$ and $h = 0.1$. The graph of the SIR epidemic model demonstrates that, with increasing time t , the susceptible population continuously decreases to nearly zero, whereas the infected population gradually increases approximately 1000 due to disease transmission dynamics. As time t increases, susceptible population slightly

increase because some of the recovered moves to susceptible class. Infected population initially increase and after a certain

period infected population decreases due to recovery. The endemic equilibrium points is locally asymptotical stable.

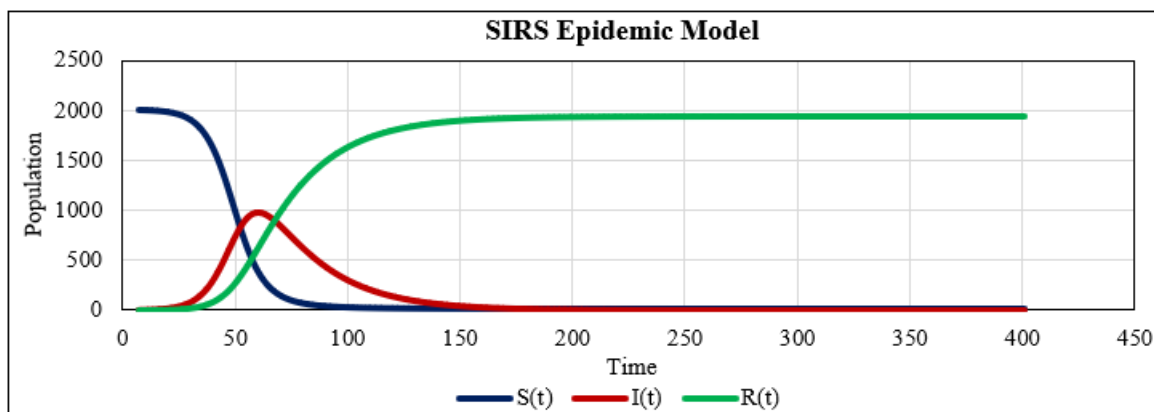


Figure 9: Graphical representation of the SIRS epidemic model

5.1.4 Comparative Analysis of Epidemic Behaviour in Classical and Data-Driven SIRS Model:

The classical SIR epidemic model assumes fixed transmission, recovery, and immunity loss rates throughout the epidemic process. However, real-world infectious disease dynamics continuously vary due to environmental conditions, vaccination effects, healthcare interventions, and behavioural changes. Therefore, constant epidemic parameters may not accurately represent practical disease transmission behaviour. To improve epidemic prediction and forecasting accuracy, data-driven techniques can be incorporated into the SIR epidemic framework. In the data-driven SIR model, the

transmission, recovery, and immunity loss parameters are dynamically estimated using epidemic data and predictive learning techniques. The data-driven based framework helps in identifying hidden epidemic patterns, improving parameter estimation, and enhancing outbreak forecasting. The comparative analysis demonstrates that the data-driven SIR model produces smoother and more adaptive epidemic behaviour compared to the classical SIR model. The data-driven framework demonstrates improved reinfection prediction, higher forecasting accuracy, and more realistic epidemic transmission dynamics compared to the traditional model.

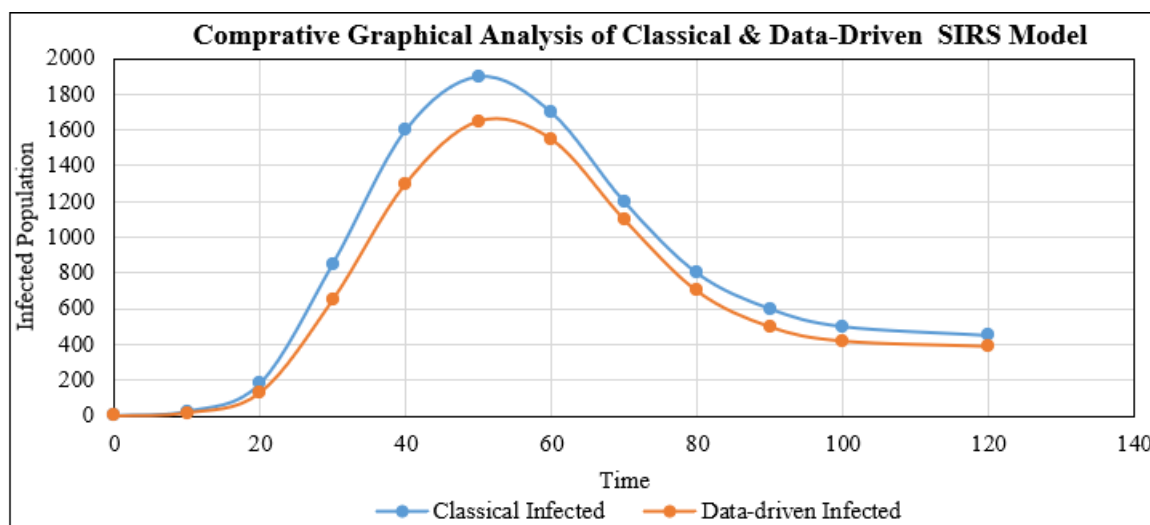


Figure 10: Comparative Graphical Analysis Representation of SIRS and Data-driven Model

5.1.5 Graphical Interpretation:

The graphical comparison between the classical SIRS model and the Data-driven SIRS model demonstrates the significant role of Artificial Intelligence in epidemic prediction and reinfection analysis. In the classical SIRS model, the infected population increases rapidly and reaches a higher epidemic peak due to fixed transmission, recovery, and immunity loss rates. However, the Data-driven SIRS framework produces smoother and more adaptive epidemic behaviour through dynamic estimation of epidemic parameters. The Data-driven based model demonstrates controlled outbreak growth, gradual stabilization, and improved reinfection forecasting. Furthermore, the comparative analysis indicates that Data-

driven enhances prediction accuracy and provides more realistic epidemic transmission dynamics compared to the traditional SIRS epidemic model.

5.1.6 Exponential Trend-Based Parameter Estimation:

The exponential trend-fitting methodology developed for the SIS model is equally applicable to the SIRS model. Therefore, the detailed parameter estimation procedure is not repeated here. The same approach may be employed to estimate the transmission rate, growth rate, and basic reproduction number from epidemic data. This demonstrates the applicability of data-driven techniques in supporting the analysis and prediction of epidemic dynamics.

Comparative Analysis of SI, SIS, and SIRS Epidemic Models

Feature	SI	SIS	SIRS
Compartments	S, I	S, I	S, I, R
Recovery	None	Yes (no immunity)	Yes (temporary immunity)
Reinfection	N/A	Yes	Yes (after immunity loss)
Steady-State	All infected	Persistent endemic state	Recurring epidemic cycles
Stability Analyzed	No	Yes, when $R_0 > 1$	Yes (endemic equilibrium)
Best suited for	Irreversible spread	Bacterial/STI-like diseases	Seasonal/recurring diseases
Data-Driven Parameter Estimation	Estimation of β from data	Estimation of β and δ from data	Estimation of β, δ and γ from data

The comparative analysis of SI, SIS, and SIRS epidemic models demonstrates different patterns of infectious disease transmission dynamics and epidemic behaviour. The SI model represents continuous infection spread without recovery, where the infected population continuously increases over time. This model is useful for analysing irreversible epidemic transmission processes. The SIS model extends the epidemic framework by incorporating recovery and reinfection dynamics. In this model, infected individuals return to the susceptible class after recovery, resulting in repeated disease transmission behaviour. The SIS framework is suitable for studying infectious diseases where permanent immunity is not developed. The SIRS model further enhances epidemic analysis by including temporary immunity loss and reinfection mechanisms. In this model, recovered individuals gradually lose immunity and become susceptible again. Therefore, the SIRS epidemic framework provides more realistic epidemic behaviour for recurring infectious diseases. Data-driven parameter estimation enhances epidemic prediction and transmission analysis in all three epidemic frameworks. Data-driven epidemic models utilize infection data to estimate transmission, recovery, and immunity-loss parameters, resulting in more adaptive epidemic behaviour compared to classical epidemic models. Comparative graphical analysis demonstrates that data-driven models improve outbreak forecasting, prediction accuracy, epidemic monitoring, and transmission dynamics analysis. Overall, the comparative study indicates that data-driven epidemic modelling provides a more realistic and effective framework for understanding infectious disease transmission dynamics and epidemic forecasting compared to traditional mathematical epidemic models.

6. Conclusion

The paper offers a well-organized, mathematically accessible introduction to SI, SIS, and SIRS epidemic models, presenting clean derivations and useful graphical illustrations. Its literature review is impressively current, citing 2025–2026 publications on data-driven epidemic forecasting. However, the paper's primary contribution data-driven epidemic modelling is not substantively realized. The equilibrium points and basic reproduction number R_0 were derived for models, and stability analysis was performed using the jacobian matrix method. The results showed that the disease-free equilibrium is stable when $R_0 < 1$, whereas the endemic equilibrium exists and becomes stable when $R_0 > 1$. Numerical simulations based on Euler's method were carried out to illustrate the behaviour of the epidemic models over time. The graphical results demonstrated the evolution of susceptible, infected, and recovered populations and supported the analytical findings obtained from the stability analysis. Furthermore, the study highlights the potential role

of data-driven parameter estimation in epidemic modelling. Data-driven techniques can improve parameter estimation, disease forecasting, and epidemic monitoring, thereby enhancing the accuracy and reliability of mathematical epidemic models. The integration of classical epidemic models with data-driven approaches provides a useful framework for understanding infectious disease dynamics and improving epidemic prediction.

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