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# Numerical solution of a system of Volterra integral equations in application to the avian human influenza epidemic model

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#### Abstract

We propose an efficient multistage method for solving a system of linear and nonlinear Volterra integral equations of the second kind. This numerical method is based on the Gauss–Legendre quadrature rule that obtains several values of unknown function at each step, and it will be shown that the order of the convergence is  $O(M^{-4})$ , where M is the number of the nodes in the time discretization. The method has also the advantages of simplicity of application, less computational time, and useful performance for large intervals. In order to show the efficiency of the method, numerical results for the avian human influenza epidemic model is obtained that is comparable with the fourth-order Runge–Kutta method.

AMS subject classifications (2020): 45D05; 65R20.

**Keywords:** The avian human influenza epidemic model; system of Volterra integral equations; Gauss–Legendre quadrature rule; convergence order.

# 1 Introduction

Numerical methods for solving a variety of system of Volterra integral equations (SVIE) are offered in many publications. Here readers may refer to [1, 3, 7, 10] and others.

In this article, we introduce a multistage numerical method for solving SVIE, and then the introduced method will be used to the avian human influenza epidemic model, which recently has been described by Iwami, Takeuchi, and Liu [6]. This mathematical model is proposed to interpret the spread of the

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avian influenza from the bird world to the human world. The avian influenza has caused the death of millions of birds (almost 100% death) and it has become a disease of great importance both for animal and human health. Fortunately, there is still no evidence that the avian influenza virus can be transmitted among humans [12], but this virus is unstable and lacks of gnomic proofreading mechanism. Therefore the small errors, which occur when the copies themselves, go undetected and uncorrected. Since the specifics of mutations and evolution of the influenza viruses cannot be predicted, it is hardly possible to know if or when a virus such as the avian influenza, might acquire the properties needed to spread easily and sustainably among humans [5]. However, experts warn about an occurrence of the so-called "mutant the avian influenza", which can be easily transmitted among humans with potentially devastating consequence. The US Congressional Budget Office has formally modeled the likely consequences of pandemic influenza and estimates that up to 2 million of the US population might die, with up to 40%of all workers ill for as long as three or more weeks [11]. Thus, it is necessary and urgent to investigate the transmission process of the avian influenza and to take efficient measures to control the spread of the avian influenza.

#### 2 Preliminaries

In this section, we introduce notations, definitions, and preliminaries facts, which are used throughout this article. Consider SVIE

$$Y(t) = G(t) + \int_0^t K(t, s, Y^t(s)) ds, \qquad 0 \le s \le t \le T,$$
(1)

where  $Y(t) = [y^{(1)}(t), y^{(2)}(t), \dots, y^{(n)}(t)]^t$  is the desired function,  $G(t) = [g^{(1)}(t), g^{(2)}(t), \dots, g^{(n)}(t)]^t$ , and

$$K(t, s, Y^{t}(s)) = \begin{bmatrix} k_{1}(t, s, y^{(1)}(t), y^{(2)}(t), \dots, y^{(n)}(t)) \\ k_{2}(t, s, y^{(1)}(t), y^{(2)}(t), \dots, y^{(n)}(t)) \\ \vdots \\ k_{n}(t, s, y^{(1)}(t), y^{(2)}(t), \dots, y^{(n)}(t)) \end{bmatrix}$$

are the source functions  $(A^t \text{ is the transposed matrix of } A)$ . Let system (1) is uniquely solvable. Necessary and sufficient conditions for the existence and uniqueness of solution (1) can be found in [9]. Therefore we assume the following conditions:

(I) The source function G(t) is continuous (i.e., each component is continuous).

(II) The kernel K(t, s, U) is a continuous function for  $0 \le s \le t \le T$  and  $0 \le ||U|| < \infty$ .

(III) The kernel K satisfies the Lipschitz condition

$$|| K(t,s,U) - K(T,s,V) || \le L || U - V ||,$$

where the norm is defined as  $\parallel U \parallel = \max_{0 \le i \le n} |u_i(t)|$ .

#### **3** Numerical procedure

Let  $I_h = \{t_m = mh, m = 0, 1, \ldots, M\}$  with  $t_M = Mh = T$  be a given uniform mesh on [0, T]. For given real numbers  $c_j$  with  $0 = c_0 < c_1 < \cdots < c_p = 1$ , we choose the set of mesh points as  $\Pi_h := \{t_{m,j} = t_m + c_jh, m = 0, 1, \ldots, M 1, j = 0, 1, \ldots, p\}$ , where  $c_j, j = 1, 2, \ldots, p - 1$ , are the roots of the (p - 1)th Legendre polynomial. The Legendre polynomials  $P_{p-1}(x)$  are orthogonal with respect to the weight functions w(x) = 1 over the interval [-1, 1], that is,

$$\int_{-1}^{1} P_m(x) P_n(x) dx = \delta_{nm},$$

where  $\delta_{mn}$  is the Kronecker delta (see, for example, [8, 4] for Legendre polynomials and [13] for funding roots of polynomials).

For simplicity, let p = 3  $(c_1 = \frac{3-\sqrt{3}}{6}, c_2 = \frac{3+\sqrt{3}}{6})$  and let n = 2 (system dimensional). Then we will have a multistep method with at least four order of convergence, which one can generalize it by increasing the Legendre polynomial degree.

Assume that  $y_{m,j}^{(i)} \approx y^{(i)}(t_{m,j}), m = 0, 1, \dots, M-1, j = 0, 1, 2, 3$  and that  $Y_{m,j} \approx Y(t_{m,j}) = [y^{(1)}(t_{m,j}), y^{(2)}(t_{m,j})]^t$ . Thus system (1) can be rewrite as

$$y^{(1)}(t_{m,j}) = g^{(1)}(t_{m,j}) + \int_{0}^{t_{m}} k_{1}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds + \int_{t_{m}}^{t_{m,j}} k_{1}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds,$$
(2)

$$y^{(2)}(t_{m,j}) = g^{(2)}(t_{m,j}) + \int_{0}^{t_{m}} k_{2}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds + \int_{t_{m}}^{t_{m,j}} k_{2}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds,$$
(3)

 $m = 0, 1, \dots, M - 1, \ j = 1, 2, 3.$ 

Note that  $Y_{0,0} = [y_{0,0}^{(1)}, y_{0,0}^{(2)}]^t = [g^{(1)}(0), g^{(2)}(0)]^t$ , and suppose that approximations  $Y_{0,1}, Y_{0,2}, Y_{1,0}, \ldots, Y_{n,0}$ , have been calculated in the previous steps. Therefore the first integral in relations (2) and (3) can be estimated by using the Gauss-Legendre quadrature rule,

$$\int_{0}^{t_{m}} k_{1}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds = \sum_{i=0}^{m-1} \int_{t_{i}}^{t_{i+1}} k_{1}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds$$

$$\approx \frac{h}{2} \sum_{i=0}^{m-1} \left[ k_{1}(t_{m,j}, t_{i,1}, y^{(1)}_{i,1}, y^{(2)}_{i,1}) + k_{1}(t_{m,j}, t_{i,2}, y^{(1)}_{i,2}, y^{(2)}_{i,2}) \right] =: A_{1}(m, j),$$

$$\int_{0}^{t_{m}} k_{2}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds = \sum_{i=0}^{m-1} \int_{t_{i}}^{t_{i+1}} k_{2}(t_{m,j}, s, y^{(1)}(s), y^{(2)}(s)) ds$$

$$\approx \frac{h}{2} \sum_{i=0}^{m-1} \left[ k_{2}(t_{m,j}, t_{i,1}, y^{(1)}_{i,1}, y^{(2)}_{i,1}) + k_{2}(t_{m,j}, t_{i,2}, y^{(1)}_{i,2}, y^{(2)}_{i,2}) \right] =: A_{2}(m, j).$$
(4)

If j = 3, then the second integral in relations (2) and (3) can be similarly approximated as

$$\int_{t_m}^{t_{m,3}} k_1(t_{m,3}, s, y^{(1)}(s), y^{(2)}(s)) ds 
\approx \frac{h}{2} \left[ k_1(t_{m,3}, t_{m,1}, y^{(1)}_{m,1}, y^{(2)}_{m,1}) + k_1(t_{m,3}, t_{m,2}, y^{(1)}_{m,2}, y^{(2)}_{m,2}) \right], 
\int_{t_m}^{t_{m,3}} k_2(t_{m,3}, s, y^{(1)}(s), y^{(2)}(s)) ds 
\approx \frac{h}{2} \left[ k_2(t_{m,3}, t_{m,1}, y^{(1)}_{m,1}, y^{(2)}_{m,1}) + k_2(t_{m,3}, t_{m,2}, y^{(1)}_{m,2}, y^{(2)}_{m,2}) \right], \quad (5)$$

and for j = 1, by using this quadrature rule, we obtain

$$\begin{split} &\int_{t_m}^{t_{m,1}} k_1(t_{m,1},s,y^{(1)}(s),y^{(2)}(s))ds \\ &\approx \frac{c_1h}{2} \left[ k_1(t_{m,1},t_m+\frac{h}{6},y^{(1)}(t_m+\frac{h}{6}),y^{(2)}(t_m+\frac{h}{6})) \right. \\ &\left. + k_1(t_{m,1},t_m+\frac{2-\sqrt{3}}{6}h,y^{(1)}(t_m+\frac{2-\sqrt{3}}{6}h),y^{(2)}(t_m+\frac{2-\sqrt{3}}{6}h)) \right], \\ &\int_{t_m}^{t_{m,1}} k_2(t_{m,1},s,y^{(1)}(s),y^{(2)}(s))ds \\ &\approx \frac{c_1h}{2} \left[ k_2(t_{m,1},t_m+\frac{h}{6},y^{(1)}(t_m+\frac{h}{6}),y^{(2)}(t_m+\frac{h}{6})) \right. \\ &\left. + k_2(t_{m,1},t_m+\frac{2-\sqrt{3}}{6}h,y^{(1)}(t_m+\frac{2-\sqrt{3}}{6}h),y^{(2)}(t_m+\frac{2-\sqrt{3}}{6}h) \right]. \end{split}$$

$$(6)$$

Finally, for j = 2, we obtain

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$$\begin{split} &\int_{t_m}^{t_{m,2}} k_1(t_{m,2},s,y^{(1)}(s),y^{(2)}(s))ds \\ &\approx \frac{c_2h}{2} \left[ k_1(t_{m,2},t_m+\frac{h}{6},y^{(1)}(t_m+\frac{h}{6}),y^{(2)}(t_m+\frac{h}{6})) + k_1(t_{m,2},t_m+\frac{2+\sqrt{3}}{6}h,y^{(1)}(t_m+\frac{2+\sqrt{3}}{6}h),y^{(2)}(t_m+\frac{2+\sqrt{3}}{6}h)) \right], \\ &\int_{t_m}^{t_{m,2}} k_2(t_{m,2},s,y^{(1)}(s),y^{(2)}(s))ds \\ &\approx \frac{c_2h}{2} \left[ k_2(t_{m,2},t_m+\frac{h}{6},y^{(1)}(t_m+\frac{h}{6}),y^{(2)}(t_m+\frac{h}{6})) + k_2(t_{m,2},t_m+\frac{2+\sqrt{3}}{6}h,y^{(1)}(t_m+\frac{2+\sqrt{3}}{6}h),y^{(2)}(t_m+\frac{2+\sqrt{3}}{6}h)) \right]. \end{split}$$

$$(7)$$

In relations (6) and (7),  $t_m + \frac{2\pm\sqrt{3}}{6}h$  and  $t_m + \frac{h}{6}$  do not belong to the mesh points  $\Pi_h$ . Then we will have a problem to computing  $y^{(i)}(t_m + \frac{2\pm\sqrt{3}}{6}h)$  and  $y^{(i)}(t_m + \frac{h}{6})$ , i = 1, 2. In order to overcome to this difficulty, we use the Lagrange interpolation

$$y^{(i)}(x) \approx \mathcal{P}_i(x) = \sum_{i'=0}^3 L_{i'}(x) y^{(i)}_{m,i'}, \qquad L_{i'}(x) = \prod_{\substack{j'=0\\j' \neq i'}}^3 \frac{x - t_{m,j'}}{c_{i'} - c_{j'}},$$

for  $x = t_m + \frac{2\pm\sqrt{3}}{6}h$  or  $x = t_m + \frac{h}{6}$ . Substituting these approximations into (2), leads to the system of algebraic equations

$$\begin{split} y_{m,1}^{(i)} = & g^{(i)}(t_{m,1}) + A_i(m,1) + \frac{c_1 h}{2} \left[ k_i(t_{m,1},t_m + \frac{h}{6},\mathcal{P}_1(t_m + \frac{h}{6}),\mathcal{P}_2(t_m + \frac{h}{6})) \right. \\ & \left. + k_i(t_{m,1},t_m + \frac{2 - \sqrt{3}}{6}h,\mathcal{P}_1(t_m + \frac{2 - \sqrt{3}}{6}h),\mathcal{P}_2(t_m + \frac{2 - \sqrt{3}}{6}h)) \right], \\ & y_{m,2}^{(i)} = & g^{(i)}(t_{m,2}) + A_i(m,2) + \frac{c_2 h}{2} \left[ k_i(t_{m,2},t_m + \frac{h}{6},\mathcal{P}_1(t_m + \frac{h}{6}),\mathcal{P}_2(t_m + \frac{h}{6})) \right. \\ & \left. + k_i(t_{m,2},t_m + \frac{2 + \sqrt{3}}{6}h,\mathcal{P}_1(t_m + \frac{2 + \sqrt{3}}{6}h),\mathcal{P}_2(t_m + \frac{2 + \sqrt{3}}{6}h)) \right], \\ & \left. y_{m,3}^{(i)} = & g^{(i)}(t_{m,3}) + A_i(m,3) \right. \\ & \left. + \frac{h}{2} \left[ k_i(t_{m,3},t_{m,1},y_{m,1}^{(1)},y_{m,1}^{(2)}) + k_i(t_{m,3},t_{m,2},y_{m,2}^{(1)},y_{m,2}^{(2)}) \right], \end{split}$$

$$i = 1, 2.$$
 (8)

This system can be solved by using an iterative method such as Newton–Raphson method or by using a suitable software package such as Maple or MATLAB

# 4 Convergence analysis

**Theorem 1.** The approximation method given by system (8) is convergent, and its order of convergence is at least 4 for the functions  $k_i$  and  $g^{(i)}$  (i = 1, 2) with at least fourth-order continuous derivatives.

*Proof.* Define  $E_{m,j} = Y_{m,j} - Y(t_{m,j})$ , where  $Y(t_{m,j}), Y_{m,j} \in \mathbb{R}^2$  denote, respectively, the exact and approximate solutions of (1) at the point  $t = t_{m,j}$ . Subtracting (6) from (2) and (3) (for j = 1) leads to

$$\begin{split} E_{m,1} = & Y_{m,1} - Y(t_{m,1}) \\ = & \frac{h}{2} \sum_{i=0}^{m-1} \left[ K(t_{m,1}, t_{i,1}, Y_{i,1}^t) + K(t_{m,1}, t_{i,2}, Y_{i,2}^t) \right] \\ & + \frac{c_1 h}{2} \left[ K(t_{m,1}, t_m + \frac{h}{6}, \mathcal{P}(t_m + \frac{h}{6})) \\ & + K(t_{m,1}, t_m + \frac{2 - \sqrt{3}}{6}h, \mathcal{P}(t_m + \frac{2 - \sqrt{3}}{6}h)) \right] \\ & - \int_0^{t_m} K(t_{m,1}, s, Y^t(s)) ds - \int_{t_m}^{t_{m,1}} K(t_{m,1}, s, Y^t(s)) ds, \end{split}$$

where  $\mathcal{P}(x) = [\mathcal{P}_1(x), \mathcal{P}_2(x)]$ . By adding and diminishing the terms

$$\frac{h}{2} \sum_{i=0}^{m-1} \left[ K(t_{m,1}, t_{i,1}, Y^t(t_{i,1})) + K(t_{m,1}, t_{i,2}, Y^t(t_{i,2})) \right],$$

and

$$\frac{c_1h}{2} \left[ K(t_{m,1}, t_m + \frac{h}{6}, Y^t(t_m + \frac{h}{6})) + K(t_{m,1}, t_m + \frac{2 - \sqrt{3}}{6}h, Y^t(t_m + \frac{2 - \sqrt{3}}{6}h)) \right],$$

we can write

$$\begin{split} ||E_{m,1}|| &\leq \frac{h}{2} \sum_{i=0}^{m-1} \left[ ||K(t_{m,1}, t_{i,1}, Y_{i,1}^t) - K(t_{m,1}, t_{i,1}, Y^t(t_{i,1}))|| \\ &+ ||K(t_{m,1}, t_{i,2}, Y_{i,2}^t) - K(t_{m,1}, t_{i,2}, Y^t(t_{i,2}))|| \right] \\ &+ \frac{c_1 h}{2} \left[ ||K(t_{m,1}, t_m + \frac{h}{6}, \mathcal{P}(t_m + \frac{h}{6})) - K(t_{m,1}, t_m + \frac{h}{6}, Y^t(t_m + \frac{h}{6}))|| \right] \end{split}$$

$$+ ||K(t_{m,1}, t_m + \frac{2 - \sqrt{3}}{6}h, \mathcal{P}(t_m + \frac{2 - \sqrt{3}}{6}h)) - K(t_{m,1}, t_m + \frac{2 - \sqrt{3}}{6}h, Y^t(t_m + \frac{2 - \sqrt{3}}{6}h))|| \right] + (m+1)||e(G)||.$$

In the previous relation, e(G) is the upper bound of the Gauss–Legendre integration error, that is,

$$\begin{split} &\|\frac{h}{2}\sum_{i=0}^{m-1}\left[K(t_{m,1},t_{i,1},Y^{t}(t_{i,1}))+K(t_{m,1},t_{i,2},Y^{t}(t_{i,2}))\right]-\sum_{i=0}^{m-1}\int_{t_{i}}^{t_{i+1}}K(t_{m,1},s,Y^{t}(s))ds||\\ &+\|\frac{c_{1}h}{2}\left(K(t_{m,1},t_{m}+\frac{h}{6},Y^{t}(t_{m}+\frac{h}{6}))+K(t_{m,1},t_{m}+\frac{2-\sqrt{3}}{6}h,Y^{t}(t_{m}+\frac{2-\sqrt{3}}{6}h))\right)\\ &-\int_{t_{m}}^{t_{m,1}}K(t_{m,1},s,Y^{t}(s))ds||\leq m||e(G)||+||e(G)||. \end{split}$$

If  $k_i \in C^4([0,1])$  (i = 1, 2), then  $e(G) = \frac{1}{4320}h^4k^{(4)}(t, \tilde{t}, Y^t(\tilde{t}))$  where  $0 < \tilde{t} < 1$ ; see [2].

In the following, by using the Lipschitz condition for the kernel K, we have

$$\begin{split} ||E_{m,1}|| &\leq \frac{hL}{2} \sum_{i=0}^{m-1} \left( ||E_{i,1}|| + ||E_{i,2}|| \right) + \frac{c_1 hL}{2} \left[ ||\mathcal{P}(t_m + \frac{h}{6})) - Y^t(t_m + \frac{h}{6}))|| \\ &+ ||\mathcal{P}(t_m + \frac{2 - \sqrt{3}}{6}h)) - Y^t(t_m + \frac{2 - \sqrt{3}}{6}h))|| \right] + (m+1)||e(G)||. \end{split}$$

Let I(t) be the Lagrange interpolation error, that is,  $I(t) = Y^t(t) - \mathcal{P}(t)$ . Thus

$$\begin{split} ||E_{m,1}|| \leq & \frac{hL}{2} \sum_{i=0}^{m-1} \left( ||E_{i,1}|| + ||E_{i,2}|| \right) \\ &+ \frac{c_1 hL}{2} \left[ ||I(t_m + \frac{h}{6}))|| + ||I(t_m + \frac{2 - \sqrt{3}}{6}h))|| \right] + (m+1)||e(G)||. \end{split}$$

Without loss of generality, assume  $\max_{j=1,2,3} ||E_{m,j}|| = ||E_{m,1}||$ . Then it is easy to see that

$$||E_{m,1}|| \le hL \sum_{i=0}^{m-1} ||E_{i,1}|| + c_1 hL||I|| + (m+1)||e(G)||,$$

where I is the maximum error of the Lagrange interpolation. Finally, from the Gronwall inequality [2], we conclude that

$$||E_{m,1}|| \le (c_1 hL||I|| + M||e(G)||) \exp(Lt_m).$$

This yields  $||E_{m,1}|| \to 0$  as  $h \to 0$  and for the functions  $k_1, k_2$ , and g with at least fourth-order continuous derivatives, we have  $e(G) = O(h^4)$  and  $I = O(h^4)$ . So we expect the error generally to be at least  $O(h^4)$  as the numerical results confirm it.

## **5** Application

#### 5.1 Description of the model

In this part, the introduced numerical method is applied to interpret the avian human influenza epidemic model. Iwami, Takeuchi, and Liu [6] proposed the following mathematical model to interpret the spread of the avian human influenza epidemic

$$X' = \eta - bX - \omega XY,$$
  

$$Y' = \omega XY - (b+m)Y,$$
  

$$S' = \lambda - \mu S - (\beta_1 Y - \beta_2 H)S,$$
  

$$B' = \beta_1 SY - (\mu + d_1 + \epsilon)B,$$
  

$$H' = \beta_2 SH + \epsilon B - (\mu + \alpha + \gamma)H,$$
  

$$R' = \gamma H - \mu R.$$
(9)

All birds and humans in the effective population are divided into six main groups, respectively, including susceptible birds (X), birds infected with the avian influenza (Y), susceptible humans (S), humans infected with the avian influenza (B), humans infected with mutant the avian influenza (H), and humans recovered from mutant the avian influenza (R). It is assumed that all birds infected with the avian influenza are dead or remain infected and can never recover. The parameter  $\eta$  and  $\lambda$  are the birth rates for birds and humans, respectively. The natural death rate is assumed to be b and  $\mu$  for birds and humans, respectively. Furthermore, m and d are the death rates infected by wild the avian influenza, respectively, for birds and humans, and  $\alpha$  is the additional death rate induced by mutant the avian influenza. The parameters  $\omega$  and  $\beta_1$  are the rate at which the avian influenza is contracted from an average infected bird,  $\beta_2$  is the transmission rate of mutant the avian influenza in humans,  $\gamma$  is the recovery rate, and  $\epsilon$  is the mutation rate.

In [6], it was investigated mathematical properties and qualitative analysis of the above model, also was defined the basic reproductive number for infected birth with the avian influenza (" $r_0$ , which is the number of newly infected birds that are produced from anyone infected bird when all birds are susceptible") and the basic reproductive number for infected humans with

mutant the avian influenza  $(R_0)$  as

$$r_0 = \frac{\eta \omega}{b(b+m)}, \qquad R_0 = \frac{\lambda \beta_2}{\mu(\mu + \alpha + \gamma)}.$$

Finally, using some theorems, global analysis to spread of the avian influenza and mutant influenza in the human world is obtained as follows:

"If  $r_0 \leq 1$  and  $R_0 < 1$ , then the avian influenza and mutant the avian influenza cannot spread in the human world. On the other hand, if  $R_0 > 1$ , then mutant the avian influenza spreads in the human world. Moreover, if  $r_0 > 1$ , then both the avian influenza and mutant the avian influenza spread in the human world."

It must be pointed that all constants are positive in the system (9) and that  $\epsilon$  is sufficiently small. Moreover, b is sufficiently larger than  $\mu$  ( $b \gg \mu$ ),  $\alpha$  is less than d, and d is less than m ( $m > d > \alpha$ ) because of the differences of the virulence [6].

#### 5.2 Solution procedure

One can transfer the system (9) to the SVIE

$$\begin{aligned} X(t) &= X(0) + \eta t - \int_0^t (b + \omega Y(s)) X(s) ds, \\ Y(t) &= Y(0) + \int_0^t (\omega X(s) - b - m) Y(s) ds, \\ S(t) &= S(0) + \lambda t - \int_0^t (\mu + \beta_1 Y(s) + \beta_2 H(s)) S(s) ds, \\ B(t) &= B(0) + \int_0^t (\beta_1 S(s) Y(s) - (\mu + d + \epsilon) B(s)) ds, \\ H(t) &= H(0) + \int_0^t (\beta_2 S(s) H(s) + \epsilon B(s) - (\mu + \alpha + \gamma) H(s)) ds, \\ R(t) &= R(0) + \int_0^t (\gamma H(s) - \mu R(s)) ds. \end{aligned}$$
(10)

In this way, we can apply the multistage method for this SVIE. In order to do it, set  $t = t_{n,i}$ . Therefore

$$\begin{aligned} X(t_{n,i}) &= X(0) + \eta t_{n,i} - \int_0^{t_n} (b + \omega Y(s)) X(s) ds - \int_{t_n}^{t_{n,i}} (b + w Y(s)) X(s) ds, \\ Y(t_{n,i}) &= Y(0) + \int_0^{t_n} (\omega X(s) - b - m) Y(s) ds + \int_{t_n}^{t_{n,i}} (w X(s) - b - m) Y(s) ds, \end{aligned}$$

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$$S(t_{n,i}) = S(0) + \lambda t_{n,i} - \int_{0}^{t_{n}} (\mu + \beta_{1}Y(s) + \beta_{2}H(s))S(s)ds - \int_{t_{n}}^{t_{n,i}} (\mu + \beta_{1}Y(s) + \beta_{2}H(s))S(s)ds, B(t_{n,i}) = B(0) + \int_{0}^{t_{n}} (\beta_{1}S(s)Y(s) - (\mu + d + \epsilon)B(s))ds + \int_{t_{n}}^{t_{n,i}} (\beta_{1}S(s)Y(s) - (\mu + d + \epsilon)B(s))ds, H(t_{n,i}) = H(0) + \int_{0}^{t_{n}} (\beta_{2}S(s)H(s) + \epsilon B(s) - (\mu + \alpha + \gamma)H(s))ds + \int_{t_{n}}^{t_{n,i}} (\beta_{2}S(s)H(s) + \epsilon B(s) - (\mu + \alpha + \gamma)H(s))ds,$$
(11)  
$$R(t_{n,i}) = R(0) + \int_{0}^{t_{n}} (\gamma H(s) - \mu R(s))ds + \int_{t_{n}}^{t_{n,i}} (\gamma H(s) - \mu R(s))ds, n = 0, 1, \dots, N - 1, i = 1, 2, 3.$$

Assume that  $X_{n,i}, Y_{n,i}, \ldots, R_{n,i}$  are approximation for exact solutions X(t),  $Y(t), \ldots, R(t)$  in the point  $t_{n,i}$ . Similar to the previous section, we can approximate the integrals in the SIVE (11). Use two points Gauss-Legendre for integration on the interval  $[0, t_n]$ . Thus

$$\begin{split} &\int_{0}^{t_{n}} (b+\omega Y(s))X(s)ds \approx \frac{h}{2}\sum_{j=0}^{n-1} \left[ (b+\omega Y_{j,1})X_{j,1} + (b+\omega Y_{j,2})X_{j,2} \right] =:A_{1}, \\ &\int_{0}^{t_{n}} (\omega X(s) - b - m)Y(s)ds \\ &\approx \frac{h}{2}\sum_{j=0}^{n-1} \left[ (\omega X_{j,1} - b - m)Y_{j,1} + (\omega X_{j,2} - b - m)Y_{j,2} \right] =:A_{2}, \\ &\vdots \\ &\int_{0}^{t_{n}} (\gamma H(s) - \mu R(s))ds \approx \frac{h}{2}\sum_{j=0}^{n-1} \left[ \gamma H_{j,1} - \mu R_{j,1} + \gamma H_{j,2} - \mu R_{j,2} \right] =:A_{6}. \end{split}$$

Continuing the same process for other integrals leads to the system of algebraic equations

$$\begin{aligned} X_{n,1} = X_0 + \eta t_{n,1} - A_1 - \frac{hc_1}{2} \left[ (b + \omega \mathcal{P}_2(t_n + \frac{2 - \sqrt{3}}{6}h)) \mathcal{P}_1(t_n + \frac{2 - \sqrt{3}}{6}h) \\ + (b + \omega \mathcal{P}_2(t_n + \frac{h}{6})) \mathcal{P}_1(t_n + \frac{h}{6}) \right], \end{aligned}$$

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$$\begin{split} X_{n,2} = & X_0 + \eta t_{n,2} - A_1 \\ & - \frac{hc_2}{2} \left[ (b + \omega \mathcal{P}_2(t_n + \frac{2 + \sqrt{3}}{6}h))\mathcal{P}_1(t_n + \frac{2 + \sqrt{3}}{6}h) \\ & + (b + \omega \mathcal{P}_2(t_n + \frac{h}{6}))\mathcal{P}_1(t_n + \frac{h}{6}) \right], \\ X_{n,3} = & X_0 + \eta t_{n,3} - A_1 \\ & - \frac{h}{2} \left[ (b + \omega Y_{n,1})X_{n,1} + (b + \omega Y_{n,2})X_{n,2} \right], \\ Y_{n,1} = & Y_0 + A_2 \\ & + \frac{hc_1}{2} \left[ (\omega \mathcal{P}_1(t_n + \frac{2 - \sqrt{3}}{6}h) - b - m)\mathcal{P}_2(t_n + \frac{2 - \sqrt{3}}{6}h) \\ & + (\omega \mathcal{P}_1(t_n + \frac{h}{6}) - b - m)\mathcal{P}_1(t_n + \frac{h}{6}) \right], \\ Y_{n,2} = & Y_0 + A_2 \\ & + \frac{hc_2}{2} \left[ (\omega \mathcal{P}_1(t_n + \frac{2 + \sqrt{3}}{6}h) - b - m)\mathcal{P}_2(t_n + \frac{2 + \sqrt{3}}{6}h) \\ & + (\omega \mathcal{P}_1(t_n + \frac{h}{6}) - b - m)\mathcal{P}_1(t_n + \frac{h}{6}) \right], \\ Y_{n,3} = & Y_0 + A_2 \\ & - \frac{h}{2} \left[ (\omega X_{n,1} - b - m)Y_{n,1} + (\omega X_{n,2})Y_{n,2} \right], \\ & \vdots \\ R_{n,1} = & R_0 + A_6 \\ & + \frac{hc_1}{2} \left[ \gamma \mathcal{P}_5(t_n + \frac{2 - \sqrt{3}}{6}h) - \mu \mathcal{P}_6(t_n + \frac{2 - \sqrt{3}}{6}h) \\ & + \gamma \mathcal{P}_5(t_n + \frac{h}{6}) - \mu \mathcal{P}_6(t_n + \frac{4}{6}) \right], \\ R_{n,2} = & R_0 + A_6 \\ & + \frac{hc_2}{2} \left[ (\gamma \mathcal{P}_5(t_n + \frac{2 + \sqrt{3}}{6}h) - \mu \mathcal{P}_6(t_n + \frac{2 + \sqrt{3}}{6}h) \\ & + \gamma \mathcal{P}_5(t_n + \frac{h}{6}) - \mu \mathcal{P}_6(t_n + \frac{4}{6}h) \right], \\ R_{n,2} = & R_0 + A_6 \\ & + \frac{hc_2}{2} \left[ (\gamma \mathcal{P}_5(t_n + \frac{2 + \sqrt{3}}{6}h) - \mu \mathcal{P}_6(t_n + \frac{2 + \sqrt{3}}{6}h) \\ & + \lambda \right] \end{split}$$

$$+\gamma \mathcal{P}_5(t_n+\frac{n}{6})-\mu \mathcal{P}_6(t_n+\frac{n}{6})\right],$$

$$R_{n,3} = R_0 + A_6$$
  
-  $\frac{h}{2} [\gamma H_{n,1} - \mu R_{n,1} + \gamma H_{n,2} - \mu R_{n,2}], \qquad n = 0, 1, \dots, N-1,$ 

where

$$X(t_n + hx) \approx \mathcal{P}_1(t_n + hx) = \sum_{j=0}^3 L_j(t_n + hx)X_{n,j},$$
$$Y(t_n + hx) \approx \mathcal{P}_2(t_n + hx) = \sum_{j=0}^3 L_j(t_n + hx)Y_{n,j},$$
$$\vdots$$
$$R(t_n + hx) \approx \mathcal{P}_6(t_n + hx) = \sum_{j=0}^3 L_j(t_n + hx)R_{n,j},$$

for the Lagrange polynomial  $L_j(t_n + hx) = \prod_{\substack{m=0 \ m \neq j}}^3 \frac{x - c_m}{c_j - c_m}$  and  $x = \frac{2 \pm \sqrt{3}}{6}$  or

 $x = \frac{1}{6}$ .

In each step (n = 0, 1, ..., N - 1), three values of unknowns functions can be obtained by solving this system.

## 6 Numerical results and discussion

In this section, we present some numerical results to investigate the spread of the avian influenza. The initial value of system (10) is fixed at X(0) = 10, Y(0) = 2, S(0) = 100, B(0) = 0, H(0) = 0, and R(0) = 0. These amounts are chosen from the region  $\Omega := \{(X, Y, S, B, H, R) : X > 0, Y > 0, S > 0, B = 0, H = 0, R = 0\}$ , which denotes that there do not exist the infected humans with the avian influenza and mutant the avian influenza.

Similar to [6], the parameters are fixed at b = 5, m = 5,  $\lambda = 3$ ,  $\mu = 0.015$ ,  $\beta_1 = 0.2$ ,  $\epsilon = 10^{-3}$ , d = 1,  $\alpha = 0.06$ , and  $\gamma = 0.01$ . We will provide numerical results of infected birds (Y) with the avian influenza, infected humans (B) with the avian influenza, and infected humans (H) with mutant the avian influenza by choosing different constants  $\eta$ ,  $\omega$ , and  $\beta_2$ .

The numerical experiments are carried out in Maple, and nonlinear systems arising from the nonlinear integral equations are solved by Maple routine fsolve.

**Example 1.** In system (10), let  $\eta = 26.5$ ,  $\omega = 2$  and  $\beta_2 = 0.003$ . Then

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$$r_0 = \frac{\eta \omega}{b(b+m)} = 1.06, \qquad R_0 = \frac{\beta_2 \lambda}{\mu(\mu + \alpha + \gamma)} \approx 7.1.$$

Figures 1 and 2:(a) describe the pandemic effect on the birds and the human world. Figure 1:(a) describes an endemic in the infected birds just after the occurrence of the avian influenza. According to the reported global analysis from [6], Figure 1:(b) shows an initially pandemic of the avian influenza and afterward pandemic level would be decreased, and Figure 2:(a) interprets that the infected humans with mutant the avian influenza outbreak and eventually keep the relatively high level of the size. It suggests that the mutant the avian influenza pandemic will occur if we do not take efficient measures to control the spread of the avian influenza. Moreover, CPU times of the computations are shown in the figures.



Figure 1: (a) The bird rate infected with avian, T = 10, M = 100, CPU time=19.5s. (b) The human rate infected with the avian influenza, T = 100, M = 1000, CPU time=408s. $r_0 = 1.06, R_0 \approx 7.1.$ 

**Example 2.** The parameters are the same as the previous example except for  $\beta_2 = 0.0015$  (the transmission rate of mutant the avian influenza is reduced by half). Therefore the basic reproduction number for the avian influenza in the bird and human world, respectively, is equal to  $r_0 = \frac{\eta \omega}{b(b+m)} = 1.06$ ,  $R_0 = \frac{\beta_2 \lambda}{\mu(\mu + \alpha + \gamma)} \approx 3.5$ .

Figures 2:(b) and 3:(a), respectively, show the endemic process in the bird world after the morbidity of the avian influenza and the occurrence of the pandemic of the avian influenza in the human world. Figure 3:(b) shows the human rate infected with mutant the avian influenza. Since  $R_0$  is relatively small, we do not have mutant the avian influenza pandemic and in this case, we have only the avian influenza pandemic.



Figure 2: (a) The rate infected with mutant the avian influenza, T = 100, M = 1000, CPU time=408s,  $r_0 = 1.06, R_0 \approx 7.1$ . (b) The bird rate infected with the avian influenza, T = 10, M = 100, CPU time=19.3s,  $r_0 = 1.06, R_0 \approx 3.5$ .

**Example 3.** Let  $\eta = 30$  and  $\omega = 1.5$ ; then  $r_0 = 0.9$  and  $R_0 \approx 7.1$ .

The numerical results for this example are shown in Figures 4 and 5. In these figures, there are two pandemic for the avian influenza and mutant the avian influenza even, when all the infected birds and humans with the avian influenza were extinct.



Figure 3: (a) The human rate infected with the avian influenza, (b) The rate infected with mutant the avian influenza.  $T = 100, M = 1000, \text{ CPU time}=398s. r_0 = 1.06, R_0 \approx 3.5.$ 



Figure 4: (a) The bird rate infected with the avian influenza, T = 10, M = 100, CPU time=18.2s. (b) The human rate infected with the avian influenza, T = 100, M = 1000, CPU time=409s.  $r_0 = 0.9, R_0 \approx 7.1$ .

From these numerical results similar to [6], we conclude the following result:

- Elimination policy of the infected birds is not necessarily useful, because the speed of spread of disease in the bird world is fast and their lifetime is shorter than humans.
- For  $r_0 < 1$ , the infected humans extinct, but there are some infected humans for  $r_0 > 1$  (see Figures 1:(a), 3:(a), 4:(b)).
- If  $R_0$  is not large enough, then the outbreak of mutant influenza will not occur (see Figures 2:(a), 3:(b), 5).

The numerical results for Examples 1–3 are comparable with the fourth-order Runge–Kutta method [6] in the whole intervals. Moreover, the presented method, in contrast to Runge–Kutta methods, did not need to computation a lot of derivations, and the computation time for this method is short. Of course, we can increase the convergence order of the method. Also, numerical results are obtained for each time interval that is one of the other advantages of the introduced method.



Figure 5: The rate infected with mutant the avian influenza, T = 100, M = 1000, CPU time=409s,  $r_0 = 0.9, R_0 \approx 7.1$ .

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