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SEIR Model in Spread Disease

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Abstract. As a country with a tropical climate, Indonesia has special problems related to tropical diseases. There are many types of this disease, it is very easy to develop and spread in tropical climates when climate change occurs. The infectious diseases discussed in this study are Measles, Hepatitis B, Influenza and Covid-19. These four diseases are deadly plagues caused by very fast-growing viruses. So its existence is very troubling for humans. Therefore we need an appropriate method to restrain the rate of development. The purpose of this study was to find out how the use of the SEIR model in mathematical models in several infectious diseases. The research method used is Literature Study, namely collecting data by conducting studies that explore several journals, books and other sources of information data. The results obtained through this study are exposure to mathematical models that can explain the spread of Measles, Hepatitis B, Influenza and Covid-19 diseases.

Keywords: SEIR Model, Measles, Hepatitis B, Influenza and Covid-19.

1 Introduction

Indonesia is a country with a tropical climate. Tropical countries have two seasons, including the dry season and the rainy season. With the existence of these two seasons, it is easy to develop a disease. In fact, there are also so-called "tropical diseases" which are diseases that are easy to attack, especially in areas with tropical climates. Tropical countries also have special problems related to tropical diseases. Included in tropical diseases are typhoid fever, tuberculosis, leprosy, tetanus, dengue, chikungunya, polio, malaria, intestinal worms, measles, hepatitis and others. These types of diseases are very easy to develop and spread, especially in areas with a tropical climate during times of climate change¹. Susilawati (2021:30) define that climate change has an impact on health, both directly and indirectly. Many types of diseases arise when the climate changes in the tropics as previously discussed. In Indonesia, there are several diseases that have become a pandemic, including Measles, Hepatitis B, Influenza and

¹Susilawati. Dampak Perubahan Iklim terhadap Kesehatan. E-SEHAD, Volume 1 Nomor 2 (2021).

Covid-19. The pandemic that occurred was caused by the spread of the virus so that many people suffered from the consequences.

Measles virus is a cause of infection. This disease is highly contagious. This virus is part of the negative, enveloped, unsegmented single-stranded RNA virus species, belonging to the genus Morbillivirus in the family Paramyxoviridae³. In Indonesia, the disease caused by the measles virus has a relatively high case history. Therefore, the government must take action to anticipate the recurrence of this virus. Measles virus transmission can occur through droplets / aerosol particles which initially infect lymphocytes, dendritic cells, and alveolar macrophages in the respiratory tract. Where the transmission time of measles is 4 days before the rash to 4 days after the appearance of the rash which begins with high fever, runny nose, cough, loss of appetite, and conjunctivitis. As a form of prevention of this virus, measles-mumps-rubella (MMR) vaccination can be done.²

In Southeast Asia, Indonesia is one of the countries with a high prevalence of hepatitis B (Kemenkes RI, 2014). Based on Riskesdas conducted by the Ministry of Health of the Republic of Indonesia, in a study conducted on PMI blood samples, 10 out of 100 Indonesians were infected with hepatitis B or C1. Therefore, extra treatment is needed to overcome the problem of hepatitis B infection.³The Indonesian Liver Research Association issued several parameters (serum HBV DNA, HBeAg status, ALT and liver histology) which were used to assess the right time to perform hepatitis therapy in order to obtain maximum results and reduce resistance rates.⁴This becomes very important because the longer hepatitis B treatment is given, the higher the prevalence of resistance, especially for antiviral types with low barrier resistance.⁵

Influenza H1N1 is an acute respiratory disease in humans that affects the nose.⁶Influenza can cause death, 0.1% of the death rate is caused by influenza virus infection. The first symptom of influenza is the body feels cold but the body has a fever with a body temperature of 39° C. In general, the symptoms of influenza include body aches, especially the joints and throat, coughing and sneezing, fever, dizziness, eye irritation, stomach pain and so on.⁷

In early 2020, the world was shocked by an outbreak of a new pneumonia that started in Wuhan, Hubei Province, which then spread rapidly to more than 190 countries and territories. This outbreak was named coronavirus disease 2019 (COVID-19) caused by Severe

²Yahmal, Princess Nuraini. Faktor-Faktor Yang Berhubungan Dengan Kejadian Campak. Jurnal Medika Hutama. Vol 03 No 01, October 2021

³Kementrian Kesehatan Republik Indonesia. Info DATIN Situasi dan Analisis Hepatitis. Jakarta: Kemenkes RI; 2014.

⁴Lesmana C, Hasan I, Gani R, Sanityoso A, Djumhana A, Setiawan P. Lesmana C, Hasan I, Gani R, Sanityoso A, Djumhana A, Setiawan P. Konsensus Nasional Penatalaksanaan Hepatitis B. Jakarta: Perhimpunan Peneliti Hati Indonesia; 2017

⁵Ghany M, Doo E. Antiviral resistance and hepatitis B therapy. Hepatology. (2009); 49(S5):S174-84

⁶Rahmadania, Beautiful and Educate Khusnul. Kontrol Optimal pada Model Penyebaran Virus Influenza Tipe A H1N1 dengan Menggunakan Prinsip Minimum Pontryagin. Limits: Journal of Mathematics and Its Applications. Volume 17 Number 1 (2020).

⁷Pratiwi, Noviana. Strategi Model Pengendalian Penyebaran Virus Influenza. Journal of Mathematics. Volume 11 Number 3. (2008).

Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2). The spread of this disease has had a wide social and economic impact.⁸

The existence of a pandemic that occurred related to the viruses previously described, made the Indonesian economy also feel the impact. Therefore, the government is trying in every way possible to reduce the number of sufferers in the hope that national stability will improve. One method that has often been used to reduce the impact of a pandemic is the SEIR Model.

The SEIR model is a mathematical model that can play a role in studying the spread of disease, commonly called an epidemiological mathematical model. The classic model of the spread of disease was formulated by Kermack in 1927, known as the SIR (Susceptible, Infected and Recovered) model. In the SIR model, the total population is divided into 3 subpopulations, namely Susceptible which states the number of healthy individuals but susceptible to infection, Infected which states the number of individuals who are infected and can transmit the disease, and Recovered which states that the subpopulation is cured. Some diseases have a latent period (incubation period), which is the time between healthy individuals who become infected and can transmit the disease. This period resulted in the emergence of a new subpopulation, namely Exposed.⁹

Based on the explanation above, it appears that the SEIR model can help analyze how a pandemic spreads and how to deal with it. The SEIR model has been widely used in analyzing an event related to a pandemic. Therefore, the researcher wants to see how the SEIR model is used in four diseases that have become pandemics in Indonesia.

2 Methods

The type of research used is literature study. The literature study method is a series of activities related to the methods of collecting library data, reading and taking notes, and managing research materials.¹⁰ Literature studies are carried out by each researcher with the main objective of finding the basis for obtaining and building theoretical foundations, frameworks of thought, and determining provisional conjectures or also known as research hypotheses.¹¹ So that researchers can classify, allocate, organize, and use a variety of literature in their fields. In this study, the SEIR model is seen in the discussion of the SEIR model disease, Measles, Hepatitis B, Influenza and Covid-19.

⁸Susilo, Adityo, et al. Coronavirus Disease 2019: Tinjauan Literatur Terkini. *Jurnal Penyakit Dalam*. Volume 7 Number 1 (2020).

⁹M. Jamah, MA Karim, and Y. Yulida. Analisis Kestabilan Model Seir Untuk Penyebaran Covid-19 Dengan Parameter Vaksinasi. *BAREKENG: J. Il. Mat. & Ter.*, vol. 15, no. 03, pp. 535-542, Sept. 2021.

¹⁰Zed, M. (2014). *Metode Penelitian Kepustakaan*. Jakarta: Yayasan Obor Indonesia.

¹¹Kartiningih, Eka Diah. *Panduan Penyusunan Studi Literatur*. Lembaga Penelitian dan Pengabdian Masyarakat Politeknik Kesehatan Majapahit Mojokerto, 2015.

3 Results and Discussion

3.1 Results

This study discusses the SEIR model disease, Measles, Hepatitis B, Swine Flu and Covid-19 through the SEIR model. For clearer conclusions based on the results of the application of the Seir Model, it can be seen in the following table.

Table 1. SEIR Model Application Table on Measles, Hepatitis B, Swine Flu and Covid-19

| Title | Disease Name | Destination | Results |
|--|--------------|---|---|
| SEIR Model of Measles With Vaccination and Migration. Mohammad Soleh and Siti Rahma | Measles | Explain about the measles spread model using the SEIR model with vaccination and migration. | If $R_0 < 1$ then the disease-free equilibrium point is asymptotically stable and if $R_0 > 1$ then the disease-endemic equilibrium point is asymptotically stable. The number of people vaccinated to prevent the spread of measles is $R_0 < 1 R_0 > 1 p_c < 1 - \frac{1}{R_0}$ |
| Analysis of the Stability of the SEIR Model for the Spread of Covid-19 with Vaccination Parameters Miftahul Jannah, Muhammad Ahsar Karim, Yuni Yulida | Covid-19 | Determining the equilibrium point and the basic reproduction number, stability analysis and simulation of the SEIR model. | Based on the SEIR model for the spread of Covid-19 by paying attention to vaccination as a model parameter, the basic reproduction number is obtained $R_0 = \frac{\alpha\beta\mu}{(\beta+\mu)(\mu+v)(\mu+1+\delta+\mu)}$ locally asymptotically stable disease-free equilibrium point at $R_0 < 1$, and an endemic equilibrium point $E_0 = \left(\frac{\mu}{\mu+v}, 0, 0, \frac{v}{\mu+v} \right) R_0$ $E^* = \left(\frac{\mu}{R_0(\mu+v)}, \frac{\mu(R_0-1)}{R_0(\beta+\mu)}, \frac{(\mu+v)(R_0-1)}{\alpha}, \frac{\delta(R_0-1)R_0(\mu+v)^2 + \alpha\mu v}{\alpha\mu R_0(\mu+v)} \right)$ which is also locally asymptotically stable at $R_0 > 1$. This is supported through numerical simulations which provide visualization that the equilibrium point E_0 and E^* each local asymptotically stable |
| Spread of Influenza Type | Influenza | Knowing the behavior of the | Spread of influenza type A (H1N1) ModelR has two equilibrium points, |

| | | | |
|---|--------------------|--|--|
| <p>A (H1n1) SEIR Model</p> <p>The Beginning of Princess Sinula's Launch</p> | | <p>system from the spread of influenza type A (H1N1) by analyzing the stability of the model of the system and determining R_0 (basic reproduction number) of the SEIR model.</p> | <p>namely: free of disease, which is a state where there is no spread of disease so that individuals are exposed to it (E), individuals infected with the disease (I_S) and asymptomatic infected individuals (I_N) does not exist or the population is zero then</p> <p>$T^0 = (S^0, E^0, I_S^0, I_N^0) = (N, 0, 0, 0)$ with</p> <p>$R_0 = 0.714$ then substitute the parameter values so that a disease-free equilibrium point is obtained</p> <p>$T^0 = (S^*, E^*, I_S^*, I_N^*) = (1, 0, 0, 0)$.</p> <p>Then, the epidemic equilibrium point is the state at which the disease will spread. So $T^* = (S^*, E^*, I_S^*, I_N^*)$ with</p> $S^* = \frac{1}{\left(\frac{\beta(-1+p)}{\gamma}\right) + \left(\frac{\beta\delta(1-p)}{\eta}\right)}$ $E^* = \frac{IS(\gamma+\mu)}{pk} - pk$ $I_S^* = \frac{kE(-1+p)}{\gamma}$ $I_N^* = \frac{kE'(1-p)}{\eta}$ <p>with $R_0 = 9.603$ after that by substituting the parameter values obtained disease</p> <p>$T^* = (0.59; 0.1; 0.1; 0.1; 0.2)$.</p> <p>Based on the stability analysis, the comparison type is in the form of an unstable saddle</p> |
| <p>SEIR Model on Hepatitis B Transmission</p> <p>Syafruddin</p> | <p>Hepatitis B</p> | <p>Discusses mathematical modeling on Hepatitis B transmission by dividing the population group into four parts, namely Susceptible, Exposed, Infected and</p> | <p>Hepatitis B transmission can be interpreted in a mathematical equation. The mathematical equation is a 4-D nonlinear differential equation system. The system of differential equations is then simplified into a 3-D non-linear system of differential equations based on the assumption that the recovered population is immune from Hepatitis B. The 3-D system of ordinary differential equations is the simplest form of mathematical modeling of hepatitis B</p> |

| | | | |
|--|--|------------------|---------------|
| | | Recovered (SEIR) | transmission. |
|--|--|------------------|---------------|

The table above summarizes the results of research using the SEIR Model on several diseases that have become pandemics in Indonesia. Of the four studies, using the SEIR model as a mathematical modeling which will later be continued in its application.

3.2 Discussion

There are four diseases discussed in this article, namely Measles, Hepatitis-B, Covid-19 and Influenza. The choice of these four diseases is because they are diseases that have become a pandemic in Indonesia. These four diseases are caused by viruses. For further, how so that these viruses can be overcome quickly and precisely, the researchers use the help of the Seir Model in their form of mathematical modeling. In the case of measles, through the help of the SEIR model, it was concluded: "Measles will disappear from the population or the population free from measles if the proportion of individuals infected with measles is $p = 1$ ".¹²

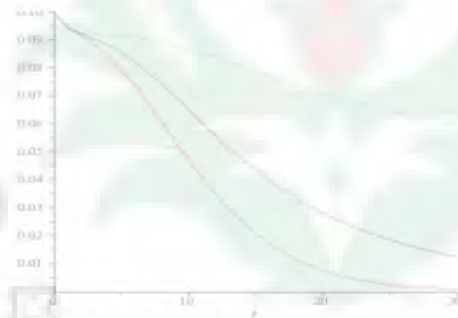


Figure 1. Proportion of Individuals in the Infected class with $p = 0,8, p = 0,9, p = 1$

Furthermore, in the case of Hepatitis-B, through the SEIR model, a mathematical model has been obtained which can assume the recovered population to be immune, so that the simplest form of the system of differential equations is described in the following system of equations.¹³

$$\frac{dx}{dt} = (1 - a)\mu x + p_1 x - (p_2 + \beta + \mu)x$$

$$\frac{du}{dt} = \beta x + p_1 u - (y + p_2 + \mu)u$$

$$\frac{dy}{dt} = \gamma u + p_1 y - (\mu + p_2 + \delta)y$$

¹²Salih, Mohammad. Model SEIR penyakit Campak dengan Vaksinasi dan Migrasi. Jurnal Sains, Teknologi dan Industri, Volume 9 Nomor 2 (2012)

¹³Sidi, Syarifuddin. Model SEIR pada penularan Hepatitis-B. Jurnal SCIENTIFIC PINISI Journal, Vol.1 No.1 October 2015

Then, the next disease that uses the SEIR model in developing its mathematical model is Covid-19. In this disease, the SEIR model has been used to see how the virus spreads by considering vaccination as a parameter. Then the mathematical model is obtained as follows.

$$R_0 = \frac{\alpha\beta\mu}{(\beta + \mu)(\mu + \nu)(\mu + \delta + \mu)}$$

With a disease-free equilibrium point $E_0 = \left(\frac{\mu}{\mu + \nu}, 0, 0, \frac{\nu}{\mu + \nu}\right)$

which is locally asymptotically stable at $R_0 < 1$, and the endemic equilibrium point R_0

$$E^* = \left(\frac{\mu}{R_0(\mu + \nu)}, \frac{\mu(R_0 - 1)}{R_0(\beta + \mu)}, \frac{(\mu + \nu)(R_0 - 1)}{\alpha}, \frac{\delta(R_0 - 1)R_0(\mu + \nu)^2 + \alpha\mu\nu}{\alpha\mu R_0(\mu + \nu)} \right)$$

which is also locally asymptotically stable at $R_0 > 1$.¹⁴

Finally, the disease that uses the SEIR model in this study is Influenza. Spread of influenza type A (H1N1) Model R has two equilibrium points, namely: disease-free, which is a condition where there is no spread of disease so that individuals are exposed (E), individuals are infected with the disease (I_S) and infected individuals without symptoms (I_N) do not exist or the population is zero then

$T^0 = (S^0, E^0, I_S^0, I_N^0) = (N, 0, 0, 0)$ with $R_0 = 0.714$ then substitute the parameter values so that a disease-free equilibrium point is obtained $T^0 = (S^*, E^*, I_S^*, I_N^*) = (1, 0, 0, 0)$. Then, the epidemic equilibrium point is the state at which the disease will spread. So $T^* = (S^*, E^*, I_S^*, I_N^*)$ with

$$S^* = \frac{1}{\left(\frac{\beta(-1+p)}{\gamma}\right) + \left(\frac{\beta\delta(1-p)}{\eta}\right)}$$

$$E^* = \frac{IS(\gamma + \mu)}{pk}$$

$$I_S^* = \frac{kE^*(-1+p)}{\gamma}$$

$$I_N^* = \frac{kE^*(1-p)}{\eta}$$

¹⁴Jannah, Miftahul, et al. Analisis Kestabilan Model SEIR untuk Penyebaran Covid-19 dengan Parameter Vaksinasi. BAREKENG Volume 15 Number 3, (2021)

with $R_0 = 9,603$ after that by substituting the parameter values obtained disease $T^* = (0.59; 0.1; 0.1; 0.1; 0.2)$. Based on the stability analysis, the comparison type is in the form of an unstable saddle.¹⁵

In addition to the four research results above, there are many other research articles that use the SEIR model. Like what Ihsan did who did the SEIRS mathematical modeling of Malaria¹⁶, Pramudito in his research with the title SEIR Model of COVID-19 Disease with Migration and Vaccination¹⁷, Kharis with his research themed on the SEIR model on Swine Flu¹⁸, Sihotang raised the theme of his research on the SEIR Model on the spread of Measles by paying attention to Immunization and MR Vaccines¹⁹ and many more.

4 Conclusion

The description that has been done above shows that the SEIR Model can be very helpful in making a mathematical model of an event, in this case the occurrence of a disease that once became a pandemic in Indonesia. The SEIR model is a mathematical model that describes the pattern of the spread of a disease that is limited by certain assumptions and parameters, so that the SEIR model is suitable for the problem of the spread of a disease that meets a pre-defined assumption.

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¹⁵Sinula, Early Launy Putri. Penyebab Penyakit Influenza Tipe A (H1N1) Model SEIR. *MATHunesa*. *MATHunesa*. Volume 6 Number 3 (2018)

¹⁶Ihsan, Hisham, et.al. Pemodelan Matematika SEIRS pada Penyebaran Penyakit Malaria di Kabupaten Mimika. *JMATHCoS* Volume 4 Number 1 (2021)

¹⁷Pramusito, M Shandy Prabowo and Budi Priyo Prawoto. Model SEIR Penyakit COVID-19 dengan adanya Migrasi dan Pemberian Vaksin. *Jurnal Ilmiah Matematika*. Volume 9 Number 2 (2021)

¹⁸Kharis, M. Model Seir Untuk Epidemi Flu Babi Pada Populasi Babi Dengan Laju Kontak Jenuh. *Indonesian Journal of Mathematics and Natural Science (IJMNS)*. Volume 35 Number 1 (2012)

¹⁹Sihotang, Wilyam Daniel, et.al. Analisis Kestabilan Model SEIR Penyebaran Penyakit Campak dengan Pengaruh Imunisasi dan Vaksin MR. *Jurnal Matematika, Statistika & Komputer*. Volume 16 Number 1 (2019)

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