SEIR Epidemic Model Analysis Using Next Generation Matrix Method

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Abstract. Epidemic model is a model that consist of mathematical equations to describe the spread of a disease in a population. To measure the magnitude of the spread of disease in a population is called the basic reproductive number (R_0), if $R_0 < 1$ declared not epidemic and if $R_0 > 1$ the condition of an epidemic is declared. One way to determine the value R_0 is using the next generation matrix, which is the use of this method depends onlu on the infected compartment, with R_0 is defined as the spectral radius of the next generation matrix. Hantavirus is a disease caused by mice, more mice become infected, then in the human population the chances of lungs or kidney infections will increase. The model that are used in this research is SEIR epidemic model on the mice population, using the next generation matrix obtained value R_0 to control the progression of the desease in the mice population.

Keywords: *SEIR deterministic model, linearization, basic reproductive number, next generation matrix method, Hantavirus*

1. Introduction

Development of science and technology in the field of medicine has an important role in preventing the spread of disease that has not spread, that is by giving a vaccine against a disease-infected population. Development of science in the field of Mathematics also gives an important role in the prevention of a disease outbreak. The role of mathematics in the form of a mathematical model, called the mathematical model of the epidemic. Epidemic mathematical model was first published by Daniel Bernoulli, and modern epidemic models developed by AG McKendrick and W.O. Kermarck (1927). [12]

In this paper, the model used is SEIR epidemic models. SEIR models are presented as a system of differential equations. System of differential equations SEIR epidemic is an outline describing the flow spread of disease spread individual subpopulations susceptible (vulnerable) and before the individual susceptible truly infected, the virus is present in a subpopulation of exposed (latent) in the body and the proliferation of the virus has not happened yet, so if durability susceptible individual body is weak, then the individual becomes infected through direct contact or other intermediaries, but if it happens otherwise, it would not susceptible individuals infected with the virus.

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Further infected individuals are able to survive the disease will be cured and into subpopulations recovered (healed).

A population that has been infected with the virus can lead to the transmission of infectious diseases from one individual to another or in other words the transmission of disease in the population , another factor that must be considered is the average number of cases of the disease if there are cases of secondary or better known as basic reproduction number R_0. This paper analyzes the model of the spread of Hantavirus disease rodent population using Next Generation Matrix method for determining R_0.

2 . Basis Theory

2.1. Epidemic Model

Mathematical modeling which model the transmission of a disease called epidemic mathematical models. In epidemic models itself many models are used to model the spread of a disease in a population. With the expansion of knowledge , there are some models that are tailored to the type of epidemic outbreaks of disease, including models of SIR, SI, SIS, SEIS, and SEIR.

Epidemic is a disease that arises as a new case in particular, within a specific time period, at a rate that exceeded estimates. In other words, the plague epidemic is occurring more rapidly than expected. Common disease that occurs in a constant rate but high enough in a population is called endemic. [4]

A disease is said to be endemic in a if the infection in the population took place without any outside influence. An infectious disease is said to be endemic if every person who contracted the disease spread to the right of another individual. If the infection is not lost and the number of people who are infected do not add up, then an infection is said to be in a state of permanent endemic (endemic steady state). An infection that began as an epidemic will eventually reach a state of endemic lost or fixed, depending on a number of factors, including the virus spreads and how the disease concerned.

Epidemic models is a mathematical model used to look at the incidence of disease in a population. Conditions epidemic occurs when there is a vulnerable individual in the population, all individuals who are in the population has the opportunity to be a population of susceptible individuals, and most likely the infection will be prevalent in this population. So in the end all potentially infected individuals in the population. Basically, the notation of class epidemiology on a model of disease that is currently being standardized, the phase Susceptibles, Infected, and Removed, defined [16]:

- The way that someone can get out of the vulnerable groups is infected. The way that someone can get out of the infected group was recovering from illness. Once a person has been recovered , the person receives immunity;

- Age, sex, social status, and race did not affect the possibility of being infected;
- There is no immunity derivatives;
- Members of the population homogeneous mixture (having the same interaction with others at the same level.

Mathematical model used in this paper is a deterministic mathematical models, deterministic mathematical model is a model that does not consider the influence of inter- individual random. [21]

2.2. Basic Reproduction Number (R_0)

In a mathematical model of the epidemic, there are parameters which have a very important role in the spread of infectious virus, the Basic Reproduction Number (R_0) which is the average number of secondary cases the endemic period. R_0 is the potential transmission of the disease in susceptible populations is the average number of individuals who will be infected directly by someone who has been infected during transmission on entirely within vulnerable populations. According Hethcote, R_0 is a ratio that shows the number of susceptible individuals who may suffer from diseases caused by a single infected individual.

The greater the value of R_0 it is increasingly difficult to control the outbreak of a disease. For a simple model , the proportion of the population who need to be vaccinated to prevent the spread of sustainable . Basic reproductive rate is influenced by several factors including the duration of infected individuals.

When $R_0 > 1$ then the infected person can spread the virus to the individuals who are susceptible class and lead to an outbreak of a disease and when $R_0 < 1$ then someone who is infected does not cause other people affected by the same disease , in other words not an epidemic in this population. [8]

Basic Reproduction Number (R_0) is equivalent to:

- Duration of disease transmission .
- The number of cases of vulnerable populations per unit time .
- The possibility of transmission of infection in a meeting with a number of susceptible individuals.

2.3. Next Generation Matrix method

From the results linearization which produces Jacobi matrix, the next step is determining the eigenvalues, which is the greatest value that will be dominant in the system eigenvalues are named as spectral radius .

If A is a matrix of size $n\ x\ n$ with eigenvalues $\lambda_1, \lambda_2, \dots, \lambda_n$, denoted by $\sigma(A)$, then the spectral radius of A is defined by [10]

$$\boldsymbol{\rho(A) = max|\lambda|, \lambda \in \sigma(A)\}} \quad (1)$$

NGM is a matrix which is constructed from sub- populations that cause infections only. For the general model with m disease compartment and $m+1$ disease-free compartments.

R_0 is defined as the expectation of the number of secondary cases generated by a particular infection in the whole population in vulnerable circumstances.

NGM methods introduced by Diekmann et al (1990) , this method is a common method R_0 decline in a case of epidemic, include some situations become diseased compartment and the compartment without the disease. For the specific implementation, the assumption is that the probability estimates between the transmission is constant or the same conditions, so the distribution of each condition is exponential. [12]

Generation on the model of an epidemic wave of secondary infections that flows from any pre-existing infections. This matrix is a matrix that is constructed from sub- populations that cause infections only. For the general model with compartments i and j compartment disease without the disease, R_0 value can be calculated for each compartment. By using the NGM, can facilitate in determining R_0 when in a model of epidemic that has more than two variables are interrelated.

As described earlier, that the application of the method NGM, only focused on the infected compartment alone . Where F is a matrix with the emerging new infections, and T is the transition matrix between sub-classes. For any nonnegative vector x, the elements of the vector T_x describe the growth rate of each infected compartment. [3]

In the formation of the next generation operator on the discussion here, because the model used is a dynamic model when discrete time, it is assumed that the value of the matrix $Q = F + T$, where T is the transition of each condition, with nonnegative elements.

F and T is a nonnegative matrix is not zero, so that all the number of columns $T < 1$, because the element (i, j) of T describes the fraction of individuals in class j that survive and move to class i at time intervals, and the elements (i, j) of F describes a new number appears on the class i alighted from a single individual in class j in the time interval.

Matrix model of population dynamics is expressed as a series of nonnegative vector $x_0, x_1, \ldots$ as much n , is defined as,

$$x_k = Qx_{k-1}, k = 1,2, \ldots \quad (2)$$

to prove that x_0 is nonzero where Q is the $n \times n$ matrix with nonnegative entries. It is assumed that

$$Q = F + T \quad (3)$$

where F and T is a nonzero nonnegative matrix such that the number of columns of T is not greater than 1 .

The probability of infection of a population is assumed

$$\lim_{k\to\infty} T^k x_0 = 0$$

for the initial conditions the population as a whole (nonnegative vector) x_0.

By examining the effect of T^k on the basis of standard unit vectors , this condition will be the same show with the system (3) in turn, it is known that the condition is the same as

$$\rho(T) < 1 \tag{4}$$

Assumption (4) describes the distribution that satisfies the conditions of the birth of a new born offspring and collected during the whole lifespan of the population x_0. Because the initial conditions, $x_0 = 0$, using MacLaurin series, in order to get [5]

$$(I - T)^{-1} = I + T + T^2 + \cdots \tag{5}$$

Because $Q = F(I - T)^{-1}$, then

$$Qx_0 = Fx_0 + FTx_0 + FT^2x_0 + \cdots \tag{6}$$

So NGM for discrete time model is [5]

$$Q = F(I - T)^{-1} \tag{7}$$

R_0 is not negartif eigenvalue with the largest eigenvalue or spectral radius of NGM, that is the number of new infections from all types of hosts in the next generation. Thus, [16]

$$R_0 = \rho(Q) \tag{8}$$

Theorem 1: [1]

System $X(t+1) = G\big(X(t)\big), G \in C^1$ has the disease-free equilibrium and linearization of the DFE system containing the system $Y(t+1) = J(Y(t))$, where matrix $J = \begin{pmatrix} F+T & O \\ A & C \end{pmatrix}$ with the matrix F and T non-negative. And T satisfy (4). Then the basic reproductive number of system $X(t+1) = G\big(X(t)\big), G \in C^1$ is defined by (8). Thus, the DFE is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

3. Discussion

3.1. Modification Model

The model used is the model for disease epidemics SEIR Hantavirus that occurs in the rodent population. Models birth given, [1]

$$B(N_m + N_f) = \frac{2bN_mN_f}{N} \quad (9)$$

where, $N_m = S_m + E_m + I_m + R_m$ and $N_f = S_f + E_f + I_f + R_f$ so $N = N_m + N_f$. B is a function of the average birth harmonic.

For a model that describes the occurrence of infection in a population , it is assumed the number of contacts between male and female rodents is a random distribution of the rodent population. Thus, the amount of contact between rodents follow a Poisson distribution.

Assuming a Poisson distribution, with

$$p(i) = \frac{\exp(-\lambda)\lambda^i}{\text{i!}}, i = 0,1,2, \ldots$$

because the only result of the inter- individual contacts infected, then the chances rodents live in vulnerable conditions become infected individual is $1 - p(0)$. [23]

Assumed that the birth and the occurrence of an infection in accordance with the density- dependent survival so it can be assumed that the density-dependent survival is a logistical nature.

Known to be modeled as a logistic growth, [1]

$$D(N) = \frac{K}{K + (b/2)N}$$

where D is the density-dependent or a function that depends on the density of population, K is the carrying capacity, and $1 + b/2$ is the exponential of the intrinsic growth rate. With an average litter size b that describes that on an individual rodents in one breeding individuals produce as much b .

b values in humans likely to generate little b above 1, there may be a twin , but rarely, and the value of b in rodents is likely to produce more value b. So that K depends on b, K will be smaller if b resulting from the proliferation slightly. And the opposite applies.

Given deterministic system of a rodent population, [1]

$$\begin{cases} S_m(t+1) = \left[\frac{B}{2} + \exp\left(-\beta_m I_m - \beta I_f\right) S_m\right] D(N) \\ E_m(t+1) = \left(\left[1 - \exp\left(-\beta_m I_m - \beta I_f\right)\right] S_m + (1-\delta) E_m\right) D(N) \\ I_m(t+1) = \left[\delta E_m + (1-\gamma_m) I_m\right] D(N) \\ R_m(t+1) = \left[\gamma_m I_m + R_m\right] D(N) \\ S_f(t+1) = \left[\frac{B}{2} + \exp\left(-\beta I_m - \beta I_f\right) S_f\right] D(N) \\ E_f(t+1) = \left(\left[1 - \exp\left(-\beta I_m - \beta I_f\right)\right] S_f + (1-\delta) E_f\right) D(N) \\ I_f(t+1) = \left[\delta E_f + (1-\gamma_f) I_f\right] D(N) \\ R_f(t+1) = \left[\gamma_f I_f + R_f\right] D(N) \end{cases} \quad (10)$$

Inisialization conditions of the system (10) non-negative,

$S_j(0) \geq 0, E_j(0) + I_j(0) > 0, R_j(0) \geq 0$, where $j = m, f$

$0 \leq \gamma_m, \gamma_f \leq 1$

$0 \leq \delta \leq 1$

$N_m = S_m + E_m + I_m + R_m$ dan $N_f = S_f + E_f + I_f + R_f$

$N = N_m + N_f$

where β_m a direct contact with male rodent male, β is a direct contact with female rodents, δ is the probability of infection, and γ is the probability of recovery from infection.

And the value of the parameters are positive, so the solution to the SEIR model is non-negative for $t \geq 0$. So that the vector of epidemic SEIR models is $X = (E_m, E_f, I_m, I_f, S_m, S_f, R_m, R_f)^T$.

3.2. Application of Method

Using the Next Generation Matrix method for determining the value of R_0 on rodent population, as it is known in advance that the NGM method is divided into two compartments, the diseased compartment, $X_0 = (E_j, I_j)$, where $j = m, f$. And compartment without disease, $X_1 = (S_j, R_j)$, where $j = m, f$. After that the linearization process system (10), the result,

$$Y(t+1) = J(Y(t))$$

with J an 8×8 matrix,

$$J = \begin{bmatrix} (1-\delta) & 0 & \overline{S_m}\beta_m \exp(-\beta_m I_m - \beta I_f) & \overline{S_m}\beta \exp(-\beta_m I_m - \beta I_f) & 1-\exp(-\beta_m I_m - \beta I_f) & 0 & 0 & 0 \\ 0 & (1-\delta) & \overline{S_f}\beta \exp(-\beta I_m - \beta I_f) & \overline{S_f}\beta \exp(-\beta I_m - \beta I_f) & 0 & 1-\exp(-\beta I_m - \beta I_f) & 0 & 0 \\ \delta & 0 & (1-\gamma_m) & 0 & 0 & 0 & 0 & 0 \\ 0 & \delta & 0 & (1-\gamma_f) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\overline{S_m}\beta_m \exp(-\beta_m I_m - \beta I_f)) & -(\overline{S_m}\beta \exp(-\beta_m I_m - \beta I_f)) & \exp(-\beta_m I_m - \beta I_f) & 0 & 0 & 0 \\ 0 & 0 & -(\overline{S_f}\beta \exp(-\beta I_m - \beta I_f)) & -(\overline{S_m}\beta_m \exp(-\beta I_m - \beta I_f)) & 0 & \exp(-\beta I_m - \beta I_f) & 0 & 0 \\ 0 & 0 & \gamma_m & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & \gamma_f & 0 & 0 & 0 & 1 \end{bmatrix} D(N)$$

(11)

Where J is the Jacobi matrix , whose entries are the first derivative of the system (10), by using the concept of a Poisson distribution, where in a population resulting only one infected contact, then it is likely that rodents live in vulnerable conditions become infected individuals is $1 - p(0)$. Transfer rate on individuals in the interaction between the two categories of the population , such as individuals vulnerable, with contact with infected individuals led to individuals who are in a vulnerable category will be infected, and the presence of the reaction processes that are infected will recover, this statement is said to be the law of mass action. [6] If the average number of contacts per infected individual susceptible individuals with an infected male or female fulfill the law of mass action, then $\lambda S = (\beta I_m + \beta I_f)S$, so that

$$1 - p(0) = 1 - \exp(-\beta_m I_m - \beta I_f) = 0$$
$$\exp(-\beta_m I_m - \beta I_f) = 1 \quad (12)$$

in relation to the level of male aggressiveness, it is assumed that the contact between males is greater than the contact between male and female or female and female, so

$$\beta_m \gg \beta > 0$$

and for that , then the Poisson distribution for vulnerable females is

$$\exp(-\beta I_m - \beta I_f) = 1 \quad (13)$$

The total population of the system (10) there is a logistic growth (Beverton-Holt growth),

$$N(t+1) \approx \frac{(1 + b/2)KN(t)}{K + (b/2)N(t)}$$

cause $\lim_{t\to\infty} N(t) = K$. [1]

From the Disease-free Equilibrium state in which it is assumed there is a spread of infection, then $E_m, E_f = I_m, I_f = R_m, R_f = 0$, known $N(t) = K$, and $N(t) = N_m(t) + N_f(t)$, as previously assumed that in a population is assumed to be entirely in a state susceptible (*S*), then $\overline{S_m} = \frac{K}{2} = \overline{S_f}$. [1]

So,

$$J = D(N)\begin{bmatrix} (1-\delta) & 0 & (K/2)\beta_m & (K/2)\beta & 0 & 0 & 0 & 0 \\ 0 & (1-\delta) & (K/2)\beta & (K/2)\beta & 0 & 0 & 0 & 0 \\ \delta & 0 & (1-\gamma_m) & 0 & 0 & 0 & 0 & 0 \\ 0 & \delta & 0 & (1-\gamma_f) & 0 & 0 & 0 & 0 \\ 0 & 0 & -((K/2)\beta_m) & -((K/2)\beta) & 1 & 0 & 0 & 0 \\ 0 & 0 & -((K/2)\beta) & -((K/2)\beta_m) & 0 & 1 & 0 & 0 \\ 0 & 0 & \gamma_m & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & \gamma_f & 0 & 0 & 0 & 1 \end{bmatrix}$$

where J is 8×8 matrix.

Because the NGM nethod only focus on the diseased compartment, $X_0 = (E_j, I_j)$, where $j = m, f$, so that

$$J = D(N)\begin{bmatrix} (1-\delta) & 0 & (K/2)\beta_m & (K/2)\beta \\ 0 & (1-\delta) & (K/2)\beta & (K/2)\beta \\ \delta & 0 & (1-\gamma_m) & 0 \\ 0 & \delta & 0 & (1-\gamma_f) \end{bmatrix} \quad (14)$$

where J is 4×4 matrix.

So that,

$$D(N) = \frac{K}{K + (b/2)N}$$

$$D(K) = \frac{K}{K + (b/2)K}$$

$$D(K) = \frac{1}{1 + (b/2)}$$

then,

$$J = \frac{1}{1+(b/2)}\begin{bmatrix} (1-\delta) & 0 & (K/2)\beta_m & (K/2)\beta \\ 0 & (1-\delta) & (K/2)\beta & (K/2)\beta \\ \delta & 0 & (1-\gamma_m) & 0 \\ 0 & \delta & 0 & (1-\gamma_f) \end{bmatrix} \quad (15)$$

where J is 4×4 matrix, that F is an emerging infection and T is a transition period of the disease, with F and T is 4×4 matrix so obtained

$$F = \frac{K/2}{1+(b/2)}\begin{bmatrix} 0 & 0 & \beta_m & \beta \\ 0 & 0 & \beta & \beta \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \text{ and}$$

$$T = \frac{1}{1+(b/2)}\begin{bmatrix} (1-\delta) & 0 & 0 & 0 \\ 0 & (1-\delta) & 0 & 0 \\ \delta & 0 & (1-\gamma_m) & 0 \\ 0 & \delta & 0 & (1-\gamma_f) \end{bmatrix} \quad (16)$$

By using NGM, where R_0 is defined as spectral radius or largest eigenvalues of the matrix Q, where Q is NGM.

$$Q = F(I-T)^{-1}$$

$$(I-T) = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} - \begin{bmatrix} \frac{(1-\delta)}{1+b/2} & 0 & 0 & 0 \\ 0 & \frac{(1-\delta)}{1+b/2} & 0 & 0 \\ \frac{\delta}{1+b/2} & 0 & \frac{(1-\gamma_m)}{1+b/2} & 0 \\ 0 & \frac{\delta}{1+b/2} & 0 & \frac{(1-\gamma_f)}{1+b/2} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{b/2+\delta}{1+b/2} & 0 & 0 & 0 \\ 0 & \frac{b/2+\delta}{1+b/2} & 0 & 0 \\ \frac{\delta}{1+b/2} & 0 & \frac{b/2-\gamma_m}{1+b/2} & 0 \\ 0 & \frac{\delta}{1+b/2} & 0 & \frac{b/2-\gamma_f}{1+b/2} \end{bmatrix} \quad (17)$$

Furthermore, it will find the inverse matrix (17) using row reduction,

$$(I-T)^{-1}=\left|\begin{matrix}\frac{b/2+\delta}{1+b/2} & 0 & 0 & 0\\ 0 & \frac{b/2+\delta}{1+b/2} & 0 & 0\\ \frac{\delta}{1+b/2} & 0 & \frac{b/2-\gamma_m}{1+b/2} & 0\\ 0 & \frac{\delta}{1+b/2} & 0 & \frac{b/2-\gamma_f}{1+b/2}\end{matrix}\right|\left|\begin{matrix}1&0&0&0\\0&1&0&0\\0&0&1&0\\0&0&0&1\end{matrix}\right|$$

$$=\left|\begin{matrix}1&0&0&0\\0&1&0&0\\0&0&1&0\\0&0&0&1\end{matrix}\right|\left|\begin{matrix}\frac{1+b/2}{b/2+\delta} & 0 & 0 & 0\\ 0 & \frac{1+b/2}{b/2+\delta} & 0 & 0\\ \frac{\delta(1+b/2)}{(b/2+\delta)(b/2+\gamma_m)} & 0 & \frac{1+b/2}{b/2+\gamma_m} & 0\\ 0 & \frac{\delta(1+b/2)}{(b/2+\delta)(b/2+\gamma_f)} & 0 & \frac{1+b/2}{b/2+\gamma_f}\end{matrix}\right|$$

$$=\left[\begin{matrix}\frac{1+b/2}{b/2+\delta} & 0 & 0 & 0\\ 0 & \frac{1+b/2}{b/2+\delta} & 0 & 0\\ \frac{\delta(1+b/2)}{(b/2+\delta)(b/2+\gamma_m)} & 0 & \frac{1+b/2}{b/2+\gamma_m} & 0\\ 0 & \frac{\delta(1+b/2)}{(b/2+\delta)(b/2+\gamma_f)} & 0 & \frac{1+b/2}{b/2+\gamma_f}\end{matrix}\right] \quad (18)$$

then,

$$Q=F(I-T)^{-1}$$

$$Q = \frac{K}{2}\begin{bmatrix} 0 & 0 & \frac{1}{1+(b/2)}\beta_m & \frac{1}{1+(b/2)}\beta \\ 0 & 0 & \frac{1}{1+(b/2)}\beta & \frac{1}{1+(b/2)}\beta \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \cdot \begin{bmatrix} \frac{1+b/2}{b/2+\delta} & 0 & 0 & 0 \\ 0 & \frac{1+b/2}{b/2+\delta} & 0 & 0 \\ \frac{\delta(1+b/2)}{(b/2+\delta)(b/2+\gamma_m)} & 0 & \frac{1+b/2}{b/2+\gamma_m} & 0 \\ 0 & \frac{\delta(1+b/2)}{(b/2+\delta)(b/2+\gamma_f)} & 0 & \frac{1+b/2}{b/2+\gamma_f} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{K}{2}\cdot\frac{\beta_m\delta}{(b/2+\delta)(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_f)} & \frac{K}{2}\cdot\frac{\beta_m}{(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_f)} \\ \frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_f)} & \frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_f)} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (19)$$

Furthermore, find eigen value from (19), bu using,

$$|\lambda I - Q| = \begin{bmatrix} \lambda & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{bmatrix} - \begin{bmatrix} \frac{K}{2}\cdot\frac{\beta_m\delta}{(b/2+\delta)(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_f)} & \frac{K}{2}\cdot\frac{\beta_m}{(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_f)} \\ \frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_f)} & \frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_m)} & \frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_f)} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$= \begin{bmatrix} \lambda - \frac{K}{2}\cdot\frac{\beta_m\delta}{(b/2+\delta)(b/2+\gamma_m)} & -\frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_f)} & -\frac{K}{2}\cdot\frac{\beta_m}{(b/2+\gamma_m)} & -\frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_f)} \\ -\frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_m)} & \lambda - \frac{K}{2}\cdot\frac{\beta\delta}{(b/2+\delta)(b/2+\gamma_f)} & -\frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_m)} & -\frac{K}{2}\cdot\frac{\beta}{(b/2+\gamma_f)} \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{bmatrix}$$

Assumed that,

$b_\delta = (b/2+\delta)$

$b_{\gamma m} = (b/2+\gamma_m)$

$b_{\gamma f} = (b/2+\gamma_f)$

So that,

$$|\lambda I - Q| = \begin{bmatrix} \lambda - \frac{K}{2}.\frac{\beta_m \delta}{b_\delta b_{\gamma_m}} & -\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}} & -\frac{K}{2}.\frac{\beta_m}{b_{\gamma_m}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_f}} \\ -\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_m}} & \lambda - \frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_m}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_f}} \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{bmatrix}$$

Because the matrix used is a $4 \times 44 \times 4$ matrix, so to find its eigenvalues using row reduction, row reduction here will be on the first line,

$$\det|\lambda I - Q| = a_{11}C_{11} + a_{12}C_{12} + a_{13}C_{13} + a_{14}C_{14} \quad (20)$$

$$M_{11} = \begin{vmatrix} \lambda - \frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_m}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_f}} \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{vmatrix}$$

$$= \lambda^3 - \lambda^2\left(\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}}\right)$$

$$C_{11} = (-1)^2 M_{11} = \lambda^3 - \lambda^2\left(\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}}\right)$$

$$M_{12} = \begin{vmatrix} -\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_m}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_m}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_f}} \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{vmatrix} = -\lambda^2\left(-\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_m}}\right)$$

$$C_{12} = (-1)^3 M_{12} = \lambda^2\left(-\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_m}}\right)$$

$$M_{13} = \begin{vmatrix} -\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_m}} & \lambda - \frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_f}} \\ 0 & 0 & 0 \\ 0 & 0 & \lambda \end{vmatrix} = 0$$

$$C_{13} = (-1)^4 M_{13} = 0$$

$$M_{14} = \begin{vmatrix} -\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_m}} & \lambda - \frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}} & -\frac{K}{2}.\frac{\beta}{b_{\gamma_m}} \\ 0 & 0 & \lambda \\ 0 & 0 & 0 \end{vmatrix} = 0$$

$$C_{14} = (-1)^5 M_{14} = 0$$

substitute to (20),

$$\det|\lambda I - Q| = (\lambda - \frac{K}{2}.\frac{\beta_m \delta}{b_\delta b_{\gamma_m}})(\lambda^3 - \lambda^2(\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}})) +$$

$$(-\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_f}})(\lambda^2(-\frac{K}{2}.\frac{\beta\delta}{b_\delta b_{\gamma_m}}))$$

$$= \lambda^2(\lambda^2 + \lambda(\frac{K}{2}(-\frac{\beta_m\delta}{b_\delta b_{\gamma_m}} - \frac{\beta\delta}{b_\delta b_{\gamma_f}})) + \frac{K}{2}((\frac{\beta_m\delta}{b_\delta b_{\gamma_m}}.\frac{\beta\delta}{b_\delta b_{\gamma_f}}) - (\frac{\beta\delta}{b_\delta b_{\gamma_m}}.\frac{\beta\delta}{b_\delta b_{\gamma_f}}))$$

$$= 0$$

or written as,

$$\lambda^2 = 0, \text{ dan}$$

$$\lambda^2 + \lambda(\frac{K}{2}(-\frac{\beta_m\delta}{b_\delta b_{\gamma_m}} - \frac{\beta\delta}{b_\delta b_{\gamma_f}})) + \frac{K}{2}(\left(\frac{\beta_m\delta}{b_\delta b_{\gamma_m}}.\frac{\beta\delta}{b_\delta b_{\gamma_f}}\right) - \left(\frac{\beta\delta}{b_\delta b_{\gamma_m}}.\frac{\beta\delta}{b_\delta b_{\gamma_f}}\right) = 0$$

by using *ABC* formula,

$$\lambda_{1,2} = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$$

$$\lambda_{1,2} = \frac{-\frac{K}{2}(-\frac{\beta_m\delta}{b_\delta b_{\gamma_m}} - \frac{\beta\delta}{b_\delta b_{\gamma_f}}) \pm \sqrt{\frac{K}{2}(-\frac{\beta_m\delta}{b_\delta b_{\gamma_m}} - \frac{\beta\delta}{b_\delta b_{\gamma_f}})^2 - 4\frac{K}{2}(\frac{\beta_m\delta}{b_\delta b_{\gamma_m}}.\frac{\beta\delta}{b_\delta b_{\gamma_f}}) - (\frac{\beta\delta}{b_\delta b_{\gamma_m}}.\frac{\beta\delta}{b_\delta b_{\gamma_f}})}}{2}$$

$$\lambda_{1,2} = \frac{\frac{K}{2}(\frac{\beta_m\delta}{b_\delta b_{\gamma_m}} + \frac{\beta\delta}{b_\delta b_{\gamma_f}}) \pm \frac{\delta}{b_\delta b_{\gamma_m} b_{\gamma_f}})\sqrt{(\beta_m b_{\gamma_f} - \beta b_{\gamma_m})^2 - 4\beta(\beta_m - \beta)b_{\gamma_m} b_{\gamma_f}}}{2}$$

$$\lambda_{1,2} = \frac{K}{4}((\frac{\beta_m\delta}{b_\delta b_{\gamma_m}} + \frac{\beta\delta}{b_\delta b_{\gamma_f}}) \pm \frac{\delta\sqrt{(\beta_m b_{\gamma_f} - \beta b_{\gamma_m})^2 - 4\beta(\beta_m - \beta)b_{\gamma_m} b_{\gamma_f}}}{b_\delta b_{\gamma_m b_{\gamma_f}}})$$

(21)

Because R_0 defined as the largest positive eigen value from Q, then

$$R_0 = \rho(Q)$$

$$R_0 = \frac{K}{4}\left(\left(\frac{\beta_m \delta}{b_\delta b_{\gamma_m}} + \frac{\beta\delta}{b_\delta b_{\gamma_f}}\right) + \frac{\delta\sqrt{(\beta_m b_{\gamma_f} - \beta b_{\gamma_m})^2 - 4\beta(\beta_m - \beta) b_{\gamma_m} b_{\gamma_f}}}{b_\delta b_{\gamma_m b_{\gamma_f}}}\right) \quad (22)$$

Results of (22) satisfy Theorem 1, with the value obtained from the linearized R_0 on the system (10), the matrix *J* is defined by (11) and the matrix *F*, *T* non-negative.

That if the value $R_0 > 1$ then the situation is not stable in other words occur endemic, whereas if the value $R_0 < 1$ then the state of the local asymptotically stable in other words do not occur endemic.

Corrolary 1: [1]

For example R_0 is defined by (22). In the SEIR model (10), $\lim_{t\to\infty} N_m(t) = \frac{K}{2} = \lim_{t\to\infty} N_f(t)$. So, if $R_0 < 1$ then the DFE in (10) is locally asymptotically stable and if $R_0 > 1$, then it is unstable.

In the epidemic SEIR model in the rodent population, will increase the value of R_0 depend on the parameters β and δ, because the parameters describing the rate of infection in a population, the greater the value of the parameter R_0 will increase, and if the value of the parameter is smaller then R_0 will decrease.

4. Simulation

4.1. SEIR Model For Disease Hantavirus

Simulations performed to describe the spread of Hantavirus disease in the rodent population, using the system (10) and in accordance with the previous discussion, it is assumed for the behavior of male rodents / male is more aggressive than female rodents, causing,

$$\beta_m \gg \beta > 0$$

can be seen in the rodent population graph for t = 5 years in Figure 1,

Table. 1. SEIR Deterministic Model Parameters

Parameter	Value
K	1000 rodent
b	2 rodent
β_m	0.4
β	0.01
γ_m	0.9
γ_f	0.5
δ	0.5

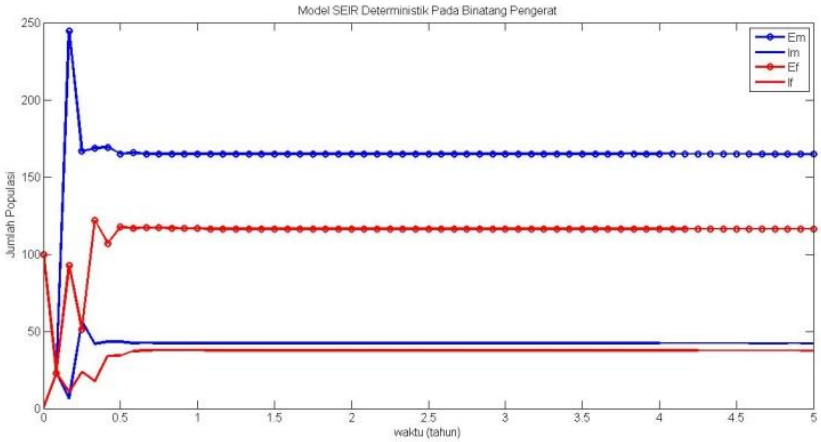


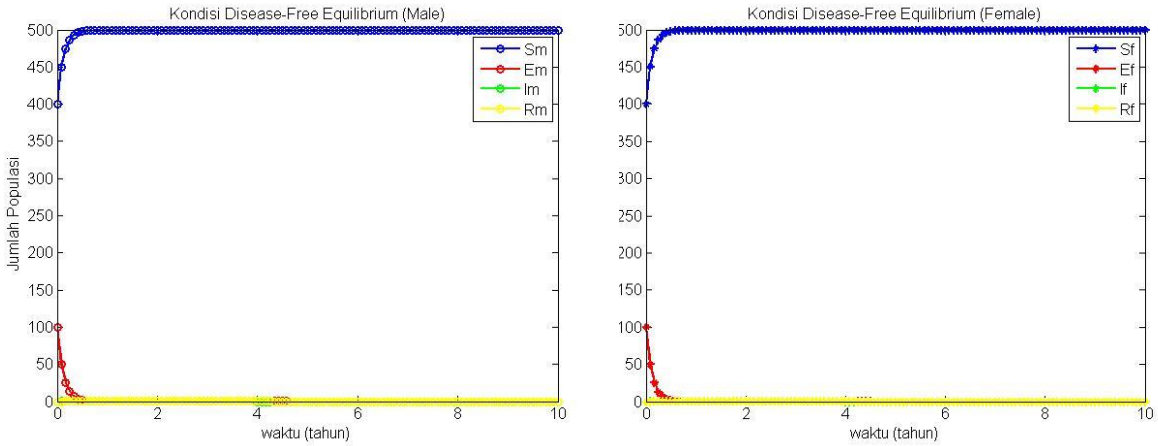
Figure 1. Exposed and Infected Individuals Charts For Seir Deterministic Model

From Figure 1 it can be seen that for t = 5, the rate of contact on male larger 3-5 fold compared to the rate of individual contacts in the female. And contacts between individual males also have larger contact rate compared with the rate of contact between the individual male and female, or female and female individuals.

When the Disease-free Equilibrium conditions, which indicates that in a population no outbreak, with $X = \{S_m, S_f, E_m, E_f, I_m, I_f R_m, R_f\}$, where X is a population of rodents so that $X = \{K/2, K/2, 0, 0, 0, 0, 0, 0\}$, to see the state role in the spread of disease DFE using the following parameter values,

Table. 2. Parameter *DFE* Value SEIR Deterministic Model

Parameter	Value
K	1000 rodent
b	2 rodent
β_m	0.01
β	0.004
γ_m	0.5
γ_f	0.5
δ	0.005



(a) (b)

Figure 2 . Graphs individual males (a) and female (b) in a state of DFE

In Figure 2 (a) and (b) shows that the number of individuals who are in a vulnerable state (S) in the time interval $0 \leq t \leq 10$ will go to a value of 500 , which is where the value is the total population of each of the male and female rodent. And the number of individuals in a state of latent/ hidden (E) which has a value initialized early $E_m = E_f = 100$ in the time interval $0 \leq t \leq 10$ will be close to the value 0, it is due to the spread of disease produced by these rodents, and for the infected state (I) did not show any disease-infected individuals. Since there are no infected individuals, resulting in no individuals who recovered (R) of the disease , it can be concluded that by using these parameters do not occur in other words not endemic outbreaks and disease will disappear. Data obtained from the analysis of the value of R_0,

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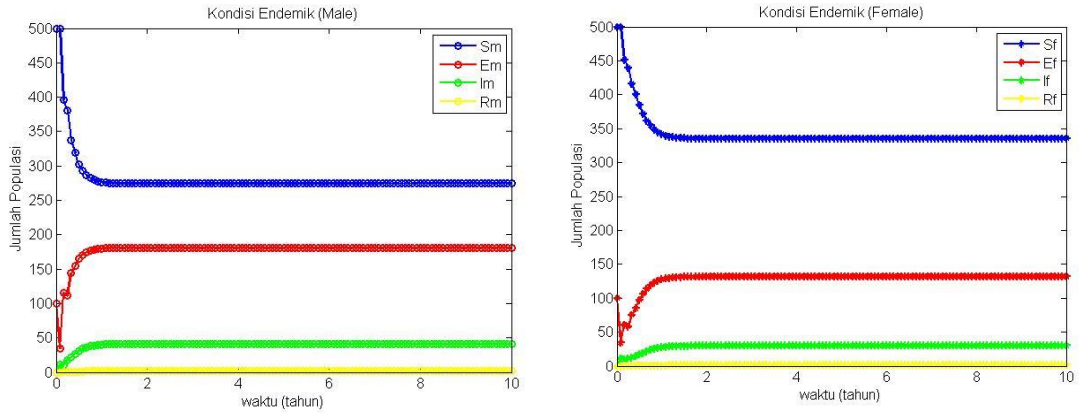
Basic Reproductive Number (R0) : 0.57214
```

because $R_0 < 1$, then the rodent population no outbreak and the system (10) is said locally asymptotically stable .
When endemic conditions, using the parameters in Table 3,

Table 3. Parameter Value Endemic SEIR Deterministic Model

Parameter	Nilai
K	1000 rodent
b	2 rodent
β_m	0.04
β	0.01
γ_m	0.05
γ_f	0.05
δ	0.25

Obtained graph depicting the endemic condition in the Figure 3,



(a) (b)

Figure 3 . Graphs individual males (a) and female (b) in a state of endemic

In Figure 3 (a) and (b) shows that the number of individuals who are in a vulnerable state (S) in the time interval $0 \leq t \leq 10$ will decrease , and the condition of latent/ hidden (E) that has previously been initialized with an initial value $E_m = E_f = 100$ in the time interval $0 \leq t \leq 10$, due to the possibility of infection rate (δ) of the population has a high enough value, thus resulting in the existence of individuals who are infected with the disease. This leads to the occurrence of endemic conditions, in other words an outbreak in the

population during the time span t. Data obtained from the analysis of the value of R_0,

```
Basic Reproductive Number (R0) : 10.463
```

because $R_0 > 1$, then the rodent population outbreak and the system (10) is said to be unstable.

To cope with so many outbreaks of disease spread to all individuals who are in the population, usually using vaccination to an individual in accordance with the level of need in this population.

4.2. Hantavirus disease and R_0

Results of analysis for determining the basic reproductive number (R_0) the system (10), using Next Generation Matrix (NGM), which is R_0 is defined as the value of the largest eigenvalues or spectral radius of the matrix *Q*. And the elements of the matrix *Q* is itself an element related to the state of the infected , the epidemic SEIR model of the state of infection is $X_0 = \{E_m, E_f, I_m, I_f\}$. For example use cases of epidemic SEIR models, the deterministic model of the disease Hantavirus SEIR, which will further analyze mathematical models of the Hantavirus epidemic itself, which is divided into two gender in a closed population, namely male and female.

From the analysis of the system (10), obtained for a R_0 value rodent population, namely

$$R_0 = \frac{K}{4}\left(\left(\frac{\beta_m \delta}{b_\delta b_{\gamma m}} + \frac{\beta\delta}{b_\delta b_{\gamma f}}\right) + \frac{\delta\sqrt{(\beta_m b_{\gamma f} - \beta b_{\gamma m})^2 - 4\beta(\beta_m - \beta) b_{\gamma m} b_{\gamma f}}}{b_\delta b_{\gamma m b_{\gamma f}}}\right)$$

where R_0 parameter has a positive value .

R_0 value is used to see how many individuals are infected in a population that is dependent on the value of R_0, using the parameters in Table 4,

Table. 4. Parameter Value Analysis R_0

Parameter	Value
K	1000 rodent
b	2 rodent
β_m	0.04
β	0.004
γ_m	0.005
γ_f	0.005
δ	0.02

graph depicting the number of infected individuals R_0,

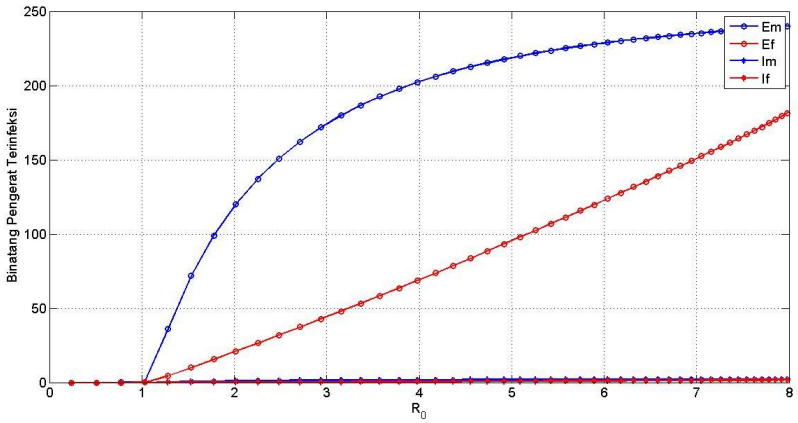


Figure 4. Graph of the number individu in Exposed and Infected to R_0

In Figure 4 it can be seen that the number of male individuals in a latent condition (E) is greater than the number of female individuals in the condition (E), as has been discussed earlier that this is the case because the contact rate (β) male individuals at a rate greater compare to contact (β) individual female. The greater the value of R_0 major impact on the number of individuals who enter into a state of E. If state E is high enough, then there are chances of infected individuals, in other words if there is not likely going to happen prevention of disease in the population .

From Figure 4, it can be seen the number of infected individuals at each value of R_0. The greater the value of R_0 , the greater the potential of individuals

in a population exists in a latent state (E) and has a chance to get in on the infected condition *(I)*. In epidemic models Seir when a population is assumed for all individuals in it are in a vulnerable condition (S), then the individual is when the body resistance is weak then he is in a latent condition (E), in other words, the individual is exposed to an infection, but infection the body has not spread , the factors supporting the spread of a disease that is a weak immune system and environmental factors, if the individuals who are in a latent condition (E) the disease has spread, then the individual is in a state of infected *(I)*, when given the vaccination in individuals infected, then with a good immune system and vaccination according to the need, in the time interval t such individuals will be in a state of recovery *(R)*.

In accordance with the analysis that has been discussed previously, that a population will not be an outbreak if $R_0 < 1$ and a population of disease outbreaks will occur if $R_0 > 1$. To measure the potential of a population in a state of disease-free equilibrium or the endemic state, the parameters that support was instrumental in spreading a disease or not, one of the parameters that influence the spread of the disease among individuals contact rate parameter (β). For the case of this Hantavirus disease, the parameter (β) depends on the gender of the population, due to gender Hantavirus disease is divided into two gender, namely male and female rodents. Previously been presented that the level of contact rodent aggressive male larger than the female, so that $\beta_m \gg \beta > 0$.

The influence of parameter β as the rate of contact between individu shown in Figure 5,

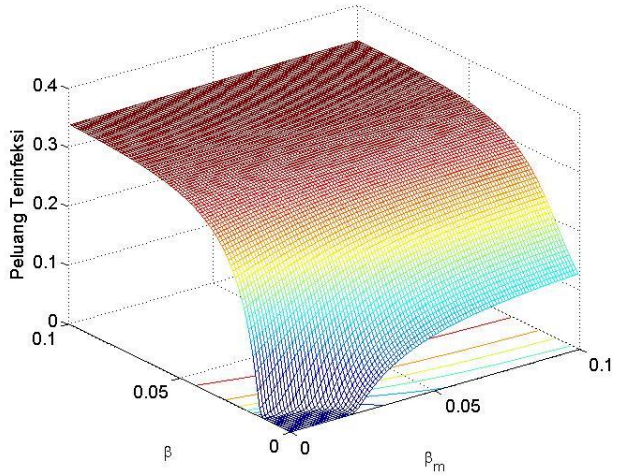


Figure 5. Graph of Parameter β_m and β to Infection Occurence Opportunities

From Figure 5 it can be seen that the value of the parameter β plays an important role for the occurrence of the disease infected opportunities in a population, the smaller the value of β, the less the possibility of infection in a population.

5 . Conclusion

Epidemic SEIR model is a mathematical model that describes the spread of a disease that is in four conditions, namely susceptible (*S*), latent (*E*), infected (*I*), and recovered (*R*). To determine the spread of a disease in a population is determined by R_0 . One way to determine the value R_0 using NGM. NGM method is a method that relies on the infected compartment, for the case of SEIR who become infected compartment is $X_0 = \{E, I\}$.

Hantavirus is a disease from rodents, commonly called rat. Hantavirus be fatal if a person infected with this virus, a disease caused by an infection of the lungs (for the Americas and Asia) and kidney (for Europe). Mode of transmission can be through air, food, or objects that have been contaminated with the virus. In the rodent population itself does not affect anything. But if more and more infected rodents, it is probable that the virus will spread to the human population. Hantavirus in this model, gender differences in rodents is very important, because the behavior of male is more aggressive than the female. By dividing the system (10) into two compartments, namely $X_0 = \{E, I\}$ and $X_1 = \{S, R\}$, and to determine the value of R_0 using the NGM obtained,

$$R_0 = \frac{K}{4}\left(\left(\frac{\beta_m \delta}{b_\delta b_{\gamma m}} + \frac{\beta\delta}{b_\delta b_{\gamma f}}\right) + \frac{\delta\sqrt{(\beta_m b_{\gamma f} - \beta b_{\gamma_m})^2 - 4\beta(\beta_m - \beta) b_{\gamma_m} b_{\gamma f}}}{b_\delta b_{\gamma_m} b_{\gamma_f}}\right)$$

Spread of a disease depends on the size of the resulting R_0 value, the greater R_0 value the greater the chances of a disease outbreak in a population, the contrary, the smaller R_0 value, then the chances are very small to outbreaks of disease in a population.

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