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## CO-INFECTION MODEL FOR COVID-19 AND RUBELLA WITH VACCINATION TREATMENT: STABILITY AND THRESHOLD

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**Abstract:** This study aimed to explore a co-infection transmission model between Covid-19 and Rubella that involves administering vaccinations for both diseases. These two diseases not only have the same characteristics, but also has the same pattern in terms of the causes of disease, spread, clinical manifestations, and vaccines as prevention efforts. This model provided answers to the question of whether one of these diseases or both will disappear from the human population through several steps in the mathematical modelling analysis, which consists of: 1) critical point analysis, 2) stability analysis, 3) next generation matrix, and 4) threshold value analysis. This research resulted in four critical points, which is a critical point of disease-free, Rubella critical point, Covid-19 critical point, and the critical point for both diseases. Based on the next generation matrix and the disease-free critical point, two basic reproduction numbers were generated, namely  $R_{01}$  for Rubella and  $R_{02}$  for Covid-19. The first condition,  $R_{01}$  less than 1 and  $R_{02}$  less than 1, the disease-free critical point will be stable such that Rubella and Covid-19 will disappear from the human population. The second condition,  $R_{01}$  greater than 1 and  $R_{02}$  less than 1, the disease-free critical point become unstable, which means that Rubella-infected people will be found in the population. The third condition,  $R_{01}$  less than 1 and  $R_{02}$  greater than 1, Covid-19 will be found in the human population.

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## 1. INTRODUCTION

Since the end of 2019, there has been a sporadic spread of the corona virus not only in tropical countries but also in sub-tropical countries. Data obtained from the official WHO report until the end of March 2021 shows no less than 3.8 million additional new cases originating from the Southeast Asia Region, West Pacific, and Africa. Brazil and the United States recorded 533,024 new cases and 421,936 patients infected with Covid-19 in the past week. Meanwhile, Indonesia as one of the countries in Southeast Asia also has a fairly high number of new cases. WHO data as of March 31, 2021 recorded an increase in new cases of 5,937 patients and 104 new deaths from 34 provinces in Indonesia. [1-2].

Since the first case was discovered in the city of Depok in early March 2020, the number of Covid-19 patients in Indonesia has been increasing rapidly. This has resulted in the government having to issue policies related to handling corona cases. The government issued circulars to study from home, work from home, and worship from home [3-4].

This case has also resulted in an increase in the function of the hospital, which is prioritized for handling Covid-19 patients. Likewise, medical personnel and medical equipment used to help treat Covid-19 patients. As a result, infectious diseases such as measles, rubella, and diphtheria are no longer the main concern of health workers. Unfortunately, at the official WHO report, Rubella is one of the diseases that occupies the highest position in Indonesia with more than 500 patients per year [5]. Unlike other infectious diseases, rubella will cause more serious problems when it attacks pregnant women. Babies born to mothers with rubella will die or experience CRS (Congenital Rubella Syndrome). This syndrome will cause the baby to have congenital defects such as impaired vision, impaired growth to impaired heart function [6]. The growth of babies with this condition is a concern for the government, therefore the Government of Indonesia has also issued a policy related to handling this disease, namely the provision of vaccines at school age.

Unfortunately, a circular from the Ministry of Education and Culture which implements education from home resulted in several government programs related to the disruption of the program. Based on an analysis of the Ministry of Health's data, it shows that during the Covid-19 pandemic there was a decline in control and surveillance performance of Diseases Preventable by Immunization (PD3I). Compared to 2019 data, the coverage from January to April 2020 shows a decline from 0.5% to 87% [7].

This research will construct a mathematical model of co-infection between Rubella disease and Covid-19. Through the mathematical model, the dynamics of the existence for these two diseases can be predicted through analytical techniques in mathematics. The advantages of mathematical models can show the possibilities that occur to the dynamics of the two diseases in a population such as when there are no two diseases, conditions when there is only rubella disease in a population, conditions when there is only Covid-19 disease, or conditions when two diseases are present. Rubella and Covid-19 can coexist in a population. These two diseases not only have the same characteristics but also have the same pattern in terms of causes, spread, clinical manifestations, and disease administration as a preventive measure.

Specifically, Covid-19 is well-known as a disease caused by the corona virus which was first discovered in the Huanan seafood wholesale market located in Wuhan City, the capital of Hubei Province, Central China. The virus that causes this disease is known as Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2). SARS-CoV-2 will attack the human respiratory system to cause severe lung infections [8-9]. According to Roethe (2020) it was reported that Covid-19 transmission can occur from individuals who have been infected with the virus or individuals who are not yet symptomatic or known as people without Symptoms [10]. Clinical manifestations of a person infected with Covid-19 will appear on the 5th to 7th day with several symptoms including fever (temperature  $> 38^{\circ}\text{C}$ ), coughing, sneezing, and shortness of breath. The spread of this disease occurs through droplets that come out when people infected with Covid-19 cough and sneeze [11-13].

Meanwhile, Rubella disease, also known as German Measles, is a disease that can be transmitted

very quickly but is not deadly. A person with this disease will recover on its own, but this disease will require more attention when infecting a pregnant woman. The disease is caused by the Rubella virus from the *Togaviridae* virus family and the *Rubivirus* genus. It has several clinical manifestations that appear after a person is infected with the rubella virus, including fever, red rash on the skin, and enlarged lymph nodes behind the ear. Symptoms of a red rash on the skin only occur in 1-5% of patients [14-16]. From the results of mathematical analysis of the developed model for both disease, this study will answer the question of whether one of these diseases or both will disappear from the human population after being given the vaccine.

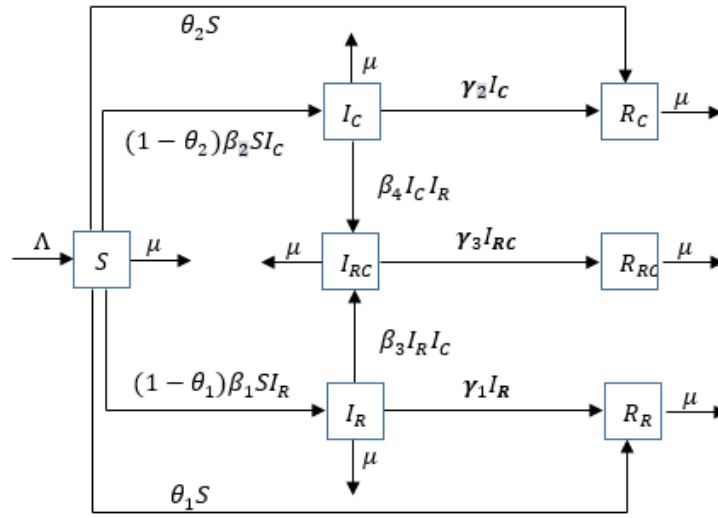
## 2. PRELIMINARIES

SIR mathematical modelling was used as a baseline in this research. At first, all the human population have been looked as healthy people but susceptible to disease. Furthermore, there is someone infected with Rubella and someone infected with Covid-19. These infected people will then infect other humans and form a sub-population of humans infected with Rubella and a sub-population of humans infected with Covid-19. With the handling of Covid-19 patients who are not really good (not self-isolated or not receiving treatment at the hospital) and Rubella patients who are no longer the main concern of treatment in hospitals, this results in the occurrence of co-infection disease between Covid-19 and Rubella. Regard to the characteristics of the two diseases that allow patients of both diseases to recover, this results in the formation of seven human sub-population compartments, namely the susceptible human sub-population ( $S$ ), the Rubella-infected human sub-population ( $I_R$ ), the Covid-19-infected human sub-population ( $I_C$ ), the infected human sub-population with Rubella and Covid-19 ( $I_{RC}$ ), sub-population of humans who recovered from Covid-19 ( $R_C$ ), sub-population of humans who recovered from Rubella ( $R_R$ ) and sub-population of humans who recovered from both diseases ( $R_{RC}$ ). By taking some assumptions that can provide limitations in making mathematical models, the pattern of the spread of the two diseases can be described in a compartment diagram as shown in Figure 1.

Moreover, some of the assumptions used to construct the mathematical model were mentioned as

follows:

1. The population is closed and constant, meaning that the modelling does not pay attention to migration (no-migration)
2. Someone who has been infected with Rubella or Covid-19 can be infected again in the future (re-infection)
3. For simplification model, there is no exposed sub-population
4. There are no deaths directly caused by Rubella and Covid-19



**Figure 1.** Compartment diagram of Co-infection Model

The rate of change for each compartment at time  $t$  is represented by the following system of nonlinear ordinary differential equations:

$$\frac{dS}{dt} = \Lambda - \theta_1S - \theta_2S - (1 - \theta_1)\beta_1SI_R - (1 - \theta_2)\beta_2SI_C - \mu S \quad (1)$$

$$\frac{dI_R}{dt} = (1 - \theta_1)\beta_1SI_R - \beta_3I_RI_C - \gamma_1I_R - \mu I_R \quad (2)$$

$$\frac{dI_C}{dt} = (1 - \theta_2)\beta_2SI_C - \beta_4I_RI_C - \gamma_2I_C - \mu I_C \quad (3)$$

$$\frac{dI_{RC}}{dt} = \beta_3I_RI_C + \beta_4I_RI_C - \gamma_3I_{RC} - \mu I_{RC} \quad (4)$$

$$\frac{dR_R}{dt} = \gamma_1I_R + \theta_1S - \mu R_R \quad (5)$$

$$\frac{dR_C}{dt} = \gamma_2 I_C + \theta_2 S - \mu R_C \quad (6)$$

$$\frac{dR_{RC}}{dt} = \gamma_3 I_{RC} - \mu R_{RC} \quad (7)$$

With the initial value for each sub-population is shown as follows

$$S(t_0) = S_0, \quad I_R(t_0) = I_{R0}, \quad I_C(t_0) = I_{C0}, \quad I_{RC}(t_0) = I_{RC0}, \quad R_R(t_0) = R_{R0}, \quad R_C(t_0) = R_{C0}, \\ R_{RC}(t_0) = R_{RC0}$$

Here,  $t \geq t_0$  represents the time in days and  $t_0$  represents the beginning of the Covid-19 and Rubella disease spread where each symbol can be described as follows.

- $\Lambda$  : Recruitment rate
- $\beta_1$  : Infection rate by Rubella disease
- $\beta_2$  : Infection rate by Covid-19
- $\beta_3$  : Infection rate by Covid-19 for sub-population Rubella-infected
- $\beta_4$  : Infection rate by Rubella for sub-population Covid-19 infected
- $\theta_1$  : Rubella vaccination rate
- $\theta_2$  : Covid-19 vaccination rate
- $\gamma_1$  : Recovery rate from Rubella disease
- $\gamma_2$  : Recovery rate from Covid-19
- $\gamma_3$  : Recovery rate co-infection disease
- $\mu$  : Natural Death rate

### 3. MAIN RESULTS

#### a. Equilibrium Point and its existence

Based on the mathematical model that had been constructed, then we determined the solution of the system of nonlinear ordinary differential equations (1) - (7). Determination of this solution had been done by taking the left-hand side for each equation equal to zero so that four critical points were obtained as follows.

- i. Disease-free equilibrium point

$$\left\{ S = \frac{\Lambda}{\mu + \theta_1 + \theta_2}, I_C = 0, I_R = 0, I_{RC} = 0, R_C = \frac{\Lambda \theta_2}{\mu(\theta_1 + \theta_2 + \mu)}, R_R = \frac{\Lambda \theta_1}{\mu(\theta_1 + \theta_2 + \mu)}, R_{RC} = 0 \right\};$$

ii. Rubella endemic equilibrium point

$$\left\{ S = -\frac{\mu + \gamma_1}{\beta_1(\theta_1 - 1)}, I_C = 0, I_R = \frac{\Lambda \beta_1 \theta_1 + \mu \theta_2 + \gamma_1 \theta_1 + \gamma_1 \theta_2 - \Lambda \beta_1 + \mu^2 + \mu \gamma_1}{\beta_1(\mu \theta_1 + \gamma_1 \theta_1 - \mu - \gamma_1)}, I_{RC} = 0, R_C = -\frac{(\mu + \gamma_1) \theta_2}{\mu \beta_1(\theta_1 - 1)}, R_R = \frac{\Lambda \beta_1 \gamma_1 \theta_1 - \Lambda \beta_1 \gamma_1 + \mu^2 \gamma_1 - \mu^2 \theta_1 + \mu \gamma_1^2 - \mu \gamma_1 \theta_1 + \mu \gamma_1 \theta_2 + \gamma_1^2 \theta_2}{\mu \beta_1(\mu \theta_1 + \gamma_1 \theta_1 - \mu - \gamma_1)}, R_{RC} = 0 \right\};$$

iii. Covid-19 endemic equilibrium point

$$\left\{ S = -\frac{\mu + \gamma_2}{\mu \beta_2(\theta_2 - 1)}, I_C = \frac{\Lambda \beta_2 \theta_2 + \mu \theta_1 + \mu \theta_2 + \gamma_2 \theta_1 + \gamma_2 \theta_2 - \Lambda \beta_2 + \mu^2 + \mu \gamma_2}{\beta_2(\mu \theta_2 + \gamma_2 \theta_2 - \mu - \gamma_2)}, I_R = 0, I_{RC} = 0, R_C = \frac{\Lambda \beta_2 \gamma_2 \theta_2 - \Lambda \beta_2 \gamma_2 + \mu^2 \gamma_2 - \mu^2 \theta_2 + \mu \gamma_2^2 + \mu \gamma_2 \theta_1 - \mu \gamma_2 \theta_2 + \gamma_2^2 \theta_1}{\mu \beta_2(\mu \theta_2 + \gamma_2 \theta_2 - \mu - \gamma_2)}, R_R = -\frac{(\mu + \gamma_2) \theta_1}{\mu \beta_2(\theta_2 - 1)}, R_{RC} = 0 \right\};$$

iv. Co-infection endemic equilibrium point

$$\{S = S^*, I_C = I_C^*, I_R = I_R^*, I_{RC} = I_{RC}^*, R_C = R_C^*, R_R = R_R^*, R_{RC} = R_{RC}^*\};$$

Due to the complexity of the result, this co-infection equilibrium could not be written in this article.

Furthermore, we analyzed the existence for each equilibrium point regard to the condition that sub-population Rubella-infected, sub population Covid-19-infected, and sub population co-infection are exist,  $I_R > 0, I_C > 0$ , and  $I_{RC} > 0$  respectively. The endemic equilibrium point for Rubella exist when this condition is met,  $\frac{\Lambda \beta_1(1 - \theta_1)}{(\mu + \gamma_1)(\theta_1 + \theta_2 + \mu)} > 1$  and  $\theta_1 < 1$ . The endemic equilibrium point for Covid-19 exist when this condition is met  $\frac{\Lambda \beta_2(1 - \theta_2)}{(\mu + \gamma_2)(\theta_1 + \theta_2 + \mu)} > 1$  and  $\theta_2 < 1$ .

Whereas, the endemic equilibrium point for co-infection exist when this condition is met

$$\frac{\Lambda \beta_1 \beta_4 (1 - \theta_1)}{(\mu + \gamma_1)((\mu + \gamma_2)(\beta_1(1 - \theta_1)) + (\mu + \gamma_1)\beta_2(1 - \theta_2) + \beta_4(\mu + \theta_1 + \theta_2))} > 1;$$

and

$$\frac{\Lambda \beta_2 \beta_3 (1 - \theta_2)}{(\mu + \gamma_2)(\beta_2(1 - \theta_2)(\mu + \gamma_1) + \beta_1(1 - \theta_1)(\mu + \gamma_2) - \beta_3(\theta_1 + \theta_2))} > 1;$$

## b. Stability Analysis

Moreover, we analyzed the stability system through the eigenvalues of Jacobian matrix from each equilibrium point. Based on the system of nonlinear ordinary differential equations (1) - (7) and the disease-free equilibrium point, we derived the Jacobian matrix as follows.

$$J_1 = \begin{pmatrix} a_{11} & a_{12} & a_{13} & 0 & 0 & 0 & 0 \\ 0 & a_{22} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & a_{33} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\mu - \gamma_3 & 0 & 0 & 0 \\ \theta_1 & \gamma_1 & 0 & 0 & -\mu & 0 & 0 \\ \theta_2 & 0 & \delta_2 & 0 & 0 & -\mu & 0 \\ 0 & 0 & 0 & \gamma_3 & 0 & 0 & -\mu \end{pmatrix}$$

where

$$a_{11} = -\mu - \mu\theta_1 - \mu\theta_2;$$

$$a_{12} = \frac{\Lambda\beta_1\theta_1 - \Lambda\beta_1}{\mu + \theta_1 + \theta_2};$$

$$a_{13} = \frac{\Lambda\beta_2\theta_2 - \Lambda\beta_2}{\mu + \theta_1 + \theta_2};$$

$$a_{22} = -\frac{\Lambda\beta_1\theta_1 + \Lambda\beta_1}{\mu + \theta_1 + \theta_2} - \mu - \gamma_1;$$

$$a_{33} = -\frac{\Lambda\beta_2\theta_2 + \Lambda\beta_2}{\mu + \theta_1 + \theta_2} - \mu - \gamma_2$$

Regard to the eigenvalues of the Jacobian matrix, it could be concluded that the disease-free equilibrium point will be asymptotically stable if  $\frac{\Lambda\beta_2(1-\theta_2)}{(\mu+\gamma_2)(\theta_1+\theta_2+\mu)} < 1$  and  $\frac{\Lambda\beta_1(1-\theta_1)}{(\mu+\gamma_1)(\theta_1+\theta_2+\mu)} < 1$ . It

means that when the conditions have been met then both disease will be disappeared from the human population forever.

Next, a stability analysis at the equilibrium point for Rubella. Substitute the equilibrium point in the Jacobian matrix in order to obtain the following matrix.

$$J_2 = \begin{pmatrix} a_{11} & -\mu - \gamma_1 & a_{13} & 0 & 0 & 0 & 0 \\ a_{21} & 0 & a_{23} & 0 & 0 & 0 & 0 \\ 0 & 0 & a_{33} & 0 & 0 & 0 & 0 \\ 0 & 0 & a_{43} & -\mu - \gamma_3 & 0 & 0 & 0 \\ \theta_1 & \gamma_1 & 0 & 0 & -\mu & 0 & 0 \\ \theta_2 & 0 & \gamma_2 & 0 & 0 & -\mu & 0 \\ 0 & 0 & 0 & \gamma_3 & 0 & 0 & -\mu \end{pmatrix}$$

$$a_{11} = \frac{(\theta_1-1)}{\mu\theta_1+\gamma_1\theta_1-\mu-\gamma_1} (\Lambda\beta_1\theta_1 - \Lambda\beta_1 + \mu^2 + \mu\gamma_1 + \mu\theta_1 + \mu\theta_2 + \gamma_1\theta_1 + \gamma_1\theta_2) - \mu - \theta_1 - \theta_2;$$

$$a_{13} = -\frac{\beta_2(\mu+\gamma_1)(\gamma_2-1)}{\beta_1(\theta_1-1)};$$

$$a_{21} = -\frac{(\theta_1-1)}{\mu\theta_1+\gamma_1\theta_1-\mu-\gamma_1} (\Lambda\beta_1\theta_1 - \Lambda\beta_1 + \mu^2 + \mu\gamma_1 + \mu\theta_1 + \mu\theta_2 + \gamma_1\theta_1 + \gamma_1\theta_2);$$



## CO-INFECTION MODEL FOR COVID-19 AND RUBELLA

$$a_{23} = -\frac{1}{\beta_1(\mu\theta_1+\gamma_1\theta_1-\mu-\gamma_1)}(\beta_3(\Lambda\beta_1\theta_1 - \Lambda\beta_1 + \mu^2 + \mu\gamma_1 + \mu\theta_1 + \mu\theta_2 + \gamma_1\theta_1 + \gamma_1\theta_2));$$

$$a_{33} = \frac{\beta_2(\mu+\gamma_1)(\theta_2-1)}{\beta_1(\theta_1-1)} - \frac{\beta_4}{\beta_1(\mu\theta_1+\gamma_1\theta_1-\mu-\gamma_1)}(\Lambda\beta_1\theta_1 - \Lambda\beta_1 + \mu^2 + \mu\gamma_1 + \mu\theta_1 + \mu\theta_2 + \gamma_1\theta_1 + \gamma_1\theta_2) - \mu - \gamma_2; a_{43} = \frac{(\beta_3+\beta_4)}{\beta_1(\mu\theta_1+\gamma_1\theta_1-\mu-\gamma_1)}(\Lambda\beta_1\theta_1 - \Lambda\beta_1 + \mu^2 + \mu\gamma_1 + \mu\theta_1 + \mu\theta_2 + \gamma_1\theta_1 + \gamma_1\theta_2)$$

Regard to the eigenvalues of the Jacobian matrix, it could be concluded that the Rubella equilibrium point will be asymptotically stable if  $\frac{\Lambda\beta_1(1-\theta_1)}{(\mu+\gamma_1)(\theta_1+\theta_2+\mu)} > 1$ ,  $\theta_1 < 1$ , and

$$\frac{\Lambda\beta_1\beta_4(1-\theta_1)}{(\mu+\gamma_1)((\mu+\gamma_2)(\beta_1(1-\theta_1))+(\mu+\gamma_1)\beta_2(1-\theta_2)+\beta_4(\mu+\theta_1+\theta_2))} < 1. \text{ It means that when the conditions have}$$

been met then Rubella disease will not be gone from human population.

Furthermore, a stability analysis was carried out at an equilibrium point for Covid-19. Substitute the equilibrium point in the Jacobian matrix in order to obtain the following matrix.

$$J_3 = \begin{pmatrix} a_{11} & a_{12} & -c & 0 & 0 & 0 & 0 \\ 0 & a_{22} & 0 & 0 & 0 & 0 & 0 \\ a_{31} & a_{32} & 0 & 0 & 0 & 0 & 0 \\ 0 & a_{42} & 0 & -\mu - \gamma_3 & 0 & 0 & 0 \\ \theta_1 & \gamma_1 & 0 & 0 & -\mu & 0 & 0 \\ \theta_2 & 0 & \gamma_2 & 0 & 0 & -\mu & 0 \\ 0 & 0 & 0 & \gamma_3 & 0 & 0 & -\mu \end{pmatrix}$$

$$a_{11} = \frac{(\theta_2-1)}{\mu\theta_2+\gamma_2\theta_2-\mu-\delta_2}(\Lambda\beta_2\theta_2 - \Lambda\beta_2 + \mu^2 + \mu\gamma_2 + \mu\theta_1 + \mu\theta_2 + \gamma_2\theta_1 + \gamma_2\theta_2) - \mu - \theta_1 - \theta_2;$$

$$a_{12} = -\frac{\beta_1(\mu+\gamma_2)(\theta_1-1)}{\beta_2(\theta_2-1)},$$

$$a_{22} = \frac{\beta_1(\mu+\gamma_2)(\theta_1-1)}{\beta_2(\theta_2-1)} - \frac{\beta_3}{\beta_2(\mu\theta_2+\gamma_2\theta_2-\mu-\gamma_2)}(\Lambda\beta_2\theta_2 - \Lambda\beta_2 + \mu^2 + \mu\gamma_2 + \mu\theta_1 + \mu\theta_2 + \gamma_2\theta_1 + \gamma_2\theta_2) - \mu - \gamma_1;$$

$$a_{31} = -\frac{(\theta_2-1)}{\mu\theta_2+\gamma_2\theta_2-\mu-\gamma_2}(\Lambda\beta_2\theta_2 - \Lambda\beta_2 + \mu^2 + \mu\gamma_2 + \mu\theta_1 + \mu\theta_2 + \gamma_2\theta_1 + \gamma_2\theta_2);$$

$$a_{32} = -\frac{1}{\beta_2(\mu\theta_2+\gamma_2\theta_2-\mu-\gamma_2)}(\beta_4(\Lambda\beta_2\theta_2 - \Lambda\beta_2 + \mu^2 + \mu\gamma_2 + \mu\theta_1 + \mu\theta_2 + \gamma_2\theta_1 + \gamma_2\theta_2));$$

$$a_{42} = \frac{(\beta_3+\beta_4)}{\beta_2(\mu\theta_2+\gamma_2\theta_2-\mu-\gamma_2)}(\Lambda\beta_2\theta_2 - \Lambda\beta_2 + \mu^2 + \mu\gamma_2 + \mu\theta_1 + \mu\theta_2 + \gamma_2\theta_1 + \gamma_2\theta_2);$$

Regard to the eigenvalues of the Jacobian matrix, it could be concluded that the Covid-19

equilibrium point will be asymptotically stable if  $\frac{\Lambda\beta_2(1-\theta_2)}{(\mu+\gamma_2)(\theta_1+\theta_2+\mu)} > 1$ ,  $\theta_2 < 1$ , and

$\frac{\Lambda\beta_2\beta_3(1-\theta_2)}{(\mu+\gamma_2)(\beta_2(1-\theta_2)(\mu+\gamma_1)+\beta_1(1-\theta_1)(\mu+\gamma_2)-\beta_3(\theta_1+\theta_2))} < 1$ . It means that when the conditions have been met then Covid-19 will stay in the human population for long time.

### c. Two Basic Reproduction Number

Furthermore, basic reproduction numbers have been obtained through *next generation matrix* which is defined as  $K = -FV^{-1}$ . It consists of  $F$  matrix as a Jacobian matrix with non-linear elements from the sub-population that can transmit the disease ( $I_R, I_C$ , and  $I_{RC}$ ) and  $V$  as a Jacobian matrix with linear elements from the sub-population that can transmit the disease ( $I_R, I_C$ , and  $I_{RC}$ ). Based on the non-linear system of ordinary equation (1) – (7), we derived these equations for  $F$ .

$$F_1 = -\beta_1 S I_R \theta_1 + \beta_1 S I_R - \beta_3 I_R I_C$$

$$F_2 = -\beta_2 S I_C \theta_2 + \beta_2 S I_C - \beta_4 I_R I_C$$

$$F_3 = \beta_3 I_R I_C + \beta_4 I_R I_C$$

While, these equation for  $V$  are as follows.

$$V_1 = -\mu I_R - \gamma_1 I_R$$

$$V_2 = -\mu I_C - \gamma_2 I_C$$

$$V_3 = -\mu I_{RC} - \gamma_3 I_{RC}$$

So that it is obtained

$$K = -FV^{-1} = \begin{pmatrix} -\frac{S\beta_1\theta_1 - S\beta_1 + I_C\beta_3}{\mu + \gamma_1} & -\frac{I_R\beta_3}{\mu + \gamma_2} & 0 \\ -\frac{I_C\beta_4}{\mu + \gamma_1} & -\frac{S\beta_2\theta_2 - S\beta_2 + I_R\beta_4}{\mu + \gamma_2} & 0 \\ -\frac{-I_C\beta_3 - I_C\beta_4}{\mu + \gamma_1} & -\frac{-I_R\beta_3 - I_R\beta_4}{\mu + \gamma_2} & 0 \end{pmatrix}$$

Moreover, we substituted the disease-free equilibrium point to the *next generation matrix* and it gave us the eigenvalue of  $K$  as follows  $\frac{\Lambda\beta_1(1-\theta_1)}{(\mu+\gamma_1)(\theta_1+\theta_2+\mu)}$ ;  $\frac{\Lambda\beta_2(1-\theta_2)}{(\mu+\gamma_2)(\theta_1+\theta_2+\mu)}$ ; and 0. The dominant eigenvalue is the basic reproduction number with the  $R_{O1}$  for Rubella disease and  $R_{O2}$  for Covid-19, which are  $\frac{\Lambda\beta_1(1-\theta_1)}{(\mu+\gamma_1)(\theta_1+\theta_2+\mu)}$  and  $\frac{\Lambda\beta_2(1-\theta_2)}{(\mu+\gamma_2)(\theta_1+\theta_2+\mu)}$ , respectively. When  $R_{O1} < 1$  and  $R_{O2} < 1$ , the disease-free equilibrium point is stable so that Rubella and Covid-19 disease will be

gone from the population. The condition  $R_{O1} > 1$  and  $R_{O2} < 1$  make the disease-free equilibrium point unstable, which means that people infected by Rubella will be found in the population. While, the condition  $R_{O1} < 1$  and  $R_{O2} > 1$  also make the disease-free equilibrium point unstable so then people infected by Covid-19 will also be found in the population.

Final step, when we substituted the co-infection equilibrium point to the *next generation matrix* (the calculation are more complex) then we derived another basic reproduction number that show the existence of co-infection for both diseases, namely  $R_{11}$  and  $R_{12}$ . These two diseases will be appeared in human population when these condition met  $R_{11} > 1$  and  $R_{12} > 1$ , where

$$R_{11} = \frac{\Lambda\beta_1\beta_4(1-\theta_1)}{(\mu+\gamma_1)((\mu+\gamma_2)(\beta_1(1-\theta_1))+(\mu+\gamma_1)\beta_2(1-\theta_2)+\beta_4(\mu+\theta_1+\theta_2))};$$

$$\text{and } R_{12} = \frac{\Lambda\beta_2\beta_3(1-\theta_2)}{(\mu+\gamma_2)(\beta_2(1-\theta_2)(\mu+\gamma_1)+\beta_1(1-\theta_1)(\mu+\gamma_2)-\beta_3(\theta_1+\theta_2))}.$$

#### 4. CONCLUSION

Co-infection model for Rubella and Covid-19 diseases have been constructed through this study and it gave four equilibrium points which are disease-free equilibrium point, Rubella endemic equilibrium point, Covid-19 endemic equilibrium point, and co-infection endemic equilibrium point. This research also gave the stability analysis for each equilibrium point, which were stable if the stability conditions have been fulfilled with the assumption that all parameters used are positive.

The next generation matrix and disease-free equilibrium gave two basic reproduction number  $R_{O1}$  and  $R_{O2}$ , whereas the next generation matrix and co-infection equilibrium point gave another basic reproduction number  $R_{11}$  and  $R_{12}$ . The condition for each pair of the basic reproduction number determined the existence for the disease in the human population.

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## CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

## REFERENCES

- [1] World Health Organization 2021 Covid-19 Weekly Epidemiological Update: Data as received by WHO from national authorities, as of 28 March 2021 10 am CET retrieved March 31 2021 from <https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---31-march-2021>
- [2] World Health Organization Indonesia 2021 Coronavirus Disease 2019 (COVID-19) Situation Report-49: 31 March 2021 retrieved March 31 2021 from <https://www.who.int/indonesia/news/novel-coronavirus>
- [3] Ihsanuddin, Jokowi: Kerja dari Rumah, Belajar dari Rumah, Ibadah di Rumah perlu digencarkan: 16/03/2020 15:45 WIB retrieved March 31 2021 from <https://nasional.kompas.com/read/2020/03/16/15454571/jokowi-kerja-dari-rumah-belajar-dari-rumah-ibadah-di-rumah-perlu-digencarkan?page=all>
- [4] D. Nurita, 9 Pesan Jokowi Soal New Normal: Pakai Masker sampai di Rumah Saja: Minggu, 5 Juli 2020 10:53 WIB retrieved March 31 2021 from <https://nasional.tempo.co/read/1361453/9-pesan-jokowi-soal-new-normal-pakai-masker-sampai-di-rumah-saja>
- [5] World Health Organization 2020 WHO vaccine-preventable diseases: monitoring system 2020 global summary: Last updated 15 July 2020 (data as of 12 October 2020) retrieved March 31 2021 from [https://apps.who.int/immunization\\_monitoring/globalsummary/countries?countrycriteria%5Bcountry%5D%5B%5D=IDN](https://apps.who.int/immunization_monitoring/globalsummary/countries?countrycriteria%5Bcountry%5D%5B%5D=IDN)
- [6] Abadi, R. Artiono, B.P. Prawoto, The effects of vaccination to the dynamics of rubella virus with seasonality, *Commun. Math. Biol. Neurosci.*, 2020 (2020), Article ID 9.
- [7] Kementerian Kesehatan Republik Indonesia, Tetap Terlindungi Di Masa Pandemi Covid-19 Buletin Surveilans PD3I & Imunisasi (2021) retrieved March 31, 2021 from [https://www.who.int/docs/default-source/searo/indonesia/sit-rep/buletin-surveilans-pd3i-dan-imunisasi-edisi-2-2020.pdf?sfvrsn=2a76da54\\_2,2020](https://www.who.int/docs/default-source/searo/indonesia/sit-rep/buletin-surveilans-pd3i-dan-imunisasi-edisi-2-2020.pdf?sfvrsn=2a76da54_2,2020).
- [8] L.A. Abdillah, Stigma Terhadap Orang Positif COVID-19 (Stigma on Positive People COVID-19) (April 22, 2020). *Pandemik COVID-19: Antara Persoalan dan Refleksi di Indonesia*, Forthcoming, Available at SSRN: <https://ssrn.com/abstract=3582624>.

- [9] A. Prastyowati, Mengenal karakteristik virus SARS-CoV-2 penyebab penyakit COVID-19 sebagai dasar upaya untuk pengembangan obat antivirus dan vaksin. *BioTrends*. 11 (2020), 1–10.
- [10] C. Rothe, M. Schunk, P. Sothmann, et al. Transmission of 2019-nCoV infection from an asymptomatic contact in Germany, *N. Engl. J. Med.* 382 (2020), 970–971.
- [11] X. Jin, J.-S. Lian, J.-H. Hu, et al. Epidemiological, clinical and virological characteristics of 74 cases of coronavirus-infected disease 2019 (COVID-19) with gastrointestinal symptoms, *Gut*. 69 (2020), 1002–1009.
- [12] C.P.E.R.E. Novel, The epidemiological characteristics of an outbreak of 2019 novel coronavirus diseases (COVID-19) in China, *Zhonghua Liu Xing Bing Xue Za Zhi*, 41(2020), 145-151. (in Chinese).
- [13] W. Wang, J. Tang, F. Wei, Updated understanding of the outbreak of 2019 novel coronavirus (2019-nCoV) in Wuhan, China, *J. Med. Virol.* 92 (2020), 441–447.
- [14] R. Artiono, B.P. Prawoto, D. Hidayat, D.N. Yuniarti, Y.P. Astuti, The dynamics of COVID-19: the effect of large-scale social restrictions, *Commun. Math. Biol. Neurosci.* 2020 (2020), Article ID 76.
- [15] W. Febriani, G.W. Nurcahyo, S. Sumijan, Diagnosa penyakit rubella menggunakan metode fuzzy tsukamoto, *Jurnal Sistim Informasi Dan Teknologi*, 1 (2019), 12–17.
- [16] G.M. Prabandari, S. BM, and A. Kusumawati, Beberapa faktor yang berhubungan dengan penerimaan ibu terhadap imunisasi measles rubella pada anak sd di desa gumpang, kecamatan kartasura, kabupaten sukoharjo, *Jurnal Kesehatan Masyarakat (Undip)*, 6 (2018), 573-581.