Mathematical fitting model and analysis in describing Covid-19 viruses outbreak in Indonesia

F Ilahi1,*, M A Ibrahim2, D Gojali3, A Akmaliyah4 and D Mashudi5

1 Department of Mathematics, Faculty of Science and Technology, UIN Sunan Gunung Djati, Bandung, Indonesia
2 Department of Islamic Finance, Faculty of Sharia, UNISBA, Bandung, Indonesia
3 Jurusan Manajemen Keungan Syariah, Fakultas Ekonomi dan Bisnis Islam, UIN Sunan Gunung Djati, Bandung, Indonesia
4 Jurusan Sastra Arab, Fakultas Adab dan Humaniora, UIN Sunan Gunung Djati, Bandung, Indonesia
5 Jurusan Perbandingan Mazhab dan Hukum, Fakultas Syariah dan Hukum, UIN Sunan Gunung Djati, Bandung, Indonesia

*fadilah.ilahi@uinsgd.ac.id

Abstract. The outbreak of novel coronavirus at the end of 2019 (covid-19) has become a global concern due to its fast transmission from human-to-human. It is first time discovered in Wuhan, Hubei Province in China. In this research, the author tries to construct epidemiological model that consist of six subpopulations such as susceptible (S), exposed (E), infected (I), isolated (Q), recovered (R), and dead (D) population. Those compartments will be analyzed to get basic reproduction number (\(R_0\)). The data used in this research is secondary data that obtained from the recent study and various news report related to the covid-19 outbreak. Fitting method will be carried out to describe the virus outbreak and see the trend of the future condition based on the real observation data and the mathematical function that has been determined. The expected result of this research is that the mathematical fitting model and its analysis helping the epidemiologist and health practitioner to determine the right treatment to stop the outbreak so that the society could be back to virgin population.

1. Introduction
Covid-19 is an infection caused by Severe Acute Respiratory Syndrome Corona Virus-2 (SARS-CoV-2). It is first discovered in the late December 2019 in Wuhan, the capital of Hubei Province in China [1-7]. The transmission of this virus is human-to-human transmission. This kind of transmission makes the spread of the disease become fast and infected in a large scale. The actual disease is caused when the virus alight on the mucous membrane in the eye, nose and/or mouth from the droplets of infected people to the susceptible people [3,4,6]. It is commonly attacked to the people with the low of immune system such as the elderly and the people that has degenerative disease. World Health Organization (WHO) declared that Covid-19 become the pandemic because its spread globally. More than 150 countries and 2 international conveyances have been affected. Right now, more than 800.000 people has infected since its first case in December 26, 2019 in all over the world [2,4,5].
Today, covid-19 itself is already become a main concern of Indonesia. The government through the media is intensively campaigned and recommended the society to do the social and physical distancing because it is believed as a right treatment before the vaccine and the medicine is found. From the 25th day of the first case in Indonesia, covid-19 has infected 1.528 people in the 31 provinces in Indonesia [5].

In this article, the authors try to construct the model for the covid-19 to see the trend of the spread of the disease. This model is include the dynamical model, construction of basic reproduction number, and fitting model to approach the real observation data.

2. Methods

In this paper, the methodology that used consist of the construction of the assumptions and the mathematical model, including the interaction diagram and also the analysis of the basic reproduction number. The fitting model will be done by least square approximation based on the real data of covid-19 in Indonesia. We will construct epidemic model based on modified SEIR model, which population consist of six subpopulations such as susceptible, exposed, infected, isolation, recovered and dead population. This model using autonomous ordinary differential equation where each compartments depends on variable of time $t$. The assumptions are also given to create the simple model but still relevant to the real life problem.

2.1. Assumptions

Before we construct the formula for the covid-19 case, we begin to make some assumptions to understand several things that really influenced on the construction of mathematical model. Assumed that population is to be closed and the total population is constant. The recruitment rate on susceptible subpopulation is constant. The exposed population brings the incubation of the virus, but they are not include to the infected yet because there is a possibility to recover by themselves such as with the immune system. The natural death for each compartment has the same value and constant but, in this article, the author tries to focus on the death caused by the infection from the subpopulation infected and quarantined (isolated), so there is a death caused by the infection. After recovered, every people have the possibilities to get the second infection that is why they move back to the susceptible population. In the following diagram, the arrow describe the addition or the subtraction the parameters from one compartment to the others. To give the overview of the assumption, here is the following interaction diagram that represents the model.

![Figure 1. Diagram interaction of each compartment.](image)

2.2. Mathematical model

Based on the diagram interaction above, here is the mathematical model that we construct for general case of covid-19.

This following table is describe all variables and parameters that has been used for the model.
Table 1. List of variables and parameters.

| Notation | Description                                | Constraint |
|----------|--------------------------------------------|------------|
| S        | Susceptible subpopulation                  | $S > 0$    |
| E        | Exposed subpopulation                      | $E > 0$    |
| I        | Infected subpopulation                     | $I > 0$    |
| Q        | Quarantined (Isolated) subpopulation       | $Q > 0$    |
| R        | Recovered subpopulation                    | $R > 0$    |
| D        | Death subpopulation                        | $D > 0$    |
| N        | Total population                           | $N > 0$    |
| A        | Recruitment rate                           | $A > 0$    |
| c        | Probability of individual in a self-quarantine | $0 < c < 1$ |
| m        | Probability of disease spread              | $0 < m < 1$ |
| $\delta$| Transition from exposed to infected subpopulation | $0 < \delta < 1$ |
| $\eta$  | Transition from infected to isolated subpopulation | $0 < \eta < 1$ |
| $\rho$  | Transition from isolated to recovered subpopulation | $0 < \rho < 1$ |
| $\gamma$| Transition from recovered to susceptible subpopulation | $0 < \gamma < 1$ |
| $\mu_I$ | Death caused by the infection from infected subpopulation | $0 < \mu_I < 1$ |
| $\mu_Q$ | Death caused by the infection from infected subpopulation | $0 < \mu_Q < 1$ |

The diagram from Figure 1 can be written as a system in mathematics formula using autonomous ordinary differential system such as:

$$
\dot{S} = A + cS - \frac{(m - c)}{N}SE - \frac{(m - c)}{N}SI + \gamma R
$$

$$
\dot{E} = -cS + \frac{(m - c)}{N}SE + \frac{(m - c)}{N}SI - \delta E
$$

$$
\dot{I} = \delta E - (\eta + \mu_I)I
\dot{Q} = \eta I - (\rho + \mu_Q)Q
\dot{R} = \rho Q - \gamma R
\dot{D} = \mu_I I + \mu_Q Q
$$

Furthermore, if there is an endemic around the population, the important thing to identify is basic reproduction number. Basic reproduction number or usually known as $R_0$ is the number that representing the average secondary infection caused by one individual infection. This number is the greatest eigen value from next generation matrix. For this model, basic reproduction number is describe as

$$
R_0 = \frac{2(m - c)}{c\delta}
$$

where $R_0 < 1$ is the condition for disease free it is achieved when the self-quarantine effort more than two times of disease spreads or mathematically when $c > \frac{2m}{\delta+2}$ while $R_0 > 1$ is the condition in for endemic that achieved when $c < \frac{2m}{\delta+2}$. According to the system (1) above and substituting the real observation data of covid-19 in Indonesia, the $R_0$ is in the value of 3.33. This value is still in the range...
of basic reproduction number according to World Health Organization (WHO) calculation that is in the interval 3-5 in once transmission. So if we had $R_0 = 3.33$ that means that every single infected person could spread the virus to three people simultaneously. By having this number of $R_0$ the spread of this disease reached the global pandemic rapidly.

3. Results
Besides construct the model by ordinary differential system, the other way to see the trend of the covid-19 case is through the fitting model. This empirical model is using least square criterion, which can be approached by linear model or non-linear model to estimate the slope and the intercept of the observation data. By this approximation, the trend of the curve could be determined and also could predict the future incidence. Perhaps, this quadratic equation is still a rough prediction because the function would be blow up in a bigger size of number as time goes by while the expectation of everybody that this covid-19 case would be decrease and the curve would be flattened. However, this is one of the method to that we could used to fit the experimental data.

The least square criterion to fit the covid-19 curve is using non-linear function such as,

$$y = ax^2$$

Where

$$a = \frac{\sum x_i^2 y_i}{\sum x_i^4}$$

The reason is because the observation data for total case, total recovery, and total death of covid-19 in Indonesia and global world is still following the exponential function and it has the curve upward-parabola-like curve. The data is observed from the first cases which is in March 2nd until April 4th 2020 (33 days after the first case). The real observation data obtain from World meters [8-12]. The slope for the covid-19 case is obtained in the value of $a = 1.7; a = 0.1; a = 0.154$ respectively for total cases, total recovery, and total death caused by the covid-19 in Indonesia.

The chart below is describing the difference of observation and fitting data.

![Figure 2. Chart for total cases of covid-19 in Indonesia.](image)

According to Figure 2, the fitting model for total case of covid-19 in Indonesia approaches the real data in the beginning seven days then it is stay away then until the 26 days. The fitting data is somehow give the higher number than the real data, but at the end of the period, it moves slower than the real observation data.
Based on the observation data, the total recovery data of covid-19 in Indonesia is kind of fluctuate, so the fitting data is quite away for the whole period of the research. It just only approaches the real data in the beginning of eight days since the first confirmed case in March 2\textsuperscript{nd}.

The observation data of the total death of covid-19 in Indonesia is still appropriate to fit by fitting model in the equation (3) even though there are so many missed data from the real data. The fitting data approaches the beginning of the period, then it diverge mostly the data. It is sometime has the higher value than the real data, but eventually the fit model get the data slower than the observation data.

4. Discussion
According to the model of the system (1) and equation (3), the covid-19 case in Indonesia can be described mathematically to find the value of $\mathcal{R}_0$ and make the difference between observation real data and the empirical data.

The $\mathcal{R}_0$ is quite high because in can spread the virus to three other people per transmission. So it is very possible to make the data follows the exponential function and it will getting higher every single day. In this model, to supress the transmission of the virus, the author include the self-quarantine in
order to decrease the disease and the peak of the exponential function. For the information, the cure and the vaccine can be found yet, so the self-quarantine is one of the right treatment to stop the transmission of covid-19.

The fitting model is determined for the three conditions such as total case, total recovery, and total death for 34 days from the first confirmed case in Indonesia on March 2nd 2020. This empirical model is quite good to fit the total case, even though there are many data has not been approached by the fitting curve. While the total recovery and total death needs some revision in determining a fitting model or function.

5. Conclusion
According to the explanation by analysis and simulation, the self-quarantine is still considered to be the effective ways to prevent the spread of covid-19 in the society before the cure and the vaccine found. However, this model is just a rough description for covid-19 case in Indonesia and the author realizes for some revision. But at least the model can be used as an initial reference for the community, practitioner, and mathematician who works in epidemiology model.

Acknowledgement
This paper is written for the 4th Annual Applied Science and Engineering Conference (AASEC) 2020 organized by Universitas Pendidikan Indonesia (UPI) and UIN Sunan Gunung Djati as a co-host. This research is fully funded and supported by Lembaga Penelitian dan Publikasi UIN Sunan Gunung Djati Bandung.

References
[1] Zhou P, Yang X-L, Wang X-G, Hu B, Zhang L, Zhang W, Si H-R, Zhu Y, Li B and Huang C-L 2020 A pneumonia outbreak associated with a new coronavirus of probable bat origin Nature 579 270–3
[2] Luo X, Feng S, Yang J, Peng X-L, Cao X, Zhang J, Yao M, Zhu H, Li M Y and Wang H 2020 Analysis of potential risk of COVID-19 infections in China based on a pairwise epidemic model
[3] Phan L T, Nguyen T V, Luong Q C, Nguyen T V, Nguyen H T, Le H Q, Nguyen T T, Cao T M and Pham Q D 2020 Importation and human-to-human transmission of a novel coronavirus in Vietnam N. Engl. J. Med. 382 872–4
[4] Li G and De Clercq E 2020 Therapeutic options for the 2019 novel coronavirus (2019-nCoV)
[5] Susilo A, Rumende C M, Pitoyo C W, Santoso W D, Yulianti M, Herikurniawan H, Sinto R, Singh G, Nainggolan L and Nelwan E J 2020 Coronavirus Disease 2019: Tinjauan Literatur Terkini J. Penyakit Dalam Indones. 7 45–67
[6] Kampf G, Todt D, Pfaender S and Steinmann E 2020 Persistence of coronaviruses on inanimate surfaces and their inactivation with biocidal agents J. Hosp. Infect. 104 246–51
[7] Peng L, Yang W, Zhang D, Zhuge C and Hong L 2020 Epidemic analysis of COVID-19 in China by dynamical modeling arXiv Prepr. arXiv2002.06563
[8] BBC News Indonesia 2020 Virus corona: Jika terkena, seberapa besar tingkat kematian dan peluang kita untuk bertahan hidup?
[9] B.M. C and R.A K 2020 Akan Sampai Kapan Perjuangan Kita Melawan Pandemi Covid-19?
[10] Lauer S A, Grantz K H, Bi Q, Jones F K, Zheng Q, Meredith H R, Azman A S, Reich N G and Lessler J 2020 The incubation period of coronavirus disease 2019 (COVID-19) from publicly reported confirmed cases: estimation and application Ann. Intern. Med. 172 577–82
[11] Soewono E 2020 On the analysis of Covid-19 transmission in Wuhan, Diamond Princess and Jakarta-cluster Commun. Biomath. Sci. 3 9–18
[12] WHO 2020 Q&A on coronaviruses (COVID-19)