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Multistage Modified Sinc Method for Solving Nonlinear Dynamical Systems

H. Pourbashash[a,*] and H. Kheiri[b]

[a] *Department of Mathematics, University of Garmsar, Iran,*
[b] *Faculty of Mathematical Sciences, University of Tabriz, Iran.*

Abstract The sinc method is known as an efficient numerical method for solving ordinary or partial differential equations but the system of differential equations has not been solved by this method which is the focus of this paper. We introduce a modified version of sinc method namely multistage modified sinc method(MMSM) for solving these systems. We illustrate that the proposed method is able to solve non-simple system while Runge-kutta method(RKM) has difficultly with these systems. It is shown that the MMSM has the advantage of giving an analytical form of the solution within each time interval which is not possible in purely numerical techniques like RKM. Moreover, Due to the great attention to mathematical models in disease, the detailed stability analysis and numerical experiments are given on the standard within-host virus infections model.

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1. Introduction

Sinc methods for the numerical solution of ordinary and partial differential equations have been extensively studied and found to be a very effective technique, particularly for problems with singular solutions and those on unbounded domains that has been developed by Frank Stenger, the pioneer of this field, and his colleagues [18]. Sinc methods have many applications in scientific and engineering applications including heat transfer [10], population growth [1], fluid mechanics[20], inverse problems [15] and medical imaging [16].

*Corresponding author. Email: h.pourbashash@ugsr.ir.

However, the sinc method(SM) has some drawbacks. By using the SM, we obtain a closed solution. This solution does not exhibit the real behaviours of the problem but gives a good approx- imation to the true solution in a very small region. Therefore, in order to accelerate the rate of convergence and improve the accuracy of the calcula- tions, it is necessary to divide the entire domain H into n subdomains. The main advantage of domain split process is that only a few terms are required to get the solution in a small time interval H_i. Therefore, the system of differential equations can then be solved in each subdomain. In the MMSM, the obtained solution in the end of interval H_i uses as initial values for interval H_{i+1}. Thus proposed method does not have the sinc methods drawbacks.

Mathematical modeling of disease are one of the efficient methods for understanding the dynamics of disease. these models are often a system of nonlinear ordinary differential equations. Testing specific hypotheses based on clinical data is often difficult since samples cannot always be taken too frequently from patients, or because detection techniques of the virus may not be accurate. This justifies the central role played by mathematical models in this area of research.

In this paper, we will revisit the standard model of within-host virus infections [12, 14] which encompasses several important infections such as HIV [13], hepatitis B [5] and C, influenza. we will introduce a new lyapunov function for proving global stability of the standard model and it will be simulated with modified sinc method and Runge-Kutta method.
Our goal is solving the nonlinear system of

$$\begin{cases} \dot{X}_1 = f_1(X_1, ..., X_N), \\ \vdots \\ \dot{X}_N = f_N(X_1, ..., X_N), \end{cases} \tag{1}$$

where $X_1(0) = X_{10}, ..., X_N(0) = X_{N0}$ over $[0, \alpha]$ with sinc method.

2. The Multistage Modified Sinc Method

Let $\mathbb{C}$ denote the set of all complex numbers and for all $z \in \mathbb{C}$ define the sinc cardinal or sinc function by

$$sinc(z) = \begin{cases} \frac{\sin(\pi z)}{\pi z}, & z \neq 0, \\ 1, & z = 0. \end{cases}$$

This function is translated with evenly spaced nodes are given as

$$S(k, h)(z) = sinc(\frac{z - kh}{h}), \ k = 0, \pm 1, \pm 2, \ldots, h > 0.$$

If $f(z)$ is analytic on a strip domain

$$|Imz| < d, \tag{2}$$

in the z-plane and $|f(z)| \to 0$ as $z \to \pm\infty$ then, the series

$$\mathcal{C}(f, h) = \sum_{k=-\infty}^{\infty} f(kh) sinc(\frac{z - kh}{h}), \tag{3}$$

converges, we call it whittaker cardinal expansion.
From [17], as $h \to 0$ we can write

$$f(z) = \mathcal{C}(f,h) + E_{sinc}, \qquad E_{sinc}(h) = O\left(\exp\left(-\frac{\pi d}{h}\right)\right),$$

where d is half width of strip domain (2).

For problems on a subinterval, Γ, of the real line we employ map ϕ for which $\phi(\Gamma) = \mathbb{R}$ Let ϕ denote a smooth one-to-one transformation of an arc Γ, with end-points a and b onto R, such that $\phi(a) = -\infty$ and $\phi(b) = \infty$. Let $\psi = \phi^{-1}$ denote the inverse map, so that

$$\Gamma = \{z \in \mathbb{C} : z = \psi(u), u \in R\}.$$

Given ϕ, ψ and a positive number h, define the sinc points z_k by

$$z_k = z_k(h) = \psi(kh), k = 0, \pm 1, \pm 2, ...$$

and a function ρ, by

$$\rho(z) = e^{\phi(z)}.$$

Observe that $\rho(z)$ increases from 0 to ∞ as z traverses Γ from a to b.
Corresponding to positive numbers α, β and d, let $L_{\alpha,\beta,d}(\phi)$ denote the family of all functions F defined on Γ for which

$$F(z) = \begin{cases} O(\rho(z)^{\alpha}) & z \to a, \\ O(\rho(z)^{-\beta}) & z \to b, \end{cases}$$

and such that the Fourier transform $\{Fo\phi^{-1}\}^{\tilde{}}$ satisfies the relation

$$\{Fo\phi^{-1}\}^{\tilde{}}(\varsigma) = O(e^{-d|\varsigma|}),$$

for all $\varsigma \in R$.
In many of applications of the sinc method transformation

$$\phi(z) = log\left(\frac{z-a}{b-z}\right), \tag{4}$$

has been used. The map ϕ carries the eye-shaped region

$$D_E = \left\{z = x + iy : \left|arg\left(\frac{z-a}{b-z}\right)\right| < d < \frac{\pi}{2}\right\},$$

on to

$$D_d = \{\xi = \xi + i\eta : |\eta| < d < \pi/2\}.$$

Define h by

$$h = \frac{2}{\sqrt{N}}.$$

The h is the mesh size in D_d for the uniform grids kh, $-\infty < k < \infty$. In real numbers the base functions on (a, b) are given by

$$S(j,h)o\phi(x) = sinc\left(\frac{\phi(x) - jh}{h}\right).$$

The sinc grid points $z \in (a, b)$ in D_E will be denoted by x because they are real. The inverse images of the equispaced grids (4) are

$$x = \phi^{-1}(t) = \psi(t) = \frac{a + be^t}{1 + e^t}.$$

For given a positive integers M and N, let D and V denote linear operators acting on functions u defined on Γ given by

$$Du = diag[u(x_{-M}), ..., u(x_N)], \tag{5}$$

$$Vu = (u(x_{-M}), ..., u(x_N))^{tr}, \tag{6}$$

where $x_j = \phi^{-1}(jh)$ denote the sinc points. Set

$$\gamma_j = S(j,h)o\phi,\ \ j = -M, ..., N,$$

$$\omega_j = \gamma_j,\ \ j = -M+1, ..., N-1,$$

$$\omega_{-M} = \frac{1}{1+\rho} - \sum_{j=-M+1}^{N} \frac{1}{1+e^{jh}}\gamma_j,$$

$$\omega_N = \frac{\rho}{1+\rho} - \sum_{j=-M}^{N-1} \frac{e^{jh}}{1+e^{jh}}\gamma_j,$$

$$\epsilon_N = N^{1/2}e^{-(\pi d\beta N)^{1/2}}.$$

The ω_j are the basis functions thus we define

$$w = (\omega_{-M}, ..., \omega_N).$$

For given f, we can now form the sinc approximation,

$$f(x) \simeq \sum_{k=-M}^{N} f(x_k)\omega_k(x),$$

or in terms of the notation defined above,

$$f \simeq wVf.$$

If define

$$\sigma_k = \int_0^k sinc(x)dx,\ k \in Z$$

$$e_k = \frac{1}{2} + \sigma_k,$$

and we define an $m \times m$ matrix $I^{(-1)} = [e_{i-j}]$, with e_{i-j} denoting the $(i,j)^{th}$ element of $I^{(-1)}$.
We define the operators $\zeta^+, \zeta^-, \zeta_m^+, \zeta_m^-$ and $m \times m$ matrices A^+ and A^-:

$$(\zeta^+ f)(x) = \int_a^x f(t)dt,$$
$$(\zeta^- f)(x) = \int_x^b f(t)dt,$$
$$(\zeta_m^+ f)(x) = w(x)A^+ Vf, \quad A^+ = hI^{(-1)}D(1/\phi'),$$
$$(\zeta_m^- f)(x) = w(x)A^- Vf, A^- = h(I^{(-1)})^T D(1/\phi'),$$

where $D(.)$ and $V(.)$ are defined as in (6) and (6). Now from [17] we can write

THEOREM 2.1 *If $f/\phi' \in L_{\alpha,\beta,d}(\phi)$, then, for all $N > 1$,*

$$\|\zeta^+ f - \zeta_m^+ f\| = O(\epsilon_N),$$
$$\|\zeta^- f - \zeta_m^- f\| = O(\epsilon_N).$$

Now we want to solve nonlinear system (1), thus we have the system

$$\begin{pmatrix} \dot{X}_1 \\ \vdots \\ \dot{X}_N \end{pmatrix} = \begin{pmatrix} f_1(X_1, ..., X_N) \\ \vdots \\ f_N(X_1, ..., X_N), \end{pmatrix}$$

which is to be solved over $[0, \alpha]$ subject to our initial conditions. Integrating each of equations over $[0, \alpha]$ and collocating, at points x_j, we get the system of equations

$$\begin{pmatrix} X_1 \\ \vdots \\ X_N \end{pmatrix} = \begin{pmatrix} X_1(0) \\ \vdots \\ X_N(0) \end{pmatrix} + \begin{pmatrix} A^+ & & \\ & \ddots & \\ & & A^+ \end{pmatrix} \begin{pmatrix} f_1(X_1, ..., X_N) \\ \vdots \\ f_N(X_1, ..., X_N), \end{pmatrix} \tag{7}$$

where $X_1, ..., X_N$, the $f_1, ..., f_N$ and the initial value vectors are column vectors of size $M + N + 1$ (with e.g.

$$X_1(0) = (X_1(0), ..., X_1(0))^{tr}$$

this being a vector of size $M + N + 1$). We can then try to solve our system via use of successive approximation, starting with

$$(X_1, ..., X_N) = (X_1(0), ..., X_N(0)).$$

In solving problems some times the successive approximation dose not converge. As mentioned in introduction section for improving the accuracy of the calculations we use MMSM to solve proposed system. for fixing the problem we can pick a positive $\beta < \alpha$ and repeat the above process. We will then eventually get a solution over $(0, \beta)$ for some sufficiently small, (because we get a contraction operator for β

sufficiently small). We can then repeat the process to get a solution over $(\beta, 2\beta)$, starting by taking the initial value of the system at β to be

$$(X_1(x_N), ..., X_N(x_N)),$$

etc.

3. The Standard Model of Within-Host Virus Infections

The standard mathematical model considered here is a system of three nonlinear ODEs. Our model [12, 14] is

$$\begin{cases} \dot{T} = f(T) - kVT, \\ \dot{T}^* = kVT - \beta T^*, \\ \dot{V} = N\beta T^* - \gamma V, \end{cases} \tag{8}$$

where T, T^* and V denote the concentrations of uninfected (healthy), infected host cells and free virus particles, respectively. Parameters k, β, N and γ are all positive constants. k is the contact rate between uninfected cells and viruses. The parameters β and γ represent the death rate of infected cells and virus particles, respectively. N is the average number of virus particles produced by an infected cell during its lifetime.
The growth rate of the uninfected cell population is modeled by the smooth function $f : \mathbb{R}_+ \to \mathbb{R}$, which is assumed to satisfy the following:

$$\exists T_0 > 0 : f(T)(T - T_0) < 0, \ \forall T \neq T_0, \quad \text{and} \quad f'(T) < 0 \ \forall T \in [0, T_0]. \tag{9}$$

The continuity of f implies that $f(T_0) = 0$, and hence $E_0 = (T_0, 0, 0)$ is an equilibrium point of system (8). Biologically, E_0 represents the disease-free equilibrium. An additional equilibrium point exists provided that the following quantities are positive,

$$\bar{T} = \frac{\gamma}{kN}, \qquad \bar{T}^* = \frac{f(\bar{T})}{\beta}, \qquad \bar{V} = \frac{f(\bar{T})}{k\bar{T}}. \tag{10}$$

Therefore, a positive equilibrium exists if and only if $f(\bar{T}) = f(\frac{\gamma}{kN}) > 0$ or by (9), if $\bar{T} = \frac{\gamma}{kN} < T_0$. Let

$$R_0 = \frac{T_0(kN)}{\gamma}, \tag{11}$$

denote the basic reproduction number. Existence of a positive equilibrium is equivalent to $R_0 > 1$. Thus we obtain our first result:

LEMMA 3.1 *If $R_0 \leqslant 1$ the equilibrium E_0 is the only equilibrium of (8), and if $R_0 > 1$ then E_0 and $E = (\bar{T}, \bar{T}^*, \bar{V})$ are two equilibrium points of system (8).*

From [3], we have

THEOREM 3.2 *If $R_0 \leqslant 1$ then the infection free equilibrium E_0 attracts all solutions in $\mathbb{R}^3_+$.*

THEOREM 3.3 *The equilibrium E is globally asymptotically stable for system (8).*

Proof Recall that the following hold:

$$k\bar{V}\bar{T} = \beta\bar{T}^*, \tag{12}$$
$$N\beta\bar{T}^* = \gamma\bar{V}. \tag{13}$$

We can write:

$$\beta = \frac{k\bar{V}\bar{T}}{\bar{T}^*}, \tag{14}$$
$$N\beta k\bar{T} = \gamma\beta. \tag{15}$$

Consider the following function on $\text{int}(\mathbb{R}^3_+)$:

$$W = \int_{\bar{T}}^{T} \left(1 - \frac{\bar{T}}{\tau}\right) d\tau + \int_{\bar{T}^*}^{T^*} \left(1 - \frac{\bar{T}^*}{\tau}\right) d\tau + \frac{k\bar{T}}{\gamma} \int_{\bar{V}}^{V} \left(1 - \frac{\bar{V}}{\tau}\right) d\tau.$$

So,

$$\frac{dW}{dt} = \left(1 - \frac{\bar{T}}{T}\right)\frac{dT}{dt} + \left(1 - \frac{\bar{T}^*}{T^*}\right)\frac{dT^*}{dt} + \frac{k\bar{T}}{\gamma}\left(1 - \frac{\bar{V}}{V}\right)\frac{dV}{dt} := A_1 + A_2 + A_3.$$

The first term, A_1, in $\dot{W}$ can be rewritten as

$$\begin{aligned} A_1 &= \left(1 - \frac{\bar{T}}{T}\right)(f(T) - kVT) \\ &= \left(1 - \frac{\bar{T}}{T}\right)(f(T) - f(\bar{T})) + \left(1 - \frac{\bar{T}}{T}\right) f(\bar{T}) - kVT + kV\bar{T} \\ &= \left(1 - \frac{\bar{T}}{T}\right)(f(T) - f(\bar{T})) + k\bar{V}\bar{T} - k\bar{V}\frac{\bar{T}^2}{T} - kVT + kV\bar{T}. \end{aligned}$$

Due to (12), the second term, A_2, in $\dot{W}$ takes the form

$$A_2 = \left(1 - \frac{\bar{T}^*}{T^*}\right)(kVT - \beta T^*) =$$
$$kVT - \beta T^* - kVT\frac{\bar{T}^*}{T^*} + k\bar{V}\bar{T}.$$

The third term, A_3, in $\dot{W}$ is

$$A_3 = \frac{k\bar{T}}{\gamma}\left(1 - \frac{\bar{V}}{V}\right)(N\beta T^* - \gamma V) =$$
$$\frac{kN\beta}{\gamma}\bar{T}T^* - k\bar{T}V - \frac{kN\beta}{\gamma}\bar{T}T^*\frac{\bar{V}}{V} + k\bar{T}\bar{V}.$$

Using (14) and (15), A_3 can be written as

$$A_3 = \beta T^* - k\bar{T}V - \beta T^* \frac{\bar{V}}{V} + k\bar{V}\bar{T} =$$

$$\beta T^* - k\bar{T}V - k\bar{V}\bar{T}\frac{T^*\bar{V}}{\bar{T}^*V} + k\bar{V}\bar{T}.$$

Combining $A_1 + A_2 + A_3$, we obtain

$$\dot{W} = \left(1 - \frac{\bar{T}}{T}\right)(f(T) - f(\bar{T})) + k_1\bar{V}\bar{T}\left(3 - \frac{\bar{T}}{T} - \frac{VT\bar{T}^*}{\bar{V}\bar{T}T^*} - \frac{T^*\bar{V}}{\bar{T}^*V}\right).$$

The first term is always non-positive due to our assumptions on f. The second term is non-positive as well due to the arithmetic-geometric mean (AM-GM) inequality. Hence, $\dot{W} \leqslant 0$ in $\text{int}(\mathbb{R}^3_+)$, and $\dot{W}$ equals zero if and only if $T = \bar{T}$ and $\bar{T}^*V = T^*\bar{V}$. Since all solutions of (8) in $\text{int}(\mathbb{R}^3_+)$ are bounded [3], the LaSalle's invariance principle implies that any ω-limit set in $\text{int}(\mathbb{R}^3_+)$ is a subset of the largest invariant set in

$$M = \{(T, T^*, V) \in \text{int}(\mathbb{R}^3_+) \mid T = \bar{T},\ \bar{T}^*V = T^*\bar{V}\}.$$

Any such invariant set in M must satisfy $\dot{T} = 0$, hence

$$0 = f(\bar{T}) - \bar{T}\frac{V}{\bar{V}}\left(k_1\bar{V} + k_2\bar{T}^*\right) = f(\bar{T})\left(1 - \frac{V}{\bar{V}}\right),$$

which implies that $V = \bar{V}$ and $T^* = \bar{T}^*$. Therefore, the largest invariant set in M is the singleton $\{E\}$, hence it attracts all solutions in $\text{int}(\mathbb{R}^3_+)$. ■

4. Numerical Examples

This section provide some examples to show the effectiveness the modified sinc method numerically.

Example 1: In system (8) we assume that: $f(T) = a - bT$ with $a = 10^4 ml^{-1}day^{-1}$ and $b = 0.01day^{-1}$ (wich implies that $T_0 = 10^6 ml^{-1}$), $k = 2.4 \times 10^{-8} mlday^{-1}, N = 3000, \gamma = 23day^{-1}, \beta = 1day^{-1}$, $T(0) = 10^6, T^*(0) = 0, V(0) = 0$(The parameters used are taken from [**?**]).

We use the MMSM first ten steps with length 1/3 and then we use 1/4. Figures 1 and 2 show that theMMSM with $M = N = 50$ and RKM have the same results. In this example $R_0 = 3.13 > 1$ thus E attracts all solutions.

Example 2: Consider

$$\begin{cases} \dot{T} = T^*V + T^*, \\ \dot{T}^* = 2\sqrt{T}^*, \\ \dot{V} = 3T^*, \end{cases} \tag{16}$$

with $T(0) = 0, T^*(0) = 0, V(0) = 1$. The exact solution is

$$\begin{cases} T = \frac{t^6}{6} + \frac{2}{3}t^3, \\ T^* = t^2, \\ V = t^3 + 1. \end{cases}$$

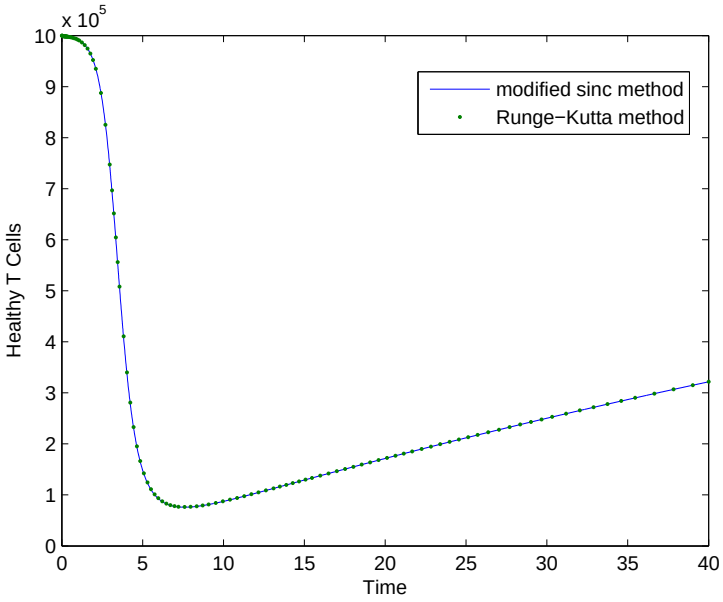

Figure 1. Healthy T-Cells graphs in example 1

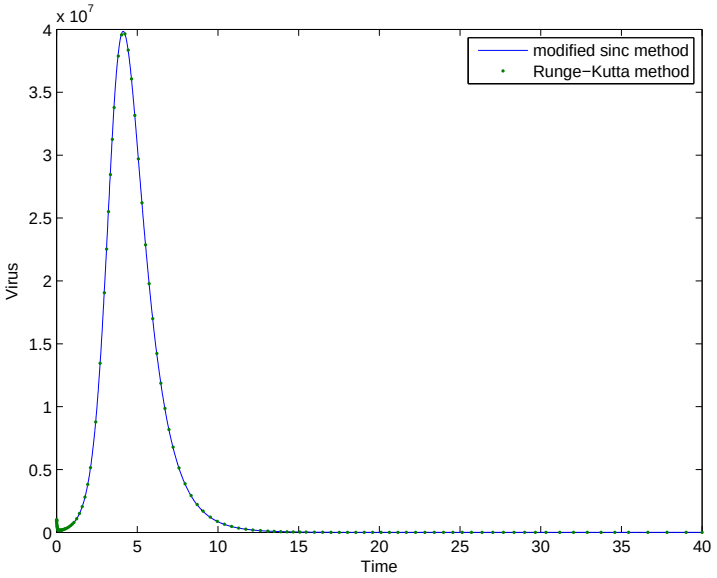

Figure 2. Virus graphs in example 1

This system is a non-simple system. The obtained results show that the MMSM is so better than the RKM for solving non-simple systems. Table 1 shows the errors of the MMSM for solving system (16) (M=N=150). We have first solved the system in [0,1] and used solution values on point 1 as an initial values for second interval and so on. Table 2 shows the errors of the RKM. These results highlight the efficiency of proposed method in comparison with the Runge-Kutta method.

Table 1
solving system (16) with MMSM

t	T Error	T* Error	V Error
0.106891754162263	6.25 * 10^(-10)	5.84 * 10^(-9)	9.37 * 10^(-10)
0.342269403147559	6.53 * 10^(-9)	1.87 * 10^(-8)	9.61 * 10^(-9)
0.693492155829498	3.06 * 10^(-8)	3.79 * 10^(-8)	3.94 * 10^(-8)
1.000000000023015	8.19 * 10^(-8)	5.46 * 10^(-8)	8.19 * 10^(-8)
1.500000000000000	3.30 * 10^(-7)	8.19 * 10^(-8)	1.84 * 10^(-7)
1.957003445514055	9.93 * 10^(-7)	1.06 * 10^(-7)	3.13 * 10^(-7)
2.500000000000000	3.00 * 10^(-6)	1.36 * 10^(-7)	5.11 * 10^(-7)
2.836579259470979	5.44 * 10^(-6)	1.54 * 10^(-7)	6.58 * 10^(-7)
3.620082391336317	1.76 * 10^(-5)	1.97 * 10^(-7)	1.07 * 10^(-6)
4.941369924115898	8.13 * 10^(-5)	2.68 * 10^(-7)	1.99 * 10^(-6)

Table 2
solving system (16) with RKM

t	T Error	T* Error	V Error
	1.0e+2*		
0.106891754162263	0.000008144678341	0.011425847107885	0.001221328840152
0.342269403147559	0.000182327200162	0.061616986880817	0.027011527725630
0.693492155829498	0.000986398793172	0.136011634999748	0.131123247147711
1.000000000023015	0.002702827471232	0.201128458244837	0.286120402047258
1.500000000000000	0.011158460878702	0.307337485146835	0.667472221287408
1.957003445514055	0.034267673988071	0.404410491643513	1.155379122170604
2.500000000000000	0.105938086448733	0.519749256914904	1.908102189135498
2.836579259470979	0.194029411806061	0.591242649667933	2.469007491337539
3.620082391336317	0.640489035099812	0.757665488742674	4.054319567845326
4.941369924115898	3.014170771060235	1.038572484952894	7.613981404402580

5. Conclusions

In this paper, We introduced multistage modified sinc method for solving system of differential equations. In examples we illustrate that the MMSM method is able to solve non-simple system while RKM has difficultly with these systems. We revisited the standard model of within-host virus infections and introduced a new lyapunov function for proving global stability of the standard model. The illustrated example shows the global stability of the endemic equilibrium with MMSM and RKM. In this example the MMSM has the same behaver as RKM.

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