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Numerical investigation of differential biological models via Gaussian RBF collocation method with genetic strategy

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In this paper, we use radial basis function collocation method for solving the system of differential equations in the area of biology. One of the challenges in RBF method is picking out an optimal value for shape parameter in Radial basis function to achieve the best result of the method because there are not any available analytical approaches for obtaining optimal shape parameter. For this reason, we design a genetic algorithm to detect a close optimal shape parameter. The population convergence figures, the residuals of the equations and the examination of the ASN2R and ARE measures all show the accurate selection of the shape parameter by the proposed genetic algorithm. Then, the experimental results show that this strategy is efficient in the systems of differential models in biology such as HIV and Influenza. Furthermore, we show that using our pseudo-combination formula for crossover in genetic strategy leads to convergence in the nearly best selection of shape parameter. Copyright © 2022 Shahid Beheshti University.

Keywords: Radial basis function; Genetic algorithm; HIV; Influenza; Shape parameter.

1. Introduction

In the past few years, various mathematical models have been used to investigate biological and clinical problems. Various examples of mathematical models have been presented hitherto, including HIV [59, 60], Influenza [37], Covid-19 [76, 66] and Ebola [10, 3]. In this paper, we will focus specifically on the simulation of HIV and Influenza models using the combination of RBF method and genetic algorithm and we show that this method is very efficient and robust for simulating biological models.

1.1. HIV Infection CD4+T Cells

Acquired Immune Deficiency Syndrome (AIDS), first-time appeared in the continent of America in 1981 [9]. The human immunodeficiency Virus (HIV) in short HIV is the cause of the illness that attacks vital cells such as Dendrite cells, helper lymphocyte particularly CD4+T cells and infects them and gradually, the immune system will be destroyed [14]. This process may take from 6 months to 10 years. The mathematical model of HIV-infected CD4+T cells described by Perelson and Nelson in 1991 [59, 60]. HIV model investigates the concentration of susceptible CD4+T cells infected by the HIV viruses. It is obvious that presenting a mathematical model is an easier study of the behavior of the system and helps the process of detecting or improving disease. Let $\mathbf{T}(t)$ be the concentration of susceptible CD4+T cells, $\mathbf{I}(t)$ be CD4+T cells infected by the HIV virus and $\mathbf{V}(t)$ be free HIV particular in the blood at the time. Thus, the mathematical model of the HIV-infected CD4+T cell on a

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couple system of the ordinary differential equation will be presented as follows:

$$\begin{cases} \frac{d}{dt} \mathbf{T}(t) = s - \alpha \mathbf{T}(t) + r \mathbf{T}(t) \left(1 - \frac{\mathbf{T}(t) + \mathbf{I}(t)}{T_{max}}\right) - k \mathbf{V}(t) \mathbf{T}(t), & \mathbf{T}(0) = T_0, \\ \frac{d}{dt} \mathbf{I}(t) = k \mathbf{V}(t) \mathbf{T}(t) - \beta \mathbf{I}(t), & \mathbf{I}(0) = I_0, \\ \frac{d}{dt} \mathbf{V}(t) = N \beta \mathbf{I}(t) - \gamma \mathbf{V}(t), & \mathbf{V}(0) = V_0, \end{cases} \quad 0 \leq t \leq R \leq \infty \quad (1)$$

where R is a positive constant and other parameters have been shown in Table 1.

Table 1. Parameters in HIV infected CD4+T cells model

α	Natural turnover rates of uninfected T cells
β	Infected T cells
γ	Virus particles
k	Infection rate
s	Rate of constructing T cells
r	Rate of T cells mitoses
N	Virus particle from each infected T cell
T_{max}	Maximum T cell concentration in the body

It is noteworthy that there is no exact solution for HIV model. Ergo, the numerical methods are used to solve it. Table 2 shows some approaches applied to this model.

Table 2. Used technique for solving HIV model

Author(s)	Method	Year
Merdan [45]	Homotopy Perturbation method(HPM)	2007
Alomari et al. [24]	Homotopy Analysis method(HAM)	2011
Merdan et al. [46]	Variational Iteration Method(VIM)	2011
Ongun [50]	Laplace Adomian Decomposition Method(LADM)	2011
Doğun [17]	Multistep Laplace Adomian Decomposition Method(MLADM)	2012
Khan et al. [41]	Iterative Homotopy Perturbation Transform Method(IHPTM)	2012
Yüzbaşı [80]	Bessel Collocation Method(BCM)	2012
Atangana et al. [5]	Homotopy Decomposition Method(HDM)	2014
Chen [11]	Padé-Adomian Decomposition Method(PADM)	2015
Venkatesh et al. [75]	Legendre Wavelets Method(LWM)	2016
Kajani et al. [23]	Müntz-Legendre Method(MLM)	2016
El-Baghdady et al. [18]	Legendre Collocation Method(LCM)	2017
Parand et al. [54]	Shifted Lagrangian Jacobi Method (SLG)	2018
Parand et al. [53]	Quasilinearization-Lagrangian Method (QLM)	2018
Parand et al. [55]	Pseudospectral Legendre Method (PLM)	2018
Parand et al. [58]	Shifted Boubaker Lagrangian Method (SBLM)	2018
Parand et al. [56]	Shifted Chebyshev Polynomial Method (SCP)	2019
Umar et al. [73]	Genetic Algorithm Active Set Method (GA-ASM)	2020
Attaullah et al. [69]	continuous GalerkinPetrov (cGP)	2020
Attaullah et al. [69]	Legendre Wavelets Collocation Method (LWCM)	2020
Oluwaseun et al. [49]	Block Method (BM)	2021
Thirumalai et al. [72]	Spectral Collocation Method (SCM)	2021
Umar et al. [74]	Neuro Swarm Intelligent Computing (NSIC)	2021
Hassani et al. [30]	Generalized Shifted Jacobi Polynomials (GSJP)	2022
Ghosh et al. [25]	New Iterative Method (NIM)	2022

1.2. Influenza

Influenza virus causes a type of disease named *Influenza* or *Flu* that is divided into four classes A, B, C and D [44]. From the perspective of the epidemic, class A is the most significant class. That is because this type is able to merge and rebuild its genes with host gene [4, 77]. The mathematical model of Susceptible-Infected-Removed (SIRC) for displaying the outbreaks of Influenza in population is defined by Kermack and McKendrick [37]. This is a system of the differential equation as follows:

$$\begin{cases} \frac{d}{dt} \mathbf{S}(t) = \mu(1 - \mathbf{S}(t)) - \beta \mathbf{S}(t) \mathbf{I}(t) - \gamma \mathbf{C}(t) & \mathbf{S}(0) = S_0, \\ \frac{d}{dt} \mathbf{I}(t) = \beta \mathbf{S}(t) \mathbf{I}(t) + \sigma \beta \mathbf{C}(t) \mathbf{I}(t) - (\mu + \theta) \mathbf{I}(t), & \mathbf{I}(0) = I_0, \\ \frac{d}{dt} \mathbf{R}(t) = (1 - \sigma) \beta \mathbf{C}(t) \mathbf{I}(t) + \theta \mathbf{I}(t) - (\mu + \delta) \mathbf{R}(t), & \mathbf{R}(0) = R_0, \\ \frac{d}{dt} \mathbf{C}(t) = \delta \mathbf{R}(t) - \beta \mathbf{C}(t) \mathbf{I}(t) - (\mu + \gamma) \mathbf{C}(t) & \mathbf{C}(0) = C_0. \end{cases} \quad (2)$$

where $\mathbf{S}(t)$, $\mathbf{I}(t)$, $\mathbf{R}(t)$ and $\mathbf{C}(t)$ mean ratio susceptible, infections, recovered and cross immune respectively. Other parameters are shown in Table 3. This model studied by Khader et al. [39] using Chebyshev spectral method in 2014. Table 4 shows the

Table 3. Parameters in Flu model

μ	Mortality rate
θ	Improve infection each year
δ	Progression from recovered to cross-immune each year
γ	Progression from recovered to susceptible each yer
σ	Rate of cross-immune into the infective
β	Contact rate

applying methods to SIRC model.

Table 4. Used techniques for solving SIRC model

Author(s)	Method	Year
El-Shahed et al. [19]	Non-standard Finite Difference(NSFDM)	2012
Ibrahim et al. [34]	Modified differential transform method(MDTM)	2013
Zeb et al. [81]	Multi-step generalized differential transform method(MGDTM)	2013
Khader et al. [39]	Chebyshev spectral method(CSM)	2014
Khader et al. [38]	Legendre spectral method(LSM)	2014
González-parra et al. [28]	Grünwald Letnikov method(GLM)	2014
Jaber-Mohammad et al. [48]	Runge-kutta 45 (RK45)	2020
Sabir et al. [63]	Genetic Algorithm Active-Set Method (GA-ASM)	2021
Sabir et al. [64]	Artificial Neural Network (ANN)	2022
Sabir et al. [65]	Morlet wavelet Neural Network (MWNN)	2022

1.3. Meshfree Method

Firstly, the Meshfree methods introduced by Monaghan and Gingold in 1977. They enlarged a Lagrangian method according to Kernel estimate method [26]. A number of meshfree methods such as smoothing particle hydrodynamic (SPH) [70, 12], Element-Free Galerkin (EFG) [42, 8], Reproducing Kernel method (RKM) [1, 7], Meshless local Petrov-Galerkin (MLPG) [61, 6], Comapctly supported radial basis function method(CSRBF) [32, 40], Radial basis function finite difference method(RBFFD) [47, 31], Radial basis function differential quadrature method(RBF-DQ) [52, 51] and Kansa method (KM) [57, 68] are used for solving differential equations (DEs). The appearance of meshfree methods was through the difficulty of the classic methods such as Finite Element method (FEM) [71, 35] and Finite Difference method (FDM) [16, 15] which require a mesh of points for solving problems. In these methods, rising problem dimensions causes increasing complexity (the order of construction of the mesh); furthermore, in meshfree we have no need to make any grid, and scattered points are used instead. RBF method as a meshfree approach utilizes as Trial functions of kind (Global/Compact support) Radial basis functions (RBFs)Table 5 demonstrates the RBF types. The main advantages of RBF method are the simplicity, high accuracy, and capability of being applicable in high dimension problems. In addition to these advantages, there exist two main challenges that all methods based on RBFs are faced with; selecting Shape parameters (SP) and distribution of collocation points. Choosing an inappropriate SP decreases the performance of method or even it will be unusable when the method is ill-conditioned. It seems that amount of optimal Shape parameter (oSP) depends on equation state, dimension and etc. Thus, any comprehensive formula not found hitherto for recognizing optimal SP in RBFs. Instead of choosing a proper SP, Many researchers offered different formulas; however, these formulas are applicable only in some special cases. In [43] SP decomposed to a dimensionless size of support domain (α_s) and a nodal spacing near the point at the center (d_c), where $c = \alpha_s d_c$. Hardy [29] suggested using (inverse) multiquadric formula as follows:

$$c = \frac{1}{0.815\epsilon}$$

Table 5. Some radial basis functions ${}_c\psi$, ($r = \|x - x_i\| = r_i$), $c > 0$

Class	Name of function	Definition
1	Multiquadrics(MQ)	$\sqrt{r^2 + c^2}$
	Inverse Multiquadrics (IMQ)	$\frac{1}{\sqrt{r^2 + c^2}}$
	Gaussian (GA)	$\exp(-c^2 r^2)$
	Inverse Quadrics (IQ)	$\frac{1}{r^2 + c^2}$
	Hyperbolic Secant (sech)	$\text{sech}(c\sqrt{r})$
2	Thin Plate Spline (TPS)	$(-1)^{k+1} r^{2k} \log(r)$
	Conical Spline	r^{2k+1}
3	Wendland _{3,0}	$(1 - r)_+^2$
	Wu _{3,3}	$(1 - r)_+^4 (16 + 29r + 20r^2 + 5r^3)$
	Oscillator _{1,3}	$(1 - r)_+^4 (1 + 4r - 15r^2)$
	Buhman ₁	$12r^4 \log r - 21r^4 + 32r^3 - 12r^2 + 1$
4	Platte _{a,b,c}	$\cos(cr) \exp(\frac{-b}{(1-r^2)^a} + b)$

where $\varepsilon = \frac{1}{N} \sum_{i=1}^N \varepsilon_i$, and ε_i is the distance of the center from its closest neighbor. Rippa [62] used the Predictive residual sum of square (PRESS) algorithm for calculating a proper SP. Leave on-out cross validation (LOOCV) approach [22] and Craven and Wahba [13] which emanated in the statistics literature used for finding optimal SP. Esmaeilbeigi et al. [2, 20] employed the genetic package of MATLAB for solving a number of DEs. The following formula is proposed in [36, 67] to calculate a reasonable SP

$$c_i = \sqrt{c_\alpha^2 \left(\frac{c_\beta}{c_\alpha}\right)^{\frac{i-1}{n-1}}}$$

where n is the number of points and c_α is the smallest and c_β is the biggest selected parameter in the domain of candidate SPs. Similarly, in [67, 79] the SP is obtained by

$$c_i = c_\alpha + (c_\beta - c_\alpha) \Delta_{rand}$$

where Δ_{rand} is a random number in arbitrary domain.

In this paper, we suggested a Meta-heuristic continuous Genetic algorithm (CGA) choose a near optimal SP, based on the average of summation of the residual 2-norm (ASN2R) and the average of summation of the relative error (ARE) for the solution of differential equation systems in Biology sciences.

1.4. Genetic Algorithm

Genetic algorithm (GA) is a search and optimization approach based on the Genetic principles and natural selection. A GA starts with processing a population of candidate solutions (called individuals or chromosomes) with different competencies. During this process (called evolution), GA changes the population and generates some solutions close to optimal competency (maximum benefit or minimum cost). John Holland invented original GA in the early 1970s [33]. He also proposed a theoretical basis for GA according to the Type theory. In the following, David E Goldberg [27] extended GA concept and applied it to encode and solve different problems in miscellaneous fields. GA has many advantages over other optimization methods like:

- Practicable on both discrete and continuous data,
- No need to derivative of objective function (fitness function),
- Usable in multivariate functions,
- High potential for parallelization,
- Calculating a set of appropriate (close to optimal) solutions,
- Expandable on experimental, analytical and numerical data.

The main objective of a meta-heuristic algorithm is finding a close-minimum to global minimum (maximum) solution by escaping from local minimum (maximum) solutions. Universally, GA is classified to DGA (Discrete GA) and CGA (Continuous GA). In this article, we use CGA to find a close to optimal SP (near-optimal Shape parameter) around a specified interval in the RBF method, where ϱ is either ASRN2 or ARE strategies.

2. Methodology

2.1. RBF approximation

Let $\psi : \mathbb{R}^+ \rightarrow \mathbb{R}$ be a continuous function with ${}_c\psi(0) \geq 0$. A radial basis function on \mathbb{R}^d is a function of the form

$${}_c\psi(\|x - x_i\|),$$

where $x, x_i \in \mathbb{R}^d$ and $\|\cdot\|$ denote the Euclidean distance between x and x_i s. By choosing N points $\{x_i\}_{i=1}^N$ in \mathbb{R}^d and by defining

$$s(x) = \sum_{i=1}^N \xi_i \psi(\|x - x_i\|); \quad \xi_i \in \mathbb{R},$$

where $s(x)$ is called a radial basis functions mesh [78, 21]. To approximate one-dimensional function $f(x)$, we can illustrate it with an RBF as

$$f(x) \approx f_n(x) = \sum_{i=1}^N \xi_i \psi_i(x) = {}_c\bar{\Psi}^T(x)\Xi, \tag{3}$$

in which,

$$\begin{aligned} {}_c\psi_i(x) &= \psi(\|x - x_i\|), \\ {}_c\bar{\Psi}^T(x) &= [{}_c\psi_1(x), {}_c\psi_2(x), \dots, {}_c\psi_N(x)], \\ \Xi &= [\xi_1, \xi_2, \dots, \xi_N], \end{aligned}$$

x is the input and ξ_i s are the collection of coefficients to be determined. By selecting N points $(x_j, j = 1, 2, \dots, N)$ in interval:

$$f_j(x) = {}_c\bar{\Psi}^T(x_j)\Xi$$

To sum up the discussion of the coefficients matrix, we define

$$\hat{\mathbf{M}}\Xi = \vec{F}, \tag{4}$$

where

$$\begin{aligned} \vec{F} &= [f_1, f_2, \dots, f_N]^T \\ \hat{\mathbf{M}} &= [{}_c\bar{\Psi}^T(x_1), {}_c\bar{\Psi}^T(x_2), \dots, {}_c\bar{\Psi}^T(x_N)]^T \end{aligned} \tag{5}$$

By solving the system(4), the unknown coefficients Ξ will be attained.

2.2. Solving models by RBF method

Both models are system of first-order differential equations, so we define the solution functions and it's first-order derivatives as follows:

$$U(t) \simeq U_N(t) = \sum_{i=0}^N a_{\#i} \psi_i(t), \tag{6}$$

$$\frac{dU(t)}{dt} \simeq \frac{dU_N(t)}{dt} = \sum_{i=0}^N a_{\#i} \psi'_i(t). \tag{7}$$

where ψ is RBF. In addition, solution function $U(t)$ and unknown coefficient $a_{\#}$ are also defined separately according to the unknown functions of the models as follows

$$T(t) \simeq T_n(t) = \sum_{i=0}^n a_{1i} \psi_i(t), \tag{8}$$

$$I(t) \simeq I_n(t) = \sum_{i=0}^n a_{2i} \psi_i(t), \tag{9}$$

$$V(t) \simeq V_n(t) = \sum_{i=0}^n a_{3i} \psi_i(t), \tag{10}$$

for HIV and

$$S(t) \simeq S_n(t) = \sum_{i=0}^n a_{1i} \psi_i(t), \tag{11}$$

$$I(t) \simeq I_n(t) = \sum_{i=0}^n a_{2i} \psi_i(t), \tag{12}$$

$$R(t) \simeq R_n(t) = \sum_{i=0}^n a_{3i} \psi_i(t), \tag{13}$$

$$C(t) \simeq C_n(t) = \sum_{i=0}^n a_{4i} \psi_i(t), \tag{14}$$

for Influenza model. Similarly, we define it's derivative according to the Eq.(7). By placing the solution functions in the 1 and 2 equations, we form the residual functions for each system of equations as follows.

$$Res_1(t) = \frac{d}{dt}T_n(t) + \alpha T_n(t) - rT_n(t)(1 - \frac{T_n(t)+I_n(t)}{T_{max}}) + kV_n(t)T_n(t) - s, \tag{15}$$

$$Res_2(t) = \frac{d}{dt}I_n(t) - kV_n(t)T_n(t) + \beta I_n(t), \tag{16}$$

$$Res_3(t) = \frac{d}{dt}V_n(t) - \eta\beta I_n(t) + \gamma V_n(t), \tag{17}$$

for HIV and

$$Res_1(t) = \frac{d}{dt}S_n(t) - \mu(1 - S_n(t)) + \beta S_n(t)I_n(t) + \gamma C_n(t), \tag{18}$$

$$Res_2(t) = \frac{d}{dt}I_n(t) - \beta S_n(t)I_n(t) - \sigma\beta C_n(t)I_n(t) + (\mu + \theta)I_n(t), \tag{19}$$

$$Res_3(t) = \frac{d}{dt}R_n(t) - (1 - \sigma)\beta C_n(t)I_n(t) - \theta I_n(t) + (\mu + \delta)R_n(t), \tag{20}$$

$$Res_4(t) = \frac{d}{dt}C_n(t) - \delta R_n(t) + \beta C_n(t)I_n(t) + (\mu + \gamma)C_n(t), \tag{21}$$

for Influenza.

We will simulate the problem in the domain (0, 1], and for this purpose we will choose the n points $t = t_1, \dots, t_n$ within the domain, where we have used equidistant points. By placing the n points in the residual functions and adding the initial conditions (IC#) as follows

$$IC1_{HIV} = T_n(0) - T_0, \tag{22}$$

$$IC2_{HIV} = I_n(0) - I_0, \tag{23}$$

$$IC3_{HIV} = V_n(0) - V_0, \tag{24}$$

$$IC1_{Influenza} = S_n(0) - S_0, \tag{25}$$

$$IC2_{Influenza} = I_n(0) - I_0, \tag{26}$$

$$IC3_{Influenza} = R_n(0) - R_0, \tag{27}$$

$$IC4_{Influenza} = C_n(0) - C_0. \tag{28}$$

We obtain $3(n + 1)$ algebraic nonlinear equations for HIV model , as well as $4(n + 1)$ algebraic nonlinear equations for Influenza model as follows

$$RES_{HIV} = (Res_1(t_1), \dots, Res_1(t_n), Res_2(t_1), \dots, Res_2(t_n), Res_3(t_1), \dots, Res_3(t_n), IC1_{HIV}, IC2_{HIV}, IC3_{HIV})_{3(n+1)}, \tag{29}$$

$$RES_{Influenza} = (Res_1(t_1), \dots, Res_1(t_n), Res_2(t_1), \dots, Res_2(t_n), Res_3(t_1), \dots, Res_3(t_n), Res_4(t_1), \dots, Res_4(t_n), IC1_{Influenza}, IC2_{Influenza}, IC3_{Influenza}, IC4_{Influenza})_{4(n+1)}, \tag{30}$$

and finally for obtaining unknown coefficients, we solve these algebraic equations by Newton-Raphson method.

2.3. Genetic algorithm to find optimal shape parameter

GA as a meta-heuristic approach employed for optimization and finding the optimal parameter in problems. In fact, solving a problem by GA includes designing some functions and subroutines which be fired in each iteration (evolution). The main required functions and subroutines are Fitness function, Selection, Crossover, and mutation. However, more detailed explanation of GA is as follows:

- 1. Generating an initial population (chromosomes):** The algorithm utilizes a population-based structure to solve the problem. Thus it is necessary to pick out an initial population from the solution domain and start the evolution. Generating the initial population is usually done by a uniformly random distribution. The commands " **sample('Uniform'(Ω_a , Ω_b), #points)**" from the library " **Statistics**" of Maple and " **rand(#points)**" in Matlab generate the mentioned population.
- 2. Fitness function:** In fitness function, the competency of each chromosome is investigated. The fitness of each individual is typically a numerical value. According to the nature of the problem, we assume that the minimum cost is zero and define our fitness function as:

$$\exp(\frac{1}{1 + \Theta})$$

where Θ is $ASN2R (\sum_{i=1}^3 \|Res_i\|_2)$ in HIV problem and $ARE (\sum_{i=1}^N |u_i - u_{RKF}|)$ in SIRC model.

- 3. Parental selection:** GA is an iterative process, with the population in each iteration called a generation. The more fit individuals (parents) are stochastically selected from the current population, and modified (recombined and possibly randomly mutated) to form a new generation (children). Then the new generation of candidate solutions are used in the next iteration of the algorithm. Our method for selecting parents is based on the fitness function and Roulette wheel technique (RWT). In RWT, the chance of an individual to be chosen as a parent has a direct relationship with its fitness value.

4. **Crossover:** When two individuals are selected as parents, the crossover subroutines combine them to produce a new individual (their child). In this regard, we define a crossover formula called "Pseudo-combination" (PCF). The PCF produces a child based on the value and fitness of its both parents. We define PCF as follows:

$$d = \frac{a+b}{2} + \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \frac{|f(a)|^\alpha - |f(b)|^\alpha}{|f(a)|^\alpha + |f(b)|^\alpha} \right)$$

where d, a, b, ϵ and α parameters are child, first parent, second parent, outer limit and strongly inclination, respectively. The convergence of this PCF can be shown by taking the limit under different conditions as follows

- (a) If $|f(b)|^\alpha < |f(a)|^\alpha$ and $a < b$ so

$$\lim_{|f(b)| \rightarrow 0} d = \frac{a+b}{2} + \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \frac{|f(a)|^\alpha}{|f(a)|^\alpha} \right) = \frac{a+b}{2} + \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \right)$$

because $a < b$ so $b - \frac{a+b}{2} > 0$

$$\begin{aligned} & \frac{a+b}{2} + \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \right) = \\ & \frac{a+b}{2} + (b - \frac{a+b}{2} + \epsilon) = b + \epsilon \\ & \lim_{|f(b)| \rightarrow 0} d = b + \epsilon. \end{aligned}$$

- (b) If $|f(b)|^\alpha < |f(a)|^\alpha$ and $a > b$ so $b - \frac{a+b}{2} < 0$

$$\begin{aligned} & \frac{a+b}{2} + \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \right) = \\ & \frac{a+b}{2} - (-b + \frac{a+b}{2} + \epsilon) = b - \epsilon \\ & \lim_{|f(b)| \rightarrow 0} d = b - \epsilon. \end{aligned}$$

- (c) If $|f(b)|^\alpha > |f(a)|^\alpha$ and $a < b$ so

$$\lim_{|f(a)| \rightarrow 0} d = \frac{a+b}{2} + \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \frac{|f(b)|^\alpha}{|f(b)|^\alpha} \right) = \frac{a+b}{2} - \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \right)$$

because $a < b$ so $b - \frac{a+b}{2} > 0$

$$\begin{aligned} & \frac{a+b}{2} - \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \right) = \\ & \frac{a+b}{2} - (b - \frac{a+b}{2} + \epsilon) = a - \epsilon \\ & \lim_{|f(a)| \rightarrow 0} d = a - \epsilon. \end{aligned}$$

- (d) If $|f(b)|^\alpha > |f(a)|^\alpha$ and $a > b$ so $b - \frac{a+b}{2} < 0$

$$\begin{aligned} & \frac{a+b}{2} - \text{sign}(b-a) \left(\left| b - \frac{a+b}{2} + \text{sign}(b-a)\epsilon \right| \right) = \\ & \frac{a+b}{2} + (-b + \frac{a+b}{2} + \epsilon) = a + \epsilon \\ & \lim_{|f(a)| \rightarrow 0} d = a + \epsilon. \end{aligned}$$

- (e) If $|f(b)|^\alpha = |f(a)|^\alpha$ so

$$\lim_{|f(a,b)| \rightarrow 0} d = \frac{a+b}{2}.$$

5. **mutation:** In mutation operation, some chromosomes are chosen randomly (according to the mutation rate) and one digit of each chromosome is replaced with a random digit. Considering elitism, we guard top three chromosomes (based on their fitness) against mutation.

Algorithm (1) presents a general form of the proposed GA.

3. Result

In this section, we set $\epsilon=0.02$, $\alpha = 0.016$ $mutation=0.2$ and $elit=3$, and solve the HIV(1) and Influenza SIRC(2) models. We used Maple 2015 for solving these models. The hardware configuration was as follows:

OS : Windows 10 (64bit)

CPU : Corei7 2.8 GHZ

RAM : 12 GB DDR3.

Algorithm 1: GA-RBF method

```

1 Initial random feasible population:  $pop \leftarrow \{c_1, c_2, \dots, c_N\}$ 
2 WHILE (iteration condition)
3   RBF method computes ASN2R (or ARE) for population
4    $Fitness \leftarrow \exp(\frac{1}{1+ASN2R(orARE)})$ 
5   Sorting the population :  $\forall c_i, c_j \in pop, i < j \iff Fitness(c_i) > Fitness(c_j)$ 
6   Elitism :  $pop' \leftarrow \{c_1, c_2, \dots, c_{elit}\}$ 
7   FOR  $i = elit + 1$  to  $N$ 
8      $\{p_1, p_2\} \leftarrow ParentalSelection(pop)$ 
9      $c'_i \leftarrow PCF(p_1, p_2)$ 
10     $c''_i \leftarrow Mutation(c'_i)$ 
11     $pop' \leftarrow pop' \cup \{c''_i\}$ 
12  END FOR
13   $pop \leftarrow pop'$ 
14 END WHILE
    
```

3.1. HIV

In HIV model by selecting $\alpha = 0.02$, $\beta = 0.3$, $\gamma = 2.4$, $r = 3$, $k = 0.0027$, $T_{max} = 1500$, $s = 0.1$, $N = 10$, $T_0 = 0.1$, $V_0 = 0.1$ and $I_0 = 0$, we approximate target functions with the classic Gaussian function and apply the average of residual functions to the fitness function. Figures 1 and 2 show given target function and residual function plots from 20 collocation points for $T(t)$, $I(t)$ and $V(t)$.

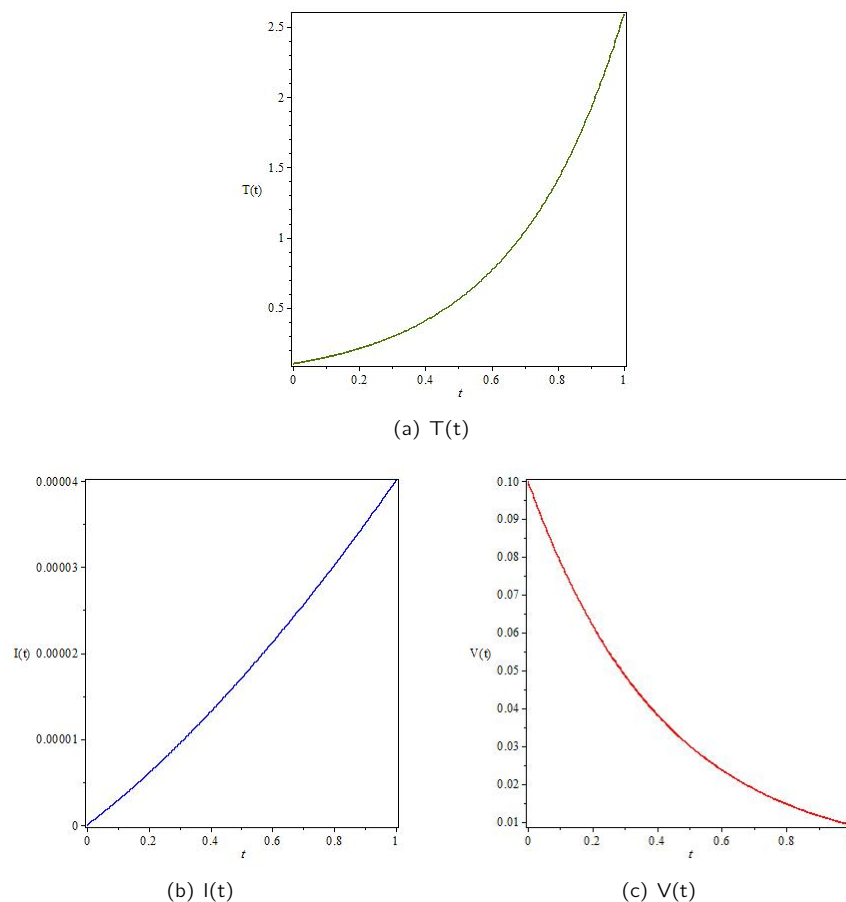


Figure 1. Plots of $T(t), I(t), V(t)$ for $N = 20$

Tables 6,7 and 8 illustrates the comparison of the presented method (with 20 collocation points) with approximated results of Bessel Collocation method (BCM) [80], Runge-Kutta method (RKM) [80], Homotopy Decomposition method (HDM) [5]

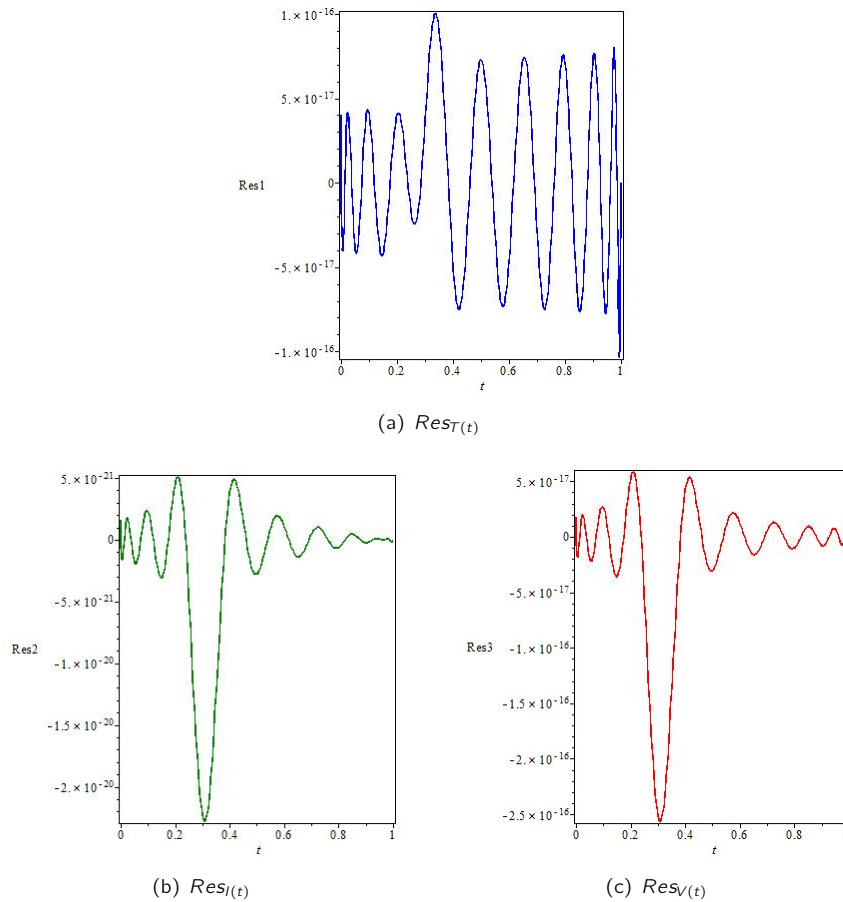


Figure 2. Plots of residual $T(t), I(t), V(t)$ for $N = 20$

and Wavelet Legendre method (WLM) [75]. The results show that the presented method and Runge-Kutta method are equal up to eight decimal places.

Table 6. Numerical results for $T(t)$

t	BCM	RKM	HDM	LWM	cGP	Present method for N=20
0.2	0.2038616561	0.2088080833	0.2088072731	0.2088073215	0.208806496	0.2088080843
0.4	0.3803309335	0.4062405393	0.4061052625	0.4061245634	0.406234784	0.4062405427
0.6	0.6954623767	0.7644238890	0.7611467713	0.7641476415	0.764408244	0.7644238985
0.8	1.2759624442	1.4140468310	1.3773198590	1.3977746217	1.414009061	1.4140468518
1.0	2.3832277428	2.5915948020	2.3291697610	2.5571462314	2.591509458	2.5915948516

Table 7. Numerical results for $I(t)$

t	BCM	Runge-Kutta	HDM	LWM	cGP	Present method for N=20
0.2	0.6247872e-5	0.6032702e-5	6.0327072e-5	0.6032704e-5	0.60325e-5	0.6032702e-5
0.4	0.1293552e-4	0.1315834e-4	1.3159161e-4	0.1316784e-4	0.13158e-4	0.1315834e-4
0.6	0.2035267e-4	0.2122378e-4	2.1268368e-4	0.2112628e-4	0.21223e-4	0.2122378e-4
0.8	0.2837302e-4	0.3017741e-4	3.0069186e-4	0.2998139e-4	0.30177e-4	0.3017742e-4
1.0	0.3690842e-4	0.4003781e-4	3.9873654e-4	0.3287654e-4	0.40037e-5	0.4003781e-4

Figures 3 and 4 show the residual functions. We used the uniform distribution library of Maple and generate 20 chromosomes as GA initial population in search domain (0.1, 5). The GA population collected on the smaller range after 20 iterations:
 5 collocation points (0.1, 5) → (0.15, 0.45)
 10 collocation points (0.1, 5) → (0.3, 0.59)

Table 8. Numerical results for $V(t)$

t	BCM	Runge-Kutta	HDM	LWM	cGP	Present method for N=20
0.2	0.0618799185	0.0618798433	0.0618799602	0.0618799076	0.061879980	0.0618798432
0.4	0.0382949349	0.0382948878	0.0383132488	0.0383234157	0.038295057	0.0382948877
0.6	0.0237043186	0.0237045501	0.0243917434	0.0238109873	0.023704707	0.0237045500
0.8	0.0146795698	0.0146803637	0.0099672189	0.0162138976	0.014680493	0.0146803636
1.0	0.0237043186	0.0091008450	0.0033050764	0.0160504423	0.009100944	0.0091008449

15 collocation points (0.1 , 5) → (0.45 , 0.75)

20 collocation points (0.1 , 5) → (0.74 , 0.95).

Figure 5 shows the condition of ASN2R based on the SP in the domain (0.1, 5). The optimal SP for 5 collocation points is in the domain (0.12, 0.35) and for 15 collocation points is in the domain (0.2, 0.8).

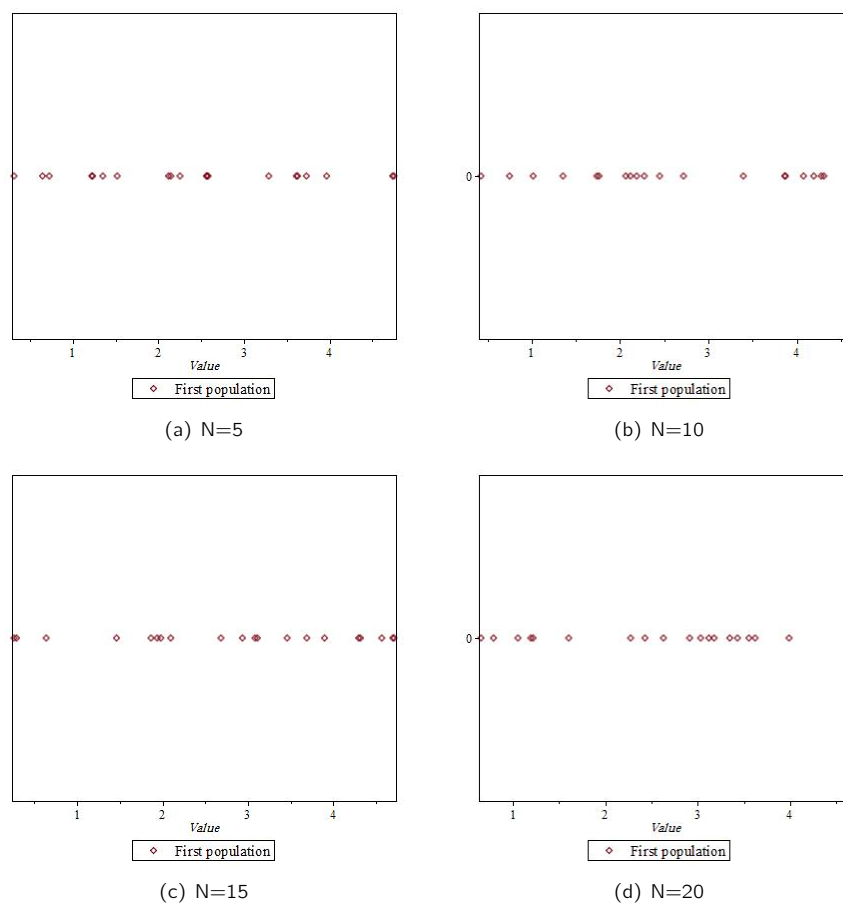


Figure 3. Initial population for SP domain

Obviously, by increasing the number of iterations in GA, in the case of the uniqueness of the optimal point, the final range will be limited again. Table 9 represents changes in the results and residuals by changing the number of collocation points. It can be seen that the results remained stable in 15 and 20 points.

In Fig. (6) and Fig. (7) display the average of value population (AVP) and the average of the residual population (ARP). After a number of steps, the AVP tended to a nonzero value, likewise, the ARP disposed to zero which indicates the convergence and productivity of our Genetic strategy.

3.2. Influenza

In this model, we applied the Gaussian function with a minor change as follows

$$c\psi = \exp(-\eta r^2) \quad \eta = \sqrt{(c^2)}, \tag{31}$$

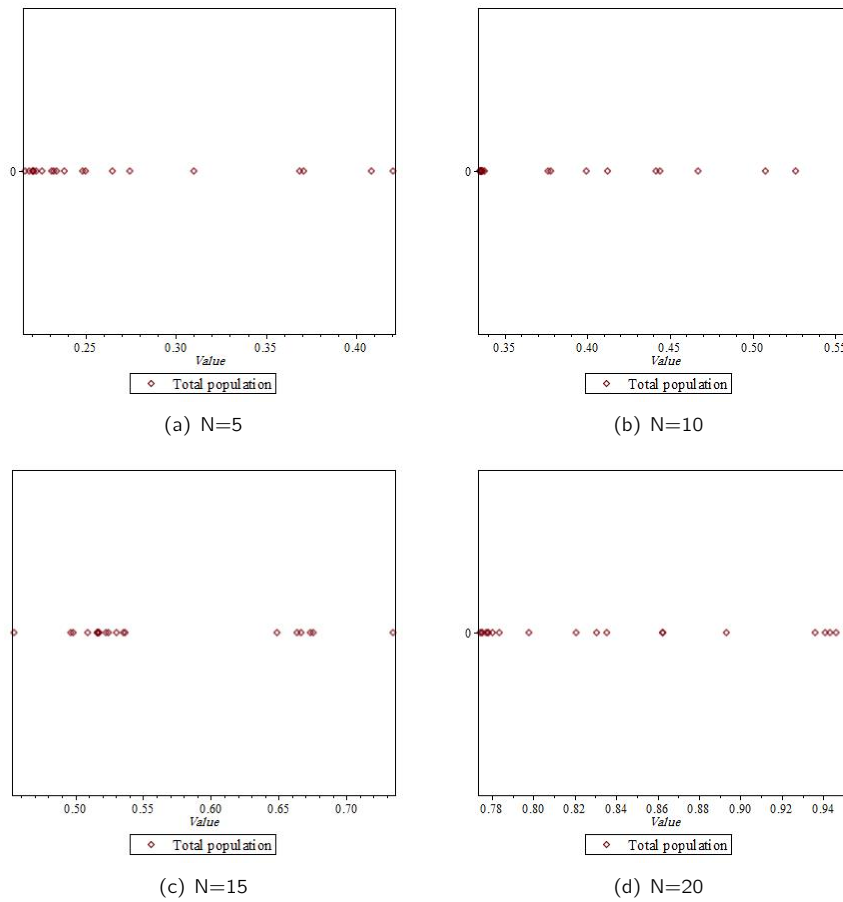


Figure 4. Total population for SP domain in latest iteration

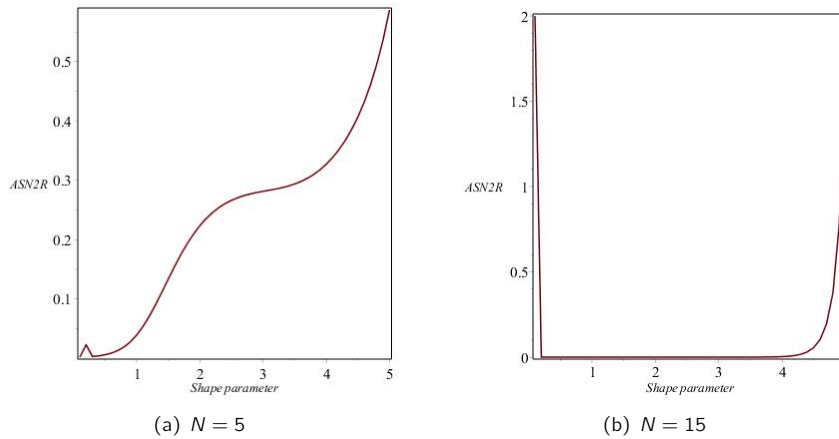


Figure 5. ASN2R condition based on Shape parameter

Moreover, the GA population is 200 randomly selected points from the real domain (1, 200). We used Maple's DSOLVE tool for calculating the fitness of chromosomes and compared our results with Runge-Kutta-Fehlberg (RKF) method. By selecting $\mu = 0.02$, $\beta = 100$, $\delta = 1$, $\gamma = 0.5$, $\sigma = 0.05$, $\theta = 73$, $S_0 = 0.8$, $I_0 = 0.1$, $R_0 = 0.05$ and $C_0 = 0.05$, four target functions have been obtained from 60 collocation points whose plots are shown in Fig.(8). In addition, in Fig. (9), treatment of functions for 20, 40 and 60 collocation points are considered. Initial and total population are presented in Fig. (10) and Fig. (11).

When we set the number of collocation points to 20, 40 and 60, the final generation collected in ranges (22, 28), (100, 140) and (120, 150) respectively. Furthermore, convergence of APN to a nonzero value is searchable in Fig.(13). Figure 12 shows the condition of ARE based on the SP selected from the domain (1, 200). For 20 collocation points, the optimal SP is in the

Table 9. Numerical comparison for $N = 5, 10, 15, 20$ in best SP

t	N=5	Res	N=10	Res	N=15	Res	N=20	Res
	c=0.21635819		c=0.33489998		c=0.51637831		c=0.77428513	
				T(t)				
0.2	0.2141496490	3.86e-03	0.2088094672	7.82e-06	0.2088080843	2.60e-13	0.2088080843	3.96e-17
0.4	0.3996040883	1.31e-01	0.4062432618	7.24e-07	0.4062405427	1.68e-13	0.4062405427	4.87e-17
0.6	0.7116524148	1.34e-01	0.7644289795	4.05e-07	0.7644238985	1.55e-13	0.7644238985	4.65e-17
0.8	1.2973641582	4.31e-03	1.4140559835	6.47e-07	1.4140468518	3.61e-13	1.4140468518	7.23e-17
1.0	2.3892259227	5.66e-92	2.5916114131	1.94e-84	2.5915948516	3.17e-80	2.5915948516	8.88e-78
	I(t)							
0.2	0.6114687e-5	2.27e-09	0.6032719e-5	2.46e-11	0.6032702e-5	3.42e-18	0.6032702e-5	4.46e-21
0.4	0.1337344e-4	8.34e-07	0.1315841e-4	5.26e-14	0.1315834e-4	6.28e-18	0.1315834e-4	3.71e-21
0.6	0.2134401e-4	1.13e-06	0.2122391e-4	6.30e-13	0.2122378e-4	5.06e-18	0.2122378e-4	1.09e-21
0.8	0.2987347e-4	3.22e-08	0.3017760e-4	1.60e-12	0.3017742e-4	7.01e-19	0.3017742e-4	6.41e-22
1.0	0.3908961e-4	6.10e-96	0.4003806e-4	4.41e-89	0.4003781e-4	9.99e-85	0.4003781e-4	1.45e-81
	V(t)							
0.2	0.0618187051	6.80e-05	0.0618798524	6.92e-08	0.0618798432	4.57e-14	0.0618798432	5.14e-17
0.4	0.0384572762	2.28e-03	0.0382948935	6.31e-09	0.0382948877	7.37e-14	0.0382948877	4.08e-17
0.6	0.0242145096	2.31e-03	0.0237045544	3.49e-09	0.0237045500	7.32e-14	0.0237045500	1.22e-17
0.8	0.0151695545	7.31e-05	0.0146803662	5.55e-09	0.0146803636	4.63e-14	0.0146803636	1.00e-17
1.0	0.0093128300	3.10e-93	0.0091008467	2.11e-86	0.0091008449	6.50e-82	0.0091008449	4.10e-79

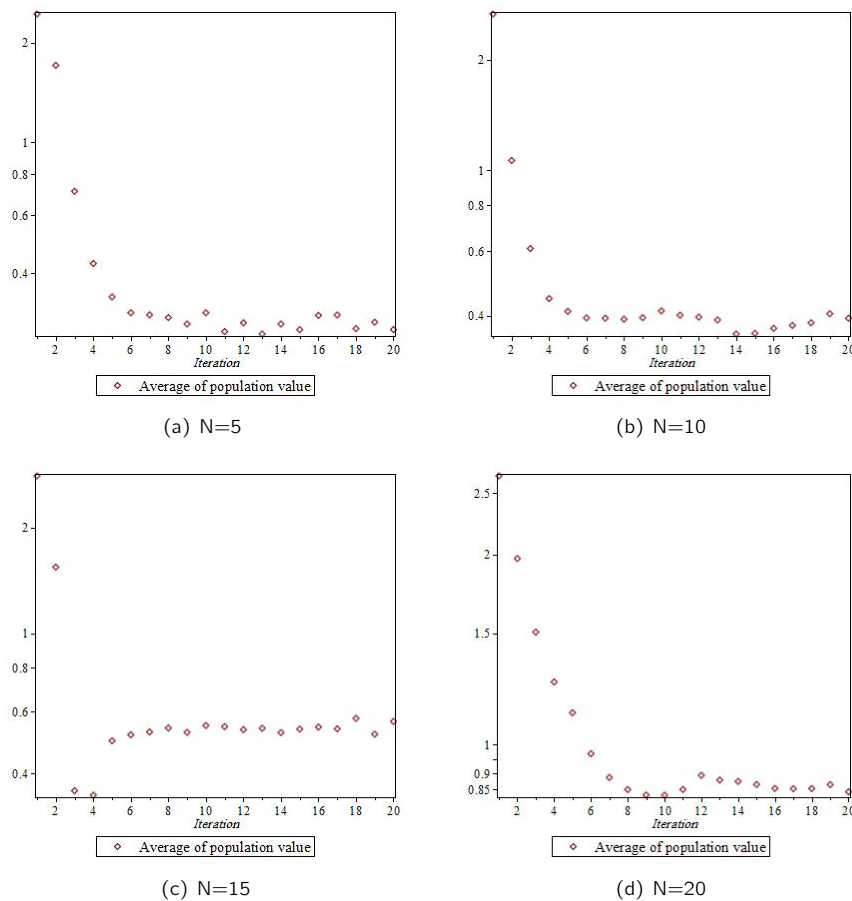


Figure 6. Average of population value in iterations

domain (20, 30) and for 40 collocation points is in the domain (100, 160).

Eventually, Tab.(10) displays the comparison of the proposed method (for 20, 40 and 60 collocation points) with RKF method. It shows that our results converge to the RKF method by increasing the number of collocation points.

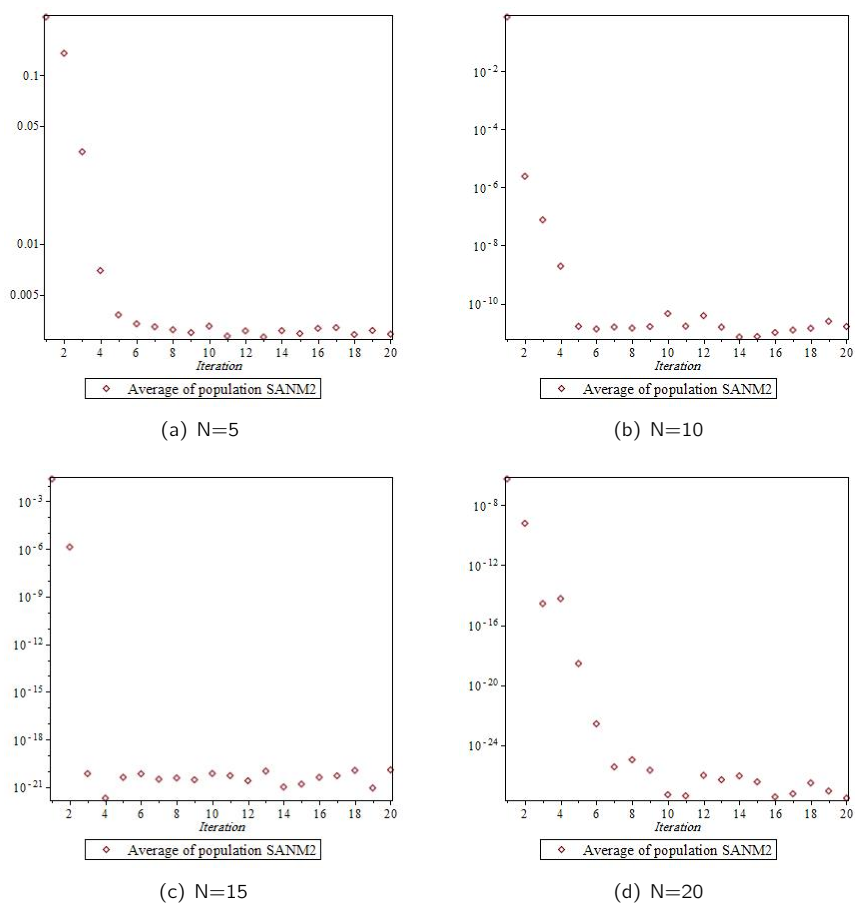


Figure 7. Average of population fitness in iterations

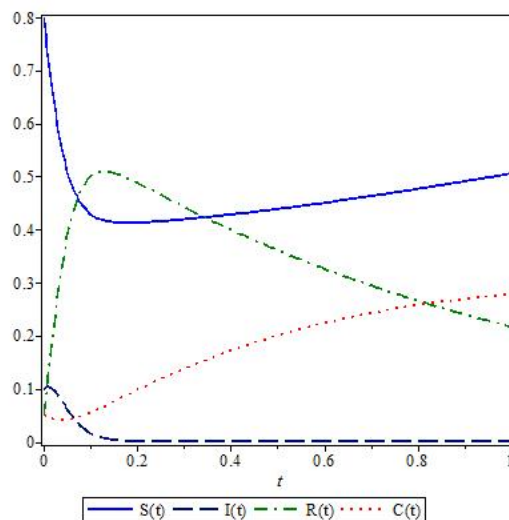


Figure 8. Plots for SIRC model

4. Conclusion

In this study we have proposed an approximation technique to solve biological equations. The method is based on the collocation method and Gaussian radial basis function. We used a Genetic strategy to overcome the challenge of searching optimal Shape parameters in RBF method. Additionally we tested ASN2R for HIV and ARE for SIRC model in fitness function and a new

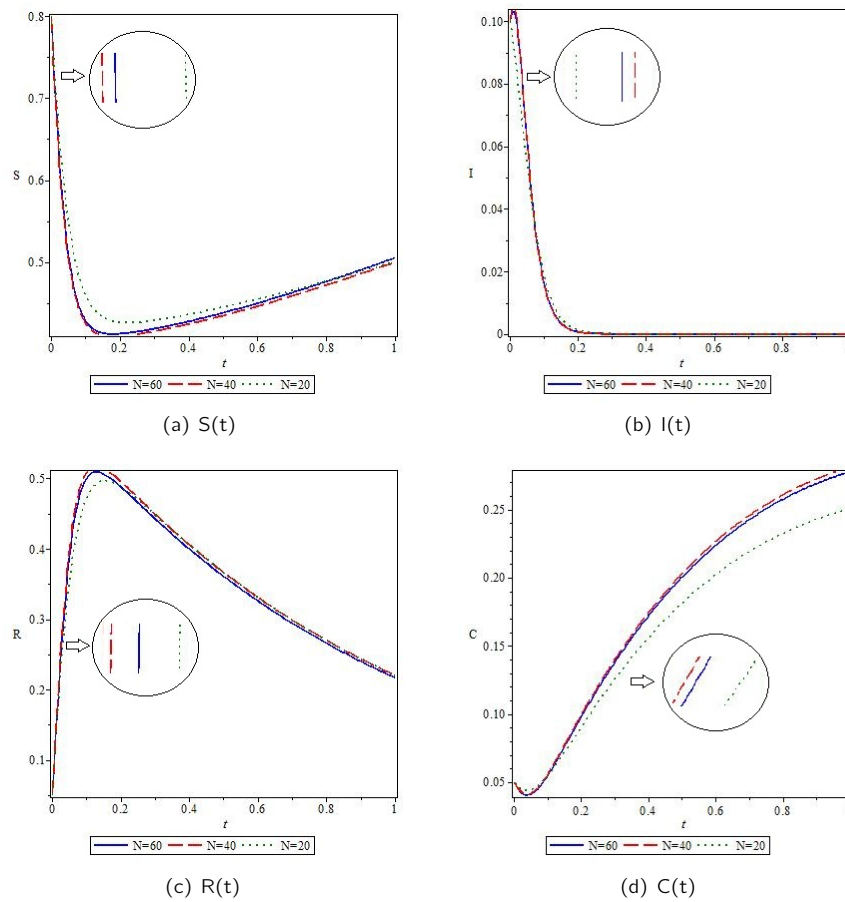


Figure 9. Gained plots for $N = 20, 40, 60$

crossover formula called Pseudo-combination defined for using the considered GA. The obtained results show that the proposed genetic algorithm has well identified the optimal shape parameter. Finally, we showed that our approach is applicable and accurate for the solving system of the differential equations such as HIV and Influenza models.

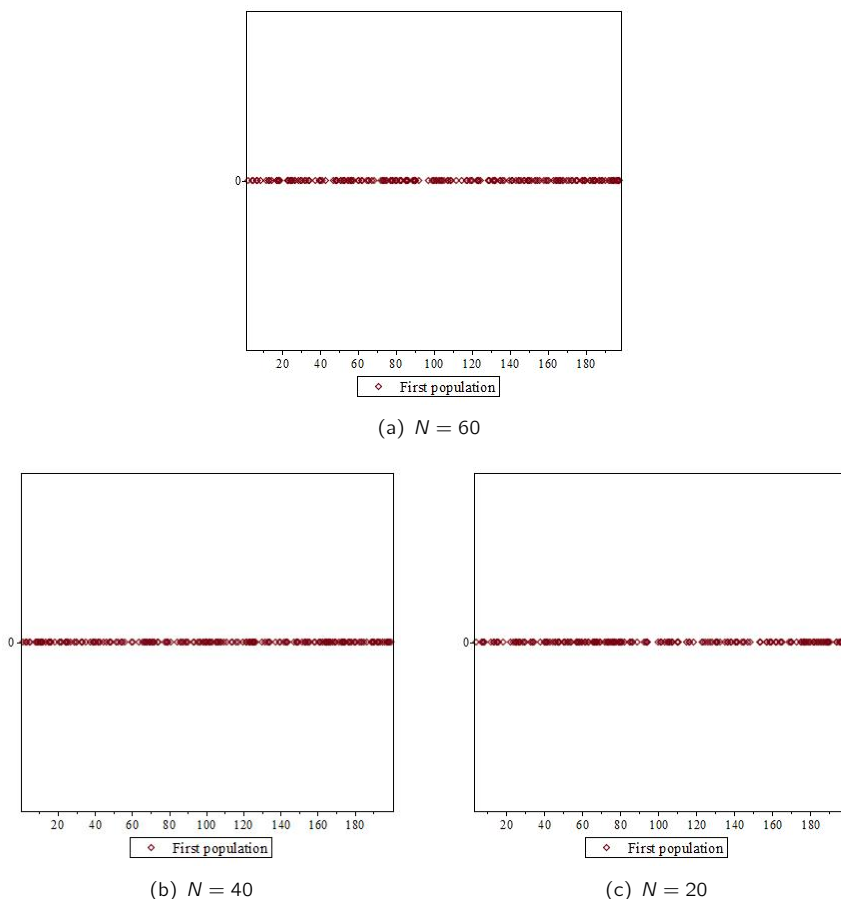


Figure 10. Initial population for SP domain

Table 10. Runge-Kutta-Fehlberg and RBF method results with $N = 20, 40, 60$

	RKFM	Presented method 20N	Presented method 40N	Presented method 60N	Relative error 60N
			S(t)		
c	-	26.800747761	137.9078869	123.44438040	-
0.2	0.4129967652	0.4270195495	0.4098921081	0.4128015008	1.952644e-04
0.4	0.4280199934	0.4363880004	0.4246103505	0.4278128844	2.071090e-04
0.6	0.4502002535	0.4549500702	0.4463055244	0.4499962534	2.040001e-04
0.8	0.4765242244	0.4766921230	0.4719383037	0.4763283175	1.959069e-04
1.0	0.5054118548	0.5003541451	0.5001004305	0.5052268175	1.850373e-04
			I(t)		
c	-	26.800747761	137.9078869	123.44438040	-
0.2	7.340828e-04	1.396989e-03	7.051238e-04	7.534934e-04	0.194106e-04
0.4	1.675623e-06	8.708980e-06	1.566126e-06	1.806640e-06	1.310170e-07
0.6	2.525609e-09	8.678259e-08	4.611322e-09	-1.672634e-09	4.198243e-09
0.8	9.855557e-10	-3.67796e-07	-2.23659e-09	-1.066306e-09	2.0518617e-09
1.0	-7.72143e-10	-2.21603e-05	-1.428391e-09	-3.324845e-08	3.2476307e-08
			R(t)		
c	-	26.800747761	137.9078869	123.44438040	-
0.2	0.4886071026	0.4886065768	0.4957432281	0.4884197981	1.873045e-04
0.4	0.4001052933	0.4061157789	0.4061422515	0.3999667848	1.385085e-04
0.6	0.3262752258	0.3313413846	0.3312018206	0.3261621289	1.130969e-04
0.8	0.2660651578	0.2702079076	0.2700828333	0.2659730573	9.210050e-05
1.0	0.2169661278	0.2203903869	0.2202819063	0.2168965849	6.954290e-05
			C(t)		
c	-	26.800747761	137.9078869	123.44438040	-
0.2	0.0976620493	0.9008003610	0.0990852949	0.0975773248	8.472450e-05
0.4	0.1718730376	0.1556924837	0.1741092475	0.1717627291	1.103085e-04
0.6	0.2235245180	0.2019667950	0.2263417601	0.2233978645	1.266535e-04
0.8	0.2574106166	0.2323192884	0.2606042265	0.2572747238	1.358928e-04
1.0	0.2776220180	0.2504052565	0.2810922415	0.2774868004	1.352176e-04

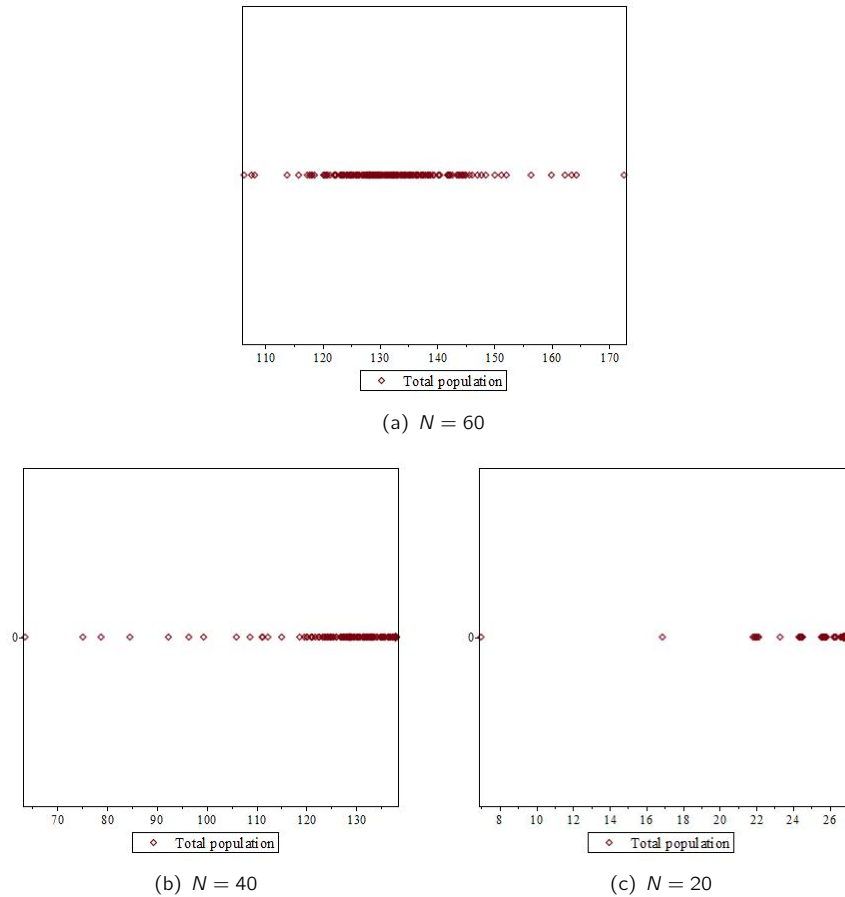


Figure 11. Total population for SP domain

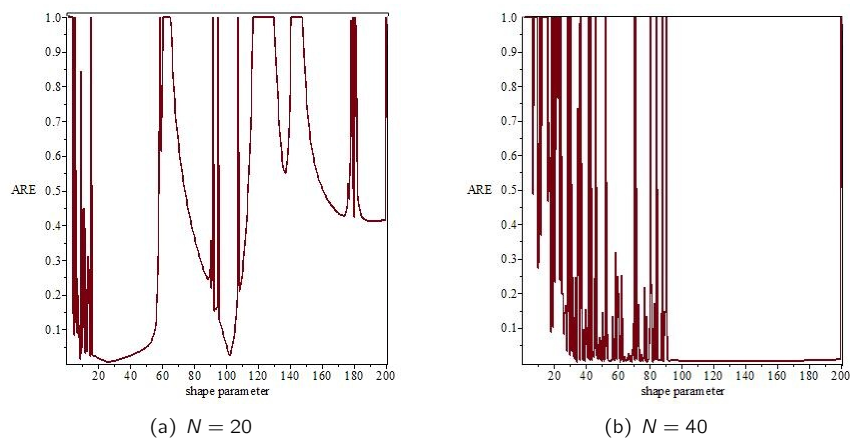


Figure 12. ARE condition based on Shape parameter

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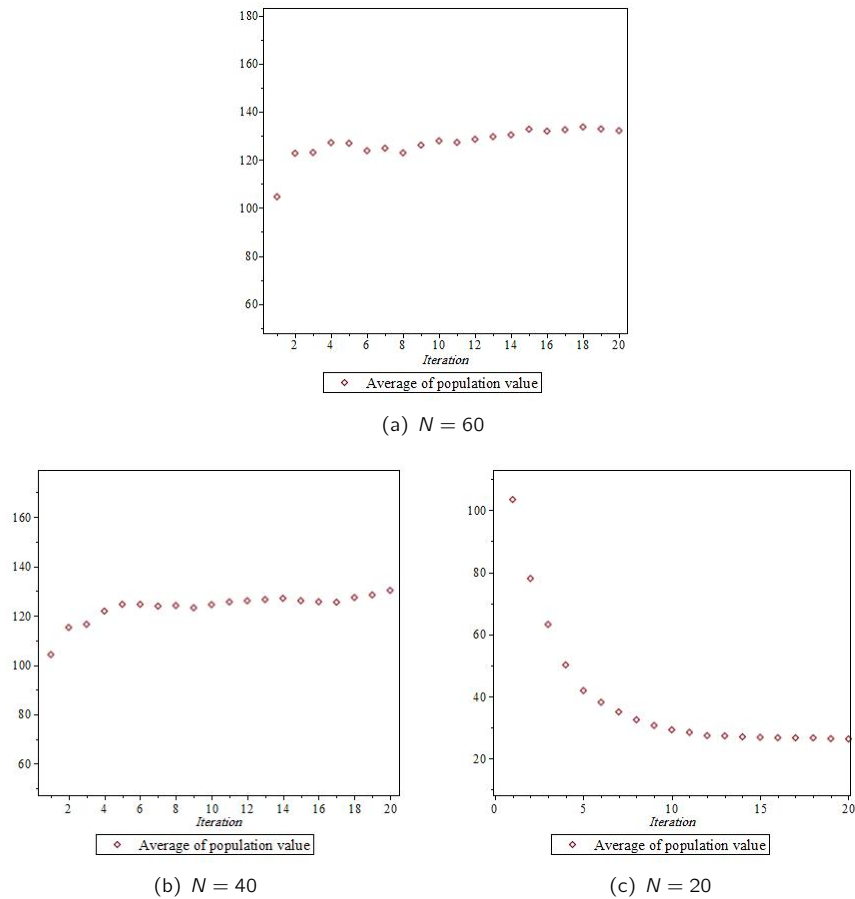


Figure 13. Average of population value in iterations

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