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The Completion of Positive Contact Distribution Models in Transmission Distribution of Viruses in Two Different Locations

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Abstract. This paper discusses the mathematical model of the spread of viruses between locations by examining population models of one species in two different locations. Each location has the same subpopulation but has a different number of species.This model assumes that H1N1 virus transmission can occur due to direct interaction with infected individuals and spatial movements in a location by each individual in the Susceptible and Expose subpopulations. Local and global movements are not only carried out by Susceptible and Expose but also by Infected subpopulations. This mathematical model is constructed based on the compartment model, then reduced, so that a positive solution can be obtained. If the growth rate of population (mortality rate minus the birth rate) is greater or equal to the constant of the individual movement proportion, then positive solution are fulfilled.

1. Introduction

The spread of diseases caused by virus attacks is a very serious threat in the field of health and social and community fields. Mathematical modeling of the spread of viruses has been built by many previous researchers. Mathematical models are in the form of ordinary differential equations by observing the spread of viruses in pigs which are expected to occur the coalition between H1N1 and H5N1 viruses [1]. Furthermore, Hyman [2] has constracted a model of the spread of geographic of the H1N1 virus for 59 cities around the world, and the results of analysis indicate that the spread of the virus in other cities correlates with the center of the spread of the virus. Most of the coastal areas in Southeast Sulawesi are close to forest areas where wild boar habitat. Therefore, this causes the spread of the H1N1 virus in pigs. Thus, people who living in coastal areas are also vulnerable to contracting the H1N1 virus. Based on these reasons, it is necessary to study mathematical modeling for the distribution of the H1N1 virus. The results of the model analysis became new knowledge for coastal communities to maintain their healthy from the dangers of the spread of the H1N1 virus.

[1], [2] has constructed a model of transmission of disease spread in two locations with the same strain and emphasized more on the infected distribution model with linear transmission functions as a form of disease spread. Furthermore, constracts a model for the spread of disease in 2 locations with different strains at each location, for example the spread of the avian influenza H5N1 globally that

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occurs in Indonesia has the potential to create a coalition with human viruses. The constraction of mathematical models on each problem.

Blyuss has constructed a mathematical model for the spread of viruses that have an incubation period in the Expose subpopulation. In this problem, the population is only in one location, namely $\Omega_1$with the size of L_1which emphasizes the spatial movements of individuals in one location or between locations. In these locations are divided into several subpopulations including Suspectible (S) which states individuals who are susceptible to viruses [1]. Expose (E) states infection incubation masses, individuals who are infected but have not been able to transmit the virus to other individuals. Infected (I) states that individuals are infected and can transmit the virus to other individuals, in this case Suspectible and Expose [1], [2], [3].

[4], [5] has assume that virus transmission can occur after the interaction or direct contact with infected individuals, and spatial movements within a location can be carried out by each individual in the subpopulation, while the movement between locations is only done by individuals Susceptible and Expose subpopulations. But in this paper, the movement between locations is not only done by individuals in Susceptible and Expose subpopulations, but individuals who are in the Infected subpopulation can also move from location 1 to location 2 or can be otherwisex

2. Methods

The method in this paper consists of several stages, namely the literature study, constructing a mathematical model based on the compartment model, and obtaining the solution of the model has been constructed.

The steps in solving the problems in this study are as follows.

2.1 Stage of Literature Study

At this stage identification of problems is carried out and uses several references that support research. In-depth understanding of the problem of functional analysis, model production and completion of the model unity.

2.2 Stage of Model Construction and Model Reduction

After conducting a literature study from several references, a transmission model for the spread of disease was formed in two locations and then reduced the model of the spread of viruses that had been formed or constructed.

2.3 Model Completion Phase

At this stage, the model that has been constructed from the differential equation then analyzes the model to obtain a positive solution [2], [6].

2.4 Stage of Conclusion

At this stage the conclusions are drawn from the model of the spread of contact distribution diseases in the transmission of the spread of the virus in two different locations.

3. Results and Discussions

The function of spatial density can be expressed as $S_1(x,t)$, $E_1(x,t)$, $I_1(x,t)$.. While the population density function can be expressed as $N_1(x,t)$. The parameters that influence the model are as follows [1], [2], [3].

β^* : transmission rate
d : death rate
b : birth rate
δ : natural healing rate
γ : the transmission rate from exposure becomes infected
$K(x,t)$: Kernel density function
S_1 : humans who are susceptible to viruses
E_1 : humans who have been infected by a virus but have not been able to transmit it to individuals around it. In this case it is in an incubation mass.

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I_1 : humans are infected by a virus and can transmit the virus.

3.1 Virus Spread Model in Location I

The following mathematical model is a mathematical system model built by [2] where the model is a development of a mathematical system model that has been built by [1].

$$\frac{\partial S_1}{\partial t} = D_1^S \frac{\partial^2 S_1}{\partial x^2} - \beta^* S_1 I_1 - dS_1 + bS_1 + \delta E_1 + \delta I_1 + \int_{\Omega 2} S_2 K(x-y)dy - S_1 \int_{\Omega 1} K(y-x)dx$$

(1)

$$\frac{\partial E_1}{\partial t} = D_1^E \frac{\partial^2 E_1}{\partial x^2} + \beta^* S_1 I_1 - \gamma E_1 - dE_1 - bE_1 + \int_{\Omega 2} E_2 K(x-y)dy - E_1 \int_{\Omega 1} K(y-x)dx - \delta E_1$$

(2)

$$\frac{\partial I_1}{\partial t} = D_1^I \frac{\partial^2 I_1}{\partial x^2} + \gamma E_1 - dI_1 - bI_1 - \delta I_1 + \int_{\Omega 2} I_2 K(x-y)dy - I_1 \int_{\Omega 1} K(y-x)dx$$

(3)

With the initial conditions

$$S_1(x,0) = S_{10} = S_1(0),\ I_1(x,0) = I_{10} = I_1(0),\ E_1(x,0) = E_{10} = E_1(0).$$

(4)

Boundary conditions

$$\frac{\partial S_1}{\partial x}(0) = \frac{\partial S_1}{\partial x}(L) = 0,\ \frac{\partial E_1}{\partial x}(0) = \frac{\partial E_1}{\partial x}(L) = 0,\ \text{and}\ \frac{\partial I_1}{\partial x}(0) = \frac{\partial I_1}{\partial x}(L) = 0$$

(5)

Suppose the population in location 1 is $N_1(t)$ or $N_1(x_1,t)$, then the total population can be determined at location 1 is

$$N_1(t) = S_1(t) + E_1(t) + I_1(t)$$

(6)

or can be written

$$N_1(x_1,t) = S_1(x_1,t) + E_1(x_1,t) + I_1(x_1,t)$$

(7)

In equations (1), (2) and (3) above $D_2^S \frac{\partial^2 S_2}{\partial x^2}$, $D_2^E \frac{\partial^2 E_2}{\partial x^2}$, and $D_2^E \frac{\partial^2 I_2}{\partial x^2}$ is local diffusion. While global diffusion is stated as follows

$$\int_{\Omega_2} S_2 K(x-y)dy - \int_{\Omega_1} S_1 K(y-x)dx$$

(8)

$$\int_{\Omega_2} E_2 K(x-y)dy - \int_{\Omega_1} E_1 K(y-x)dx$$

(9)

$$\int_{\Omega_2} I_2 K(x-y)dy - \int_{\Omega_1} I_1 K(y-x)dx$$

(10)

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From equations (8), (9) and (10) above, in terms of positive terms each indicates an individual movement from location 2 to location 1, so that there is an addition to location 1. The tribe is negative indicates the existence of individual transfers from location 1 out to location 2, so that the impact of a reduction in location 1.

3.2 Model Analysis to Obtain Positive Resolution

Each individual in the Susceptible, Expose and Infected subpopulations can make changes between locations. This is made clear by [1] which states that location Ω_1 and location Ω_2 are domains that are limited to $[0, L]$, so that individual movements in subpopulations that move on their own location or that move between locations depend on the status of the subpopulation.

This status has an impact by utilizing the Kernel density function $K(x,t)$. Kernel density functions are expressed as Laplace functions, namely:

$$K(x,t) = e^{-x}$$

(11)

with $S_1(x,t)$ stating the movement in location 1, then obtained:

$$\int_{\Omega_1} S_1(x,t) K(y-x) dx = \int_{\Omega_1} S_1(x,t)\, e^{-x} dx$$

(12)

Equation (12) is solved using partial integrals, with general rules as follows.

$$\int_{\Omega_1} u \quad dv = uv \int_{\Omega_1} v \quad du$$

(13)

Example:

$$u = S_1(x,t); \quad dv = e^{-x}; \quad v = -e^{-x}; \quad du = \frac{\partial S_1(x,t)}{\partial t} dx$$

From the example obtained as follows:

$$\int_{\Omega_1} S_1(x,t)\, e^{-x} dx = -S_1(x,t)\, e^{-x} \Big|_0^{L_1} + \int_{\Omega_1} e^{-x} \frac{\partial S_1(x,t)}{\partial t}\, dx$$

$$= -S_1(L_1,t)\, e^{-L_1} + S_1(0,t) + \int_{\Omega_1} e^{-x} \frac{\partial S_1(x,t)}{\partial t}\, dx$$

So get it,

$$\int_{\Omega_1} S_1(x,t)\, e^{-x} dx = -S_1(L_1,t)\, e^{-L_1} + S_1(0,t)$$

(14)

Because

$$-S_1(L_1,t)\, e^{-L_1} + S_1(0,t) > 0$$

then,

$$e^{-L_1} < \frac{S_1(0,t)}{S_1(L_1,t)}$$

and

$$S_1(L_1,t) < S_1(0,t) \qquad \forall t \in [0,\infty)$$

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Suppose $\frac{S_1(0,t)}{S_1(L_1,t)} = k$ is a rational then $e^{-L_1} < k$ which is a function of the individual movement of subpopulations both localized and between locations because $0 < K(x,t) < 1, \quad \forall t \in [0,\infty)$ and $\forall x \in \Omega$.

Suppose the constant proportions of individual displacement globally are expressed as μ. It is assumed that the symptoms of infection can inhibit infected individual mobility of $0 \le \sigma \le 1$ while Suspectible and Exposed Individuals can move to another location with the same level of mobility.

Other assumptions:

1. $\int_{\Omega} K(x,t) = 1$
2. $\int_{\Omega_2} K(x-y) S_2(y,t)dy = \mu S_1(x,t), \quad \forall x \in \Omega_1, \quad y \in \Omega_2$ and $0 < \mu < 1$ i.e. declare the shift between locations $S_2(y,t)$ from the position $y \in \Omega_2$ to the position $x \in \Omega_1$ then the individual $S_2(y,t)$ will be part $S_1(x,t)$ at location 1.
   $S_1(x,t)\int_{\Omega_1} K(y-x)dx = \mu S_2(y,t), \quad \forall x \in \Omega_1, \quad y \in \Omega_2$ and $0 < \mu < 1$ which states the movement between locations $S_1(x,t)$ from position $x \in \Omega_1$ to position $y \in \Omega_2$ then the individual $S_1(x,t)$ will be part $S_2(y,t)$ at location 2.
3. $\int_{\Omega_2} K(x-y) E_2(y,t)dy = \mu E_1(x,t), \quad \forall x \in \Omega_1, \quad y \in \Omega_2$ and $0 < \mu < 1$ that is declare the shift between locations $E_2(y,t)$ from position $y \in \Omega_2$ to position $x \in \Omega_1$ then individual $E_2(y,t)$ will be part $E_2(y,t)$ at location 1.
   $E_1(x,t)\int_{\Omega_1} K(y-x)dx = \mu E_2(y,t), \quad \forall x \in \Omega_1, \quad y \in \Omega_2$ and $0 < \mu < 1$ which is the movement between locations $E_1(x,t)$ from position $x \in \Omega_1$ to position $y \in \Omega_2$ then individual $E_1(x,t)$ will be part $E_2(y,t)$ at location 2.
4. $\int_{\Omega_2} K(x-y) I_2(y,t)dy = \mu I_1(x,t), \quad \forall x \in \Omega_1, \quad y \in \Omega_2$ and $0 < \mu < 1$ that is declare the shift between locations $I_2(y,t)$ from the position $y \in \Omega_2$ to the position $x \in \Omega_1$ then the individual $I_2(y,t)$ will be part $I_1(x,t)$ at location 1.
   $I_1(x,t)\int_{\Omega_1} K(y-x)dx = \mu I_2(y,t), \quad \forall x \in \Omega_1, \quad y \in \Omega_2$ and $0 < \mu < 1$ which is the movement between locations $I_1(x,t)$ from position $x \in \Omega_1$ to position $y \in \Omega_2$ then individual $I_1(x,t)$ will be part $I_2(y,t)$ at location 2.

Thus after observing the assumptions that exist, the system models in equations (1), (2) and (3) can be reduced to

$$\frac{\partial S_1}{\partial t} = D_1^S \frac{\partial^2 S_1}{\partial x^2} - \beta * S_1 I_1 - dS_1 + bS_1 + \delta E_1 + \delta I_1 - \mu S_1 + \mu S_2$$

(15)

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$$\frac{\partial E_1}{\partial t} = D_1^E \frac{\partial^2 E_1}{\partial x^2} + \beta * S_1 I_1 - \gamma E_1 - dE_1 - bE_1 - \mu E_1 + \mu E_2 - \delta E_1$$
(16)

$$\frac{\partial I_1}{\partial t} = D_1^I \frac{\partial^2 I_1}{\partial x^2} - \gamma E_1 - dI_1 - bI_1 - \delta I_1 - \mu \sigma I_1 + \mu \sigma I_2$$
(17)

The total population in location 1, has been shown in equation (6), that is

$$N_1(t) = S_1(t) + E_1(t) + I_1(t) = \int_{\Omega_1} S_1(x,t)dx + \int_{\Omega_1} E_1(x,t)dx + \int_{\Omega_1} I_1(x,t)dx$$

So that it is obtained,

$$\begin{aligned}
\frac{dN_1(t)}{dt} &= \frac{\partial}{\partial t}\left[\int_{\Omega_1} S_1(x,t)dx + \int_{\Omega_1} E_1(x,t)dx + \int_{\Omega_1} I_1(x,t)dx\right] \\
&= \int_{\Omega_1}\left\{\frac{\partial S_1(x,t)}{\partial t} + \frac{\partial E_1(x,t)}{\partial t} + \frac{\partial I_1(x,t)}{\partial t}\right\}dx \\
&= \int_{\Omega_1}\left\{\begin{array}{l} D_1^S \frac{\partial^2 S_1}{\partial x^2} - \beta * S_1 I_1 - dS_1 + bS_1 + \delta E_1 + \delta I_1 - \mu S_1 + \mu S_2 + \\ D_1^E \frac{\partial^2 E_1}{\partial x^2} + \beta * S_1 I_1 - \gamma E_1 - dE_1 - bE_1 - \mu E_1 + \mu E_2 - \delta E_1 + \\ D_1^I \frac{\partial^2 I_1}{\partial x^2} + \gamma E_1 - dI_1 - bI_1 - \delta I_1 - \mu \sigma I_1 + \mu \sigma I_2 \end{array}\right\}dx \\
&= D_1^S \frac{\partial^2 S_1}{\partial x^2}\Bigg|_0^L + D_1^S \frac{\partial^2 E_1}{\partial x^2}\Bigg|_0^L + D_1^S \frac{\partial^2 I_1}{\partial x^2}\Bigg|_0^L + (b-d)N_1(t) \\
&\quad - \mu\{S_1(x,t) + E_1(x,t) + \sigma I_1(x,t)\} \\
&\quad + \mu\{S_2(x,t) + E_2(x,t) + \sigma I_2(x,t)\}
\end{aligned}$$
(18)

Using the boundary conditions in equation (5), equation (18) becomes

$$\frac{dN_1(t)}{dt} = (b-d)N_1(t) - \mu\{S_1(x,t) + E_1(x,t) + \sigma I_1(x,t)\} + \mu\{S_2(x,t) + E_2(x,t) + \sigma I_2(x,t)\}$$
(19)

From equation (19) it can be assumed that the birth rate is greater than the mortality rate, so that $b > d$.

Definition

1. The form $(b-d)N(t)$ in equation (19) states that the initial population is in location 1, obtained from the number of births minus the number of deaths in the population time t.
2. Form $\mu\{S_1(x,t) + E_1(x,t) + \sigma I_1(x,t)\}$ the number of pushing populations from location 1 to location 2.

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3. Form $\mu\{S_2(x,t)+E_2(x,t)+\sigma I_2(x,t)\}$ the number of pushing populations from location 2 to location 1.

Theorem

If (S_1, E_2, I_1) *is a settlement of subsystems in equations (1), (2) and (3) and there are numbers* $b>0$, $d>0$ *and* $0<\mu<1$ *such that* $b-d\geq\mu$ *then subsystem of the equation (1) - (3) have a positive solution*

Proof:

It will be shown that $\frac{dN_1(t)}{dt}$ has a positive solution.

Suppose $\frac{dN_1(t)}{dt}=k$, with $k>0$, then from equation (19) is obtained

$$\frac{dN_1(t)}{dt}=(b-d)N_1(t)+\mu\{S_2(x,t)+E_2(x,t)+\sigma I_2(x,t)\}>\mu\{S_1(x,t)+E_1(x,t)+\sigma I_1(x,t)\}$$
(20)

From the equation (20) above, it is known that $\frac{dN_1(t)}{dt}$ has a positive solution if the initial population number 1 is added to the population that enters location 1 must be greater than the number of population coming out to location 2. For example taken $\sigma=1$, then the equation (20) becomes:

$$\frac{dN_1(t)}{dt}=(b-d)N_1(t)+\mu\{S_2(x,t)+E_2(x,t)+I_2(x,t)\}>\mu\{S_1(x,t)+E_1(x,t)+I_1(x,t)\}$$

Or it can be written

$$\frac{dN_1(t)}{dt}=(b-d)N_1(t)+\mu N_2(t)>\mu N_1(t)$$
(21)

with $0<\mu<1$.

1. Untuk $\mu\approx 0$

   $(b-d)N_1+0>0$, can be written

   $(b-d)N_1>0$

   (22)

Then inequality (21) is fulfilled

2. Untuk $\mu\approx 1$

   $(b-d)N_1+\mu N_2(t)>\mu N_1(t)$

Equation (21) can be fulfilled if

$b-d\geq\mu$

(23)

Thus, the system has a positive solution if the population growth rate (birth rate is reduced by the death rate) is greater or equal to the proportion of the individual displacement constantn. It means that the established system can provide knowledge to coastal communities in Southeast Sulawesi about overcoming the spread of the H1N1 virus.

4. Conclusion

Based on the discussion in the previous chapter, the results of this study can be summarized as follows The Susceptible *(S)* subpopulation, Expose *(E)* and Infected *(I)* can move globally which has the same proportion of each subpopulation in each location and The system model in equations (1), (2), and (3)

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has a positive solution with numbers $b > 0$, $d > 0$ and $0 < \mu < 1$ such that $b - d \geq \mu$. In other words, the system has a positive solution if the population growth rate is greater or equal to the constant proportion of individual movements.

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