



Analysis of COVID-19 Disease Using Fractional Order SEIR Model

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Abstract: In this study, the spread of COVID-19 pandemic disease model is analyzed using fractional order SEIR model. Fractional order is concept of calculus such as derivative and integral that is measured by using non-natural order that recently being used in various applications in real-world such as engineering, physics, chemistry, biology etc. Starting from this concept, the mathematical model is used in this study is in the form of a dynamical system consisting of nonlinear fractional differential equations with order one. These equations represent four compartments with certain health conditions. Those four compartments are susceptible, exposed, infected and recovered that are considered to have a significant influence in the development of COVID-19 infectious diseases. Having described the model, some analysis in terms of region of the solutions, the equilibrium points and reproduction number are measured in which is useful in describing qualitatively the stability of the system described. This dynamical system is solved numerically and simultaneously by using a modification of the Euler method. The results obtained are the graphs that describe the behaviour of four compartments in which giving predictive results about how the disease behaves with various orders. This approach has the advantage in terms of giving flexibility in approaching the real case that is happening in the world.

Keywords: SEIR Model, Fractional Calculus, Dynamical System

1. Introduction

In early 2019, COVID-19 is first reported in Wuhan, China. Then in the following weeks, the transmission spread widely to mainland China, other countries including Indonesia, causing a global panic. On April 19, 2020, Globally recorded [18] 2,548,185 people infected with the coronavirus with a total of 173,959 deaths and 778,537 have recovered. COVID-19 as well as influenza has a presentation resulting in respiratory disorders, which appear as a variety of diseases ranging from asymptomatic or mild to severe illness and death. The spread of this virus can occur because of the close distance between individuals, from the respiratory tract such as sneezing and coughing splashes and contact with objects that are often touched. It is therefore important to know the mathematical model of the development of COVID-19 specifically, such as the prevalence and duration of a pandemic and its impact on a

population. With the knowledge of the COVID-19 development model it is expected that it can help policymakers in the health sector to determine the best strategies when dealing with this infectious disease, such as mass vaccination programs, use of antiviral drugs, pest control, disinfection as well as establishing isolation and quarantine rules. Mathematical modeling is used to describe reality or make prediction of possibilities that transpire in the future scientifically. Nevertheless, mathematical modeling is somewhat limited in representing a problem due to the limited ability to estimate with a large number of input parameters. For instance, when modeling infectious diseases there is usually a number of parameters that might affect such as weather conditions, healthier per individual in a population that can be ignored. Consequently, it is essential to identify which

parameters have a significant impact on modeling to reduce errors that occur and simultaneously have an appropriate picture of the evolution of a disease. In an epidemic mathematical model, the spread of infectious diseases is distributed into compartments in a population, each group representing a particular health condition with an increasing infectious agent. This model is quite dynamic because the number of individuals from each compartment can fluctuate over time by changing health conditions. This concept has an important role in the process of spreading diseases such as COVID-19 in a certain period.

- Susceptible: The group of population that possibly can be infected
- Exposed: The group of population who have been infected but not yet infectious
- Infected: The group of population that have been infected, who are capable of transmitting the disease
- Removed: The group of population that have cured or dead and buried.

According on the assumed compartments, there are various other epidemic models, such as the SIS model [7], the SIRS model [11]. Epidemic models have been implemented successfully against various infectious diseases such as HIV / AIDS [14], Ebola Latha et al. [12], Influenza and Cancer [8], and COVID-19 [4]. Currently, fractional derivatives have been used to describe epidemic models and are proven to be accurate in certain cases, when compared to classical orders (natural number orders) such as SIR model [16], SEIR model [5], SIRC model [6, 1] and others. This study analyzed the spread of the COVID-19 pandemic using the fractional order SEIR method, where the spread of this disease is described into a dynamical system in the form of nonlinear differential equations with fractional order. The use of this fractional order is considered to be more advantageous because the fractional derivative is a non-local operator and also the fractional order is any positive number α , which can be chosen which order is closest in describing the graph of an infectious disease. This dynamical system is transformed and the solution is numerically obtained using Euler's Method.

2. Fractional Calculus

Fractional calculus is an extension of the ordinary calculus, by considering integrals and derivatives of arbitrary real or complex order [10, 15]. Currently there are various kinds of definitions for fractional derivatives, some which are the Riemann, Caputo [13], and conformable [9] which are generalized from the natural order of classical calculus. In this section presents some important definitions of Fractional Calculus.

Definition 1. The Riemann- Liouville fractional Integral of order $\alpha \in (0, 1]$ is defined as:

$$J^\alpha f(t) = \frac{1}{\Gamma(\alpha)} \int_0^t (t-u)^{\alpha-1} f(u) du,$$

for $t > 0$.

Definition 2. The Riemann- Liouville fractional derivatives of order $\alpha \in (0, 1]$ is defined as

$$D_t^\alpha = \frac{d}{dt} J^{1-\alpha} f(t)$$

Definition 3. The Caputo fractional derivatives of order $\alpha \in (0, 1]$ is defined as

$$D_t^\alpha = \frac{d}{dt} J^{1-\alpha} f(t)$$

If m and n are integers such that $m > n$, then n -th order derivative of t^m (using Euler's Gamma Function) is

$$\frac{d^n}{dt^n} t^m = \frac{\Gamma(m+1)}{\Gamma(m-n+1)} t^{m-n}$$

3. Model Analysis

This section discusses model description that is used to analysis the disease, the region of solutions where the solutions remain invariant, equilibria of the system defined, the reproduction number which is the average number of the secondary cases generated by a typical infective within a populatin with no immunity to the disesase, and stability analysis of the system.

3.1. Model Analysis

The model in this paper is a fractional order SEIR epidemic model with fractional order. The population $N(t)$ is partitioned into four compartments which are susceptible, exposed, infected and removed denoted by $S(t), E(t), I(t), R(t)$, respectively:

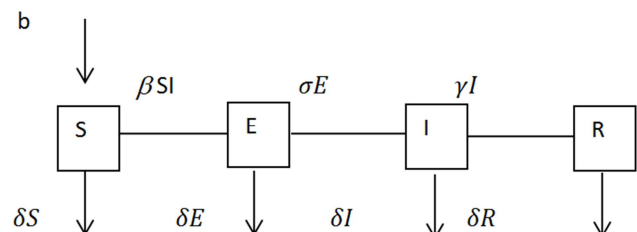


Figure 1. SEIR DIAGRAM.

- 1) Susceptible: Number of susceptible individuals, who can be infected
- 2) Exposed: Number of exposed individuals, who have been infected but not yet infectious
- 3) Infected: Number of infectious cases in the community, who are capable of transmitting the disease
- 4) Removed: Number of individuals removed from the chain of transmission. (cured or dead and buried)
- 5) b : constant influx of new susceptibles
- 6) δ : The death rate
- 7) βSI : The bilinear incidence term
- 8) σ : The incubation rate
- 9) γ : The recovery rate

The model of this problem is [3]

$$\begin{cases} D^\alpha S(t) = b - \beta SI - \delta S \\ D^\alpha E(t) = \beta SI - \sigma E - \delta E \\ D^\alpha I(t) = \sigma E - \delta I - \gamma I \\ D^\alpha R(t) = \gamma I - \delta R \end{cases} \quad (1)$$

with the initial conditions

$$S(0) = S_0, E(0) = E_0, I(0) = I_0, R(0) = R_0 \quad (2)$$

Where

$$N(t) = S(t) + E(t) + I(t) + R(t),$$

In (1) D^α denotes the fractional Derivative having order $\alpha \in (0, 1]$ if $\alpha = 1$, then the system becomes the Classical derivative with first order.

3.2. Region of the Solutions

Theorem 1. There exists a unique solution for the initial value problem given by (1)-(2) and the solution belongs to

$$\mathbb{R}_+^4 = \{S, E, I, R \in \mathbb{R}^4: S, E, I, R \geq 0\}.$$

To prove the theorem 1, the mean value theorem [17] is established

Theorem 2. Let $f \in C[a, b]$ and $D^\alpha f(x) \in C[a, b]$ with $\alpha \in (0, 1]$, then

$$f(x) = f(a) + \frac{1}{\Gamma(\alpha)} D^\alpha f(\zeta)(x - a)^\alpha$$

where $\zeta \in [a, x]$, for all $x \in (a, b]$

Proof. The proof is available in [17].

Proof of Theorem 1. Based on the theorem (2) let $f \in C[a, b]$ and $D^\alpha f(x) \in C[a, b]$ with $\alpha \in (0, 1]$. If $D^\alpha f(x) \geq 0$ for all $x \in (0, b)$, then f is monotonically increasing and if $D^\alpha f(x) \leq 0$ for all $x \in (0, b)$, then f is monotonically decreasing. Thus, there exists unique solution for system (3.1) and the solution belongs to \mathbb{R}_+^4 .

3.3. Equilibria, Reproduction Number and Stability

Theorem 3. The system (1) has at most two categories equilibrium points:

- A disease free equilibrium point $E_f = (\frac{b}{\delta}, 0, 0, 0)$
- A endemic equilibrium point $E_e = (S^*, E^*, I^*, R^*)$, with

$$\begin{aligned} S^* &= \frac{(\sigma + \delta)(\gamma + \delta)}{\beta\sigma} \\ E^* &= \frac{b\sigma\beta - \delta^3 - \delta^2\gamma - \delta\gamma\sigma}{\beta\sigma(\delta + \sigma)} \\ I^* &= \frac{b\sigma\beta - \delta^3 - \delta^2\gamma - \delta\gamma\sigma}{\beta(\delta + \gamma)(\delta + \sigma)} \end{aligned}$$

$$S(t_i + 1) = S(t_i) + \frac{h^\alpha}{\Gamma(\alpha + 1)} (b - \beta S(t_i)I(t_i) - \delta S(t_i))$$

$$E^* = \frac{b\sigma\beta - \delta^3 - \delta^2\gamma - \delta\gamma\sigma}{\delta\beta(\delta + \gamma)(\delta + \sigma)}.$$

Proof. The equilibrium points are computed by evaluating the right hand sides of the four equations given in (3.1) equal to zero.

Theorem 4. The system (3.1) has the reproduction number

$$R_0 = \frac{b\beta\sigma}{(\gamma + \delta)(\sigma + \gamma)}.$$

Proof. Using Next Generation Method (NGM) given by

$$K = FV^{-1}$$

Where

$$F = \begin{pmatrix} 0 & b\beta \\ 0 & 0 \end{pmatrix}$$

And

$$V^{-1} = \begin{pmatrix} \frac{\delta + \gamma}{(\delta + \gamma)(\delta + \sigma)} & 0 \\ \frac{\sigma}{(\delta + \gamma)(\delta + \sigma)} & \frac{\delta + \sigma}{(\delta + \gamma)(\delta + \sigma)} \end{pmatrix}$$

Therefore,

$$K = \begin{pmatrix} \frac{b\beta\sigma}{(\delta + \gamma)(\delta + \sigma)} & \frac{b\beta(\delta + \sigma)}{(\delta + \gamma)(\delta + \sigma)} \\ 0 & 0 \end{pmatrix}$$

This is Next generation Operator. Taking the largest eigenvalue of this matrix, then the reproduction number is obtained as follows,

$$R_0 = \frac{b\beta\sigma}{(\gamma + \delta)(\sigma + \gamma)}.$$

The disease free equilibrium E_f of system (1) is locally asymptotically stable if

$$\frac{b\beta\sigma}{(\gamma + \delta)(\sigma + \gamma)} < 1$$

and the endemic equilibrium E_e of system (1) is locally asymptotically stable if

$$\frac{b\beta\sigma}{(\gamma + \delta)(\sigma + \gamma)} > 1$$

4. Numerical Results

The method used in determining the solution of the system (1) is the Euler method [17]:

$$E(t_i + 1) = E(t_i) + \frac{h^\alpha}{\Gamma(\alpha + 1)} (\beta S(t_i) I(t_i) - \sigma E(t_i) - \delta E(t_i))$$

$$I(t_i + 1) = I(t_i) + \frac{h^\alpha}{\Gamma(\alpha + 1)} (\sigma E(t_i) - \delta I(t_i) - \gamma I(t_i))$$

$$R(t_i + 1) = R(t_i) + \frac{h^\alpha}{\Gamma(\alpha + 1)} (\gamma I(t_i) - \delta R(t_i)).$$

Models simulations are performed using *Python* software. The initial values (started from 02 March 2020) $S(0), E(0), I(0), R(0)$ and parameter values of the models used in this simulation are presented in Table below [18, 2], with basic reproduction number R_0 obtained above.

Table 1. PARAMETER / VARIABLE VALUES.

PARAMETER / VARIABLE	ESTIMATED VALUE
$S(0)$	$N(0) - E(0) - I(0) - R(0)$
$E(0)$	2
$I(0)$	0
$R(0)$	0
b	1.845×10^{-2}
δ	6.25×10^{-3}
β	2.3×10^{-2}
σ	2×10^{-1}
γ	6.65×10^{-4}

Using the Generalized *Euler's Method*, the following results from Figure 2- Figure 4 were obtained.

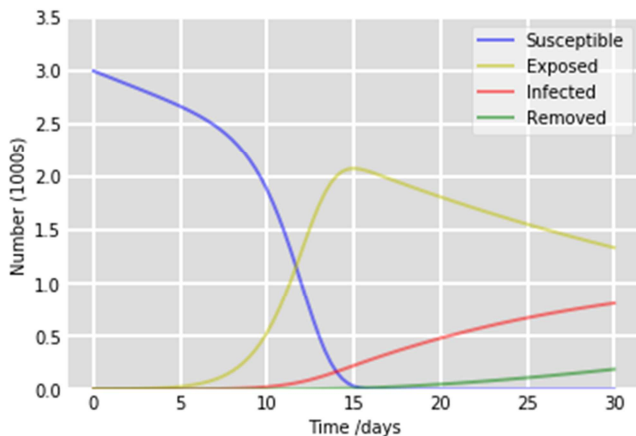


Figure 2. ORDER $\alpha = 1$.

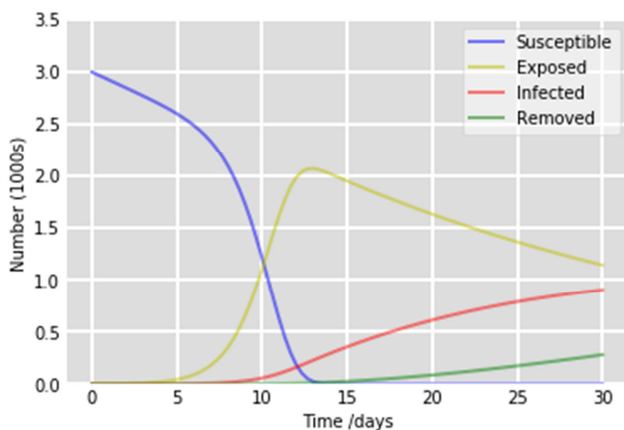


Figure 3. ORDER $\alpha = 0.9$.

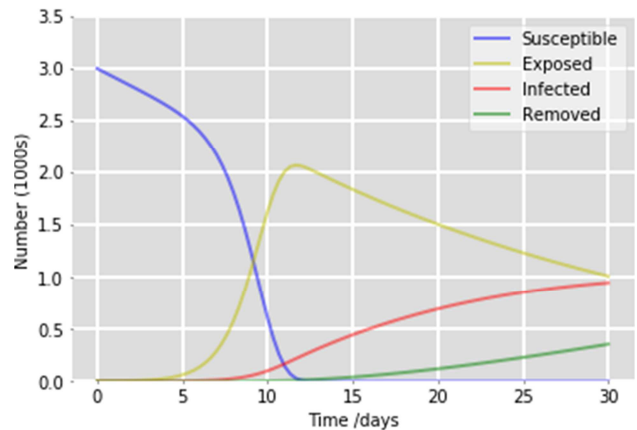


Figure 4. ORDER $\alpha = 0.8$.

These are the simulation results of various fractional order variations in 30 days per 3000 population. It can be seen in the figure that there are differences by applying for each ORDER. Those who are susceptible are people who contract the disease will reach the minimum point on the nearly 20-25th day for each order. In other words, on that day there may be no more people who intentionally contract the disease. Furthermore, in the exposed category on the first day to the 20-25th day, the cases continued to increase and reached a peak on that day and then decreased on the next day. Then in the infected category, each order has a monotonically increasing graph it is nearly on interval 750-1000. Then, in the category of Removed each or nearly 200-300 populations that were categorized as Removed on the last day which has shown us it is growing up slowly. In this case, it shows that the fractional order has flexibility in approximating the problem.

5. Conclusion and Future Work

This research is to study and analyze the Spread of the COVID-19 Pandemic in Indonesia using Fractional Order SEIR Model. This mathematical model is in the form of a dynamic system consisting of nonlinear fractional differential equations. These equations are compartments with certain health conditions that are considered to have a significant influence on the development of the COVID-19 infectious disease. This dynamical system is transformed and the solution is numerically obtained using a Generalized Euler's method. Numerical results obtained with Python software. Using Fractional order varied predictions has been obtained regarding the development of the spread of the COVID-19

infectious disease depending on time for the value of its parameters. In the future, there are many extension can be used to make better measurement in studying the spread of COVID-19 or generally any diseases such as adding the compartment of the population, extending the deterministic model by using stochastic models, or using a better modification method in solving the model.

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