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An effective new one-step block integrator for the numerical solution of system of first order differential equation arising from epidemiology models

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Abstract

This paper proposes an effective new one-step block integrator for the solution of system of first-order ordinary differential equation that arise from models in epidemiology in life science. Showing the performance of this method, SIR, SEIR and more compartmental models are solve numerically and thus comparing with the classical Runge-Kutta to reveal its accuracy. The numerical results obtained clearly shows that the proposed method is more efficient and robust for obtaining the numerical solution of mathematical models in epidemiology.

1 Introduction

Its not contentious that first order differential equation are models of many physical phenomenons. In science and engineering, usually mathematical models are developed to help in the understanding of physical phenomena. These models especially in economics, medicine, chemical, electrical, and mechanical engineering, physics, and mathematical biology, often yields equations of first order with certain initial condition. In mathematical biology especially in the study of spread of diseases in epidemiology, mathematical models formulated form system of first-order ordinary differential equations (ODEs) with prescribed initial conditions. Motivated by this life applications, the following initial value problem (IVP) is considered in this work:

$$\frac{\bar{y}}{dx} = \bar{f}(\bar{x}, \bar{y}), \quad \bar{y}(a) = \bar{y}_0 \quad a \leq x \leq b, \quad (1)$$

where $\bar{y} = (y_1, y_2, \dots, y_n)^T$, $\bar{f} = (f_1, f_2, \dots, f_n)^T$, and $\bar{x} = (x_1, x_2, \dots, x_n)^T$, with $\bar{y}$ being unknown vectors or real vector functions which are at least one time differentiable in $\mathbf{R}$, $F \in \mathbf{R}^n \times \mathbf{R}^m$ and a, b are real constants. It is assumed that $f_i, i = 1, \dots, n$ are continuous and each f_i satisfies the following Lipschitz conditions:

$$|f_i(x, y_{j1}) - f_i(x, y_{j2})| \leq \gamma |y_{j1} - y_{j2}| \quad (2)$$

for some positive γ thus guaranteeing the existence and uniqueness of solution of the system (1) in $\mathbf{R}$.

In literature, there are diverse numerical methods for solving scalar form of (1). There are numerous numerical method for the numerical solution of the system in (1). One available approach is the Runge-Kutta method. This method has a very wide range of applicability in terms of nature of problems being solved ranging from oscillatory to stiff problem and thus obtaining good good approximation of solution with appreciable absolute and relative errors [1, 2]. In many cases, some of the system may

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be stiff, that is, the solution varies rapidly over a short time. In this case, Runge-Kutta methods are mostly inappropriate for dealing with such differential systems. Other numerical approaches for solving (1) includes the Differential Transform Method (DTM) as seen in [3, 4, 5], Adomian Decomposition Method (ADM) have been used in [6, 7, 8], Homotopy Perturbation Method (HPM) applied in [9]. There exists other methods are in the literature for the numerical solution of (1). In this paper, Linear Multistep Block method based on collocation techniques is applied. In this approach a one-step block method is derived. This method has the advantage of being self-starting, i.e, they do not require a staring value to kick-start their implementation. They also have the advantage of producing smaller global errors (at the end of the range of integration) than those produced by the step-by-step methods due to the presence of accumulated errors at each step in the step-by-step method. This paper is structured as follows: Section 2 explains the derivation of the method and section 3 presets the characteristics of the derived method. the implementation of the derived method with epidemiological model in literature is presented in section 4, and section 5 summarizes and concludes the work.

2 Derivation of the Method

The derivation of a continuous implicit three off-step hybrid block method is described in this section. Consider an approximate solution $y(x)$ of (1) over the integration subinterval $[x_n, x_{n+1}]$ with the polynomial given as

$$y(x) \approx T(x) = \sum_{k=0}^7 \rho_k x^k \quad (3)$$

with the first derivative

$$f(x)y'(x) \approx T'(x) = \sum_{k=1}^7 \rho_k k x^{k-1} = f(x) \quad (4)$$

where ρ_k , $k = 0(1)7$ are unknown parameters to be determined with the method of collocation/interpolation.

Considering a one-step method in the interval $[x_n, x_{n+1}]$, the p_i , $i = 1(1)5$ off-grid points in the interval $[0, 1]$ such that $0 < p_1 < p_2 < p_3 < p_4 < p_5 < 1$ with x_n and x_{n+1} being the points of interpolations while the points of interpolation are x_n, x_{n+p_i} , $i = 1(1)5$ and x_{n+1} , thereby obtaining the following system of equations $T(x_n) = y_n$; $T(x_{n+p_i}) = y_{n+p_i}$; $T'(x_n) = f_n$; $T'(x_{n+p_i}) = f_{n+p_i}$, $i = 1(1)5$; $T'(x_{n+1}) = f_{n+1}$, where $y_{n+p_i} \simeq y(x_{n+p_i})$, $f_{n+p_i} \simeq f(x_{n+p_i})$, $y(x_{n+p_i})$.

Solving the above system using a computer algebraic system (cas) in Mathematica we obtain the values of the coefficients ρ_k $k = 0(1)7$ (not included here). Substituting these values of ρ_k 's into the polynomial (3), the following is obtained:

$$T(x_n + th) = y_n + h(\beta_0 f_n + \beta_{p_1} f_{n+p_1} + \beta_{p_2} f_{n+p_2} + \beta_{p_3} f_{n+p_3} + \beta_{p_4} f_{n+p_4} + \beta_{p_5} f_{n+p_5} + \beta_1 f_{n+1}) \quad (5)$$

where $p_1 = \frac{1}{10}$, $p_2 = \frac{1}{4}$, $p_3 = \frac{1}{2}$, $p_4 = \frac{13}{20}$, $p_5 = \frac{9}{10}$. Evaluating (5) at the points $t = \frac{1}{10}, \frac{1}{4}, \frac{1}{2}, \frac{13}{20}, \frac{9}{10}, 1$ and after simplifying, the following formulas are obtained

$$\begin{aligned} y_{n+p_1} &= y_n + h \left(\frac{4484209}{122850000} f_n + \frac{97247}{1247400} f_{n+p_1} - \frac{307313}{15356250} f_{n+p_2} + \frac{68659}{6300000} f_{n+p_3} - \frac{103193}{15765750} f_{n+p_4} + \frac{18247}{9828000} f_{n+p_5} - \frac{130681}{198450000} f_{n+1} \right), \\ y_{n+p_2} &= y_n + h \left(\frac{18383}{628992} f_n + \frac{1972625}{12773376} f_{n+p_1} + \frac{11131}{157248} f_{n+p_2} - \frac{473}{64512} f_{n+p_3} + \frac{13675}{4036032} f_{n+p_4} - \frac{3775}{5031936} f_{n+p_5} + \frac{253}{1016064} f_{n+1} \right), \\ y_{n+p_3} &= y_n + h \left(\frac{55}{1456} f_n + \frac{5875}{49896} f_{n+p_1} + \frac{1075}{4914} f_{n+p_2} + \frac{109}{7835347} f_{n+p_3} - \frac{42042}{16690609} f_{n+p_4} + \frac{2912}{412009} f_{n+p_5} - \frac{63504}{7267} f_{n+1} \right), \\ y_{n+p_4} &= y_n + h \left(\frac{5600000}{198243} f_n + \frac{319334400}{15400} f_{n+p_1} + \frac{142749}{568750} f_{n+p_2} + \frac{101979}{700000} f_{n+p_3} + \frac{450927}{1751750} f_{n+p_4} + \frac{45189}{364000} f_{n+p_5} - \frac{4716959}{3175200000} f_{n+1} \right), \\ y_{n+p_5} &= y_n + h \left(\frac{198243}{4550000} f_n + \frac{1503}{15400} f_{n+p_1} + \frac{142749}{568750} f_{n+p_2} + \frac{101979}{700000} f_{n+p_3} + \frac{450927}{1751750} f_{n+p_4} + \frac{45189}{364000} f_{n+p_5} - \frac{4716959}{3175200000} f_{n+1} \right), \\ y_{n+1} &= y_n + h \left(\frac{205}{4914} f_n + \frac{10375}{99792} f_{n+p_1} + \frac{592}{2457} f_{n+p_2} + \frac{83}{504} f_{n+p_3} + \frac{14800}{63063} f_{n+p_4} + \frac{7675}{39312} f_{n+p_5} + \frac{149}{7938} f_{n+1} \right) \end{aligned} \quad (6)$$

The above formulas together constitute the required block integrator for the direct approximation of the (1).

3 Analysis of the Block Integrator

For any numerical scheme, It is very important to know the order of accuracy and the nature of the local error in the implementation of the scheme. We thus introduce the difference operator corresponding

to each of the formula in (6) as

$$\mathcal{L}[y(x); h] = y(x) - h \left(\beta_0 y'(x_n) + \beta_1 y'(x_{n+1}) + \sum_{j=1}^5 \beta_j y'(x_{n+p_j}) \right) \quad (7)$$

where $y'(x_{n+p_j}) = f(x_{n+p_j})$ and $y(x) \in C[a, b]$. Expanding (6) in Taylor series about x_n , and after collecting all the terms in h the following local truncation errors (LTEs) are obtained

$$\left(\frac{1247969y^{(8)}(x_n)h^8}{846720000000000}, -\frac{9799y^{(8)}(x_n)h^8}{34681651200000}, \frac{383y^{(8)}(x_n)h^8}{90316800000}, \right. \\ \left. \frac{104583791y^{(8)}(x_n)h^8}{361267200000000000}, \frac{354483y^{(8)}(x_n)h^8}{313600000000000}, \frac{37y^{(8)}(x_n)h^8}{4233600000} \right)^T$$

The block method in (6) takes the matrix form

$$A_1 Y_{n+p} = A_0 Y_n + h(B_0 F_n + B_1 F_{n+p}) \quad (8)$$

where

$$Y_{n+p} = (y_{n+p_1}, y_{n+p_2}, y_{n+p_3}, y_{n+p_4}, y_{n+p_5}, y_{n+1})^T$$

$$Y_n = (y_n, y_{n-p_1}, y_{n-p_2}, y_{n-p_3}, y_{n-p_4}, y_{n+p_5})^T$$

$$F_{n+p} = (f_{n+p_1}, y_{n+p_2}, y_{n+p_3}, y_{n+p_4}, y_{n+p_5}, y_{n+1})^T$$

$$F_n = (f_n, f_{n-p_1}, f_{n-p_2}, f_{n-p_3}, f_{n-p_4}, f_{n+p_5})^T$$

The zero-stability refers to stability of the difference system in (7) as $h \rightarrow 0$. As such, if $h \rightarrow 0$ in (7) and by extension the the matrix representation in (8), we obtain

$$A_1 Y_{n+p} = A_0 Y_n \quad (9)$$

where A_1 is $I_{6 \times 6}$ identity matrix and $A_0 = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$ The characteristic equation of

(9) is given as $\lambda^5(\lambda - 1)$, which yields $\lambda_r = 0$, for $r = 1, 2, \dots, 5$ and $\lambda_6 = 1$. The block method (6) is 0-stable since the root of the first characteristic polynomial in (9), that is $p(\lambda) = 0$ satisfies the strict root condition, i.e, all its roots lie inside the unit circle, $|r| < 1$ and with those on the boundary being simple, see [2].

The block method in (6) has the property of consistency since it has accuracy greater than one as seen in its LTEs and it satisfies zero stability. Then, the method is concluded to be convergent.

3.1 Linear stability

For the linear stability of the NOSBI, the following test problem is adopted

$$y'(x) = -\xi y(x) \quad (10)$$

where $\xi \in \mathbb{C}$. It can be easily seen that (10) has a bounded solution for $\xi \geq 0$ as $x \rightarrow \infty$. Substituting (10) into (5) and (6), we obtain

$$\bar{Y}_{n+\tau} = \Omega(\omega) \bar{Y}_n \quad (11)$$

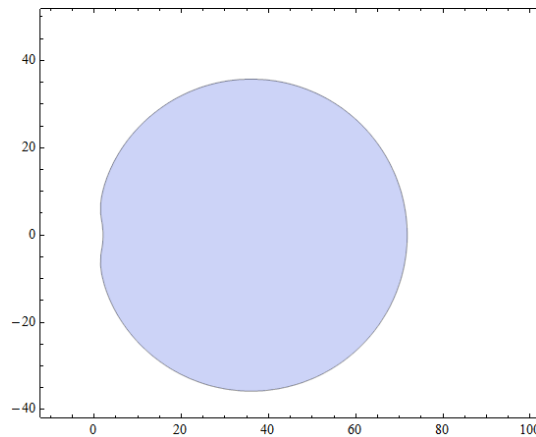


Figure 1: Region of absolute stability of the NOSBI

where $\omega = \xi h$ and the matrix $\Omega(\omega)$ is the amplification matrix or the stability matrix defined as

$$\Omega(\omega) = (A_0 + \omega B)^{-1}(A_1 + \omega C) \quad (12)$$

with

$$A_0 = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}; \quad A_1 = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix}$$

$$B = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & \frac{4484209}{122850000} \\ 0 & 0 & 0 & 0 & 0 & \frac{18383}{628992} \\ 0 & 0 & 0 & 0 & 0 & \frac{55}{1456} \\ 0 & 0 & 0 & 0 & 0 & \frac{202501}{5600000} \\ 0 & 0 & 0 & 0 & 0 & \frac{198243}{4550000} \\ 0 & 0 & 0 & 0 & 0 & \frac{205}{4914} \end{pmatrix}$$

$$C = \begin{pmatrix} \frac{97247}{1247400} & -\frac{307313}{15356250} & \frac{68659}{6300000} & -\frac{103193}{15765750} & \frac{18247}{9828000} & -\frac{130681}{198450000} \\ \frac{12773376}{5875} & \frac{157248}{1075} & -\frac{64512}{109} & \frac{4036032}{1775} & -\frac{5031936}{25} & \frac{1016064}{181} \\ \frac{49896}{16690609} & \frac{4914}{7835347} & \frac{672}{16690609} & -\frac{42042}{412009} & \frac{2912}{7267} & -\frac{63504}{4716959} \\ \frac{67200000}{1503} & \frac{37800000}{142749} & \frac{67200000}{101979} & \frac{12936000}{450927} & \frac{1792000}{45189} & -\frac{317520000}{47529} \\ \frac{15400}{10375} & \frac{568750}{592} & \frac{700000}{83} & \frac{1751750}{14800} & \frac{364000}{7675} & -\frac{2450000}{149} \\ \frac{99792}{2457} & & \frac{504}{63063} & & \frac{39312}{7938} & \end{pmatrix}$$

Hence obtaining the the following eigenvalues

$$\Omega(\omega) = \left(0, 0, 0, 0, 0, \frac{3(26880000 + 138240\omega - 3265600\omega^2 + 459552\omega^3)}{8064000 - 391680\omega + 8644800\omega^2 + 1122144\omega^3} \right); \quad (13)$$

The values in (13) shows the stability of the NOSBI entirely described by the amplification matrix $\Omega(\omega)$, whose region of absolute stability is is given as by $|\xi\Omega(\omega)| \leq 1$. The stability interval is thus (0, 71.795). The region of absolute stability is thus given in Figure 1

4 Computational procedure

The proposed method is implemented in a fixed step-size block mode in such that, on the each block interval of the form $[x_n, x_{n+1}]$, $n = 0, 1, N-1$, where N is the number of subinterval of the integration

interval $[a, b]$. Applying the proposed method to system of m first order ODEs, we have the following procedure

$$Y' = F(X, Y^T), \quad Y(a) = Y_0, \quad [X_0, X_N]$$

where

$$Y = (y_1, y_2, \dots, y_m)^T,$$

$$F(X, Y^T) = (f_1(x, Y^T), f_2(x, Y^T), \dots, f_m(x, Y^T))^T$$

and

$$Y_0 = (y_{1,0}, y_{2,0}, \dots, y_{m,0})^T, \quad)^T.$$

The method is applied to each of the scalar equations in the differential system so that a total of $6 \times m$ are obtained. This is solved using the Newton's method.

5 Numerical experiments

In this section, the implementation of the proposed method is performed on modeled problems rising from diseases in human population. The comparison of the proposed method is done with the classical fourth-order Runge-Kutta (RK) method.

Model Problem 1. Consider a three compartmental model of a disease epidemic discussed in [3]

$$\begin{aligned} \frac{dS}{dt} &= \beta - \alpha SI - (\rho + \mu)S + \sigma R \\ \frac{dI}{dt} &= \alpha SI - (\gamma + \delta + \mu)I \\ \frac{dR}{dt} &= \gamma I - (\mu + \sigma)R + \rho S \end{aligned} \quad (14)$$

where the state variables S , I and R are susceptible, infected and recovered population with their respective initial state given as $S(0) = 300$, $I(0) = 200$ and $R(0) = 100$. Here, α , β , γ , δ , μ , ρ and σ are parameters which describes how human migrates from one compartment to another. The following values are obtained in [3]: $\alpha = 0.0011$, $\beta = 10^8$, $\gamma = 0.01$, $\delta = 0.013$, $\mu = 0.02$, $\rho = 0.33$ and $\sigma = 0.44$. Solving (14) with the developed NOSBI and the classical Runge-Kutta method, the following figure shows how efficient and accurate the new method performed.

In Figure 2, the continuous line indicates solution using the classical Runge-Kutta method while the dots show the solution obtained using the NOSBI. These two methods agree which indicate the suitability of NOSBI for solving similar epidemiological models.

Model Problem 2. Consider the solution for a mathematical model of the SEIR COVID-19 outbreak that includes partially and fully vaccinated individual discussed in [6].

$$\begin{aligned} \frac{dS}{dt} &= A - \alpha SI - \mu S - V_p S - V_f S \\ \frac{dE}{dt} &= \alpha SI - \mu E - \delta E + V_p S \\ \frac{dI}{dt} &= \delta E - \mu I - \mu_1 I - \gamma I \\ \frac{dR}{dt} &= V_f S + \gamma I - \mu R \end{aligned} \quad (15)$$

with the following descriptions with respect to [6]:

$A(= 33.595)$ - recruitment rate; $\alpha(= 10^{-5})$ - rate of interaction between susceptible and infected population; $\mu(= 0.143)$ - death rate; $V_p(= 0.2522)$ - partially vaccinated population; $V_f(= 0.1517)$ - fully

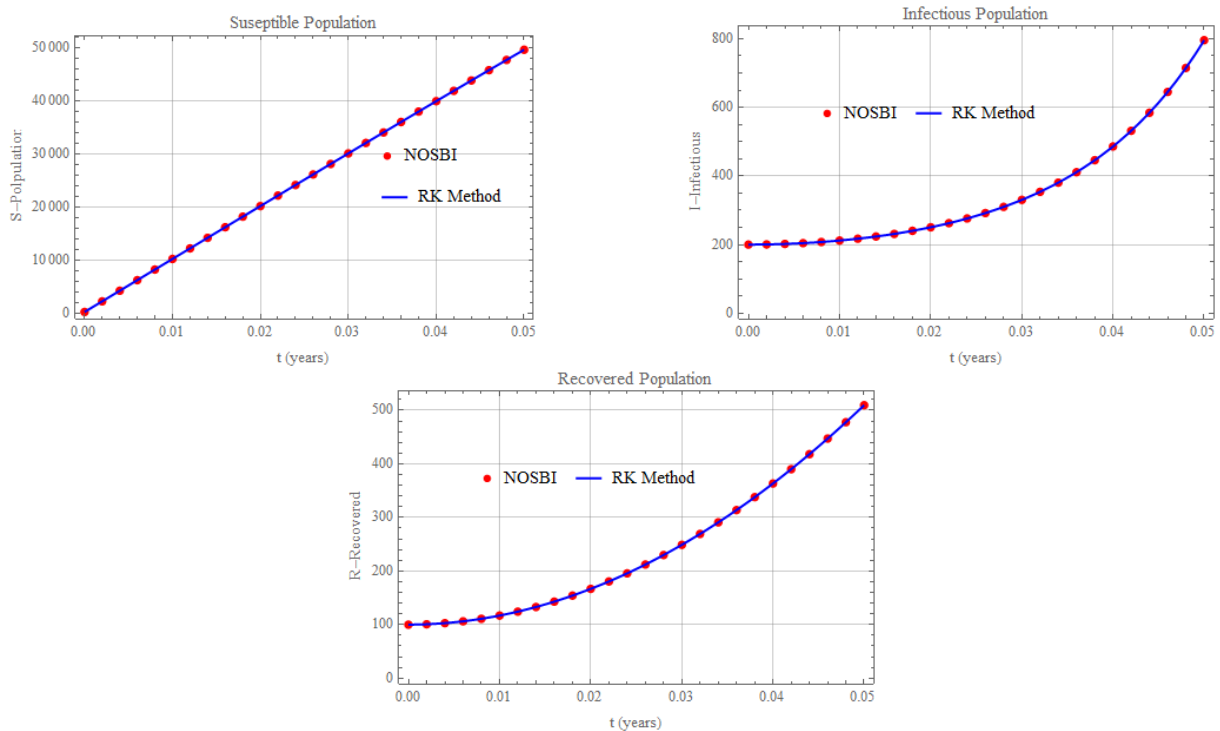


Figure 2: Both NOSBI and the classical Runge-Kutta numerical method

vaccinated population; $\delta (= 1.01)$ - rate of infection by exposed population; $\mu_1 (= 0.1595)$ - disease-related rate; $\gamma (= 0.9)$ - rate of recovery. The state variables at time $t_0 = 0$ (in days) are as follows: $S(t_0) = 1,661,987$; $E(t_0) = 1,661$; $I(t_0) = 481$; $R(t_0) = 487$. The developed NOSBI and the classical fourth-order Runge-Kutta method was used to solve [14](#) numerically. The table below shows curves of the solutions of $S(t)$, $E(t)$, $I(t)$, $R(t)$.

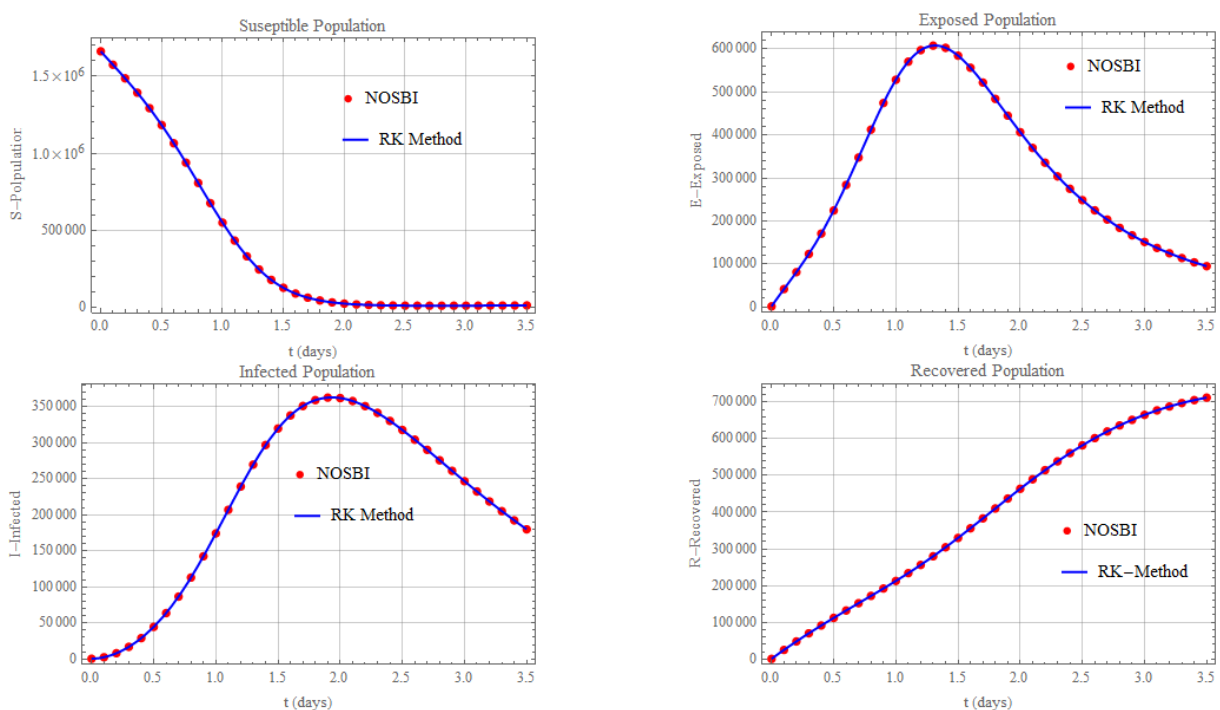


Figure 3: NOSBI and the classical Runge-Kutta numerical method

Model Problem 3. In this experiment, a nonlinear malaria transmission epidemic model discussed in [10] is considered.

$$\begin{aligned}
 \frac{dS}{dt} &= \Omega - \tau SI - \phi S \\
 \frac{dE}{dt} &= \tau SI - (\sigma_1 + \phi)E \\
 \frac{dI}{dt} &= \sigma_1 E - (\sigma_2 + \phi + \theta)I \\
 \frac{dR}{dt} &= \sigma_2 I - \phi R
 \end{aligned} \tag{16}$$

where the state variables are Susceptible (S), Exposed (E), Infected (I), and Removed (R). Here, Ω is susceptible recruitment rate, τ is infection rate (effective infection rate), σ_1 is the increasing rate of exposed (human) being infectious, σ_2 is human recovery rate (removal rate), ϕ is natural mortality rate and θ is the Increase in death rate.

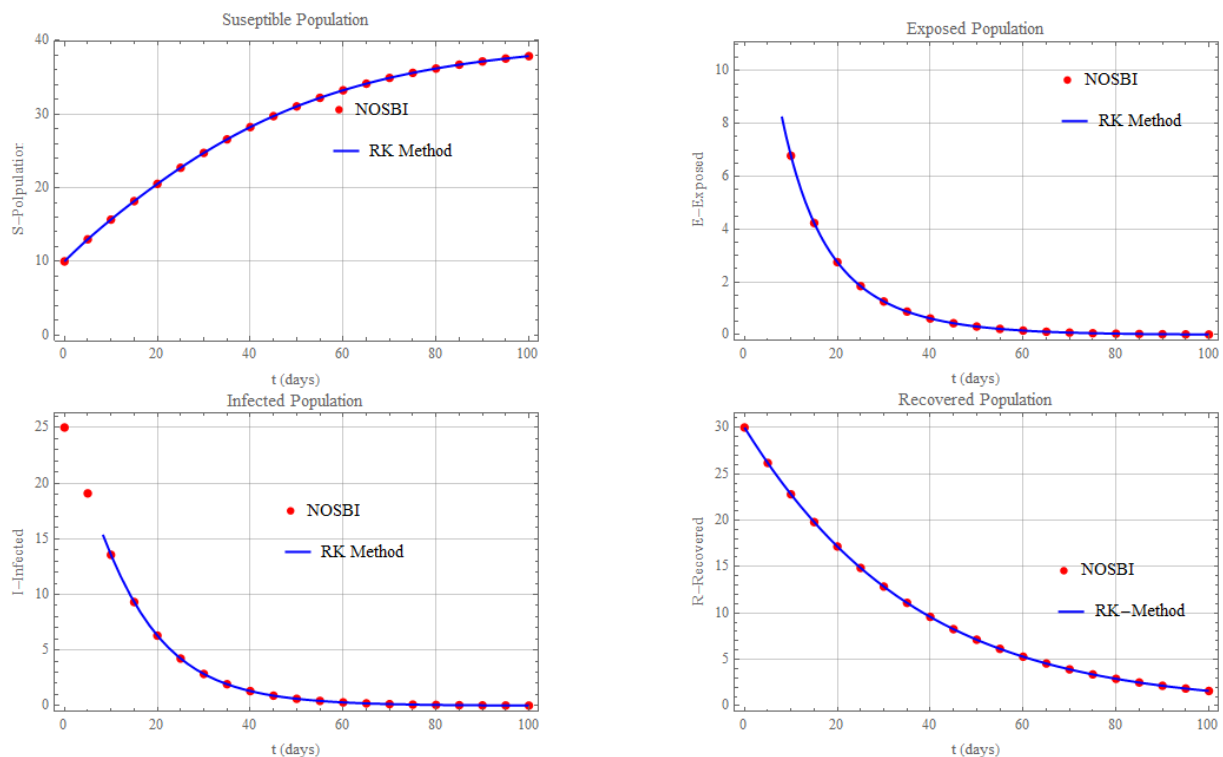


Figure 4: NOSBI and the classical Runge-Kutta numerical method

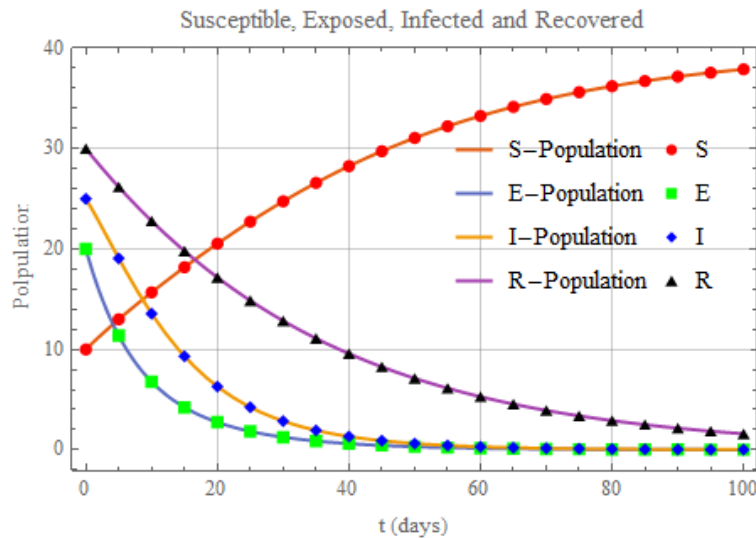


Figure 5: NOSBI and the classical Runge-Kutta numerical method

The following parameter values and initial conditions are used for this experiment. $S(0) = 10$, $E(0) = 20$, $I(0) = 25$, $R(0) = 30$, with $\Omega = 1.2$, $\tau = 0.001$, $\phi = 0.03$, $\sigma_1 = 0.1$, $\sigma_2 = 0.0035$, $\theta = 0.089$.

Generally, it can be clearly seen that, apart from the Runge-Kutta method, this method proves better approximation of the solution of the model so far presented. The effectiveness of the NOSBI is seen in the highly nonlinear model that follows.

Model Problem 4. In this experiment, a mathematical model to cholera transmission with vaccination strategy discussed in [10] is considered.

$$\begin{aligned}
 \frac{dS}{dt} &= \Lambda - (1 - \omega) \left(\frac{\beta_e B}{B + k} + \beta_h I \right) S - \mu S - \psi S \\
 \frac{dV}{dt} &= \psi S - p(1 - \omega) \left(\frac{\beta_e B}{B + k} + \beta_h I \right) V - \mu V \\
 \frac{dI}{dt} &= (1 - \omega) \left(\frac{\beta_e B}{B + k} + \beta_h I \right) S + p \left(\frac{\beta_e B}{B + k} + \beta_h I \right) (1 - \omega) V - I(\delta + \mu + \epsilon) \\
 \frac{dQ}{dt} &= \epsilon I - Q(\delta + \eta + \mu) \\
 \frac{dR}{dt} &= \eta Q - \mu R \\
 \frac{dB}{dt} &= \alpha(1 - \omega)I - \sigma B
 \end{aligned} \tag{17}$$

Here the physical meaning of the parameters and state values for (17) as stated in [10] are as follows:

$S(t)$ -susceptible population, $V(t)$ -vaccinated population, $I(t)$ -infected population, $Q(t)$ -quarantined population and $R(t)$ -Recovered population and $B(t)$ -is the vibrio cholerae.

Λ : Rate of human Population recruited in susceptible compartment with the value 15.1854/day;

$1/\mu$: Average life expectancy with value 60 years;

δ : Death rate from cholera infection with value 0.015/day;

β_e : Human-to-human interaction rate with value 0.2143/day;

β_h : Vibrios ingestion rate from the Surroundings with value 0.0040963/day;

ω : Measure of education campaign and treatment efficacy with value 0.39;

k : Concentration of the bacterium *Vibrio cholerae* with value 10^9 cells/L;

ϵ : Quarantine rate of cholera patients with value 0.00331428/day;

η : Rate of quarantine individual recover through treatment with value 0.003/day

α : Contribution rate of infected persons to *Vibrio cholerae* amount in the environment with value 10

cells/ml-day;

σ : Decay rate of *Vibrio cholerae* from the atmosphere with value 0.00174478/day;

ψ : The rate at which Susceptible class is Vaccinated 0.07/day;

p : Modification Parameter with value 0.0186821.

The following initial conditions are considered: $S(0) = 15$, $V(0) = 20$, $I(0) = 50$, $Q(0) = 75$, $R(0) = 30$, $B(0) = 0$.

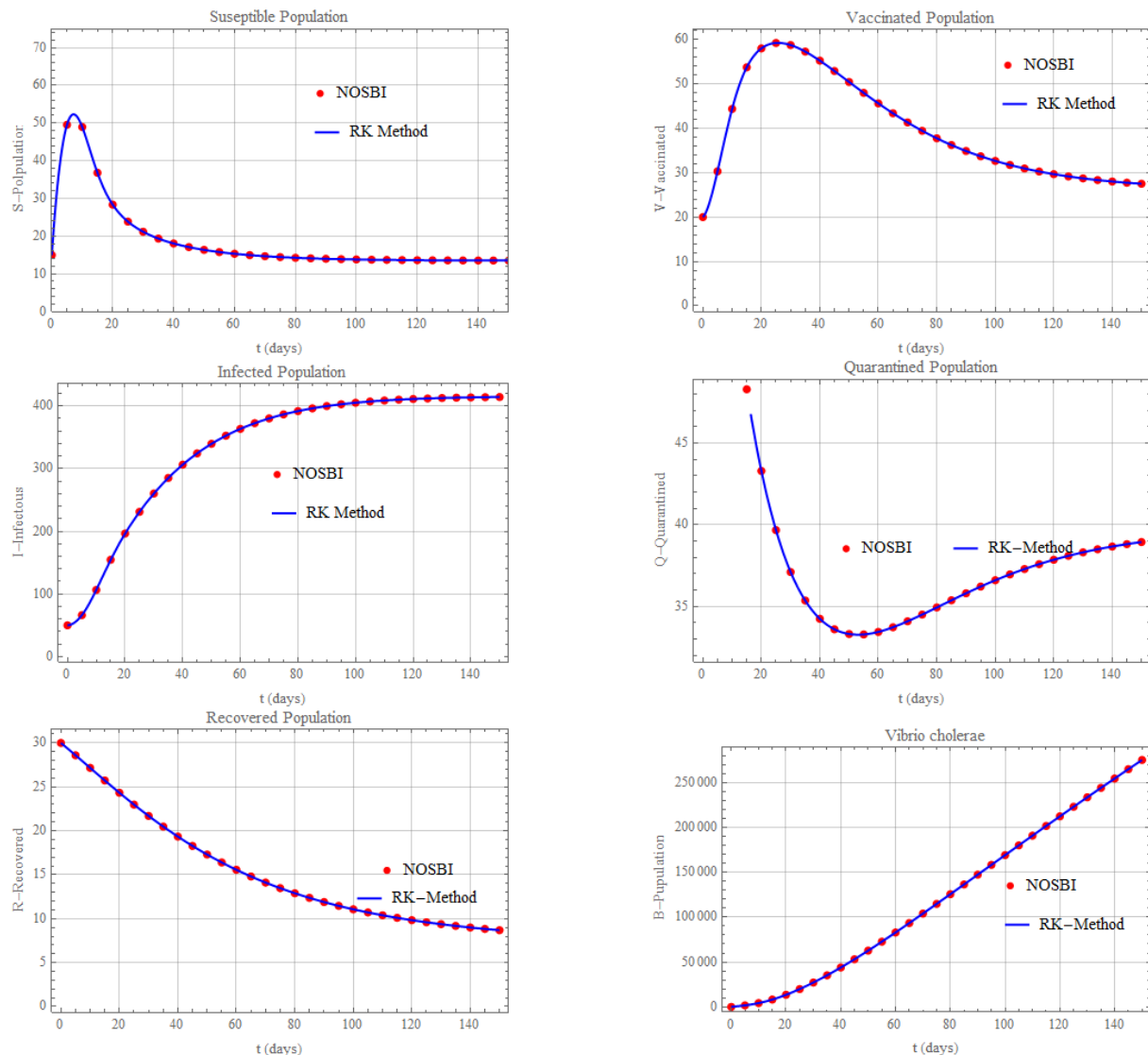


Figure 6: NOSBI and the classical Runge-Kutta numerical method

The applicability of the NOSBI to epidemiological models can not be over emphasized as can be seen in the numerical solution of model problem (17) shown by the graph in Figure 6. It clearly agrees with the RK-4 method and invariable with other methods as described in literatures. The numerical experiments shown in the Figures above demonstrate the robustness of the derived NOSBI.

6 Conclusion

Linear multistep method has been shown in several literature to have a good performance in obtaining the numerical solutions of a very large range of problems both scalar and in the case of this work, system of ordinary differential equation. The key advantages of the NOSBI are demonstrated its ease of derivation and implementation. The theoretical properties of the developed scheme shows the robust-

ness in real application to epidemiological dynamics even with large time step sizes. This is a significant implementation and computational advantage.

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