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HEALTH PROMOTION ANALYSIS AND SIMULATION ON INCREASING VACCINATION WITH USING THE SRV MODEL IN PINRANG REGENCY

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ABSTRACT

This study discusses the SRV mathematical model of the rate of people refusing vaccination. The data used is primary data in the form of questionnaire data taken directly from the community in Pinrang Regency related to the rate of people who refuse vaccination. This research starts from building an SRV model to then perform analysis and simulation of increased vaccination as a result of the role of the Health Promotion section, determining the balance point, analyzing the stability of the model, determining the value of the basic reproductive number (R_0)*, conducting model simulations using Maple21 software, and interpreting the simulation results. In this article, a mathematical model of SRV is obtained from the analysis and simulation of increased vaccination as the role of the Health Promotion section; two balance points, namely the free balance point to refuse vaccination and the balance point to refuse vaccination; and the basic reproduction rate* $R_0 = 0.4472$ *indicates that the population refuses vaccination is decreasing.*

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1. INTRODUCTION

Pinrang is one of the regencies in Indonesia. Bumi Lasinrang is the city with the largest population in Pinrang Regency. Based on data from the Central Statistics Agency of Pinrang Regency, the population of Makassar City in 2021 was 407,882 people. The area of Pinrang Regency is 1,961.77 km² and is divided into 12 sub-districts, which include 68 villages and 36 urban villages and consists of 86 neighborhoods and 189 hamlets. However, with the characteristics of the Bumi Lasinrang area, it does not guarantee that it will be free from virus attacks.

Previously, a new virus that can cause an increase in pneumonia first appeared in Wuhan, China, in early December 2019 [1]. According to WHO monitoring until February 2021 [2], Coronavirus Disease-19 (COVID-19) is the latest type of coronavirus found in the city of Wuhan, China in December 2019 [3]. The number of cases of coronavirus infection that causes Covid-19 continues to increase in various parts of the world. The rate of increase, both for the number of cases of infection, death and cure, varies in each region. Each country also has its own policy to curb the spread of the virus that occurs in its territory. According to data compiled by John Hopkins University, as of March 23, 2020, the total number of Covid-19 cases worldwide has reached 331,273 cases, with 14,450 deaths, and 97,847 patients declared cured [4]. Previously, there were several types of coronaviruses, including in 2002 the Severe Acute Respiratory Syndrome Coronavirus or known as SARS-CoV and the Middle East Respiratory Syndrome Coronavirus or known as MERS-CoV in 2012 [5], [6]. Confirmed patients have reached 106 million infected patients and patients died from COVID-19 totaling 2.3 million population [7], Meanwhile, according to data from the Ministry of Health updated on February 19, 2021, the total number of COVID-19 cases in Indonesia reached 1,263. 299 cases with total recovered cases and deaths were 34,152 cases and 34,152 cases, respectively [5]. In Pinrang Regency alone, it has reached 53,569 [8]. In this case, the government in various countries around the world, including the Unitary State of the Republic of Indonesia, took decisive steps to prevent further spread. At the end of March 2020, the President of Indonesia announced large-scale social restrictions that were useful to minimize the transmission of the coronavirus [5], so that in this case Covid-19 could cause our country, without exception, Pinrang Regency, to experience a crisis both morally and financially. In this case, one of the moral crises we mean is that it is easy for the public to receive information that does not have a clear source, thus encouraging people to do things that deviate from government policies, one of which is refusing the Covid-19 vaccination.

This is supported by the development of information technology that occurs in Indonesia, making everyone have the freedom to exchange information via internet. In this digital era, people are free to have personal accounts as a place to channel their aspirations either verbally, in printed media, or in electronic media. The current spread of hoaxes can only be suppressed by the government, but it is not completely eradicated because as long as the motive for spreading hoaxes persists, the perpetrators of hoax spreaders will continue to emerge. The government's role in this case, specifically the Health Office of the Pinrang Regency, is to provide counseling and educational socialization about valid information related to this case, namely the Covid-19 vaccination, to the public so that rejection of vaccination can be suppressed. However, the Health Office does not know about the rate of effectiveness of the program that has been run in educating the public to vaccinate, so as a student, they have an important role in conducting research by making mathematical models that will be a solution to the problems faced by the Health Office of Pinrang Regency [8].

The mathematical model that has been formed will be analyzed, so that the model made is representative of the problems discussed [9]. In this case, we as students have an important role in finding solutions to problems by analyzing and simulating the main problems faced by people in the real world using mathematical models. In developing the model, we refer to several journals: Analysis and simulation of mathematical model for typhus disease in Makassar [4]; SEIAS-SEI model on asymptomatic and super infection malaria with imperfect vaccination [10]; SEIRS model analysis for online game addiction problem of mathematics students [11]; Analysis and Solution of The SEIRS Model for The Rubella Transmission with Vaccination Effect using Runge-Kutta Method [12]; SEIRI Model analysis using the mathematical graph as a solution for Hepatitis B disease in Makassar [13]; Numerical Solution of SIRS model for Dengue Fever Transmission in Makassar City with Runge-Kutta Method [14]; A mathematical model for the novel coronavirus epidemic in Wuhan, China [15]; Review on COVID19 disease so far [16]. With these references, the SRV mathematical model has been successfully developed so that it can find the best solution in dealing with social problems that refuse vaccination in Pinrang Regency.

2. RESEARCH METHODS

This research is a type of theoretical and applied research, namely by reviewing the literature on mathematical modeling and psychology and communication science related to the dissemination of information and the influence of information on individuals. The data used in this study is primary data on the number of people in Pinrang Regency who have or have not ben vaccinated against Covid-19. The population in this study is the entire community in the Pinrang Regency, totaling 351.118 people, it is necessary to draw a research sample. Sampling was carried out using the Sloving technique as the minimum number of samples, then dividing the sample evenly in each health center so that a total sample of 425 samples was produced spread over several health centers in Pinrang Regency as follows:

Table 1. The spread sample in every health centre in Pinrang Regency

Health Centre	Amount
Suppa	25
Mattiro Deceng	25
Lanrisang	25
Mattiro Bulu	25
Batulappa	25
Teppo	25
Cempa	25
Sulili	25
Salo	25
Mattombong	25
Bungi	25
Lampa	25
Tadang Palie	25
Ujung Lero	25
Tuppu	25
Salimbongan	25
Leppangang	25

The steps taken in this study are, first, to build an SRV model for refusing vaccination by determining the assumptions, variables, and parameters used for the SVR model and forming an SRV model for refusing vaccination. Next, analyze the SRV model against vaccination, determine the equilibrium point of the SRV model, determine the type of stability of the balance point based on the eigenvalues, and determine the basic reproduction number (R_0). Then simulating the SRV model against vaccination using Maple21 software, followed by collecting data on the community rejecting COVID-19 vaccination by partnering with the Health Service, and 17 Puskesmas spread across Pinrang Regency with the role of Puskesmas as partners collecting questionnaire data directly from the people of Pinrang regency, inputting community data against vaccination due to COVID-19, inputting model analysis results into software, analyzing simulation results, and drawing conclusions.

3. RESULTS AND DISCUSSION

3.1 SVR Model Refusing Vaccination

In this study, the population in the model is divided into four classes, namely Susceptible (S) class which represents a class of individuals who have the potential to refuse COVID-19 vaccination, Refuse Vaccination (R) class which indicates a class of individuals who refuse COVID-19 vaccination, and vaccination class (V) which states that the individual class has been vaccinated against Covid-19. There are several assumptions used in making the model, namely people who live and domiciled in Pinrang Regency, there are people who have the potential to refuse COVID-19 vaccination, there are people who refuse Covid-19 vaccination, there are people who have vaccinated Covid-19, people who entering the class with the potential to refuse the COVID-19 vaccination (Susceptible) are those who belong to the Pinrang Regency community and have the potential to refuse the Covid-19 vaccination, the people who enter the class rejecting the COVID-19 vaccination (Refuse Vaccination) are those who belong to the Pinrang Regency community and have refuse to vaccinate Covid-19, people who enter the class who have vaccinated against COVID-19 (Vaccination) are those who belong to the community of Pinrang Regency and have vaccinated against

Covid-19, the community took the initiative to vaccinate after hearing socialization from the Health Promotion from the local Health Center, Department of Health, or the government, people want to vaccinate, because they are invited by friends, neighbors or family. The scheme of the SRV model refuse vaccination can be seen in **Figure 1** below.

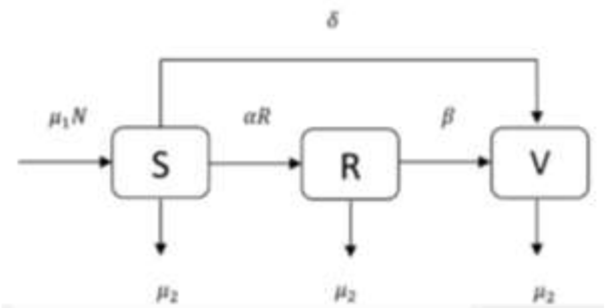

Figure 1. The scheme of the SRV model refuse vaccination

Figure 1 can also be interpreted into a mathematical model which is a nonlinear differential equation as follows:

$$\frac{dS}{dt} = \mu_1 N - \alpha SR - \delta S - \mu_2 S \tag{1}$$

$$\frac{dR}{dt} = \alpha SR + \varepsilon V - (\beta + \mu_2)R \tag{2}$$

$$\frac{dV}{dt} = \beta R + \delta S - (\varepsilon + \mu_2)V \tag{3}$$

Table 2. Variables and parameters in the refuse vaccination SRV model

Variable/ Parameter	Information
S	People who have the potential to refuse vaccination
R	People who refuse vaccination
V	People who have been vaccinated
μ_1	Birth rate that has reached vaccination age
μ_2	Death Rate
α	The rate of movement of people from the community class that has the potential to refuse vaccination to a class of society that refuses the Covid-19 vaccination
β	The rate of people moving from a class of people who refuse vaccination to a class of people who want to vaccinate
δ	The rate of movement of people from the community class has the potential to refuse vaccination to a class of people who want to vaccinate
ε	The rate of people moving from a class of people who want to vaccinate to a class of people who refuse vaccination

where $N = S + R + V$ is the total population under study.

3.2 Analysis of SVR Model Refusing Vaccination

Equilibrium Point

The initial step in determining the vaccination equilibrium point and the point of rejecting vaccination is to simplify **Equations (1-3)** by dividing by N $\left(S = \frac{s}{N}, R = \frac{r}{N}, V = v\right)$, so that the **Equations (4-6)**

$$\frac{ds}{dt} = \mu_1 - \alpha sr - (\delta + \mu_2)s \tag{4}$$

$$\frac{dR}{dt} = \alpha sr - (\beta + \mu_2)r \quad (5)$$
$$\frac{dV}{dt} = \beta r + \delta s - \mu_2 v \quad (6)$$

to determine the vaccination equilibrium point and the point of rejecting vaccination, each equation in **Equations (4-6)**, must be equal to zero, namely $\left(\frac{dS}{dt}, \frac{dP}{dt}, \frac{dR}{dt}\right) = (0,0,0)$, so that the **Equations (7-9)** is obtained.

$$\mu_1 - \alpha sr - (\delta + \mu_2)s = 0 \quad (7)$$
$$\alpha sr - (\beta + \mu_2)r = 0 \quad (8)$$
$$\beta r + \delta s - \mu_2 \mathrm{v} = 0 \quad (9)$$

Furthermore, by using a simple substitution method, the values of S, R, and V will be determined for the vaccination equilibrium point and the SRV model reject point. The vaccination balance point is a condition where there is no mental disorder in the population, so P = 0. By doing a little algebraic manipulation in **Equations (7-9)**, the following **Equations (10-12)** is obtained.

$$s = \mu_1 - \alpha sr - (\delta + \mu_2)s \quad (10)$$
$$r = \alpha sr - (\beta + \mu_2)r \quad (11)$$
$$v = \beta r + \delta s - \mu_2 v \quad (12)$$

By substituting each equation in **Equation (10-12)** by first determining the value of P = 0 then the vaccination equilibrium point for the SRV model of the distribution of individuals who refuse vaccination in Pinrang Regency is obtained, namely

$$(s, r, v) = \left(\frac{\mu_1}{\mu_2 + \delta}, 0, \frac{\delta \mu_1}{\mu_2{}^2 + \mu_2 \delta}\right) \quad (13)$$

Furthermore, in the same way, by substituting each equation in **Equations (10-12)**, the point value of refusing vaccination for the SRV model is the distribution of individuals who refuse vaccination in Pinrang Regency, namely

$$(s, r, v) = \begin{pmatrix} \frac{\beta + \mu_2}{\alpha}, \\ \frac{\alpha\mu - \beta\mu_2 - \delta\beta - \mu_2{}^2 - \upsilon\mu_2}{\alpha(\beta + \mu_2)}, \\ \frac{\alpha\beta\mu - \beta^2\mu_2 - \beta\mu_2{}^2 + \delta\beta^2 - \delta\beta\mu_2 - \mu_2{}^2\delta}{\alpha(\beta + \mu_2)\mu_2} \end{pmatrix} \quad (14)$$

Basic Reproduction Number

The basic reproduction number can be found using the next generation matrix method. This matrix was formed by taking into account the positive and negative parts of the transmission rate of the infected population, namely the refuse vaccination population. The formula for determining the basic reproduction number can be seen in **Equation (15)**.

$$R = F' \cdot (V')^{-1} \quad (15)$$

Based on **Equation (2)**, then:

$$\frac{dP}{dt} = \alpha sr - \beta r - \mu_2 v$$

To obtain

$$F = [\alpha sr], F' = [\alpha s] \quad (16)$$
$$V = [\beta r + \mu_2 r - \alpha sr], V' = [\beta + \mu_2] \quad (17)$$

Then we get the inverse of the matrix **Equation (13)**, namely

$$(V')^{-1} = \left[\frac{1}{\beta + \mu_2}\right] \quad (18)$$

Next, the eigenvalues of the matrix R will be determined, based on **Equation (15)**

$$R = [\alpha s]\left[\frac{1}{\beta+\mu_2}\right]$$
$$R = \left[\frac{\alpha s}{\beta+\mu_2}\right] \quad (19)$$

After obtaining the R matrix in **Equation (19)**, then the eigenvalues will be searched using the formula $Det(\lambda I - R) =$, where I is the identity matrix. The basic reproduction number will be determined based on the largest eigenvalue (λ).

$$|\lambda I - J| = \left|\left(\lambda[1] - \left[\frac{\alpha s}{\beta+\mu_2}\right]\right)\right| = 0 \quad (20)$$

So that the eigenvalues are obtained based on **Equation (20)**, namely

$$\lambda = \frac{\alpha s}{\beta+\mu_2}$$

Then the eigenvalues are obtained, namely $\lambda = \frac{\alpha s}{\beta+\mu_2}$

So that the basic reproduction number is obtained:

$$R_0 = \frac{\mu_1 \alpha}{(\beta+\mu_2)(\mu_2+\delta)} \quad (21)$$

Equilibrium Point Stability Analysis

Based on **Equation (1-3)**, the following Jacobian matrix (J) can be formed:

$$J = \begin{bmatrix} -\alpha r - \mu_2 - \delta & -\alpha s & 0 \\ \alpha r & -\beta - \mu_2 & 0 \\ \delta & \beta & -\mu_2 \end{bmatrix} \quad (22)$$

Theorem 1 Equilibrium point of refusing vaccination mathematical model of refusal to vaccinate spread is said to be stable if $R_0 \leq 1$ and unstable if $R_0 > 1$.

Proof. Substitution of the equilibrium point against vaccination into the J matrix of **Equation (22)**, so that a new matrix is obtained as in **Equation (23)**

$$J = \begin{bmatrix} -\alpha r - \mu_2 - \delta & -\alpha s & 0 \\ \alpha r & -\beta - \mu_2 & 0 \\ \delta & \beta & -\mu_2 \end{bmatrix} \quad (23)$$

Then look for the eigenvalues of the **Equation (23)** with the following description:

$$|\lambda I - J| = 0$$
$$|\lambda I - J| = \left|\left(\lambda\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} - \begin{bmatrix} -\alpha r - \mu_2 - \delta & -\alpha s & 0 \\ \alpha r & -\beta - \mu_2 & 0 \\ \delta & \beta & -\mu_2 \end{bmatrix}\right)\right| = 0$$
$$|\lambda I - J| = \left|\begin{bmatrix} -\alpha r - \mu_2 - \delta - \lambda & -\alpha s & 0 \\ \alpha r & -\beta - \mu_2 - \lambda & 0 \\ \delta & \beta & -\mu_2 - \lambda \end{bmatrix}\right| = 0 \quad (24)$$

Next, substitute S in **Equation (24)** so that

$$|\lambda I - J| = \left|\begin{bmatrix} -\alpha r - \mu_2 - \delta - \lambda & -\alpha s & 0 \\ \alpha r & -\beta - \mu_2 - \lambda & 0 \\ \delta & \beta & -\mu_2 - \lambda \end{bmatrix}\right| = 0$$
$$\Rightarrow (\lambda + \mu_2)(\lambda + \mu_2 + \delta)[\lambda^2 + (\beta + \mu_2)\lambda + (\beta + \mu_2) - R_0] = 0 \quad (25)$$

According to Descartes' sign rule, **Equation (25)** will have all negative roots if all the signs of each term are positive. So, it can be concluded that the vaccination equilibrium point is said to be stable if $R_0 \leq 1$ and unstable if $R_0 > 1$.

Theorem 2. Equilibrium point rejects vaccination mathematical model of spread resists vaccination asymptotically stable.

Proof. The point of rejecting vaccination applies to I ≠ 0, then based on the J matrix in **Equation (18)**, a new matrix is obtained as in **Equation (26)**

$$J = \begin{bmatrix} -\alpha i - \mu_2 - \upsilon(t-\tau) & -\alpha s & 0 \\ \alpha i & -\beta(t-\tau) - \mu_2 & 0 \\ \upsilon(t-\tau) & \beta(t-\tau) & -\mu_2 \end{bmatrix} \quad (26)$$

Then look for the eigenvalues with the following description:

$$|\lambda I - J| = 0$$

$$|\lambda I - J| = \begin{bmatrix} -\alpha r - \mu_2 - \delta - \lambda & -\alpha s & 0 \\ \alpha r & -\beta - \mu_2 - \lambda & 0 \\ \delta & \beta & -\mu_2 - \lambda \end{bmatrix} = 0$$

To obtain

$$= (\lambda + \mu)\big(\lambda + (\alpha r + \mu_2 + \delta)\big) \begin{bmatrix} \big(\lambda^2 + (\beta + \mu_2)\lambda + (\beta + \mu_2)\big) \\ -\alpha\beta s \\ +\alpha^2\beta^2 sr \end{bmatrix}$$

Next, substitute the equilibrium point value against vaccination, so we get

$$= (\lambda + \mu)\left(\lambda + \begin{pmatrix} \frac{\alpha\mu - \beta\mu_2 - \delta\beta - \mu_2{}^2 - \delta\mu_2}{(\beta + \mu_2)} \\ +\mu_2 + \delta \end{pmatrix}\right) \begin{bmatrix} \big(\lambda^2 + (\beta + \mu_2)\lambda + (\beta + \mu_2)\big) \\ -\alpha\beta \frac{\beta + \mu_2}{\alpha} \\ +\alpha\beta^2(\beta + \mu_2) + \\ \left(\frac{\alpha\mu - \beta\mu_2 - \delta\beta - \mu_2{}^2 - \delta\mu_2}{(\beta + \mu_2)}\right) \end{bmatrix} \tag{27}$$

According to Descartes' sign rule, if all the roots of the characteristic equation (λ) are positive, it can be concluded that the equilibrium point is asymptotically stable with the condition that:

$$\alpha\mu - \beta\mu_2 - \delta\beta - \mu_2{}^2 - \delta\mu_2 > \mu_2 + \delta \text{ , dan } \frac{\alpha\mu - \beta\mu_2 - \delta\beta - \mu_2{}^2 - \delta\mu_2}{\mu_2 + \upsilon(t - \tau)} > 1$$

Eigen Values

Based on **Equation (27)** it will be obtained the eigenvalues obtained $\lambda =$ -$\mu_2 - \delta$, $\lambda = -\beta - \mu_2$, dan $\lambda = -\mu_2$. The values of obtained at the equilibrium point (14) are real and have a negative sign. Referring to **[17]**, **[18]** stability properties, the type of stability at this equilibrium point is asymptotic stable.

3.2 Health Promotion SRV Model Simulation

The simulation is carried out using Maple 2021 software and by providing a value for each parameter. Furthermore, given the initial value of the sample who entered the class susceptible to refusing the S(0) vaccination was 34 samples, the sample that entered the class refused the R(0) vaccination was 85 samples, and the sample that entered the vaccination group or recovered from refusing the V(0) vaccination was 306 samples. The total sample studied (N) is 425 samples.

Table 3. Distribution of samples in every health center in Pinrang Regency

Variable/Parameter	Information
S	0,08
R	0,0588
V	0,72
α	0,3688
β	0,2941
δ	0,4511
μ_1	0,0170
μ_2	0,0100

The Analysis of Equilibrium Point Stability

The balance point is determined using the SRV model set with the parameters for the Pinrang Regency that have been determined. Then to determine the fixed point, the system of **Equation (1-3)** is equated with zero, then the system for the model in this equation is solved using Maple 2021 software and gives the value of the model balance points is (S, R,V) = (0,528129; 0.009896; 38.277771).

These balance points explain that the number of people who have the potential to experience refusing vaccination due to COVID-19 is 51.81% of the total population and the number of people who experience refusal of vaccination is 0.9% of the total population. The people who managed to recover or were free from refusing vaccination were 3827% of the total sample population.

The Stability of Health Promotion SRV Model

Substitute the equilibrium point (0.528129; 0.009896; 38.277771) so that the eigenvalues of λ_1;="-0.0198" , $\lambda_2 = -1.36549 \times 10^{-8}$, and $\lambda_3 = -3.4516 \times 10^{-6}$. The values of obtained at the equilibrium point (0.528129; 0.009896; 38.277771) are real and have a negative sign. Refering to **[19]** the nature of stability, the type of stability at this equilibrium point is asymptotically stable.

The Result of Health Promotion SRV Model Simulation

The simulation of the Health Promotion Mathematical model in Pinrang Regency was carried out using the Maple 2021 software. The initial values of S, R, V and the parameter values of the model used in this simulation have been presented in **Table 2**. Furthermore, simulations were carried out with 2 different conditions, namely the SRV mathematical model against the effect of health promotion in Pinrang Regency. The following are the simulation results of the SRV model on the effect of health promotion in Pinrang Regency.

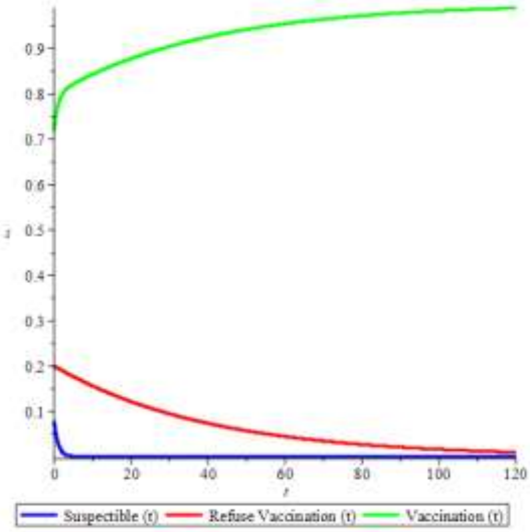

Figure 2. The graph of health promotion SRV model

Based on **Figure 2**, it can be seen that in the distribution model of the health promotion model, the value in the community has decreased from 9% of the community to 0% in the first 5 months and is constant for the next 10 years. The population that refuses vaccination has decreased from 20% of the population to almost 0% at 10 years. People who vaccinated significantly increased from 74% of people to 82% of people in the first 3 months and experienced a normal increase to almost 100% of people who were vaccinated in 10 years. So that the effect of health promotion on increasing vaccination in Pinrang Regency is more than 20% in the total population.

In general, the simulation results of the Pinrang Regency Health Promotion SRV mathematical model can be seen that the values of the basic reproductive number or R_0 are numbers that can explain the potential spread in a population. In the SRV model, the spread of refusing vaccination obtained a value of $R_0 = 0.44721$, which means that the process of refusing vaccination occurs, where everyone can influence others with a 44% probability of happening. So that it can be interpreted that the spread of refusing vaccination based on the equilibrium points tends to be stable and the potential for spread will be low.

In its development, many studies have emerged related to measuring the characteristics of the rate of an object in measuring the speed of the object in the future. The relevant research is analysis and simulation of mathematical model for typhus disease in Makassar [4]; Analysis and solution of the SEIRS model for the Rubella transmission with vaccination effect using Runge-Kutta Method [12], but the studies that have been mentioned are only limited in the process of spreading the disease and there is no mathematical model to measure the rate of refusing vaccination in the people of Pinrang Regency. So that in this study using the SRV model, researchers conducted research related to the level of distribution of people who refused vaccination and the effect of health promotion on increasing people who wanted to vaccinate. The peak point for the spread of people who refused vaccination was at the beginning, after 120 months later people who refused to vaccinate approached 0% of the total community. The increase in population vaccinating will be almost 100% after 120 months and the population refusing vaccination will disappear in less than 10 months.

The SVR Model for the Spread of Tuberculosis obtained a value of $R_0 = 0.44721$ which means that the process of spreading the virus occurs, where each individual can spread the virus to other individuals with a 40% probability of occurring during the period. So, it can be concluded that the spread that occurs in the population will have a low level of spread, by looking at the people who will vaccinate almost 100% in 10 years.

4. CONCLUSIONS

Based on the discussion that has been carried out, it is concluded that the following SRV mathematical model is produced on the spread of people rejecting vaccination with the effect of health promotion in Pinrang Regency with a 4-dimensional differential equation. The SRV mathematical model on the spread of people rejecting vaccination with the influence of health promotion in Pinrang Regency produces two balance points, namely the balance point for refusing vaccination and the balance point for vaccination, both of which are stable. Occurs, where every person who refuses to vaccinate can affect a 44% probability of another person. So that it can be interpreted that the spread of refusing vaccination based on the equilibrium points tends to be stable, and the potential for spread will be low by looking at the people who will vaccinate almost 100% in 10 years.

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REFERENCES

[1] M. Abdy, S. Side, S. Annas, W. Nur, and W. Sanusi, "An SIR epidemic model for COVID-19 spread with fuzzy parameter: the case of Indonesia," *Adv. Differ. Equ.*, vol. 2021, no. 1, p. 105, Feb. 2021, doi: 10.1186/s13662-021-03263-6.

[2] "COVID Live - Coronavirus Statistics - Worldometer." https://www.worldometers.info/coronavirus/ (accessed Dec. 16, 2022).

[3] O. Torrealba-Rodriguez, R. A. Conde-Gutiérrez, and A. L. Hernández-Javier, "Modeling and prediction of COVID-19 in Mexico applying mathematical and computational models," *Chaos Solitons Fractals*, vol. 138, p. 109946, Sep. 2020, doi: 10.1016/j.chaos.2020.109946.

[4] S. Annas, Muh. Isbar Pratama, Muh. Rifandi, W. Sanusi, and S. Side, "Stability analysis and numerical simulation of SEIR model for pandemic COVID-19 spread in Indonesia," *Chaos Solitons Fractals*, vol. 139, p. 110072, Oct. 2020, doi: 10.1016/j.chaos.2020.110072.

[5] "COVID-19 infection: Origin, transmission, and characteristics of human coronaviruses | Elsevier Enhanced Reader." https://reader.elsevier.com/reader/sd/pii/S2090123220300540?token=2BE53B78D0D5CA6241A59A9D2CA26E57437F840A239C6EC31CA73C2805922B8A2806BE0CEF5526407E90DDBF383002EB&originRegion=eu-west-1&originCreation=20221216094200 (accessed Dec. 16, 2022).

[6] Y. Yulida and M. A. Karim, "PEMODELAN MATEMATIKA PENYEBARAN COVID-19 DI PROVINSI KALIMANTAN SELATAN," *MEDIA BINA Ilm.*, vol. 14, no. 10, Art. no. 10, May 2020, doi: 10.33758/mbi.v14i10.572.

[7] I. CNN, "WHO Umumkan Virus Corona Sebagai Pandemi." https://www.cnnindonesia.com/internasional/20200312000124-134-482676/who-umumkan-virus-corona-sebagai-pandemi (accessed Oct. 30, 2022).

[8] Dinas Kesehatan Provinsi Kabupaten Pinrang, "Sulsel Tanggap COVID-19," 2021. https://covid19.sulselprov.go.id/Data (accessed Dec. 16, 2022).
[9] S. Side, W. Sanusi, M. K. Aidid, and S. Sidjara, "Global Stability of SIR and SEIR Model for Tuberculosis Disease Transmission with Lyapunov Function Method," *Asian J. Appl. Sci.*, vol. 9, no. 3, pp. 87–96, Jun. 2016, doi: 10.3923/ajaps.2016.87.96.
[10] H. Maryam, M. Abdy, Alimuddin, and S. Side, "SEIAS-SEI model on asymptomatic and super infection malaria with imperfect vaccination," *J. Phys. Conf. Ser.*, vol. 1918, no. 4, p. 042028, Jun. 2021, doi: 10.1088/1742-6596/1918/4/042028.
[11] A. Anwar, R. Syam, M. I. Pratama, and S. Side, "SEIRS model analysis for online game addiction problem of mathematics students," *J. Phys. Conf. Ser.*, vol. 1918, no. 4, p. 042024, Jun. 2021, doi: 10.1088/1742-6596/1918/4/042024.
[12] M. Asri, S. Sidjara, W. Sanusi, S. Side, and M. I. Pratama, "Analysis and Solution of the SEIRS Model for the Rubella Transmission with Vaccination Effect using Runge-Kutta Method," *J. Phys. Conf. Ser.*, vol. 1899, no. 1, p. 012090, May 2021, doi: 10.1088/1742-6596/1899/1/012090.
[13] S. Side, M. Abdy, F. Arwadi, and W. Sanusi, "SEIRI Model analysis using the mathematical graph as a solution for Hepatitis B disease in Makassar," *J. Phys. Conf. Ser.*, vol. 1899, no. 1, p. 012091, May 2021, doi: 10.1088/1742-6596/1899/1/012091.
[14] W. Sanusi, M. I. Pratama, M. Rifandi, S. Sidjara, Irwan, and S. Side, "Numerical Solution of SIRS model for Dengue Fever Transmission in Makassar Citywith Runge Kutta Method," *J. Phys. Conf. Ser.*, vol. 1752, no. 1, p. 012004, Feb. 2021, doi: 10.1088/1742-6596/1752/1/012004.
[15] C. Yang and J. Wang, "A mathematical model for the novel coronavirus epidemic in Wuhan, China," *Math. Biosci. Eng. MBE*, vol. 17, no. 3, pp. 2708–2724, Mar. 2020, doi: 10.3934/mbe.2020148.
[16] T. Singhal, "A Review of Coronavirus Disease-2019 (COVID-19)," *Indian J. Pediatr.*, vol. 87, no. 4, pp. 281–286, 2020, doi: 10.1007/s12098-020-03263-6.
[17] Nurhaeda, S. Annas, and S. Side, "Analysis and simulation of mathematical model for typhus disease in Makassar," *J. Phys. Conf. Ser.*, vol. 1918, no. 4, p. 042025, Jun. 2021, doi: 10.1088/1742-6596/1918/4/042025.
[18] W. Nur, H. Rachman, N. M. Abdal, M. Abdy, and S. Side, "SIR Model Analysis for Transmission of Dengue Fever Disease with Climate Factors Using Lyapunov Function," *J. Phys. Conf. Ser.*, vol. 1028, no. 1, p. 012117, Jun. 2018, doi: 10.1088/1742-6596/1028/1/012117.
[19] S. Side, N. A. Muzakir, D. Pebriani, and S. N. Utari, "Model SEIR Kecanduan Game Online pada Siswa di SMP Negeri 3 Makassar," *Sainsmat J. Ilm. Ilmu Pengetah. Alam*, vol. 9, no. 1, Art. no. 1, Mar. 2020, doi: 10.35580/sainsmat91199042020.