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ORIGINAL PAPER

Novel analytical and numerical techniques for fractional temporal SEIR measles model

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Abstract In this paper, a fractional temporal SEIR measles model is considered. The model consists of four coupled time fractional ordinary differential equations. The time-fractional derivative is defined in the Caputo sense. Firstly, we solve this model by solving an approximate model that linearizes the four time fractional ordinary differential equations (TFODE) at each time step. Secondly, we derive an analytical solution of the single TFODE. Then, we can obtain analytical solutions of the four coupled TFODE at each time step, respectively. Thirdly, a computationally effective fractional Predictor-Corrector method (FPCM) is proposed for simulating the single TFODE. And the error analysis for the fractional predictor-corrector method is also given. It can be shown that the fractional model provides an interesting technique to describe measles spreading dynamics. We conclude that the analytical and Predictor-Corrector schemes derived are easy to implement and can be extended to other fractional models. Fourthly, for demonstrating the accuracy of analytical solution for fractional decoupled measles model, we applied GMMP Scheme (Gorenflo-Mainardi-Moretti-Paradisi) to the original fractional equations. The comparison of

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the numerical simulations indicates that the solution of the decoupled and linearized system is close enough to the solution of the original system. And it also indicates that the linearizing technique is correct and effective.

Keywords Time fractional model · SEIR measles model · Analytical solution · Predictor-corrector method · GMMP Scheme

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1 Introduction

Health issues are considered a serious threat for public health throughout the world. As such, epidemiology study has gained popularity and importance due to its growing needs in assessing and predicting numerous epidemics or any disease outbreak. Furthermore, it leads the health researcher to determine the nature of the disease and suggest recommended actions.

Several approaches have been adopted to study the dynamics of epidemics and one consists of models that include derivatives of ordinary differential equations. As known, ordinary differential models have certain restrictions due to local operator properties [1]. Therefore, modification is needed and it is seen that fractional calculus plays an important role in turning classical ordinary derivatives into fractional ordinary derivatives. The fractional system can be represented by operator symbol D^{α}; $\alpha = 1$ coincides with the ordinary differential operator [2]. Suitability of fractional derivatives in modeling certain complex dynamics lies in the property exhibited by the non-locality of the systems that means that the processes dynamics has a certain degree of memory, as opposed to ordinary derivative. This makes the system possess hereditary properties—a powerful instrument in a fractional model [3–6]. In addition, fractional calculus has an important role in superdiffusive and subdiffusive processes that also makes it a useful tool in epidemiology [7].

The theory of derivatives of non-integer order originated from the de l'Hospital letter to Leibniz discussing the meaning of the derivative or "what does the derivative of order $1/3$ or $\sqrt{2}$ of a function mean?" in 1695. Leading from that, it has caught the interest of mathematicians during eighteenth to nineteenth centuries to study this area. A well-known scientist, Abel in 1823 has become the first scientist to implicitly apply fractional calculus for investigating tautochrone problems [1]. Later, several fundamental works on various aspects of fractional calculus have appeared [2, 8–10].

As one would expect, since fractional order differential equation systems allow greater degrees of freedom and incorporate memory effect in the model, they have become an excellent tool in modeling epidemiology properties. Although the fractional derivative is more complicated than the classical model, there exist several numerical methods for solving such systems [11, 12]. Several works on modeling epidemiology systems can be seen in [13–19].

Here, the focus is devoted on establishing a mathematical model to control measles diseases. Measles, also known as rubeola, is a highly contagious respiratory infection that is caused by a Paramyxovirus virus and has higher incidence if there

is no high coverage in vaccination [20]. Measles is also one of the causes of death for young children despite the presence of an effective vaccine [20]. The disease has been known to be highly contagious and can be easily transmitted by coughing and sneezing or direct contact with infected nasal secretions [20]. Much research has been attempted to reveal the biological and dynamical processes of measles such as [21–23]. These studies respectively investigated the measles dynamics using bifurcation theory [21] and studied the effect of vaccination and area on measles transmission dynamics [22, 23]. There are also other studies that use metapopulation models to control measles and other infectious diseases [20, 24, 25]. These studies focused on dynamics of individuals between patches which may be towns, cities, and so forth. Generally, the model is described in the form of ordinary differential equations to describe disease spread in an environment divided by patches. Following previous work on a SEIR metapopulation model, [25] has then extended the system into a fractional SEIR metapopulation model. However, they did not justify the order parameter used in their fractional model.

In this recent work, we follow [25], who described a metapopulation measles model by a fractional order differential equation system. Their work is motivated by measles outbreak in New Zealand. The outbreak is believed to have originated in the Philippines, arriving in New Zealand via a dance competition in Sydney, which was attended by a South Auckland 18-year-old [26]. In Australia, measles is considered rare due to widespread use of vaccine; however, cases still occur [27]. Although the cases are under control, infections will still happen from persons' travel and spreading infection to others over wide distances. A basic measles model was developed in New Zealand by a group of researchers in 1996 and it successfully predicted the 1997 measles epidemic; the model was later enhanced to become a prediction/prevention model [28]. It turned out that fractional calculus used in [25] is able to represent the well-posedness of the measles dynamics.

Actually, one of the difficulties in a fractional derivative model is due to its analytical investigation. As a matter of fact, this limits the understanding to the dynamics of the fractional model itself. Several works have been devoted to constructing analytical methods, for instance in 2012, [29, 30] have proposed an idea for deriving analytical solutions for time-fractional diffusion equations. Recently, [31] have derived an approximate analytic method called the fractional reduced differential transform method for solving time fractional order biological population models. As far as we are aware, there are no relevant papers in the published literature discussing the derivation of analytical solutions to the measles model. Furthermore, [25] has only derived a numerical approximation to the model with no analytical solution attached to it.

Next, the essential part of this paper is to construct an analytical technique scheme that is applicable to solve the defined model. Firstly, we solve this model by linearizing technique the four time fractional ordinary differential equations (TFODE) at each time step. This linearizing technique has been used for numerical simulating of complex dynamical systems [32] and assured that the solutions of the coupling system is in agreement with the original system. Secondly, we derive an analytical solution of the single TFODE. Then, we can obtain analytical solutions of the four TFODE at each time step, respectively. The analytical solution technique proposed

in this manuscript is compared to numerical solutions in order to show that it has good agreement and furthermore, this analytical technique can be considered as an alternative and well-organized technique in attaining analytical solutions not only for fractional time measles model, but other time-fractional model as well. These analytical solutions are only involved in two-parameter function of the Mittag-Leffler type, which can be calculated by MATLAB.

Furthermore, for demonstrating the accuracy of analytical solution for fractional decoupled measles model, we applied GMMP scheme (Gorenflo-Mainardi-Moretti-Paradisi) and Newton method to the original fractional ordinary differential equations (TFODE). Then, the comparison of the numerical simulations indicates that the solution of the decoupled and linearized system is close enough to the solution of the original system. And it also indicates that the linearizing technique is correct and effective.

Here, we limit the interpretation to the order of the fractional system as our main intention is to propose an analytical solution technique for time fractional systems. We believe that the results will be very helpful for a number of fractional epidemic applications.

The remainder of the paper is arranged as follows. In Section 2, an introduction to the basic SEIR measles model is given. In Section 3, we give some preliminaries that are useful throughout the paper. In Section 4, we derive analytical solutions of the decoupled model. In Section 5, a computationally effective fractional Predictor-Corrector method (FPCM) is constructed for this decoupled model. The error analysis for the fractional predictor-corrector method is carried out in Section 6. Comparisons using GMMP scheme and the analytical solution for fractional temporal model are given in Section 7. Some results from numerical and analytical findings are given to compare and illustrate the behavior of the solution in Section 8. We then extend the developed techniques into two examples in epidemiology areas. Finally, some discussions and conclusions are given.

2 Basic metapopulation model

In this model, a population is divided into different classes, disjoint and based on their disease status. At time t, $S = S(t)$ is the fraction of population representing individuals susceptible to measles, $E = E(t)$ is the fraction of population representing individuals exposed to measles, $I = I(t)$ is the fraction of populations representing individuals infectious with measles, and $R = R(t)$ is the fraction of population representing individuals recovered from measles. The recruitment is done by birth to the susceptible class and occurs at constant birth rate b. The constant rate for nondisease-related death is μ, with $\frac{1}{\mu}$ referring to the average lifetime. In this case, standard mass balance is used $\beta(t)SI$ to indicate successful transmission of measles due to effective contact dynamics by the infectious individuals. Once infected, a fraction of exposed people becomes infectious with a constant rate σ, so that $\frac{1}{\sigma}$ is the average incubation period. Some infected individuals will recover after treatment or over a certain period of time at a constant rate ζ, making $\frac{1}{\zeta}$ the average infectious period. The model is called metapopulation dynamics because the population is spatially spread into patches. In this model, the population is spatially spread into four

patches representing four cities. We consider the set $\wp = \{A, B, W, D\}$ representing four patches. The m^c_{xy} is the rate of travel from city x to city y in compartment c with $c = S, E, I, R$ which represents the transfer rate of individuals in the compartment c of city x moving to the same compartment c in city y. It is clear that $m^c_{xx} = 0$, for all $x \in \wp$ and $c \in \{S, E, I, R\}$.

The basic metapopulation model is given by

$$\frac{dS_x}{dt} = b_x - (\beta_x(t)I_x + \mu_x)S_x + \sum_{y\in\wp} S_y m^S_{yx} - S_x \sum_{y\in\wp} m^S_{xy}, \tag{1}$$

$$\frac{dE_x}{dt} = \beta_x(t)S_x I_x - (\sigma_x + \mu_x)E_x + \sum_{y\in\wp} E_y m^E_{yx} - E_x \sum_{y\in\wp} m^E_{xy}, \tag{2}$$

$$\frac{dI_x}{dt} = \sigma_x E_x - (\zeta_x + \mu_x)I_x + \sum_{y\in\wp} I_y m^I_{yx} - I_x \sum_{y\in\wp} m^I_{xy}, \tag{3}$$

$$\frac{dR_x}{dt} = \zeta_x I_x - \mu_x R_x + \sum_{y\in\wp} R_y m^R_{yx} - R_x \sum_{y\in\wp} m^R_{xy}. \tag{4}$$

The fractional temporal model is formulated by the following differential equations [25]

$${}^cD^\alpha_t S_x = b_x - (\beta_x(t)I_x + \mu_x)S_x + \sum_{y\in\wp} S_y m^S_{yx} - S_x \sum_{y\in\wp} m^S_{xy}, \tag{5}$$

$${}^cD^\alpha_t E_x = \beta_x(t)S_x I_x - (\sigma_x + \mu_x)E_x + \sum_{y\in\wp} E_y m^E_{yx} - E_x \sum_{y\in\wp} m^E_{xy}, \tag{6}$$

$${}^cD^\alpha_t I_x = \sigma_x E_x - (\zeta_x + \mu_x)I_x + \sum_{y\in\wp} I_y m^I_{yx} - I_x \sum_{y\in\wp} m^I_{xy}, \tag{7}$$

$${}^cD^\alpha_t R_x = \zeta_x I_x - \mu_x R_x + \sum_{y\in\wp} R_y m^R_{yx} - R_x \sum_{y\in\wp} m^R_{xy}. \tag{8}$$

where

$${}^cD^\alpha_t u(t) = \frac{1}{\Gamma(1-\alpha)} \int_0^t \frac{u'(r)}{(t-r)^\alpha} dr, \tag{9}$$

with $0 \leq \alpha < 1$ the fractional derivative of the function $u(t)$ in the sense of Caputo and Γ is the Gamma function.

3 Preliminaries

This section will outline important definitions and lemmas used throughout the paper.

Definition 1 A two-parameter function of the Mittag-Leffler type is defined by the series expansions [2]

$$E_{\alpha,\beta}(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k + \beta)}, \quad (\alpha > 0, \beta > 0).$$

For a one-parameter generalization, the Mittag-Leffler function can be denoted by [2]

$$E_\alpha(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k + 1)} \equiv E_{\alpha,1}(z), \quad (\alpha > 0).$$

Definition 2 Let $\mathbf{A} \in \mathbb{R}^{n\times n}$. The matrix $\alpha-$Exponential function $e_\alpha^{z\mathbf{A}}$ is defined by [2]

$$e_\alpha^{z\mathbf{A}} \equiv z^{\alpha-1} E_{\alpha,\alpha}(z^\alpha \mathbf{A}) = z^{\alpha-1} \sum_{k=0}^{\infty} \frac{\mathbf{A}^k z^{\alpha k}}{\Gamma(\alpha k + \alpha)}.$$

Definition 3 The definition of function spaces are based on ([35]). Let $f(t),\ t > 0$ be a real or complex-valued function. The function is said to be in the space C_ρ, $\rho \in \Re$, if there exists a real number s, $s > \rho$, such that

$$f(t) = t^s f_1(t), \quad t > 0,$$

with a function $f_1(t)$ in $C[0, \infty)$. Obviously, C_ρ is a vector space and the set of spaces C_ρ is ordered according to

$$C_\rho \subset C_\beta \Leftrightarrow \rho \geq \beta.$$

Definition 4 A function $f(t),\ t > 0$, is said to be in the space C_ρ^m, $m \in \mathbb{N}_0 = \mathbb{N} \cup \{0\}$, iff $f^m \in C_\rho$.

Lemma 1 *(see [29, 35]) Let $\mu > \mu_1 > \cdots > \mu_n \geq 0, m_i - 1 < \mu_i \leq m_i, m_i \in N_0 = N \cup \{0\}, d_i \in R, i = 1, \ldots, n$. Consider the initial value problem*

$$\left\{ \begin{array}{l} ({}^c D_t^\mu y)(x) - \sum_{i=1}^n d_i ({}^c D_t^{\mu_i} y)(x) = g(x), \\ y^{(k)}(0) = c_k \in R, \qquad k = 0, \ldots, m-1,\ m-1 < \mu \leq m, \end{array} \right\} \tag{10}$$

where the function $g(x)$ is assumed to lie in C_{-1} if $\mu \in N$, in C_{-1}^1 if $\mu \notin N$, and the unknown function $y(x)$ is to be determined in the space C_{-1}^m. For the definition of C_{-1}, C_{-1}^1 and C_{-1}^m, we refer to ([35]). This has solution

$$y(x) = y_g(x) + \sum_{k=0}^{m-1} c_k u_k(x), \qquad x \geq 0, \tag{11}$$

where

$$y_g(x) = \int_0^x t^{\mu-1} E_{(.),\mu}(t) g(x-t) dt, \tag{12}$$

and

$$u_k(x) = \frac{x^k}{k!} + \sum_{i=l_k+1}^{n} d_i x^{k+\mu-\mu_i} E_{(.),k+1+\mu-\mu_i}(x), \qquad k = 0, \ldots, m-1, \tag{13}$$

fulfills the initial conditions $u_k^{(l)}(0) = \delta_{kl}, k, l = 0, \ldots, m-1$. The function

$$E_{(.),\beta}(x) = E_{\mu-\mu_1,\ldots,\mu-\mu_n,\beta}(d_1 x^{\mu-\mu_1}, \cdots, d_n x^{\mu-\mu_n}) \tag{14}$$

is a particular case of the multivariate Mittag-Leffler function (see [35]*) and the natural numbers* $l_k, k = 0, \ldots, m-1$*, are determined from the condition*

$$\begin{cases} m_{l_k} \geq k+1, \\ m_{l_k+1} \quad \leq k. \end{cases} \tag{15}$$

In the case $m_i \leq k, i = 1, \ldots, n$*, we set* $l_k := 0$*, and if* $m_i \geq k+1, i = 1, \ldots, n$*, then* $l_k := n$*.*

Lemma 2 *For the case of single* μ*, let* $\mu \geq 0$ *and consider the initial value problem*

$$\left\{ \begin{array}{r} ({}^c D_t^{\mu} y)(x) - dy(x) = g(x), \\ y(0) = c \in R. \end{array} \right\}. \tag{16}$$

This has solution

$$y(x) = y_g(x) + cu(x), \tag{17}$$

where

$$y_g(x) = \int_0^x t^{\mu-1} E_{\mu,\mu}(t) g(x-t) dt, \tag{18}$$

and

$$u(x) = 1 + dx^{\mu} E_{\mu,1+\mu}(x). \tag{19}$$

Here the function

$$E_{(\mu),\beta}(x) = E_{\mu,\beta}(dx^{\mu}). \tag{20}$$

4 Analytical solution of a decoupled model

In this section, an analytical solution for fractional decoupled measles model will be constructed.

Let

$$\begin{pmatrix} S_x(t) \\ E_x(t) \\ I_x(t) \\ R_x(t) \end{pmatrix} = H = \begin{pmatrix} H_{1x}(t) \\ H_{2x}(t) \\ H_{3x}(t) \\ H_{4x}(t) \end{pmatrix}, \ t = t_0, t_1, \ldots, t_N, \ x \in \wp = \{A, B, W, D\}. \tag{21}$$

Rewriting the system in (5)–(8), we have

$$
\begin{aligned}
{}^{c}D_t^{\alpha} H_{1x}(t) &= -(\beta_x(t) H_{3x}(t) + \mu_x + \sum_{y \in \wp} m_{xy}^{H_1}) H_{1x}(t) \\
&\quad + \sum_{y \in \wp} H_{1y}(t) m_{yx}^{H_1} + b_x, \qquad (22) \\
{}^{c}D_t^{\alpha} H_{2x}(t) &= \beta_x(t) H_{3x}(t) H_{1x}(t) - (\sigma_x + \mu_x + \sum_{y \in \wp} m_{xy}^{H_2}) H_{2x}(t) \\
&\quad + \sum_{y \in \wp} H_{2y}(t) m_{yx}^{H_2}, \qquad (23) \\
{}^{c}D_t^{\alpha} H_{3x}(t) &= \sigma_x H_{2x}(t) - (\zeta_x + \mu_x + \sum_{y \in \wp} m_{xy}^{H_3}) H_{3x}(t) + \sum_{y \in \wp} H_{3y}(t) m_{yx}^{H_3}, \qquad (24) \\
{}^{c}D_t^{\alpha} H_{4x}(t) &= \zeta_x H_{3x}(t) - (\mu_x + \sum_{y \in \wp} m_{xy}^{H_4}) H_{4x}(t) + \sum_{y \in \wp} H_{4y}(t) m_{yx}^{H_4}. \qquad (25)
\end{aligned}
$$

The model consists of four coupled time fractional ordinary differential equations (TFODE). Firstly, we solve this model by linearizing technique the four time fractional ordinary differential equations (TFODE) at each time step, i.e., we solve a single TFODE at each time level $t = t_n$:

$$
\begin{aligned}
{}^{c}D_t^{\alpha} H_{1x}(t_n) &= -(\beta_x(t) H_{3x}(t_{n-1}) + \mu_x + \sum_{y \in \wp} m_{xy}^{H_1}) H_{1x}(t_n) \\
&\quad + \sum_{y \in \wp} H_{1y}(t_n) m_{yx}^{H_1} + b_x, \qquad (26) \\
{}^{c}D_t^{\alpha} H_{2x}(t_n) &= \beta_x(t) H_{3x}(t_{n-1}) H_{1x}(t_n) - (\sigma_x + \mu_x + \sum_{y \in \wp} m_{xy}^{H_2}) H_{2x}(t_n) \\
&\quad + \sum_{y \in \wp} H_{2y}(t_n) m_{yx}^{H_2}, \qquad (27) \\
{}^{c}D_t^{\alpha} H_{3x}(t_n) &= \sigma_x H_{2x}(t_n) - (\zeta_x + \mu_x + \sum_{y \in \wp} m_{xy}^{H_3}) H_{3x}(t_n) \\
&\quad + \sum_{y \in \wp} H_{3y}(t_n) m_{yx}^{H_3}, \qquad (28) \\
{}^{c}D_t^{\alpha} H_{4x}(t_n) &= \zeta_x H_{3x}(t_n) - (\mu_x + \sum_{y \in \wp} m_{xy}^{H_4}) H_{4x}(t_n) + \sum_{y \in \wp} H_{4y}(t_n) m_{yx}^{H_4}, \qquad (29) \\
n &= 1, 2, \ldots, N.
\end{aligned}
$$

We can simplify each of the above equations in the following form as

$$
{}^{c}D_t^{\alpha} H_{ix}(t_n) = \mathbf{a_i} H_{ix}(t_n) + \mathbf{g_i}; \quad i = 1, 2, 3, 4; \ 0 < \alpha \leq 1, \qquad (30)
$$

where $\mathbf{a_1}, \mathbf{a_2}, \mathbf{a_3}, \mathbf{a_4}$ and $\mathbf{g_1}, \mathbf{g_2}, \mathbf{g_3}, \mathbf{g_4}$ are given as

$$\mathbf{a_1} = -(\beta_x(t)H_{3x}(t_{n-1}) + \mu_x + \sum_{y\in\wp} m_{xy}^{H_1}); \quad \mathbf{g_1} = \sum_{y\in\wp} H_{1y}(t_n)m_{yx}^{H_1} + b_x; \tag{31}$$

$$\mathbf{a_2} = -(\sigma_x + \mu_x + \sum_{y\in\wp} m_{xy}^{H_2}); \quad \mathbf{g_2} = \sum_{y\in\wp} H_{2y}(t_n)m_{yx}^{H_2} + \beta_x(t)H_{3x}(t_{n-1})H_{1x}(t_n); \tag{32}$$

$$\mathbf{a_3} = -(\zeta_x + \mu_x + \sum_{y\in\wp} m_{xy}^{H_3}); \quad \mathbf{g_3} = \sum_{y\in\wp} H_{3y}(t_n)m_{yx}^{H_3} + \sigma_x H_{2x}(t_n); \tag{33}$$

$$\mathbf{a_4} = -(\mu_x + \sum_{y\in\wp} m_{xy}^{H_4}); \quad \mathbf{g_4} = \sum_{y\in\wp} H_{4y}(t_n)m_{yx}^{H_4} + \zeta_x H_{3x}(t_n). \tag{34}$$

In our case, the equation in (30) is in the form of single TFODE:

$$^{c}D_t^{\alpha} H_{ix}(t) - \mathbf{a_i} H_{ix}(t) = \mathbf{g_i}; \tag{35}$$

$$H_i x(0) = \mathbf{c_i} \in \Re, \quad i = 1, 2, 3, 4;\ 0 < \alpha \leq 1, t \geq 0. \tag{36}$$

Using Lemma 1, the analytical solution of the single TFODE (35) with initial condition (36) is derived as the following form:

$$H_{ix}(t) = H_{ix,\mathbf{g_i}}(t) + \mathbf{c_i}\mathbf{u_i}(t) \tag{37}$$

where

$$H_{ix,\mathbf{g_i}}(t) = \int_0^t \tau^{\alpha-1} E_{\alpha,\alpha}(\tau)\mathbf{g_i}(t-\tau)d\tau \tag{38}$$

and

$$\mathbf{u_i}(t) = 1 + \mathbf{a_i} t^{\alpha} E_{\alpha,1+\alpha}(\mathbf{a_i} t^{\alpha}). \tag{39}$$

Finally, the full analytical solutions at $t = t_n$ $(n = 1, 2, \ldots, N)$ for (26)–(29) are

$$H_{1x}(t_n) = \left[\int_0^{t_n} \tau^{\alpha-1} E_{\alpha,\alpha}(\tau)\mathbf{g_1} d\tau\right] + \left[\mathbf{c_1}(1 + \mathbf{a_1} t_n^{\alpha} E_{\alpha,1+\alpha}(\mathbf{a_1} t_n^{\alpha}))\right], \tag{40}$$

$$H_{2x}(t_n) = \left[\int_0^{t_n} \tau^{\alpha-1} E_{\alpha,\alpha}(\tau)\mathbf{g_2} d\tau\right] + \left[\mathbf{c_2}(1 + \mathbf{a_2} t_n^{\alpha} E_{\alpha,1+\alpha}(\mathbf{a_2} t_n^{\alpha}))\right], \tag{41}$$

$$H_{3x}(t_n) = \left[\int_0^{t_n} \tau^{\alpha-1} E_{\alpha,\alpha}(\tau)\mathbf{g_3} d\tau\right] + \left[\mathbf{c_3}(1 + \mathbf{a_3} t_n^{\alpha} E_{\alpha,1+\alpha}(\mathbf{a_3} t_n^{\alpha}))\right], \tag{42}$$

$$H_{4x}(t_n) = \left[\int_0^{t_n} \tau^{\alpha-1} E_{\alpha,\alpha}(\tau)\mathbf{g_4} d\tau\right] + \left[\mathbf{c_4}(1 + \mathbf{a_4} t_n^{\alpha} E_{\alpha,1+\alpha}(\mathbf{a_4} t_n^{\alpha}))\right], \tag{43}$$

where $\mathbf{a_1}, \mathbf{a_2}, \mathbf{a_3}, \mathbf{a_4}$ and $\mathbf{g_1}, \mathbf{g_2}, \mathbf{g_3}, \mathbf{g_4}$ are based on (31)–(34). Plots for analytical solutions are shown in Section 7 using Matlab mathematical software version 7.0.

5 A fractional predictor-corrector technique

In this section, we suggest the use of the predictor-corrector technique of Adams-Bashforth-Moulton formula where, for the sake of simplicity, we assume that we are

working on a uniform grid $t_n = n\tau,\ n = 0, 1, \ldots, N$ with integer N and $\tau = T/N$ where T represents the final time.

The following is the time fractional measles model

$$D_t^{\alpha} H_{ix}(t) = \mathbf{a_i} H_{ix}(t) + \mathbf{g_i}; \qquad H_{ix}(0) = H_{ix}^{\#},\ \ i = 1, 2, 3, 4.$$

It is known that the classical Adams-Bashforth-Moulton method for first-order ordinary differential equations is reasonable and practical in the sense that its stability properties allow for a safe application to mildly stiff equations without undue propagation of rounding error, whereas the implementation does not require extremely time consuming elements [38]. Thus, a fractional Adams-Bashforth and a fractional Adams-Moulton scheme are chosen as our predictor and corrector formulas.

The predictor $H_{ix,k+1}^{P}$ is determined by the fractional Adams-Bashforth method [12, 39]:

$$H_{ix,k+1}^{P} = H_{ix,0}^{\#} + \frac{1}{\Gamma(\alpha)} \sum_{n=0}^{k} b_{n,k+1}[\mathbf{a_i} H_{ix,n} + \mathbf{g}_i(t_n)], \tag{44}$$

where

$$b_{n,k+1} = \frac{\tau^{\alpha}}{\alpha}[(k+1-n)^{\alpha} - (k-n)^{\alpha}].$$

The fractional Adams-Moulton method determines the corrector formula [12, 39]:

$$H_{ix,k+1} = H_{ix,0}^{\#} + \frac{1}{\Gamma(\alpha)} \left(\sum_{n=0}^{k} a_{n,k+1}[\mathbf{a_i} H_{ix,n} + \mathbf{g}_i(t_n)] + a_{k+1,k+1}[\mathbf{a_i} H_{ix,k+1}^{P} + \mathbf{g}_i(t_{k+1})] \right), \tag{45}$$

where

$$a_{n,k+1} = \frac{\tau^{\alpha}}{\alpha(\alpha+1)} \begin{cases} k^{\alpha+1} - (k-\alpha)(k+1)^{\alpha}, & \text{if } n = 0, \\ (k-n+2)^{\alpha+1} + (k-n)^{\alpha+1} - 2(k-n+1)^{\alpha+1}, & \text{if } 1 \le n \le k, \\ 1 & \text{if } n = k+1. \end{cases} \tag{46}$$

Therefore, we obtain the following fractional predictor-corrector method for solving the system (5)–(8).

$$H_{ix,k+1}^{P} = H_{ix,0}^{\#} + \frac{1}{\Gamma(\alpha)} \sum_{n=0}^{k} b_{n,k+1}[\mathbf{a_i} H_{ix,n} + \mathbf{g}_i(t_n)],\ \ i = 1, 2, 3, 4.$$

$$H_{ix,k+1} = H_{ix,0}^{\#} + \frac{1}{\Gamma(\alpha)} \left(\sum_{n=0}^{k} a_{n,k+1}[\mathbf{a_i} H_{ix,n} + \mathbf{g}_i(t_n)] + a_{k+1,k+1}[\mathbf{a_i} H_{ix,k+1}^{P} + \mathbf{g}_i(t_{k+1})] \right), \tag{47}$$

where $\mathbf{a_1}, \mathbf{a_2}, \mathbf{a_3}, \mathbf{a_4}$ and $\mathbf{g_1}, \mathbf{g_2}, \mathbf{g_3}, \mathbf{g_4}$ are referring to (31)–(34). The plots for the numerical solution of (47) are exhibited in the next section using Matlab 7.0.

6 Error analysis for the fractional predictor-corrector method

In this section, we present the theorems concerning the error of our fractional predictor-corrector method.

Lemma 3 *Let $z \in C^1[0, T]$, then*

$$\left| \int_0^{t_{k+1}} (t_{k+1} - t) z(t) dt - \sum_{n=0}^{k} b_{n,k+1} z(t_n) \right| \leq \frac{1}{\alpha} ||z'||_\infty t_{k+1}^\alpha \tau. \tag{48}$$

Proof See [40]. □

Lemma 4 *If $z \in C^2[0, T]$, then there is a constant C_α depending only on α such that*

$$\left| \int_0^{t_{k+1}} (t_{k+1} - t) z(t) dt - \sum_{n=0}^{k+1} a_{n,k+1} z(t_n) \right| \leq C_\alpha ||z''||_\infty t_{k+1}^\alpha \tau^2. \tag{49}$$

Proof See [40]. □

Theorem 1 *If ${}^c D_t^\alpha H_{ix} \in C^2[0, t]$, $(i = 1, 2, 3, 4)$, then*

$$\max_{0 \leq n \leq N} \left| H_{ix}(t_n) - H_{ix,n} \right| = O(\tau^{1+\alpha}). \tag{50}$$

Proof Using given condition ${}^c D_t^\alpha H_{ix} \in C^2[0, T]$, $(i = 1, 2, 3, 4)$, Lemma 4 and Lemma 5, we have

$$\left| \int_0^{t_{k+1}} (t_{k+1} - t)^c D_t^\alpha H_{ix}(t) dt - \sum_{n=0}^{k} b_{n,k+1} {}^c D_t^\alpha H_{ix}(t_n) \right| \leq C_1 t_{k+1}^\alpha \tau, \tag{51}$$

and

$$\left| \int_0^{t_{k+1}} (t_{k+1} - t)^c D_t^\alpha H_{ix}(t) dt - \sum_{n=0}^{k+1} a_{n,k+1} {}^c D_t^\alpha H_{ix}(t_n) \right| \leq C_2 t_{k+1}^\alpha \tau^2. \tag{52}$$

We show that, for sufficiently small $\tau = T/N$,

$$\max_{0 \leq n \leq N} \left| H_{ix}(t_n) - H_{ix,n} \right| = O(\tau^{1+\alpha}). \tag{53}$$

The proof will be based on mathematical induction. In view of the given initial condition, the induction basis ($n = 0$) is presupposed.

Now assume that (53) is true for $n = 0, 1, \ldots, k$ ($k \leq N - 1$), that is

$$\max_{0 \leq n \leq N} \left| H_{ix}(t_n) - H_{ix,n} \right| = O(\tau^{1+\alpha}). \tag{54}$$

We must then prove that the inequality also holds for $n = k+1$. To do this, we look at the error of the predictor $H_{ix,k+1}^P$, $i = 1, 2, 3, 4$. By construction of the predictor formula, using (51), assumption (54), and [6]

$$\sum_{n=0}^{k} b_{n,k+1} = \int_0^{t_{k+1}} (t_{k+1} - t)^{\alpha-1} dt = \frac{1}{\alpha} t_{k+1}^\alpha \leq \frac{1}{\alpha} T^\alpha, \tag{55}$$

we find that

$$\left|H_{ix}(t_{k+1}) - H^{P}_{ix,k+1}\right| \leq \frac{C_1 T^{\alpha}}{\Gamma(\alpha)}\tau + \frac{C_0 T^{\alpha}}{\Gamma(1+\alpha)}\tau^{1+\alpha}, \quad i = 1, 2, 3, 4. \tag{56}$$

Now we begin the analysis of the corrector error. For $j = k + 1$, arguing in a similar way to the above, by construction of the predictor formula, using (52), (56), assumption (54), and [6]

$$\sum_{n=0}^{k} a_{n,k+1} = \int_0^{t_k} (t_k - t)^{\alpha-1} dt = \frac{1}{\alpha} t_k^{\alpha} \leq \frac{1}{\alpha} T^{\alpha}, \tag{57}$$

we find that

$$\begin{aligned}
&\left|H_{ix}(t_{k+1}) - H_{ix,k+1}\right| \\
&\leq \Big(\frac{C_2 T^{\alpha}}{\Gamma(\alpha)} + \frac{C_0 T^{\alpha}}{\Gamma(1+\alpha)} + \frac{C_1 T^{\alpha}}{\Gamma(\alpha)\Gamma(\alpha+2)} + \frac{C_0 T^{\alpha}}{\Gamma(\alpha+1)\Gamma(\alpha+2)}\tau^{\alpha}\Big)\tau^{1+\alpha}, \\
&\leq C\tau^{1+\alpha}, \qquad i = 1, 2, 3, 4.
\end{aligned} \tag{58}$$

This completes the proof. □

We obtain not only an approximation for the solution $H_i(t)$ but also approximations for its (Caputo type) derivatives of order α. Apart from this useful feature, the method has simple structure and easy to implement to other fractional models.

7 Comparisons using GMMP scheme and the analytical solution for fractional temporal model

For demonstrating the accuracy of analytical solution for fractional decoupled measles model, we applied GMMP scheme (Gorenflo-Mainardi-Moretti-Paradisi) [47] to the original fractional ordinary differential equations (TFODE) (22–25). Then, the comparison of the numerical simulations indicates that the solution of the decoupled and linearized system is close enough to the solution of the original system.

For the sake of simplicity, we assume that we are working on a uniform grid $t_j = a + jh$, $j = 0, 1, 2, \cdots, N$, $Nh = t - a$. Then, Riemann-Liouville and Grünwald-Letnikov fractional derivative can be approximated using the following formula,

$${}^{RL}_{a}D^{\alpha}_{t} f(t) = {}^{GL}_{a}D^{\alpha}_{t} f(t) = \lim_{h\to 0} \frac{1}{h^{\alpha}} \sum_{k=0}^{N} c^{\alpha}_{k} f(t_{N-k}) \approx \frac{1}{h^{\alpha}} \sum_{k=0}^{N} c^{\alpha}_{k} f(t_{N-k}), \tag{59}$$

and the Caputo fractional derivative can be approximated using the following relation

$${}^{C}_{a}D^{\alpha}_{t} f(t) \approx \frac{1}{h^{\alpha}} \sum_{k=0}^{N} c^{\alpha}_{k} \left(f(t_{N-k}) - \sum_{j=0}^{n-1} \frac{(t-a)^{j} f^{(j)}(a)}{j!} \right), \tag{60}$$

where $c^{\alpha}_{k} = (-1)^{k}\binom{\alpha}{j}$ are binomial coefficients.

This scheme is first introduced in [47] and known as GMMP scheme [48]. Based on this GMMP scheme (60), numerical techniques for simulating fractional order differential equations are presented. For explaining this method, we consider the following fractional order nonlinear equation:

$$\begin{aligned} {}_a^C D_t^\alpha x(t) &= f(t, x(t)), \quad 0 \le t \le T, \\ x^{(k)}(a) &= x_0^{(k)}, \quad k = 0, 1, \cdots, n-1, \end{aligned} \tag{61}$$

where ${}_a^C D_t^\alpha$ denotes the fractional derivative of Caputo definition.

It follows from formula (60) that

$$\sum_{k=0}^{N} c_k^\alpha \left(x(t_{N-k}) - \sum_{j=0}^{n-1} \frac{(t-a)^j x^{(j)}(a)}{j!} \right) = h^\alpha f(t_N, x(t_N)), \tag{62}$$

i.e.

$$x(t_N) = h^\alpha f(t_N, x(t_N)) + \sum_{j=0}^{n-1} \frac{(t-a)^j x^{(j)}(a)}{j!} - \sum_{k=1}^{N} c_k^\alpha \left(x(t_{N-k}) - \sum_{j=0}^{n-1} \frac{(t-a)^j x^{(j)}(a)}{j!} \right). \tag{63}$$

Especially, let $0 < \alpha \le 1$, the formula (63) can be simplified as follows:

$$x(t_N) = h^\alpha f(t_N, x(t_N)) + x(a) - \sum_{k=1}^{N} c_k^\alpha \left(x(t_{N-k}) - x(a) \right). \tag{64}$$

Based on the Grünwald-Letnikov formula, an implicit difference scheme (64) has been presented. We can consider the formula (64) as an equation with respect to an unknown variable $x(t_N)$, which is in both sides of the nonlinear equation. As we known, the Newton method is a quick and effective method of solving nonlinear equations. In the following, the GMMP scheme and Newton method are used to obtain the numerical solution of the fractional differential (22–25). With the $\alpha = 0.85, t \in [0, 17]$ and initial condition $[H_{1x}(0) = 15, H_{2x}(0) = 15, H_{3x}(0) = 0, H_{4x}(0) = 0]^T$; $\beta_x = 0.4, \zeta_x = 0.14, \mu_x = 0, \sigma_x = 0.09, b_x = 0$ and $k = 1$], Fig. 1 gives the comparisons using the GMMP scheme form and the analytical solution (40)–(43), which demonstrates the validity of analytical solution of the decoupled and linearized system.

8 Numerical results

This section will provide comparisons for solutions derived from (40) to (43) and numerical solutions with the predictor-corrector technique in (47).

Example 1 Comparisons for analytical and numerical solutions in (40)–(43) and (47) for system in (5)–(8).

Figure 2 shows the numerical plots with $\alpha = 0.85, t = [0, 17]$ with initial conditions $[H_{1x}(0) = 15, H_{2x}(0) = 15, H_{3x}(0) = 0, H_{4x}(0) = 0]^T$; $\beta_x = 0.4, \zeta_x =$

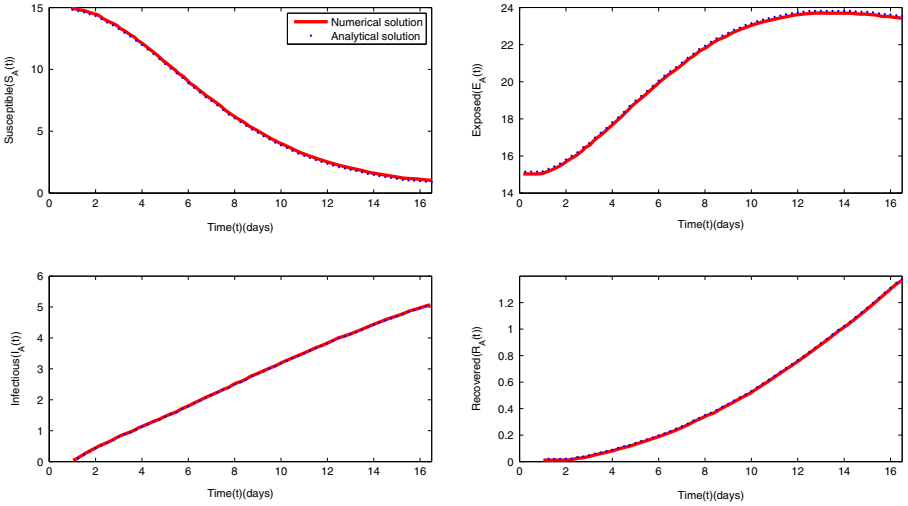

Fig. 1 Comparisons using GMMP scheme from 64 and the analytical solution (40)–(43) for the decoupled problem

0.14, $\mu_x = 0, \sigma_x = 0.09, b_x = 0$ and $k = 1$ [25]. Note that, in this simulation, we only consider the evolutions of the disease in the city $x = A$ (Auckland) as an example for the four compartments with $\alpha = 0.85$.

We display some of the results in Tables 1, 2, 3, and 4 for the measles model in the case of $\alpha = 0.85$. In each table, the leftmost column shows the step size used; the next column gives the maximum error of analytical and predictor-corrector schemes, and the third column gives the convergence rate values. According to our theoretical

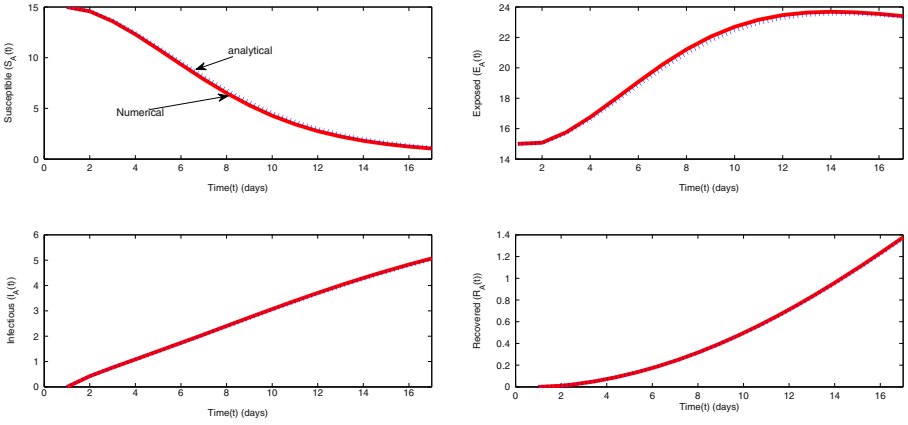

Fig. 2 Comparisons using predictor-corrector scheme from (47) and the analytical solution (40)–(43) for the decoupled problem

Table 1 Errors for H_1 with $\alpha = 0.85$

τ	$\|\|E\|\|_{max}$	Convergence rate
1/4	0.0576	
1/8	0.0154	1.91
1/16	0.00392	1.97
1/32	0.000947	2.04

consideration, we can conclude that the behavior of the maximum error displayed in Tables 1–4 behave as

$$||E||_{max} \leq C(\tau^{1+\alpha})$$

Figure 2 shows the numerical approximations converge rapidly to the analytical solutions. Apparently, we need to use smaller values for step size to increase the accuracy of the numerical solution. We have also tested the predictor corrector scheme with a variety of α values for $t = [0, 17]$ as shown in Fig. 3. Obviously, different α affects the behavior of measles transmission to every compartment in the model.

Next, we give two numerical examples using Matlab to illustrate the applicability of the developed scheme. As mentioned in the objective of this paper, this method and technique can be extended to other epidemic models. By considering two examples from HIV/AIDS model and Bovine babesiosis and tick populations model, we can demonstrate the usefulness of this technique.

Example 2 Consider the homogeneous-mixing population model for HIV proposed by [15], is given by

$$D^{\alpha}S = \Pi - \frac{c\beta_1 SI}{N} - \xi S - \mu S + \gamma V, \tag{65}$$

$$D^{\alpha}V = \xi S - \frac{c\beta_2 VI}{N} - \mu V - \gamma V, \tag{66}$$

$$D^{\alpha}I = \frac{c\beta_1 SI}{N} + \frac{c\beta_2 VI}{N} - (\mu + \tau)I, \tag{67}$$

where α is the order of the model, S, V ,and I denote the numbers of susceptible, vaccinated, infected at time t, respectively. Here, γ is the ratio converting to susceptible people due to losing efficacy, N denotes the total population size at time t, Π is the rate of recruitment of individuals per unit time, c is the number of the contact partners per unit time, β_1 is the transmission probability of a susceptible (S) by the infectious fraction (I/N), μ is their death rate and ξ denotes the fraction of

Table 2 Errors for H_2 with $\alpha = 0.85$

τ	$\|\|E\|\|_{max}$	Convergence rate
1/4	0.0646	
1/8	0.0204	1.66
1/16	0.00485	2.07
1/32	0.000972	2.32

Table 3 Errors for H_3 with $\alpha = 0.85$

τ	$\|\|E\|\|_{max}$	Convergence rate
1/4	0.0480	
1/8	0.0158	1.603
1/16	0.00362	2.12
1/32	0.000795	2.18

the vaccinated population. In this model, it is assumed that the vaccines do not offer total protection against infection, vaccinated individuals also acquire infection from symptomatic individuals. In this case, β_2, ($\beta_2 \leq \beta_1$) is a transmission probability of a vaccinated (V) by the infectious fraction (I/N), τ is the rate of progression to full-blown AIDS. This model incorporates anti-HIV preventive vaccines to exhibit the efficiency of vaccines for controlling HIV/AIDS.

Using Matlab, numerical simulations for (65), (66), and (67) using a predictor-corrector scheme are established. We consider **Example 2** with the following parameters $\Pi = 20, c = 10, \beta_1 = 0.06, \xi = 0.12, \mu = 0.02, \gamma = 0.003, \beta_2 = 0.007, \tau = 0.125$. Simulations are then performed with $t \in [0, 500]$ and $S(0) = 400, V(0) = 400$ and $I(0) = 400$ number of individuals as their initial conditions with varying α values. Figure 4 exhibits the dynamics of this model.

Example 3 Consider the fractional-order model for Bovine babesiosis disease and tick population by [16]. The system is described as

$$D^{\theta}\bar{S}_B(t) = \mu_B(\bar{S}_B(t) + \bar{C}_B(t)) + \alpha_B\bar{C}_B(t) - \mu_B\bar{S}_B(t) - \beta_B\bar{S}_B(t)\frac{\bar{I}_T(t)}{\bar{N}_T(t)}, \tag{68}$$

$$D^{\theta}\bar{I}_B(t) = \mu_B\bar{I}_B(t) + \beta_B\bar{S}_B(t)\frac{\bar{I}_T(t)}{\bar{N}_T(t)} - \mu_B\bar{I}_B(t) - \lambda_B\bar{I}_B(t), \tag{69}$$

$$D^{\theta}\bar{C}_B(t) = \lambda_B\bar{I}_B(t) - [\mu_B + \alpha_B]\bar{C}_B(t), \tag{70}$$

$$D^{\theta}\bar{S}_T(t) = \mu_T(\bar{S}_T(t) + p\bar{I}_T(t)) - \beta_T\bar{S}_T(t)\frac{\bar{I}_B(t)}{\bar{N}_B(t)} - \mu_T\bar{S}_T(t), \tag{71}$$

$$D^{\theta}\bar{I}_T(t) = \beta_T\bar{S}_T(t)\frac{\bar{I}_B(t)}{\bar{N}_B(t)} + (1-p)\mu_T\bar{I}_T(t) - \mu_T\bar{I}_T(t). \tag{72}$$

Table 4 Errors for H_4 with $\alpha = 0.85$

τ	$\|\|E\|\|_{max}$	Convergence rate
1/4	0.0221	
1/8	0.0085	1.37
1/16	0.00257	2.44
1/32	0.000465	2.46

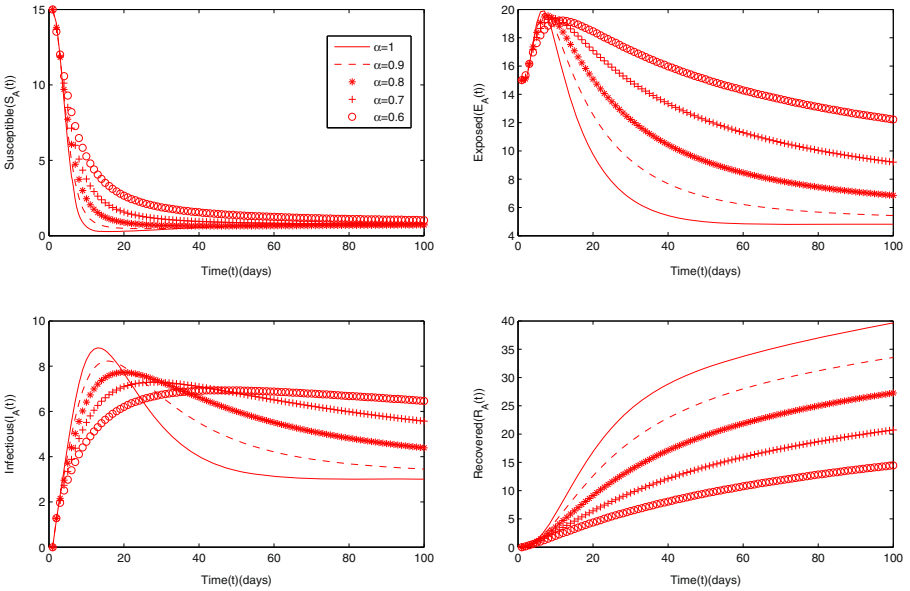

Fig. 3 Comparisons of solution for different values of α using the predictor-corrector scheme from (47)

In this model, the total of bovine population $N_B(t)$ is divided into three subpopulations, susceptible bovine $\bar{S}_B(t)$, bovine infected by Babesia parasite $\bar{I}_B(t)$, and treated bovine $\bar{C}_B(t)$.

The parameter μ_B is the birth rate of bovine and assume to be equal to natural death. The total population of ticks $N_T(t)$ is comprised of susceptible ticks $S_T(t)$ and ticks infected by Babesia parasite $I_T(t)$. The parameter μ_T is the ticks birth rate that is assumed to be equal to death rate. Other parameters are β_B the transmission rate of infected ticks, β_T the transmission rate from infected bovine, p is the probability that a susceptible tick was born from the infected one, λ_B is the controlled infected

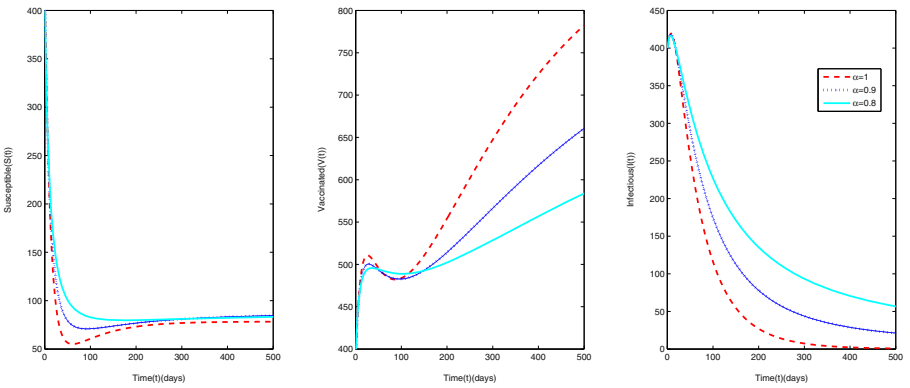

Fig. 4 The HIV model with $S(0) = 400$, $V(0) = 400$, $I(0) = 400$, and varying α values using predictor-corrector scheme

bovine against Babesia parasite and α_B, is the fraction of controlled bovine that may return to the susceptible state.

Based on [16], they simplified the (68)–(72) by taking the bovine populations constant equal to $\bar{N}_B$ and the tick populations equal to $\bar{N}_T$ and introduce the following proportions

$$S_B(t) = \frac{\bar{S}_B(t)}{\bar{N}_B(t)}; \quad I_B(t) = \frac{\bar{I}_B(t)}{\bar{N}_B(t)}; \quad C_B(t) = \frac{\bar{C}_B(t)}{\bar{N}_B(t)};$$
$$S_T(t) = \frac{\bar{S}_T(t)}{\bar{N}_T(t)}; \quad I_T(t) = \frac{\bar{I}_T(t)}{\bar{N}_T(t)}. \tag{73}$$

Finally, the resulting fractional system is given by

$$D^\theta S_B(t) = (\mu_B + \alpha_B)(1 - S_B(t) - I_B(t)) - \beta_B S_B(t) I_T(t), \tag{74}$$
$$D^\theta I_B(t) = \beta_B S_B(t) I_T(t) - \lambda_B I_B(t), \tag{75}$$
$$D^\theta I_T(t) = \beta_T (1 - I_T(t)) I_B(t) - \mu_T p I_T(t), \tag{76}$$

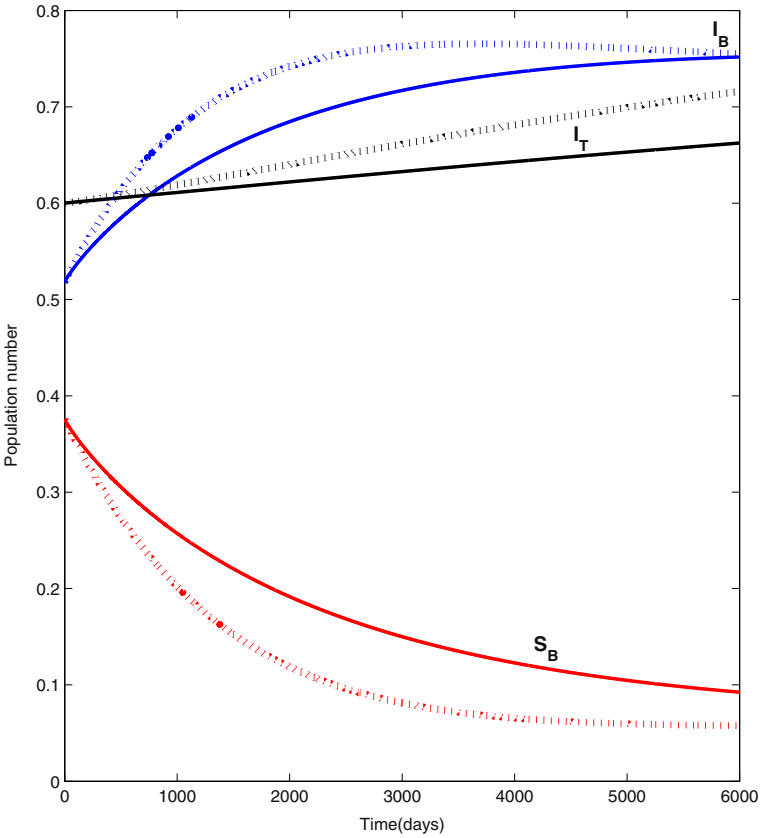

Fig. 5 Dynamics of Bovine babesiosis disease and tick populations for $t \in [0, 6000]$ with $\theta = 1$ (continuous line) and $\theta = 0.85$ (dotted line) based on (74)–(76) using the predictor-corrector scheme

with $\theta \in (0, 1)$ and defined in the region $\Omega = \{S_B, I_B, I_T : 0 \leq S_B + I_B \leq 1,\ 0 \leq I_T \leq 1\}$ [16].

Here, Fig. 5 shows the dynamics of the bovine Babesiosis disease and tick with initial conditions of $S_B = 0.3756$, $I_B = 0.5184$, and $I_T = 0.6$ [16]. The comparison between two different values of fractional order (θ) is also given in Fig. 4, with the following parameters $\mu_B = 0.0002999, \alpha_B = 0.001, \beta_B = 0.006, \lambda_B = 0.000265, \beta_T = 0.00048, \mu_T = 0.001609$, and $p = 0.1$ All initial conditions and parameters are based on [16]. For both cases of θ, the disease transmission goes to the endemic equilibrium point but gets slower as θ decreases.

9 Discussions and conclusions

For example 1, in the case of Susceptibles, Infectious and Exposed, there is a correspondingly heavier tail in the solution with much slower convergence to a steady state as α decreases from 1. We also see that for the Infectious individuals the peak arrives slightly later as α decreases, with much slower convergence. In the case of the Recovered individuals, decreasing α slows the rate of recovery.

In the second example, there is a much less pronounced dip for both Susceptible and Vaccinated as α decreases. Furthermore, as α decreases, both the rate of Vaccinated and the rate of Infectious slows with heavier tails in the latter. In the third example, we are looking at the dynamics of the bovine babesiosis disease and it was found that the system will decay to its equilibrium condition similar to the power $t^{-\theta}$ [16].

Epidemiology has become an important research area due to existence of many 'new' diseases and health problems nowadays. The transmission of diseases and concomitant health problems needs to be properly managed as it can impact people's well-being. As part of this effort, researchers have introduced epidemiological modeling systems that can describe real problems in disease transmission. Apparently, some established epidemiological modeling are not capable of describing properly the dynamics behavior and need some modification. Fractional differential equations are then proposed as a modification to the original integer model. However, analytical techniques available in the literature for fractional models are quite complicated and hard to implement. Therefore, from this work, we have proposed a simple and effective analytical technique for fractional model systems by first linearizing the time fractional ordinary differential equations model. Of course, further analysis is needed to show under what circumstances the full model and the coupling model are close in terms of the solutions.

In this paper, the fractional measles model is used to construct the analytical technique and predictor-corrector scheme. We also explore the average error estimates for the measles model to verify with the theoretical analysis. We use the GMMP scheme to show the accuracy of the analytical solution for the time coupled fractional differential equations. The best features of the techniques proposed in this work are that they can be easily extended to other fractional epidemic models. As outlined in the introduction, we limit the discussions on the effect of differential order but put more effort into constructing a simple and effective analytical technique that can be

easily applied to other fractional models. We present two problems in epidemiology areas—HIV/AIDS and Bovine babesiosis disease models. The displayed results from the given examples show the applicability of the derived techniques. In some circumstances, the solutions from the derived techniques can also help to understand the underlying mechanisms that influence the epidemic pattern. Finally, it can be concluded that the analytical technique presented in this paper is reliable and yet an alternative for the analytical evaluation to other time fractional differential equations models.

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