Transmission Analysis and Future Trend Prediction of Deyr City's B1H3 Virus by SIR Modelling

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Abstract: This study analysed the transmission dynamics of a virus using data from bat monitoring and hospital testing. This research investigated the positivity rate and infection spread in bat populations and human patients. The study employed a Poisson distribution model to evaluate bat infection rates and a linear regression model to estimate the virus's doubling time and basic reproduction number R_0 Additionally, an epidemic branching process simulation was conducted to predict future virus transmission paths. The Susceptible-Infectious-Recovered (SIR) model was utilized to understand and predict epidemic dynamics. The results indicate a moderate transmission potential with a doubling time of 41.6232 days and R_0 of 1.1665. The simulation emphasized the importance of early detection and intervention, providing valuable insights for public health strategies. By integrating various statistical and mathematical models, this research offers a comprehensive approach to understanding the transmission mechanisms of the virus. The findings highlight the interconnectedness of bat and human infections, underscoring the necessity of a holistic approach that considers the health of humans, animals, and the environment. The methodology in this research can also be applied to other zoonotic diseases, aiding in the development of robust monitoring and response systems. Future research should focus on refining models with more granular data and exploring the impacts of different intervention strategies on controlling virus spread.

1 INTRODUCTION

In December 2019, a novel strain of Coronavirus (SARS-CoV-2) was identified. This virus led to a severe and potentially deadly respiratory syndrome called COVID-19. As it spread rapidly worldwide, the World Health Organization (WHO) declared it a pandemic on March 11, 2020 (Xing et al., 2024; Zhen and Sun, 2020 & Chen et al., 2023). The unparalleled global impact of the COVID-19 pandemic has highlighted the essential need for early detection and effective management of infectious diseases. Since the onset of COVID-19, various mathematical modelling approaches have been utilized to simulate the disease's progression. Although artificial intelligence-based models are promising, their reliability can be questioned without sufficient training datasets due to their dependency on extensive learning processes. Another method, day-level forecasting based on time-series data, merely follows previous patterns and fails to predict trend changes (Zhou and Huang, 2024). In response to the ongoing threat of new zoonotic diseases, particularly in regions with dense wildlife populations, enhanced surveillance systems have been established. One such initiative is the sentinel system in Deyr, a city in the Bergia region of Sordland, known for its significant bat population and frequent zoonotic spillovers.

The mathematical modelling of epidemics has been extensively studied over the past century (Diekmann and Heesterbeek, 2000). This paper aims to apply epidemiological models to predict and manage potential outbreaks resulting from these interactions. The main goal of this research is to use mathematical modeling to analyze and forecast the transmission dynamics of diseases in Deyr. Specifically, the study employs methods to calculate the early infection growth rate, which is crucial for understanding the initial stages of an outbreak. Additionally, the Susceptible-Infected-Recovered (SIR) model, a well-established tool in epidemiology, will be utilized to project the potential spread of the disease within the human population (Wang, Luo and Hu, 2020). Among the significant mathematical models for epidemics, the SIR model, originally proposed by Kermack and McKendrick, holds great historical importance.

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This research builds on the foundational work in epidemiological modelling, which dates back to the early 20th century (Mao and Liu, 2023). The use of models such as the SIR model has evolved significantly, providing insights into the mechanisms of disease spread and the effectiveness of control measures (Satsuma et al., 2004). In Deyr, the recent increase in cases detected through the sentinel system has raised concerns about a possible escalation into a more severe outbreak. This situation mirrors historical precedents where initial outbreaks were either contained or evolved into widespread epidemics based on the interactions between susceptible and infected populations. By calculating the early growth rate and applying the SIR model, this study aims to provide actionable insights that can inform public health strategies. These models will help predict the trajectory of the outbreak and assess the potential impact of intervention measures. The analysis will also consider the accuracy of the models and the reliability of the data from the sentinel system, ensuring that the predictions are both scientifically robust and practically applicable.

The findings from this research are intended to guide public health decisions in Deyr and could serve as a reference for other regions facing similar challenges. By advancing the application of epidemiological models in real-world scenarios (Rodrigues, 2016). This study contributes to the broader field of public health, enhancing the ability to respond effectively to emerging infectious diseases.

2 METHODOLOGY

2.1 Data Sources and Description

This study utilizes two primary databases: `bat_monitoring.db` and `hospital_testing.db`. The `bat_monitoring.db` contains data on bat monitoring at different stations, including station names, monitoring dates, total bats detected, and the number of positive bats. The `hospital_testing.db` includes data on positive patients detected in hospitals, such as detection dates and patients' dates of birth. Relevant data were extracted from these databases for subsequent processing and analysis.

2.2 Indicator Description

The positivity rate in bat monitoring data was calculated as the ratio of positive bats to the total number of bats detected at each station. The positivity rate in hospital testing data was calculated as the ratio of positive patients to the total number of patients tested in hospitals. The virus transmission rate R_0 was calculated based on detection data and epidemiological models to evaluate the virus's potential spread within the population. The duration of illness was estimated by analyzing the duration of symptoms in positive patients. The doubling time was calculated using a linear regression model to evaluate the speed of virus spread within the population.

2.3 Method Description

Data were extracted from `bat_monitoring.db` and `hospital_testing.db` using SQLite.Date fields were converted to standard date formats for time series analysis. Data were sorted and filtered to ensure completeness and consistency. Histograms and time series plots were used to visualize bat monitoring data and hospital testing data. The positivity rate in bat monitoring data was calculated and the data were fitted using a Poisson distribution model. A weekly analysis of hospital testing data was performed to calculate the trend in the number of positive patients detected each week. Based on hospital testing data, a linear regression model was used to calculate the doubling time and basic reproduction number R_0 of the virus. Bat monitoring data and hospital testing data were combined to evaluate the virus's transmission characteristics in different populations.

To understand and predict the dynamics of epidemic spread, the article employed the Susceptible-Infectious-Recovered model. The simplicity and robustness of the model make it an ideal choice for simulating epidemic processes and understanding the underlying mechanisms of disease transmission.

The dynamics of the SIR model can be defined by these ODEs:

$$\frac{dS}{dt} = -\beta SI \quad (1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

In these equations: equation (1) represents the changing rate of the susceptible population, which decreases as susceptible individuals become infected. Equation (2) represents the rate of change of the infectious population, which increases as susceptible individuals become infected and decreases as infected individuals recover. Equation (3) represents the rate of change of the recovered population, which increases as infected individuals recover. Moreover, the key parameters in the model are the infection rate (β) and the recovery rate (γ). As for the Infection

Rate (β) , this parameter indicates how many susceptible individuals get infected per infectious individual per unit time. It is influenced by factors such as the transmission rate of the disease and the contact rate between individuals. This parameter Recovery Rate represents the rate at which infectious individuals recover and move to the recovered category. It is the inverse of the average infectious period. The infection rate can be further detailed as:

$$\beta = \gamma + \frac{r}{7} \quad (4)$$

where (r) is the rate of new infections per week. The basic reproduction number (R_0), a critical threshold parameter, is defined as:

$$R_0 = \frac{\beta}{\gamma} \quad (5)$$

The equation (5) represented the average number of secondary infections produced by a single infectious individual in a completely susceptible population. If $R_0 > 1$, the disease is expected to spread; if $R_0 < 1$, the disease will eventually die out.

To simulate the epidemic process, the paper initialized the model with a predefined number of infected individuals. The simulation ran for 100 repetitions over 60 times steps, capturing the stochastic nature of disease transmission. Besides, each simulation iteration involved the following steps:

First was to set initial values for S, I, and R. Then this paper updated the values of S, I, and R at each time step using the SIR equations. Finally, the basic reproduction number R_0 and doubling time were calculated and provided a measure of the disease's transmissibility and a forecast over next 60 days will be beneficial to understand the spread of the virus more intuitively.

3 RESULTS AND DISCUSSION

The research extracted the monitoring data for station H1, converting the dates to a standard format and sorting the data by date. This allowed us to visualize the detected bats and positive bats over time. The plot showed fluctuations in these numbers, which provided a basis for further analysis.

3.1 Positivity Rate Analysis

By analysing the monitoring data of station H1 from, then the following figure was plotted:

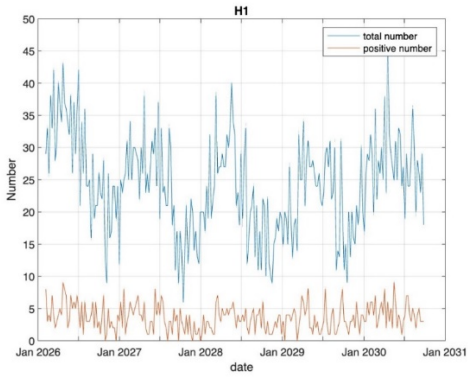

Figure 1. Positive number and total number of bats.

The results of Figure 1 showed fluctuations in the total number of bats detected and the number of positive bats over time at station H1. Then, to analyse the positivity rate, the distribution of positive bats was plotted and fitted a Poisson distribution model. The positivity rate p was calculated as the ratio of the total positive bats to the total number of bats detected. The Poisson model helped to understand the expected distribution of positive bats and evaluate the infection spread in the bat population in Figure 2.

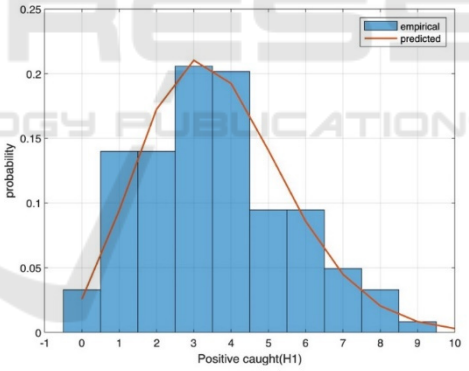

Figure 2. Positive caught and probability.

The analysis shows that the distribution of positive bats at station H1 fits well with the Poisson distribution, with a positivity rate of p.

3.2 Hospital Testing Data Analysis

Next, the research focused on analysing the hospital testing data from the `hospital_testing.db` database. Here are the steps and explanations: By analysing the hospital testing data from the hospital_testing.db database, then the number of positive cases detected each week was calculated and plotted the following Figure 3:

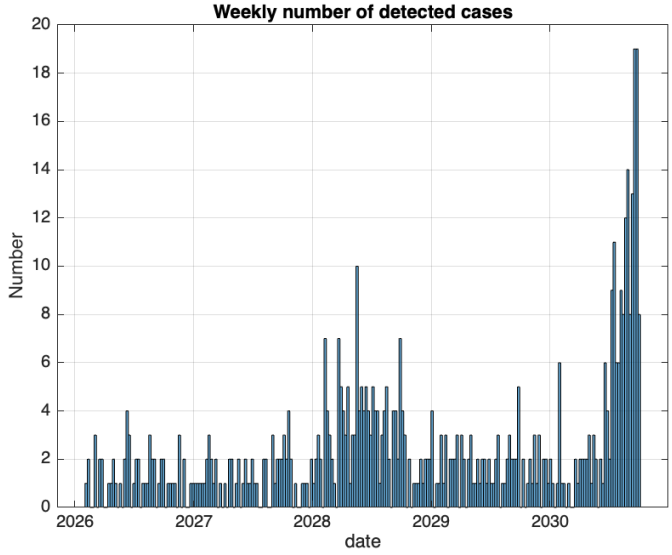

Figure 3. Weekly number of detected cases.

The result showed a clear temporal trend in the number of positive cases detected each week.

3.3 Simulation of Epidemic Branching Process

Using a linear regression model, the research fitted the data to calculate the virus's doubling time and basic reproduction number R_0 shown in Figure 4.

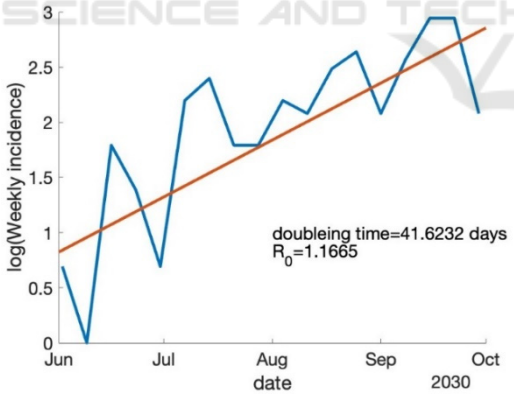

Figure 4. Reproduction number and doubling time.

The analysis of bat monitoring data and hospital testing data provided insights into the virus's transmission dynamics. The positivity rate and the distribution of positive cases in bats helped us understand the infection spread in wildlife, while the hospital data gave a clear picture of human infections. The epidemiological modelling revealed the virus's potential to spread, as indicated by the R_0 value and the doubling time. The doubling time was found to be 41.6232 days, and R_0 was calculated as 1.1665, indicating a moderate transmission potential.

The following Figure 5 presented the forecast with the mean and 90% prediction intervals over the next 60 days.

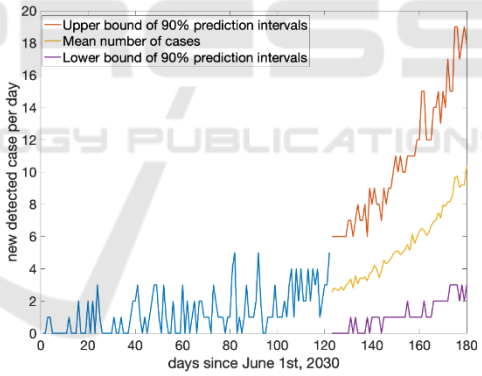

Figure 5. Forecast over the next 60 days.

The simulation of the epidemic branching process further illustrated the possible trajectories of virus transmission, highlighting the importance of early detection and intervention. These results are crucial for informing public health strategies and mitigating the impact of future outbreaks.

4 CONCLUSION

This paper conducted a comprehensive analysis of the transmission dynamics of the B1H3 virus in Deyr City, revealing the complex patterns of infection

spread between wildlife and human populations, and highlighting the importance of wildlife as reservoirs and vectors of disease. The positivity rates and case distribution in bats indicated heterogeneity in infection across different locations, possibly due to ecological factors, which is crucial for preventing potential spillovers to humans. Meanwhile, the analysis of hospital data provided a clear view of infection trends in humans, identifying patterns critical for early detection and intervention through the statistical data of weekly positive cases. Additionally, the SIR model was used to predict the disease's potential spread with considerable accuracy by calculating $\boldsymbol{R_0}$ and doubling time, quantifying the virus's transmission potential. The model highlighted the effectiveness of potential intervention strategies. The calculated $\boldsymbol{R_0}$ value of 1.1665 indicated a moderate potential for transmission, while a doubling time of 41.6232 days provided a critical window for implementing public health measures. The paper's simulation predicted the possible trajectory of the disease over the next 60 days, providing guidance for public health strategies. In summary, the study, through exhaustive methodologies and empirical analysis, offered valuable insights for addressing similar infectious threats and underscored the importance of continuous monitoring and timely intervention to effectively manage future outbreak.

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