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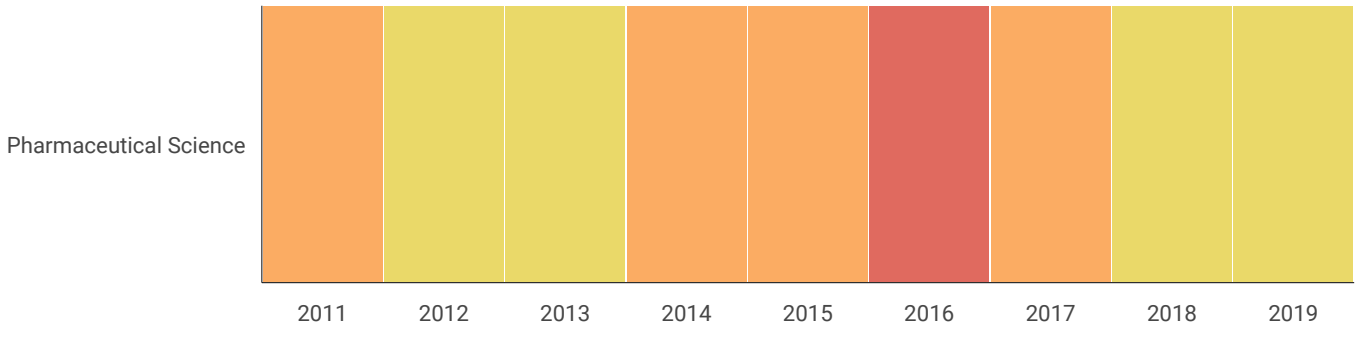

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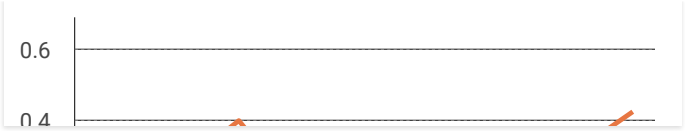

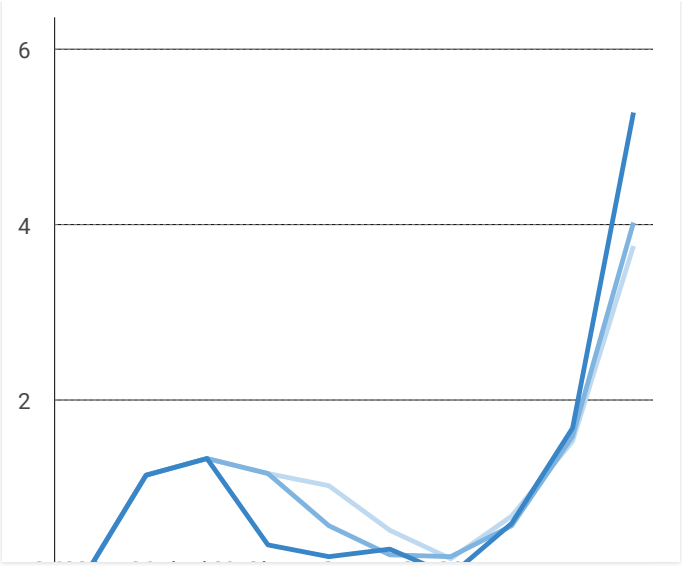

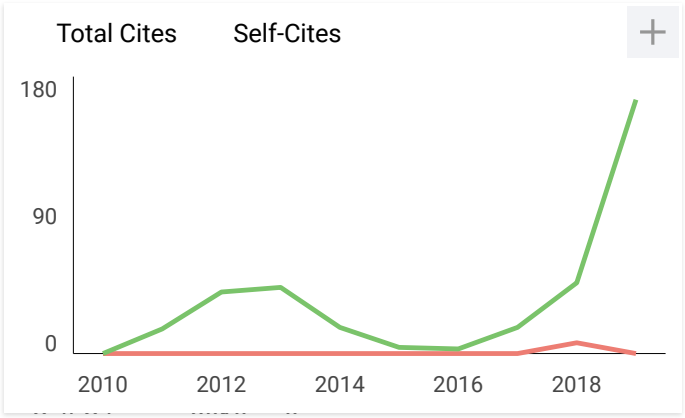

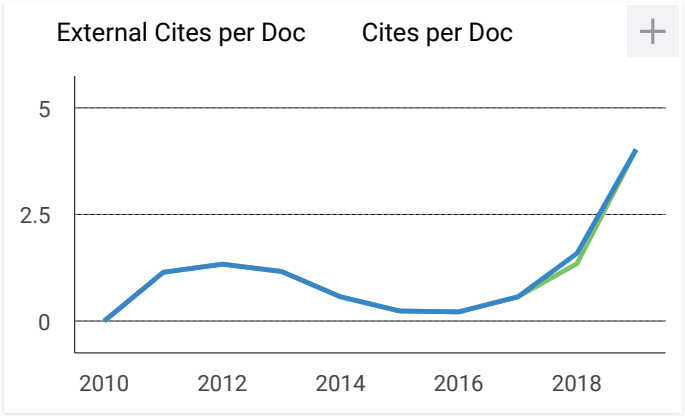

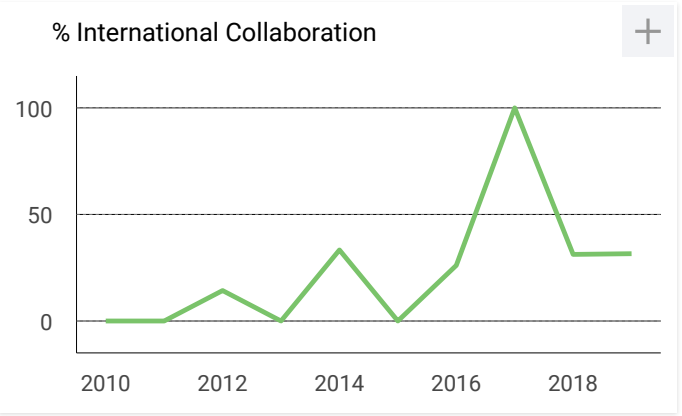

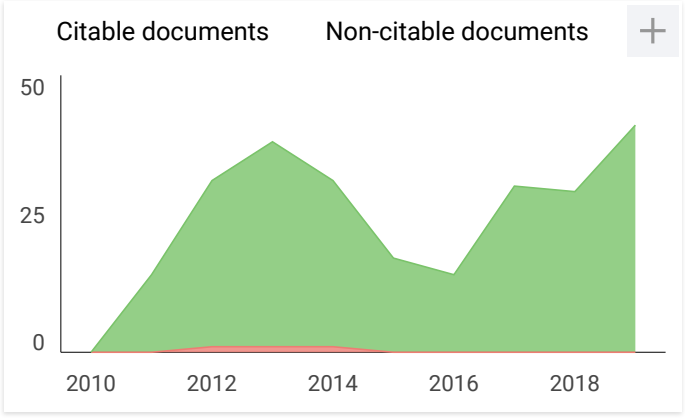

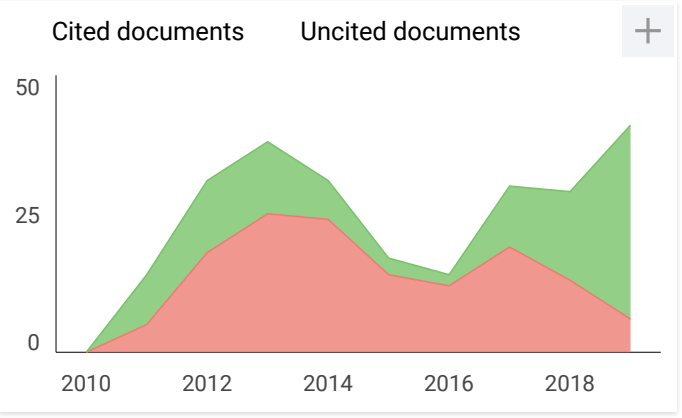

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Model of Spread of Infectious Diseases

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ABSTRACT
The Model of infectious diseases continues to develop along with the development of the disease. With the dynamic spread of disease, ongoing research is needed. This study developed the SIR model by taking into account the spread of disease in the presence of Reproductive Number or R_0. This study proposes an epidemic model of infectious diseases in dynamic networks for SIRS types, the standard mean-field model is used as a basic framework.

Keywords: Model of Spread, Infectious Disease, Modeling
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INTRODUCTION

Indonesia as a developing country, health issues are still important to get serious attention. In particular, the problem of infectious diseases because in Indonesia alone infectious diseases that occur until the end of 2017 and are still a hot topic of discussion are diphtheria. Although it sounds like a common cold or fever, diphtheria in fact has a high mortality rate and can be transmitted quickly. Until now, the vaccination program is still believed to be the most effective way in suppressing the spread of diphtheria. One branch of modern mathematics which is important and has a wide scope of research areas is differential equations.

Differential equations are branches of mathematics that are quite strategic because they relate to the central parts of Algebra, Analysis, Geometry, and others that will play a major role in the introduction of concepts and problem solving relating to the real world (Waluya, 2006).

This study aims to build a model of the spread of infectious diseases in dynamic SIRS type networks for heterogeneous populations. The model will be built using the basic framework of a mathematical model to investigate a parameter known as a basic reproductive number in detail, especially if the basic assumption of the model, mixing homogeneous populations, does not apply. In the SIRS model, this parameter has a very important role as a notification of a disease outbreak. The model that will be investigated in this study is based on a standard mean-field model. The main parameters that serve as measures for controlling epidemics, known as basic reproductive numbers with the mean-field model, will be investigated in more detail in the context of developing the model. The mean-field modification model produced essentially contains implicitly some important effects of heterogeneous mixing in contact tissue in the epidemic for vaccine allocation.

METHOD

SI epidemic model

The simplest mathematical model in epidemiology is known as the Ross Epidemic Model or SI, which was developed in 1911. In the SI model, the population is divided into two parts (subgroups), namely susceptible = S populations against disease transmission and infectious populations = I) against a disease. The assumptions used in this model are: that the vulnerable population remains in close contact with the infected population all the time $t \geq 0$, the number of populations is constant as N with N = (S (t) + I (t)) where S and I are mutually exclusive and mixing the population homogeneously so that each individual has an equal chance of infection. If $\beta \geq 0$ is the average constant (the proportion) of subgroup contact that results in a new infection the unity of time from the original state is susceptible (or also called the transmission rate constant).

SIS epidemic model

The assumptions used in this model are: that the vulnerable population remains in close contact with the infected population throughout the time ≥ 0, the number of populations is constant as N with N = (S (t) + I (t)) where S and I are mutually exclusive and homogeneous mixing of the population so that each individual has an equal chance of infection. However, the number or size of the infected population can decrease as the movement of infected individuals changes status to be susceptible to reuniting time with proportions σ.

SIR epidemic model

The SIR model is the basis for most of the deterministic models that are still used today. This model was first developed by Kermack and McKendrik in 1927. The SIR model has the same structure and assumptions as the SI model, the extension is that in the SIR model it is possible for the infected population / community members to recover and the total population of N to be divided into three subgroups mutually exclusive; susceptible subgroups (Susceptibles) symbolized S (t), infectious / infected subgroups I (t) and moved (Removed) subgroups symbolized R (t). R (t) represents individuals who died of illness, recovered from infection and now have permanent immunity or individuals who have been exiled from the rest of the population. So in this last subgroup, it no longer contributes to the spread of disease / epidemic. However, it is 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 I also assume that individuals who enter R (t) cannot be re-infected. Assuming that α is a constant proportion of the condition of the infected individual subsequently is removed unity of time. Then the differential

equation model that represents the rate of change of the population that is susceptible to constant unity of time as in the SI model, as in equation (3). This is because there is no direct transfer of 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 infected people and recover.

RESULT

Model Epidemi SI

The simplest mathematical model in epidemiology is known as the Ross'Epidemic Model or SI, which was developed in 1911. In the SI model, the population is divided into two parts (subgroups), namely susceptible (S) populations to disease transmission and infected populations (infected) infectious = I) to a disease. In Figure 1 this model is the same as SIR but without the R compartment.

The assumptions used in this model are: that the vulnerable population remains in close contact with the infected population all the time $t \geq 0$, the number of populations is constant as N with N = (S (t) + I (t)) where S and I are mutually exclusive and mixing the population homogeneously so that each individual has an equal chance of infection.

If $\beta \geq 0$ is the average constant (the proportion) of subgroup contact that results in a new infection the time unity from the original state that is vulnerable (or also called the transmission rate constant). Furthermore, by using the law of Mass action, the SI Model can be described as:

$$\frac{d\,S(t)}{dt} = -\beta S(t) I(t) \quad (1)$$

and

$$\frac{dI(t)}{dt} = \beta S(t) I(t) \quad (2)$$

hereafter written:

$$\frac{d\,S}{dt} = -\beta S\, I \quad (3)$$

$$\frac{dI}{dt} = \beta S\, I \quad (4)$$

with initial conditions S(0) = S_0 and $I(0) = I_0$.

In the SI model it can be said that the rate of change of contracting is positive, so the number of infected individuals will continue to increase until S (t) = 0.

The completion of this SI model, by changing equation (4) to:

$$\frac{dI}{dt} = \beta(N - I)I$$

Furthermore, with the separation of variables and integrated with a limit from 0 to t as follows: $\int_{I(0)}^{I(t)} \frac{1}{I(N-I)} dI = \int_0^t \beta dt$

was obtained: $I(t) = \frac{I(0)N}{I(0) + (N - I(0))e^{-\beta N_t}}$

or written : $I(t) = \frac{I_0 N}{I_0 + (N - I_0)e^{-\beta N_t}}$

observe that I (t) increases with increasing t and for t→ ∞, $e^{-\beta N_t} \to 0$

so that I(t) $\to \frac{I_0 N}{I_0} = N$

This last model states that as time goes by, the number of infected populations will increase, eventually all populations will become infected.

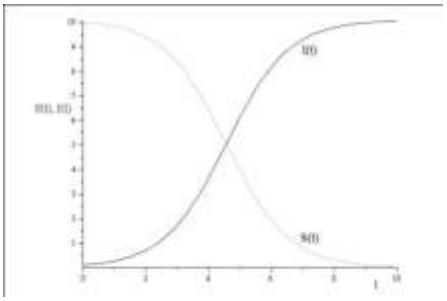

Figure 1: Model SI with $\beta = 0{,}1$ and initial value S(0) =10, I(0) = 0,1

Classic Model (SIR Model)

The SIR model is the basis for most of the deterministic models that are still used today. This model was first developed by Kermack and McKendrik in 1927. The SIR model has the same structure and assumptions as the SI model, the extension is that in the SIR model it is possible for the infected population / community members to recover and the total population of N to be divided into three subgroups mutually exclusive; susceptible subgroups (Susceptibles) are symbolized S (t), infectious / infected subgroups are symbolized I (t) and recovered subgroups are symbolized R (t). R (t) represents individuals who died of illness, recovered from infection and now have permanent immunity or individuals who have been exiled from the rest of the population. So in this last subgroup, they no longer contribute to the spread of disease / epidemic. However, it is still maintained as a member of a total population of N even though there is a possibility that some of them have died. In this model it is also assumed that individuals who enter R (t) cannot be re-infected. Assuming that α is a constant proportion of the condition of the infected individual subsequently is removed unity of time.

Then the differential equation model that represents the rate of change of the population that is susceptible to constant unity of time as in the SI model, as in equation (3). This is because there is no direct transfer of 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. When the amount moved is proportional to the amount that is infected with each unit of time, then the differential equation model becomes:

$$dI/dt = \beta SI - \alpha I$$

While the rate of change in the number of removals per unit time is:

$$\frac{dR}{dt} = \alpha I$$

with initial conditions: R (0) = R0, so that the complete differential equation model which is the SIR model is:

$$\frac{DS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \alpha I \quad (5)$$

$$\frac{dR}{dt} = \alpha I\,,$$

with initial conditions: S(0) = S_0, $I(0) = I_0$, R(0) = R_0 dan S(t) + I(t) + R(t) = N.

The SIR model above has two parameters α and β which are determined from the results of the analysis of the observed data. The average αI cure is related to the exponential waiting time "waiting time" $e^{\alpha I}$ and $\frac{1}{\alpha}$ = average period of contracting.

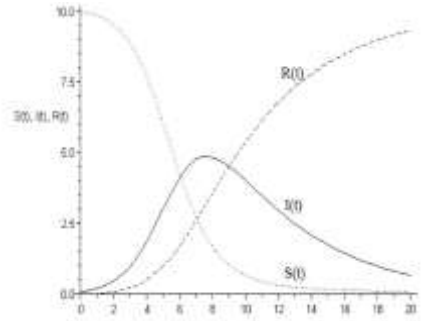

Figure 2: SIR model with $\gamma = 0{,}2$ $\beta = 0{,}1$ dan nilai awal S(0) =10, I(0) = 0,1 and R(0) = 0

SIRS Model

Not all diseases result in permanent immunity or death. Some diseases have a healing period and after time the recovered individual can be re-infected. Mathematically this means that a proportion of the subgroups that move the union of time ($\lambda \geq 0$) are again vulnerable. So the SIR model is modified to meodel SIRS as follows:

$$\frac{DS}{dt} = -\beta SI + \lambda R$$
$$\frac{dI}{dt} = \beta SI - \alpha I \qquad (6)$$
$$\frac{dR}{dt} = \alpha I - \lambda R$$

with initial conditions: S(0) = S_0, $I(0) = I_0$, R(0) = R_0 dan S(t) + I(t) + R(t) = N.

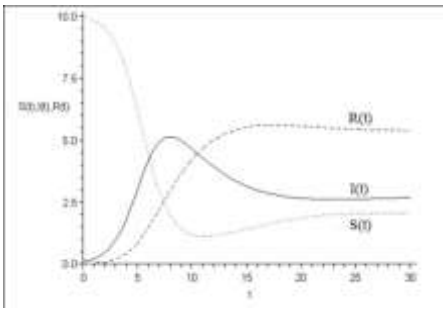

Figure 3: SIRS model with $\alpha = 0{,}2$, $\beta = 0{,}1$, $\lambda = 0{,}2$ and initial value S(0) =10, I(0) = 0,1 and R(0) = 0

CONSTRUCTION R0

Basic Reproduction Number (R0)

R0 which is usually called the Basic Reproduction Number is the average number of secondary infections produced when an infected individual is entered into the host population where each individual is in a susceptible condition. In most deterministic models, an infection begins fully if and only if R0> 1, and otherwise if R0 <1 then the number of infections will decrease and eventually become extinct. So the basic reproduction number is often seen as a threshold quantity that determines when an infection can attack and survive in a new host population.

If it is assumed that all pairs of individuals have contact at the same time so as to produce a new infected individual ie ,

The average rate of infected individuals has contact with susceptible individuals and then susceptible individuals become infected with time unity ie α, $\alpha \geq 0$.

R0 construction in the SIRS model, i.e.:

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

Growth of infection will take place if $\beta SI - \alpha I > 0$ or $\beta SI > \alpha I$ $\beta S > \alpha$ with S(0) = N so $(\beta N/\alpha) > 1$. Then thus $R_0 = \beta N/\alpha$

Logistics Equations in Epidemiology

Logistics equations are most often discussed when we study population dynamics with densities dependent on birth and death.

CONCLUSION

This study proposes an epidemic model of infectious diseases in dynamic networks for SIRS types, the standard mean-field model is used as a basic framework. In this SIRS epidemic model, a very basic parameter in discussing a disease epidemic is R0 (basic reproductive number). R0 has the main role as a threshold of an outbreak, on the relevance of testing control measures.

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Model of Spread of Infectious Diseases

Hamidah Nasution, Herlina Jusuf, Evi Ramadhani, Ismail Husein.

ABSTRACT

Abstract

The Model of infectious diseases continues to develop along with the development of the disease. With the dynamic spread of disease, ongoing research is needed. This study developed the SIR model by taking into account the spread of disease in the presence of Reproductive Number or R0. This study proposes an epidemic model of infectious diseases in dynamic networks for SIRS types, the standard mean-field model is used as a basic framework.

Key words: Model of Spread, Infectious Disease, Modeling

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Web Style

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Harvard Style

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MLA (The Modern Language Association) Style

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APA (American Psychological Association) Style

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