We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

4,800
Open access books available

122,000
International authors and editors

135M
Downloads

Our authors are among the

154
Countries delivered to

TOP 1%
most cited scientists

12.2%
Contributors from top 500 universities

CLARIVATE ANALYTICS BOOK CITATION INDEX INDEXED

WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com

Chapter 4

On New High Order Iterative Schemes for Solving Initial Value Problems in Epidemiology

Sandile Motsa and Stanford Shateyi

Additional information is available at the end of the chapter

http://dx.doi.org/10.5772/48264

1. Introduction

Most problems arising from mathematical epidemiology are often described in terms of differential equations. However, it is often very difficult to obtain closed form solutions of such equations, especially those that are nonlinear. In most cases, attempts are made to obtain only approximate or numerical solutions. In this work, we revisit the SIR epidemic model with constant vaccination strategy that was considered in [11], where the Adomian decomposition method was used to solve the governing system of nonlinear initial value differential equations.

In this work we develop new accurate iterative schemes which are based on extending Taylor series based linearization method to obtain accurate and fast converging sequence of hybrid iteration schemes. At first order, the hybrid iteration scheme reduces to quasilinearization method (QLM) which was originally developed in [1]. More recently Mandelzweig and his co-workers [8–10] have extended the application of the QLM to a wide variety of nonlinear BVPs and established that the method converges quadratically. In this work we demonstrate that the proposed hybrid iteration schemes are more accurate and converge faster than the QLM approach.

To implement the method we consider the SIR model that describes the temporal dynamics of a childhood disease in the presence of a preventive vaccine. In SIR models the population is assumed to be divided into the standard three classes namely, the susceptibles (S), who can catch the infection but are so far uninfected, the infectives (I), those who have the disease and can transmit it to the susceptibles, and the removed (R), who have either died or who have recovered and are therefore immune.

The governing equations for the problem are described [11] by

$$\frac{dS}{dt} = (1-P)\pi N - \beta\frac{SI}{N} - \mu S, \tag{1}$$

$$\frac{dI}{dt} = \beta\frac{SI}{N} - (\kappa+\mu)I, \tag{2}$$

$$\frac{dR}{dt} = P\pi N + \kappa I - \mu R, \tag{3}$$

where $S(t)$, $I(t)$ and $R(t)$ denote the susceptibles, infectives and the removed classes respectively.

The total population is denoted by $N = S + I + R$, μ is the death rate, P is the fraction of citizens vaccinated at birth each year, β is the average contact rate, π is the constant birth rate, and κ is the rate at which an individual recovers from the disease and enters the removed group which also contains vaccinated individuals. Equations (1 - 3) are solved using the new hybrid iteration schemes and the results are compared with results from the Runge-Kutta MATLAB in-built solver `ode45`.

2. Numerical solution

To simplify the formulation of the solution, equations (1) - (3) are scaled by dividing by N. We define new variables $z_1 = S/N$, $z_2 = I/N$ and $z_3 = R/N$. This leads to $z_1 + z_2 + z_3 = 1$ and if we assume that $\pi = \mu$, the scaled new system becomes

$$z_1'(t) = (1-P)\pi - \beta z_1(t) z_2(t) - \pi z_1(t), \quad z_1(0) = s_0, \tag{4}$$
$$z_2'(t) = \beta z_1(t) z_2(t) - (\pi + \kappa) z_2(t), \quad z_2(0) = i_0, \tag{5}$$

where s_0 and i_0 are given constants. The solution for $z_3(t)$ can be obtained from $z_3 = 1 - z_1 - z_2$.

Previous studies [4–7, 12] have shown that the long term behaviour of systems like (4) - (5) can be classified into two categories namely, endemic or eradication. From the long term behaviour of $z_1(t)$ and $z_2(t)$ it holds that the solution asymptotically approaches a disease free equilibrium (DFE) or the endemic equilibrium (EE) where

$$\lim_{t\to+\infty}(z_1(t), z_2(t)) = \text{DFE} = (1-P, 0), \tag{6}$$

$$\lim_{t\to+\infty}(z_1(t), z_2(t)) = \text{EE} = \left(\frac{1-P}{R_v}, \frac{\pi}{\beta}(R_v - 1)\right). \tag{7}$$

Here R_v, the vaccination reproduction number, is the threshold that determines the stability of the equilibria and is defined by

$$R_v = \frac{\beta(1-P)}{\gamma + \pi}. \tag{8}$$

It was shown in [11] that the DFE is locally stable if $R_v < 1$ and the EE is locally stable provided $1 < R_v \leq 4(\kappa + \pi)/\pi$. In this work, we use develop new iteration schemes to solve the system (4) - (5) using parameters that yield both the DFE and EE.

3. Method of solution

To develop the method of solution, we assume that the true solution of (4 - 5) is $z_{s,\alpha}$ $(s = 1, 2)$ and $z_{s,\gamma}$ are the initial approximations. We introduce the following coupled system,

$$L_j z_j + f_j(z_{1,\gamma}, z_{2,\gamma}) + \sum_{s=1}^{2}(z_s - z_{s,\gamma})\frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}) + g_j(z_1, z_2) = \Psi_j, \tag{9}$$

$$g_j(z_1, z_2) = f_j(z_1, z_2) - f_j(z_{1,\gamma}, z_{2,\gamma}) - \sum_{s=1}^{2}(z_s - z_{s,\gamma})\frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}), \tag{10}$$

where

$$L_1 z_1 = z_1' + \pi z_1, \quad L_2 z_2 = z_2' + (\pi + \kappa) z_2, \tag{11}$$

$$f_1(z_1, z_2) = \beta z_1 z_2, \quad f_2(z_1, z_2) = -\beta z_1 z_2, \quad \Psi_1 = (1 - P)\pi, \quad \Psi_2 = 0. \tag{12}$$

This idea of introducing the coupled equations of the form (9-10) have previously been used in [3] the construction of Newton-like iteration formulae for the computation of the solutions of nonlinear equations of the form $f(x) = 0$.

We write equation (9) as

$$L_j z_j + \sum_{s=1}^{2} z_s \frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}) + g_j(z_1, z_2) = \Phi_j(z_{1,\gamma}, z_{2,\gamma}), \tag{13}$$

where

$$\Phi_j(z_{1,\gamma}, z_{2,\gamma}) = \Psi_j + \sum_{s=1}^{2} z_{s,\gamma} \frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}) - f_j(z_{1,\gamma}, z_{2,\gamma}). \tag{14}$$

We use the quasilinearization method (QLM) of Bellman and Kalaba [1] to solve equation (13). The QLM determines the $(i+1)$th iterative approximation $z_{j,i+1}$ as the solution of the differential equation

$$L_j z_{j,i+1} + \sum_{s=1}^{2} z_{s,i+1} \frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}) + g_j(z_{1,i}, z_{2,i}) + \sum_{s=1}^{2}(z_{s,i+1} - z_{s,i})\frac{\partial g_j}{\partial z_s}(z_{1,i}, z_{2,i}) = \Phi_j(z_{1,\gamma}, z_{2,\gamma}), \tag{15}$$

which can be written as

$$L_j z_{j,i+1} + \sum_{s=1}^{2}\left[\frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}) + \frac{\partial g_j}{\partial z_s}(z_{1,i}, z_{2,i})\right] z_{s,i+1} = \tag{16}$$

$$\sum_{s=1}^{2} z_{s,i}\frac{\partial g_j}{\partial z_s}(z_{1,i}, z_{2,i}) - g_j(z_{1,i}, z_{2,i}) + \Phi_j(z_{1,\gamma}, z_{2,\gamma}),$$

subject to

$$z_{1,i+1} = s_0, \quad z_{2,i+1} = i_0. \tag{17}$$

We assume that $z_{j,0}$ is obtained as a solution of the linear part of equation (13) given by

$$L_j z_{j,0} + \sum_{s=1}^{2} z_{s,0} \frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}) = \Phi_j(z_{1,\gamma}, z_{2,\gamma}), \tag{18}$$

which yields the iteration scheme

$$L_j z_{j,r+1} + \sum_{s=1}^{2} z_{s,r+1} \frac{\partial f_j}{\partial z_s}(z_{1,r}, z_{2,r}) = \Phi_j(z_{1,r}, z_{2,r}). \tag{19}$$

We note that equation (19) is the standard QLM iteration scheme for solving (4 - 5).

When $i = 0$ in (16) we can approximate z_j as

$$z_j \approx z_{j,1}. \tag{20}$$

Thus, setting $i = 0$ in (16) we obtain

$$L_j z_{j,1} + \sum_{s=1}^{2} \left[\frac{\partial f_j}{\partial z_s}(z_{1,\gamma}, z_{2,\gamma}) + \frac{\partial g_j}{\partial z_s}(z_{1,0}, z_{2,0}) \right] z_{s,1} = \sum_{s=1}^{2} z_{s,0} \frac{\partial g_j}{\partial z_s}(z_{1,0}, z_{2,0}) - g_j(z_{1,0}, z_{2,0}) + \Phi_j(z_{1,\gamma}, z_{2,\gamma}), \tag{21}$$

which yields the iteration scheme

$$L_j z_{j,r+1} + \sum_{s=1}^{2} \left[\frac{\partial f_j}{\partial z_s}(z_{1,r}, z_{2,r}) + \frac{\partial g_j}{\partial z_s}(z_{1,r+1}^{(0)}, z_{2,r+1}^{(0)}) \right] z_{s,r+1} = \sum_{s=1}^{2} z_{s,r+1}^{(0)} \frac{\partial g_j}{\partial z_s}(z_{1,r+1}^{(0)}, z_{2,r+1}^{(0)}) - g_j(z_{1,r+1}^{(0)}, z_{2,r+1}^{(0)}) + \Phi_j(z_{1,r}, z_{2,r}), \tag{22}$$

where $z_{j,r+1}^{(0)}$ is the solution of

$$L_j z_{j,r+1}^{(0)} + \sum_{s=1}^{2} z_{s,r+1}^{(0)} \frac{\partial f_j}{\partial z_s}(z_{1,r}, z_{2,r}) = \Phi_j(z_{1,r}, z_{2,r}). \tag{23}$$

The general iteration scheme obtained by setting $i = m$ ($m \geq 2$) in equation (16), hereinafter referred to as scheme-m is

$$L_j z_{j,r+1} + \sum_{s=1}^{2} \left[\frac{\partial f_j}{\partial z_s}(z_{1,r}, z_{2,r}) + \frac{\partial g_j}{\partial z_s}(z_{1,r+1}^{(m-1)}, z_{2,r+1}^{(m-1)}) \right] z_{s,r+1} = \sum_{s=1}^{2} z_{s,r+1}^{(m-1)} \frac{\partial g_j}{\partial z_s}(z_{1,r+1}^{(m-1)}, z_{2,r+1}^{(m-1)}) - g_j(z_{1,r+1}^{(m-1)}, z_{2,r+1}^{(m-1)}) + \Phi_j(z_{1,r}, z_{2,r}), \tag{24}$$

where $z_{j,r+1}^{(m-1)}$ is obtained as the solution of

$$L_j z_{j,r+1}^{(m-1)} + \sum_{s=1}^{2} \left[\frac{\partial f_j}{\partial z_s}(z_{1,r}, z_{2,r}) + \frac{\partial g_j}{\partial z_s}(z_{1,r+1}^{(m-2)}, z_{2,r+1}^{(m-2)}) \right] z_{s,r+1}^{(m-1)} = \sum_{s=1}^{2} z_{s,r+1}^{(m-2)} \frac{\partial g_j}{\partial z_s}(z_{1,r+1}^{(m-2)}, z_{2,r+1}^{(m-2)}) - g_j(z_{1,r+1}^{(m-2)}, z_{2,r+1}^{(m-2)}) + \Phi_j(z_{1,r}, z_{2,r}). \tag{25}$$

The initial approximation for solving the iteration algorithms, scheme-m is obtained by solving the linear part of the governing equations (4 - 5). This gives

$$z_{1,0} = (1 - P)(1 - e^{-\pi t}) + s_0 e^{-\pi t}, \qquad z_{2,0} = i_0 e^{-(\pi+\kappa)t}. \tag{26}$$

The iteration schemes (19),(24 - 25) can be solved numerically using standard methods such as finite difference, finite elements, spline collocation methods,etc. In this study we use the Chebyshev spectral collocation method to solve the iteration schemes. For brevity, we omit the details of the spectral methods, and refer interested readers to ([2, 13]). Before applying the spectral method, it is convenient to transform the domain on which the governing equation is

defined to the interval [-1,1] on which the spectral method can be implemented. We use the transformation $t = t_F(\tau + 1)/2$ to map the interval $[0, t_F]$ to [-1,1], where t_F is a finite time. The basic idea behind the spectral collocation method is the introduction of a differentiation matrix D which is used to approximate the derivatives of the unknown variables z at the collocation points as the matrix vector product

$$\frac{dz}{dt} = \sum_{k=0}^{N} \mathbf{D}_{jk} z(\tau_k) = \mathbf{DZ}, \qquad j = 0, 1, \ldots, N, \tag{27}$$

where $N + 1$ is the number of collocation points (grid points), $\mathbf{D} = 2D/t_F$, and $\mathbf{Z} = [z(\tau_0), z(\tau_1), \ldots, z(\tau_N)]^T$ is the vector function at the collocation points τ_j.

Applying the Chebyshev spectral method to (19), for instance, gives

$$\left[\begin{array}{c|c} \mathbf{D} + \pi I + \mathbf{a}_{11} & \mathbf{a}_{12} \\ \hline \mathbf{a}_{21} & \mathbf{D} + (\pi + \kappa) I + \mathbf{a}_{22} \end{array}\right] \begin{bmatrix} z_{1,r+1}(\tau_0) \\ z_{1,r+1}(\tau_1) \\ \vdots \\ z_{1,r+1}(\tau_N) \\ \hline z_{2,r+1}(\tau_0) \\ z_{2,r+1}(\tau_1) \\ \vdots \\ z_{2,r+1}(\tau_N) \end{bmatrix} = \begin{bmatrix} \Phi_{1,r+1}(\tau_0) \\ \Phi_{1,r+1}(\tau_1) \\ \vdots \\ \Phi_{1,r+1}(\tau_N) \\ \hline \Phi_{2,r+1}(\tau_0) \\ \Phi_{2,r+1}(\tau_1) \\ \vdots \\ \Phi_{2,r+1}(\tau_N) \end{bmatrix}, \tag{28}$$

where

$$\mathbf{a}_{ji} = \frac{\partial f_i}{\partial z_i} \tag{29}$$

and I is an $(N + 1) \times (N + 1)$ identity matrix.

4. Results and discussion

In this section we present the results of solving the governing equations (4-5) using the iteration scheme-m. For illustration purposes we present the results for $m = 0, 1, 2$ to illustrate the effect of increasing m in the accuracy and convergence of the iteration schemes. The number of collocations points in all the results presented here is $N = 40$. In order to assess the accuracy of the proposed method, the present numerical results were compared against results generated using the MATLAB initial value solver `ode45`. In the numerical simulations presented here, following [11], the governing parameters were carefully selected in order to represent the cases which give rise to both the disease free equilibrium (DFE) and endemic equilibrium (EE). We consider the following cases

1. Case 1: $s_0 = 1$, $i_0 = 0$, $\beta = 0.8$, $\kappa = 0.03$, $\pi = 0.4$, $P = 0.9$.
   In this case we observe that $R_v = 0.186 < 1$, hence we expect the disease to be eradicated from the population after some time.
2. Case 2: $s_0 = 0.8$, $i_0 = 0.2$ $\beta = 0.8$, $\kappa = 0.03$, $\pi = 0.4$, $P = 0.9$.
   In this case we observe that $R_v = 0.186 < 1$ and as expected, using these parameters, the disease should be eradicated as $t \to \infty$.

3. Case 3: $s_0 = 0.8,\ \ i_0 = 0.2\ \ \beta = 0.8,\ \ \kappa = 0.03,\ \ \pi = 0.4,\ \ P = 0.$
   In this case$R_v = 1.86 > 1$ which leads to the endemic equilibrium (no disease eradication).
4. Case 4: $s_0 = 0.8,\ \ i_0 = 0.2\ \ \beta = 0.8,\ \ \kappa = 0.03,\ \ \pi = 0.4,\ \ P = 0.3.$
   In this case $R_v = 1.32 > 1$ which leads to the endemic equilibrium (no disease eradication).

The results for Case 1 are shown on Figs. 1 - 2. In this case, the initial guess and the first few iterations match the numerical solution all the iterative schemes in the plots of $s(t), r(t)$. We observe that $s(t)$ decreases monotonically with time while $r(t)$ increases with time. The graph of the profile for $i(t)$ is not shown because $i(t) = 0$ in this particular case.

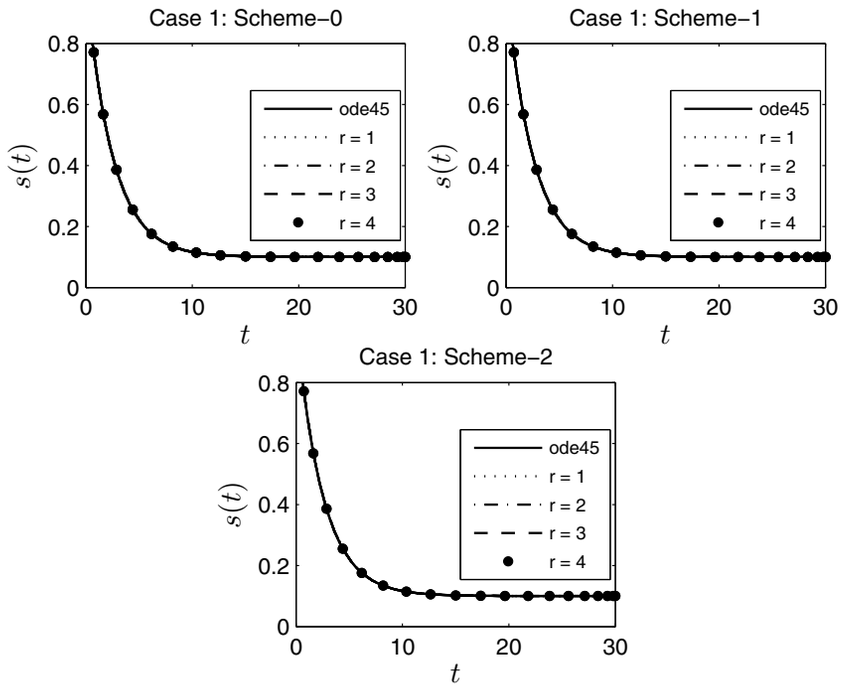

Figure 1. Case 1: Comparison of the numerical solution of the population fractions $s(t)$ against the results from the iteration schemes-0, 1 and 2

Figs. 3 - 5 show the numerical approximation of the profiles of the different classes for Case 2. Again, all the iterative schemes rapidly converge to the numerical solution. The population of the susceptibles decreases with time and that of the removed (those recovered with immunity) increases with time. The infected population initially increases and reaches a maximum, then gradually decreases to zero as $t \to \infty$.

Figs. 6 - 8 show the numerical approximation of the profiles of the different classes for Case 3. It can be noted from the graphs that the Scheme-2 converges fastest towards the numerical results. Only 10 iterations are required for full convergence in Scheme-2 compared to 14 iterations in Scheme-1 and 28 iterations in Scheme-1.

Figs. 8 - 11 shows the variation all the population groups with time for Case 4. Again, we observe that Scheme-2 converges fastest towards the numerical results. Only 5 iterations are required for full convergence in Scheme-2 compared to 6 iterations in Scheme-1 and 12 iterations in Scheme-1.

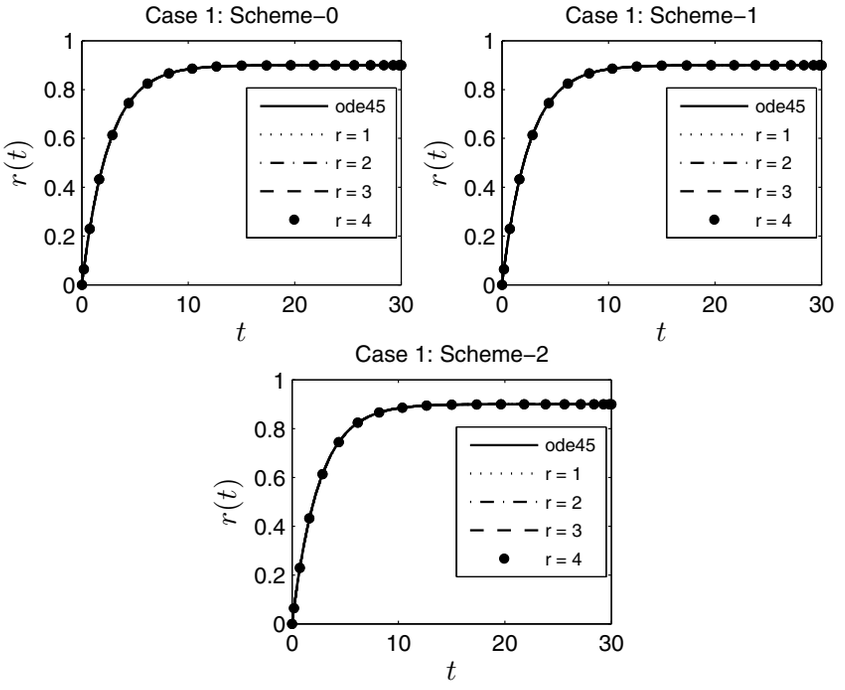

Figure 2. Case 1: Comparison of the numerical solution of the population fractions $r(t)$ against the results from the iteration schemes-0, 1 and 2

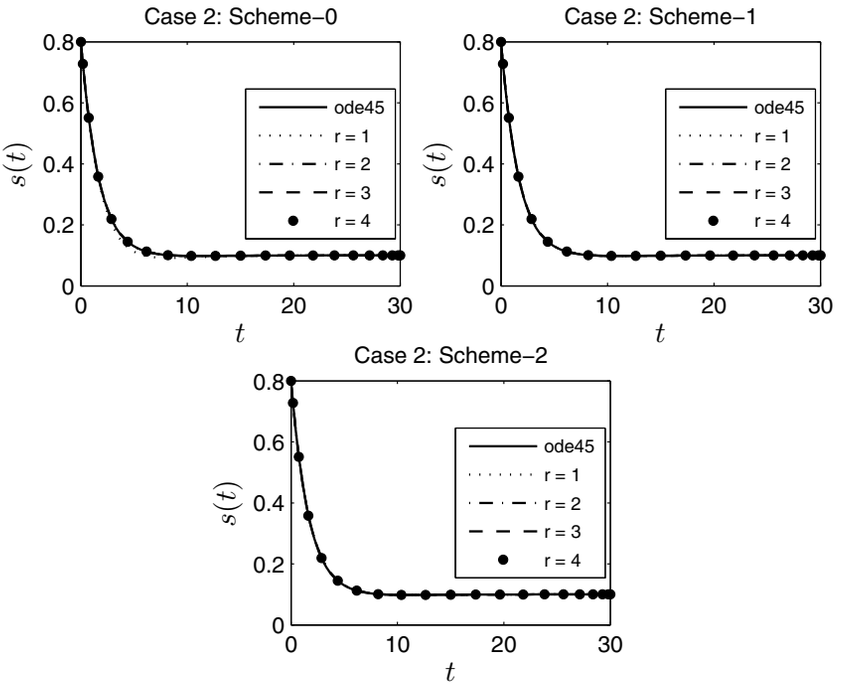

Figure 3. Case 2: Comparison of the numerical solution of the population fractions $s(t)$ against the results from the iteration schemes-0, 1 and 2

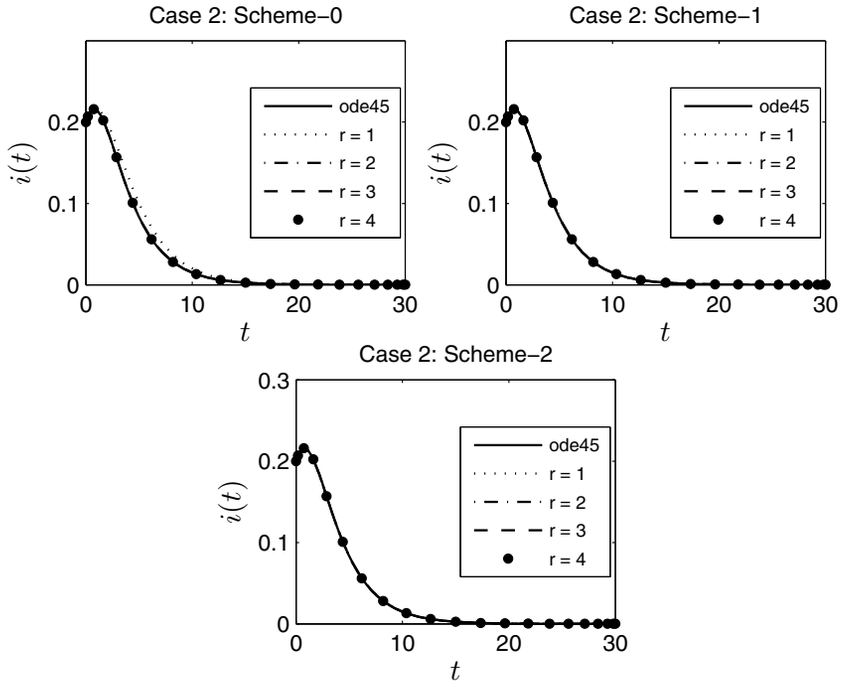

Figure 4. Case 2: Comparison of the numerical solution of the population fractions $i(t)$ against the results from the iteration schemes-0, 1 and 2

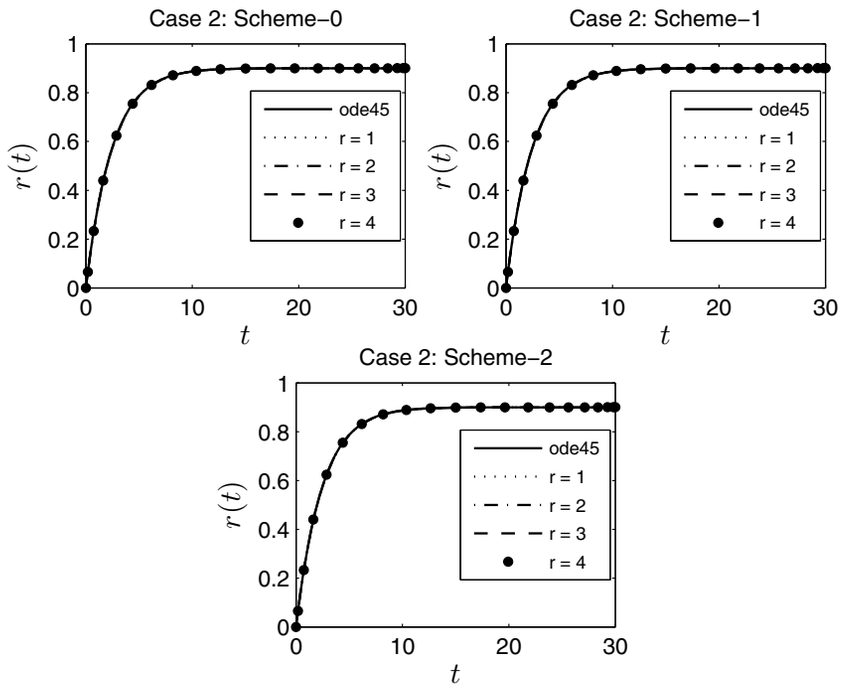

Figure 5. Case 2: Comparison of the numerical solution of the population fractions $r(t)$ against the results from the iteration schemes-0, 1 and 2

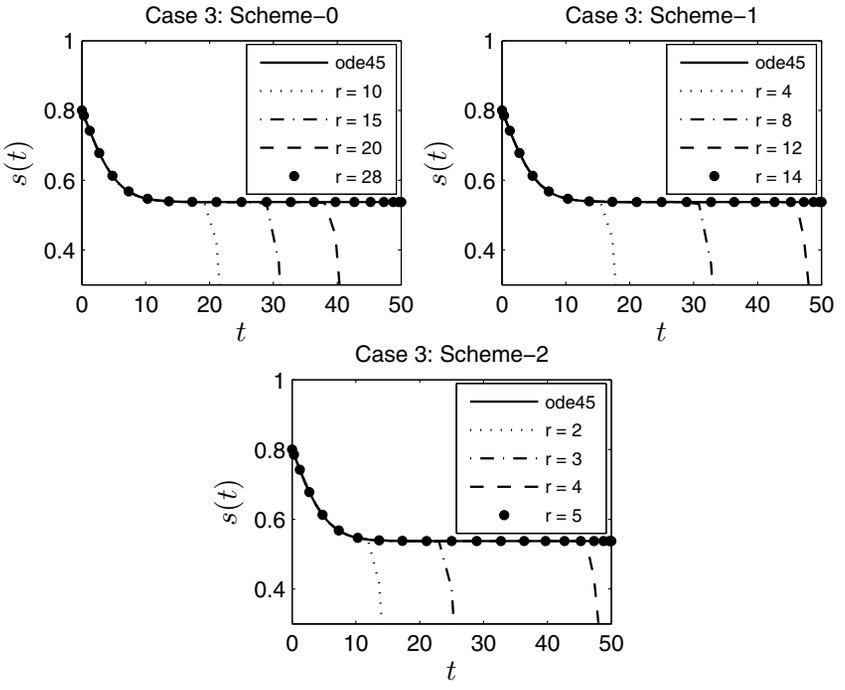

Figure 6. Case 3: Comparison of the numerical solution of the population fractions $s(t)$ against the results from the iteration schemes-0, 1 and 2

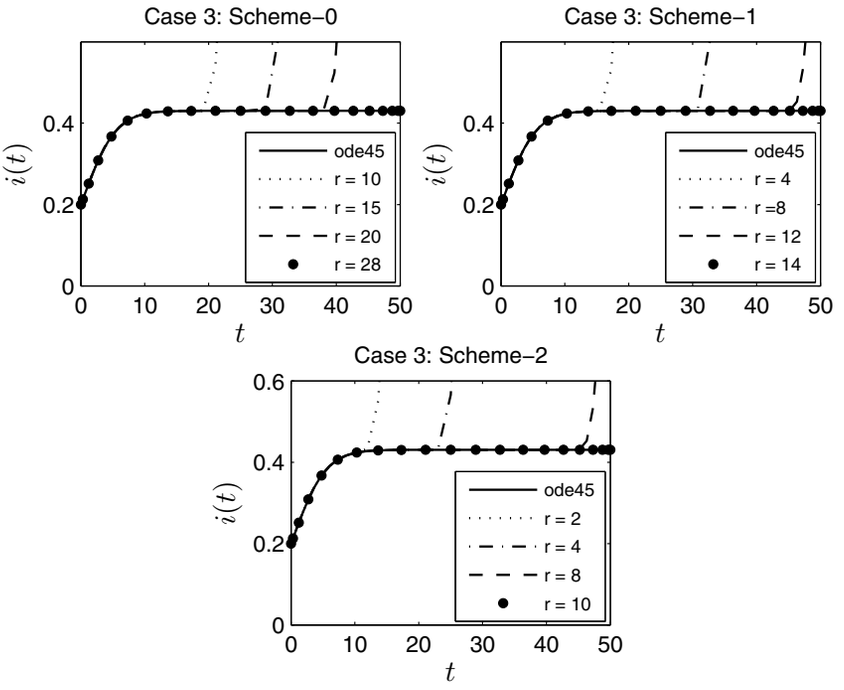

Figure 7. Case 3: Comparison of the numerical solution of the population fractions $i(t)$ against the results from the iteration schemes-0, 1 and 2

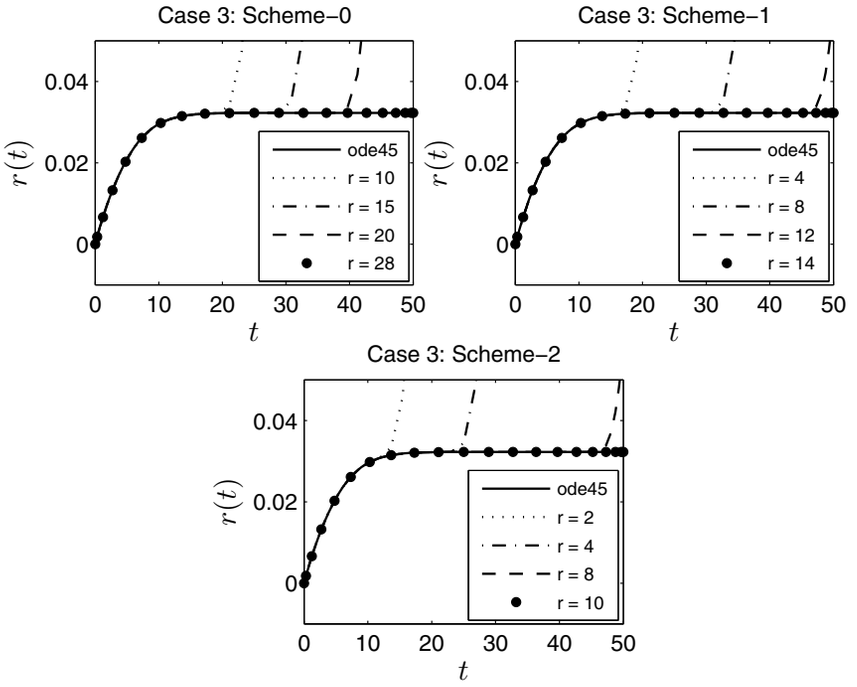

Figure 8. Case 3: Comparison of the numerical solution of the population fractions $r(t)$ against the results from the iteration schemes-0, 1 and 2

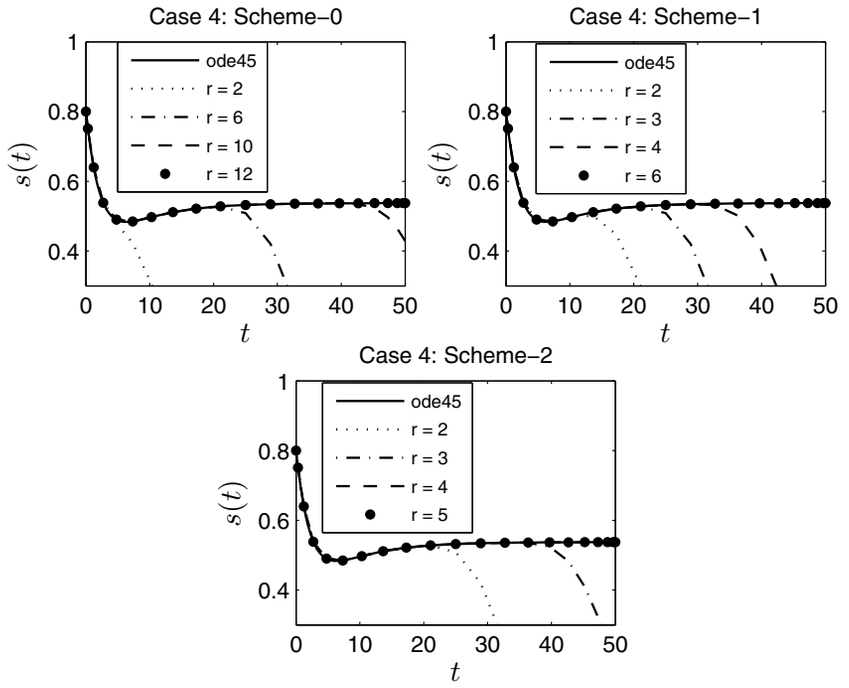

Figure 9. Case 4: Comparison of the numerical solution of the population fractions $s(t)$ against the results from the iteration schemes-0, 1 and 2

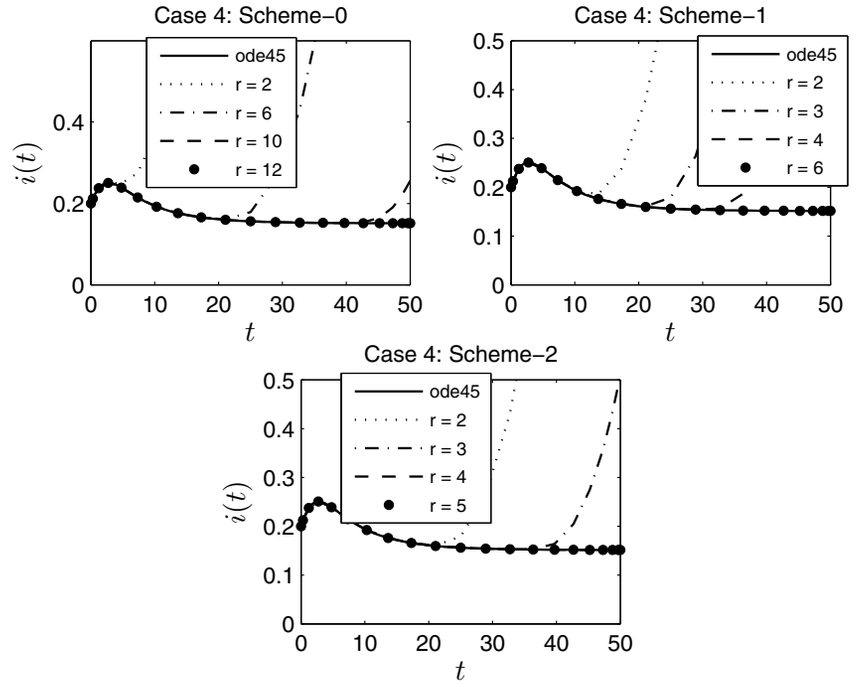

Figure 10. Case 4: Comparison of the numerical solution of the population fractions $i(t)$ against the results from the iteration schemes-0, 1 and 2

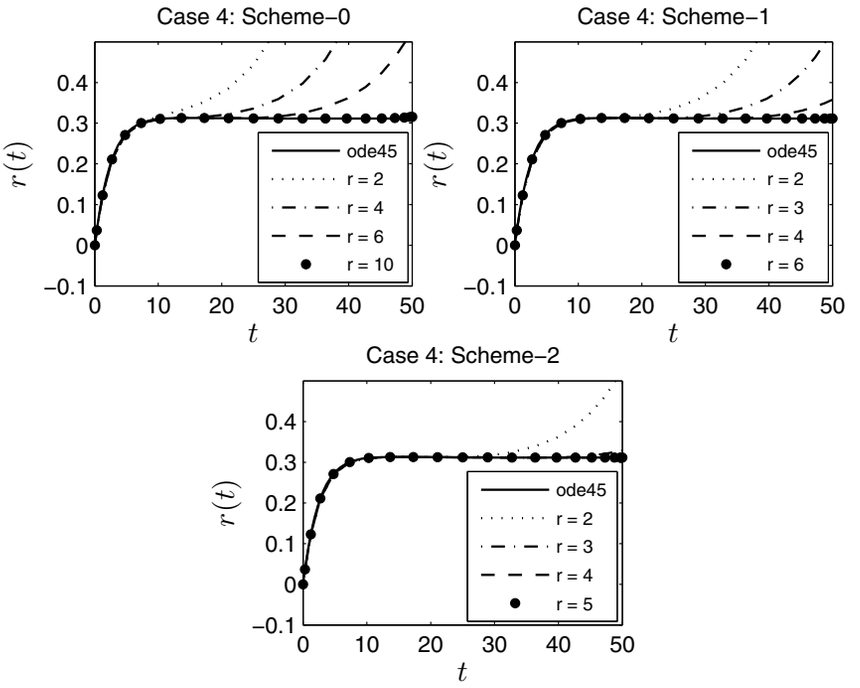

Figure 11. Case 4: Comparison of the numerical solution of the population fractions $r(t)$ against the results from the iteration schemes-0, 1 and 2

5. Conclusion

In this work, a sequence of new iteration schemes for solving nonlinear differential equations is used to solve the SIR epidemic model with constant vaccination strategy. The proposed iteration schemes are derived as an extension to the quasi-linearization method to obtain hybrid iteration schemes which converge very rapidly. The accuracy and validity of the proposed schemes is confirmed by comparing with the `ode45` MATLAB routine for solving initial value problems. It is hoped that the proposed method of solution will spawn further interest in computational analysis of differential equations in epidemiology and other areas of science.

Author details

Sandile Sydney Motsa
School of Mathematics, Computer Science and Statistics, University of KwaZulu Natal, Private Bag X01, Scottsville 3209, Pietermaritzburg, South Africa

Stanford Shateyi
University of Venda, Department of Mathematics, Private Bag X5050, Thohoyandou 0950, South Africa

6. References

[1] R.E. Bellman and R.E. Kalaba, (1965) Quasilinearization and Nonlinear Boundary-Value Problems, Elsevier, New York.
[2] C. Canuto, M.Y. Hussaini, A. Quarteroni, and T.A. Zang (1988). Spectral Methods in Fluid Dynamics, Springer-Verlag, Berlin.
[3] C. Chun, (2005) Iterative methods: Improving Newton's method by the Decomposition method, Computers and Mathematics with Applications, Vol 50, pg 1559–1568.
[4] H. Khan, R.N. Mohapatra, K.Vajravelu, and S.J. Liao, Explicit series solution of SIR and SIS epidemic models, Appl. Math.Comput, doi:10.1016/j.amc.2009.05.051(2009).
[5] W.O. Kermack and A.G. McKendrick,(1927) Contribution to the mathematical theory of epidemics, Proc. Roy. Soc, A115:700-721.
[6] H. W. Hethcote, (2000) The mathematics of infectious diseases, SIAM Review, 42(4):599–653.
[7] R. Casagrandi, L. Bolzoni, S.A. Levin. V. Andreasen, (2006) The SIRC model and influenza A, Math. BioSc. Vol 200, pg 152–169.
[8] R. Krivec, V.B. Mandelzweig, (2001) Numerical investigation of quasilinearization method in quantum mechanics, Computer Physics Communications Vol 138, pg 69–79
[9] V.B. Mandelzweig, F. Tabakin, (2001) Quasilinearization approach to nonlinear problems in physics with application to nonlinear ODEs, Computer Physics Communications, Vol 141, pg 268–281
[10] V. B. Mandelzweig, (2005) Quasilinearization Method: Nonperturbative Approach to Physical Problems, Physics of Atomic Nuclei, Vol 68(7) pg 1227–1258.
[11] O. D. Makinde, (2007) Adomian decomposition approach to a SIR epidemic model with constant vaccination strategy, Appl. Math.Comput, Vol 184, pg 842-848.
[12] Murray, J.D. Mathematical Biology, Springer-Verlag, 3rd.ed., 2001.
[13] Trefethen,L.N., (2000) Spectral Methods in MATLAB, SIAM.