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Stability Analysis Of Susceptible Infected Treatment Recovered Model On COVID-19 Spread With Vaccination

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Abstract – In this paper, we analyzes the fixed point stability of the susceptible infected treatment recovered (SITR) model on COVID-19 spread with vaccination was given to susceptible sub populations. In this model, the susceptible is further divided two sub populations, the first parts is those from normal individuals and the second parts is individuals who are elderly or co morbid. The model being constructed is a nonlinear system by assuming that individuals who have been vaccinated already have strong immunity, so that them cannot be infected by COVID-19. This model has two fixed points, the disease-free fixed point and the endemic fixed point. Furthermore, a stability analysis is carried out on the two fixed points, which shows that the disease-free fixed point is asymptotically stable if $I > 0$ and the endemic fixed point is asymptotically stable if $I = 0$. To observe the implementation of the model, numerical simulation is conducted using the 4th order Runge Kutta method and the help of Matlab.

Keywords – SITR model, Stability, Vaccination

I. INTRODUCTION

Coronavirus Disease 2019 (COVID-19) is an infectious disease that was caused by the *Severe Acute Respiratory Syndrome Coronavirus 2* (SARS-CoV-2) [13]. SARS-CoV-2 is a new strain of coronavirus, that has not been previously identified in humans. The disease can be more dangerous if suffered by the elderly or those with co morbid diseases. Some co morbid diseases that can increase the risk factors for COVID-19 include is hypertension, diabetes, heart disease, asthma, and cancer [5]. A method to explain this COVID-19 problem is with mathematical modeling. The basic model of disease spread is SIR, where the population is divided into sub populations Susceptible, Infected, and Recovered. That model as used by some researchers, refers to [3], [7], [8], [9], and [14]. Sanchez et al in [12] also introduced a mathematical model of COVID-19. that is SITR (Susceptible, Infected, Treatment , and Recovered) model. Which is the susceptible population is further divided into two sub populations, The first sub population S_1 indicates those individuals, who are from the normal individuals, while the second sub population S_2 represents those individuals who are elderly or co morbid [13]. Rafik et al. [10], continued the research of [11] by analyzing the stability of the fixed point and looking at the numerical scheme of the SITR model. Recently, several researchers began to develop mathematical models on COVID-19 by considering vaccination, as reported by [2] and [11].

In this study, the *model* in [10] is modified by adding vaccination factor. In this model, we assumed that individuals who have been vaccinated have strong immunity, so that them cannot to be infected by COVID-19. Furthermore, the fixed point stability of the model is analyze. At the end, numerical simulations are carried out with the help of MATLAB software.

II. MATHEMATICS MODEL

An attempt to *reduce the* amount of infected sub population is by giving vaccines to susceptible individuals so that it increases the individual's immunity. The flow diagram of the SITR model of COVID-19 spread with vaccination is as follows :

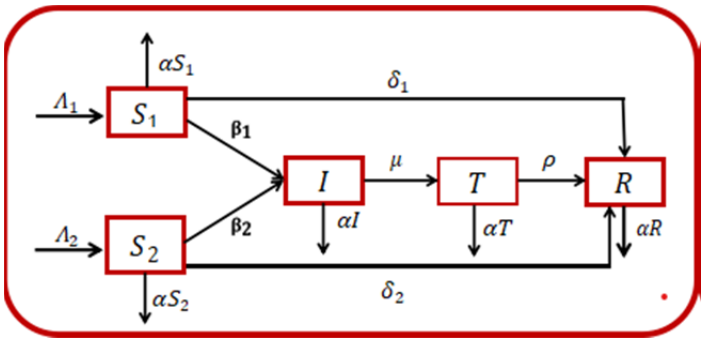

Fig.1 Flow Diagram of the SITR model on COVID-19 spreads with vaccination

From the schematic Fig. 1 above, the distribution of the SITR model on COVID-19 spreads can be modeled in the form of a non-linear system of differential equations as follows

$$\dot{S}_1 = \Lambda_1 - \beta_1 I S_1 - (\alpha + \delta_1) S_1,$$

$$\begin{aligned} \dot{S}_2 &= \Lambda_2 - \beta_2 I S_2 - (\alpha + \delta_2) S_2 , \\ \dot{I} &= \beta_1 I S_1 + \beta_2 I S_2 - (a + \mu)\, I, \\ \dot{T} &= \mu I - (a + \rho) T, \\ \dot{R} &= \delta_1 S_1 + \delta_2 S_2 - aR. \end{aligned} \tag{1}$$

Base on the system (1) above, $S_1 = S_1(t)$ denote the number of susceptible individuals who are from the normal individuals at any time t, $S_2 = S_2(t)$ denote the number of susceptible individuals who are from the elderly or co morbid at any time t, $I = I(t)$ is used to denote the number infected individuals from COVID-19 at any time t, $T = T(t)$ is used denote the number of individuals undergoing some treatment at any time t, and $R = R(t)$ is used to denote the number recovered individuals from the COVID-19 at any time t. The definition of the related parameters, Λ_1 is influx rate of S_1, Λ_2 is influx rate of S_2, α is the natural mortality rate, β_1 is the infection rate of S_1, β_2 is the infection rate of S_2, μ is the treatment rate, ρ is the recovered rate, δ_1 is the vaccination rate of S_1, and δ_2 is the vaccination rate of S_2. The initial values of system (1) is $S_1(0) \geq 0$, $S_2(0) \geq 0, I(0) \geq 0, T(0) \geq 0, R(0) \geq 0$. We assumed that the COVID-19 spreads in populations with constant diffusion and the total populations is

$$N = S_1 + S_2 + I + T + R. \tag{2}$$

III. Results And Discussion

3.1. Determination of Fixed Points

There are two kinds of fixed points that describe the state of system in epidemiological theory, namely disease-free fixed points obtained by assuming $I = 0$, and endemic fixed points obtained by assuming $I > 0$ [1]. The disease-free fixed points of system (1) denoted is

$$C^0 = ({S_1}^0, {S_2}^0, I^0, T^0, R^0) = \left(\frac{\Lambda_1}{(\alpha+\delta_1)}, \frac{\Lambda_2}{(\alpha+\delta_2)}, 0, 0, \frac{\delta_1\Lambda_1}{\alpha(\alpha+\delta_1)} + \frac{\delta_2\Lambda_2}{\alpha(\alpha+\delta_2)}\right),$$

and the endemic fixed points denoted is $C^* = ({S_1}^*, {S_2}^*, I^*, T^*, R^*)$, with

$${S_1}^* = \left(\frac{\Lambda_1}{\beta_1 I^* + (\alpha + \delta_1)}\right),$$

$${S_2}^* = \left(\frac{\Lambda_2}{\beta_2 I^* + (\alpha + \delta_2)}\right),$$

$$I^* = \left(\frac{B + \sqrt{B^2 + 4BC}}{2A}\right),$$

$$T^* = \left(\frac{\mu I^*}{(\alpha + \rho)}\right),$$

$${S_2}^* = \left(\frac{\delta_1 {S_1}^* + \delta_2 {S_2}^* + \rho T^*}{\alpha}\right),$$

with

$$A = 1,$$

$$B = \left(\frac{\Lambda_1 + \Lambda_2}{(\alpha + \mu)} - \frac{(\alpha + \delta_2)\beta_1}{\beta_2} - \frac{(\alpha + \delta_1)\beta_2}{\beta_1}\right),$$

$$C = \left(\frac{\Lambda_1 (\alpha + \delta_2)}{(\alpha + \mu)\beta_2} + \frac{\Lambda_2(\alpha + \delta_1)}{(\alpha + \mu)\beta_1} - \frac{(\alpha + \delta_1)(\alpha + \delta_2)}{\beta_1\beta_2}\right).$$

3.2. Fixed Point Stability Analysis

The model (1) is a nonlinear system of differential equations. Therefore, to determine the stability of the system (1) at the disease-free fixed point and the endemic fixed point, the system (1) needs to be linearized using the Jacobian matrix as

follows [6].

$$J = \begin{pmatrix} -(\beta_1 I + (\alpha + \delta_1)) & 0 & -\beta_1 S_1 & 0 & 0 \\ 0 & -(\beta_2 I + (\alpha + \delta_2)) & -\beta_2 S_2 & 0 & 0 \\ \beta_1 I & \beta_1 I & (\beta_1 S_1 + \beta_2 S_2) - (\alpha + \mu) & 0 & 0 \\ 0 & 0 & \mu & -(\alpha + \rho) & 0 \\ \delta_1 & \delta_1 & 0 & \rho & -\alpha \end{pmatrix} \quad (3)$$

Furthermore, by substituting the disease-free fixed points C^0 into (3). The eigenvalues are obtained by solving the equation $\det(J_{C^0} - \lambda I_5)$, where I_5 is identity matrix of order 5×5. So that the characteristic equation is obtained as follows:

$$[-\alpha - \lambda][-(\alpha + \rho) - \lambda][-(\alpha + \delta_1) - \lambda][(-(\alpha + \delta_2) - \lambda)][(\beta_1 {S_1}^0 + \beta_2 {S_2}^0 - (\alpha + \mu)) - \lambda] = 0. \quad (4)$$

From equation (4) , the eigen value of the matrix J_{C^0} is

$$\lambda_1 = \alpha, \lambda_2 = (\alpha + \rho), \lambda_3 = (\alpha + \delta_1), \lambda_4 = (\alpha + \delta_2), \quad \lambda_5 = (\beta_1 {S_1}^0 + \beta_2 {S_2}^0 - (\alpha + \mu)).$$

Base on the stability criteria, the fixed point is asymptotically stable if $\lambda_5 < 0$, then

$$\frac{(\beta_1 {S_1}^0 + \beta_2 {S_2}^0)}{(\alpha + \mu)} < 1.$$

Hence the disease-free fixed point C^0 is asymptotically stable .

At the endemic fixed points C^* into (3). The eigenvalues are obtained by solving the equation $\det(J_{C^*} - \lambda I_5)$, where I_5 is identity matrix of order 5×5. So that the characteristic equation is obtained as follows:

$$\begin{aligned} &[-\alpha - \lambda]\,[-(\alpha + \rho) - \lambda][\lambda^3 + \left((\alpha + \mu) + (\beta_1 {S_1}^* + \beta_2 {S_2}^*) - \left(\frac{\Lambda_1}{{S_1}^*} + \frac{\Lambda_2}{{S_2}^*}\right)\right)\lambda^2 \\ &+((\alpha + \mu)\left(\frac{\Lambda_1}{{S_1}^*} + \frac{\Lambda_2}{{S_2}^*}\right) - (\beta_1 \Lambda_1 + \beta_2 \Lambda_2) - \left(\frac{\Lambda_1 \beta_2 {S_2}^*}{{S_2}^*} + \frac{\Lambda_2 \beta_1 {S_1}^*}{{S_1}^*}\right) + \frac{\Lambda_1 \Lambda_2}{{S_1}^* {S_2}^*} \\ &-(\beta_1{}^2 {S_1}^* + \beta_2{}^2 {S_2}^* \mathrm{I}^*)\lambda + (((\alpha + \mu) + \beta_1 {S_1}^* + \beta_2 {S_2}^*)\frac{\Lambda_1 \Lambda_2}{{S_1}^* {S_2}^*} \\ &+\left(\frac{\Lambda_1 \beta_2{}^2 {S_2}^*}{{S_2}^*} + \frac{\Lambda_2 \beta_1{}^2 {S_1}^*}{{S_1}^*}\right)\mathrm{I}^*)] = 0. \end{aligned} \quad (5)$$

From equation (5), the eigen values of matrix J_{C^*} are obtained $\lambda_1 = \alpha, \lambda_2 = (\alpha + \rho), \lambda_3, \lambda_4,$ and λ_5 the roots of the polynomial

$$\begin{aligned} &\lambda^3 + \left((\alpha + \mu) + (\beta_1 {S_1}^* + \beta_2 {S_2}^*) - \left(\frac{\Lambda_1}{{S_1}^*} + \frac{\Lambda_2}{{S_2}^*}\right)\right)\lambda^2 + ((\alpha + \mu)\left(\frac{\Lambda_1}{{S_1}^*} + \frac{\Lambda_2}{{S_2}^*}\right) - (\beta_1 \Lambda_1 + \beta_2 \Lambda_2) \\ &-\left(\frac{\Lambda_1 \beta_2 {S_2}^*}{{S_2}^*} + \frac{\Lambda_2 \beta_1 {S_1}^*}{{S_1}^*}\right) + \frac{\Lambda_1 \Lambda_2}{{S_1}^* {S_2}^*} - (\beta_1{}^2 {S_1}^* + \beta_2{}^2 {S_2}^* \mathrm{I}^*)\lambda + (((\alpha + \mu) + \beta_1 {S_1}^* + \beta_2 {S_2}^*)\frac{\Lambda_1 \Lambda_2}{{S_1}^* {S_2}^*} \\ &+\left(\frac{\Lambda_1 \beta_2{}^2 {S_2}^*}{{S_2}^*} + \frac{\Lambda_2 \beta_1{}^2 {S_1}^*}{{S_1}^*}\right)\mathrm{I}^*) = 0. \end{aligned} \quad (6)$$

Let $U = (\alpha + \mu) + \beta_1 {S_1}^* + \beta_2 {S_2}^*, V = \Lambda_1 {S_1}^* + \Lambda_2 {S_2}^*, W = \Lambda_1 \beta_1 + \Lambda_2 \beta_2, X = \beta_1{}^2 {S_1}^* + \beta_2{}^2 {S_2}^*, Y = \Lambda_2 \beta_1 (S_1^*)^2 + \Lambda_1 \beta_2 (S_2^*)^2, Z = \Lambda_2 \beta_1{}^2 + \Lambda_1 \beta_2{}^2$. Based on the Routh-Hurwitz text [4], the polynomial (6) have negative real part if and only if

$$\frac{U(S_1^* S_2^*)}{V} > 1,$$

$$\frac{V(\alpha+\mu)+\Lambda_1\Lambda_2}{S_1^* S_2^*(W+XI^*+Y)} > 1,$$

$$(\mathrm{X}+(\alpha+\mu))\Lambda_1\Lambda_2 + Z(S_1^* S_2^* I^*) > 0,$$

$$\frac{A(S_1^* S_2^* - 1)\Lambda_1\Lambda_2 + ABS_1^* S_2^*(\alpha+\mu)}{S_1^* S_2^*(B((\alpha+\mu)B+\Lambda_1\Lambda_2)+((A-B)(C+DI^*+FI^*)S_1^* S_2^*} > 1.$$

Hence the endemic fixed point C^* is asymptotically stable.

3.3. Numerical Simulation

In this section, a numerical simulation is carried out with the help of MATLAB software which is simulated using the Runge Kutta method of order 4 to see the population changes for cases $\mathrm{I} = 0$ and $\mathrm{I} > 0$.

3.3.1. Simulation for disease-free fixed points

The initial value used is $S_1(0) = 0.45, S_2(0) = 0.15, I(0) = 0.1, T(0) = 0.2, R(0) = 0.1$ [13]. All parameter values are $\Lambda_1 = 0.2, \Lambda_2 = 0.05, \beta_1 = 0.2, \beta_2 = 0.4, \alpha = 0.25, \mu = 0.1, \rho = 0.3$ [10, 12], and we assumed the values of parameters $\delta_1 = 0.007$, and $\delta_2 = 0.006$. In the simulation, the initial time $t_0 = 0$ day and the end time $t_n = 100$ were used. The graph of the SITR model on COVID-19 spreads without vaccination and with vaccination is obtained as follows

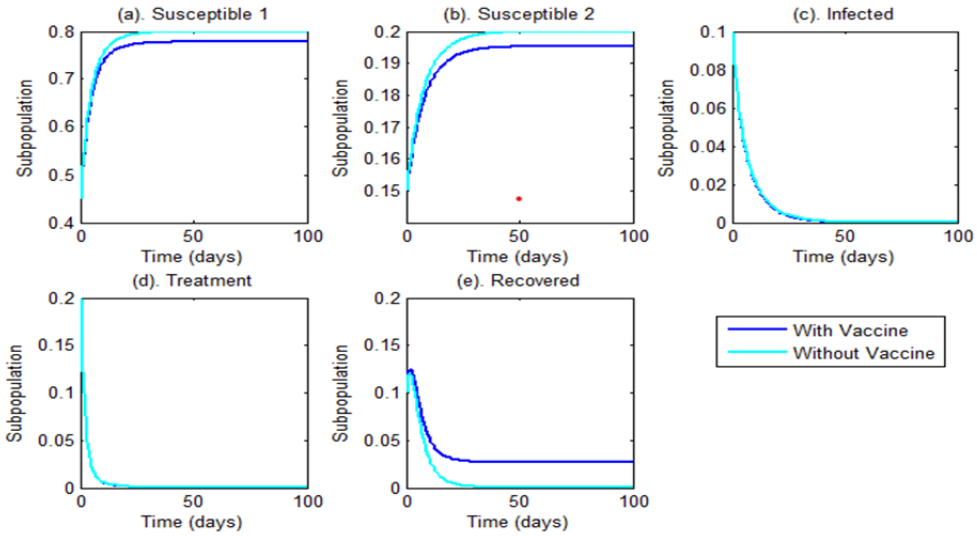

Fig. 2 Effect of vaccination rate on SITR sub populations for disease-free fixed point.

Base on the Fig. 3 the disease-free fixed point is $C^0 = (0.7782, 0.1953, 0, 0, 0.0265)$, it can be seen that the population is stable with $\mathrm{I} = 0$. Fig. 2 also exhibit the effect of vaccinations on SITR sub populations which is evidently seen that an increase in the recovered sub population.

3.3.2. Simulation for endemic fixed points

The initial value used is $S_1(0) = 0.45, S_2(0) = 0.15, I(0) = 0.1, T(0) = 0.2, R(0) = 0.1$ [13]. All parameter values are $\Lambda_1 = 0.2, \Lambda_2 = 0.05, \beta_1 = 0.3, \beta_2 = 0.6, \alpha = 0.25, \mu = 0.1, \rho = 0.3$ [10, 112], and we assumed the values of parameters $\delta_1 = 0.0075$, and $\delta_2 = 0.0065$. In the simulation, the initial time $t_0 = 0$ day and the end time $t_n = 100$ were used. The graph of the SITR model on COVID-19 spreads without vaccination and with vaccination is obtained as follows

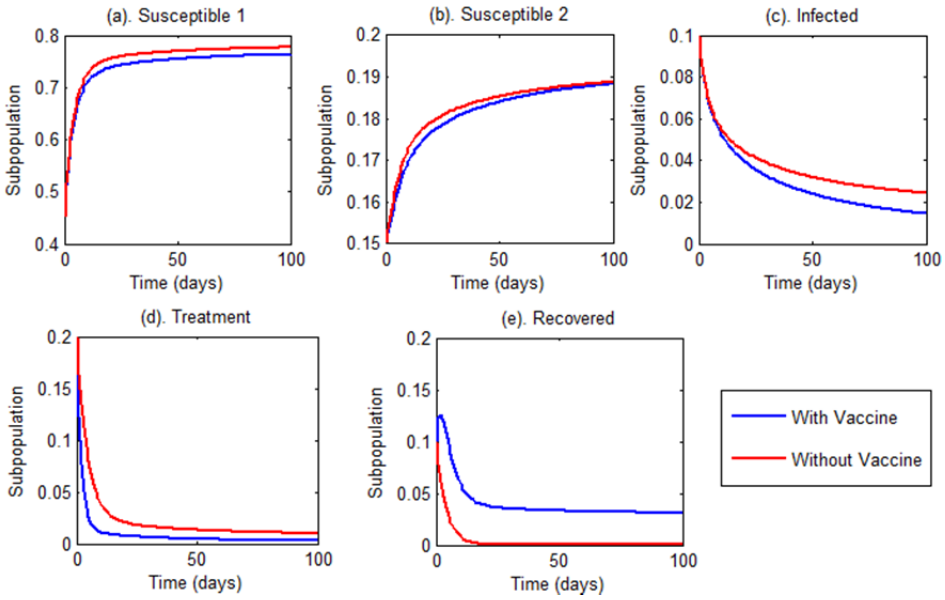

Fig. 3 Effect of vaccination rate on SITR sub populations for endemic fixed point.

Base on the Fig. 3 the endemic fixed point is C^* = (0.7165, 0.1668, 0.0721, 0.0131, 0.0416), it can be seen that the population is stable with $I = 0$. Fig. 3 also exhibit the effect of vaccinations rate on SITR sub populations, which is it can be decrease the infected sub population and treatment sub population, and also evidently seen that an increase in the recovered sub population.

IV. CONCLUSIONS

The distribution of SITR model on COVID-19 spreads with vaccination produces asymptotically stable disease-free fixed point when $I = 0$and asymptotically stable endemic fixed point when $I > 0$.

REFERENCES

[1] Beaglehole. R, R. Bonita, Basic Epidemiology, World Health Organization: Geneva , 1993

[2] Diagne. M. L., H. Rwezaura, S. Y. Tchoumi, and J. M. Tchuenche, "A Mathematical Model of COVID-19 with Vaccination and Treatment," vol. 2021. Hindawi Computational and Mathematical Methods in Medicine, Senegal, 2021, pp. 1 – 16.

[3] Din. Rahim ud, and Ebrahem A, Algehyne, "On Mathematical analysis of COVID-19 by using SIR model with convex incidence rate," Vol. 23, Elsevier B.V. 2021, pp. 1 – 6.

[4] Fisher. S, Complex Variables: Second Edition. Dover Publications Inc: New York, 1990

[5] Iskandar. H, et al, Pengendalian COVID-19 dengan 3M, 3T, Vaksinasi, Disiplin, Kompak, dan Konsisten Buku 2. Kementerian Kesehatan RI: Jakarta Selatan, 2021

[6] Lynch. Stephen, Dynamical System With Applications Using Mathematica. Birkhauser: Boston, 2007

[7] Mitra. A, "Covid-19 in India and Sir Model," vol. 15. J. Mech. Contin. Math. Sci , 2020, pp. 1 – 8.

[8] Mohsen. ahmed. A., Hassan F. AL-Husseiny, Xueyong Zhou, and Khalid Hattaf, "Global stability of COVID-19 model involving the quarantine strategy and media coverage effects," vol. 7, AIMS Public Health, 2020, pp. 587-605.

[9] P. Y. Mardiana, Muhafzan, and A. I. Baqi, "Aplikasi Teori Kontrol Optimal Pada Model Infeksi Virus Hepatitis B ," vol. 10, J. Mathematics Unand: Padang, 2021, pp. 260-267.

[10] Rafiq. M., Javaid. A., M. B. Riaz, and Jan. A, "Numerical Analysis of a Bimodal COVID-19 SITR Model." vol. 61, Alexandria Engineering Journal, 2022, pp. 227 – 235.

[11] Resmawan. Lailany, Y., Revandi, S.P, Hasan S.P, and Agusyarif. R. N, "Dynamic Analysis of COVID-19 Spread Model with Vaccination," vol. 3, Jambura Journal of Biomathematics, 2022, pp. 29 – 38.

[12] Sanchez. Y. G., Z. Sabir, and J. L. G. Guirao, "Design of A Nonlinear *SITR* Fractal Model Based On The Dynamics of A novel Coronavirus (COVID -19),", vol. 28. World Scientific, 2020, pp. 1 – 6.

[13] Sugihantonni. A.,et al, Guidelines for the Prevention and Control of Coronavirus Disease (COVID-19). 5th Edition. Kementerian Kesehatan RI : Jakarta Selatan, 2021

[14] T. R. Wulandari, Muhafzan, and Zulakmal, "Model Penyebaran Penyakit Tuberkolosis dengan Kontrol Vaksinasi," vol. 10. J. Mathematics Unand: Padang, 2021, pp. 280-287.