International Journal of Analysis and Applications

Practical Aspects for Applying Picard Iterations to the SIR Model Using Actual Data

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Abstract. The updated version of the Picard method for solving systems of differential equations is employed to solve the SIR system. A local performance of the Picard iteration algorithm combined with the Gauss-Seidel approach is applied to the SIR model. The integral form of the SIR model, in addition to the use of Gauss-Seidel philosophy (using the most recent calculated values), achieved more accuracy in the computational work than those obtained using the differential forms. Documented data regarding the spread of corona virus 19 in the Kingdom of Saudi Arabia region from April to the end of December 2020 were used to calculate the corresponding actual values for the parameters and the initial conditions. Due to efficient management and to obtain representable behaviours, we restricted the size of the study to only 1% of the population. The global characteristics of the integral formulation have affected the calculations accurately. The initial conditions and the model's parameters are established depending on the documented data. The results illustrate the superiority of the updated Picard formulation over the classical Picard within their domain of convergence. The results of this study illuminate and validate the importance of mathematical modeling. These findings can provide valuable insights into mathematical modeling for those involved in environmental health research, especially those responsible for devising strategic plans.

1. Introduction

In recent years, humanity has lived through the experience of the spread of Covid-19 disease. It was announced that it appeared for the first time in the Chinese city of Wuhan. It was a harsh experience in which human societies experienced conflicting feelings between gratitude for scientific progress at the speed of information transfer and the temporary inability of science to resist disease spread. Among the indications of concern in many countries was the arrival of hospitals to the peak of absorptive capacity and the large number of critical health cases and deaths. In this work, we concentrate on the Saudi Arabia case. The Kingdom of Saudi Arabia is character-

In this work, we concentrate on the Saudi Arabia case. The Kingdom of Saudi Arabia is characterized by its large area relative to the number of its population. Despite this, the Kingdom of Saudi Arabia has areas that are considered to have the highest population densities in the world. The

Received: Dec. 15, 2023.

²⁰²⁰ Mathematics Subject Classification. 47J26.

Key words and phrases. SIR Model; Picard iteration; updated Picard iteration; COVID-19.

Kingdom of Saudi Arabia is characterized by the abundance and diversity of visitors of different nationalities, most of the nationalities of the world, and more than that, visitors are transported to visit the holy places. Therefore, the Kingdom of Saudi Arabia is interested in implementing preventive measures in strict ways, which has had a clear impact in controlling epidemic diseases, and the Corona Covid-19 pandemic is considered the best evidence of this. In this work, we focus on applying the SIR model to study the spread of Corona 19, setting the model parameters, choosing the appropriate initial conditions, as well as the available solution methods, using documented data during the period from April 1, 2020, until the end of December 2020, the period when there are no vaccinations.

The scientific development has contributed effectively to the speedy work of statistics and the circulation and documentation of data, which will be the base for future research work. Scientists presented temporary and rapid solutions to control the spread of the disease through the rapid publication of data and infection transmission methods. Everyone has realized the role of science and scientists from all disciplines in participating in the work of the necessary studies to confront such pandemics. Mathematical models are among the most valuable sciences that can be employed to face such epidemics in advance and develop priority scenarios to meet the expected situation.



FIGURE 1. The components of the community and the flow direction.

The SIR (Susceptible - Infected - Removed) model is considered one of the oldest mathematical representations that can be used to determine the number of active infected cases at any time I(t), provided that the other unknowns and parameters of the model are correctly selected [1–5]. When studying and solving the SIR model, we look at the study community with fixed size N as consisting of three separate groups, as shown in Fig. 1. The first S(t) is the group that has not been infected but is susceptible to infection, the second I(t) is the active infected group and the third R(t) is the group that was removed from the infected group whether by recovery or death, such that at any time we have,

$$S(t) + I(t) + R(t) = N.$$
 (1.1)

The SIR model established by Kermack and McKendrick, 1927 – 1933, is one of the simplest epidemiological mathematical models based on the bilinear incidence rate. The model considers the rate of change in the size of each group. The SIR model is a system of three nonlinear ordinary differential equations of the form:

$$S'(t) = -\beta SI,$$

$$I'(t) = \beta SI - \alpha I,$$

$$R'(t) = \alpha I,$$

(1.2)

subject to the initial conditions: $S(t_0) = S_0$, $I(t_0) = I_0$, $R(t_0) = R_0$.

This system contains five non-negate parameters β , α , S_0 , I_0 and R_0 . The parameter α is the recovery coefficient, and the parameter β is the transmission coefficient. Solving the SIR model requires the determination of the five parameters; the solutions are parameter-dependent [1–3]. In any solution R(t), must be an increasing function, and S(t) must be a decreasing function. Numerical methods are the most practical techniques for such systems because of their nonlinearities. The first numerical technique is the Euler method, which, despite its low accuracy, is the simplest among all numerical techniques for solving systems of differential equations. The fourth-order Runge-Kutta method is the most acceptable technique and gives reliable results, so it is the calibration technique in many research papers [3,6–9]. Solving the SIR model can help understand and predict how diseases can spread out through the community under consideration. Accordingly, the policymakers can generate applicable decisions in controlling disease propagation. Due to the system's non-linearity, solution methods are restricted towards numerical or semi-analytical techniques [3,6–9]. The credibility of the results does not depend on the model itself but also on the solution technique and the system's data (the coefficients β , α , and the initial conditions) [10–13]. In this work, we use actual documented data from the Kingdom of Saudi Arabia to determine the model parameters related to the study area and use these parameter values in solving the model [3,14]. In a previous work [3], we considered the documented data of the Kingdom of Saudi Arabia from April 2020 to the end of December 2020, as shown in Figs. (2A and 2B). we found that the documented international statistics and reports have illustrated that the Kingdom of Saudi Arabia has managed the pandemic efficiently. In this work, we present a numerical implementation of the Picard iteration algorithm combined with Gauss-Seidel iteration [6] to the SIR Model (1.2) subject to the documented data of Saudi Arabia data during the period from April 2020 to the end of December 2020, as shown in Figs. (2A and 2B). We recalculate the values of the parameters using a more accurate numerical integration technique (Simpson's rule) than the Rectangle rule used in [3]. Also, we use different solution techniques alternative forms of Picard iterations [6]. Applying the Picard technique for studying differential equations depends on reformulating the given differential forms into an equivalent integral form through simple integration and using fixed point recurrence techniques, the same as in algebraic cases. Undoubtedly, integral representation considers the global behaviours of the system instead of the local attitudes of the differential forms [6,15]. Moreover, for systems of differential equations, the updated Picard form introduced in [6], which uses Gauss-Seidel treatment for algebraic systems, can be employed. It was established that the updated Picard iteration form for systems of differential equations converges faster than the classical Picard within its domain of convergence, like the algebraic cases. Also, it is important to remember that outside the domain of convergence, the divergence of the updated Picard iteration will be faster.



FIGURE 2. (A) Total daily active infected cases I(t), (B) Accumulative daily removed cases R(t).

The remainder of the paper is organized as follows: In section 2, Material and Methods is subdivided into four subsections in which we introduce the classical Picard formulation of the *SIR* model, the updated Picard formulation of the SIR model, the choice of the initial conditions and the tactic of determining the parameters. In section 3, results, we introduce the parameter values, Table 1, the implementation of the classical Picard, the updated Picard, Table 2. Comparison with the fourth-order Runge-Kutta method in addition to the documented data as shown in Fig. (4)–Fig. (9). Section 4, Discussion, discusses our results compared with the published works and the documented data. In section 5, based on our results and dissection, some concluding points are mentioned.

2. MATERIAL AND METHODS

The Picard fixed point approach is a constructive technique used to prove the existence and uniqueness of solutions of initial value problems of differential equations. With the rapid developments in symbolic computation and computer algebra systems, Picard iteration has become an acceptable solution technique. Due to the use of the corresponding integral forms [6, 15] for the initial value problem, the results of Picard iteration give accurate results provided sufficient terms are considered. Moreover, the updated Picard iteration method [6] gives more accurate results. The feature of this technique is that it provides a scheme for solving any problem without any transformations or linearization, provided the included integrals are computable.

2.1. **Classical Picard formulation of the SIR model.** The Picard iteration formulation of the *SIR* model can be written in the form:

$$S_{n}(t) = S(t_{0}) - \beta \int_{t_{0}}^{t} S_{n-1}(t) I_{n-1}(t) dt,$$

$$I_{n}(t) = I(t_{0}) + \int_{t_{0}}^{t} I_{n-1}(t) \{\beta S_{n-1}(t) - \alpha\} dt,$$

$$R_{n}(t) = R(t_{0}) + \alpha \int_{t_{0}}^{t} I_{n-1}(t) dt, \quad n = 1, 2, \cdots.$$
(2.1)

So, a series solution for the unknowns S(t), I(t) and R(t) can be calculated up to the required order.

2.2. **Updated Picard formulation of the SIR model.** The updated Picard iteration formulation of the *SIR* model can be written in the form:

$$S_{n}(t) = S(t_{0}) - \beta \int_{t_{0}}^{t} S_{n-1}(t) I_{n-1}(t) dt,$$

$$I_{n}(t) = I(t_{0}) + \int_{t_{0}}^{t} I_{n-1}(t) \{\beta S_{n}(t) - \alpha\} dt,$$

$$R_{n}(t) = R(t_{0}) + \alpha \int_{t_{0}}^{t} I_{n}(t) dt, \quad n = 1, 2, \cdots.$$
(2.2)

In this formulation, the principle of using Seidel's approach, using the most recent calculated data introduced in the Gauss-Seidel method for solving linear systems is employed, [6] as shown in the last two equations, the suffix *n* instead of (n - 1). Accordingly, a series solution for the unknowns S(t), I(t) and R(t) can be calculated up to the required order. The series solution contains more terms (powers) than the corresponding terms in the classical forms accordingly the convergence within the domain of convergence will be rapid.

2.3. Initial Conditions. Suitable initial or boundary conditions must be associated with the given set of differential equations to solve differential equations. For the SIR model, we use the actual documented real data of the unknowns at any starting time as initial conditions, $I(t_0)$, and $R(t_0)$ and for the value of $S(t_0)$ the size of susceptible group usually is taken to be the overall size of population at the beginning of the study (approximately forty million the population of the Kingdom of Saudia Arabia). The size of the susceptible group can be taken as a significant subsize of the overall population according to the expected spread of the disease, the experience of researcher and policymaker expectations such that the relation $S(t_0) + I(t_0) + R(t_0) = N$. So, we considered the size of our study to be 1% of the population of the Kingdom of Saudia Arabia which is 400000 (at first, we assumed the size to be 10% but due to the effective restriction which successfully controlled the spread of the disease and to make graphs readable we have to reduce the size of the sample to be only 1%). The period of our study is 275 days from the first of April to the end of December 2020. Different initial conditions lead to different results, small changes in the initial conditions may give major results for occurrence outcomes [10–12]. Also, the choice of $S(t_0)$ will affect the calculated values of the parameters.

2.4. **The Parameters of the Model.** The reliability of the calculated results of the SIR model depends on how realistic the parameter values used. In a previous work [3], we have used and re-proposed two formulas to calculate the parameter values α and β from the daily published documented data of the kingdom of Saudia Arabia.

$$R(t_n) - R(t_m) = \alpha \int_{t_m}^{t_n} I(t) dt.$$
(2.3)

$$\ln\left(S\left(t_{m}\right)/S\left(t_{n}\right)\right) = \beta \int_{t_{m}}^{t_{n}} I(t)dt$$
(2.4)

The calculation depends on evaluating only one integral, $\int_{t_m}^{t_n} I(t) dt$ in this work we use the Simpson's standard numerical integration technique in the evaluation process. Simpson's Rule for calculating the integral $\int_{t_m}^{t_n} I(t)$ appears in equations (2.3) and (2.4) take the form:

$$\int_{t_1}^{t_{11}} I(t)dt = \frac{1}{3} \left\{ (I_1 + I_{11}) + 4 \left(I_2 + I_4 + \dots + I_{10} \right) + 2 \left(I_3 + \dots + I_9 \right) \right\}.$$
 (2.5)

We use the data for the first eleven days of the month to determine the parameters and then use the parameter values in the SIR model over the month, Figures [7-9]. Where t_i is the day number *i* of the considered month and I_i denotes to the number of active infected cases at day number *i*. Accordingly, the parameter values corresponding to the Saudi Arabia published data can be calculated accurately Table 1 . Also, this approach can be adopted for the overall period.

$$\int_{t_1}^{t_{275}} I(t)dt = \frac{1}{3} \left\{ (I_1 + I_{275}) + 4 \left(I_2 + I_4 + \dots + I_{274} \right) + 2 \left(I_3 + \dots + I_{273} \right) \right\}$$
(2.6)

3. Results

In anticipation of establishing a suitable framework for applying epidemic disease spread models to the context of the Kingdom of Saudi Arabia, particularly concerning the initial phase of the COVID-19 pandemic before vaccine availability (April - December 2020), we focused our work on utilizing the SIR model (1.2) due to its simplicity and satisfactory outcomes. We established the model's parameters (formulas (2.3) and (2.4)), fine-turned the initial conditions, and carefully selected solution technique (2.1) and (2.2) to yield pertinent results. Our study involved a comparative analysis of three solution methods: the classical Picard (2.1), an updated Picard (2.2), and the fourth order Runge-Kutta [3].

In the following we summarize our results of implementation in connection with the actual documented daily values. The calculated parameter values are summarized in Table 1.

	Total	Total	Total			Recovery
2020	number of	number of	number of	α	$\beta * 10^{-7}$	Day's
	confirmed	recovered	deaths			$\frac{1}{\alpha}$
	cases	cases				
April	21190	2998	152	0.0234	2.771	43
May	62508	59279	341	0.0374	1.858	27
June	105562	68324	1146	0.059	3.562	17
July	85082	104892	1217	0.055	3.105	19
August	39867	55138	1031	0.052	3.530	20
September	18833	28358	871	0.0483	4.848	21
October	12677	14688	634	0.0599	6.824	17
November	10078	12960	494	0.0597	10.744	17
December	5381	7051	327	0.0773	12.011	13
Mean						$\frac{1}{\alpha_{mean}}$
Values				0.05234	5.4724	= 19
Overall period calculations				0.0611	4.0253	17

TABLE 1. documented values and the calculated parameter values.

Using the values of the parameters in Table 1, and the recognized initial conditions, a power series solution for the unknowns in the SIR model was generated. In the following we present the detailed results for May 2020.

The initial conditions for the first of May are:

$$S(0) = 375903, I(0) = 20373, R(0) = 3724, \alpha = 0.0374$$
 and $\beta = 1.858 \times 10^{-7}$.
 $S(0) + I(0) + R(0) = 400000, (1\% of the overall population).$

TABLE 2. The generated series solution for the active infected cases during May 2020 as a sample for our results, $I_n^{CP}(t)$ represents the output of iteration number n, obtained from the application of the classical Picard iteration (2.1), $I_n^{UP}(t)$ represents the output of iteration number n, obtained from the application of the updated Picard iteration (2.2).

п	$I_n^{CP}(t)$ Classical Picard	$I_n^{UP}(t)$ Updated Picard
1	$I_1^{CP}(t) = 20373 + 660.957t$	$I_1^{UP}(t) = 20373 + 660.957t - 2.69307t^2$
2	$I_2^{CP}(t) = 20373 + 660.95t + 8.029t^2$	$I_2^{UP}(t) = 20373 + 660.957t + 8.029t^2 - 0.0504t^3$
	$-0.058t^3$	$-0.0005t^4 + 2.836(10^{-6})t^5 - 3.643(10^{-9})t^6$
3	$I_3^{CP}(t)$	$I_3^{UP}(t)$
4	$I_4^{CP}(t)$	$I_4^{UP}(t)$

$$\begin{split} I_{3}^{CP}(t) =& 20373 + 660.957t + 8.029t^{2} + 0.0029t^{3} - 0.0016t^{4} - \\& 1.57\left(10^{-6}\right)t^{5} + 5.126\left(10^{-8}\right)t^{6} - 9.005\left(10^{-11}\right)t^{7}, \\ I_{3}^{UP}(t) =& 20373 + 660.957t + 8.029t^{2} + 0.0029t^{3} - 0.0018t^{4} - \\& 2.5\left(10^{-7}\right)t^{5} + 3.772\left(10^{-8}\right)t^{6} + 6.623\left(10^{-10}\right)t^{7} - \\& 2.875\left(10^{-12}\right)t^{8} - 2.622\left(10^{-14}\right)t^{9} + 1.592\left(10^{-16}\right)t^{10} + \\& 1.56\left(10^{-19}\right)t^{11} - 3.338\left(10^{-21}\right)t^{12} + 1.065\left(10^{-23}\right)t^{13} - \\& 1.475\left(10^{-26}\right)t^{14} + 7.903\left(10^{-30}\right)t^{15}, \\ I_{4}^{CP}(t) =& 20373 + 660.957t + 8.029t^{2} + 0.0029t^{3} - 0.0012t^{4} - 0.00002t^{5} \\& + 7.781 \times 10^{-8}t^{6} + 1.592 \times 10^{-9}t^{7} + 2.138 \times 10^{-12}t^{8} \\& - 9.16 \times 10^{-14}t^{9} - 1.611 \times 10^{-16}t^{10} + 3.316 \times 10^{-18}t^{11} \\& -2.653 \times 10^{-21}t^{12} - 4.16 \times 10^{-23}t^{13} + 1.23 \times 10^{-25}t^{14} \\& -1.005 \times 10^{-28}t^{15} \\ I_{4}^{UP}(t) =& 20373 + 660.957t + 8.029t^{2} + 0.0029t^{3} - 0.0012t^{4} - 0.000016t^{5} \\& + 7.033 \times 10^{-8}t^{6} + 1.989 \times 10^{-9}t^{7} + 2.762 \times 10^{-12}t^{8} \\& - 8.506 \times 10^{-14}t^{9} - 1.282 \times 10^{-15}t^{10} + 2.84 \times 10^{-18}t^{11} \\& + 9.305 \times 10^{-20}t^{12} + 1.52 \times 10^{-22}t^{13} - 4.901 \times 10^{-24}t^{14} \\& -2.1001 \times 10^{-26}t^{15} + 2.255 \times 10^{-28}t^{16} + 9.917 \times 10^{-31}t^{17} \\& -6.921 \times 10^{-33}t^{18} - 4.366 \times 10^{-35}t^{19} + 2.088 \times 10^{-37}t^{20} \\& + 1.708 \times 10^{-39}t^{21} - 9.773 \times 10^{-42}t^{22} - 3.042 \times 10^{-44}t^{23} \\& + 3.379 \times 10^{-46}t^{24} - 4.077 \times 10^{-49}t^{25} - 4.684 \times 10^{-51}t^{26} \\& + 2.199 \times 10^{-53}t^{27} - 1.72 \times 10^{-56}t^{28} - 1.749 \times 10^{-58}t^{29} \\& + 8.131 \times 10^{-61}t^{30} - 1.863 \times 10^{-3}t^{31} + 2.6381 \times 10^{-66}t^{32} \\& -2.353 \times 10^{-69}t^{33} + 1.223 \times 10^{-72}t^{44} - 2.847 \times 10^{-76}t^{35} \end{split}$$

From Fig. (6), the classical Picard or the updated Picard give acceptable results even with low iterations along small intervals one month, but from Figs. (7, 8 and 9) one have to update the parameter values after at most forty days as shown in Fig. (9) in order to guarantee convergence of the obtained series solutions.



FIGURE 3. The performance of $I_1^{CP}(t)$, $I_1^{UP}(t)$, Fourth order Runge and the documented data.



FIGURE 4. The performance of $I_2^{CP}(t)$, $I_2^{UP}(t)$, Fourth order Runge and the documented data.



FIGURE 5. The performance of $I_3^{CP}(t)$, $I_3^{UP}(t)$, Fourth order Runge and the documented data.



FIGURE 6. The performance of the active daily infected cases $I_4^{CP}(t)$, $I_4^{UP}(t)$, Fourth order Runge and the documented data, calculations according to May data in table 1.



FIGURE 7. The performance of the active daily infected cases $I_4^{CP}(t)$, $I_4^{UP}(t)$, Fourth order Runge and the documented data, calculations according to June data in table 1.



FIGURE 8. The performance of the active daily infected cases $I_4^{CP}(t)$, $I_4^{UP}(t)$, Fourth order Runge and the documented data, calculations according to July data in table 1.



FIGURE 9. The performance of the active daily infected cases $I_4^{CP}(t)$, $I_4^{UP}(t)$, Fourth order Runge and the documented data, calculations according to August data in table 1.

The results of this work offer valuable perspectives on the investigation of epidemic diseases within the Kingdom of Saudi Arabia, as we will explore in the forthcoming discussion section. There is a need for additional research to delve deeper into the specific dynamics that drive these patterns.

4. DISCUSSION

The efficiency of solving mathematical models used in studying epidemic diseases depends on many factors, including the size of the study sample, the accuracy of the parameter values used, the initial conditions and the solution method itself. Epidemic models are typically fitted for shortterm applications, where the consequence of reinfection outlooks remains restricted. Usually, the spread of epidemic diseases begins quickly, which requires the use of solution techniques for the mathematical models with high reliability in small periods. SIR models provide understanding insights into the dynamics of epidemic diseases [10], as demonstrated in various case studies conducted in different regions [16–19]. However, when employed over extended time periods, the results of SIR models may suffer from reduced accuracy even if the solution technique is accurate due to the cumulative impacts of errors arising from different sources. Our results not only confirm the existing theory and the documented data but also consider the global behaviors through the integral representations of the SIR model. The progresses in the application of epidemic mathematical models are based on three tracks: The first track: is the mathematical models used and the dynamics on which they are based we considered the integral form of the SIR model because of its simplicity reliability Figs. (4-9), the differential form of the SIR model gives acceptable results in different applications [3,4,7–9]. The updated Picard converges faster than the classical Picard Table 2. The second track: is the initial conditions of the model at the beginning of study, S(0), I(0), and R(0). Both I(0), and R(0) are documented data, and the value of S(0) is chosen to be a significant subset of the population, we had chosen the size of the susceptible study to be 400000 (1% of the population). The size of susceptible study is effective in the determination of the parameters α and β , formulas (2.3), (2.4) and Table 1. Also, the size of the susceptible study is effective in final graph output. The third track: the solution technique considered the Picard method plays an essential role in studying differential equations, especially in proving the existence of a solution. Although it was not typically used as a solution method due to the nature of the calculations involved, it has gained importance with the rapid development of scientific calculation devices and systems. With the advent of symbolic calculation systems such as MATHEMATICA, the Picard method, particularly with the updated formula (2.1), had become a reliable method of solution. This is due to the mathematical structure of the "fixed point theory". It is important to note that Picard or updated Picard might not converge for all systems of differential equations if the problem has stiff behavior or the initial guess (initial conditions) are far from the true solution which are not our case, the initial conditions are taken from the documented data. Also, the coefficients of the system are determined efficiently (the parameters of the model). As shown in the result section and based on the check of the difference between consecutive iterates, we used the fourth iteration as our solution. According to our results, we extend our sincere thanks to the relevant authorities in the Kingdom of Saudi Arabia for controlling the spread of the epidemic by implementing social distancing in an effective manner and quickly providing the required vaccines as soon as they appear.

5. Conclusion

Differential equations are the most mathematical concepts used in modeling epidemic diseases. Mathematical simulations of epidemics are important tools for identifying, expecting and organizing infectious diseases. The calculations give an overestimation, this is an acceptable situation because of the daily progress in applying lockdown and prevention methods which daily affect the calculated values of the parameters. Despite their restricted domain of convergence, the Picard techniques give accurate results within their convergence domains which makes Picard techniques a good choice at the beginning, and this is suitable for solving epidemic models. The values of the parameters are related to the size of the sample of study not general values. In studying epidemic diseases the size of the sample study should be chosen carefully relative to the expected spread down of the disease in order to obtain actual representation of the values of the parameters and accordingly solutions can be good approximations to the documented data(we have changed our size of study from 10% to only 1%). Decisions related to epidemics should be deeply revised by highly qualified specialists. All thanks to the health organizations that helped maintain community safety by spreading the culture of prevention and control of the spread of diseases and ensuring social distancing despite its international costs.

Acknowledgments: This research paper is supported by Deanship of Scientific Research, Islamic University of Madinah. Many thanks to our colleagues in Deanship of Scientific Research, Islamic University of Madinah for their cooperation and complete support to achieve this work.

Conflicts of Interest: The authors declare that there are no conflicts of interest regarding the publication of this paper.

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