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STUDY THE DYNAMICS OF HUMAN INFECTION BY AVIAN INFLUENZA: CASE STUDY IN THE CENTRAL JAVA PROVINCE OF INDONESIA

KARTONO, WIDOWATI AND R HERI SU

Abstract. Mathematical modeling can be used for designing programs to control rapidly spreading infection diseases such as avian influenza. In this paper, we present a deterministic mathematical model that monitor the dynamics of three subpopulations, namely: Susceptible (S), Infected (I) and Recovered (R). To gain an insight into the critical factors associated with the control of avian influenza in a community, we develop a dynamic model to study an avian influenza epidemic in the Central Java Province of Indonesia.

Key words and Phrases : an avian influenza, dynamic model, epidemic.

1. Introduction

Human influenza viruses are classified into three serotypes: A, B, and C. Among these types, the virus A is epidemiologically the most important for humans, since it can recombine its genes with those of strains circulating in animal populations (birds, swine and horses) (R Casagrandi *et al,* 2006). The influenza A viruses are known to infect and multiply in avian influenza (Davis C, 2008). Studies have shown that direct contact with diseases poultry was the source of infection and found no evidence of person-to-person spread of the virus (A. Handel *el al,* 2007).

In reality, influenza is an important problem for the public health system. Just to give an idea of the social cost due to morbidity, we point out that the excess hospitalizations for pneumonia and influenza during the recent epidemic in the Central Java Province of Indonesia have been estimated to have very expensive cost (Central Java Province Public Health, 2009). This amount should be increased by the cost of workdays lost by the people infected, vaccines, antiviral drugs and so on. The Central Java Province is one of the provinces in Indonesia that reported in 2005 – 2009 as the avian influenza epidemic region. Of course not everyone dies from an avian influenza, thus the data do not count all instances of the avian influenza. Our goal for recent will be to attempt to devise a model that will describe this data. In this paper, we develop a mathematical model in order to study the dynamic of human infection by an avian influenza in the Central Java Province of Indonesia.

There are some mathematical models have been used for infectious diseases in influenza, namely SIR model (Anderson, 2006), SEIR model (M. Y. Li *et al,* 1995), SIRC model (R Casagrandi *et al,* 2006) or SEIRJQ (Susceptible

S, Asymptomatic E, Symptomatic I, Quarantined Q, Isolated J. Recovered R) model (A.B. Gumel *et al,* 2004) and $SIRS_bI_b$ model for an avian influenza (M. Derouich *et al*, 2008). In generally, these models were used to study the dynamics of human infectious by influenza and determine the best strategies at preventing and controlling influenza epidemics.

2. Main Results

In the introduction we mentioned that we are interested in the spread of an infectious diseases by an avian influenza. As an example we consider the data from an influenza epidemic in the Central Java Province of Indonesia in 2005-2009 where individuals may be susceptible to the disease, may be currently infected with diseases, or may be recovered from the disease. Thus we have three classes in which we can place individuals. Let us begin with some notations: S_t , I_t , R_t are respectively the number of susceptible individuals, infected individuals, and recovered individuals in the population at time t. Correspondingly define the three classes as fraction of the total population N, then notation s_t , i_t , r_t are respectively the susceptible, infected and recovered fraction of the population at time t. Note that each individual in the population is in one of the three classes, thus $s_t + i_t + r_t = 1$. The dynamical transfer of hosts among compartments can be demonstrated in a Fig.1:

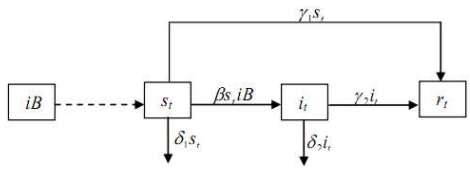

Fig.1: Schematic diagram: compartments of human populations

The resulting model is of SIR type with ignore the natural births. The term iB denotes the infected fraction of the birds population and iB is assumed constant. The daily contact rate β is the average number of adequate contacts of a human susceptible with infected birds per day. The term $\beta s_t iB$ is the human incidence i.e. the rate at which susceptible become infectious. Definitions of the other parameters of the model are δ_1 denotes natural death rate constant, δ_2 denotes disease-related death rate constant, γ_1 denotes natural recovery rate constant and γ_2 denotes disease-related recovery rate constant.

We can now write a series of difference equations that describe the motion of the SIR system in terms of the population fractions. In period $t + 1$ we have

$$s_{t+1} = s_t - \beta s_t iB - \delta_1 s_t - \gamma_1 s_t \quad (1)$$

$$i_{t+1} = i_t + \beta s_t iB - \delta_2 i_t - \gamma_2 i_t \quad (2)$$

$$r_{t+1} = r_t + \delta_2 i_t + \gamma_1 s_t \quad (3)$$

According to the series of difference equations (1), (2), and (3), we develop the dynamic model that will describe the spread of an avian influenza in the Central Java Province of Indonesia. We have

$$\frac{ds}{dt} = -(\beta iB + \delta_1 + \gamma_1)s \quad (4)$$

$$\frac{di}{dt} = \beta s iB - (\delta_2 + \gamma_2) i \quad (5)$$

$$\frac{dr}{dt} = \delta_2 i + \gamma_1 s \quad (6)$$

with initial conditions : $s(0) = 1$, $i(0) = 0$ and $r(0) = 0$. (7).

We start with no people infected, this system (4), (5), (6), (7) have a solution

$$s_t = e^{(-(\beta iB+\gamma_1+\delta_1)t)} \quad (8)$$

$$i_t = \left(\frac{\beta iB\, e^{(-(\beta iB+\gamma_1+\delta_1)t+(\delta_2+\gamma_2)t)}}{-\beta iB - \gamma_1 - \delta_1 + \delta_2 + \gamma_2} + \frac{\beta iB}{\beta iB + \gamma_1 + \delta_1 - \delta_2 - \gamma_2}\right) e^{(-(\delta_2+\gamma_2)t)}$$

and

$$r_t = \frac{1}{\beta iB + \gamma_1 + \delta_1 - \delta_2 - \gamma_2} \int_0^t (\beta iB(A(\gamma_1 - \gamma_2 + \gamma_1^2 - \gamma_1\gamma_2 + \gamma_1\delta_1 - \gamma_1\delta_2) + \gamma_2 C)dz$$

where $A = e^{-(\beta iB+\gamma_1+\delta_1)z}$, $C = e^{-(\gamma_2+\delta_2)z}$

This solution (8) describe that s_t , i_t and r_t as function of iB. If $iB > 0$ and the daily contact rate $\beta > 0$ (there is contact with the infected birds population) then the human incidence $\beta iB > 0$. The result shows that direct contact with diseased poultry was the source of infection. Thus parameters such as the average number of adequate contacts of a human susceptible with infected birds in determining the incidence of the disease are seen as important tools for preventive strategies. If β is increasing then i_t is increasing and decreasing whenever β is decreasing.

If $iB = 0$ then the susceptible population will remove just by the natural death or natural recovery and the results indicates that the infected population will always disappear. Thus we can destroy all of the infected birds population. We can also quarantine people for this disease.
The other result, $i_t = 0$ only if

$$\beta = \frac{\delta_2 - \gamma_1 - \delta_1}{iB} \tag{9}$$

Equation (9) describes that the daily contact rate and the rate of removal are parameters of the social structure of population and the disease of interest. There is nothing that we can do about $\delta_2, \gamma_1, \delta_1$ since it is a function of biology and physiology (well, doctors and medical researchers can work on this problem

but for most part we cannot since very costly). Thus we would like to be able to provide safety from the disease at the lowest possible cost. We do have some control over the β since it is a function of the infected birds population iB. Therefore the best strategy for controlling the spread of infectious an avian influenza is decreasing the daily contact rate β.

To get a better feel for how the model works, we used the data of avian influenza epidemic in the Central Java province of Indonesia to view the dynamic of the epidemic. According to the data, we have $\gamma_1 = 0.76$, $\delta_1 = 0.14$, $\gamma_2 = 0.08$, $\delta_2 = 0.92$, $\beta = 0.9$. In this paper, simulation was carried out with values of the parameters. In Figure 2, the typical behavior of solution indicates that the rate of human susceptible, infectious and recovered approaches asymptotically. The dynamics of the disease is mainly determined by the average number of adequate contact of a human susceptible with infected birds. This parameter constitutes an essential key to preventive strategies against the epidemics.

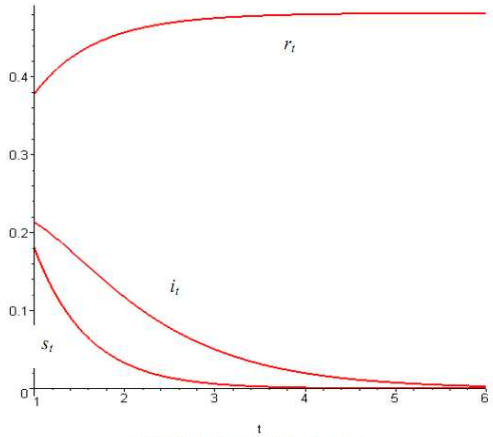

Figure 2: behavior of s_t , i_t and r_t

3. Concluding Remarks

Despite all medical advances, infectious disease outbreaks still pose a significant threat to the health and economics of our society. Since future infectious disease outbreaks- caused either by naturally emerging or deliberately introduced pathogens- are virtually certain to occur, it is utmost

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Despite all medical advances, infectious disease outbreaks still pose a significant threat to the health and economics of our society. Since future infectious disease outbreaks- caused either by naturally emerging or deliberately introduced pathogens- are virtually certain to occur, it is utmost importance to investigate effective control strategies that can minimize the impact of such outbreaks, especially the optimal strategy against an avian influenza. Effective control of infectious disease outbreaks is an important public health goal. We hope that the ideas presented here will stimulate

further studies on how to best implement the effective outbreaks control.

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