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MODELLING INFECTIOUS DISEASE IN DYNAMIC NETWORKS CONSIDERING VACCINE

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ABSTRACT

The model of spread of infectious diseases is research that must be done continuously as the development of infectious diseases. Although medical measures can reduce the consequences of infectious diseases, preventing the spread of infectious diseases is the main action that must be taken. Vaccination is a method commonly used to control the spread of communicable diseases today. This study aims to develop an epidemic model that warts proposed by Kermark and Mc Kendrick in 1927 in the form of S, I and R. compartments. The method used was an experiment by adding V compartment which is a vaccination. The results show that the point remains disease free to become asymptotically stable when the number of basic reproduction is less than one which means that the disease will not spread in the population and eventually the disease will disappear from the population. Whereas the endemic point will be asymptotically stable when the number of basic reproduction is more than one which means that the disease Exists. This study can be concluded that based on the stability analysis shows that the vaccination process is entirely dependent on the basic reproduction rate.

Keywords: Modeling, Infectious Diseases, Dynamic Networks

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LITERATURE REVIEW

2.1 Several Epidemic Models

An epidemic is a pestilence of a disease in a short time. A diseases is called endemic if the disease persists in a population. So the epidemic model is used for describe fast outbreaks that occur in a short amount of time, whereas endemic models are used to study disease over a longer period of time long, as long as there are additions that are vulnerable due to abnormalities or healing from immunity, while the spread of infectious diseases involves not only disease-related factors, for example infectious agents, modes of transmission, latent period, transmission period, vulnerability and endurance, but also a factor social, cultural, demographic, economic and geographic.

2.1. a S I Model

The simplest mathematical model in epidemiology is known as the Ross Epidemic Model or SI, which was developed in 1911. On SI model, the population is divided into two parts (subgroups) namely population susceptible (susceptible = S) to disease transmission and infected population (infectious = I) to a disease. The assumptions used in this model is: that vulnerable populations remain in close contact with the population infected all the time $t > 0$, the total population is constant at N with $N = (S(t) + I(t))$ where S and I are mutually exclusive and mixing homogeneous population so that each individual has the same opportunity occurrence of infection. If 3> 0 is the average (proportion) constant of the subgroup contact that results in a new infection the time unity of the situation originally namely vulnerable (or also called the transmission rate constant).

2.1 b. SIS Epidemic Model

The assumptions used in this model are: that the population is vulnerable keep in close contact with the infected population all the time $t > 0$, the total population is constant as N where $N = (S(t) + I(t))$ where S and I are mutually exclusive and the population is mixed homogeneously so that each individuals have the same chance of infection. But the amount or the size of the infected population can decrease with migration Infected individuals change status to be vulnerable again to unity of time in proportion to a. Then the SIS model can be constructed as:

$$\frac{dS}{dt} = -\beta SI + \sigma I$$
$$\frac{dI}{dt} = -\beta SI - \sigma I \qquad (2.1)$$

with initial condition $S(0) = S_0$ dan $I(0) = I_0$

2.1. c.SIR Epidemic Model

The SIR model is the basis for most of the still deterministic models used to date. This model was first developed by Kermack and McKendrik in 1927. The SIR model has structure and assumptions the same as the SI model, the extension is that in the SIR model it is possible for infected populations / members of the community to recover as well the total population of N is divided into three interrelated subgroups exclusive; vulnerable subgroups (Susceptibles) symbolized $S(t)$, subgroups in infected / infected (symbolized) symbolized $I(t)$ and moved subgroup (Removed) symbolized $R(t)$.

$R(t)$ Represents individuals who died of illness, recovering from infection and now have permanent immunity or individual who already exiled from the rest of the population. So in this last subgroup, no again contributing to the spread of disease / epidemic. But still maintained as a member of a total population of N , although there is a possibility that some of them have died. In this model it is assumed also that individuals who enter $R(t)$ cannot be re-infected. Assuming that is a constant proportion of the state of the infected individual then it is removed per unit time. Then the differential equation model represents the level changes in populations that are vulnerable to a constant unity of time as in the SI model as in the equation above. This is because there is no direct transfer from individuals from subgroups vulnerable to moving subgroups. However, the differential equation model of the infected subgroup needs to be modified to take into account the number of individuals infected and recovered.

So that the differential equation model the complete SIR model is:

$$\frac{dS}{dt} = \beta SI$$
$$\frac{dI}{dt} = \beta SI - \sigma I$$
$$\frac{dR}{dt} = \sigma I$$

2.1.d. Model SVIR and Continue Vaccination Strategy (CVS)

Alexander et al. (2004) and Shim (2006) use a model SVIR to study the dynamics model of influenza (flu) disease by vaccination. All of the continuous models above assume that the individual gets immunity after being vaccinated and the time for the individual to get immunity or the time to complete the vaccination process is ignored. In fact as soon as a vulnerable individual starts the vaccination process, that individual will different from vulnerable individuals but vaccinated individuals must be distinguish it from individuals who recover because they have acquired immunity from it vaccinated or immune after recovering from the disease.

Xianning et al. (2007) introduce a continuous vaccination strategy in the SVIR epidemic model. The continuous vaccination strategy in the SVIR model is mathematically is the addition of V compartment to the SIR base model, where V is new groups that are divided from group S and show the density of individual who has started the vaccination process. Individuals in V need time to get the level of protection against disease during the vaccination process and will move to R when getting immunity.

2.2 Fixed Point

For example, given a system of DE (differential equations) as follows

$x = f(x), x\,E\ !R^n$

The point x is called a fixed point or a critical point or also called an equilibrium point if $f(x) = 0$. (Tu 1994)

2.3. Stable Fixed Points

Suppose x is a fixed point at system of DE and $x(t)$ is a solution with an initial value $x(0) = xo$ with $xo = x$. Point x is said to remain stable, if for each $e > 0$, there is $r > 0$, such that $|\, xo - x\,| < r$, then the solution $x(t) = x$ meet $|\, x(t) - x\,| < e$ for each $t > 0$ (Vershulst 1990)

2.4. Local Asymptotic Stable Fixed Point

Point x is said to be asymptotically stable if point x is stable and is present $e > 0$ such that $||\, x - xo\,|| < e$ then lim $x(t) = x$, where $xo = x(0)$.

(Szidarovzky & Bahill 1998)

2.5 Eigen Value and Eigen Vector

Let A be a matrix $n \times n$, a nonzero vector x in Rn is called eigenvector of A , if a scalar A called the eigenvalue of A applies:

$Ax = Ax$

The vector x is called the eigenvector which corresponds to the eigenvalue A which is of size $n \times n$, so the equation $Ax = Ax$ can be written as follows:

$(A - AI)x = 0$

where I is the identity matrix. The equation $Ax = Ax$ has a solution zero if and only if $\det(A - XI) = 0$ is called the equation characteristics. (Anton 1995)

2.6 Fixed Point Stability Analysis

Stability analysis for each fixed point is different for each eigenvalue, namely:

1. The system $x = Ax$ is stable if and only if each eigenvalue of A the real part is negative.
2. System $x = Ax$ is unstable if and only if at least one value the eigenvalue of A in the real part is positive.

(Borrelli & Coleman 1998)

2.7 Routh Hurwitz Condition

For example $a_1, a_2, a_3, \ldots, a_k$ real numbers, $a_j = 0$ if $j > k$. All eigenvalues of the characteristic equation $p(x) = X_k + a_1 X(k-1) + a_x X(-2) + \ldots + a_k = 0$ has a negative real part if the determinant of the H_j matrix is positive. Furthermore, Hurwitz Hj's matrix is defined as follows

$$H_j = \begin{pmatrix} a_1 & 1 & 0 & 0 & \ldots & 0 \\ a_3 & a_2 & a_1 & 1 & \ldots & 0 \\ a_5 & a_4 & a_3 & a_2 & \ldots & 0 \\ \vdots & \vdots & \vdots & \vdots & \ldots & \vdots \\ a_{2j-1} & a_{2j-2} & a_{2j-3} & a_{2j-4} & \ldots & a_j \end{pmatrix}$$

all eigenvalues of the characteristic equation have a real part which is negative (fixed point x stable) if and only if the determinants of all matrices Positive Hurwitz, namely: $H_j > 0$, for $j = 1, 2, \ldots, k$ so according to conditions Routh-Hurwitz for a k , $k = 2, 3, 4$ states that the point remains x stable if and only if (for $k = 2, 3, 4$),

1. $k = 2, a_1 > 0, a_2 > 0$
2. $k = 3, a_1 > 0, a_3 > 0, a_1 a_2 > a_3$

3. $k = 4, a_1 > 0, a_3 > 0, a_4 > 0, a_1 a_2 a_3 > a_1 a_4$

Edelstein-Keshet 1998

2.8 Basic Reproductive Number (R_0)

Basic Reproductive Numbers (R0) is the average number of vulnerable individuals infected directly by another infected individual if the infected individual enters the population that is still entirely susceptible.

The conditions that will arise are one of the following possibilities:

1. If $R_0 < 1$, then the disease will disappear.

2. If $R_0 = 1$, then the disease will persist (endemic).

3. If $R_0 > 1$, then the disease will increase to an outbreak.

(Blyuss & Kyrychko 2005)

METHODOLOGY

3.1. Research Methods

Methods used in this study as follows:

1. Determine the assumptions and define the parameters used in SIR model assuming vaccination.
2. Draw a transfer diagram to form a mathematical model. In-transfer functions to form a system of differential equations.
3. Complete the system of differential equations.
4. Finding the equilibrium point of the model. The equilibrium point to be searched is disease-free equilibrium point and disease endemic equilibrium point.
5. Analyzing the stability of the equilibrium point.
6. Interpreting the results obtained to determine the number of individuals who must be vaccinated so that there is no endemic disease
7. Simulate the model by defining parameter values and illustrating it using MATLAB software.

This section briefly presents the topology of the disease infection model which is based on the transmission route on SIR which will be developed later with the addition of compartment V. Transmission route of disease infection can be described in the form of a compartment pattern as shown in the following:

RESULT

4.1 Basic Reproductive Numbers (R_0)

R_0 construction in SIRS compartment model with closed population, that is:

$$\frac{dI}{dt} = -\beta SI + \sigma I$$

Growth of infection will occur if $\beta SI \alpha I > 0$ or $\alpha I \beta S > \alpha$ with $S(0) = N$, then $\beta N / \alpha > 1$. Then $R_0 = \beta N / a\alpha$

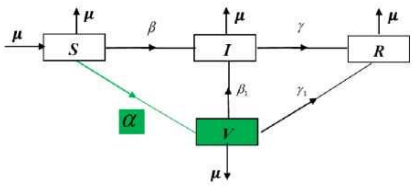
4.2 Social Network

The development of a probability networking model is work prove and parameterize complicated systematics in the structure of the network Therefore, it starts with several notations and some related definitions. The main basic concept in talks about social networks is graph and directed graph. The following descriptions are based on Wasserman and Faust (1994) and Bollobas (1998).

4.3 Model of Infectious Diseases

Xianning et al. (2007) introduce a continuous vaccination strategy in SVIR epidemic model. The continuous vaccination strategy in the SVIR model mathematically is the addition of compartment V to the basic SIR model, where V is a new group that is divided from group S and shows to- and individuals who have started the vaccination process. Individuals in V require time to get the level of protection against disease during the vaccination process and will move to R when getting immunity. Therefore, based on the SIR model compartment transfer diagram it can be illustrated compartment model transfer diagram as follows assuming:

1. α is the rate at which vulnerable individuals are moved into the process vaccination.
2. 7i is the average rate (1 / YI is the average time) for individuals who are undergoing a vaccination process to obtain immunity
3. Before gaining immunity, individuals still have possibilities infected with a transmission rate of 3n Assumed 31 is smaller than because individuals who get vaccinated may have immunity partial during the vaccination process.



4.5. Determination of Fixed Point

The assumptions above can be written in the form of the following differential equation:

$$\frac{dS}{dt} = \mu - \mu S - \beta SI - \alpha S$$
$$\frac{dV}{dt} = \alpha S - \beta_1 VI - \gamma_1 V - \mu N$$
$$\frac{dI}{dt} = \beta SI + \beta_1 VI - \gamma_1 - \mu_1$$
$$\frac{dR}{dt} = \gamma_1 V + \gamma I - \mu R$$

4.6. Stability Analysis

Fixed point analysis on the system of differential equations is often used to determine a solution that does not change with time (constant solution). The fixed point of the differential equation above will be obtained by specify $d \mid = 0, dV = 0$. $dt = 0$ And $dR = 0$ dR = 0. Because the equation dS, dV, ddt is not depending on the dR dR equation, it can be reduced to:

$$\frac{dS}{dt} = \mu - \mu S - \beta SI - \alpha S$$
$$\frac{dV}{dt} = \alpha S - \beta_1 VI - \gamma_1 V - \mu N$$
$$\frac{dI}{dt} = \beta SI + \beta_1 VI - \gamma_1 - \mu_1$$

So we will get

$$\frac{dS}{dt} = \mu - \mu S - \beta SI - \alpha S = 0$$
$$\frac{dV}{dt} = \alpha S - \mu S - \beta_1 VI - \gamma_1 V - \mu V = 0$$
$$\frac{dI}{dt} = \beta SI + \beta_1 VI - \gamma I - \mu I = 0$$

By completing simultaneously, two points will be obtained fixed ie disease-free fixed point and endemic fixed point

1. The point remains disease free

$$E_0 = (S_0, V_0, I_0) = \left(\frac{\mu}{\mu + \alpha}, \frac{\alpha\mu}{\mu + \gamma_1 + \mu + \alpha}, 0 \right)$$

2. Fixed point Endemic

$$S_+ = \frac{\mu}{\mu + \alpha + \beta I_+}, V_+ = \frac{\alpha S_+}{\mu + \gamma_1 + \beta_1 I_+} = \frac{\alpha\mu}{\mu + \alpha + \beta I_+ \ \mu + \gamma_1 + \beta_1 I_+}$$

And I_+ is the positive root of $g(I) = A_1 I^2 + A_2 I + A_3$ with :

$$A_1 = (\mu + \gamma)\beta\beta_1$$
$$A_2 = (\mu + \gamma)(\mu + \alpha)\beta_1 + (\mu + \gamma_1)\beta - \mu\beta\beta_1$$
$$A_3 = (\mu + \gamma)(\mu + \alpha)(\mu + \gamma_1) - \beta\mu(\mu + \gamma_1) + \beta_1\alpha\mu$$

4.7. Stability of Endemic Fixed Point

Let the differential equation is denoted as follows

$$f(S,V,I) = \mu - \mu S - \beta SI - \alpha S$$
$$g(S,V,I) = \alpha S - \beta_1 VI - \gamma_1 V - \mu V$$
$$h(S,V,I) = \beta SI + \beta_1 VI - \gamma I - \mu$$

By linearized the equations above we will get the Jacobi matrix as follows:

$$J(S,V,I) = \begin{bmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial V} & \frac{\partial f}{\partial I} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial V} & \frac{\partial g}{\partial I} \\ \frac{\partial h}{\partial S} & \frac{\partial h}{\partial V} & \frac{\partial h}{\partial I} \end{bmatrix}$$

$$= \begin{bmatrix} -\mu - \beta I - \alpha & 0 & -\beta S \\ \alpha & -\beta_1 I - \gamma_1 - \mu & -\beta_1 V \\ \beta I & \beta_1 I & \beta S + \beta_1 V - \gamma - \mu \end{bmatrix}$$

4.8 Transmition Model at Dynamic Network

Linearized at a fixed point $E+$ will produce the Jacobi matrix as the following:

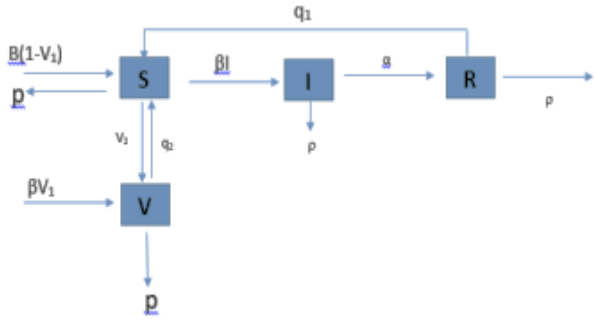
$$JE_+ = \begin{bmatrix} -\mu - \alpha - \beta I_+ & 0 & -\beta S_+ \\ \alpha & -\gamma - \mu - \beta_1 I_+ & -\beta_1 V_+ \\ \beta I_+ & \beta_1 I_+ & \beta S_+ + \beta_1 V_+ - \gamma - \mu \end{bmatrix}$$

$$= \begin{bmatrix} -\frac{\mu}{S_+} & 0 & -\beta S_+ \\ \alpha & -\frac{\alpha S_+}{V_+} & -\beta_1 V_+ \\ \beta I_+ & \beta_1 I_+ & 0 \end{bmatrix}$$

4.8.3 Mean-Field Modification Model

Suppose a SIR model in the presence of vaccination. In this model the birth rate B and the death rate p are included. Suppose there are 2 types vaccination v_1 of vaccinated babies and v_2 vaccination rates of individuals who are susceptible (susceptible). It is also assumed that protection against infection is not lifetime. Recovered individuals can be vulnerable again at the rate of q_1 someone vaccinated at q_2 .

The compartment model can be scheduled as a schedule as follows:



$$\frac{dS}{dt} = \beta(1 - VI) - \beta SI - V_2 S + q_1 R + q_2 V - pS$$
$$\frac{dI}{dt} = \beta SI - \alpha I - pI$$
$$\frac{dR}{dt} = \alpha I - q_1 R - pR$$
$$\frac{dv}{dt} = \beta VI + V_2 S - q_2 V - pV$$

ρ = infection rate

α = the rate of recovery from infection

p = death rate

β = birth rate

V_1 = percentage of vaccinated babies

V_2 = the rate of vaccination of vulnerable individuals

q_1 = conversion rate from cured

q_2 = the conversion rate from vaccinated becomes vulnerable

CONCLUSION

Vaccination strategy mathematical models obtained two fixed points, namely the point remains disease free and the point remains endemic. From the stability analysis, the dynamics of the Vaccination Strategy are entirely dependent on reproduction numbers basic. When the basic reproduction number is less than one, the fixed point disease free will be asymptotically stable which means that the disease will not spread in the population or eventually the disease will disappear from the population. If the basic reproduction number is more than one, the dot remains endemic will be asymptotically stable which means that the disease will persist and spread in the population.

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