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On the Extension of Sir Model on the Spread of Covid 19 by Assuming Two Types of Viruses

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ABSTRACT
This paper will model the spread of the Covid-19 by assuming two types of viruses using the SIR model extension. Furthermore, it will also be discussed about the analysis of the fixed-point stability of the model. The fixed-point stability analysis result shows that the fixed-points are disease-free, disease-free symptomatic-cases-but-endemic-asymptomatic-cases, and disease-free asymptomatic-cases-but-endemic-symptomatic-cases are locally asymptotically stable, but the endemic fixed-point is stable.

***Keywords**: Covid-19, SIR model, Fixed-point.*

1. INTRODUCTION

Since Covid-19 infects most societies worldwide, WHO has taken a measure by declaring Covid-19 as a pandemic [8-12], mathematicians have tried to model the spread of this virus by using the SIR model as practised by [2-3,5-7]. From the simulation model, some predictions are obtained that the reach of this virus will halt at a specific time, but as for the end of 2020, the number is still growing, and the growth chart has not been flattened. Therefore, the question arises whether the Covid-19 pandemic will end. The question is what inspired this research. In our opinion, the question is less crucial and essential. The underlying issue is when this symptomatic COVID-19 pandemic will end? We take the term symptomatic Covid-19 form that Covid-19 patients are divided into two cases: symptomatic (patients who develop the COVID-19 symptoms) and asymptomatic (patients who do not produce the COVID-19 symptoms).

This study assumes that what distinguishes symptomatic and asymptomatic patients is the virus itself due to mutation [13]. Over the period, some of these mutations do not replicate that fast. A doctor discovered this fact in Italy, who mentioned that the covid virus he studied did not reproduce as quickly as it used to when the COVID-19 first appeared [14]. In addition, what reinforces our assumption is the results of a study by doctors in China on Asymptomatic Covid patients who state that the immune resistance is not strong enough to fight the virus [4]. The thing that distinguishes symptomatic patients with asymptomatic is not in the patients' immune system or immune system. Still, indeed the covid virus that attacks him does not multiply much in his body.

Throughout this paper, for brevity, we will use the term S virus for a group of covid viruses that cause patients to be symptomatic and A virus for a group of covid viruses that make patients asymptomatic. Our assumption is that S virus and A virus are from the same virus family, the Covid virus. However, the A virus is the result of a mutation from the S virus. If a person is infected with the A virus and recovers, that person will be immune to the S virus (because of one family). However, if a person is exposed to the S virus and recovers, it is still possible to be exposed to the A virus. This is because the A virus is a new mutation from the S virus, and the body has not yet formed antibodies against the S virus. Even though the A virus is the mutation S of a virus, S virus is still spreading in the population when A virus appears.

In this paper, we aim to model the spread of the Covid-19 virus based on these assumptions. The usual SIR model will not cover these assumptions. Therefore, we will modify the SIR model to meet the expected conditions and the extension of the SIR model will be obtained. Furthermore, we will analyze the model. And at the end, we will also discuss the dynamical simulation of the model.

2. ECTENSION THE SIR MODEL

2.1. Assumptions

Some of the assumptions used in this model are:

1. S virus is a virus that causes symptomatic cases
2. A virus is a virus that causes asymptomatic cases
3. Emerging virus A is the result of mutation of the S virus
4. S virus and A virus are both spreading in the population, but A virus spread first.
5. The rate of spread of virus A is greater than the rate of reach of the S virus
6. Those who have been exposed to virus A and have recovered will be immune to the S virus and vice versa (Those who are affected by the S virus and successfully recovered, it is still possible to be exposed (not immune) to the S virus).

2.2. $SI_SR_SI_AR_A$ Model

From the above assumptions, it can be stated in the $SI_SR_SI_AR_A$ model. In this $SI_SR_SI_AR_A$ model, the overall population is divided into five compartments: $S(t)$: Susceptible subpopulation; $I_S(t)$: Symptomatic Infected subpopulation; $I_A(t)$: Asymptomatic Infected subpopulation; $R_S(t)$: Symptomatic recovered subpopulation; and$R_A(t)$: Asymptomatic recovered subpopulation.
In general, the interactions among those subpopulations describe in the following diagram:

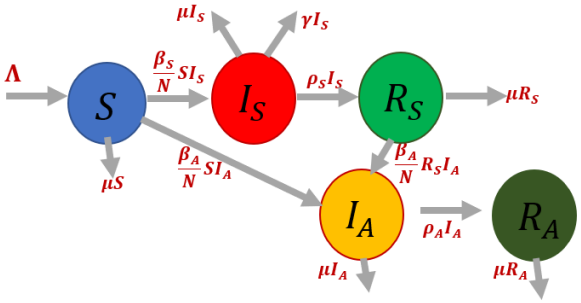

Figure 1 the diagram of $SI_S\ R_S\ I_A\ R_A$ Model.

From the diagram, it is obtained the following system of ODE

$$\frac{dS}{dt} = \Lambda - \frac{\beta_S}{N} SI_S - \frac{\beta_A}{N} SI_A - \mu S$$

$$\frac{dI_S}{dt} = \frac{\beta_S}{N} SI_S - \rho_S I_S - \gamma I_S - \mu I_S$$

$$\frac{dR_S}{dt} = \rho_S I_S - \frac{\beta_A}{N} R_S I_A - \mu R_s$$

$$\frac{dI_A}{dt} = \frac{\beta_A}{N} SI_A + \frac{\beta_A}{N} R_S I_A - \rho_A I_A - \mu I_A$$

$$\frac{dR_A}{dt} = \rho_A I_A - \mu R_A$$

$$\beta_S < \beta_A$$

With $S(t)$ is the number of healthy people in the population but prone to infection; $I_S(t)$ is the number of people infected with symptomatic cases; $R_S(t)$ is the number of people recovering from illness with symptomatic cases; $I_A(t)$ is the number of people infected with asymptomatic cases; $R_A(t)$ is the number of people recovering from asymptomatic case infections cases; Λ is the number of recruitment; μ is the rate of natural death; γ is the rate of death due to Covid-19 symptomatic cases; β_S is the rate at which the infection spreads symptomatic cases; ρ_S is the rate of recovery from the disease of symptomatic cases; β_A is the rate of spread of disease of asymptomatic cases; ρ_A is the rate of recovery from infection of asymptomatic patients; and$N$ is the large population. Therefore,

$$N = S(t) + I_S(t) + R_S(t) + I_A(t) + R_A(t).$$

2.3. Fixed-Points

The fixed-point occurs when $\frac{dS(t)}{dt} = 0$, $\frac{dI_S(t)}{dt} = 0$, $\frac{dR_S(t)}{dt} = 0$, $\frac{dI_A(t)}{dt} = 0$, and $\frac{dR_A(t)}{dt} = 0$

If substituted to the system, it is obtained

$$\Lambda - \frac{\beta_S}{N} SI_S - \frac{\beta_A}{N} SI_A - \mu S = 0 \quad \text{(a)}$$

$$\frac{\beta_S}{N} SI_S - \rho_S I_S - \gamma I_S - \mu I_S = 0 \quad \text{(b)}$$

$$\rho_S I_S - \frac{\beta_A}{N} R_S I_A - \mu R_s = 0 \quad \text{(c)}$$

$$\frac{\beta_A}{N} (S + R_S) I_A - \rho_A I_A - \mu I_A = 0 \quad \text{(d)}$$

$$\rho_A I_A - \mu R_A = 0 \quad \text{(e)}$$

From (b) and (d) obtained

$$I_S\left(\frac{\beta_S}{N}S-\rho_S-\gamma-\mu\right)=0$$

$$I_A\left(\frac{\beta_A}{N}(S+R_S)-\rho_A-\mu\right)=0$$

which means that $I_S=0$ or $\frac{\beta_S}{N}S-\rho_S-\gamma-\mu=0$, and $I_A=0$ or $\frac{\beta_A}{N}(S+R_S)-\rho_A-\mu=0$, and has three fixed-points, i.e., a fixed point without disease (X) a fixed-point endemic to asymptomatic cases (X^*), and a fixed-point endemic to symptomatic cases (X^{**})

2.4. Disease-free fixed-point

The disease-free fixed-point means that Covid-19 disease (both symptomatic and asymptomatic cases) will disappear from the population. It occurs if $I_S=0$ and $I_A=0$, then the equation (a) gives $\Lambda-\mu S=0$, therefore $S=\frac{\Lambda}{\mu}$. Whereas the equations (c) and (e) give $R_S=0$ and $R_A=0$. So that the fixed-point is $X=(S,I_S,R_S,I_A,R_A)=\left(\frac{\Lambda}{\mu},0,0,0,0\right)$

2.5. Symptomatic-free-but-endemic-asymptomatic fixed point

If $I_S=0$ but $I_A\neq 0$, then the equation (d) gives $\frac{\beta_A}{N}(S+R_S)-\rho_A-\mu=0$. By substituting $I_S=0$ to the equation (c), it is obtained $-\mu R_S-\frac{\beta_A}{N}R_S I_A=0$ or $R_S\left(\mu+\frac{\beta_A}{N}I_A\right)=0$. That is, $R_S=0$ or $\mu+\frac{\beta_A}{N}I_A=0$. Suppose $\mu+\frac{\beta_A}{N}I_A=0$ then $\mu=-\frac{\beta_A}{N}I_A<0$. This is not satisfied, so it has to be $R_S=0$. From the equation (d) obtained $\frac{\beta_A}{N}S-\rho_A-\mu=0$ or $S=\frac{N}{\beta_A}(\rho_A+\mu)$. Furthermore, substitution to the equation (a) is obtained

$$\Lambda-\frac{\beta_A}{N}\left(\frac{N}{\beta_A}(\rho_A+\mu)\right)I_A-\mu\left(\frac{N}{\beta_A}(\rho_A+\mu)\right)=0.$$

So $I_A=\frac{\left[\Lambda-\mu\left(\frac{N}{\beta_A}(\rho_A+\mu)\right)\right]}{(\rho_A+\mu)}=\frac{\Lambda}{(\rho_A+\mu)}-\frac{\mu N}{\beta_A}$.

From the equation (e), it is obtained $R_A=\frac{\rho_A}{\mu}\left(\frac{\Lambda}{(\rho_A+\mu)}-\frac{\mu N}{\beta_A}\right)$

So that the fixed point is

$$X^*=(S^*,I_S^*,R_S^*,I_A^*,R_A^*)=\left(\frac{N}{\beta_A}(\rho_A+\mu),0,0,\frac{\Lambda}{(\rho_A+\mu)}-\frac{\mu N}{\beta_A},\frac{\rho_A}{\mu}\left(\frac{\Lambda}{(\rho_A+\mu)}-\frac{\mu N}{\beta_A}\right)\right).$$

Under condition $\frac{\Lambda}{(\rho_A+\mu)}-\frac{\mu N}{\beta_A}>0$ or $\frac{\beta_A\Lambda}{\mu N(\rho_A+\mu)}>1$

2.6. Endemic-symptomatic-but-asymptomatic-free fixed point

If $I_A=0$ but $I_S\neq 0$, then the equation (e) gives $R_A=0$ and the equation (b) gives $S=\frac{N}{\beta_S}(\rho_S+\gamma+\mu)$. Equation (a) becomes

$$\frac{\Lambda}{\frac{N}{\beta_S}(\rho_S+\gamma+\mu)}-\frac{\beta_S}{N}I_S-\mu=0.$$

Therefore

$$I_S=\frac{N}{\beta_S}\left(\frac{\Lambda}{\frac{N}{\beta_S}(\rho_S+\gamma+\mu)}-\mu\right)=\frac{\Lambda}{(\rho_S+\gamma+\mu)}-\frac{N\mu}{\beta_S}$$

The equation (c) provides

$$R_S=\frac{\rho_S}{\mu}\left(\frac{\Lambda}{(\rho_S+\gamma+\mu)}-\frac{N\mu}{\beta_S}\right)$$

$$\rho_S I_S-\mu R_s=0$$

The fixed-point is

$$X^{**}=(S^{**},I_S^{**},R_S^{**},I_A^{**},R_A^{**})=\left(\frac{N}{\beta_S}(\rho_S+\gamma+\mu),\frac{\Lambda}{(\rho_S+\gamma+\mu)}-\frac{N\mu}{\beta_S},\frac{\rho_S}{\mu}\left(\frac{\Lambda}{(\rho_S+\gamma+\mu)}-\frac{N\mu}{\beta_S}\right),0,0\right).$$

by the existence condition that is $\frac{\Lambda}{(\rho_S+\gamma+\mu)}-\frac{N\mu}{\beta_S}>0$ or $\frac{\beta_S\Lambda}{\mu N(\rho_S+\gamma+\mu)}>1$

2.7. Endemic fixed-point

If $I_A \neq 0$ but $I_S \neq 0$, then the equation (b) gives $S = \frac{N}{\beta_S}(\rho_S + \gamma + \mu)$ and the equation (d) gives $(S + R_S) = \frac{N}{\beta_A}(\rho_A + \mu)$.

As a result, $R_S = \frac{N}{\beta_A}(\rho_A + \mu) - \frac{N}{\beta_S}(\rho_S + \gamma + \mu)\frac{N}{\beta_A}(\rho_A + \mu) - \frac{N}{\beta_S}(\rho_S + \gamma + \mu) > 0$ or $\frac{\beta_S(\rho_A+\mu)}{\beta_A(\rho_S+\gamma+\mu)} > 1$.

Equation (a) becomes

$$\frac{\Lambda}{\frac{N}{\beta_S}(\rho_S + \gamma + \mu)} - \frac{\beta_S}{N}I_S - \frac{\beta_A}{N}I_A - \mu = 0 \quad \text{(f)}$$

The equation (c) becomes

$$\frac{\rho_S I_S}{\frac{N}{\beta_A}(\rho_A + \mu) - \frac{N}{\beta_S}(\rho_S + \gamma + \mu)} - \frac{\beta_A}{N}I_A - \mu = 0 \quad \text{(g)}$$

From (f) and (g) obtained

$$\frac{\Lambda}{\frac{N}{\beta_S}(\rho_S + \gamma + \mu)} = \frac{\beta_S}{N}I_S + \frac{\rho_S I_S}{\frac{N}{\beta_A}(\rho_A + \mu) - \frac{N}{\beta_S}(\rho_S + \gamma + \mu)}$$

So, it is obtained

$$I_S = \frac{\left(\frac{\Lambda}{(\rho_S + \gamma + \mu)}\right)}{\left(1 + \frac{\rho_S}{\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu)}\right)} = \frac{\left(\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu)\right)\Lambda}{\left(\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu) + \rho_S\right)(\rho_S + \gamma + \mu)}.$$

As a result $I_A = \frac{\beta_S}{\beta_A}\left(\frac{\rho_S\Lambda}{\left(\frac{\beta_S}{\beta_A}(\rho_A+\mu)-(\rho_S+\gamma+\mu)+\rho_S\right)(\rho_S+\gamma+\mu)}\right) - \frac{\mu N}{\beta_A}$

with

$\frac{\beta_S}{\beta_A}\left(\frac{\rho_S\Lambda}{\left(\frac{\beta_S}{\beta_A}(\rho_A+\mu)-(\rho_S+\gamma+\mu)+\rho_S\right)(\rho_S+\gamma+\mu)}\right) - \frac{\mu N}{\beta_A} > 0$ or $\frac{\Lambda\beta_S}{\mu N(\rho_S+\gamma+\mu)}\left(\frac{\rho_S}{\left(\frac{\beta_S}{\beta_A}(\rho_A+\mu)-(\rho_S+\gamma+\mu)+\rho_S\right)}\right) > 1$

Because $\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu) > 0$ then $\frac{\Lambda\beta_S}{\mu N(\rho_S+\gamma+\mu)} > 1$

From the equation (e) obtained

$$R_A = \frac{\beta_S}{\mu\beta_A}\left(\frac{\rho_A\rho_S\Lambda}{\left(\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu) + \rho_S\right)(\rho_S + \gamma + \mu)}\right) - \frac{N\rho_A}{\beta_A}.$$

So that the fixed point is

$$X^{***} = (S^{***}, I_S^{***}, R_S^{***}, I_A^{***}, R_A^{***}) = \left(\frac{N}{\beta_S}(\rho_S + \gamma + \mu), \frac{\left(\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu)\right)\Lambda}{\left(\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu) + \rho_S\right)(\rho_S + \gamma + \mu)}, \frac{N}{\beta_A}(\rho_A + \mu) - \frac{N}{\beta_S}(\rho_S + \gamma + \mu), \frac{\beta_S}{\beta_A}\left(\frac{\rho_S\Lambda}{\left(\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu) + \rho_S\right)(\rho_S + \gamma + \mu)}\right) - \frac{\mu N}{\beta_A}, \frac{\beta_S}{\mu\beta_A}\left(\frac{\rho_A\rho_S\Lambda}{\left(\frac{\beta_S}{\beta_A}(\rho_A + \mu) - (\rho_S + \gamma + \mu) + \rho_S\right)(\rho_S + \gamma + \mu)}\right) - \frac{N\rho_A}{\beta_A}\right).$$

with the condition $\frac{\Lambda\beta_S}{\mu N(\rho_S+\gamma+\mu)} > 1$ and $\frac{\beta_S(\rho_A+\mu)}{\beta_A(\rho_S+\gamma+\mu)} > 1$.

From these terms, $\frac{\Lambda\beta_S}{\mu N(\rho_S+\gamma+\mu)} > 1$, we obtain:

$$1 < \frac{\beta_S(\rho_A+\mu)}{\beta_A(\rho_S+\gamma+\mu)} = \left(\frac{\Lambda\beta_S}{\mu N(\rho_S+\gamma+\mu)}\right)\left(\frac{\mu N(\rho_A+\mu)}{\Lambda\beta_A}\right)$$

$$1 < \frac{\Lambda\beta_A}{\mu N(\rho_A+\mu)} < \frac{\Lambda\beta_S}{\mu N(\rho_S+\gamma+\mu)}$$

2.8. Basic Reproduction Number

The primary reproduction number ($\mathcal{R}_0$) is the average number of individuals in a newly infected population produced directly or indirectly from an infected individual during the spread of the disease in a vulnerable population. By determining this primary reproduction number, we can find out if the Coronavirus will spread or not. The value of the base reproduction number is the most considerable eigenvalue of the NGM matrix, obtained

$$\mathcal{R}_0 = \max\left\{\frac{\Lambda\beta_S}{\mu N(\rho_S+\gamma+\mu)}, \frac{\Lambda\beta_A}{\mu N(\rho_A+\mu)}\right\}$$

2.9. Stability Analysis

The stability analysis of the model can be seen at the following theorems.

Theorem 1. If $\mathcal{R}_0 < 1$ then the disease-free equilibrium point is locally asymptotically stable

Proof*:* Jacobian matrix:

$$J(S, I_S, I_A) = \begin{bmatrix} -\frac{\beta_S}{N}I_S - \frac{\beta_A}{N}I_A - \mu & -\frac{\beta_S}{N}S & -\frac{\beta_A}{N}S \\ \frac{\beta_S}{N}I_S & \frac{\beta_S}{N}S - \rho_S - \gamma - \mu & 0 \\ \frac{\beta_A}{N}I_A & 0 & \frac{\beta_A}{N}(S+R_S) - \rho_A - \mu \end{bmatrix}$$

$$J\left(\left(\frac{\Lambda}{\mu}\right), 0, 0\right) = \begin{bmatrix} -\mu & -\frac{\beta_S}{N}\left(\frac{\Lambda}{\mu}\right) & -\frac{\beta_A}{N}\left(\frac{\Lambda}{\mu}\right) \\ 0 & \frac{\beta_S}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_S - \gamma - \mu & 0 \\ 0 & 0 & \frac{\beta_A}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_A - \mu \end{bmatrix}$$

The characteristic equation of the matrix is

$$(-\mu-\lambda)\left(\frac{\beta_S}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_S - \gamma - \mu - \lambda\right)\left(\frac{\beta_A}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_A - \mu - \lambda\right) = 0$$

So eigenvalues are obtained as follows

$\lambda_1 = -\mu, \lambda_2 = \frac{\beta_S}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_S - \gamma - \mu, \lambda_3 = \frac{\beta_A}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_A - \mu$

Because $\mathcal{R}_0 < 1$ then $\frac{\beta_S\Lambda}{\mu N(\rho_S+\gamma+\mu)} < 1$ and $\frac{\beta_A\Lambda}{\mu N(\rho_A+\mu)} < 1$. It applies that $\frac{\beta_S}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_S - \gamma - \mu < 0$ and $\frac{\beta_A}{N}\left(\frac{\Lambda}{\mu}\right) - \rho_A - \mu < 0$. As a result, the eigenvalue is always negative which implies that the equilibrium point is locally asymptotically stable.

Theorem 2. If $\mathcal{R}_0 = \frac{\beta_A\Lambda}{\mu N(\rho_A+\mu)} > 1$ then the equilibrium points disease-free symptomatic-cases-but-endemic-asymptomatic-cases is locally asymptotically stable.

Theorem 3. If $\mathcal{R}_0 = \frac{\beta_S \Lambda}{\mu N(\rho_S+\gamma+\mu)} > 1$and $\frac{\beta_A \Lambda}{\mu N(\rho_A+\mu)} < \left(1 - \frac{\beta_A(\gamma+\mu)}{\beta_S(\rho_A+\mu)}\right)\left(\frac{\rho_S+\gamma+\mu}{\rho_S}\right)$ then the disease-free fixed-point asymptomatic-case-but-endemic-symptomatic-cases is locally asymptotically stable.

Theorem 4. If $\mathcal{R}_0 = \frac{\beta_S \Lambda}{\mu N(\rho_S+\gamma+\mu)} > 1$ and $\frac{\Lambda \beta_A}{\mu N(\rho_A+\mu)} > \left(1 - \frac{\beta_A(\gamma+\mu)}{\beta_S(\rho_A+\mu)}\right)\left(\frac{\rho_S+\gamma+\mu}{\rho_S}\right)$ then the endemic fixed-point is stable

3. DYNAMICAL SIMULATION AND DISCUSSION

The dynamical simulation is carried out by taking any data that meets the stability requirements both in endemic and disease-free conditions. Keep in mind that endemic conditions occurred when $\mathcal{R}_0 > 1$ while disease-free conditions occur when $\mathcal{R}_0 < 1$.

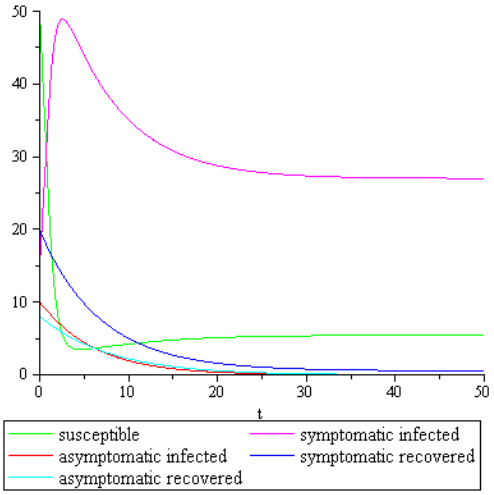

Figure 2 Endemic simulation with $\Lambda = 5, \beta_S = 0.95, \beta_A = 0.01, \mu = 0.15, \rho_S = 0.003, \gamma = 0.002, \rho_A = 0.02$ with $\mathcal{R}_0 = 6.13$.

Based on Figure 2, the symptomatic infected subpopulation has the highest number than any other subpopulation. This is occurred because this subpopulation has more opportunity to be reinfected by both variant of viruses. Basic reproduction number in this case reach 6.13 which is in accordance with the real basic reproduction number of covid-19 on interval of 5-8. The symptomatic recovered, symptomatic infected, and asymptomatic infected are remain constant and converges to the small number close to zero. All the subpopulations are constant around $t = 40$ (unit time).

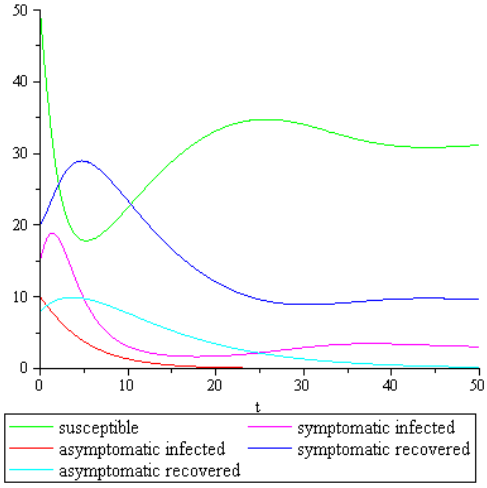

Figure 3 Disease-free simulation with $\Lambda = 5, \beta_S = 0.95, \beta_A = 0.1, \mu = 0.15, \rho_S = 0.3, \gamma = 0.2, \rho_A = 0.2$ with $\mathcal{R}_0 = 0.58$.

The Figure 3 represents the disease-free condition when the basic reproduction number is 0.58. In this case, the dominant subpopulation showed by susceptible subpopulation. It is described that the community is still in under control because the number of recovered subpopulations for symptomatic patients continues in higher number than infected subpopulation both for symptomatic and asymptomatic infected populations. Furthermore, the behavior of asymptomatic infected and recovered are remain constant in zero at $t = 24$ and $t = 45$ respectively and all population in stable condition after $t = 50$.

4. CONCLUSION

We have successfully obtained the mathematical model of the spread of Covid19 by assuming two types of viruses using the extension of SIR model called $I_S R_S I_A R_A$. Furthermore, it is also obtained that the system has 4 fixed-points (disease-free, disease-free symptomatic cases but endemic asymptomatic cases, disease-free asymptomatic cases but endemic symptomatic cases, and endemic). The results of the fixed-point stability analysis shows that the fixed-points are disease-free, disease-free symptomatic-cases-but-endemic-asymptomatic-cases, and disease-free asymptomatic-cases-but-endemic-symptomatic-cases are locally asymptotically stable, but the

endemic fixed-point is stable. Based on the analysis of equilibrium points and basic reproduction number, the variant of S virus has more dominant role than A virus on transmission of covid-19 in the society. It is assumed that symptomatic cases widely spread in population but the endemic condition could be suppressed by the highly rate of recovery from infection of these cases. Furthermore, the rate of spread of disease in symptomatic cases should be decreasing in order to make the population gradually back to virgin.

AUTHORS' CONTRIBUTION

All authors conceived and designed this study. All authors contributed to the process of revising the manuscript, and at the end all authors have approved the final version of this manuscript.

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