Solution of the Fractional Epidemic Model by a Modified Approach of the Fractional Variation Iterative Method Using a Radial Basis Functions

M. Al-Towaiq, Ahmed A. Ababnah, and Safaa Al-Dalahmeh

***Abstract*—In this paper, we propose an efficient modification of the variation iteration method called the fractional interpolated variation iteration method, which uses a radial basis functions to find an approximate solution to a fractional differential equation. We used the fractional-order epidemic problem as a case study. Numerical results show that the proposed method is very efficient, accurate, applicable, and more accurate than some existing methods in the literature.**

***Index Terms*—Differential equations, mathematical modelling, numerical analysis, variation iterative method.**

I. Introduction

Fractional differential equations appear in various areas of engineering, science, finance, applied mathematics, and bioengineering [1]-[4]. For example, we consider the simple Susceptible, Infected, and Recovered (SIR) model, [5]-[8].

Let S: denotes the Susceptible which refers to hosts that are not exposed to the disease, I: denotes the Infected which refers to hosts that are exposed and not recovered, and R: denotes the

Recovered which refers to those individuals that cleared the infection. In the SIR model there are only two transitions; S → I and I → R. However, other transitions are possible with more complex models. The dynamics of the above groups with respect to time are summarized in the following system of fractional differential equations:

$$\begin{aligned} D^{\alpha}S(t) &= -\beta S I, & S(0)>0 \\ D^{\alpha}I(t) &= \beta S I - \gamma I, & I(0)>0 \\ D^{\alpha}R(t) &= \gamma I, & R(0)>0 \end{aligned} \quad (1)$$

where $0<\alpha<1$. The parameter β is a rate that encompasses both the contact and transmission rates between the *S* and *I* groups. The γ term indicates the recovery rate. It is obvious that as γ decreases, we will have more and individuals in the *I* group which is inversely proportional to the average infectious period (i.e. $1/\gamma$). With the assumption of a closed system, we have an additional constraint on the system $S+I+R=N_T$, where N_T is the size of the population.

Many researchers proposed and developed numerical approaches to find an approximate solutions to the fractional SIR model problem [9]-[12].

The paper organized as follows: in section two we introduce the proposed method, the Fractional Interpolated Variation Iteration Method (FIVIM). In section three we give numerical experiments to illustrate the efficiency, validity, and applicability of our proposed technique. We conclude the paper in section four.

II. The Proposed Fractional Interpolated VIM (FIVIM)

In this section, first we present the basic idea of the VIM and the fractional VIM (FVIM), then we introduce our proposed modification of the FVIM method. The proposed method uses a set of radial basis functions to simplify the evaluation of the correctional FVIM formula.

A. The VIM

In this section, we illustrate the basic idea of the VIM using the following IVP:

$$u'(t) = f(t,u(t)), \quad u(a) = u_a, t \in [t_i, t_f] \quad (2)$$

Then, the differential equation solution is calculated iteratively by turning the solution into a sequence of approximate functions whose limit, if it exists, is the equation's solution. So, the VIM correctional formula is given by

$$u_{m+1}(t) = u_m(t) + \int_a^t \lambda(s,t)(u_m'(s) - f(s,u_m(s))ds, \; m = 0,1,2,.... \quad (3)$$

Integrate the integral term in (3) by parts, we get

$$u_{m+1}(t) = G_m(t) - \int_a^t H_m(s,t)ds, \; m = 0,1,2,.... \quad (4)$$

where the function $G_m(t)$ and $H_m(s,t)$ are defined as follows: $G_m(t) = (1+\lambda(t,t))u_m(t) - \lambda(a,t)u_m(a)$

$$H_m(s,t) = \frac{\partial \lambda(s,t)}{\partial s} u_m(s) + \lambda(s,t) f(s,u_m(s))$$

See [13] for the existence of the solution and the convergence of the VIM to the exact solution.

Now, we will illustrate the FVIM method by considering the following IVP:

$$\begin{aligned} D_t^{\alpha}u(x,t) &= D_x u(x,t) + p(x,t), \; t>0, \; x \in R, \\ u(x,0) &= f(x), \; 0<\alpha<1, \end{aligned} \quad (5)$$

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M. Al-Towaiq, Ahmed A. Ababnah, and Safaa Al-Dalahmeh are with Jordan University of Science and Technology, P.O.Box 3030, Irbid 22110, Jordan (e-mail: towaiq@just.edu.jo, aaababnah@just.edu.jo, aldalahmehs@yahoo.com).

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where D_t^α is the fractional differential operator in *t*, D_x is some differential operator in *x*, and *p*(*x*,*t*) is some continuous function.

In general the operator $D_t^\alpha(.)$ follows the fractional Riemann-Liuoville definition [2]:

$$I_x^\alpha f(x) = \frac{1}{\Gamma(\alpha)} \int_0^x (x-\zeta)^{\alpha-1} f(\zeta) d\zeta, \alpha > 0. \quad (6)$$

Referring to (5), the FVIM uses the following correction formula:

$$u_{m+1}(x,t) = u_m(x,t) + I_t^\alpha [\lambda(D_t^\alpha u(x,t) - D_x u(x,t) - p(x,t))] \quad (7)$$

From (6) and (7) we obtain:

$$u_{m+1}(x,t) = u_m(x,t) + \frac{1}{\Gamma(\alpha)} \int_0^t (x-\zeta)^{\alpha-1} \lambda(\zeta) (D_t^\alpha u_m(x,\zeta) - D_x u_m(x,\zeta) - p(x,\zeta)) d\zeta \quad (8)$$

One of the drawbacks of the FVIM is its high computational complexity, especially when the problem is nonlinear. To overcome this problem, we propose the Interpolated FVIM (FIVIM) Using a radial basis functions (RBF).

The IVIM proceeds by dividing the interval [*a*, *T*], where *T* is the end point, into *n* subintervals each of length *h* = (*T*-*a*)/*n*. Thus, we have *n* grid nodal points on the *t*-axis, dented by $t_i = a + ih, i = 0, 1, \ldots, n$. In the IVIM, nodal points used in conjunction with a set of *K* radial basis functions (RBFs), [14]. (In particular, in the FIVIM we use either the Gaussian $e^{(-\varepsilon r)^2}$ or the multiquadric $\sqrt{1+(\varepsilon r)^2}$ functions). The RBF value at the point *s* is given by

$$\psi_k(s) = \phi_k(\| s - c_k \|), \quad (9)$$

where c_k is the center of the k^{th} basis function.

Now, let X_k = span $\phi_i(t)$, i =1, 2, …, n, then every v^k in X_k is a piecewise linear function of the form $v^k(t) = \sum_{i=1}^n \alpha_i \phi_i(t), t \in [a,T]$ and $\alpha_i = v^k(t_i)$.

Then, we obtain the following interpolating formula:

$$u_{m+1}^k(t) = \sum_{r=1}^n u_{m+1}(t_i) \varphi_r(t), t \in [a,T]$$

And the piecewise linear function of $H_m(s,t_i)$ in X_k is given by:

$$H_m^k(s,t_i) = \sum_{r=1}^n H_m(t_r,t_i) \phi_r(s), s \in [a,t_i], i = 1,2,\ldots,n. \quad (10)$$

Replacing $H_m(s,t_i)$ by $H_m^k(s,t_i)$ in equation (4), we get

$$u_{m+1}(t_i) \cong G_m(t_i) - \sum_{r=2}^n H_m(t_r,t_i) \int_a^{t_i} \phi_r(t) dt.$$

From (9) and (10), we obtain

$$H_m(s,t_i) = \sum_{k=1}^K \lambda_{k,m}^i \psi_k(s),$$

Therefore, the approximate of $u_{m+1}(t_i)$ is given by

$$\begin{aligned} u_{m+1}(t_i) &= G(t_i) - I_s^\alpha (H_m(s,t_i)) \\ &= G(t_i) - I_s^\alpha \left(\sum_{k=1}^K \lambda_{k,m}^i \psi_k(s)\right) \\ &= G(t_i) - \sum_{k=1}^K \lambda_{k,m}^i I_s^\alpha (\psi_k(s)). \end{aligned} \quad (11)$$

Now, we summarize the process of the FIVIM in the following algorithm:

Algorithm 1 for the FIVIM

- *Using the points* $\{t_i\}_{i=1}^n$ *and center points* $\{c_k\}_{k=1}^K$ *to calculate matrix* $\boldsymbol{\Psi}$ *and its inverse* $\boldsymbol{\Psi}^{-1}$.
- *For m = 1 : M % number of sequence calculations*
  For i = 1 : n
    For j = 1 : n
      Compute the entries $H_m(t_i,t_j)$ *of matrix* $\mathbf{H}_m$.
    End j loop
  End i loop
  For i = 1 : n
    Compute the weights γ_m^i *associated with the* t_i *points*
    $\gamma_m^i = \Psi^{-1} H_m^i$, *where the* H_m^i *is the i- the column of matrix* $\mathbf{H}_m$
    For k = 1 : K
      Compute $I_s^\alpha(\psi_k(s))$ *for* $s \in [t_{initial}, t_i]$
    End k loop
    Compute $\sum_{k=1}^K \gamma_{k,m}^i I_s^\alpha(\psi_k(s))$
    Compute $u_{m+1}(t_i)$ *using* (11)
  End i loop
End m loop.

III. Numerical Experiments

In this section, we examine the accuracy of the solution provided by the proposed RBF-based FIVIM method. As a case study, we investigate the solution of the SIR model. We compare our proposed technique with the FVIM with B-spline functions because it is being shown in [7] that using six iterations of the VIM produced a comparable result to both the Adomian Decomposition Method and Homotopy

Perturbation Method.

In order to compare our work with other techniques appeared in the literature, the same parameters and values of the SIR model, (1), used in [5], [7]-[8] are employed. Let N_1=20, N_2=15, N_3 =10 and β = 0.01, γ = 0.02.We assume the following initial values: $S_0 = N_1$=20, $I_0 = N_2$=15, and $R_0 = N_3$ =10.

In the following experiments, we first compare the error of the approximate solution of different methods for α = 0.5. Next, we investigate the effect of the number *K* of RBF functions used on the accuracy of the solution. In the third experiment, we examine the shape parameter (ε) range that can be used to provide a good approximate solution. Finally, we examine the convergence of the solution provided by the proposed RBF-based FIVIM.

A. Comparison for $\alpha = 0.5$

In this experiment, we compare the error performance of the approximate solutions of S, I and R components of the SIR problem. Fig. 1 shows the relative error on using the FVIM with B-spline functions, and the proposed MQ and Gaussian RBF's- FIVIM solutions of the SIR problem with $\alpha = 0.5$. Note that the proposed method gives better solution than the FVIM with B-spline functions.

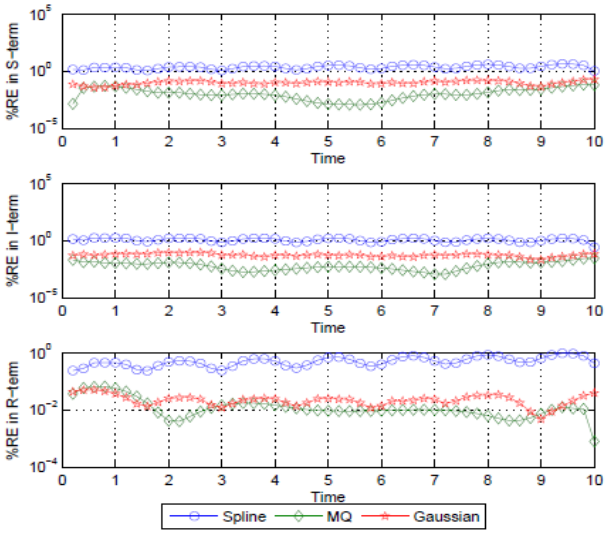

Fig. 1. Relative error using FVIM with B-spline functions vs. FIVIM with MQ and Gaussian RBF with α = 0.5.

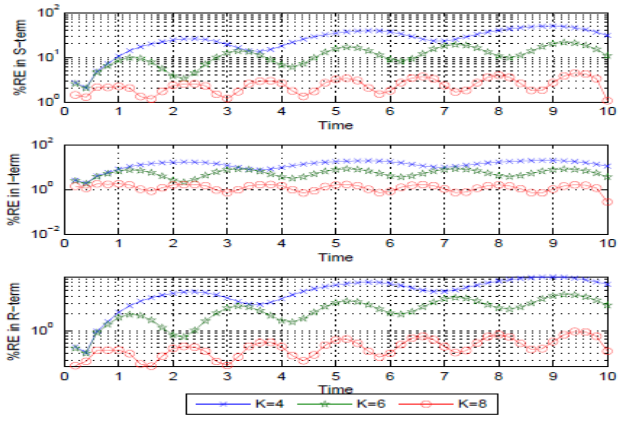

Fig. 2. Relative error of Spline-FVIM vs. Time for different values of K

B. Effect of Number (K) of RBF Functions

In this section, we examine the effect of the number *K* of RBF interpolating functions on the solution's accuracy for the B-Spline , MQ and Gaussian FIVIM. Results in Figs. 2, 3, and 4 indicate that both the B-Spline and the Gaussian RBF-based method are sensitive to changes in *K*. As *K* is reduced, we notice significant degradation in the solution accuracy. On the other hand, the Multiquadric-FIVIM shows robustness (i.e., less sensitive) to variations in the value of *K*, see Fig. 3.

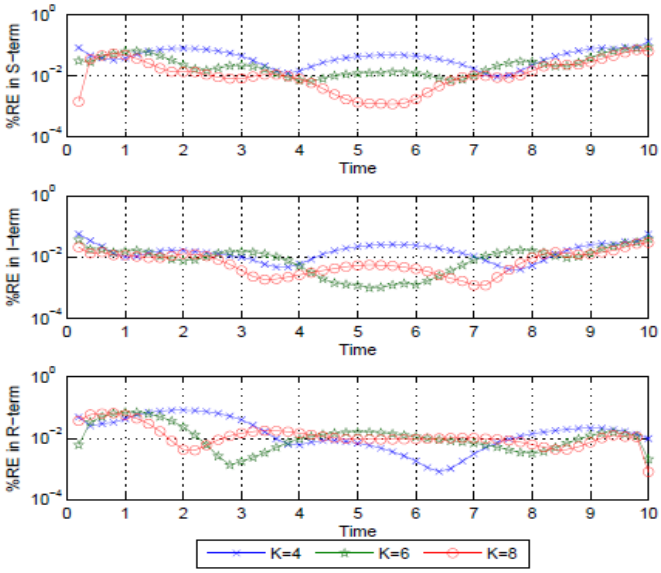

Fig. 3. Relative error of MQ-FIVIM vs. Time for different values of K

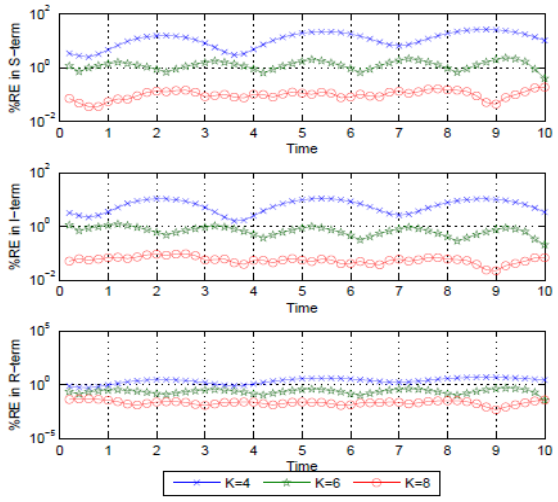

Fig. 4. Relative error of gaussian-FIVIM vs. time for different values of K.

C. Effect of the Shape Parameter ε

The problem of setting the value of the shape parameter ε remains in question within the RBF interpolation. In this section we investigate the performance of the MQ and Gaussian RBF-FIVIM as we vary the shape parameter. Fig. 5 shows that the Multiquadric-based FIVIM displays more robustness with respect to ε. Varying ε from 0.5 to 30 does not have a significant effect on the solution accuracy. This in contrast to the Gaussian-based FIVIM which is sensitive to the value of ε. We note that changing ε from 0.5 to 2.5 as in Fig. 6 results in a significant degradation of the error performance of the FIVIM.

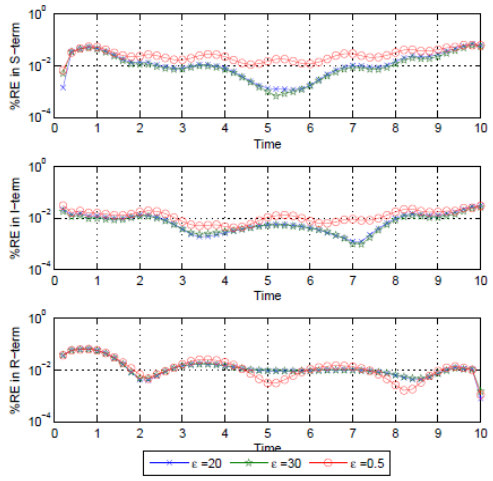

Fig. 5. Relative error vs. Time for different values of ε in the multiquadric RBF.

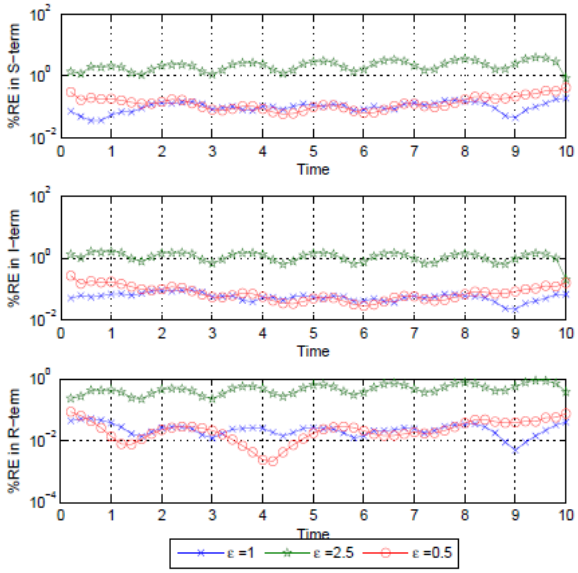

Fig. 6. Relative error vs. Time for different values of ε in the gaussian RBF.

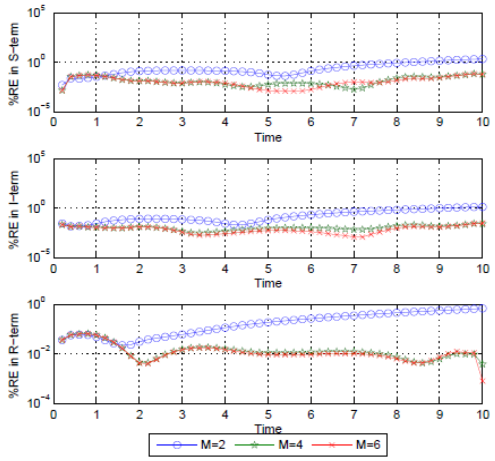

Fig. 7. Relative error vs. Time for different values of M in the multiquadric RBF.

D. Convergence of the RBF-FIVIM

In this experiment, we investigate the convergence of both the MQ and Gaussian-RBF FIVIM with respect to the number of iterations (m) (see Figs. 7 and 8). We notice that both of the proposed RBF methods converge rapidly as the number of iterations increases from m=2 to 6. In fact, our results indicate that little improvement can be achieved after 5 iterations.

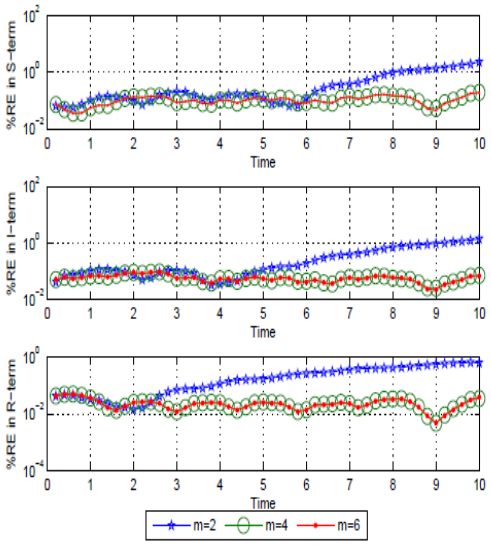

Fig. 8. Relative error vs. Time for different values of M in the Gaussian RBF

IV. Conclusion

In this paper, we proposed a RBF-based fractional interpolated variation iteration method (FIVIM) with the goal of reducing the computational complexity of the FVIM. In particular, we used the multiquadric (MQ) and Gaussian functions as radial basis functions. The proposed methods were used to solve both the integer and fractional SIR epidemic problems. The numerical results indicate the effectiveness, validity and the applicability of the proposed method. Both the MQ and Gaussian RBF showed a superior performance in comparison with the B-Spline VIM proposed in the literature. However, the MQ showed more robustness with respect to several factors (e.g., number of RBF functions and shape parameter).

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Mohammad Al-Towaiq received a diploma in mathematics from Amman Teachers Training Institute, Jordan (1971), the BSc. in mathematics from William Paterson coll of State of New Jersey, USA (1981), the M.Sc. and the Ph.D in applied mathematics and Statistics from SUNY at Stony Brook, USA (1983, degree awarded in 1985), and 1985 respectively.

He is currently holding a professor position in the Department of Mathematics and Statistics jointly with the Computer Science Department at Jordan University of Science and Technology. His areas of interest include Numerical Analysis, Parallel Computing, and Mathematical Modeling.

Ahmed A. Ababnah received BSc. in electrical engineering from Mutah University, Jordan (2003), the MSc in electrical engineering from Arizona State University, USA (2007), and the PhD in electrical engineering from Kansas State University (2010).

He is currently holding an associate professor position in the Electrical Engineering Dept. at Jordan University of Science & Technology.

His areas of research including Optimal control theory MIMO communications, MIMO radar, and convex optimization.

Safaa Al-Dalahmeh received the BSc. in mathematics from Yarmouk University, Jordan (2009) and the MSc. in mathematics from Jordan University of Science and Technology (2017).

Her area of research is the solutions of the initial and boundary value problems.