

# Stability Analysis On Models Of Spreading H1N1 And H5N1 Virus In Two Locations

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**Abstract**—The dynamics of population mobility are occurring in a population. This phenomena can expand the area of the spread of a virus. Allowing the occurrence of a pandemic of a coalition between the H5N1-p virus and H5N1. In this paper, we analyze the stability of the model of the spread of H1N1 and H5N1-p. Based on the basic reproduction number  $R_0$ , which is then simulated using the Matlab software, we conclude that when  $R_0 < 1$  the system is stable, whereas when  $R_0 > 1$  the system is unstable.

**Index Terms**—Basic reproduction number, stability.

## I. INTRODUCTION

INFLUENZA spreads around the world in seasonal epidemics and caused the deaths of hundreds of thousands and even millions of people in pandemic years. Genetic of influenza viruses change constantly. This is very worrying, because the virus H1N1 and H5N1-p will definitely be more easily transmitted among humans. To better understand the spreading dynamics of a disease, we need the basic reproduction number  $R_0$ , which is a number that could be used to determine whether a population is epidemic or not. By using the value of  $R_0$  we can analyze the stability of a model, which is important to determine the dynamical stability.

Previous research used kernel density function  $K(y, t) = e^{-\beta^* y}$  declared as a monotonically decreasing function, while this paper uses kernel density function  $K(y, t) = e^{\beta^* y^2}$ , by assuming that the occurrence rate of virus transmissions is very high, so the individual needs to be evacuated or quarantined to restrict the mobility of the population. Beside that, in previous research, the evolutionary model is built based on any possibilities that may occur due to the interaction between the susceptible individual to an infected individual, whereas in this study, by considering the characteristics of the virus, we assume that any susceptible individual ( $S_{jm}$ ) that interacts with individuals infected by H1N1-p virus ( $I_{1jm}$ ) will directly become part of exposed sub-populations ( $E_{1jm}$ ), and susceptible individuals, both poultry and humans, who interact with birds infected by H5N1 ( $I_{2ju}$ ) will be directly affected. Thus, the evolutionary model obtained will be different, and the basic reproductive number obtained is also different.

With attention to genetic changes of the individual populations, which happens due to the interaction between individuals, as well as characteristics of the virus itself, then we obtain

a spreading model of influenza viruses H1N1 and H5N1-p at two locations, as follows:

$$\begin{aligned}\frac{\partial S_{jm}}{\partial t} &= D_j^S \frac{\partial^2 S_{jm}}{\partial x^2} - kE_{1jm} - aI_{2jm} - dS_{jm} + bS_{jm} + \\ &\quad \mu_1 S_{km} - \mu_2 S_{jm} + oS_{jm} + q_1 S_{jm} + q_2 S_{jm} \\ \frac{\partial E_{1jm}}{\partial t} &= D_{1j}^E \frac{\partial^2 E_{1jm}}{\partial x^2} + kE_{1jm} - pI_{1jm} - dE_{1jm} - \\ &\quad bE_{1jm} + \mu_1 \sigma E_{1km} - \mu_2 E_{1jm} - nE_{1jm} \\ \frac{\partial I_{1jm}}{\partial t} &= (D_{1j}^I + D_{2j}^I) \frac{\partial^2 I_{1jm}}{\partial x^2} + aI_{2jm} + pI_{1jm} - dI_{1jm} - \\ &\quad bI_{1jm} - uI_{1jm} - vI_{2jm} \\ \frac{\partial S_{2ju}}{\partial t} &= D_{2j}^S \frac{\partial^2 S_{2ju}}{\partial x^2} - sI_{2ju} - dS_{2ju} + bS_{2ju} + \\ &\quad \mu_1 S_{2ku} - \mu_2 S_{2ju} \\ \frac{\partial I_{2ju}}{\partial t} &= D_{2j}^I \frac{\partial^2 I_{2ju}}{\partial x^2} + sI_{2ju} - dI_{2ju} - bI_{2ju}\end{aligned}$$

with initial conditions:

$$\begin{aligned}S_{jm}(x, 0) &= \sigma, & I_{1jm}(x, 0) &= I_{1jm0}, \\ E_{1jm}(x, 0) &= E_{1jm0}, & S_{2ju}(x, 0) &= S_{u0}, & I_{2ju} &= I_{u0}\end{aligned}$$

and Neumann boundary conditions, as follows:

$$\begin{aligned}\frac{\partial S_{jm}}{\partial x}(0) &= \frac{\partial S_{jm}}{\partial x}(L) = 0, & \frac{\partial S_{2ju}}{\partial x}(0) &= \frac{\partial S_{2ju}}{\partial x}(L) = 0, \\ \frac{\partial E_{1jm}}{\partial x}(0) &= \frac{\partial E_{1jm}}{\partial x}(L) = 0, & \frac{\partial I_{1jm}}{\partial x}(0) &= \frac{\partial I_{1jm}}{\partial x}(L) = 0, \\ \frac{\partial^2 I_{1jm}}{\partial x^2}(L) &> 0, & \frac{\partial I_{2ju}}{\partial x}(0) &= \frac{\partial I_{2ju}}{\partial x}(L) = 0, & \frac{\partial^2 I_{2ju}}{\partial x^2}(L) &> 0\end{aligned}$$

with total population

$$\begin{aligned}N_{jm}(t) &= S_{jm}(t) + E_{1jm}(t) + I_{1jm}(t) + I_{2jm}(t) \\ N_{2ju}(t) &= S_{2ju}(t) + I_{2ju}(t)\end{aligned}$$

Index  $i$  expresses influenza virus, where  $i = 1$  for H1N1-p virus and  $i = 2$  for the H5N1 virus. Index  $j = 1, 2$  expresses the location, where  $j = 1$  for location 1 and  $j = 2$  for location 2. Index  $m$  and  $u$ , express the population of individuals, where  $m$  denotes humans, and  $u$  for poultry.

## II. METHODOLOGY

In our work, we use the following methodology to obtain the results.

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### A. Construction of Matrix $F_i(X, t)$ and $V_i(X, t)$ of the existing models

Determination of basic reproductive number of the system equation begins by formulating Jacobian matrix. Before forming Jacobian matrix, first we construct matrix  $F_i$  and  $V_i$  whose elements represent newly infected individual and individual changes in each subpopulation.

### B. Proving that Matrix $F_i$ and $V_i$ fulfill five basic assumptions of Van Driessche and proving that matrix $V$ is $M$ -nonsingular matrix

After obtaining the Jacobian matrix of the existing model, we prove that matrices  $F_i$  and  $V_i$  fulfill five basic assumptions of Van Driessche and  $V$  is non-singular  $M$ -matrix.

### C. Calculate $R_0$ of H1N1-p of Virus, H5N1 of human and H5N1 in Poultry

By using the Jacobian matrix of the matrices  $F_i$  and  $V_i$ , we can calculate  $R_0$  of each virus, as the spectral radius of the matrix  $FV^{-1}$ .

### D. Simulations and interpretations of the model

The obtained system is then simulated by using the fourth-order Runge-Kutta method to make sure that results are in accordance with the analysis result. The simulation program is run by varying the parameters that fulfill two conditions, namely when  $R_0 < 1$  and  $R_0 > 1$ .

## III. MAIN RESULTS

Basic reproduction number ( $R_0$ ) is a number that specifies the average of secondary infected individuals to primary infected individuals that take place in susceptible populations.

By seeing the population ( $S_{jm}, E_{1jm}, I_{1jm}$ ) of the existing system of equations, we have matrix  $F_i$  and  $V_i$ , as follows:

$$F_i = \begin{bmatrix} 0 \\ kE_{1jm} \\ pI_{1jm} \end{bmatrix}$$

$$V_i = \begin{bmatrix} kE_{1jm} + dS_{jm} - bS_{jm} - \mu_2S_{jm} - oS_{jm} - q_1S_{jm} \\ pI_{1jm} + dE_{1jm} + bE_{1jm} - \mu\sigma E_m + \mu E_m + nE_m \\ dI_{1jm} + bI_{1jm} + uI_{1jm} \end{bmatrix}$$

Let  $x = (S_{jm}, E_{1jm}, I_{1jm})$  with  $(S_{jm}, E_{1jm}, I_{1jm}) \geq 0$ , then it can be shown that matrix  $F_i$  and  $V_i$  fulfill five basic assumptions of Van Driessche and matrix  $V$  is as follows:

$$V = \begin{bmatrix} d - b + \mu_2 - o - q_1 & k & 0 \\ 0 & d + b + n + \mu_2 & p \\ 0 & 0 & d + b + u \end{bmatrix}$$

Notice that  $V$  is a non-singular  $M$ -matrix.

Then, the three basic reproduction numbers:  $R_0$  from H1N1-p virus, H5N1 virus in humans and H5N1 in poultry, are obtained as the spectral radius of the matrix  $FV^{-1}$ , as follows:

$$R_{0_{H1N1-p}} = \frac{p}{d + b + u}, \quad R_{0_{H1N1-p-m}} = \frac{a}{d + b + v},$$

$$R_{0_{H1N1-p-u}} = \frac{s}{d + b}$$

From the existing spreading model of H1N1-p and H5N1 virus at two locations above, we acquire disease-free equilibrium point  $E_0 = (S_{jm}, 0, 0, 0, S_{2ju}, 0)$  and the endemic equilibrium point  $E_0 = (x_4, x_5, x_1, x_2, x_3, x_6)$  where:

$$x_1 = I_{1jm}$$

$$x_2 = I_{2jm}$$

$$x_3 = I_{2ju}$$

$$x_4 = \frac{ax_2 + \frac{kpx_1}{k - d - b + \mu\sigma - \mu - n}}{b - d + o + q_1 + q_2}$$

$$x_5 = \frac{px_1}{k - d - b + \mu\sigma - \mu - n}$$

$$x_6 = \frac{sx_3}{b - d}$$

From the simulation results we can obtain a full description of each subpopulation comparison conditions when  $R_0 < 1$  and  $R_0 > 1$ , as shown by Figs. 1 and 2 below: We can see

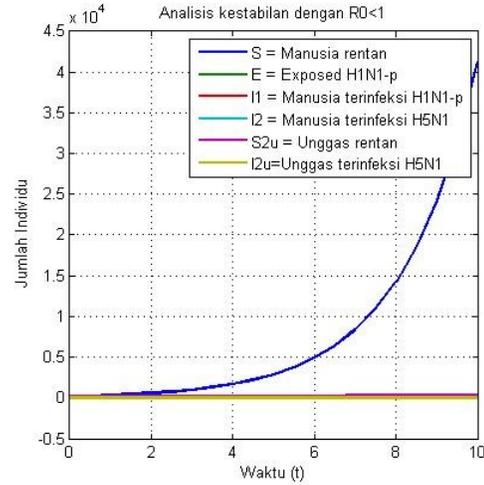


Fig. 1. Stability of the system when  $R_0 < 1$ .

that when  $R_0 < 1$ , the system is in a stable condition for a disease-free equilibrium point. This means no transmission of the disease occurs in the system. Therefore the number of populations ( $E_{1jm}$ ,  $I_{1jm}$ , and  $I_{2ju}$ ) decreases continuously, while the number  $I$  and  $S_{ju}$  increasing continuously. The influence of virus H5N1 to the system is less when the density of susceptible populations is equal to the density of infected populations.

From Fig. 2, we can see that when  $R_0 > 1$ , and when the mortality rate is bigger than the birth rate ( $d > b$ ), natural recovery rate is very small, and H1N1 virus infection rate ( $k$  and  $p$ ) is high enough the system is in an unstable state. The spread of the virus occurred in a very short time, resulting in transmission of the virus H1N1 and H5N1-p in the system. It is shown in the increasing number of infected individuals, both in human and poultry subpopulations. The number of susceptible subpopulations and exposed continue to decrease and the number of infected human populations is increased.

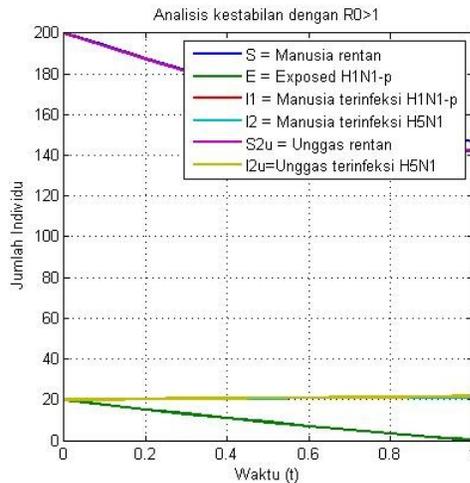


Fig. 2. Stability of the system when  $R_0 > 1$ .

#### IV. CONCLUSIONS

From the discussions, the research is concluded as follows. The system is stable when  $R_0 < 1$ , which is a condition when the average infected individuals produce less than one new infected individual. In other words, transmission of the virus does not happen in the system. Thus it does not cause endemic. In this condition, the mortality rate is equal to the birth rate ( $d = b$ ), and virus H5N1 is still affecting the change of the system even less influence if the density of susceptible populations is equal to the density of infected populations.

Besides that, the system is unstable when  $R_0 > 1$ , which is a condition when the average infected individuals produce more than one infected individual. In other words, there is a transmission virus in very large quantities. Thus this condition causes endemic and endanger the survival of the individual in the system. In this condition, the mortality rate is bigger than the birth rate ( $d > b$ ), natural recovery rate is very small, and H1N1 virus infection rate ( $k$  and  $p$ ) is high enough.

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