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# Dynamical analysis of a mathematical model on the spread of diphtheria disease with vaccination completeness factor

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## Abstract

Pandemi COVID-19 telah mempengaruhi banyak aspek dalam kehidupan, termasuk layanan imunisasi. Akibat adanya gangguan dalam layanan ini, puluhan juta anak di seluruh dunia berisiko terjangkit difteri, ratusan ribu bayi tidak menerima imunisasi DPT secara lengkap, dan lebih dari satu juta bayi tidak mendapatkan vaksin BCG saat lahir. Selama tiga tahun terakhir, terdapat peningkatan angka kematian terhadap penyakit difteri, yakni mencapai 10,6% pada tahun 2022. Selain itu, jumlah kasus difteri pada tahun 2022 adalah dua kali lipat lebih banyak jika dibandingkan tahun 2021. Untuk mengatasi mewabahnya kembali difteri berbagai penelitian dilakukan, salah satunya melalui pemodelan matematika, yang mana dapat bermanfaat dalam memprediksi dinamika penyebaran penyakit dan mengatur strategi untuk mengatasinya. Penelitian ini mengembangkan model matematika untuk menggambarkan dinamika penyebaran difteri dengan pengaruh kelengkapan vaksinasi. Metode yang digunakan dalam analisis dinamik adalah dengan menganalisa nilai eigen dan perhitungan numerik, sedangkan simulasi numerik dilakukan menggunakan metode Runge-Kutta Orde Empat. Hasil dari analisis dinamik dan simulasi numerik menunjukkan bahwa titik keseimbangan bebas penyakit stabil jika bilangan reproduksi dasar $R_0 < 1$, dan titik keseimbangan endemik fisibel dan stabil jika $R_0 > 1$. Selain itu, dengan meningkatkan faktor kelengkapan vaksinasi dalam suatu populasi dapat membantu upaya pencegahan penyebaran difteri. Berdasarkan simulasi dalam skenario yang dibangun dalam penelitian ini, difteri tidak akan menjadi endemi ketika faktor kelengkapan vaksin mencapai 90% dengan tingkat perawatan 30%.

The COVID-19 pandemic has impacted many aspects of life, including immunization services. As a result of disruptions in these services, tens of millions of children worldwide are at risk of contracting diphtheria, hundreds of thousands of infants did not receive complete DPT immunization, and more than a million infants missed BCG vaccination at birth. Over the past three years, there has been an increase in mortality rates, reaching 10.6% in 2022. Additionally, the number of diphtheria cases in 2022 was more than twice that of 2021. To address the re-emerging of diphtheria, various studies have been conducted, one of which is through mathematical modeling, which can be useful in predicting the dynamics of disease spread and devising strategies to control it. This study developed a mathematical model to describe the dynamics of diphtheria spread with the influence of vaccination completeness. The dynamical

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analysis method used is by analyzing the eigenvalues and numerical calculation, while numerical simulations employ Fourth Order Runge-Kutta Method. Results from the dynamical analysis and numerical simulations indicate that the disease-free equilibrium point is stable if basic reproduction number $R_0 < 1$, and the endemic equilibrium point is feasible and stable if $R_0 > 1$. Moreover, increasing the vaccination completeness factor within a given population can aid in efforts to prevent the spread of diphtheria. Based on the simulation of the scenarios developed in this study, diphtheria will not become endemic when the vaccination completeness factor reaches 90% and the treatment rate reaches 30%.

**Keywords**: Diphtheria, Dynamical Analysis, Mathematical Model, Vaccination Completeness.



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## INTRODUCTION

Diphtheria is a disease that affects the respiratory tract and skin of humans. This disease is transmitted through droplets from individuals infected with the bacteria Corynebacterium diphtheriae. Diphtheria is a dangerous contagious disease that can lead to death if the infected individual is not treated promptly. The death is usually caused by obstruction of the airway, damage to the heart muscles, and abnormalities in the central nervous system and kidneys (Direktorat Surveilans dan Karantina Kesehatan & Direktorat Pencegahan dan Pengendalian Penyakit, 2017). Preventive measures against diphtheria can be taken by maintaining environmental hygiene, boosting the immune system, and participating in immunization programs.

**Table 1**. The Case Fatality Rate (CFR) of Diphtheria in Indonesia from 2020 to 2023

| Year | Diphtheria Case | Mortality Case | CFR |
|---|---|---|---|
| 2020 | 259 | 13 | 5,02% |
| 2021 | 235 | 25 | 10,64% |
| 2022 | 541 | 46 | 8,50% |
| 2023 | 949 | 68 | 7,17% |

Indonesia began implementing the DPT immunization program in 1976. Nevertheless, cases of diphtheria continue to occur year after year. In the last three years, according to data from the Indonesian Ministry of Health (2023), there were 259

cases in 2020, 235 cases in 2021, and an increase to 540 cases in 2022. The number of diphtheria cases in 2021 decreased compared to the previous year, but the number of deaths due to diphtheria showed a significant increase compared to the previous year (Kementerian Kesehatan RI, 2021). Data from 2022 also indicated that 10.6 percent of diphtheria cases were reported to have resulted in death, a proportion that is twice as high as in 2020 (Direktorat Statistik Kesejahteraan Rakyat, 2023). The case fatality rate (CFR) of diphtheria in the last four years is given by Table 1. CFR itself is defined by comparison between the total number of deaths due to a spesicific disease in one year and the total number of individuals affected by the disease.

An analysis of the increase in diphtheria cases indicates that the presence of vulnerable populations at high risk of outbreaks occurs among unimmunized children due to various reasons. One of the reasons is the COVID-19 pandemic, which affected immunization services. As a result, 80 million children under the age of 1 year old worldwide are at risk of suffering from diphtheria due to disruptions in routine immunization services during the COVID-19 pandemic. The impact of the pandemic and the decline in immunization coverage resulted in 373,200 infants aged 0-11 months not receiving complete DPT immunization, thus not achieving optimal immunity. By the end of 2021, there were 1,716,323 infants who did not receive BCG immunization at birth. Data from 2022 showed that the highest incidence of diphtheria suspects occurred in the age group of children under 1 to 4 years old (see Figure 1) (Direktorat Jenderal Pencegahan dan Pengendalian Penyakit, 2023). To learn more about the re-emerging of diphtheria, researches on the outbreak of diphtheria during and post-COVID has also been conducted, such as in Nigeria (Denue, et al., 2024; Olayiwola & Alaje, 2024; Egbune, et al., 2024), Thailand (Wanlapakorn, et al., 2024), Australia (Hendry, et al., 2024), and regions in Europe (Maugeri, et al., 2024).

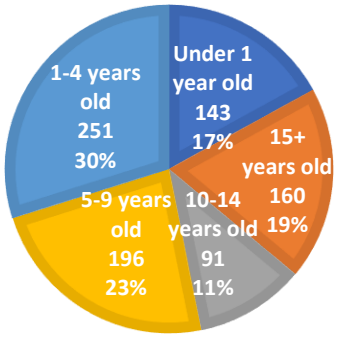


**Figure 1**. Distribution of Diphtheria Suspects by Age in 33 Provinces in Indonesia in 2022


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Strategies for addressing the spread of diphtheria can be conducted through a mathematical approach, i.e. modeling. Previous studies discussing mathematical modeling of diphtheria spread include: Puspita et al. (2017) discussed SIQR model of diphtheria; Ilahi and Widiana (2018) discussing the effectiveness of vaccines during diphtheria outbreaks; Izzati et al. (2020) designing optimal control problems in the SIQR model with prevention and management measures such as vaccination and quarantine; Putra and Rosha (2022) also utilizing the SIQR model. The results showed that the higher the vaccination rate, the fewer diphtheria cases there were, and the faster diphtheria disappeared from the population. Additionally, each infected individual must be quarantined to prevent the disease from spreading; Izzati and Andriani (2021) discussed the SEIQR model considering the influence of complete immunization coverage and natural immunity levels on diphtheria spread. Izzati & Andriani (2021) further applied optimal control problems to the model, showing that optimal control successfully reduced the number of exposed and infected individuals. Ghani et al. (2023) then developed the model into a fractional order SEIQR model. Ahmed et al. (2024) also studying a fractional order SEIQR model of diphtheria. Saltina et al. (2022) also used SEIQR model, finding that increasing the proportion of vaccinated and quarantined individuals significantly reduced the basic reproduction number; Aryani and Widyaningsih (2020) discussed the SVIR model, with simulation results indicating that diphtheria cases would still exist in 2030, suggesting that the goal of being diphtheria-free has not yet been achieved; Rahayu (2020) used the MSEIVR model to analyze diphtheria spread while considering the immune system of each individual.

Numerical simulation results indicated that diphtheria would not become endemic if vaccination continued consistently, meaning that vaccination could be an effective diphtheria control strategy; Nurhana and Abadi (2023) discussed the SVIQR model, showing that disease spread or endemicity could be prevented if the vaccines administered do not easily lose their efficacy; Lestari (2023) discussed the SEIQVR model, concluding that measures to prevent diphtheria outbreaks include reducing direct contact with infected individuals and maintaining hygiene; Ayinla & Ayinla (2024) using SEITR model showed that case detection is one of the important factors in preventing and handling a diphtheria outbreak. Madubueze et al. (2023) discuss dynamic analysis and optimal control issues in a diphtheria model considering booster

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vaccines. Fauzi et al. (2024) also consider booster vaccines for mapping high-risk zones in the spread of diphtheria. There are also models that take into account asymptomatic infected individuals (Madubueze, et al., 2023; Gourram, et al., 2024; Johnson, et al., 2024). And Islam et al. (2024) consider migration factors in their model. Meanwhile Hendry et al. (2024) discussed vaccination coverage of diphtheria-tetanus-pertussis in Australia, and Wanlapakorn et al. (2024) considered various age groups model in Thailand.

In previous studies, none have considered how the status of vaccination completeness affects the immunity acquired by individuals. Motivated by this, this research aims to contribute by providing a dynamic overview of the spread of diphtheria with the influence of vaccination completeness through mathematical modeling. And by providing the dynamical overview, further prevention and management measures for diphtheria spread could be made and applied.

## METHODS

The research flow is described descriptively as follows. The first step is data collection. In this step, a literature review is conducted to obtain data and references related to diphtheria, including its causes, transmission, treatment, and prevention. Data and references can be sourced from scientific articles, research studies, books, annual reports, and others (Kementerian PPN/BAPPENAS, 2013; Direktorat Surveilans dan Karantina Kesehatan & Direktorat Pencegahan dan Pengendalian Penyakit, 2017; Kementerian Kesehatan RI, 2021; Direktorat Jenderal Pencegahan dan Pengendalian Penyakit, 2023; Direktorat Statistik Kesejahteraan Rakyat, 2023). In addition to the literature review, data is also collected through interviews with health practitioners. The second step is model construction with the influence of vaccination completeness. After the model is constructed, the next step is dynamic analysis. In this third step, equilibrium points and the basic reproduction number of the system are sought. Dynamical analysis is performed to determine the stability properties of the equilibrium points. The stability properties could be determined by analyzing the eigenvalues of the characteristic equation. In addition, numerical analysis is also used due to algebraically lengthy characteristic equation, which would be relatively difficult to solve using the eigenvalue method. Following that, the fourth step involves simulation to obtain the

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trajectory of numerical solutions from the model. Numerical simulations are performed using Maple 2022 software with Fourth Order Runge-Kutta Method. The Fourth Order Runge-Kutta method provides high accuracy and good stability in the numerical computation of ordinary differential equations. Maple is used as a tool in this research because it can perform both symbolic and numerical calculations, which is useful for verifying analytical computations and providing graphical representations of the numerical solutions to systems of differential equations. Maple also offers a command option to implement the Fourth Order Runge-Kutta method. The combination of both enables effective and efficient simulations of differential equation systems. In numerical simulations, the stability properties of the equilibrium points obtained analytically can be verified against the results of numerical simulations. The results of the numerical simulations are then interpreted and conclusions are drawn. Next, the fifth step is model validation. Model validation is conducted with the assistance of health practitioners to ensure that the obtained mathematical model is appropriate and reasonable from a medical perspective. Once assessed as suitable, the next step is to write the results obtained in this research in a scientific article manuscript.

## RESULT AND DISCUSSION

This section discusses the construction of the model, stability analysis of the equilibrium points, and its numerical simulation.

### Construction of the Model

The assumptions established in the model are as follows:

- In a total population $N$, there are five subpopulations based on their status regarding the spread of diphtheria, namely $S$ (Susceptible), $E$ (Exposed), $I$ (Infected), $Q$ (Quarantined), and $R$ (Recovered).
- Susceptible refers to the subpopulation that is vulnerable to diphtheria. Exposed is the subpopulation that has been exposed to diphtheria due to contact with the infected subpopulation, referred to as Infected. Quarantined is the subpopulation that is infected and subsequently receives treatment in quarantine. Recovered is the subpopulation that has recovered from diphtheria.
- There is natural growth and natural death within the total population.


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- Individuals who receive complete vaccinations are assumed to be immune, meaning they will not contract diphtheria, and are included in the Recovered subpopulation, i.e. $v\mu N$. In contrast, individuals who do not receive complete vaccinations, or are not vaccinated at all, fall into the Susceptible subpopulation, i.e. $(1-v)\mu N$. This model does not take into account natural immunity, so individuals who do not receive full vaccination are categorized as Susceptible.
- There are deaths caused by diphtheria.

Based on the established assumptions, a compartment diagram is created as shown in Figure 2.

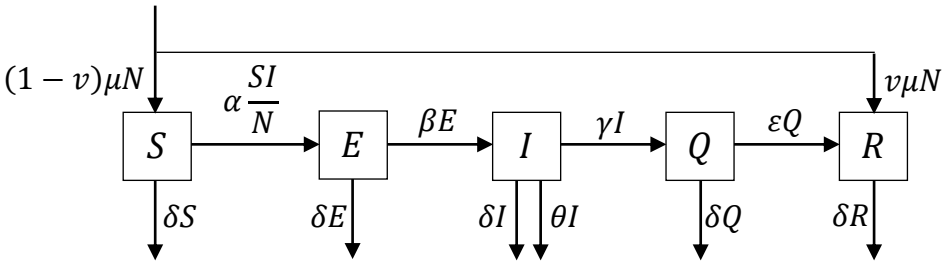


**Figure 2**. Compartment Diagram of the Mathematical Model on the Spread of Diphtheria Disease with Vaccination Completeness Factor

Based on the compartment diagram in Figure 2, the mathematical model for the spread of diphtheria disease with vaccination completeness factor can be expressed mathematically as a system of ordinary differential equations (1).

$$\frac{dS}{dt} = (1-v)\mu N - \frac{\alpha SI}{N} - \delta S$$

$$\frac{dE}{dt} = \frac{\alpha SI}{N} - \beta E - \delta E$$

$$\frac{dI}{dt} = \beta E - \gamma I - \delta I - \theta I \qquad (1)$$

$$\frac{dQ}{dt} = \gamma I - \varepsilon Q - \delta Q$$

$$\frac{dR}{dt} = v\mu N + \varepsilon Q - \delta R$$

where $N = S + E + I + Q + R$, with the parameters

$\mu$: natural growth rate (birth rate)

$v$: proportion of individuals receiving complete vaccination


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$\alpha$: transmission rate (interaction rate between the susceptible and infected subpopulations)

$\beta$: rate at which the exposed subpopulation transitions to the infected subpopulation

$\gamma$: rate of management and treatment of the infected subpopulation in quarantine

$\delta$: natural death rate

$\varepsilon$: recovery rate of the subpopulation in quarantine

$\theta$: death rate due to diphtheria

*Non-dimensional*

Let $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, $q = \frac{Q}{N}$, and $r = \frac{R}{N}$ be non-dimensional variables, representing the proportion of individuals in each subpopulation, then the system of equations (1) can be expressed as the system of equations (2).

$$\frac{ds}{dt} = (1-v)\mu - \alpha si - \delta s$$

$$\frac{de}{dt} = \alpha si - \beta e - \delta e$$

$$\frac{di}{dt} = \beta e - \gamma i - \delta i - \theta i \qquad (2)$$

$$\frac{dq}{dt} = \gamma i - \varepsilon q - \delta q$$

$$\frac{dr}{dt} = v\mu + \varepsilon q - \delta r$$

**Equilibrium points**

By solving $\frac{ds}{dt} = \frac{de}{dt} = \frac{di}{dt} = \frac{dq}{dt} = \frac{dr}{dt} = 0$ referring to the system of equations (2), two equilibrium points are obtained, i.e. the disease-free equilibrium point and the endemic equilibrium point. The disease-free equilibrium point is obtained when $i = 0$, namely $T_1\left(\frac{(1-v)\mu}{\delta}, 0,0,0, \frac{v\mu}{\delta}\right)$. Meanwhile, the endemic equilibrium point is obtained when $i \neq 0$, namely $T_2(s^*, e^*, i^*, q^*, r^*)$,where $s^* = \frac{(\beta+\delta)(\gamma+\delta+\theta)}{\alpha\beta}$, $e^* = \frac{\gamma+\delta+\theta}{\beta} i^*$, $i^* = \frac{(1-v)\mu\beta}{(\beta+\delta)(\gamma+\delta+\theta)} - \frac{\delta}{\alpha}$, $q^* = \frac{\gamma}{\varepsilon+\delta} i^*$, $r^* = \frac{v\mu}{\delta} + \left(\frac{\varepsilon\gamma}{\delta\varepsilon+\delta^2}\right) i^*$. From the obtained endemic equilibrium point, it can be seen that $e^*$, $q^*$ and $r^*$ depend on the value of $i^*$. This means that the proportion of the exposed diphtheria subpopulation, the proportion of the

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quarantined subpopulation, and the proportion of the recovered subpopulation depend on the proportion of the diphtheria-infected subpopulation. Additionally, it is also evident that the feasibility of the endemic equilibrium point depends on the value of $i^*$, with the condition for the feasibility of the endemic equilibrium point being $\frac{(1-v)\mu\beta}{(\beta+\delta)(\gamma+\delta+\theta)} > \frac{\delta}{\alpha}$.

## Basic Reproduction Number

To determine $R_0$, the derivatives of the affected subpopulations in the system of equations (2) are taken, namely $\frac{de}{dt}$ and $\frac{di}{dt}$. Let $x = (e, i)$ and $\frac{dx}{dt} = F - V$, where $F = \begin{pmatrix} \alpha si \\ 0 \end{pmatrix}$ and $V = \begin{pmatrix} (\beta+\delta)e \\ -\beta E + (\gamma+\delta+\theta)i \end{pmatrix}$. Thus, the Jacobian matrix of $F$ and $V$ is obtained as follows.

$$J_F = \begin{pmatrix} 0 & \alpha s \\ 0 & 0 \end{pmatrix}$$

$$J_V = \begin{pmatrix} \beta+\delta & 0 \\ -\beta & \gamma+\delta+\theta \end{pmatrix}$$

Substituting the disease-free equilibrium point $T_1$ into the Jacobian matrices $J_F$ and $J_V$ results in $\boldsymbol{F} = \begin{pmatrix} 0 & \frac{\alpha(1-v)\mu}{\delta} \\ 0 & 0 \end{pmatrix}$ and $\boldsymbol{V} = \begin{pmatrix} \beta+\delta & 0 \\ -\beta & \gamma+\delta+\theta \end{pmatrix}$, respectively. Where $\boldsymbol{F}$ is the matrix of secondary rates of affected individuals and $\boldsymbol{V}$ is the matrix of transmission rates.

Next, the dominant eigenvalue of $\boldsymbol{FV}^{-1}$ is determined to find the value of $R_0$, where

$\boldsymbol{FV}^{-1} = \begin{pmatrix} \frac{\alpha\beta(1-v)\mu}{\delta(\beta+\delta)(\gamma+\delta+\theta)} & \frac{\alpha(1-v)\mu}{\delta(\gamma+\delta+\theta)} \\ 0 & 0 \end{pmatrix}$. By solving $|\boldsymbol{FV}^{-1} - \lambda I| = 0$, the eigenvalues of $\boldsymbol{FV}^{-1}$ are obtained, namely $\lambda = \frac{\alpha\beta(1-v)\mu}{\delta(\beta+\delta)(\gamma+\delta+\theta)}$ and $\lambda = 0$. Thus, it is known that the basic reproduction number of the system is $R_0 = \frac{\alpha\beta(1-v)\mu}{\delta(\beta+\delta)(\gamma+\delta+\theta)}$.

## Stability of the Equilibrium Points

The Jacobian matrix of the system (2) is represented by matrix (3).


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$$J = \begin{bmatrix} -\alpha i - \delta & 0 & -\alpha s & 0 & 0 \\ \alpha i & -\beta - \delta & \alpha s & 0 & 0 \\ 0 & \beta & -\gamma - \delta - \theta & 0 & 0 \\ 0 & 0 & \gamma & -\varepsilon - \delta & 0 \\ 0 & 0 & 0 & \varepsilon & -\delta \end{bmatrix} \quad (3)$$

*Stability of the disease-free equilibrium point*

Substituting the disease-free equilibrium point $T_1\left(\frac{(1-v)\mu}{\delta}, 0,0,0, \frac{v\mu}{\delta}\right)$ into matrix (3) yields matrix (4).

$$J_{T_1} = \begin{bmatrix} -\delta & 0 & -\frac{\alpha(1-v)\mu}{\delta} & 0 & 0 \\ 0 & -\beta - \delta & \frac{\alpha(1-v)\mu}{\delta} & 0 & 0 \\ 0 & \beta & -\gamma - \delta - \theta & 0 & 0 \\ 0 & 0 & \gamma & -\varepsilon - \delta & 0 \\ 0 & 0 & 0 & \varepsilon & -\delta \end{bmatrix} \quad (4)$$

Then, the equation $\left|J_{T_1} - \lambda I\right| = 0$ will be solved to obtain the characteristic equation (5).

$$(-\delta - \lambda)(-\varepsilon - \delta - \lambda)(-\delta - \lambda)\left[\lambda^2 + (\beta + 2\delta + \gamma + \theta)\lambda + (\beta + \delta)(\gamma + \delta + \theta) - \frac{\alpha\beta(1-v)\mu}{\delta}\right] = 0 \quad (5)$$

Based on equation (5), it is known that $\lambda_{1,2} = -\delta$, and $\lambda_3 = -\varepsilon - \delta$, while $\lambda_4$ and $\lambda_5$ are obtained from the quadratic equation (6).

$$\frac{1}{(\beta + \delta)(\gamma + \delta + \theta)}\lambda^2 + \frac{(\beta + 2\delta + \gamma + \theta)}{(\beta + \delta)(\gamma + \delta + \theta)}\lambda + 1 - R_0 = 0 \quad (6)$$

The roots of equation (6) are negative if $1 - R_0 > 0$, or $R_0 < 1$. Thus, it is known that the disease-free equilibrium point $T_1$ is asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

*Stability of the endemic equilibrium point*

As mentioned in the subsection discussing equilibrium points, the endemic equilibrium point $T_2$ is not always feasible. The conditions for its feasibility are $\frac{(1-v)\mu\beta}{(\beta+\delta)(\gamma+\delta+\theta)} > \frac{\delta}{\alpha} \Leftrightarrow \frac{\alpha(1-v)\mu\beta}{\delta(\beta+\delta)(\gamma+\delta+\theta)} > 1 \Leftrightarrow R_0 > 1$.

In other words, the endemic equilibrium point $T_2$ is feasible if $R_0 > 1$. The analytical solution for the endemic equilibrium point $T_2$ is relatively lengthy; therefore, further


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analysis of the equilibrium point $T_2$ is conducted through numerical simulation.

## Numerical Simulations

In this study, numerical simulations were conducted using Maple 2022 software. The numerical simulations were performed to verify the eigenvalues and their stability properties. Additionally, several scenarios were discussed through numerical simulations to illustrate the dynamics occurring in the system. Some parameter values used in the numerical simulations refer to previous studies (see Table 2), while others were chosen hypothetically in the elaborated scenarios. Three scenarios were simulated, each having three different cases. These scenarios were simulated to determine the impact of vaccination completeness on three different conditions of managing the diphtheria-infected subpopulation.

**Table 2**. Parameter that Refers to Previous Research

| Parameter | Value | Source |
|---|---|---|
| $\alpha$ | 0.57 | (Puspita et al., 2017) |
| $\beta$ | 0.23 | (Fathoni et al., 2014) |
| $\varepsilon$ | 0.5 | (Puspita et al., 2017) |
| $\mu$ | 0.019 | (Kementerian PPN/BAPPENAS, 2013) |
| $\delta$ | 0.006 | (Kementerian PPN/BAPPENAS, 2013) |
| $\theta$ | 0.05 | (Direktorat Surveilans dan Karantina Kesehatan & Direktorat Pencegahan dan Pengendalian Penyakit, 2017) |

**Table 3**. Results of the Numerical Simulations

| Parameter | Scenario I | | | Scenario II | | | Scenario III | | |
|---|---|---|---|---|---|---|---|---|---|
| | Case A | Case B | Case C | Case A | Case B | Case C | Case A | Case B | Case C |
| $v$ | 0 | 0 | 0 | 0.3 | 0.3 | 0.3 | 0.9 | 0.9 | 0.9 |
| $\gamma$ | 0 | 0.3 | 0.9 | 0 | 0.3 | 0.9 | 0 | 0.3 | 0.9 |
| $R_0$ | 31.413 | 4.941 | 1.840 | 21.989 | 3.459 | 1.289 | 3.141 | 0.494 | 0.184 |
| Feasible Equilibrium Point | $T_1, T_2$ | $T_1, T_2$ | $T_1, T_2$ | $T_1, T_2$ | $T_1, T_2$ | $T_1, T_2$ | $T_1, T_2$ | $T_1$ | $T_1$ |
| Stable Equilibrium Point | $T_2$ | $T_2$ | $T_2$ | $T_2$ | $T_2$ | $T_2$ | $T_2$ | $T_1$ | $T_1$ |
| $s_f$ | 0.101 | 0.641 | 1.721 | 0.101 | 0.641 | 1.721 | 0.101 | 0.317 | 0.317 |


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| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| $e_f$ | 0.078 | 0.064 | 0.037 | 0.054 | 0.040 | 0.013 | 0.006 | 0 | 0 |
| $i_f$ | 0.320 | 0.042 | 0.009 | 0.221 | 0.026 | 0.003 | 0.023 | 0 | 0 |
| $q_f$ | 0 | 0.025 | 0.016 | 0 | 0.015 | 0.005 | 0 | 0 | 0 |
| $r_f$ | 0 | 2.050 | 1.311 | 0.950 | 2.229 | 1.399 | 2.850 | 2.850 | 2.850 |
| Total Population | 0.499 | 2.822 | 3.094 | 1.326 | 2.951 | 3.141 | 2.98 | 3.167 | 3.167 |

In Scenario I, the value $v = 0$ is chosen, meaning that no individuals receive complete vaccination. In Scenario II, $v = 0.3$ is selected to represent that the proportion of individuals receiving complete vaccination is 30% of the total natural growth. In Scenario III, $v = 0.9$ is chosen to illustrate a situation where the proportion of individuals receiving complete vaccination is 90%. Similarly, the parameter $\gamma$ is selected for three different conditions of managing the diphtheria-infected subpopulation, namely $\gamma = 0$, $\gamma = 0.3$, and $\gamma = 0.9$. The value $\gamma = 0$ means there is no management at all for the infected subpopulation. The value $\gamma = 0.3$ indicates that 30% of the infected subpopulation receives treatment in quarantine. The value $\gamma = 0.9$ means that 90% of the infected subpopulation is quarantined. The results of the simulated scenarios are shown in Table 3.

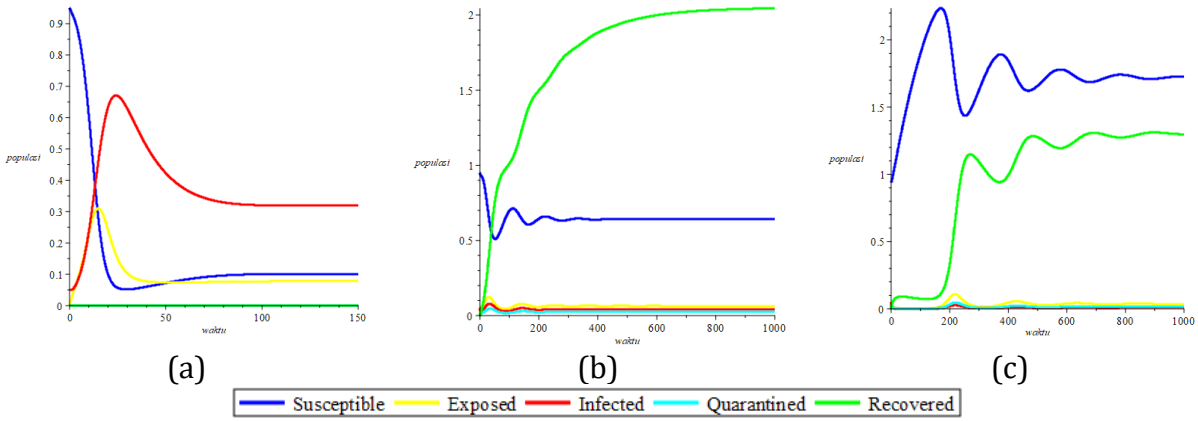


**Figure 3**. Population dynamics in the mathematical model of diphtheria spread with vaccination completeness $v = 0$ (a) $\gamma = 0$ (b) $\gamma = 0.3$ (c) $\gamma = 0.9$

In Scenario I, the population dynamics of the model are shown in Figure 3. Figure 3a illustrates the population dynamics when no individuals receive complete vaccination and there is no management of diphtheria. It is observed that in Case A, the number of exposed subpopulations increases, followed by an increase in the number of infected subpopulations, before finally decreasing and stabilizing towards the endemic


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equilibrium point (0.101, 0.078, 0.320, 0, 0). This means that in Case A, the number of individuals treated in quarantine and those who recover is zero. For Figure 3b, no individuals receive complete vaccination, but there is management of diphtheria amounting to 30% of the total infected. The results show that over time, the population dynamics stabilize towards (0.641, 0.064, 0.042, 0.025, 2.050). Similarly, in Case C, there is also management, but at a higher level of 90% of the total infected subpopulation. Over time, the population dynamics shown in Figure 3c stabilize towards (1.721, 0.037, 0.009, 0.016, 1.311). The difference between Case B and Case C is that, in addition to the $R_0$ value in Case C being lower than in Case B, the number of individuals exposed and infected with diphtheria in Case C is smaller, resulting in fewer recoveries compared to Case B.

Similarly, for Scenario II, the interpretation is akin to Scenario I. The difference lies in the $R_0$ value obtained in Scenario II, which is smaller than the $R_0$ in Scenario I. This is due to the higher vaccination completeness factor ($v = 0.3$) compared to that in Scenario I ($v = 0$).

In Scenario III, the situation is discussed where the vaccination completeness factor is $v = 0.9$ and there is no treatment. In Case A (see Figure 5a), the value of $R_0 = 3.141$ is obtained. Over time, the population dynamics stabilize towards the endemic equilibrium point (0.101, 0.006, 0.023, 0, 2.850). Because there is no treatment, the value $q_f = 0$ and the value $r_f$ is derived from individuals who are immune to diphtheria due to complete vaccination. In Case B (see Figure 5b), the value of $R_0 = 0.494$ is obtained. In this scenario, the endemic equilibrium point is not feasible. Over time, the population dynamics stabilize towards the disease-free equilibrium point (0.317, 0, 0, 0, 2.850). This means that there are no more individuals exposed, infected, or quarantined due to diphtheria. Case C is similar to Case B, with the difference being that the value of $R_0 = 0.184$ in Case C is smaller than in Case B. Looking at the population dynamics shown in Figure 5c (compare with Figure 5b), the time taken for the exposed, infected, and quarantined subpopulations to reach zero is faster in Case C compared to Case B.


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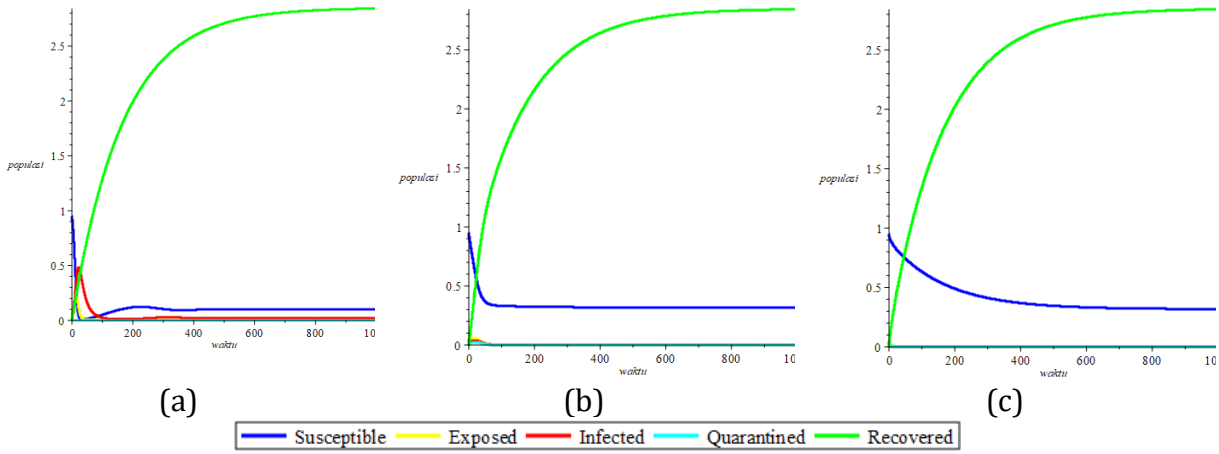


**Figure 5**. Population dynamics in the mathematical model of diphtheria spread with vaccination completeness $v = 0.9$ (a) $\gamma = 0$ (b) $\gamma = 0.3$ (c) $\gamma = 0.9$

Figure 6 shows that the $R_0$ values in all three cases, i.e Case A ($\gamma = 0$), Case B ($\gamma = 0.3$), and Case C ($\gamma = 0.9$), decreases as the vaccination completeness factor increases. The level of treatment ($\gamma$) also plays a role in the resulting $R_0$ value, as shown by the graph of Case C, which is lower than the graph of Case B, and the graph of Case B, which is lower than Case A. Sensitivity analysis of $v$ and $\gamma$ on infected population also support these results, which show the larger the values of $v$ and $\gamma$, the fewer the number of infected individuals (see Figure 7).

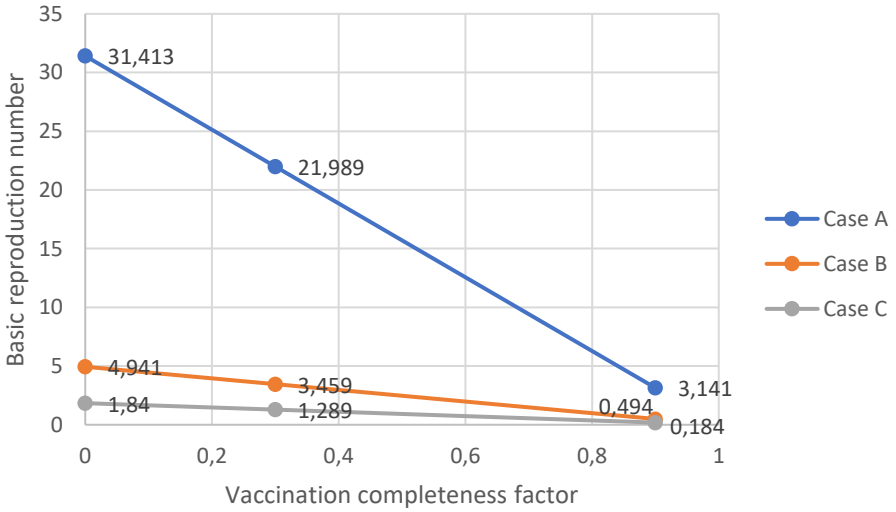


**Figure 6**. Changes of Basic Reproduction Number ($R_0$) Value over the Vaccination Completeness Factor in Case A, B, and C


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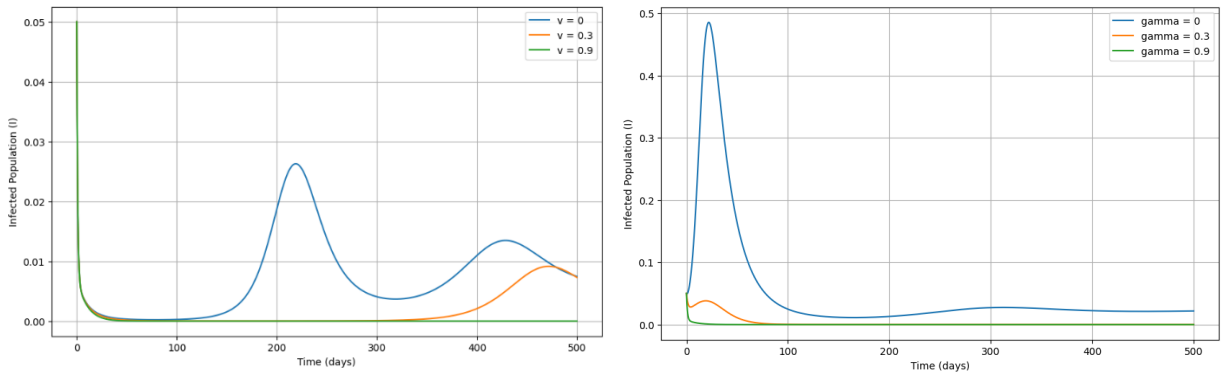


(a) (b)

**Figure 7**. Effect of Vaccination Completeness Factor ($v$) on Infected Population (a) and Effect of Treatment Rate ($\gamma$) on Infected Population (b)

## CONCLUSION

Based on the results and discussion, several conclusions can be drawn from this study. First, the higher the vaccination completeness in the total population, the lower the resulting basic reproduction number. Second, as the basic reproduction number increases, the number of individuals exposed, infected, and quarantined in the total population also increases. The model will be disease-free when $R_0 < 1$, and an epidemic will occur when $R_0 > 1$. This study's findings indicate that the vaccination completeness factor within a population can influence the response to the spread of diphtheria as modeled. Therefore, vaccination completeness is a factor that needs to be considered in the strategy to prevent the re-emerging of diphtheria. One way to achieve this is by promoting immunization campaigns. This study only discusses vaccination completeness factor in a simple manner, further research can be conducted by considering factors such as age structure, individual mobility, the presence of booster vaccines, and many others.

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## CONFLICTS OF INTEREST

The authors hereby declare that there are no conflicts of interest regarding the research and publication of this work. All funding and support received were disclosed, and no financial or personal relationships influenced the outcomes of this study.

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## AUTHOR CONTRIBUTIONS

**Nailul Izzati:** Conceptualization, writing - original draft, editing, and visualization;

**Nanndo Yannuansa:** Formal analysis;

**Imamatul Ummah:** Methodology;

**Dian Anisa Rokhmah Wati:** Resources;

**Elly Indahwati:** Resources;

**Silviana Maya Purwasih:** Validation;

**Nur Kholis:** Writing - review & editing, Supervision.

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