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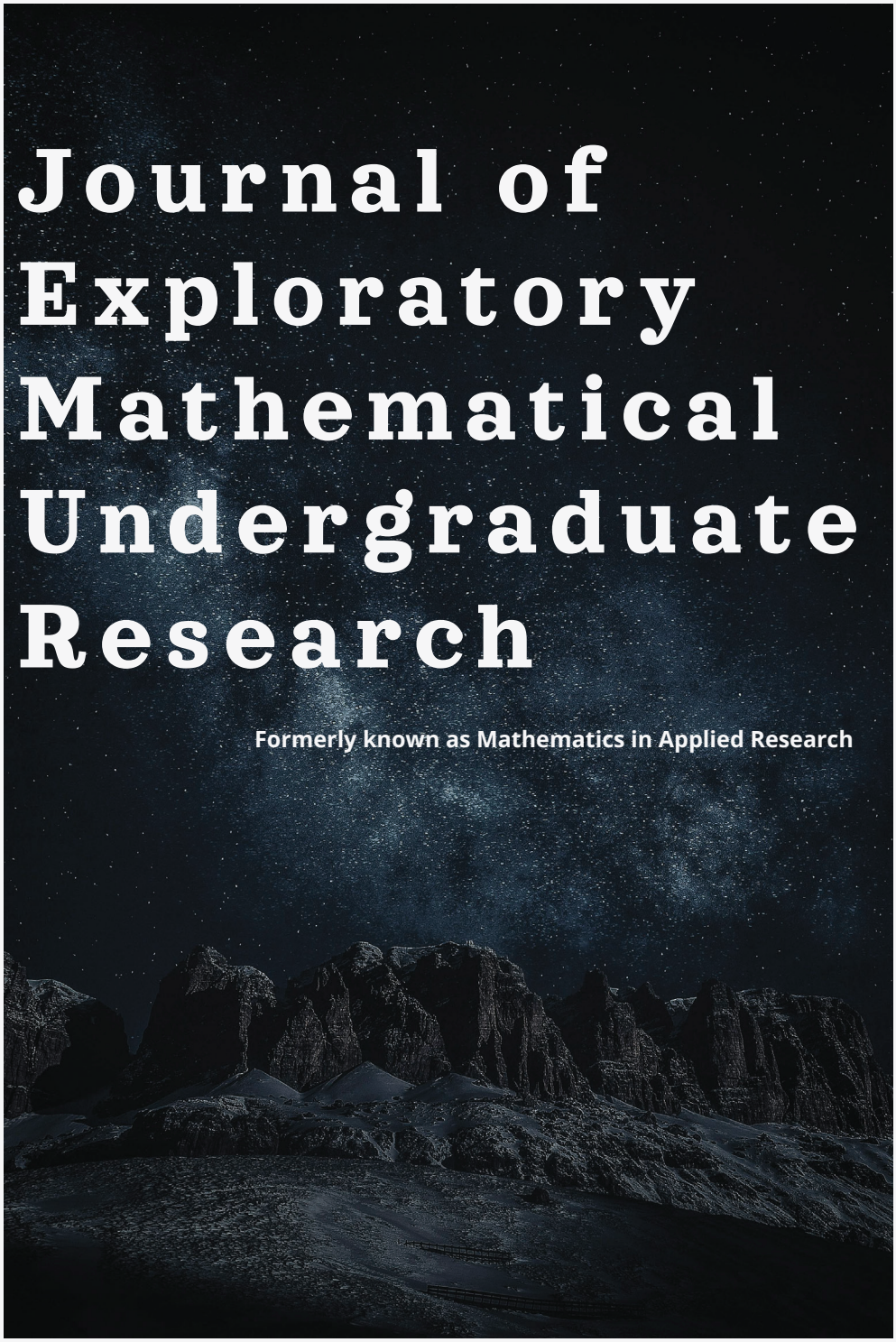

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BANACH CONTRACTION METHOD FOR SOLVING THE EPIDEMIC MODEL WITH CONSTANT VACCINATION

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Abstract

In this study, we employed the Runge-Kutta Fourth Order (RK4) method and the Banach Contraction Method (BCM) to simulate an epidemiological model with constant vaccination, utilizing parameters and initial conditions established according to Fauzi et al. (2021). The solutions for susceptible (S), infected (I), and recovered (R) individuals were obtained and compared between RK4 and BCM over a time range of 0 to 2. Although an exact solution reference was unavailable, our comparative analysis revealed consistent results between RK4 and BCM at the initial time steps for all variables. However, as time progressed, minor differences emerged between the solutions obtained from RK4 and BCM, albeit these differences were relatively small. While the variations observed may not be significant in magnitude, they underscore the importance of selecting appropriate numerical techniques in epidemiological modeling to ensure accurate predictions over time.

Keywords: Banach Contraction Method; SIR epidemic model; Runge-Kutta method; Maximum error remainder.

1. Introduction

Simulating infectious illnesses is important to control them and reduce the epidemic. Constant vaccination is a crucial method for controlling infectious diseases. As individuals get vaccinated, they move from the susceptible to the immune compartment, reducing potential hosts. This strategy maintains high immunity, limits disease transmission, and mitigates epidemic impact. Following a standard constant vaccination strategy, vaccines should be administered to susceptible newborns. In the past, diligent vaccination campaigns have resulted in high levels of permanent immunity against the childhood diseases prevalent among the population (Kumar and Kumar, 2014).

The Susceptible Infectious Recovered (SIR) model, a foundational mathematical framework, was among the earliest models created to elucidate the transmission of infectious diseases within a population. According to Magal and Webb (2018) SIR model was introduced by Kermack and McKendrick in 1927, it describes disease transmission through individuals, utilizing basic notations like susceptible (S), infectious (I), recovered (R), and population size (N). In this model, the population is assumed to be constant so that the birth rate and death rate are equal, and the efficacy of the vaccine is 100% (Kumar and Kumar, 2014). This model has significantly contributed to shaping the understanding of epidemics, offering key insights into the dynamics of disease spread.

Nonlinear functional equations, such as the SIR model, are prevalent in various scientific fields and require iterative and numerical methods for precise solutions. An iterative method based on the Banach contraction principle was proposed by Daftardar-Gejji and Bhalekar (2009) to solve the general nonlinear functional equation in the form, $u = f+N(u)$, where f is a known function and N is a nonlinear operator. BCM is useful for solving general nonlinear functional equations, proving the existence and uniqueness of solutions in various mathematical models. The primary goal of this study is to solve SIR with constant vaccines using BCM and validate its accuracy and efficiency, as few studies have solved this epidemic model using BCM. This involves evaluating how well BCM performs compared to other methods in dealing with the SIR epidemic model.

In recent research by Marinov and Marinova (2022), the SIR epidemic model underwent analysis using the Variational Iteration Method, specifically focusing on formulating and solving the inverse equation through the Method of Variational Embedding. This study aimed to demonstrate the effectiveness of an inverse approach in identifying time-dependent functions and parameters of the SIR model, utilizing COVID-19 data from Israel, the United States, and Japan. Additionally, both Mungkasi (2021) and

Rafei et al. (2007) recognized and employed the variational iteration method in their respective investigations of the SIR epidemic model. Mungkasi conducted a comparative analysis with the successive approximation method, incorporating Lagrange multipliers through variational theory. Rafei et al. followed a similar approach, emphasizing the method's accuracy and reduced computational requirements, supporting findings consistent with Mungkasi's assertions.

Several previous studies demonstrate the application of BCM in various contexts. In the most recent publication by Raslan and Entesar (2022), the authors explore the use of BCM to solve the Drinfeld-Sokolov-Wilson system. The results, assessed through absolute maximum error (MAE) and mean square error (MSE) in comparison to an exact solution, affirm the efficiency of BCM. Meanwhile, Ghitheeth and Mahmood (2021) addresses the solution of partial differential equations using BCM, enhancing results through the integration of the trapezoidal rule. The hybridization of BCM with the trapezoid base proves effective in solving non-linear partial difference equations, with the efficiency validated through calculated MSE and MAE. Additionally, Al-Jawary et al. (2018) demonstrates the applicability of BCM in solving nonlinear initial value problems. Their study focuses on the thin film problem of a non-Newtonian fluid on a moving belt, proposing a method based on Banach's contraction principle. The accuracy of the obtained solutions is determined by comparing them with results from other authors who utilized methods such as Runge-Kutta and Newton-Rhapson-Euler-based solutions.

2. Banach Contraction Method

We start this section by stating some basic concepts(Daftardar-Gejji and Bhalekar, 2009).

Definition 2.1. Let X_1 and X_2 be two metrics and F be a mapping from X_1 into X_2. F is said to be Lipschitz if there exists a real number $r \geq 0$ for all $x_1, x_2 \in X$ such that the distance between $d(Fx_1, Fx_2) \leq rd(x_1, x_2)$. If the Lipschitz $r < 1$, the F is termed as a contraction mapping.

Theorem 2.2. *Let F be contraction mapping with a Lipschitz constant r, of a complete metric space X, then F has a unique fixed point u within the space X. An addition, if x_0 is an arbitrary point in X and x is defined by $x_{n+1} = F(x_n), n = 0, 1, 2, ...$, the $\lim_{x\to\infty} x_n = u$ and $d(x_n, u) \leq \frac{r^n}{1-r} d(x_1, x_0)$.*

Theorem 2.3. *Let F be a mapping of a complete metric space X into itself such that F^k is a contraction mapping of X for some positive integer k, then F has a unique fixed point in X.*

To illustrate the basic concept of BCPM, we introduce the following nonlinear equation

$$L(u(x)) + N(u(x)) + g(x) = 0, \quad x > 0 \tag{1}$$

where x represents the independents variable, $u(x)$ is the unknown function, $g(x)$ is a given function, L is the linear operator defined as $L = \frac{d^n}{dx^n}$, $n \in \mathbb{N}$, N is the nonlinear operator, subject to initial conditions

$$u^{(k)}(0) = c_k, \quad k = 0, 1, 2, \cdots, n-1 \tag{2}$$

where c_k's are real numbers. Performing the integral operator with n fold with respect to x, denoted by I_x^n, to (1), with the initial conditions (2) we obtained the following general functional equation:

$$u(x) = f(x) + I_x^n[N(u(x))] \tag{3}$$

where $f(x)$ is a known analytic function that represents the sum of the available initial conditions and the result of integrating the function $g(x)$ (if such function is available). To implement the BCPM, we define successive approximations as the following

$$\begin{aligned} u_0(x) &= f \qquad (4)\\ u_1(x) &= u_0(x) + I_x^n[N(u_0(x))] \\ u_2(x) &= u_0(x) + I_x^n[N(u_1(x))] \\ &\vdots \\ u_n(x) &= u_0(x) + I_x^n[N(u_{n-1}(x))], \quad n = 1, 2, ... \qquad (5) \end{aligned}$$

Therefore, the solution for the equation (1) will be obtained by

$$u(x) = \lim_{n\to\infty} u_n(x) \tag{6}$$

2.1. *Solving SIR model by BCM*

We examine the epidemic model incorporating constant vaccination, formulated as:

$$\begin{aligned}\frac{dS}{dt} &= (1-P)\pi - \beta si - \pi s \\ \frac{dI}{dt} &= \beta si - (\gamma+\pi)i \\ \frac{dR}{dt} &= P\pi + \gamma i - \pi r\end{aligned}$$

Here, S represents susceptible individuals, I denotes infected individuals, and R stands for recovered individuals. By applying BCM to the SIR epidemic model with constant vaccination, we have:

$$\begin{aligned}s_1(t) &= s_0(t) + \int (1-P)\pi - \beta s_0 i_0 - \pi s_0 \, dt \\ i_1(t) &= i_0(t) + \int \beta s_0 i_0 - (\gamma+\pi) i_0 \, dt \\ r_1(t) &= r_0(t) + \int P\pi + \gamma i_0 - \pi r_0 \, dt \\ &\vdots \\ s_{n+1}(t) &= s_0(t) + \int (1-P)\pi - \beta s_n i_n - \pi s_n \, dt \\ i_{n+1}(t) &= i_0(t) + \int \beta s_n i_n - (\gamma+\pi) i_n \, dt \\ r_{n+1}(t) &= r_0(t) + \int P\pi + \gamma i_n - \pi r_n \, dt \end{aligned} \tag{7}$$

3. Numerical Results and Discussion

The parameters are determined according to Fauzi et al. (2021), with $\beta = 0.8$, $\gamma = 0.03$, $\pi = 0.4$, and $P = 0.9$. Initial conditions are $S(0) = 0.8$, $I(0) = 0.2$, and $R(0) = 0$.

The first few solutions for *S(t)*, *I(t)* and *R(t)*:

$$\begin{aligned}S_0(t) &= 0.8 \\ S_1(t) &= 0.8 - 0.408t \\ S_2(t) &= 0.8 - 0.408t + 0.1008t^2 + 0.0045696t^3 \\ &\vdots \end{aligned}$$

$$\begin{aligned}I_0(t) &= 0.2 \\ I_1(t) &= 0.2 + 0.042t \\ I_2(t) &= 0.2 + 0.042t - 0.02823t^2 - 0.0045696t^3 \\ &\vdots \end{aligned}$$

$$\begin{aligned}R_0(t) &= 0 \\ R_1(t) &= 0.366t \\ R_2(t) &= 0.366t - 0.07257t^2 \\ &\vdots \end{aligned}$$

Table 1 presents a comparison of solutions for $S(t)$ obtained using the Runge-Kutta Fourth Order (RK4) method and the BCM. Each line corresponds to a specific time (t) between 0 to 2, with an additional step of 0.2. RK4 and BCM solutions are provided for each time point, allowing a direct comparison between the two methods. Notably, at $t = 0$, both RK4 and BCM produce the same result of 0.8 for $S(t)$, indicating agreement between the methods at early time steps. As time passes, small differences between the RK4 and BCM solutions become apparent, as evidenced by the small absolute differences in the final column. These differences, although negligible in magnitude, suggest little variation in the predicted susceptible population as predicted by the two methods over the specified time intervals.

Meanwhile, in Table 2, a similar comparative analysis is conducted for the $I(t)$ solution obtained using RK4 and BCM. As in Table 1, solutions are provided for time points between 0 and 2, allowing a comprehensive assessment of the agreement between methods. Again, at $t = 0$, both RK4 and BCM produce the same result of 0.2 for $I(t)$, indicating consistency between the methods at early time steps. However, as time passes, small differences appear between the RK4 and BCM solutions, resulting in small absolute differences. This difference, although still small, suggests a slight discrepancy in the predicted number of infected individuals between the two methods in the specified time range.

Table 3, on the other hand, provides a comparison of the solution for $R(t)$ obtained using RK4 and BCM. Similar to Tables 1 and 2, solutions are presented for time points between 0 and 2, facilitating a comprehensive comparison between methods. At $t = 0$, both RK4 and BCM produce the same result 0 for $R(t)$, indicating agreement between the methods at early time steps. However, as time passes, small differences between the RK4 and BCM solutions become apparent, leading to small absolute differences. This difference, although relatively small, suggests little variation in the predicted amount of recovered individuals between the two methods over the specified time interval. Overall, the table provides valuable insight into the agreement and discrepancy between the solutions obtained using RK4 and BCM for susceptible, infected and recovered individuals in epidemiological models.

Table 1: Comparison of solution for $S(t)$ between RK4 with BCM

t	RK4	BCM	$\lvert u(t) - s(t)\rvert$
0	0.8	0.8	0
0.2	0.722363409	0.722363409	$4.60199e^{-12}$
0.4	0.652358747	0.652358748	$6.07521e^{-10}$
0.6	0.589504728	0.589504738	$1.07339e^{-8}$
0.8	0.533282313	0.533282396	$8.33227e^{-8}$
1.0	0.48315286	0.483153272	$4.12181e^{-7}$
1.2	0.438574997	0.43857653	$1.53256e^{-6}$
1.4	0.399018893	0.399023568	$4.675e^{-6}$
1.6	0.363977304	0.363989627	$1.2323e^{-5}$
1.8	0.33297338	0.333002398	$2.90182e^{-5}$
2.0	0.305565507	0.305627945	$6.24387e^{-5}$

Table 2: Comparison of solution for $I(t)$ between RK4 with BCM

t	RK4	BCM	$\lvert u(t) - s(t)\rvert$
0	0.2	0.2	0
0.2	0.207265729	0.207265729	$1.39999e^{-12}$
0.4	0.212274615	0.212274615	$2.08049e^{-10}$
0.6	0.215107503	0.215107499	$4.08616e^{-9}$
0.8	0.215913103	0.215913068	$3.48537e^{-8}$
1.0	0.214887196	0.214887009	$1.87379e^{-7}$
1.2	0.212253434	0.212252685	$7.49343e^{-7}$
1.4	0.208247027	0.208244593	$2.43475e^{-6}$
1.6	0.203101889	0.203095114	$6.77524e^{-6}$
1.8	0.197041235	0.197024528	$1.67072e^{-5}$
2.0	0.190271305	0.19023393	$3.73743e^{-5}$

Table 3: Comparison of solution for $R(t)$ between RK4 with BCM

t	RK4	BCM	$\lvert u(t) - s(t)\rvert$
0	0	0	0
0.2	0.068019715	0.070370862	0.002351147
0.4	0.130774542	0.135366637	0.004592095
0.6	0.188682081	0.195387762	0.006705681
0.8	0.242127149	0.250804536	0.008677387
1.0	0.291463973	0.30195972	0.010495747
1.2	0.337018326	0.349170786	0.01215246
1.4	0.379089605	0.39273184	0.013642235
1.6	0.41795283	0.432915259	0.01496243
1.8	0.453860554	0.469973074	0.01611252
2.0	0.487044676	0.504138124	0.017093448

The comparison between RK4 and BCM results can be visualized through graphs. The figures 1, 2 and 3 below illustrate the comparison of $S(t)$, $I(t)$, and $R(t)$ between RK4 and BCM.

Figure 1 depicts a contrast between the susceptible population, derived from both BCM and RK4 methods. Notably, during the initial phase, there is minimal disparity between the two solutions. Nevertheless, discrepancies become more pronounced as time progresses. This pattern is similarly observed in the solutions for infected individuals and recovered individuals, as illustrated in Figures 2 and 3, respectively.

Therefore, the comparison of solutions for $S(t)$, $I(t)$, and $R(t)$ obtained by both BCM and RK4 methods revealed significant findings. At first, there is little discernible difference between the solutions. However, with the progress of time, the variation between the two methods became more and more apparent. This emphasizes the importance of choosing an appropriate numerical technique, as it can significantly affect the accuracy and behavior of simulation results in epidemiological modeling.

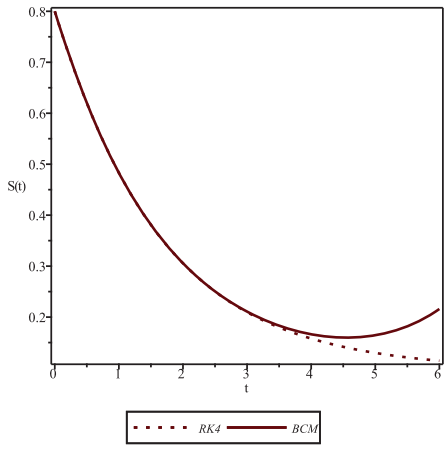

Figure 1: Comparison of RK4 method with BCM for *S(t)*

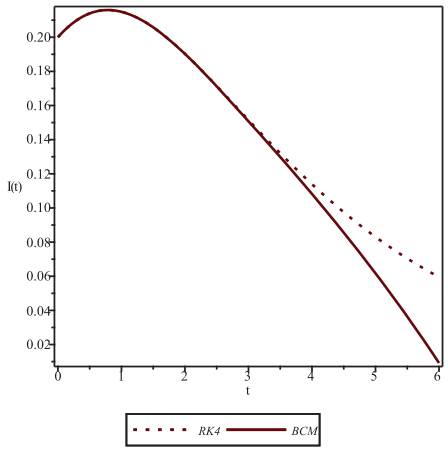

Figure 2: Comparison of RK4 method with BCM for *I(t)*

4. Conclusion and Recommendation

In this study, we used the Runge-Kutta Fourth Order (RK4) method and the Banach Contraction Method (BCM) to simulate an epidemiological model with continuous vaccination, using parameters and initial conditions set according to Fauzi et al. (2021). Solutions for $S(t)$, $I(t)$, and $R(t)$ were obtained and compared between RK4 and BCM in the time range 0 to 2. Although exact solution references are not available, our comparative analysis revealed consistent results between RK4 and BCM at the initial time step for all variables. However, as time passes, small differences appear between the solutions obtained from RK4 and BCM, although these differences are relatively small. Although the observed variations may not be significant in magnitude, they emphasize the importance of choosing appropriate numerical techniques in epidemiological modeling to ensure accurate predictions over time.

For future studies, it is recommended to explore additional numerical methods and techniques to solve epidemiological models, beyond RK4 and BCM, to further evaluate their accuracy and efficiency in capturing the dynamics of the spread of infectious diseases. Additionally, the effect of varying model parameters and initial conditions on the results should be investigated to gain insight into the sensitivity of model predictions. Additionally, efforts should be directed toward validating model results using real-world epidemiological data, where available, to improve the reliability and applicability of simulations. Furthermore, conducting sensitivity analyzes and uncertainty quantification studies can provide valuable information about the robustness of model predictions and assist in identifying critical factors that in-

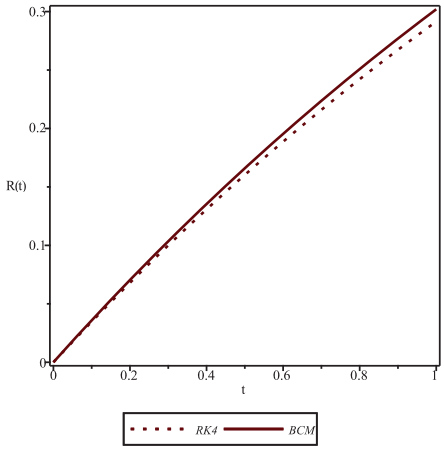

Figure 3: Comparison of RK4 method with BCM for *R(t)*

fluence disease transmission dynamics. Overall, by addressing these recommendations, future research efforts may contribute to advancing the understanding and predictive capabilities of epidemiological models, thereby facilitating more effective public health interventions and strategies.

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