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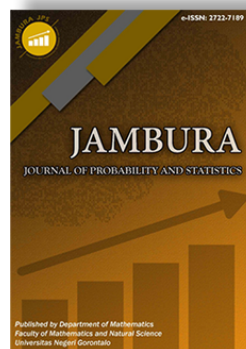
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Research Article

Exploring of Homotopy Perturbation Method (HPM) for Solving Spread of COVID-19

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ABSTRACT. *This article discusses the solution to the non-linear differential equation system for the spread of COVID-19 with SEIR (Susceptible, Exposed, Infected, Recovered) model using the Homotopy Perturbation Method. Specifically, this article examines the impact of moving the recovered subpopulation back to the susceptible subpopulation on the spread of COVID-19 in the city of Medan. The data used is real data for the city of Medan in 2021. The results of constructing a model for the spread of COVID-19 were analyzed to obtain a disease-free critical point. By using the Next Generation Matrix method, the Basic Reproduction number $R_0 = 4.61$ is obtained, this indicates that COVID-19 is still possible to spread in Medan City. Simulations using the Homotopy Perturbation Method numerical approach and the results compared with the Runge Kutte Order 4 method show results that accurately describe the dynamics of the spread of COVID-19 in Medan City. The very small error indicates that the Homotopy Perturbation Method is very suitable for use in solving non-linear differential equation systems, especially in the SEIRS model of the spread of COVID-19. The simulation results show that the impact of the movement of recovered sub-populations to susceptible sub-populations results in accelerated transmission of COVID-19. The greater the number of movements higher the rate of spread of COVID-19.*

1. Introduction

At the end of 2019, the international community was shocked by the emergence of the SARS-COV-2 virus, known as COVID-19, which is an infectious virus that attacks anyone, including babies, children, and adults. This virus spread rapidly throughout the world, so the World Health Organization (WHO) established COVID-19 as a global pandemic on March 8, 2020 [1]. How the COVID-19 spread system can be represented in mathematical modeling [2–5].

Mathematical modeling is one way of describing a real phenomenon or system using mathematical language. Through mathematical models, complex problems can be described more simply and easily understood. Mathematical modeling can also be used to analyze and predict system behavior through the use of mathematical concepts, principles, and and equations [6]. Mathematical modeling helps us predict the best way to control disease by taking into account how the disease spreads [7, 8]. Through the analysis of mathematical models, we can describe the dynamics of disease spread, determine critical points, test stability, determine the basic reproductive number (R_o), and examine the parameters that are most influential in the spread of disease. Many researchers use mathematical modeling to study the spread of infectious diseases. [9–14].

In general, in a system of non-linear differential equations, the analytic solution is difficult to find; therefore, a numerical approach is very appropriate to use to produce a solution. A nu-merical approach is a technique used to formulate mathematical problems so that they can be solved by ordinary arithmetic calculation operations or counting by using numbers [15]. The Homotopy Perturbation Method (HPM) is one of the various semi-analytical methods that serves to find solutions to various linear and nonlinear differential equations and linear and non-linear partial differential equations [16]. The result of the method is in the form of an infinite series [17]. The advantage of this method compared to other analytical methods is that HPM is a series expansion method that provides convergent series solutions, and the perturbation equation is easy to construct [18]. The Homotopy Perturbation Method (HPM), with the properties of accuracy and accuracy in determining exact solutions, is very suitable to be applied to modeling the spread of infectious diseases [19].

Some previous researchers have applied the Homotopy Perturbation Method (HPM) to infectious disease-spread problems, including: The analysis of the homotopy perturbation method (HPM) and its application for solving infectious disease models [19] discusses HPM as an effective approach to overcoming mathematical models that are difficult to solve analytically. The homotopy perturbation method for solving the SIR infectious disease model by incorporating vaccination discusses analytical solutions with HPM in the SIR model showing disease extinction within a certain period of time [20]. In Ayoade's research using the Homotopy Perturbation method on the dynamics of the spread of the mumps disease SIR model, the results confirm that HPM is able to solve the epidemic model [21].

This article discusses the spread of the COVID-19 SEIR

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model (Susceptible, Exposed, Infected, Recovered). By using real data for Medan City in 2021. In this study, a modified SEIR mathematical model was constructed by involving the parameter of moving the recovered sub-population back to the susceptible sub-population. The dynamic model is analyzed to see the dynamics of the spread of COVID-19 and how much impact the return of the cured sub-population to the susceptible sub-population has on the spread of COVID-19 in Medan City. The parameter values used in the simulation of the spread of COVID-19 refer to the mathematical model that has been studied by [22], and some parameter values used refer to previous researchers. Calculations and simulations were carried out with Matlab and Maple software, applying the homotopy perturbation method and the 4th-order Runge Kutta method.This article is divided into six sections. The first section reveals the background. Section two explains the theory of the Homotopy Perturbation Method and SEIR Model; section three discusses the process of analyzing the SEIR model and constructing the numerical scheme of the Homotopy Perturbation Method; section four, simulation and discussion; section five, conclusion; and acknowledgments in section six, submitted to Medan State University as the funder of this research.

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2. Homotopy Perturbation Method and Mathematical SEIR Model

2.1. Homotopy

Homotopy in mathematics is an approach used to classify geometric regions based on the different types of paths that can be formed within those regions. When two continuous functions can be continuously transformed into each other while maintaining the stability of their endpoints and remaining within the specified region, this is known as a homotopy between the two functions.

Consider X and Y as topological spaces, and f and g as continuous maps from X to Y. A homotopy between f and g is a continuous function $F : X \times [0, 1] \to Y$ that satisfies $F(x, 0) = f(x)$ and $F(x, 1) = g(x)$ for all x in X. If such a homotopy exists, we say that f is homotopic to g, denoted as $f \approx g$. If f is homotopic to a constant map, denoted as $f \approx \text{const}_y$, where y is an element in Y, then we say that f is nullhomotopic.

2.2. Homotopy Perturbation Method

The Homotopy Perturbation Method is an analytical technique used to solve both linear and nonlinear differential equations. It utilizes the concept of homotopy from topology to generate a series solution that converges and transforms the nonlinearities present in the system of differential equations into a homotopy-Maclaurin series. This method employs a power series expansion, which effectively converts the nonlinear terms into a sequence of linear equations. By employing the homotopy-

Maclaurin series, the Homotopy Perturbation Method enables the handling of the system's nonlinearities. When two continuous functions transition from one topological space to another and one transforms into the other, it is considered to be homotopic.

In accordance with [23], the homotopy perturbation technique involves introducing a parameter p, known as the homotopy parameter, which ranges from 0 to 1. As we begin the calculations, at $p = 0$, the system of equations simplifies to a basic form, resulting in a straightforward solution. As p increases towards 1, the system undergoes deformation, and the solutions mimic the progressive stages of deformation. At $p = 1$, the system assumes its unique equation form, and in the final stage of deformation, the desired solution to the system of equations is obtained. An important characteristic of the HPM is that typically only a few perturbation terms are needed to achieve an accurate solution.

Let's consider the following functions:

$$A(u) - f(r) = 0 \text{ where } r \in \Phi. \tag{1}$$

Subject to boundary conditions:

$$B\left(u, \frac{\partial u}{\partial n}\right) = 0 \text{ with } r \in D.$$

Here, we have $A, B, f(r)$, and D representing a general differential operator, a boundary operator, a known analytic function, and a boundary of the domain (Φ), respectively. The operator A is further divided into two components: the linear part (L) and the nonlinear part (N). With this information, eq. (1) can be written as follows:

$$L(u) + N(u) - f(r) = 0.$$

By using the homotopy technique, proposed by [24], we construct a homotopy: $(r, p) : \Phi \times [0, 1] \to R$ which satisfies:

$$K(v, p) = (1-p)[L(v) - L(v_0)] + p[L(v) + N(v) - f(r)] = 0 \tag{2}$$

and

$$K(v, p) = L(v) - L(u_0) + pL(u_0) + p[N(v) - f(r)] = 0. \tag{3}$$

Here, u_0 is an initial approximation of eq. (3) which satisfies the given conditions. Thus:

- At $p = 0$ then

$$K(v, 0) = L(v) - L(u_0).$$

- And at $p = 1$

$$K(v, 1) = A(v) - f(r) = 0.$$

As the parameter p changes from 0 to 1 then $(r, p$ changes from $u_0(r)$ to r this is called deformation in topology, and $L(v) - L(u_0)$ and $A(v) - f(r)$ are homotopic to each other. As $p \in [0, 1]$ is a small parameter, consider the solution of eq. (2) as a power series in p as indicated as:

$$v = v_0 + pv_1 + p^2v_2 + \cdots. \tag{4}$$

The solution of eq. (1) can also be obtained approximately as:

$$u = \lim_{p>1} v = v_0 + pv_1 + p^2v_2 + \cdots.$$

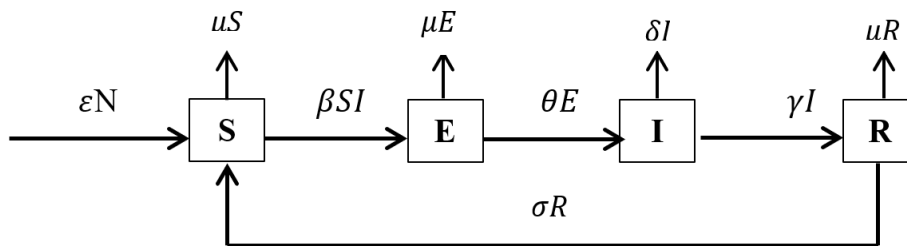Which represents the convergent series solution.

Figure 1. A Schematic Representation of SEIR Model

2.3. SEIR Model

The compartment model shown in Figure 1 is used to formulate a system of nonlinear differential equations, which is then incorporated into the Homotopy Perturbation Method. The obtained equations are subsequently solved to find analytical solutions for each compartment. In this research, a four-compartmental model is developed to study the dynamics of diarrhea transmission using ordinary differential equations [25].

Let N denote the total population of a specific region, the total population at a given time t can be expressed as:

From Figure 1, it can be classified that the *Susceptible* (S) population indicates that the presence of individuals in the human population who can contract the disease. The *Susceptible* population increases due to the population recruitment rate ε, and the population decreases because of *Susceptible* individuals who become infected with COVID-19 through effective contact with already infected individuals, where β is the *infective* contact rate. The population also increases due to individuals who recover after treatment, where σ is rate of movement of recovered sub populations to susceptible sub populations. However, the number of *Susceptible* individuals decreases due to natural death at the rate μ and formulated as:

$$\frac{dS}{dt} = \varepsilon N - (\beta I + \mu)S + \sigma R.$$

The *Exposed* individuals (E) are carriers of the virus but cannot infect *Susceptible* individuals. The population grows due to new infections from *susceptible* individuals who contract diarrhea through effective contact with people *infected* with COVID-19, where β represents the effective contact rate. The population declines due to the natural death rate μ and the transition from the *exposed* class to the *infected* class at the rate θ and formulated:

$$\frac{dE}{dt} = \beta SI - (\theta + \mu)E.$$

An *infected* individual (I) is defined as any person who has the pathogen and exhibits disease symptoms. This population is supplied by the *exposed* population, which becomes symptomatic at an infective rate θ. However, the *infected* population is reduced by the natural death rate θ, disease-induced death rate δ, and the treatment rate of *infected* individuals γ and formulated :

$$\frac{dI}{dt} = \theta E - (\gamma + \delta)I.$$

The *Recovered* individuals (R) are those who have *recovered* from the disease. Here, immunity is not permanent. The *Recovered* compartment is influenced by the treatment rate of *infected*

individuals, denoted by τ. Additionally, the population in this compartment also experiences a decline due to the natural death rate μ and the σ treatment waves and formulated :

$$\frac{dR}{dt} = \gamma I - (\tau + \mu)R.$$

The SEIR system dynamic model in Figure 1 can be written as follows :

$$\begin{aligned}
\frac{dS}{dt} &= \varepsilon N - (\beta I + \mu)S + \sigma R, \\
\frac{dE}{dt} &= \beta SI - (\theta + \mu)E, \\
\frac{dI}{dt} &= \theta E - (\gamma + \delta)I, \\
\frac{dR}{dt} &= \gamma I - (\sigma + \mu)R.
\end{aligned} \tag{5}$$

Where $N(t) = S(t) + E(t) + I(t) + R(t)$ and SEIR model can be simplified by assuming: $\frac{S}{N} = S; \frac{E}{N} = e; \frac{I}{N} = i; \frac{R}{N} = r$, so eq. (5) can be written:

$$\begin{aligned}
\frac{ds}{dt} &= \varepsilon - (\beta i + \mu)s + \sigma r, \\
\frac{de}{dt} &= \beta si - (\theta + \mu)e, \\
\frac{di}{dt} &= \theta e - (\gamma + \delta)i, \\
\frac{dr}{dt} &= \gamma i - (\sigma + \mu)r.
\end{aligned} \tag{6}$$

And the initial conditions or approximation are as follows; $S_0(0) = s_0; E_0(0) = e_0; I_0(0) = i_0; R_0(0) = r_0$.

Table 1 is a table of parameters, variables, and sources used in the SEIR model, based on real data for Medan City and references to previous articles and assumptions. Real data for Medan City refers to [26] with details of the total population of Medan City as of 2021 of $2,460,858$ people. The number of COVID-19 cases was 49,416; the number of recoveries was $48,436$, the number of deaths due to COVID-19 is 965 people. So it was obtained that for the suspect subpopulation $(s) = 0.9289920$, infected $(i) = 0.0200808$, the recovered $(r) = 0.0196820$.

3. MATHEMATICAL RESULTS

3.1. Reproduction Number Ratio (R_0)

The Reproduction Number Ratio (R_0) is a number that expresses the average number of infected individuals due to an infection that will infect other individuals [27]. By constructing the Next Generation Matrix from the infected sub-system

Variable/Parameter	Description	Mark	Source
s	Total Susceptible sub population	0.9289920	[26]
e	Total exposed subpopulation size	0.0304790	Asumtion
i	Total infected subpopulation	0.0200808	[26]
r	Subpopulation Recovered	0.0196820	[26]
ε	Birth Rate	0.0004600	[26]
β	The exposed Rate	[0-1]	Asumtion
θ	The infected rate	[0-1]	Asumtion
μ	Natural death rate	0.000460	[26]
δ	COVID-19 death rate	0.000054	[26]
γ	Recover rate	0.086	[26]
σ	The rate at which recovered individuals move to susceptible	[0-1]	Asumtion

equation, R_0 can be obtained. Before calculating (R_0), first determine the disease-free equilibrium point of eq. (2). Assume $\frac{ds}{dt} = \frac{de}{dt} = \frac{di}{dt} = \frac{dr}{dt} = 0$, then the disease-free equilibrium point is obtained:

$$\begin{aligned}
\varepsilon - (\beta i + \mu)S + \sigma r &= 0 \\
\beta si - (\theta + \mu)e &= 0 \\
\theta e - (\gamma + \delta)i &= 0 \\
\gamma i - (\sigma + \mu)r &= 0
\end{aligned} \tag{7}$$

The disease-free equilibrium point states the condition that there are no infected individuals in the population $(i = 0)$. From the eq. (7) obtained: $s = \frac{\varepsilon}{\mu}; e = 0; i = 0$ and $r = 0$ so that the disease-free equilibrium point is:

$$E_0 = (s, e, i, r) = \left(\frac{\varepsilon}{\mu}, 0, 0, 0 \right).$$

Next, to construct the reproduction number ratio (R_0) where :

$$R_0 = \rho(FV^{-1}),$$

with the Next Geneteration Matrix method from the infected subsystem equation in eq. (6), namely: $\frac{de}{dt} = \beta si - (\theta + \mu)e$ and $\frac{di}{dt} = \theta e - (\gamma + \delta)i$ obtained:

$$\begin{aligned}
T &= (\beta si, 0) \text{ and } -\Sigma = ((\theta + \mu)e, -\theta e + (\gamma + \delta)i), \\
F &= J_T = \begin{bmatrix} 0 & \beta s \\ 0 & 0 \end{bmatrix} \text{ and } V = J_\Sigma \begin{bmatrix} \theta + \mu & 0 \\ -\theta & \gamma + \delta \end{bmatrix}, \\
V^{-1} &= \frac{1}{(\theta+\mu)(\gamma+\delta)} \begin{bmatrix} \theta + \mu & 0 \\ -\theta & \gamma + \delta \end{bmatrix}, \\
R_0 &= \rho(FV^{-1}) = \rho \left(\begin{bmatrix} \theta + \mu & 0 \\ -\theta & \gamma + \delta \end{bmatrix} \frac{1}{(\theta+\mu)(\gamma+\delta)} \begin{bmatrix} \theta + \mu & 0 \\ -\theta & \gamma + \delta \end{bmatrix} \right).
\end{aligned}$$

Results obtained:

$$R_0 = \frac{\beta \varepsilon \theta}{\mu(\theta + \mu)(\gamma + \delta)}$$

3.2. Application of the Homotopy Perturbation Method to the Compartmental Disease SEIR Model

The Homotopy Perturbation Method is utilized to find the approximate solution for eq. (6) employing the homotopy constructor equation.

$$K(v, p) = (1 - p)[L(v) - L(v_0)] + p[L(v) + N(v) - f(r)] = 0$$

The procedure to derive the analytical or approximate solution of the model begins with the assumption of the Homotopy Perturbation Method in eq. (4), relying on this assumption

$$\begin{aligned}
s(t) &= s_o + ps_1 + p^2 s_2 + \cdots, \\
e(t) &= e_o + pe_1 + p^2 e_2 + \cdots, \\
i(t) &= i_o + pi_1 + p^2 i_2 + \cdots, \\
r(t) &= r_o + pr_1 + p^2 r_2 + \cdots.
\end{aligned} \tag{8}$$

Having the initial conditions specified as $s_1(0) = 0, e_1(0) = 0, i_1(0) = 0, r_1(0) = 0; \forall_i = 1, 2, 3, \cdots$ then substitution one by one of eq. (6) to eq. (7), we find:

$$\begin{aligned}
(1 - p)\left(\frac{ds}{dt} - \frac{ds_0}{dt} \right) + p\left(\frac{ds}{dt} - (\varepsilon + \sigma r) + (\beta i + \mu)s \right) &= 0, \\
(1 - p)\left(\frac{de}{dt} - \frac{de_0}{dt} \right) + p\left(\frac{de}{dt} - \beta is + (\theta + \mu)e \right) &= 0, \\
(1 - p)\left(\frac{di}{dt} - \frac{di_0}{dt} \right) + p\left(\frac{di}{dt} - \theta e + (\gamma + \delta)i \right) &= 0, \\
(1 - p)\left(\frac{dr}{dt} - \frac{dr_0}{dt} \right) + p\left(\frac{dr}{dt} - \gamma i + (\sigma + \mu)r \right) &= 0.
\end{aligned} \tag{9}$$

$p \in [0, 1]$ is a parameter and s_0, e_0, i_0, and r_0 are the initial approach values of the system solution. If eq. (8) is subtitled to eq. (9).

$$\begin{aligned}
(1 - p)\left[\frac{ds_0}{dt} + p\frac{ds_1}{dt} + p^2 \frac{ds_2}{dt} + \cdots - \frac{ds_0}{dt} \right] + p\left[\frac{ds_0}{dt} + p\frac{ds_1}{dt} \right. \\
+ p^2 \frac{ds_2}{dt} + \cdots - \varepsilon - \sigma(r_0 + pr_1 + p^2 r_2 + \cdots) + \beta(i_0 + pi + p^2 i_2 \\
\left. + \cdots)(s_0 + ps_1 + p^2 s_2 + \cdots) + \mu(s_0 + ps_1 + p^2 s_2 + \cdots) \right] = 0,
\end{aligned} \tag{10}$$

eq. (10) can be written:

$$\begin{aligned}
0 =& \left(\frac{ds_0}{dt} - \frac{ds_0}{dt} \right)p^0 + \left(\frac{ds_1}{dt} + \frac{ds_0}{dt} - \varepsilon + \beta s_0 i_0 + \mu s_0 - \sigma r_0 \right)p^1 \\
&+ \left(\frac{ds_2}{dt} + \beta(s_0 i_1 + s_1 i_0) + \mu s_1 - \sigma r_1 \right)p^2 + \left(\frac{ds_3}{dt} + \beta(s_0 i_2 \right. \\
&\left. + s_1 i_1 + s_2 i_0) + \mu s_2 - \sigma r_2 \right)p^3 + \left(\frac{ds_4}{dt} + \beta(s_0 i_3 + s_1 i_2 + s_2 i_1 \right. \\
&\left. + s_3 i_0) + \mu s_3 - \sigma r_3 \right)p^4 + \cdots,
\end{aligned}$$

$$\begin{aligned}
0 =& (1 - p)\left[\frac{de_0}{dt} + p\frac{de_1}{dt} + p^2 \frac{de_2}{dt} + \cdots - \frac{de_0}{dt} \right] + p\left[\frac{de_0}{dt} + p\frac{de_1}{dt} \right. \\
&+ p^2 \frac{de_2}{dt} + p^3 \frac{de_3}{dt} + \cdots - \beta(s_0 + ps_1 + p^2 s_2 + p^3 s_3 + \cdots)(i_0 \\
&+ pi_1 + p^2 i_2 + p^3 i_3 + \cdots) + (\theta + \mu)(e_0 + pe_1 + p^2 e_2 + p^3 e_3 \\
&\left. + \cdots) \right].
\end{aligned}$$

Or:

$$
\begin{aligned}
0 = & \left(\frac{de_0}{dt} - \frac{de_0}{dt}\right)p^0 + \left(\frac{de_1}{dt} + \frac{de_0}{dt} - \beta s_0 i_0 + (\theta + \mu)e_0\right)p^1 \\
& + \left(\frac{de_2}{dt} - \beta(s_0 i_1 + s_1 i_0) + (\theta + \mu)e_1\right)p^2 + \left(\frac{de_3}{dt} - \beta(s_0 i_2\right. \\
& \left. + s_1 i_1 + s_2 i_0) + (\theta + \mu)e_1\right)p^3 + \left(\frac{dS_4}{dt} - \beta(s_0 i_3 + s_1 i_2 + s_2 i_1\right. \\
& \left. + s_3 i_0) + (\theta + \mu)e_3\right)p^4 \cdots,
\end{aligned}
$$

$$
\begin{aligned}
0 = & (1-P)\left[\frac{di_0}{dt} + p\frac{di_1}{dt} + p^2\frac{di_2}{dt} + \cdots - \frac{di_0}{dt}\right] + p\left[\frac{di_0}{dt} + p\frac{di_1}{dt}\right. \\
& + p^2\frac{di_2}{dt} + p^3\frac{di_3}{dt} + \cdots - \theta\left(e_0 + pe_1 + p^2 e_2 + p^3 e_3 + \cdots\right) \\
& \left. + (\gamma + \delta)(i_0 + pi_1 + p^2 i_2 + p^3 i_{3+\cdots})\right].
\end{aligned}
$$

Or

$$
\begin{aligned}
0 = & \left(\frac{di_0}{dt} - \frac{di_0}{dt}\right)p^0 + \left(\frac{di_1}{dt} + \frac{di}{dt} - \theta e_0 + (\gamma + \delta)i_0\right)p^1 \\
& + \left(\frac{di_2}{dt} - \theta e_1 + (\gamma + \delta)i_1\right)p^2 + \left(\frac{di_3}{dt} - \theta e_2\right. \\
& \left. + (\gamma + \delta)i_2\right)p^3 + \left(\frac{di_4}{dt} - \theta e_3 + (\gamma + \delta)i_3\right)p^4 + \cdots.
\end{aligned}
$$

Or

$$
\begin{aligned}
0 = & \left(\frac{dr_0}{dt} - \frac{dr_0}{dt}\right)p^0 + \left(\frac{dr_1}{dt} - \frac{dr_0}{dt} - \gamma i_0 + (\mu + \sigma)r_0\right)p^1 \\
& + \left(\frac{dr_2}{dt} + (\mu + \sigma)r_1\right)p^2 + \left(\frac{dr_3}{dt} + (\mu + \sigma)r_2\right)p^3 \\
& + \left(\frac{dr_4}{dt} + (\mu + \sigma)r_3\right)p^4 + \cdots.
\end{aligned}
$$

The order p^1 gives the equation:

$$
\begin{aligned}
\frac{ds_1}{dt} + \frac{ds_0}{dt} - \varepsilon + \beta s_0 i_0 + \mu s_0 - \sigma r_0 &= 0, \\
\frac{de_1}{dt} + \frac{de_0}{dt} - \beta s_0 i_0 + (\theta + \mu)e_0 &= 0, \\
\frac{di_1}{dt} + \frac{di_0}{dt} - \theta e_0 + (\gamma + \delta)i_0 &= 0, \\
\frac{dr_1}{dt} + \frac{dr_0}{dt} - \gamma i_0 + (\mu + \sigma)r_0 &= 0,
\end{aligned}
$$

with the initial condition $s_1(0) = 0, e_1(0) = 0, i_1(0) = 0$ and $r_1(0) = 0$.
The order p^2 gives the equation:

$$
\begin{aligned}
\frac{ds_2}{dt} + \beta(s_0 i_1 + s_1 i_0) + \mu s_1 - \sigma r_1 &= 0, \\
\frac{de_2}{dt} - \beta(s_0 i_1 + s_1 i_0) + (\theta + \mu)e_1 &= 0, \\
\frac{di_2}{dt} - \theta e_1 + (\gamma + \delta)i_1 &= 0, \\
\frac{dr_2}{dt} - \gamma i_1 + (\mu + \sigma)r_1 &= 0,
\end{aligned}
$$

with the initial condition $s_2(0) = 0, e_2(0) = 0, i_2(0) = 0$ and $r_2(0) = 0$.
The order p^3 gives the equation:

$$
\begin{aligned}
\frac{ds_3}{dt} + \beta(s_0 i_2 + s_1 i_1 + s_2 i_0) + \mu s_2 - \sigma r_2 &= 0, \\
\frac{de_3}{dt} - \beta(s_0 i_2 + s_1 i_1 + s_2 i_0) + (\theta + \mu)e_2 &= 0, \\
\frac{di_3}{dt} - \theta e_2 + (\gamma + \delta)i_2 &= 0, \\
\frac{dr_3}{dt} - \gamma i_2 + (\mu + \sigma)r_2 &= 0,
\end{aligned}
$$

with the initial condition $s_3(0) = 0, e_3(0) = 0, i_3(0) = 0$ and $r_3(0) = 0$.
The order p^4 gives the equation:

$$
\begin{aligned}
\frac{ds_4}{dt} + \beta(s_0 i_3 + s_1 i_2 + s_2 i_1 + s_3 i_0) + \mu s_3 - \sigma r_3 &= 0, \\
\frac{de_4}{dt} - \beta(s_0 i_3 + s_1 i_2 + s_2 i_1 + s_3 i_0) + (\theta + \mu)e_3 &= 0, \\
\frac{di_4}{dt} - \theta e_3 + (\gamma + \delta)i_3 &= 0, \\
\frac{dr_4}{dt} - \gamma i_3 + (\mu + \sigma)r_3 &= 0,
\end{aligned}
$$

with the initial condition $s_4(0) = 0, e_4(0) = 0, i_4(0) = 0$ and $r_4(0) = 0$.
In the same way, a system of differential equations for the next order can be obtained. In this section the system is obtained to order p^5, For initial values and parameter values, the values used refer to Table 1, with $s(0) = 0.9289920, e(0) = e(0) = 0.0304790, i(0) = 0.0200808, r(0) = 0.0196820, \mu = 0.00046, \varepsilon = 0.00046, \delta = 0.000054, \beta = 0, 2, \theta = 0.02, \gamma = 0.026, \sigma = 0.1$.
To approximate the solution, time will be obtained, so that by using the initial values and parameter values above, a numerical scheme will be obtained which is an approximate solution in each order starting from the following order $\rho \to 1, \rho^2, \rho^3, \cdots, \rho^2$ as follows:

• order ρ^2:

$$
\begin{aligned}
s(t) &= 0,9289920 - 0.0000506836538t - 0.001238392250t^2, \\
e(t) &= 0,0304790 - 0.0000506836538t - 0.001238392250t^2, \\
i(t) &= 0,0200808 + 0.0037788374t - 0.0004760264314t^2, \\
r(t) &= 0,0196820 - 0.00000127074t + 0.0001870527436t^2.
\end{aligned}
$$

In the same way it is obtained ρ^3

• order ρ^4:

$$
\begin{aligned}
s(t) &= 00,9289920 - 0.0000506836538t - 0.001238392250t^2 \\
& \quad + 0.0001042725438t^3 - 0.00001160448639t^4, \\
e(t) &= 0,0304790 - 0.003732231486t + 0.001444535053t^2 \\
& \quad - 0.0001572704377t^3 + 0.00001593551819t^4, \\
i(t) &= 0.0200808 + 0.0037788374t - 0.0004760264314t^2 \\
& \quad + 0.00007570448116t^3 - 0.000007037050074t^4, \\
r(t) &= 0,0196820 - 0.00000127074t + 0.0001870527436t^2 \\
& \quad - 0.00001573755366t^3 + 0.000001875495728t^4.
\end{aligned}
$$

• order ρ^5:

$$
\begin{aligned}
s(t) &= 0,9289920 - 0.0000506836538t - 0.001238392250t^2 \\
& \quad + 0.0001042725438t^3 - 0.00001160448639t^4 \\
& \quad + 0.0000007865847958t^5, \\
e(t) &= 0,0304790 - 0.003732231486t + 0.001444535053t^2 \\
& \quad - 0.0001572704377t^3 + 0.00001593551819t^4 \\
& \quad - 0.000001137564652t^5, \\
i(t) &= 0,0200808 + 0.0037788374t - 0.0004760264314t^2 \\
& \quad + 0.00007570448116t^3 - 0.000007037050074t^4 \\
& \quad + 0.0000005522632554t^5, \\
r(t) &= 0,0196820 - 0.00000127074t + 0.0001870527436t^2 \\
& \quad - 0.00001573755366t^3 + 0.000001875495728t^4 \\
& \quad - 0.0000001395061371t^5.
\end{aligned}
$$

3.3. Simulation

Below is a simulation using the HPM up to order 5, the simulation results are in the form of graphs compared with the Runge Kutta 4th order (RK 4th). The variables and parameters used are in accordance with the real data for the city of Medan which is displayed in Table 1. From the calculations, the value $R_0 = 4.61$ or $R_0 > 1$, the value indicates that COVID-19 in the city of Medan is still endemic or not yet extinct, there is still a possibility that it will spread again. The following simulation takes the value $\sigma = 0.1$, the following is a graphic image of the results of numerical simulations using the HPM and RK 4 approaches for $R_0 > 1$.

Figure 4. The Infection of COVID-19 Spread

Figure 2. The Susceptibility of COVID-19 Spread

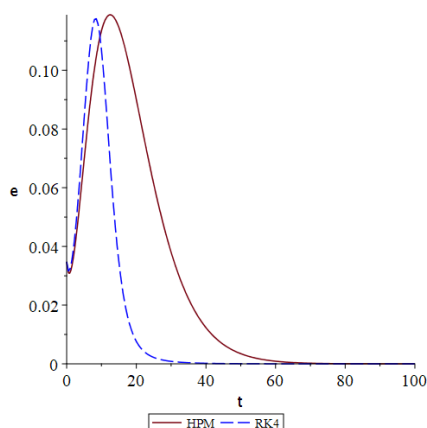**Figure 5.** The Recovered of COVID-19 Spread

Figure 3. The Exposed of COVID-19 Spread

The plot in Figure 2 is a plot of the susceptible subpopulation (s), which is plotted using RK 4th and the HPM approximation solution. The result is that the population decreases as the Susceptable subpopulation moves to the Exposed subpopulation. The figure shows that the HPM method has a longer time to reach stability than using the RK 4th method. For the HPM method, the stability for the Susceptable subpopulation is at a point $t > 40$ .While for the RK 4th stability point at $t > 20$. In Figure 3 is a plot of the Exposed subpopulation (e), the results obtained are that the subpopulation an increase from and decreases as it moves to the subpopulation infected and stable values towards zero, the behavior of the HPM and RK 4th method solutions is almost the same, the difference is that the HPM method has a longer
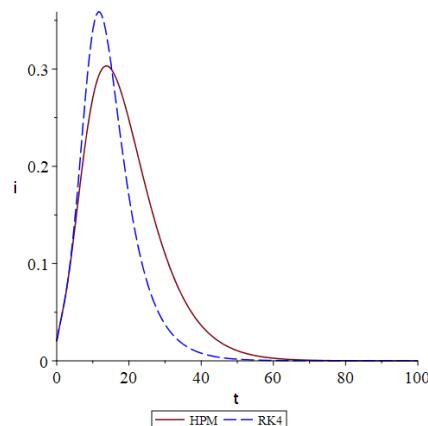
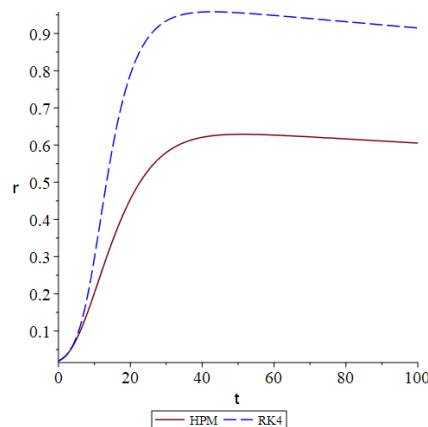time to reach stability compared to the RK 4th method. In Figure 4 is a plot of the infected subpopulation (i), in the dynamics of the spread of disease the infected subpopulation is of concern specifically, because in the infected subpopulation, each infected individual can infect other healthy individuals. The simulations using the HPM and RK 4th methods show that the largest number of infected cases is at $10 < t < 15$, the number of subpopulations infected with HPM is less than with the RK 4th method and the spread of COVID-19 in Medan City takes longer to reach stability and It also takes a longer time for the disease to disappear or be destroyed. The time required for the HPM method until COVID-19 is destroyed is $t \geq 60$ while the RK 4th method is $t > 40$. In Figure 5, the dynamics of the recovered subpopulation can be seen that HPM can approach the solution from the RK 4th method, the recovery pattern in the HPM method is almost the same as the recovery pattern in the RK 4 method. And the time needed to reach stability is also almost the same.

From the simulation obtained, it can be obtained that Homotopy Pertubation Method (HPM) can be used to solve systems of nonlinear differential equations. This can be seen from the simulation where the HPM results graph is close to the numerical simulation using RK 4th. Furthermore, in the simulation above it can also be seen that the higher the order used, the better the results obtained. As in the simulation where the 5th order is very close to the numerical solution. Apart from that, it was also found that the higher the time, the higher order HPM approximation is

required.

Following shown is a simulation of the effect of moving the recovered subpopulation to the susceptible subpopulation on the dynamics of the spread of COVID-19 in Medan City with parameter variations $\sigma = 0, 0.01, 0.1$ dan 0.5
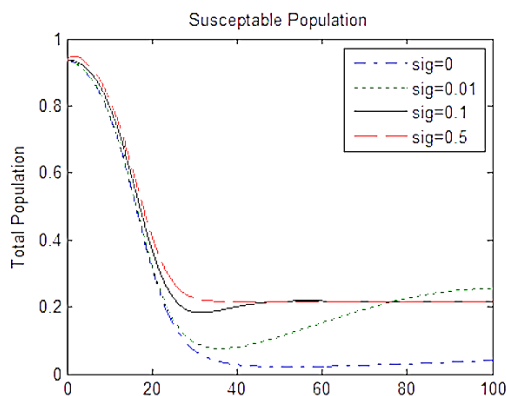

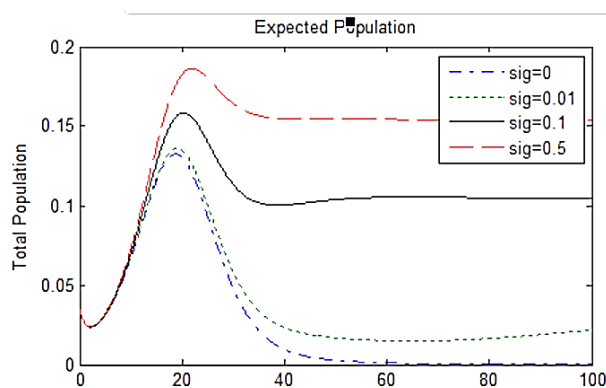**Figure 6.** The Susceptibility of COVID-19 Spread with variation sigma

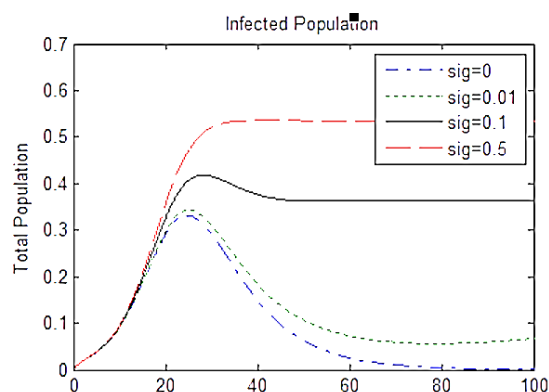**Figure 7.** The Exposed of COVID-19 Spread with variation sigma

Figure 8. The Infected of COVID-19 Spread with variation sigma

The plot in Figure 6 is a susceptable subpopulation plot with sigma variations. The results show that the displacement rate value sigma $(\sigma) = 0$, the subpopulation decreases and is
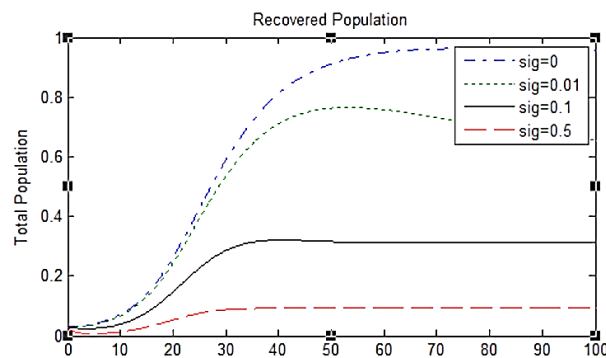

Figure 9. The Recovered of COVID-19 Spread with variation sigma

constant towards zero. For the $\sigma = 0.01$, the subpopulation is susceptible to decline, the value is above zero, which is greater than $\sigma = 0$. And the greater the sigma value, there is a tendency for the susceptible subpopulation to decrease further away from the zero value. The plot in Figure 6 is a plot of the exposed subpopulation. The simulation results show that there is an influence on the rate of movement of the recovered subpopulation on the exposed subpopulation. The graph in Figure 7 shows that the rate of movement of the exposed subpopulation initially shows an increase and finally decreases and stabilizes towards zero. Furthermore, if the displacement rate is increased, the dynamics of the exposed subpopulation after the increase decreases until the constant value moves away from zero. A larger value causes a smaller decrease in the exposed subpopulation. The plot in Figure 8 is a plot of the infected subpopulation, the results show an increase in the rate of movement of the recovered subpopulation to the susceptible subpopulation resulting in an increase in the infected subpopulation. The greater the value, the greater the increase in the infected subpopulation. The plot in Figure 9 is a recovered subpopulation plot, the results show that the greater the rate of movement of recovered subpopulations to susceptible subpopulations, the smaller the number of recovered subpopulations, this is the opposite of other subpopulations. It can be concluded that the rate of movement of the recovered subpopulation to the suspect subpopulation has a negative effect on the spread of COVID-19 in Medan City. The greater the number of movements, the higher the rate of spread of COVID-19 in Medan City. To reduce the rate of spread of COVID-19, the authorities need to anticipate the movement of recovered subpopulations to susceptible subpopulations.

4. Conclusion

The results of research using real data for the city of Medan in 2021 obtained values $R_0 = 4.61$ or $R_0 > 1$ or indicates that COVID-19 in the city of Medan is still endemic or not yet extinct. The constructed mathematical model is analyzed and simulated using Homotopy Pertubation Method (HPM) results are compared with Runge Kutta RK 4th order (RK 4th). From the simulation it can be obtained that the Homotopy Pertubation Method (HPM) can be used to solve systems of nonlinear differential equations. This can be seen from the simulation where the HPM results graph is close to the numerical simulation using RK 4th. The research results also show that there is a negative influence of the

movement of recovered subpopulations to susceptible subpopulations on the dynamics of the spread of COVID-19. The simulation results show that the greater the number of movements, the higher the spread of COVID-19 in Medan City. To reduce the rate of spread of COVID-19, the authorities need to anticipate the movement of recovered subpopulations to susceptible subpopulations.

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