SEIR model simulation on the spreading of Ebola virus between two regions

by Awawin Mustana Rohmah

Submission date: 10-Aug-2022 03:15AM (UTC-0400)
Submission ID: 1880935593
File name: SEIR_model_simulation.pdf (981.46K)
Word count: 2590
Character count: 13253

Journal of Physics: Conference Series

PAPER · OPEN ACCESS

SEIR model simulation on the spreading of Ebola virus between two regions

To cite this article: A M Rohmah and D Rahmalia 2021 *J. Phys.: Conf. Ser.* **1882** 012038

SEIR model simulation on the spreading of Ebola virus between two regions

A M Rohmah[1] and D Rahmalia[1]

[1] Department of Mathematics, Universitas Islam Darul 'Ulum Lamongan

E-mail: awawin.emer@unisda.ac.id

Abstract. In this study, we formed one of epidemic models that describe the spread of Ebola virus disease between two regions in the mathematical model known as SEIR epidemic model. For constructing the mathematical model, it is necessary to understand the phenomenon of the spread of the Ebola virus such as that the number of infected populations in one region does not only depend on the number of infected individuals in one region but also by individuals traveling from one region to another. Based on this phenomenon, we constructed the SEIR mathematical model to determine the dynamics of the spreading virus. We computed the Basic Reproduction Number to determine the stability of the spreading virus. We applied the numerical simulation using the Runge-Kutta Order 4 method to illustrate the results obtained. The simulation results show that region B has a higher spread than region A, because the number virus transmission in region B is higher than that in region A based on the Basic Reproduction Numbers.

1. Introduction

Ebola disease is a virus that can spread through direct contact with individuals through damaged skin or mucous membranes with blood, secretions, organs or other body fluids from an infected person, or it can also occur in infected individuals due to contact with contaminated objects and the clothing contaminated with liquids. The spread of the virus is from bats infected with the virus, where people in West Africa still frequently have directly contact with the infected animals, resulting many infected individual [1].

The spread of Ebola virus occurs when the people in the region B and region A do trade and transactions with people in region A who are infected with the Ebola virus, resulting the spread of virus in region B. The virus has an incubation period during 2-21 days. Based on this incident, WHO and Health Experts conducted census on cities where individuals in these cities are suspected of having contracted the virus [2].

The development of science in the medical field has an important role in the spread of the Ebola virus, but in the field of mathematics, it has a role in knowing the phenomenon of the spread of the Ebola virus. Mathematical models are the method that can be used to study dynamics and predict the behavior of the spread of infectious diseases such as the Ebola virus. This phenomenon is modelled by differential equation with a continuous time process representation. Some examples of mathematical models used to determine the pattern of disease spread are Susceptible Infected (SI) model, the Susceptible Infected Susceptible (SIS) model, the Susceptible Infected Recovery (SIR) model, the Susceptible Exposed Infected Recovery (SEIR) model, and so on.

Hadianto and Budiantara [3] constructed pre-coalition model between H1N1-p and H5N1 influenza virus that attack poultry and humans. The model was formed based on transitions and genetic changes in individual populations, the co-existence of the two viral transmissions was analyzed. Atangana and Goufo [4] constructed mathematical model on the spread of the Ebola virus in West Africa. Li and Teng [5] analyzed the epidemic model of the Susceptible Exposed Infected Treatment (SEIT) with the Ebola virus transmission application in Guinea and estimated the parameters of the model using the Least Square method. Mathematical model by simulating the spread of the Ebola virus between two countries has constructed by Rohmah [6].

In contrast to previous studies, this study develops SEIR (Susceptible Exposed Infected Removed) type mathematical model which describes the transmission of the Ebola virus spread between two regions in West Africa, namely region A and region B. The model is constructed with individuals traveling between two region. This study is conducted because the number of infected subpopulations in an area is not only caused by individuals in one area but also it can be caused by individuals from other regions traveling, so that individuals infected with the Ebola virus can infect susceptible individuals in an area. Dynamical system analysis is performed to determine the stability of virus spread based on the Basic Reproduction Numbers. In the final section, numerical simulations are applied by Matlab software with the Runge Kutta Order 4 method which aims to determine the effect of individual movement between regions on the spread of the virus.

2. Method

This method used to achieve the objectives of this study is to determine the Basic Reproduction Number to determine the flow of a virus. For determining the Basic Reproduction Number, it uses the next generation matrix, namely $A = FV^{-1}$ and the Basic Reproduction Number can be written as $R_0 = \rho\,(FV^{-1}) = \rho\,(A)$, where $\rho\,(A)$ is spectral radius of matrix A, which is the maximum modulus of the eigenvalues of matrix A. The steps taken are as follows: For calculating the reproduction number R_0, the first thing to do is the formation of the matrix $F_i(x)$ and the matrix$V_i(x)$. It is defined that the matrix $F_i(x)$ is a matrix whose component is the rate of emergence of new infections in compartment i. Meanwhile the matrix $V_i(x)$ is a matrix whose component is the rate of individual displacement V_i^{-x} and the rate of individual displacement into V_i^{+x} to compartment i. After obtaining the $F_i(x)$ and $V_i(x)$ matrices with partial derivatives of the Jacobi matrix, the F and V matrices are obtained. Based on the F and V matrices, the next step is to find the value of FV^{-1} so that it can be determined the Basic Reproduction Number$R_0 = \rho\,(FV^{-1}) = \rho(A)$. For the spread of the Ebola virus, a simulation using the Runge kutta order 4 method using Matlab software is used.

2.1. Mathematical Model

Based on the development of research [6], in this model the population is divided into four subpopulations, namely Susceptible (S) subpopulation, Exposed (E) subpopulation, Infected (I) subpopulation, and Removed (R) subpopulation. The change in each subpopulation is influenced by the interaction between susceptible individuals and infected individuals or (s_i, i_i) with i = 1,2. If β_i is the rate of virus transmission in one area and the chance of contact is θ_i , then $\theta_i\beta_i s_i \frac{i_i}{N_1}$ is the number of contacts of susceptible individuals interacting with infected individuals, so that $\sum_{i=1}^{2} \theta_i\beta_i s_i \frac{i_i}{N_1} = \theta\beta S \frac{I}{N}$. The interaction of susceptible subpopulation with the possibility of the subpopulation is infected in region A is $\theta_1\beta_1 S_1 \frac{I_1}{N_1}$ and for region B is $\theta_2\beta_2 S_2 \frac{I_2}{N_2}$. However, there is also contact between exposed individuals and susceptible individuals or (s_i, e_j) with j = 2.1 where ω_i is the rate of virus transmission between regions and the number of contacts is θ_i, so that $\theta_i\omega_i \frac{s_i}{N_i} e_j$ is the number of exposed individuals who interact with susceptible individuals. Therefore, the number of individuals can be written as

$\sum_{i=1}^{2} \theta_i \omega_i \frac{s_i}{N_i}, e_j = \theta\omega \frac{S}{N} E$. The presence of exposed subpopulation interactions that interact with the chances of a susceptible subpopulation in region A is $\theta_1\omega_1 \frac{S_1}{N_1} E_2$ and for region B is $\theta_2\omega_2 \frac{S_2}{N_2} E_1$. The parameter α_i represents the traveling rate, the b_i parameter is the death rate, the rate for exposed infected individuals is γ_i, and the cure rate is k_i.

Based on the identification of these problems, the phenomena that occur in region A and region B can be formed a mathematical model. This case begins from susceptible individuals who have directly contact (touching, sweat, saliva, clothing, etc.) with infected individuals who have not shown clinical signs (any cases suspected by a general practitioner and have not been confirmed by laboratory tests of Ebola virus disease). When an individual is tested as positive for infection during laboratory tests, the individual becomes infected with the Ebola virus. In infected individuals, they will decrease if healing is done, but until now there is no treatment.

The SEIR type mathematical model can represent the phenomena that occur in the spread of the Ebola virus. The incubation period is the time between the entry of the virus into the body and symptoms. The Ebola virus ranges from 2-21 days. Ebola virus transmission occurs when symptoms appear, for example vomiting, internal bleeding through the mouth, nose and ears. The compartment diagram of the Ebola virus spread can be seen in figure 1.

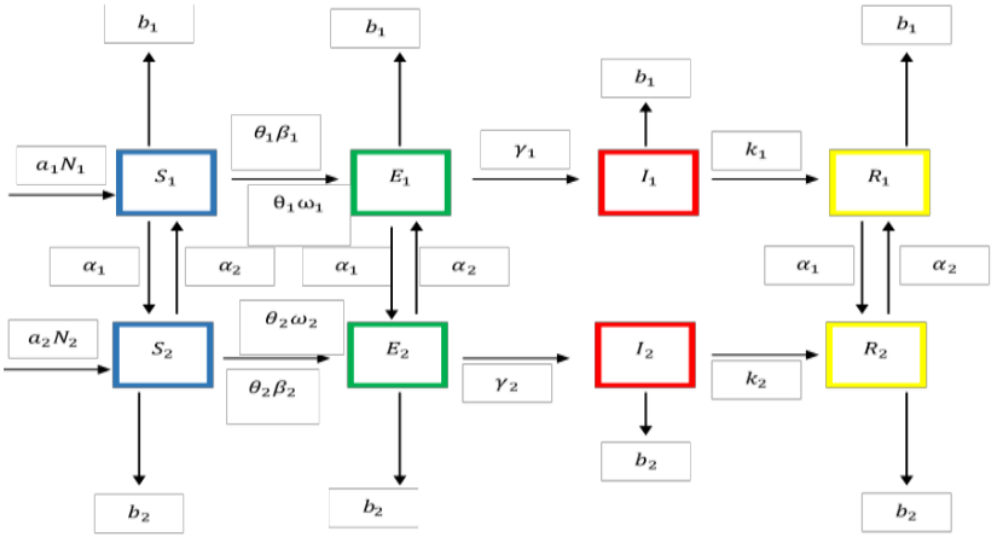

Figure 1. Compartment diagram.

In this way, each of these subpopulations can be formed in a mathematical model in equation (1) – (8).

$$\frac{dS_1}{dt} = a_1N_1 - b_1S_1 - \theta_1\beta_1S_1\frac{I_1}{N_1} - \alpha_1S_1 + \alpha_2S_2 - \theta_1\omega_1E_2\frac{S_1}{N_1} \quad (1)$$

$$\frac{dS_2}{dt} = a_2N_2 - b_2S_2 - \theta_2\beta_2S_2\frac{I_2}{N_2} - \alpha_2S_2 + \alpha_1S_1 - \theta_2\omega_2E_1\frac{S_2}{N_2} \quad (2)$$

$$\frac{dE_1}{dt} = \theta_1\beta_1S_1\frac{I_1}{N_1} - \gamma_1E_1 - b_1E_1 - \alpha_1E_1 + \alpha_2E_2 + \theta_1\omega_1E_2\frac{S_1}{N_1} \quad (3)$$

$$\frac{dE_2}{dt} = \theta_2\beta_2S_2\frac{I_2}{N_2} - \gamma_2E_2 - b_2E_2 - \alpha_2E_2 + \alpha_1E_1 + \theta_2\omega_2E_1\frac{S_2}{N_2} \quad (4)$$

$$\frac{dI_1}{dt} = \gamma_1 E_1 - b_1 I_1 - k_1 I_1 \quad (5)$$

$$\frac{dI_2}{dt} = \gamma_2 E_1 - b_2 I_1 - k_2 I_2 \quad (6)$$

$$\frac{dR_1}{dt} = k_1 I_1 - b_1 R_1 - \alpha_1 R_1 + \alpha_2 R_2 \quad (7)$$

$$\frac{dR_2}{dt} = k_2 I_2 - b_2 R_2 - \alpha_2 R_2 + \alpha_1 R_1 \quad (8)$$

2.2. Basic Reproduction Number

Basic Reproduction Number can be used to show the number of new infections caused by infected individual [7]. Based on equation (1), the Basic Reproduction Number with FV^{-1} is determined in equation (9).

$$FV^{-1} = \begin{pmatrix} \frac{(\theta_1\omega_1\alpha_1 CD + (\theta_1\beta_1\gamma_1)BD)}{H} & \frac{(\theta_1\omega_1)ACD - (\theta_2\alpha_2\beta_2\gamma_2)D}{H} \\ \frac{(\theta_2\omega_2)ACD - (\theta_1\beta_1\gamma_1)BC}{H} & \frac{(\theta_2\omega_2\alpha_2)CD + (\theta_2\beta_2\gamma_2)AC}{H} \\ 0 & 0 \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{(\theta_1\beta_1)ABD - (\theta_1\beta_1)ED}{H} & 0 \\ 0 & \frac{(\theta_2\beta_2)ABC - (\theta_2\beta_2)CE}{H} \\ 0 & 0 \\ 0 & 0 \end{pmatrix} \quad (9)$$

with

$$\gamma_1 + b_1 + f_1 + \alpha_1 = A, \qquad b_2 + k_2 = D,$$
$$\gamma_2 + b_2 + f_2 + \alpha_2 = B, \qquad \alpha_1\alpha_2 = E, \text{ and}$$
$$b_1 + k_1 = C, \qquad ABCD + CDE = H$$

Next, we determine the Eigenvalue of the FV^{-1} matrix until the Basic Reproduction Number $(\mathcal{R}_0)$ is obtained. To fulfill $(\mathcal{R}_0) < 1$, where the conditions in region A and B are disease free and to fulfill $(\mathcal{R}_0) > 1$, namely where the conditions in region A and region B are endemic. $(\mathcal{R}_0)$ is obtained in equation (10).

$$\mathcal{R}_0 = \frac{(\theta_1\omega_1\alpha_1)\prod_{i=1}^{2}(b_i + k_i) + (\theta_1\beta_1\gamma_1)(\gamma_2 + b_2 + \alpha_2)(b_2 + k_2)}{\prod_{i=1}^{2}\left((\gamma_i + b_i + \alpha_i)(b_i + k_i)\right) + (\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i + k_i)} + \frac{(\theta_2\omega_2\alpha_2)\prod_{i=1}^{2}(b_i + k_i) + (\theta_2\beta_2\gamma_2)(\gamma_1 + b_1 + \alpha_1)(b_1 + k_1)}{\prod_{i=1}^{2}\left((\gamma_i + b_i + \alpha_i)(b_i + k_i)\right) + (\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i + k_i)} \quad (10)$$

$$\frac{\sqrt{\left(\frac{(\theta_1\omega_1\alpha_1)\prod_{i=1}^{2}(b_i+k_i)+(\theta_1\beta_1\gamma_1)(\gamma_2+b_2+\alpha_2)(b_2+k_2)}{\prod_{i=1}^{2}\left((\gamma_i+b_i+\alpha_i)(b_i+k_i)\right)+(\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i+k_i)}\right.}+}{2}$$

$$\frac{\left.\left(\frac{(\theta_2\omega_2\alpha_2)\prod_{i=1}^{2}(b_i+k_i)+(\theta_2\beta_2\gamma_2)(\gamma_1+b_1+\alpha_1)(b_1+k_1)}{\prod_{i=1}^{2}\left((\gamma_i+b_i+\alpha_i)(b_i+k_i)\right)+(\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i+k_i)}\right)^2}{}$$

$$\frac{4\left((\theta_1\omega_1\alpha_1)\prod_{i=1}^{2}(b_i+k_i)+(\theta_1\beta_1\gamma_1)(\gamma_2+b_2+\alpha_2)(b_2+k_2)\right)}{\prod_{i=1}^{2}\left((\gamma_i+b_i+\alpha_i)(b_i+k_i)\right)+(\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i+k_i)}$$

$$\frac{(\theta_2\omega_2\alpha_2)\prod_{i=1}^{2}(b_i+k_i)+(\theta_2\beta_2\gamma_2)(\gamma_1+b_1+\alpha_1)(b_1+k_1)}{\prod_{i=1}^{2}\left((\gamma_i+b_i+\alpha_i)(b_i+k_i)\right)+(\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i+k_i)}$$

$$\frac{(\theta_1\omega_1)(\gamma_1+b_1+\alpha_1)\prod_{i=1}^{2}(b_i+k_i)-(\theta_2\alpha_2\beta_2\gamma_2)(b_2+k_2)}{\prod_{i=1}^{2}\left((\gamma_i+b_i+\alpha_i)(b_i+k_i)\right)+(\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i+k_i)}$$

$$\frac{(\theta_2\omega_2)(\gamma_1+b_1+\alpha_1)\prod_{i=1}^{2}(b_i+k_i)-(\theta_1\beta_1\gamma_1)(\gamma_2+b_2+\alpha_2)(b_1+k_1)}{\prod_{i=1}^{2}\left((\gamma_i+b_i+\alpha_i)(b_i+k_i)\right)+(\alpha_1\alpha_2)\prod_{i=1}^{2}(b_i+k_i)}$$

3. Results and Discussions

The numerical simulations are applied by Matlab software aiming to see the spread of the virus visually so that it is easy to analyze the system based on reproduction numbers and persistence analysis is obtained from the virus spread model between two regions. In this simulation, the 4th order Runge Kutta method is used. Parameters used are initial value as in table 1 and parameters of virus spread as in table 2.

Based on equation (1), the initial values and parameter values in table 1 and table 2 are simulated with the Runge Kutta Order 4, so that the following graphs are obtained.

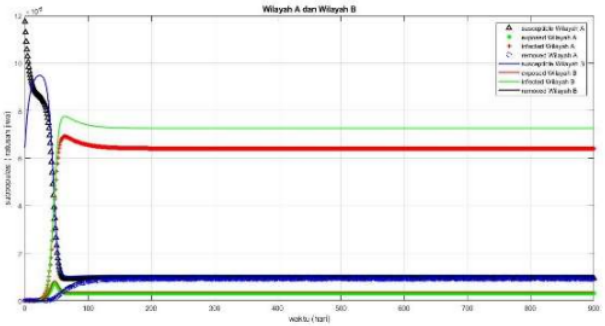

Figure 2. Changes in subpopulation in region A and region B.

Based on figure 2, changes in subpopulations in regions A and region B experienced an increase in the infected subpopulation. It occurs because the virus transmission rate is very high and the transmission rate in region B is greater than region A. In days 200 to 900, they begin to show a stable state. Region A and region B are endemic state with $R_0 > 1$, namely $R_0 = 3.0245747$.

Table 1. Initial value of region A and region B.

Subpopulation at $t=0$	Initial value	Subpopulation at $t=0$	Initial value	Subpopulation at $t=0$	Nilai awal	Subpopulation at $t=0$	Initial value
S_1	11.744.951	S_2	6.440.000	I_1	127	I_2	130
E_1	113	E_2	119	R_1	87	R_2	89

Table 2. Parameters of region A and region B.

Parameter	Region A	Parameter	Region B
a_1	0.03692	a_2	0.03658
b_1	0.03692	b_2	0.03658
θ_1	1	θ_2	1
β_1	0.4	β_2	0.4
ω_1	9.3133×10^{-8}	ω_2	9.3133×10^{-8}
γ_1	0.9	γ_2	0.9
k_1	0.005140	k_2	0.005140
α_1	0.09	α_2	0.08

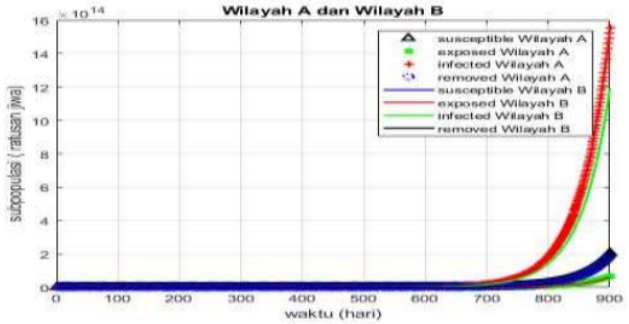

Figure 3. Region A and region B where the death rate is lower than the birth rate.

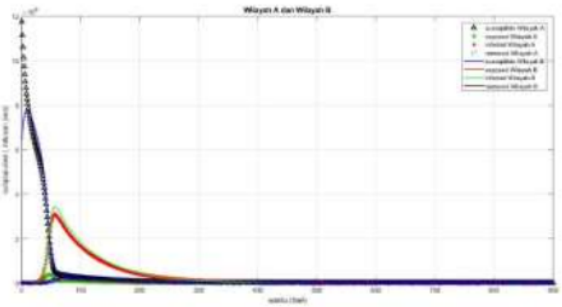

Figure 4. Region A and region B where the death rate is higher than the birth rate.

Based on figure 3, region A and region B have experienced an increase starting from day 700. This is due to the low mortality rate, resulting the spread of the virus which continues to increase. It can be seen that the infected subpopulation has experienced a very high increase. Based on figure 4, region A and

region B have decreased to near zero (0). This is because the death rate is higher than the defeat rate. So that each subpopulation has experienced a decline that is almost extinct.

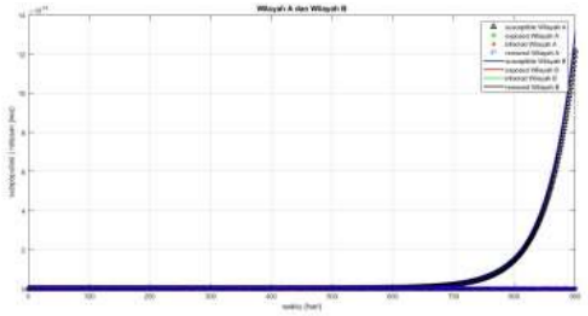

Figure 5. Region A and region B are disease Free.

Based on figure 5, regions A and region B do not have the spread of a disease. This is because there is no spread of the virus in the two regions. So that the susceptible subpopulation has increased and the subpopulation of exposed, infected, and removed has decreased to zero.

4. Conclusion

Based on results and discussion, they can be concluded that in the model of Ebola virus spread between two regions, there is Basic Reproduction Number as the threshold for stability at the disease-free equilibrium point. If $R_0 < 1$ then the disease-free equilibrium point is stable. If $R_0 > 1$ then the disease-free equilibrium point is unstable. The Basic Reproduction Number obtained is to determine the flow of virus spread. In the simulation, it is found that region B has a higher spread than region A, because there is a higher transmission of the virus in region B than in region A according to the graph of cases of the spread of the Ebola virus.

Acknowledgement

The author would like to thank the Ministry of Research and Technology (National Research and Innovation Agency of the Republic of Indonesia) for funding the publication of this scientific article in year 2020.

References

[1] Bray M dan Chertow D S 2015 *Epidemiology and Pathogenesis of Ebola Virus Disease* www.uptodate.com/contents/epidemiology-and-phatogenesis-of-ebola-disease, accessed on 25 August 2019

[2] WHO (World Health Organization) 2015 *Ebola Situation Report* http://www.who.int/ accessed on 25 August 2019

[3] Hariyanto, Widodo B and Budiantara I N 2013 The Construction of a model pre-coalition between H1N1-p and H5N1 influenza virus in Indonesia *Journal of Applied Mathematical Sciences, Hikari Ltd.* **7** 4899-4907

[4] Atangana A and Goufo E F D 2014 On mathematical analysis of Ebola haemorrhagic fever: deathly infection disease in West African countries *Journal of Biomed Research International* **2014** 261383 1-11

[5] Li Z, Teng Z, Feng X, Li Y and Zhang H 2015 Dynamical analysis of an SEIT epidemic model with application to Ebola virus transmission in Guinea *Journal of Computational and Mathematical Methods in Medicine* **2015** 582625

[6] Rohmah A M, Hariyanto, Imron C, Kisnosaputra R A 2017 Simulasi model penyebaran virus Ebola antar dua Negara dengan Runge Kutta orde 4 *Prosiding Seminar Nasional Matematika dan Pembelajarannya 2017* **3** 32-38
[7] Driessche P V and Wetmough J 2002 Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission *Journal of Mathematical Biosciences* **180** 29-48

SEIR model simulation on the spreading of Ebola virus between two regions

ORIGINALITY REPORT

19%	16%	12%	5%
SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS

PRIMARY SOURCES

1	centaur.reading.ac.uk Internet Source	2%
2	R Ratianingsih, H Hajar, A A Rahmah, A I Jaya. "The sensitivity of Covid-19 spread model parameter: an effort to point out the importance of the detection program", Journal of Physics: Conference Series, 2021 Publication	2%
3	G Saini, Seema, K Mor. "Machine Learning and Prophecy of Behavior: A Breakthrough in Artificial Intelligence", IOP Conference Series: Materials Science and Engineering, 2021 Publication	1%
4	digitalcommons.pvamu.edu Internet Source	1%
5	www.science.gov Internet Source	1%
6	eprints.unmus.ac.id Internet Source	1%

7	www.gssrr.org Internet Source	1 %
8	china.iopscience.iop.org Internet Source	1 %
9	www.teses.usp.br Internet Source	1 %
10	sinta3.ristekdikti.go.id Internet Source	1 %
11	Submitted to Kaplan International Colleges Student Paper	1 %
12	Www.medicalnewstoday.com Internet Source	1 %
13	libtreasures.utdallas.edu Internet Source	1 %
14	Teguh Herlambang, Dinita Rahmalia, Nur Aini, Denis Fidita Karya. "Predator-prey dynamical model with infected prey by virus and its optimal control using pesticide", AIP Publishing, 2022 Publication	<1 %
15	Arief Yuswanto Nugroho, Fatichatur Rachmaniyah. "FENOMENA PERKEMBANGAN CROWDFUNDING DI INDONESIA", Ekonika : Jurnal ekonomi universitas kadiri, 2019 Publication	<1 %

16	Submitted to Indian Institute of Technology Student Paper	<1%
17	istina.ipmnet.ru Internet Source	<1%
18	Allen, L.J.S.. "The dynamics of two viral infections in a single host population with applications to hantavirus", Mathematical Biosciences, 200312 Publication	<1%
19	Pubs.asahq.org Internet Source	<1%
20	eprints.utm.my Internet Source	<1%
21	Hariyanto, Lukman Hanafi, Suhud Wahyudi. "Density and persistence analyze on the spreading models multi-regions multi-patchs", AIP Publishing, 2017 Publication	<1%
22	advancesindifferenceequations.springeropen.com Internet Source	<1%
23	ejournal.unsrat.ac.id Internet Source	<1%
24	soar.wichita.edu Internet Source	<1%

25	Hariyanto, Basuki Widodo, I Nyoman Budiantara, C.A. Nidom. "The construction of a model of pre-coalition between H1N1-p and H5N1 influenza virus in Indonesia", Applied Mathematical Sciences, 2013 Publication	<1 %
26	Afina Azizah, Purnami Widyaningsih, Dewi Retno Sari Saputro. " Spread of Ebola disease with susceptible exposed infected isolated recovered (SEII R) model ", Journal of Physics: Conference Series, 2017 Publication	<1 %
27	Faïçal Ndaïrou, Delfim F. M. Torres. "Mathematical Analysis of a Fractional COVID-19 Model Applied to Wuhan, Spain and Portugal", Axioms, 2021 Publication	<1 %
28	Jon Michael Gran. "Growth rates in epidemic models: Application to a model for HIV/AIDS progression", Statistics in Medicine, 10/15/2008 Publication	<1 %

Exclude quotes	Off	Exclude matches	Off
Exclude bibliography	On		

SEIR model simulation on the spreading of Ebola virus between two regions

GRADEMARK REPORT

FINAL GRADE

/0

GENERAL COMMENTS

Instructor

PAGE 1

PAGE 2

PAGE 3

PAGE 4

PAGE 5

PAGE 6

PAGE 7

PAGE 8

PAGE 9