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Stability Analysis of Monkeypox Transmission Model by Administering Vaccine

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Abstract

Monkeypox is an infectious disease that affects mammals, including humans and some primates. Monkeypox transmission can be prevented by administering vaccinations to the human population. This study aims to construct and analyze the monkeypox transmission model's stability with vaccination. There are six sub-populations: Vaccinated humans (V_m), Susceptible humans (S_m), Infected human (I_m), Recovered human (R_m), Susceptible animal (S_h), and Infected human $I(_h)$. Several steps are literature study, formulating assumptions, constructing models, finding equilibrium points, searching for reproduction numbers by next-generation matrix, analyzing stability, and numerical simulations using Matlab R02023b. From the model, three equilibria are obtained: disease-free equilibrium points, first endemic equilibrium points, and second endemic equilibrium points. Disease-free equilibrium point $E_0^* = (\frac{\Lambda_m \eta}{\mu_1(\sigma+\eta+\mu_1)}, \frac{\Lambda_m(\mu_1+\sigma)}{\mu_1(\sigma+\eta+\mu_1)}, 0, 0, \frac{\Lambda_h}{\mu_2}, 0)$ will be asymptotically stable at the vaccination rates $\eta > \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and the animal transmission rate of the animal at the rate of $\alpha_3 < (\delta_2 + \mu_2)$. The first endemic equilibrium point $E_1^* = (\frac{\eta N_m(\gamma_1+\mu_1+\delta_1)}{\alpha_2(\sigma+\mu_1)}, \frac{N_m(\gamma_1+\mu_1+\delta_1)}{\alpha_2}, Im*, Rm*, \frac{\Lambda_h}{\mu_2}, 0)$ will be stable for $\eta < \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 < (\delta_2 + \mu_2)$. The second endemic equilibrium point $(E_2^*) = (V_{m_2}^*, S_{m_2}^*, I_{m_2}^*, R_{m_2}^*, S_{h_2}^*, I_{h_2}^*)$ will be stable for $\eta < \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 > (\delta_2 + \mu_2)$. Based on numerical simulation results, it is obtained that the higher the vaccination rate and the lower the transmission rate in animals, the faster the transmission of monkeypox infections.

INTRODUCTION

After the COVID-19 pandemic in early 2020, it has not been completed until now. The World Health Organization has stated that monkeypox is an emergency that will concern global health and has predicted that more cases will be identified [1]. In Indonesia, the Ministry of Health of the Republic of Indonesia explained that the case of monkey smallpox was first identified in Indonesia. A 27-year-old Indonesian citizen was confirmed positive for smallpox with a history of overseas travel believed to be transmitted through close contact with an infected

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person [2]. On 15 September 2022, 2 suspected and 63 cured cases were transmitted across 10 Indonesian provinces [3].

The monkeypox virus is a family of *poxviridae* and subfamily *chordboxvirinae* with the genus orthopoxvirus found in a colony of monkey animals treated for research purposes, hence the monkey pox [4]. It is known that the first human cases were identified in the Democratic Republic of the Congo in 1970 and occurred in rural endemic areas, tropical forests of the Congo Basin, and West Africa [5].

Early symptoms of monkeypox are fever, severe headaches, muscle pain, back pain, limp, swelling of lymph nodes in the neck, armpit, or groin, and rashes or skin lesions. Rashes usually begin within one to three days of fever [6]. The lesions on the skin develop into red spots such as smallpox, clear fluid blisters, pus-filled blisters, and then harden or scabbard and fall out [7]. Rashes are usually concentrated on the face, palms, and soles of the feet and can be found in the mouth, genitalia, and eyes [8]. Although symptoms can heal within 2-4 weeks, they can cause medical complications and death in some people [9]. Therefore, contact your doctor immediately if you experience these symptoms [5].

Monkeypox virus is transmission from animal to human through bites or scabs of infected animals, processing of game animals or products contaminated with viruses, and through contact with body fluids or wounds in infected people [6]. Monkeypox can also be contagious from human to human by direct contact with infectious wounds, gore, bodily fluids, and respiratory droplets [10]. Although known as monkeypox, monkeys are not the main reservoir. Various animal species can be infected with the virus, but further research is needed on its natural history and reservoirs [4]. Vaccination is one way to reduce the transmission of the monkeypox virus. To deal with the current monkeypox outbreak, three vaccines can be used: a second-generation vaccine called ACAM2000 and two third-generation vaccines known as MVA BN or JYNNEOS [3].

A study by Te Winkel on the transmission of the Monkeypox virus used the SIR model in human and animal populations as a vector of viruses. The human population is divided into Susceptible humans. (S_h), Infected humans (I_h), and Recovered humans (R_h), while the animal population is divided into Susceptible animals (S_a), Infected animals (I_a), and Recovered animals (R_a) [11].

The mathematical model of SIR disease can consider the prevention factor of vaccination. In his research, a minimal proportion of vaccinations could reduce or eliminate the number of infected people [12] [13]. In this model, a search will be performed to find disease-free and endemic equilibrium points for each compartment and calculate basic reproductive numbers to determine whether or not they are endemic. In addition, it will analyze the most significant parameters against the primary reproduction number. Next, a model simulation will be performed to dynamically visualize the stability of equilibrium points and see the changes occurring in each population class in the model.

METHOD

The study focused on the transmission of monkeypox in the presence of vaccination. Data taken for parameter estimation are data used by the previous article. Based on the above research steps, the following flow chart study can be obtained:

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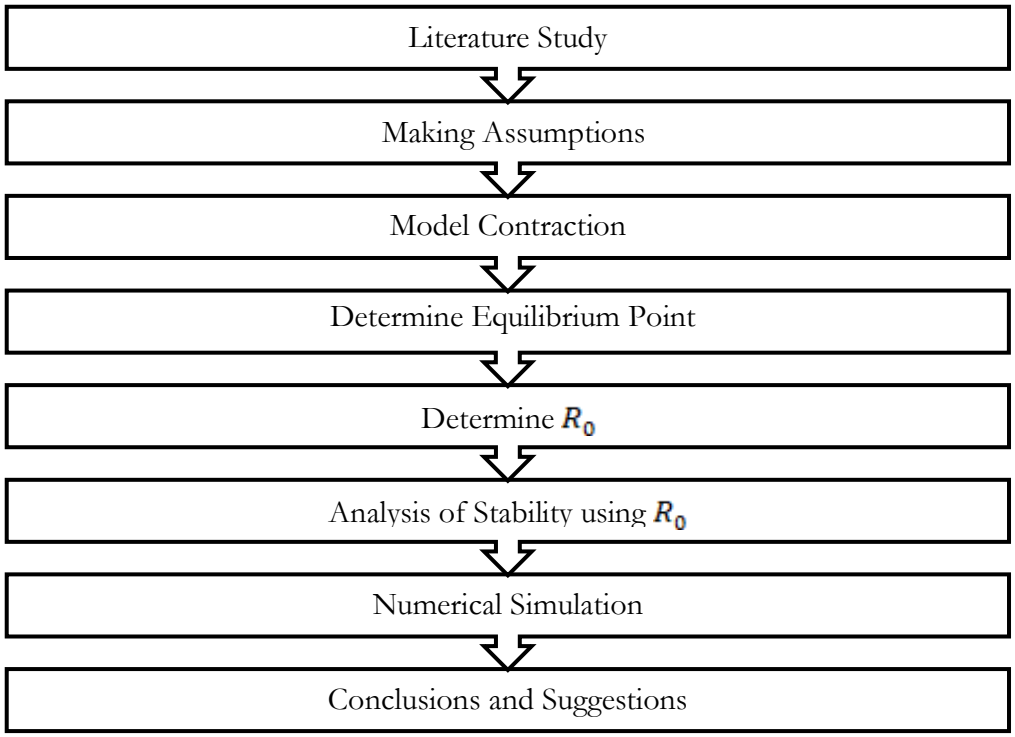

Diagram 1. Flow Chart Study

In this study, there are research steps taken. The steps are as follows:

1. Literature Study
   This step is done with literature on the model for transmitting monkey pox disease. This literature study was conducted to obtain information about problems to be used as a reference in later writings. Literature studies conducted included the identification of monkey smallpox, the method of transmission of monkey smallpox, the mathematical model of transmission smallpox, and the parameter values of the population.
2. Making Assumptions
   Every mathematical model of disease transmission begins with assumptions. The assumption is the foundation of a mathematical model [14]. The assumption is used to simplify the problem. The model's scope will fall within the limits of the problem researchers want to study. The model was created based on assumptions that supported the research problem, as seen in the model created in this study. If at least one assumption is added or omitted, this will impact the form of the model obtained.
3. Model Contraction
   This process was performed to create a comprehensive diagram of a mathematical model describing the transmission of monkeypox disease by vaccination. Next, create a differential equation for the model [15].
4. Set an Equilibrium Point
   This process is performed to find the equilibrium point of a system of differential equations or models formed. To find the equilibrium point using differential equations or from the

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model form obtained with $f(x) = 0$ [16], the value of each sub-population is the equilibrium point of the monkeypox transmission model.

5. Searching For Number Reproduction
   This step is performed to obtain the equilibrium point requirements. Stability tests are performed using the Next Generation Matrix of the interaction model formed [17]. From the Next Generation Matrix, a basic reproduction number R_0 can be found to determine the stability point requirements.
6. Analysis of Stability
   Analysis of stability and equilibrium points obtained by using R_0 [18],
7. Numerical Simulation
   This step is performed using the help of the Matlab software. So a plot of the transmission model of monkey pox disease showed results.
8. Conclusions and Suggestion
   The model analysis results with the equilibrium points obtained by concluding the previous discussion were described at this stage.

RESULTS AND DISCUSSION

The model used in the transmission of monkeypox disease is a VSIR model developed by dividing two populations (human and animal) into six compartments: vaccinated humans $V_m(t)$, Susceptible humans $S_m(t)$, Infected humans $I_m(t)$, Recovered humans (t), Susceptible animals $S_h(t)$ Infected animals $I_h(t)$. The total human population is given as $N_m(t) = S_m(t) + V_m(t) + I_m(t) + R_m(t)$, and the total animal population is given as $N_h(t) = S_h(t) + I_h(t)$.

The population is assumed to be closed, and no migration. Newborn individuals enter the susceptible population with the number of births λ_m (for the human population) and λ_h (for the animal population). The population is assumed to be homogeneous, where every susceptible individual has the same chance of contracting the virus. The disease can lead to death with rates of δ_1 to human and δ_2 animals. Susceptible human individuals who have been successfully vaccinated enter the population of vaccinated individuals at a rate of η. Individuals who fail to be vaccinated due to vaccine effectiveness decline into susceptible human populations at a rate of σ. A susceptible human makes contact with an infected human at a rate of α_2. Susceptible humans to contact with infected animals can contract the virus at a rate of α_1. People who recover will be immune to disease and not become susceptible again at a rate of γ_1. Susceptible animals to contact with infected animals can be infected at a rate α_3. Individual animals infected with the Monkeypox virus cannot be cured. Each sub-population died naturally at the rate of μ_1 humans and μ_2 animals.

Figure 1 shows a compartment diagram of a mathematical model of the transmission of monkey pox disease in the presence of vaccination based on previously determined assumptions.

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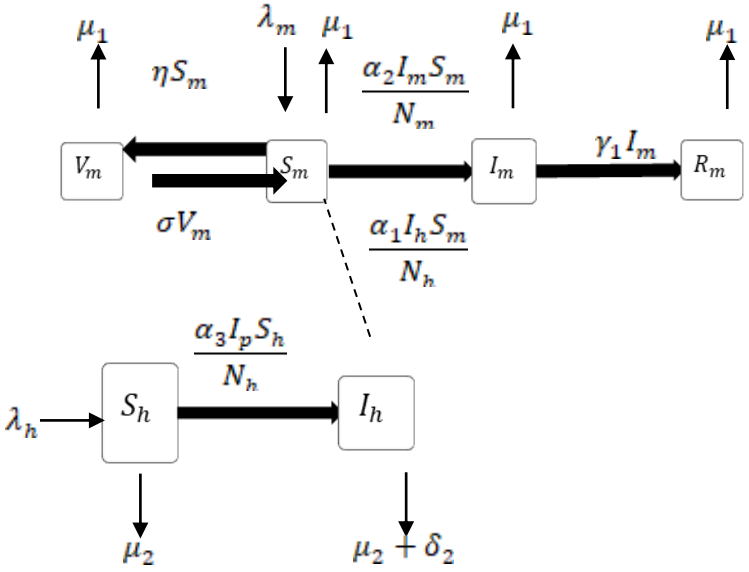

Figure 1. The mathematical model of the distribution of smallpox but with vaccination

The description of the compartment diagram in Figure 1 is as follows:

1) Human Vaccinated sub-population changes ($\boldsymbol{V_m}$) over time (t)

Human Vaccinated sub-populations ($\boldsymbol{V_m}$) increase due to decreased vaccination rates of human Susceptible sub-populations ($\boldsymbol{S_m}$) with a rate of η. The sub-population $\boldsymbol{V_m}$ decreases as the vaccine's effectiveness decreases from the sub-population $\boldsymbol{V_m}$ by a rate of σ. The sub-population $\boldsymbol{V_m}$ decreases due to the natural mortality of the sub-population $\boldsymbol{V_m}$ with a rate of $\boldsymbol{\mu_1}$. The mathematical model is

$$\frac{dV}{d_t} = \eta S_m - (\mu_1 + \sigma) V_m$$

2) Human Susceptible sub-population changes (S_m) over time (t)

Human Susceptible sub-populations (S_m) increase due to the vaccination rate of the sub-population V_m with a specific rate serta as well as the birth rate Λ_m. The sub-population S_m decreases due to the natural mortality of the population S_m μ_1. At the same time, it decreases if direct transmission from Sub-population S_m interacts with the human Infected sub-population (I_m) at a rate of α_2 and decreases if direct transmission from Sub-population S_m with sub-population Infected animals (I_p) at a rate of α_3. In addition to transmission, this decrease in sub-population is due to natural deaths from S_m sub-populations μ_1 and decreases due to disease deaths from $S_m$populations δ_1. The mathematical model is

$$\frac{dS_m(t)}{dt} = \Lambda_m + \sigma V_m - \frac{\alpha_1 I_h S_m}{N_h} - \frac{\alpha_2 I_m S_m}{N_m} - \eta S_m - \mu_1 S_m$$

3) Human Infected sub-population changes (I_m) over time (t)

Human Infected sub-populations (I_m) increase as direct transmission from S_m sub-populations interacts with I_m sub-populations at a rate of α_2 and increases in the case of direct

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transmission of S_m Infected animal sub-populations (I_p) at a rate of α_3. In addition to transmission, this decrease in sub-population is due to natural deaths from sub-population I_m of μ_1 and decreases due to disease deaths from population S_m of δ_1 and recovery from sub-population I_m of degree γ_1. The mathematical model is

$$\frac{dI_m(t)}{dt} = \frac{\alpha_1 I_h S_m}{N_h} + \frac{\alpha_2 I_m S_m}{N_m} - \gamma_1 I_m - \mu_1 I_m - \delta_1 I_m$$

4) Human Recovered sub-population changes (R_m) over time (t)

The recovered human sub-population (R_m) increases due to the recovery of the sub-population I_m by a rate of γ_1 and the decrease of this sub-population by natural death from sub-population R_m by a rate of μ_1. The mathematical model is

$$\frac{dR_m(t)}{dt} = \gamma_1 I_m - \mu_1 R_m$$

5) Animal Susceptible sub-population changes (S_h) over time (t)

Animal Susceptible sub-populations (S_h) increase due to birth rate Λ_h. Whereas it decreases if the direct transmission from Sub-population S_h interacts with the sub-population of Infected animals (I_h) at a rate of α_3 , and this decrease in sub-population due to natural death from sub-population S_h at a rate of μ_2. The mathematical model is

$$\frac{dS_h(t)}{dt} = \Lambda_h - \frac{\alpha_3 S_h I_h}{N_h} - \mu_2 S_h$$

6) Animal Infected Sub-population change (I_h) over time (t)

The sub-population of Infected animals (I_h) increases as direct transmission from Sub-population S_h interacts with sub-population I_h at a rate of α_3. In addition to transmission, this decrease in sub-population is due to natural deaths from sub-population I_h μ_1 and decreases due to disease deaths from population I_h of δ_1. The mathematical model is

$$\frac{dIh(t)}{dt} = \frac{\alpha_3 S_h I_h}{N_h} - (\delta_2 + \mu_2) I_h$$

With the above explanation, it can be concluded that the spread of monkey pox disease can be represented by a system of differential equations in the form of a mathematical model as follows [10];

$$\begin{aligned}
\frac{dV_m}{d_t} &= \eta S_m - (\mu_1 + \sigma) V_m \\
\frac{dS_m(t)}{dt} &= \Lambda_m + \sigma V_m - (\frac{\alpha_1 I_h S_m}{N_m} + \frac{\alpha_2 I_m S_m}{N_m}) - (\eta + \mu_1) S_m \\
\frac{dI_m(t)}{dt} &= \frac{\alpha_1 I_h S_m}{N_m} + \frac{\alpha_2 I_m S_m}{N_m} - (\gamma_1 + \mu_1 + \delta_1 +) I_m \\
\frac{dR_m(t)}{dt} &= \gamma_1 I_m - \mu_1 R_m \\
\frac{dS_h(t)}{dt} &= \Lambda_h - \frac{\alpha_3 S_h I_h}{N_h} - \mu_2 S_h
\end{aligned} \tag{1}$$

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$$\frac{dIh(t)}{dt} = \frac{\alpha_3 S_h I_h}{N_h} - (\delta_2 + \mu_2) I_h$$

Table 1. Variable definitions and model parameters for the transmission of monkeypox disease

No	Symbol	Definition
1.	$N_m(t)$	The total human population at the time *t*
2.	$N_h(t)$	The total number of animal populations at the time *t*
3.	$V_m(t)$	Number of vaccinated humans at the time *t*
4.	$S_m(t)$	Number of susceptible humans at the time *t*
5.	$I_m(t)$	Number of infected humans at the time *t*
6.	$R_m(t)$	Number of recovered humans at the time *t*
7.	$S_h(t)$	Number of susceptible animals at the time *t*
8.	$I_h(t)$	Number of infected animals at the time *t*
9.	μ_1	The natural death rate of human
10.	μ_2	The natural death rate of animals
11.	λ_m	Recruitment into susceptible human
12.	λ_h	Recruitment into a susceptible animal
13.	α_1	Animal-to-human contact rate
14.	α_2	Human-to-human contact rate
15.	α_3	Animal-to-animal contact rate
16.	γ_1	The recovery rate of human
17.	δ_1	The disease-induced death rate for human
18.	δ_2	The disease-induced death rate for animal
19.	σ	Effectiveness of vaccination
20.	η	Vaccine of Susceptible

1. Equilibrium point

The $(V_m, S_m, I_m, R_m, S_h, I_h)$ point is the equilibrium point of the system of equation 12 if it satisfies the equation $\frac{dV_m}{dt} = 0, \frac{dS_m}{dt} = 0, \frac{dI_m}{dt} = 0, \frac{dR_m}{dt} = 0, \frac{dS_h}{dt} = 0, \frac{dI_h}{dt} = 0$ referred to [11]. We get three kinds of equilibrium points that are disease-free equilibrium points $(E_0^*) = (V_{m_0}, S_{m_0}, I_{m_0}, R_{m_0}, S_{h_0}, I_{m_0})$, First endemic populations $(E_1^*) = (V_{m_1}, S_{m_1}, I_{m_1}, R_{m_1}, S_{h_1}, I_{m_1})$, two endemic populations $(E_2^*) = (V_{m_2}^*, S_{m_2}^*, I_{m_2}^*, R_{m_2}^*, S_{h_2}^*, I_{h_2}^*)$, the following:

$$E_0^* = \left(\frac{\Lambda_m \eta}{\mu_1(\sigma + \eta + \mu_1)}, \frac{\Lambda_m(\mu_1 + \sigma)}{\mu_1(\sigma + \eta + \mu_1)}, 0, 0, \frac{\Lambda_h}{\mu_2}, 0\right) \quad (2)$$

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$$E_1^* = \left(\frac{\eta N_m(\gamma_1+\mu_1+\delta_1)}{\alpha_2(\sigma+\mu_1)}, \frac{N_m(\gamma_1+\mu_1+\delta_1)}{\alpha_2}, \frac{-(-\lambda_m\alpha_2\sigma-\lambda_m\alpha_2\mu_1+\mu_1N_m\sigma\gamma_1+\mu_1^2N_m\sigma+\mu_1N_m\sigma\delta_1+\mu_1^2N_m\gamma_1+\mu_1^3N_m}{\alpha_2(\sigma+\mu_1)(\gamma_1+\mu_1+\delta_1)}\right.$$
$$\left.\frac{+\mu_1^2N_m\delta_1+\eta N_m\mu_1\gamma_1+\eta N_m\mu_1^2+\eta N_m\mu_1\delta_1)}{\alpha_2(\sigma+\mu_1)(\gamma_1+\mu_1+\delta_1)}, \frac{-\gamma_1(-\lambda_m\alpha_2\sigma-\lambda_m\alpha_2\mu_1+\mu_1N_m\sigma\gamma_1+\mu_1^2N_m\sigma+\mu_1N_m\sigma\delta_1+\mu_1^2N_m\gamma_1}{\alpha_2(\sigma+\mu_1)(\gamma_1+\mu_1+\delta_1)}\right.$$
$$\left.\frac{+\mu_1^2N_m+\mu_1^2N_m\delta_1+\eta N_m\mu_1\gamma_1+\eta N_m\mu_1^2+\eta N_m\mu_1\delta_1)}{\alpha_2(\sigma+\mu_1)(\gamma_1+\mu_1+\delta_1)\mu_1}, \frac{\Lambda_h}{\mu_2}, 0\right)$$

$$(E_2^*) = \left(V_{m2}^*, S_{m2}^*, I_{m2}^*, R_{m2}^*, S_{h2}^*, I_{h2}^*\right)$$

2. Basic Reproduction Number (R_0)

The basic Reproduction Number (R_0) was found using the system's method Next Generation Matrix [17] (1). This model places the compartment of infection in the human-infected sub-population (I_m), and the animal-infected sub-population (I_h). Based on the system of equation (1) containing the infected sub-population is

$$\frac{dI_m(t)}{dt} = \frac{\alpha_1 I_h S_m}{N_m} + \frac{\alpha_2 I_m S_m}{N_m} - (\gamma_1+\mu_1+\delta_1+)I_m \quad (3)$$
$$\frac{dIh(t)}{dt} = \frac{\alpha_3 S_h I_h}{N_h} - (\delta_2+\mu_2)I_h$$

If $x = [I_m, I_h]^T$, then, the subset (3) can be expressed in the form. $\dot{x} = (F+V)x$

Matrix F is the transmission vector, and V is the transition vector. Vector F and V are as follows.

$$F = \begin{pmatrix} \frac{\alpha_1 I_h S_m}{N_h} + \frac{\alpha_2 I_m S_m}{N_m} \\ \frac{\alpha_3 S_h I_h}{N_h} \end{pmatrix}, V = \begin{pmatrix} -\gamma_1 I_m - \mu_1 I_m - \delta_1 I_m \\ -\delta_2 I_h - \mu_2 I_h \end{pmatrix} \quad (4)$$

The Jacobian matrix of equation (4) is expressed in the form of a matrix $F = J(f)$ and $V = J(f)$

$$F = \begin{pmatrix} \frac{\alpha_2 S_m}{N_m} & \frac{\alpha_1 S_m}{N_h} \\ 0 & \frac{\alpha_3 S_h}{N_h} \end{pmatrix}, V = \begin{pmatrix} -\gamma_1 - \mu_1 - \delta_1 & 0 \\ 0 & -\delta_2 - \mu_2 \end{pmatrix} \quad (5)$$

Next Generation Matrix (K) is defined by equation (5) as

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

$$K = \begin{pmatrix} \frac{\alpha_2 S_m}{(\gamma_1+\mu_1+\delta_1)N_m} & -\frac{\alpha_1 S_m}{(\delta_2+\mu_2)N_h} \\ 0 & \frac{\alpha_3 S_h}{(\delta_2+\mu_2)N_h} \end{pmatrix}$$

The Basic Reproduction Number, (R_0) defined as the eigenvalues of the matrix, $R_0 = \rho(K)$ can be calculated $\rho(K)$. To determine the eigenvalues, we can find the characteristics $\det(KI) = 0$ obtained [19].

$$\left| \begin{pmatrix} \frac{\alpha_2 S_m}{(\gamma_1+\mu_1+\delta_1)N_m} - \lambda & -\frac{\alpha_1 S_m}{(\delta_2+\mu_2)N_h} \\ 0 & \frac{\alpha_3 S_h}{(\delta_2+\mu_2)N_h} - \lambda \end{pmatrix} \right| = 0 \quad (6)$$

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$$\left|\left(\frac{\alpha_2 S_m}{(\gamma_1+\mu_1+\delta_1)N_m}-\lambda\right)\left(\frac{\alpha_3 S_h}{(\delta_2+\mu_2)N_h}-\lambda\right)-(0)(0)\right|=0$$

In equation (6), the eigenvalues are obtained.

$$\lambda_1=\frac{\alpha_2 S_m}{(\gamma_1+\mu_1+\delta_1)N_m} \tag{7}$$

$$\lambda_2=\frac{\alpha_3 S_h}{(\delta_2+\mu_2)N_h}$$

That way, we get two eigenvalues of the K matrix, which is

$$R_{0_1}=\frac{\alpha_2 S_m}{(\gamma_1+\mu_1+\delta_1)N_m} \tag{8}$$

$$R_{0_2}=\frac{\alpha_3 S_h}{(\delta_2+\mu_2)N_h}$$

3. Stability Analysis

Stability analysis is obtained by means $\boldsymbol{R_0}$ [17]. Two values $\boldsymbol{R_0}$ are human population $(\boldsymbol{R_{0_1}})$ and animal population $(\mathbf{r_0})$. The analysis is obtained by setting the parameter η or proportion of vaccination $\boldsymbol{R_{0_1}}$ and the parameter α_3 or the infection rate $\mathbf{r_0}$. Analysis of three different population conditions based on existing equilibrium points. Three conditions, including.

a. Disease-free population

The condition of the disease-free population is shown when $\boldsymbol{I_m=0}$ and $\boldsymbol{I_h=0}$ where the conditions to be met are $\boldsymbol{R_{01}<0}$ and $\boldsymbol{R_{02}<0}$. $\boldsymbol{R_{01}<0}$ will be obtained if $\boldsymbol{\eta>\frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}}$ and $\boldsymbol{R_{02}<0}$ will be obtained if $\boldsymbol{\alpha_3<(\delta_2+\mu_2)}$.

b. First endemic population

The condition of the first endemic population is shown when $\boldsymbol{I_m\neq 0}$ and $\boldsymbol{I_h=0}$ where the conditions to be met are $\boldsymbol{\lambda_1>0}$ $\boldsymbol{\lambda_2<0}$. Then get $\boldsymbol{\eta<\frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}}$ and $\boldsymbol{\alpha_3<(\delta_2+\mu_2)}$, To achieve conditions where the population is disease-free, then the conditions are met when $\boldsymbol{\eta<\frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}}$ and $\boldsymbol{\alpha_3<(\delta_2+\mu_2)}$

c. Second endemic population

The condition of the second endemic population is shown when $\boldsymbol{I_m\neq 0}$ dan $\boldsymbol{I_h=0}$, where the conditions to be met, are $\boldsymbol{\lambda_1>0}$ and $\boldsymbol{\lambda_2<0}$. So $\boldsymbol{\eta<\frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}}$ dan $\boldsymbol{\alpha_3>(\delta_2+\mu_2)}$, To achieve conditions where the population

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is disease-free, then the conditions are met when $\eta < \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 > (\delta_2 + \mu_2)$

4. Numerical Simulation

At this stage, disease transmission dynamics are observed using stability analysis. Requirements are obtained under three different conditions. Then, numerical simulations are performed to visually look at the stability properties of equilibrium points and see dynamic changes in each population class in the model. Initial values and parameter values in Table 2

Table 2. Variable values and parameters for transmission of monkeypox disease

Value/month	Parameter	Description	Source
1000	$N_m(t)$	The total human population at the time t	Asummed
150	$N_h(t)$	The total number of animal populations at the time t	Asummed
150	$V_m(t)$	Number of vaccinated humans at the time t	Asummed
600	$S_m(t)$	Number of susceptible humans at the time t	Asummed
50	$I_m(t)$	Number of infected humans at the time t	Asummed
200	$R_m(t)$	Number of recovered humans at the time t	Asummed
100	$S_h(t)$	Number of susceptible animals at the time t	Asummed
50	$I_h(t)$	Number of infected animals at the time t	Asummed
0. 166666667	μ_1	The natural death rate of human	[20]
0. 125	μ_2	The natural death rate of animals	[20]
200	λ_m	Recruitment into susceptible human	Asummed
30	λ_h	Recruitment into a susceptible animal	Asummed
0. 3416666667	α_1	Animal-to-human contact rate	[11]
1. 29166667	α_2	Human-to-human contact rate	[11]
0. 5	α_3	Animal-to-animal contact rate	Asummed
0. 7083333	γ_1	The recovery rate of human	[11]
0. 125	δ_1	The disease-induced death rate for human	[11]
0. 033333	δ_2	The disease-induced death rate for animal	[11]
0. 5	σ	Effectiveness of vaccination	Asummed
0. 8	η	Vaccine of Susceptible	Asummed

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a. Disease-free population

In the case of populations when disease-free if values $\eta > \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 < (\delta_2+\mu_2)$. Get conditions parameter are $\eta > 0.19444447518056$ dan $\alpha_3 < 0.15833333$, after substituting the values in table 2. We will perform numerical simulations using the values of the parameters that satisfy the conditions $\eta = 0.8$ dan $\alpha_3 = 0.05$. Graphic drawings of the resulting simulation will be similar to the following:

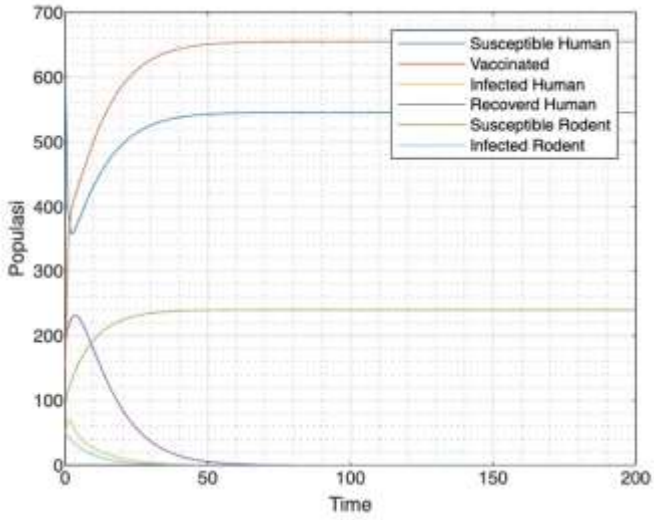

Figure 2. The simulation graph of the disease-free population with $\eta = 0.8$ and $\alpha_3 = 0.05$ in the time $t = 200$

Using the parameter values for the disease-free population, we can calculate the R_0 values obtained that are $R_{0_1} = 0.5871212332$, and $r_0 = 0.3157901385$ because of $R_{0_1} < 1$ and $r_0 < 1$. This suggests that the system is asymptotically stable and disease-free[21].

Figure 2 shows a simulation at the time $t = 200$, where the infection line goes I_m in yellow and I_h light blue. This suggests that the number of individuals infected by both variants tends to decrease over time. Meanwhile, the results obtained from maple were obtained from the disease-free point$S_m = 545.4545445$, $S_h = 240$, $V_m = 654.5454531$, $I_m = 0$, $I_h = 0$, dan $R_m = 0$.

b. First endemic population

In the case of populations when disease-free if values $\eta < \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 < (\delta_2+\mu_2)$. Get conditions parameter are $\eta < 0.19444447518056$ dan $\alpha_3 < 0.15833333$, after substituting the values in table 2. We will perform numerical simulations using the values of the parameters that satisfy the conditions $\eta = 0.05$ dan $\alpha_3 = 0.05$. Graphic drawings of the resulting simulation will be similar to the following:

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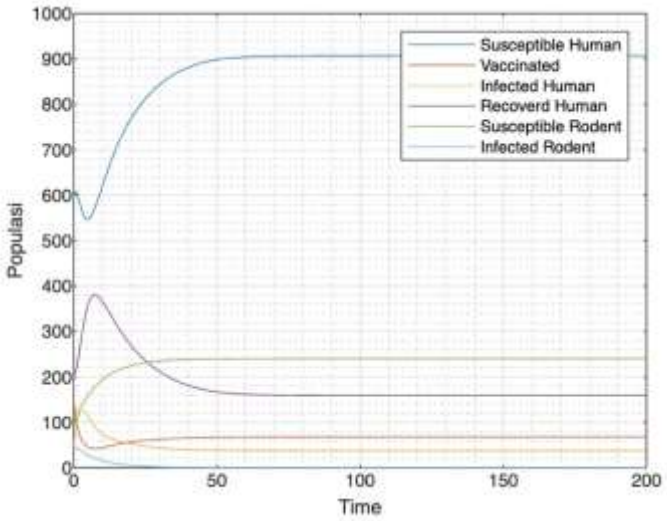

Figure 3. The simulation graph of the disease-free population with η = 0.05 and α_3 = 0.05 in the time $\mathbf{t = 200}$

Using the parameter values for the first endemic population equilibrium point, we can calculate the R_0 values obtained that are $R_0 = 1.049479205$, and $r_0 = 0.3157901385$ because of $R_0 > 1$, and $r_0 < 1$. This suggests that the system is unstable for human sub-populations and stable for animal sub-populations [21].

Figure 2 shows a simulation at the time $t = 200$where the yellow line I_m decreases but is constant at a given number of infections, and the light blue line I_h goes to zero. This suggests that the number of individuals infected by animals tends to decrease over time, and individuals infected by humans tend to decrease but are constant at a certain amount of time. Meanwhile, the results obtained from maple were obtained from the first endemic population equilibrium point $S_m = 774.1935441$, $S_h = 240$, $V_m = 58.06451578$, $I_m = 61.29032327$, $I_h = 0$, dan $R_m = 260.4838721$.

c. Second endemic population

In the case of populations when disease-free if values $\eta < \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 > (\delta_2 + \mu_2)$. Get conditions parameter are $\eta < 0.19444447518056$ dan $\alpha_3 > 0.15833333$, after substituting the values in table 2. We will perform numerical simulations using the values of the parameters that satisfy the conditions η = 0.05 dan α_3 = 0.5. Graphic drawings of the resulting simulation will be similar to the following:

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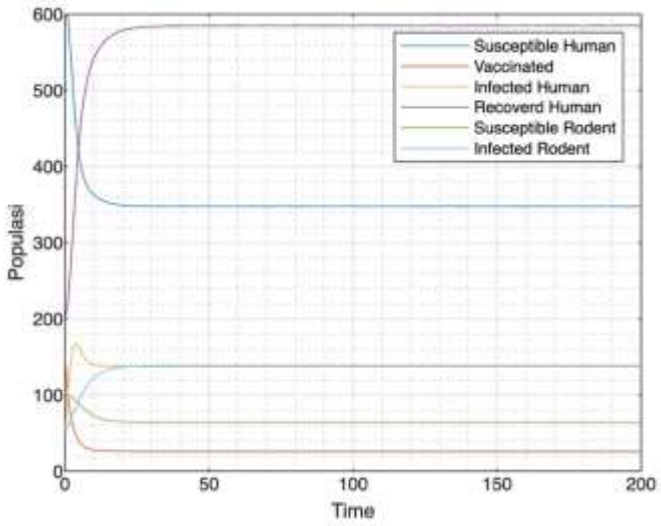

Figure 4. The simulation graph of the disease-free population with $\eta = 0.05$ and $\alpha_3 = 0.5$ in the time $t = 200$

Using the parameter values for the second endemic population equilibrium point, we can calculate the R_0 values obtained that are $R_0 = 1.049479205$, and $r_0 = 3.157901385$ because of $R_0 > 1$, and $r_0 > 1$. This indicates that the system is unstable.

Figure 4 shows a simulation at the time $t = 200$, where the line of infection yellow I_m and light blue I_h decreases but is constant at a given number of infections. This suggests that the number of individuals infected by humans and animals remains. Meanwhile, the results obtained from maple were obtained from the second endemic population equilibrium point $S_m = 278.0415653$, $S_h = 47.49999900$, $V_m = 20.85311739$, $I_m = 150.1842199$, $I_h = 151.9736882$, dan $R_m = 638.28293031$

CONCLUSION AND SUGGESTION

In this study, discussions can be concluded by giving rise to vaccinations as follows:

$$\frac{dV_m}{d_t} = \eta S_m - (\mu_1 + \sigma)V_m$$

$$\frac{dS_m(t)}{dt} = \Lambda_m + \sigma V_m - (\frac{\alpha_1 I_h S_m}{N_m} + \frac{\alpha_2 I_m S_m}{N_m}) - (\eta + \mu_1)S_m$$

$$\frac{dI_m(t)}{dt} = \frac{\alpha_1 I_h S_m}{N_m} + \frac{\alpha_2 I_m S_m}{N_m} - (\gamma_1 + \mu_1 + \delta_1 +)I_m$$

$$\frac{dR_m(t)}{dt} = \gamma_1 I_m - \mu_1 R_m$$

$$\frac{dS_h(t)}{dt} = \Lambda_h - \frac{\alpha_3 S_h I_h}{N_h} - \mu_2 S_h$$

$$\frac{dIh(t)}{dt} = \frac{\alpha_3 S_h I_h}{N_h} - (\delta_2 + \mu_2)I_h$$

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From the model, We get three different types of equilibrium points. The first point of disease-free equilibrium will be stable if the value is greater than the value $\eta > \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 < (\delta_2 + \mu_2)$ then gets $R_0 < 1$ and $r_0 < 1$ values. The first endemic equilibrium point will be stable if the value equals the value $\eta < \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 < (\delta_2 + \mu_2)$ then gets $R_0 > 1$ and $r_0 > 1$ values. The second endemic equilibrium point will be stable if the value equals the value $\eta < \frac{(\sigma+\mu_1)(\alpha_2-\gamma_1-\mu_1-\delta_1)}{(\gamma_1+\mu_1+\delta_1)}$ and $\alpha_3 > (\delta_2 + \mu_2)$ then gets $R_0 < 1$ and $r_0 > 1$ values.

Numerical simulations show that an increase in vaccination rates can cause the basic reproductive numbers to decrease, thus reducing the transmission of monkey pox disease in humans but only affecting the human population. A decrease in the rate of animal-to-animal infections can reduce the number of human and animal-infected populations. Subsequent studies may develop or add new parameters and variables.

The study [14] had only a SIR compartment in human and animal populations, while this study added a vaccinated Human compartment (V_m). Through this reference article, this study analyzed the value R_0 by adding stability conditions with reference parameters η tingkat vaccination rate in humans and α_3 transmission rate in animals. In the study [14], the number of infected people at t = 200 was 70.000. The results of this study were obtained for the number of infected people when η = 0.8 at t = 200, which was 61.29032. In this study, the effect of vaccination rates η showed that the higher the vaccination rates, the faster the number of individuals infected with monkeypox disease.

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