**SIR, SIRS, and SEIRS Models for Pertussis Cases in Eastern Visayas**

**Abstract**

This study analyzed the effectiveness of the Susceptible-Infected-Recovered (SIR), Susceptible-Infected-Recovered-Susceptible (SIRS), and Susceptible-Exposed-Infected-Recovered-Susceptible (SEIRS) models in predicting pertussis incidence in Eastern Visayas, Philippines. The research aimed to compare the accuracy of these models using real-world data on weekly pertussis cases for the year 2024. The study utilized a mathematical modeling approach, employing differential equations to simulate disease transmission dynamics. Baseline parameter values for each model were obtained from existing literature, and these parameters were later refined through estimation techniques, specifically by using least squares optimization to fit the models to the observed data. The models were implemented using MS Excel, and their performance was evaluated using the Root Mean Square Error (RMSE) metric. The results of the study showed that the SIR model, with final estimated parameters β = 13.5968 and γ = 13.5496, provided the most accurate prediction of pertussis incidence the region, with the lowest RMSE of 9.07. In contrast, the SIRS and SEIRS models, while incorporating more complex disease dynamics such as waning immunity and an exposed period, exhibited higher RMSE values of 12.694 and 12.74, respectively, indicating less accurate predictions. These findings suggest that traditional models like SIR may be more practical for short-term pertussis forecasting in the context of Eastern Visayas in 2024. This study also highlighted the importance of model calibration and validation using local real-world data.

**Keywords**: Mathematical modeling, Pertussis, Root Mean Square Error (RMSE), SIR model, SIRS model, SEIRS model

**Introduction**

Pertussis, also known as whooping cough, is an acute infectious disease caused by the bacterium *Bordetella pertussis* and, more rarely, by *Bordetella parapertussis*. Outbreaks of pertussis were first described in the 16th century by Guillaume de Baillou. Jules Bordet and Octave Gengou first isolated the organism in 1906 [1]. This pertussis bacteria spreads easily from person to person through droplets released when an infected person coughs, sneezes, or breathes very close to someone. Transmission can also occur by touching the mouth or nose after contact with contaminated surfaces. Since these droplets have limited airborne travel, they typically infect only nearby individuals. During the first three weeks of coughing or the full five days of antibiotic treatment, whichever comes first, a person with pertussis can infect others [2].

During the 20th century, pertussis was one of the most prevalent pediatric illnesses and a significant contributor to childhood mortality in the US alone [1]. At that same time, before vaccines were widely used, epidemics of whooping cough, such as pertussis, were observed to recur at intervals of 2–3 years [3]. Since the introduction of vaccination in the late 90s, the incidence of pertussis has strongly decreased. However, even in countries with high vaccination coverage, pertussis shows epidemic peaks every 3–4 years [4] [5].

According to the World Health Organization (WHO) data, there were more than 151,000 cases of pertussis globally in 2018. In 2022, there were more than 62,500 cases of pertussis globally, and nearly 39,000 cases were reported in the Western Pacific Region. Despite being preventable by vaccination for several decades, pertussis remains one of the top ten causes of death worldwide in childhood, mainly in unvaccinated children. Even in countries with strong vaccination programs, the infection continues to kill young children [6].

Outbreaks of whooping cough were [reported](https://www.pna.gov.ph/articles/1221651) across the Philippines, including Quezon City, Iloilo, and Cavite, in 2024. Philippine Department of Health (DOH) has reported more than 1,000 cases of whooping cough in the first quarter of 2024 alone, a substantial increase from the 32 cases reported during the same period in 2023; 54 people have also died during this same period. Of these total cases, 77% were children under five years old. Meanwhile, adults aged 20 and above accounted for only around 4% of the cases [7]. Despite the overall increase, there was a decreasing trend in new cases during the latter part of 2024. From May 12 to May 25, the DOH recorded 187 cases, a 38% decrease from the 301 cases reported between April 28 and May 11, and from November 17 to 30, 2024, 36 cases were logged, compared to 44 cases from November 3 to 16, indicating a downward trend. This declined can be attributed to the intensified vaccination campaigns of DOH. However, despite this, on December 14, 2024, the Department of Health (DOH) reported a total of 4,518 pertussis cases nationwide, a significant increase compared to the 760 cases recorded during the same period in 2023. This represents nearly a six-fold rise in cases. The DOH also noted 144 deaths attributed to pertussis, which is almost three times higher than the 51 deaths reported in the previous year [8].

In Eastern Visayas, there was also a significant increase in pertussis cases in early 2024. Two hundred fifty 250 pertussis cases were reported, with over half affecting infants under one-year old. This was a significant increase from the 31 cases recorded earlier in the same year [9] [10]. Despite the nationwide decline, Eastern Visayas continued to experience a rise in cases during the same period. This suggests that while efforts were effective on a larger scale, certain regions like Eastern Visayas still needed more targeted interventions.

In view of the unusual spike in cases in Eastern Visayas despite national trends showing a decline, there is a crucial need to explore the transmission dynamics of the region. Understanding these localized outbreaks requires tools that capture how the disease spread over time and across populations. In this context, mathematical modeling appears to be a valuable approach to describe and simulate the transmission patterns of pertussis in Eastern Visayas.

Mathematical modeling has gained much attention in the scientific community as it helps describe real problems and enables a better understanding of the system. It has been used to model problems in various fields, including, but not limited to, physics, biology, chemistry, and economics. More specifically, mathematical models have been used to model infectious diseases and help public health decision-makers obtain more insights into the dynamic spread and controllability of various infectious diseases. Among these diseases is pertussis, which is highly contagious, fatal, re-emergent, and circulates worldwide [11].

Kermack and Mackendrick developed the foundational SIR (Susceptible, Infected, Removed) model that mathematically describes how disease spreads in a population. The model divides the population into three compartments: Susceptible (S), who can catch the disease; Infectious (I), who can transmit it; and Recovered (R), who has gained immunity. The model uses a system of differential equations to describe the rates at which individuals move between these compartments. Their work demonstrated how the interaction between infection and recovery rates determines whether an outbreak will die out or escalate, setting the stage for modern epidemiological modeling [12].

While the foundational SIR model is much credited to the work of Kermack and McKendrick, the introduction and formal study of the SIRS (Susceptible-Infected-Recovered-Susceptible) model came later. Hethcote [13] formally developed and analyzed the SIRS model in the mid-1970s. Specifically, his research provided a rigorous mathematical framework for the SIRS model as a system of ordinary differential equations. The SIRS model was explicitly defined by introducing a flow of individuals from the Recovered (R) compartment back to the Susceptible (S) compartment. This rate represented the loss of immunity over time. By formally incorporating the loss of immunity, Hethcote's work provided a theoretical basis for understanding the recurrence of infectious diseases. The analysis also highlighted the critical role of the basic reproduction number (R0 = indicates the number of secondary infections an infected individual can produce in a susceptible population) in determining the long-term behavior of the SIRS model. Conditions related to R0 were established to determine whether an epidemic can occur and whether the disease will eventually disappear or become endemic.

The development of SEIRS was a more gradual process within epidemiological modeling. It was built upon the SIR and SEIR [14], adding an Exposed compartment for the latent period while incorporating the loss of immunity, allowing recovered individuals to become susceptible again [15]. The model has been utilized in various studies, particularly for diseases like influenza, where immunity is temporary [16].

Given the need for a reliable region-specific model for Pertussis in the Philippines, this study implemented, simulated, and compared the SIR, SIRS, and SEIRS models using real-world data in Eastern Visayas. By analyzing their accuracy and error using the Root Mean Square Error (RMSE), this research determined the most effective model for forecasting Pertussis incidence in the region.

**Objectives of the Study**

This study aimed to implement and simulate the SIR, SIRS, and SEIRS models. Specifically, it aimed to:

1. investigate the effectiveness of SIR, SIRS, and SEIRS models in predicting pertussis incidence in Eastern Visayas. and
2. compare the accuracy of these models using Root Mean Square Error and identify the most suitable epidemiological model for forecasting regional pertussis outbreaks.

**Significance of the Study**

This study would benefit various individuals and agencies. For local health agencies, particularly public health officials and policymakers in Eastern Visayas, the findings can enhance pertussis control strategies, such as modifying vaccination schedules or focusing efforts on high-risk populations. Additionally, future researchers may find value in this study as it offers a framework that can be adapted for modeling other infectious diseases or applied to different regions experiencing similar epidemiological concerns.

**Scope and Delimitations of the Study**

This study focused on the mathematical modeling of pertussis transmission in Eastern Visayas using three epidemiological models: SIR, SIRS, and SEIRS. It covered the simulation and evaluation of these models based on real-world weekly reported pertussis cases from the region for 2024. Baseline parameters were initially sourced from existing literature and later refined through estimation techniques. The model assumed a closed population with homogeneous mixing, where individuals have equal contact rates.

The research was limited to deterministic compartmental models, and stochastic variations are not considered. The study does not incorporate external factors like vaccination campaigns and environmental influences.

Furthermore, the study assessed model performance using Root Mean Square Error (RMSE) as the primary statistical error metric. The study does not account for the population's spatial variations or demographic changes.

**Review of Related Literature**

Mathematical models play a vital role in understanding the dynamics of infectious diseases, aiding in prediction and control strategies. This section reviews relevant literature on the SIR, SIRS, and SEIRS models, focusing on their applications in predicting Pertussis incidence. The studies considered provide insights into these models' accuracy assessment and error analysis.

Overview of Pertussis and Its Epidemiology

Pertussis, or whooping cough, is an acute infectious disease primarily caused by the bacterium *Bordetella pertussis*. The disease is characterized by severe coughing spells, often followed by a "whooping" sound during inhalation. Historical records indicate that pertussis outbreaks were first documented in the 16th century, with significant contributions to our understanding of the disease by researchers such as Jules Bordet and Octave Gengou, who isolated the bacterium in 1906 [1]. The disease is transmitted through respiratory droplets, making it highly contagious, particularly among close contacts. Despite introducing vaccines, pertussis remains a significant public health concern, with the WHO reporting over 151,000 cases globally in 2018 [2]. Recent reports, such as those from the DOH, indicate ongoing pertussis outbreaks in regions like Eastern Visayas, highlighting the continued relevance of studying its dynamics [8] [9].

Mathematical Modeling of Infectious Diseases

Mathematical modeling has become essential in understanding the dynamics of infectious diseases, including pertussis. Various models, such as the SIR (Susceptible-Infectious-Recovered), SIRS (Susceptible-Infectious-Recovered-Susceptible), and SEIRS (Susceptible-Exposed-Infectious-Recovered-Susceptible) models, have been employed to simulate disease spread and evaluate control strategies. These models provide valuable insights for public health officials, enabling them to predict outbreak patterns and assess the impact of vaccination programs [11].

Epidemiological Modeling of Infectious Diseases

Epidemiological models are fundamental tools for analyzing infectious disease transmission. The study [17] by Heesterbeek et al. (2015) provides a comprehensive discussion on modeling infectious disease dynamics, emphasizing the importance of incorporating real-world complexities such as demographic factors, spatial heterogeneity, and intervention strategies. The authors highlight how compartmental models, including the SIR, SIRS, and SEIRS frameworks, contribute to understanding disease spread and predicting outbreaks under varying conditions.

The SIR, SIRS, and SEIRS Models

The SIR, SIRS, and SEIRS models are compartmental models that divide a population into distinct groups based on their disease status:

SIR Model

This model divides the population into Susceptible (S), Infectious (I), and Recovered (R) compartments. It assumes that individuals in the recovered compartment have permanent immunity [14].

SIRS Model

This model is an extension of the SIR model, where recovered individuals can lose their immunity and become susceptible again. This waning immunity is critical for diseases like pertussis, where reinfection can occur [18].

SEIRS Model

This model includes an Exposed (E) compartment, representing individuals who have been infected but are not yet infectious. This model is valuable for diseases with an incubation period, such as pertussis [19].

The selection of these models for this research is appropriate because they capture key aspects of pertussis epidemiology. The SIR model provides a basic framework, while the SIRS model accounts for the possibility of waning immunity, a known characteristic of pertussis [20]. The SEIRS model further refines the analysis by incorporating the incubation period, which is essential for understanding the transmission dynamics of the disease.

Several studies have utilized SIR, SIRS, and SEIRS models to investigate pertussis dynamics. The study of Yang [35] explores the application of the SEIR model that describe how pertussis spreads. This study uses a recursive point process, a refined version of the Hawkes point process, and compares its performance against the SEIR model in fitting historical pertussis data from Nevada. It suggests that while the recursive point process showed better predictive accuracy, the SEIR model remains valuable due to its common use in epidemiological studies. Other studies like from Rohani [21] have focused on the role of waning immunity in pertussis resurgence, demonstrating the need for models like SIRS that account for this phenomenon.

The study by Thisyakorn et al. [20] provides valuable insights into Pertussis epidemiology, particularly regarding vaccination and immunity waning. The authors emphasize the need for robust modeling approaches that account for reinfection risks and vaccine-derived immunity decay. Their findings support using SIRS and SEIRS models for more accurate infectious disease incidence predictions.

Evaluating the accuracy of error analysis in epidemiological modeling is crucial for ensuring reliable predictions. Several studies emphasize the importance of using statistical error metrics to assess model performance. Common metrics include Root Mean Square Error (RMSE), Mean Absolute Error (MAE), and Mean Absolute Percentage Error (MAPE) [23]. These metrics quantify the difference between the model's predictions and the observed data, measuring the model's predictive accuracy. The study of Pascual et al. [24] also suggest parameter sensitivity analysis and model calibration against real-world data are essential for improving model accuracy.

The reviewed literature provides a strong foundation for implementing and evaluating SIR, SIRS, and SEIRS models for Pertussis incidence in Eastern Visayas. Several studies suggest the importance of waning immunity and incubation periods in modeling pertussis transmission. Furthermore, the emphasis on accuracy assessment and error analysis underscores the need for rigorous model validation. This research aims to contribute to a better understanding of pertussis dynamics in Eastern Visayas, which could inform public health strategies and improve outbreak preparedness in the region.

**Methodology**

This study utilized a mathematical modeling approach to analyze, describe, and possibly predict the spread of Pertussis in Eastern Visayas, Philippines. The three compartmental models, SEIRS, SIR, and SIRS, were implemented to assess the spread of Pertussis in the region. The research aimed to determine which best fits the real-world incidence data of pertussis in Eastern Visayas by comparing the performance of the three models. The modeling process involved differential equations, parameter estimation techniques, and numerical methods to simulate the behavior of the disease.

Data Collection

The data for this study came from two primary sources:

Existing Literature: baseline parameter values for the SIR, SIRS, and SEIRS models was obtained from peer-reviewed scientific literature. This will be the basis for model implementation and initial simulations.

Official Health Reports: Real-world data on the number of Pertussis cases were acquired from official surveillance reports published by the public health agency and official health websites. A formal data request was submitted via email to ensure access to the most accurate and up-to-date information available. The data obtained was used for model fitting and validation. The data is in weekly intervals.

Model Formulation

The study used the following compartmental models:

SIR Model

The SIR (Susceptible-Infected-Recovered) model divides the population into three compartments:

S: Susceptible individuals

I: Infected individuals

R: Recovered individuals with immunity

The model is governed by a system of ordinary differential equations (ODEs) [14]. The SIR model can be written as:

Where:

N = the total population size,

β = rate of transmission,

γ = rate of recovery.

SIRS Model

The SIRS (Susceptible-Infected-Recovered) model is the modified model of the SIR, it divides the population into three compartments:

S: Susceptible individuals

I: Infected individuals

R: Recovered individuals

The model includes a waning immunity term. Individuals in the Recovered (R) class return to the Susceptible (S) class over time [18]. The model is governed by the following system of ordinary differential equations (ODEs). The SIRS model can be written as:

Where:

N = the total population size,

β = rate of transmission,

γ = rate of recovery, and

ω = rate of loss of immunity.

SEIRS Model

The SEIRS (Susceptible-Exposed-Infected-Recovered) model is also the modified model of the SIR. It divides the population into four compartments:

S: Susceptible individuals

E: Exposed individuals

I: Infected individuals

R: Recovered individuals

The model introduces an Exposed (E) compartment to account for latency before becoming infectious [19]. The model is governed by a set of ordinary differential equations (ODEs).

The SEIRS model can be written as:

Where:

N = the total population size,

β = transmission or infectious rate,

γ = recovery rates,

ω = rate of loss of immunity, and

α = rate of which individuals become infectious

Parameter Estimation

Baseline parameters for model fitting, including transmission rate (β), recovery rate (γ), waning immunity rate (ω) and rate of which individuals become infectious (α) were obtained using available literature and were later estimated for model fitting using the real-world data for the number of Pertussis cases from official health reports. Least squares optimization was used to fit the model to observed incidence trends.

Model Simulation & Numerical Method

The models' differential equations were solved using Euler’s Method implemented in MS Excel spreadsheet software. Simulations were conducted over a predefined period, with the available data being in a weekly interval. From the model’s differential equations, we derived a numerical approximation using Euler’s Method to numerically solve the system:

SIR Model (Euler’s approximation)

SIRS Model

SEIRS Model

Where:

N = the total population size;

β = transmission or infectious rate;

γ = recovery rates;

ω = rate of loss of immunity; and

α = rate of which individuals become infectious

i = 0, 1, 2, 3, …, n – 1;

S = Susceptible individual;

I = Infected individual;

R = Recovered individual;

E = Exposed individual;

dt = time step (7 days, since data is weekly);

**Results & Discussion**

The researchers present the data collected on pertussis incidence in Eastern Visayas, Philippines, and the results of the SIR, SIRS, and SEIRS models' simulations. It further provides a comparative analysis of the model's performance in predicting pertussis outbreaks, using Root Mean Square Error (RMSE) as the key metric.

Pertussis Incidence Data

            Weekly data on pertussis cases in Eastern Visayas in the year 2024 were obtained from official surveillance reports published by the DOH Eastern Visayas, Philippines. A formal data request was submitted via email to ensure access to the most accurate and up-to-date information. Table 1 presents the summary of the pertussis incidence data.

**Table 1. Summary of Pertussis Cases in Eastern Visayas 2024**

|  |  |
| --- | --- |
| Statistic | Value |
| Total Cases | 409 |
| Mean Weekly Cases | 7.87 |
| Median | 5 |
| Minimum Weekly cases | 0 |
| Maximum Weekly cases | 70 |
| Standard Deviation | 10.8 |

In Fig.1, a total of 409 pertussis cases were reported in Eastern Visayas in a span of 52 weeks, yielding an average of approximately 7.87 cases per week. The median number of cases per week was 5. Weekly cases ranged from a minimum of 0 to a maximum of 70, with the highest spike occurring in Week 18. The data displayed a right-skewed distribution, suggesting occasional high-incidence weeks amidst generally low numbers. See Table A.1 in Appendix A for the complete list of weekly cases in 2024.

**Fig. 1. Actual weekly Pertussis cases in Eastern Visayas**

Initial Parameters

To guide the model development, baseline parameters for transmission rate (β), recovery rate (γ), rate of loss of immunity (ω), and rate of becoming infectious (α) were initially used from existing literature. These values on Table 2.

The recovery rate (γ) was obtained using the inverse of the average infectious period of 21 days [1], the transmission rate (β) = 0.24 was obtained by multiplying the reproduction number (R0) which is 5 [25] to the recovery rate, the rate loss of immunity (ω) = 0.00027 was obtained by inversing the average duration of immunity of 10 years [26], and the rate of becoming infectious (α) = 0.14 was obtained by inversing the average incubation period of 7 days [1]. The summary of the obtained parameter values is shown below.

**Table 2. Baseline Parameters from Literature**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | β  (Transmission rate) | γ  (Recovery rate) | ω  (Loss of immunity) | α  (Incubation rate) |
| SIR | 0.24 | 0.048 |  |  |
| SIRS | 0.24 | 0.048 | 0.00027 |  |
| SEIRS | 0.24 | 0.048 | 0.00027 | 0.14 |

Model Simulation Results

The SIR, SIRS, and SEIRS models, as described in the Methodology, were implemented using the collected pertussis incidence data and baseline parameter values. Initial parameter values were obtained from the literature and through model fitting, the simulation results for each model are presented below.

For all model simulations, the initial conditions were set as follows:

N = 4,000,000

t = 7 days (data is on weekly interval)

S0 = 3,999,999

I0 = 1

R0 = 0

E0 = 0 (for SEIRS)

β = 0.24

γ = 0.048

ω = 0.00027

α = 0.14

SIR Model Results

The graph in Fig. 2 presents the comparison between actual Pertussis cases and the simulated infected population using the SIR model in Eastern Visayas for 2024. From the baseline literature parameters (β = 0.24, γ = 0.048) and actual data, and from the initial model simulation, the model was calibrated to final estimated values of β = 13.5968 and γ = 13.5496. The root mean square error (RMSE) of the SIR model is 9.07, indicating a relatively good fit to the actual data. While the SIR model underestimates the sudden peak in week 19, it effectively captures the overall trend of the outbreak, including the gradual rise, peak, and decline in cases. This suggests that the SIR model provides a strong approximation of the disease dynamics.

**Fig. 2. Comparison of Actual vs. SIR Model Predicted Weekly Pertussis Cases with Parameters β = 13.5968, γ = 13.5496**

SIRS Model Results

The SIRS model incorporates waning immunity, simulating reinfection potential. Its results show a gradual increase in infections, differing from the real data's peaks. The graph in Fig. 3 shows the weekly Pertussis cases in Eastern Visayas for 2024 compared with the simulated infected population using the SIRS model. The baseline parameters from the literature were β = 0.24, γ = 0.048, and ω = 0.00027. After fitting the initial model simulation, the final estimated parameters were β = 0.1230, γ = 0.1174, and ω = 0.0002692, resulting in a Root Mean Square Error (RMSE) of 12.694. While the model captures the presence of reinfection over time, the predicted infected curve remains relatively flat and underestimates both the timing and magnitude of the epidemic peak seen around week 19. And due to its higher RMSE, it is less accurate than the SIR model in this case.

**Fig. 3. Comparison of Actual vs. SIRS Model Predicted Weekly Pertussis cases with parameters β = 0.1230, γ = 0.1174, ω = 0.0002692**

SEIRS Model Results

The SEIRS model includes an exposed (latent) compartment, representing the incubation phase before symptoms appear. The graph in Fig.4 illustrates the weekly actual pertussis cases in Eastern Visayas alongside the simulated infected population using an SEIRS model. The baseline parameters were used (γ = 0.048, β = 0.24, ω = 0.00027, and α = 0.14) and the initial model simulations were used. After model fitting, the final estimated parameters were γ = 0.1208, β = 0.1335, ω = 0.0002690, and α = 0.10, with a Root of Mean Squared Error (RMSE) of 12.74. The model simulation depicts a flat infected curve, remaining below 10 cases throughout the entire 52-week period. While the SEIRS model incorporates an exposed and a loss of immunity compartment, with the fitted parameters, it significantly underestimates the magnitude and timing of the observed epidemic peak. Despite accounting for a latent period and waning immunity, it appears to be a poor fit for describing the outbreak dynamics of pertussis in Eastern Visayas.

**Fig. 4. Comparison of Actual vs. SEIRS Model Predicted Weekly Pertussis Cases with parameters γ = 0.1208, β = 0.1335, ω = 0.0002690, and α = 0.10**

Summary of the Estimated Parameters from Model Fitting

The least square method was used as an optimization method to estimate the parameters that minimize prediction error. The transmission rate (β) reflects the rate at which susceptible individuals contract pertussis upon contact with infectious individuals. The SIR model yielded the highest transmission rate at β = 13.5968, which may suggest an overestimation due to the model’s lack of re-infection or latency components. In contrast, the SIRS and SEIRS models produced significantly lower and more realistic β values (0.1230 and 0.1335, respectively), aligning more closely with the known epidemiological behavior of pertussis.

The recovery rate (γ) across the three models remained relatively consistent, with values ranging from 0.1174 (SIRS) to 13.5496 (SIR). Again, the unusually high γ in the SIR model may reflect its structural limitations in accurately modeling pertussis, particularly its exclusion of waning immunity.

The loss of immunity rate (ω) was incorporated in the SIRS and SEIRS models and was approximately 0.000269 for both. This low value suggests that immunity wanes very slowly, a behavior consistent with pertussis, where immunity (from infection or vaccination) is not lifelong.

The incubation rate (α) was only applicable in the SEIRS model. With a value of 0.10, it indicates a moderate transition rate from exposed to infectious. This inclusion allows SEIRS to better model diseases like pertussis that involve a latent period, potentially contributing to improved forecasting accuracy.

The final values are shown below:

**Table 3. Estimated Parameters for SIR, SIRS, and SEIRS Models**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | β  (Transmission rate) | γ  (Recovery rate) | ω  (Loss of immunity) | α  (Incubation rate) |
| SIR | 13.5968 | 13.5496 |  |  |
| SIRS | 0.1230 | 0.1174 | 0.0002692 |  |
| SEIRS | 0.1335 | 0.1208 | 0.0002690 | 0.10 |

Model Accuracy Comparison Using RMSE

To objectively evaluate prediction accuracy, the Root Mean Square Error (RMSE) was computed for each model. Table 4 shows the Model RMSE Comparison of each model. The RMSE values indicate that the SIR model has the lowest error of 9.07, suggesting that it comparatively provides the most accurate prediction of pertussis incidence in Eastern Visayas. Despite simplicity, it outperformed the more complex models in fitting 2024 data. The SEIRS model has the highest error of 12.74, indicating the least accurate prediction. In contrast, the SIRS and SEIRS models, which include additional biological mechanisms such as loss of immunity (ω) and an exposed/incubation class (α), resulted in slightly higher RMSEs—12.69 and 12.74, respectively. These results may indicate that while these models are theoretically more realistic, their additional complexity did not translate into better short-term predictive performance for this specific dataset and region.

**Table 4. Model RMSE Comparison**

|  |  |
| --- | --- |
| Model | RMSE |
| SIR | 9.07 |
| SIRS | 12.69 |
| SEIRS | 12.74 |

Summary of Findings

The analysis revealed that all three models captured general pertussis dynamics, but to varying degrees of accuracy. The SIR model achieved the lowest RMSE value of 9.07, indicating the best fit among the three. It effectively modeled the sharp rise and decline in cases, closely matching real outbreak behavior. Meanwhile, the SIRS and SEIRS models, although more biologically detailed, showed smoother curves that were less reflective of the actual case, resulting in higher RMSE values of 12.694 and 12.74, respectively. The results may suggest that dynamics like reinfection and latent period may not be a major influence of pertussis transmission in Eastern Visayas context. Thus, the SIR model is a better fit. This suggests that during the year 2024, immunity loss may have had a limited effect over the year.

**Conclusion**

          Based on the findings of this study, the following conclusions were drawn:

The SIR model demonstrated better accuracy in predicting pertussis incidence in Eastern Visayas for 2024 than the SIRS and SEIRS models. Its simplicity and ability to capture the essential dynamics of the outbreak, including the rise and decline in cases, make it a valuable tool for epidemiological forecasting in the region. This study reaffirms the utility of the classical SIR model in modeling infectious disease dynamics. As shown by Salimipour *et al.* [28], even a simplified random walk-based SIR model effectively captures infection trends and estimates key epidemiological parameters.

This study highlighted the importance of model calibration and validation using real-world data. The baseline parameter values obtained from the literature and later refined through model fitting and parameter estimation techniques demonstrate the need to tailor models to specific regions. This finding is consistent with Wearing *et al.* [29] who emphasized that selecting appropriate models and calibrating them using specific outbreak data is crucial to accurately represent the dynamics of infectious diseases and improving prediction reliability. The Root Mean Square Error (RMSE) proved to be an effective metric for comparing the predictive accuracy of the different epidemiological models. The lower RMSE value for the model confirms its better performance in this study. As supported by Chai and Draxler [30], RMSE remains one of the most widely used metrics for quantifying model prediction errors, offering straightforward interpretation and comparability across different models.

**Recommendations**

          The following recommendations were made for future research and practical applications:

Future research could incorporate other factors influencing pertussis transmission dynamics, such as vaccination campaigns and population demographics. These factors could potentially improve the accuracy of the two models, the SIRS and SEIRS models.

Given the accuracy of the SIR model in this study, local health agencies in Eastern Visayas could utilize it as a tool for forecasting pertussis outbreaks and informing public health decision-making. This could aid in the timely planning and implementation of effective health measures.

Future studies should consider using other epidemic models, such as agent-based or network models, and account for spatial variations or demographic changes in the population.

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