Numerical investigation of Differential Biological-Models via GA-Kansa Method Inclusive Genetic Strategy

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Abstract

In this paper, we use Kansa method for solving the system of differential equations in the area of biology. One of the challenges in Kansa method is picking out an optimum 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 optimum Shape parameter. For this reason, we design a genetic algorithm to detect a close optimum Shape parameter. The experimental results show that this strategy is efficient in the systems of differential models in biology such as HIV and Influenza. Furthermore, we prove that using our pseudo-combination formula for crossover in genetic strategy leads to convergence in the nearly best selection of Shape parameter.

Keywords: Biological Models, Kansa Method, Radial Basis Function, Genetic Strategy, Systems of Differential Equation

1. Introduction

1.1. Mathematical Models

1.1.1. HIV Infection CD4+T Cells

Acquired Immune Deficiency Syndrome (AIDS), first-time appeared in the continent of America in 1981\textsuperscript{[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\textsuperscript{[13]}. 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\textsuperscript{[53, 54]}. 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 \( T(t) \) be the concentration of susceptible CD4+T cells, \( I(t) \) be CD4+T cells infected by the HIV virus and \( V(t) \) be free HIV particular in the blood at the time. Thus, the mathematical model of the HIV-infected CD4+T cell on a couple system of the ordinary differential equation will be presented as follows:

\[
\begin{align*}
\frac{dT}{dt} &= s - \alpha T(t) + \gamma T(t)(1 - \frac{T(t) + I(t)}{T_{\text{max}}}) - kV(t)T(t), & T(0) = T_0, \\
\frac{dI}{dt} &= kV(t)T(t) - \beta I(t), & I(0) = I_0, \quad 0 \leq t \leq R < \infty \\
\frac{dV}{dt} &= \gamma T(t) - \gamma V(t), & V(0) = V_0,
\end{align*}
\]

where \( R \) is a positive constant and other parameters have been shown in table\textsuperscript{[1]}. Unfortunately, there is no exact solution for HIV model. Ergo, the numerical methods are used to solve it. Table\textsuperscript{[2]} shows some approaches applied to this model.

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1.1.2. Influenza

Influenza virus causes a type of disease named Influenza or Flu that is divided into four classes A, B, C and D[28]. 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[3, 67]. The mathematical model of Susceptible-Infected-Removed (SIRC) for displaying the outbreaks of Influenza in population is defined by Kermack and McKendrick [35]. This is a system of the fractional differential equation as follows:

\[
\begin{align*}
D^\alpha S(t) &= \mu(1 - S(t)) - \beta S(t)I(t) - \gamma C(t), \quad S(0) = S_0, \\
D^\alpha I(t) &= \beta S(t)I(t) + \sigma C(t)I(t) - (\mu + \theta)I(t), \quad I(0) = I_0, \\
D^\alpha R(t) &= (1 - \sigma)\beta C(t)I(t) + \theta I(t) - (\mu + \delta)R(t), \quad R(0) = R_0, \\
D^\alpha C(t) &= \delta R(t) - \beta C(t)I(t) - (\mu + \gamma)C(t), \quad C(0) = C_0.
\end{align*}
\]

Forasmuch as the \( \eta = 1 \), standard model of Flu is defined by

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

where \( S(t), I(t), R(t) \) and \( C(t) \) mean ratio susceptible, infections, recovered and cross immune respectively. Other parameters are shown in table[3]. This model studied by Khader et al.[37] using Chebyshev spectral method in 2014. Table 1 shows the applying methods to SIRC model. We consider the standard Flu model to be the second sample.

| Author(s)          | Method                                | Year |
|--------------------|---------------------------------------|------|
| Merdan[42]         | Homotopy Perturbation method (HPM)    | 2007 |
| Alomari et al.[23] | Homotopy Analysis method (HAM)        | 2011 |
| Merdan et al. [43] | variational Iteration Method (VIM)    | 2011 |
| Ogunniyi[44]       | Laplace Adomian Decomposition Method (LADM) | 2011 |
| Doğan[16]          | Multistep Laplace Adomian Decomposition Method (MLADM) | 2012 |
| Khan et al.[38]    | Iterative Homotopy Perturbation Transform Method (IHPTM) | 2012 |
| Yüzbaşi[71]        | Bessel Collocation Method (BCM)       | 2012 |
| Atangana et al. [4] | Homotopy Decomposition Method (HDM)   | 2014 |
| Chen[10]           | Padé-Adomian Decomposition Method (PADM) | 2015 |
| Venkatesh et al. [66]| Legendre Wavelets method (LWM)       | 2016 |
| Kajani et al. [22] | Müntz-Legendre Method (MLM)           | 2016 |
| El-Baghdady et al. [17]| Legendre collocation method (LCM)     | 2017 |
Table 3: Parameters in Flu model

| Symbol | Description                          |
|--------|--------------------------------------|
| $\mu$  | Mortality rate                       |
| $\theta$ | Improve infection each year         |
| $\delta$ | Progression from recovered to cross-immune each year |
| $\gamma$ | Progression from recovered to susceptible each year |
| $\sigma$ | Rate of cross-immune into the infective |
| $\beta$ | Contact rate                        |

Table 4: Used techniques for solving SIRC model

| Author(s)                | Method                                      | Year |
|--------------------------|---------------------------------------------|------|
| El-Shahed et al. [18]   | Non-standard Finite Difference (NSFDM)      | 2012 |
| Ibrahim et al. [30]     | Modified differential transform method (MDTM) | 2013 |
| Zeb et al. [72]         | Multi-step generalized differential transform method (MGDTM) | 2013 |
| Khader et al. [37]      | Chebyshev spectral method (CSM)             | 2014 |
| Khader et al. [36]      | Legendre spectral method (LSM)              | 2014 |
| González-parra et al. [26] | Grünwald Letnikov method (GLM)             | 2014 |

1.2. Meshfree Method

Firstly, the Meshfree methods introduced by Monaghan and Gingold in 1977. They enlarged a Lagrangian method according to Kernel estimate method [24]. A number of meshfree methods such as smoothing particle hydrodynamic (SPH) [11, 64], Element-Free Galerkin (EFG) [8, 39], Reproducing Kernel method (RKM) [1, 7], Meshless local Petrov-Galerkin (MLPG) [8, 55], Comapctly supported radial basis function method (CSRBFS) [48, 49], Radial basis function differential quadrature method (RBF-DQ) [47, 63] and Kansa method (KM) [51, 61] 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) [31, 65] and Finite Difference method (FDM) [14, 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. Diagram (1) shows a general category of methods applied for solving DEs [6, 33, 34, 45, 46, 50, 52, 56, 57, 60, 62, 70]. Kansa 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 Kansa 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.
Table 5: Some radial basis functions, $\psi_c (r = \|x - x_i\| = r_i), c > 0$

| 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 Quadratics (IQ) | $\frac{1}{c^2 + r^2}$ |
|       | Hyperbolic Secant (sech) | $\text{sec} h(c \sqrt{r})$ |
| 2     | Thin Plate Spline (TPS) | $(-1)^{k+1} r^k \log(r)$ |
|       | Conical Spline | $\frac{r^k}{(k+1)}$ |
| 3     | Wendland$_{3,0}$ | $(1 - r)^3$ |
|       | Wu$_{3,3}$ | $(1 - r)^3 (16 + 29r + 20r^2 + 5r^3)$ |
|       | Oscillator$_{1,3}$ | $(1 - r)^2 (1 + 4r - 15r^2)$ |
|       | Buhman$_{1}$ | $12r^4 \log r - 21r^4 + 32r^3 - 12r^2 + 1$ |
| 4     | Platte$_{a,b,c}$ | $\cos(cr) \exp \left( \frac{-n}{(1-r)^b} + b \right)$ |

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 optimum 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 [40] SP decomposed to a dimensionless size of support domain ($\alpha_s$) and a nodal spacing near the point at the center ($d_c$), where $c = \alpha_s d_c$. Hardy [27] suggested using (inverse) multiquadric formula as follows:

$$c = 1.0815 \varepsilon$$

where $\varepsilon = \frac{1}{N} \sum_{i=1}^{N} e_i$, and $e_i$ is the distance of the center from its closest neighbor. Rippa [58] used the Predictive residual sum of square (PRESS) algorithm for calculating a proper SP. Leave on-out cross validation (LOOCV) approach [21] and Craven and Wahba [12] which emanated in the statistics literature used for finding optimal SP. Esmaeilbeigi et al. [2, 19] employed the genetic package of MATLAB for solving a number of DEs. The following formula is proposed in [32, 59] to calculate a reasonable SP

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

where $n$ is the number of points and $c_a$ is the smallest and $c_\beta$ is the biggest selected parameter in the domain of candidate SPs. Similarly, in [59, 69] the SP is obtained by

$$c_i = c_a + (c_\beta - c_a) \Delta_{\text{rand}},$$

where $\Delta_{\text{rand}}$ is a random number in arbitrary domain.

In this paper, we suggested a Meta-heuristic continues 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.

1.3. 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 [29]. He also proposed a theoretical basis for GA according to the Type theory. In the following, David E Goldberg [25] 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.

As shown in Fig (2), GA is a class of evolutionary meta-heuristic algorithms. 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 (ερ-optimal Shape parameter) around a specified interval in the Kansa method, where ρ is either ASRN2 or ARE strategies.

2. Methodology

2.1. Kansa method

2.1.1. RBF approximation

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

\[
e^\psi(||x - x_i||),
\]

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

\[
s(x) = \sum_{i=1}^N \xi_i \psi(||x - x_i||); \ \xi_i \in \mathbb{R},
\]
where \( s(x) \) is called a radial basis functions mesh [20, 68]. To approximate one-dimensional function \( f(x) \), we can illustrate it with an RBF as

\[
f(x) \approx f_\alpha(x) = \sum_{i=1}^{N} \xi_i \psi_i(x) = \xi^T \Psi(x),
\]

where

\[
\xi = [\xi_1, \xi_2, \cdots, \xi_N],
\]

\( \Psi(x) = [\psi_1(x), \psi_2(x), \cdots, \psi_N(x)] \),

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

\[
f_j(x) = \xi^T \Psi(x_j)
\]

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

\[
\hat{M} \hat{\xi} = \tilde{F},
\]

where

\[
\tilde{F} = [f_1, f_2, \cdots, f_N]^T
\]

\[
\hat{M} = [\Psi^T(x_1), \Psi^T(x_2), \cdots, \Psi^T(x_N)]^T
\]

By solving the system [4], the unknown coefficients \( \hat{\xi} \) will be attained.

### 2.1.2. Solving models

Consider the following non-coupled linear boundary value systems (BVS)

\[
\mathcal{L}_1 u_1(x) = g_{[1,1]} \quad \mathcal{L}_2 u_2(x) = g_{[2,1]} \quad \cdots \quad \mathcal{L}_n u_n(x) = g_{[n,1]} \quad x \in \Omega,
\]

\[
u_1(x_i) = g_{[1,2]} \quad u_2(x_k) = g_{[2,2]} \quad \cdots \quad u_n(x_s) = g_{[n,2]} \quad x \in \partial \Omega,
\]

\[
\frac{d^{\nu}}{dx^\nu} u_1(x) = g_{[1,n]} \quad \frac{d^{\nu}}{dx^\nu} u_2(x) = g_{[2,n]} \quad \cdots \quad \frac{d^{\nu}}{dx^\nu} u_n(x) = g_{[n,n]} \quad x \in \partial \Omega,
\]

where \( \mathcal{L}_i \) indicates the differential operator. We approximate functions \( u_1, u_2, \cdots, u_n \) by a linear combination of the RBFs in the form

\[
\tilde{U}_1(x) = \xi^T \Psi(1) \quad \tilde{U}_2(x) = \xi^T \Psi(2) \quad \cdots \quad \tilde{U}_n(x) = \xi^T \Psi(n)
\]

Substituting Eq [9] in Eqs [6, 7, 8] leads to outcomes algebraic equation system

\[
\hat{A} \hat{\xi} = \tilde{b},
\]

where

\[
\hat{A} = \begin{pmatrix}
\tilde{T}_1 & 0 & \cdots & 0 \\
0 & \tilde{T}_2 & \cdots & 0 \\
\vdots & \ddots & \ddots & \vdots \\
0 & 0 & 0 & \tilde{T}_n
\end{pmatrix}
\]

\[
\tilde{T}_i = (\mathcal{L}_i \tilde{U}_i(x) \quad \frac{d^{\nu}}{dx^\nu} \tilde{U}_i(x))^T
\]

\[
\tilde{b} = [g_{[1,1]} \quad g_{[2,1]} \quad \cdots \quad g_{[n,1]}]^T
\]

\[
G_i = [g_{[1,2]} \quad g_{[2,2]} \quad \cdots \quad g_{[n,2]}]^T
\]
We are to mention

\[ \text{Res}_i = \mathcal{L}[\hat{U}_i(x)] - g_{[i,1]} \]  

After solving Eq(11) and obtaining coefficients \( \xi_i \), the approximated functions could be calculated by Eq(9).

2.2. Genetic strategy

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_α, Ω_p),#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:

\[
\text{exp}(\frac{1}{1 + \Theta})
\]

where \( \Theta \) is ASN2R \( \sum_3^N |\text{Res}_i| \) in HIV problem and ARE \( \sum_3^N |k_{n-\text{next}}| \) 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 and prove its convergence as follows:

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

where \( d, a, b, \epsilon \) and \( \alpha \) parameters are child, first parent, second parent, outer limit and strongly inclination, respectively.

**Proof.** (a) If \( |f(b)|^\alpha < |f(a)|^\alpha \) and \( a < b \) so

\[
\lim_{|f(b)|\to0} d = \frac{a + b}{2} + \text{sign}(b - a)(|b - \frac{a + b}{2} + \text{sign}(b - a)\epsilon|) \frac{|f(a)|^\alpha - |f(b)|^\alpha}{|f(a)|^\alpha + |f(b)|^\alpha} = \frac{a + b}{2} + \text{sign}(b - a)(|b - \frac{a + b}{2} + \text{sign}(b - a)\epsilon|)
\]

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

\[
\frac{a + b}{2} + \text{sign}(b - a)(|b - \frac{a + b}{2} + \text{sign}(b - a)\epsilon|) = \frac{a + b}{2} + (b - \frac{a + b}{2} + \epsilon) = b + \epsilon
\]

\[
\lim_{|f(b)|\to0} d = b + \epsilon.
\]
3. Solving Systems

Algorithm (1) presents a general form of the proposed GA. The results show that the presented method and approximated results of Bessel Collocation method (BCM) [71], Runge-Kutta method (RKM) [71], Homotopy Decomposition method (HDM) [4] and Wavelet Legendre method (WLM) [66]. The hardware configuration was as follows:

- OS: Windows 7 (64bit)
- CPU: Corei5 2.8 GHZ
- RAM: 16 GB DDR3.

In this section, we set \( \varepsilon = 0.02 \), \( \alpha = 0.016 \) \( \text{mutation}=0.2 \) and \( \text{elit}=3 \), and solve the HIV [1] and Influenza SIRC [2] models. We used Maple 2015 for solving HIV model and Matlab 2010 for solving Influenza SIRC model. The hardware configuration was as follows:

- OS: Windows 7 (64bit)
- CPU: Corei5 2.8 GHZ
- RAM: 16 GB DDR3.

### 3.1. HIV

In HIV model, we approximate target functions with the classic Gaussian function and apply the average of residual functions to the fitness function. Figures (3,4) show given target function and residual function plots from 20 collocation points for \( T(t), I(t) \) and \( V(t) \).

#### 3.1.1. HIV

- If \( |f(b)|^p < |f(a)|^p \) and \( a > b \) so \( b - \frac{a + b}{2} < 0 \)
  
  \[
  \frac{a + b}{2} + \text{sign}(b-a)(|b - \frac{a + b}{2} + \text{sign}(b-a)|) = \frac{a + b}{2} - (-b + \frac{a + b}{2} + \varepsilon) = b - \varepsilon
  \]
  
  
  \[
  \lim_{|f(b)|^p \to 0} d = b - \varepsilon.
  \]

- If \( |f(b)|^p > |f(a)|^p \) and \( a < b \) so \( a - \frac{a + b}{2} > 0 \)
  
  \[
  \frac{a + b}{2} - \text{sign}(b-a)(|b - \frac{a + b}{2} + \text{sign}(b-a)|) = \frac{a + b}{2} - (-b + \frac{a + b}{2} + \varepsilon) = a - \varepsilon
  \]
  
  \[
  \lim_{|f(a)|^p \to 0} d = a - \varepsilon.
  \]

- If \( |f(b)|^p > |f(a)|^p \) and \( a > b \) so \( b - \frac{a + b}{2} < 0 \)
  
  \[
  \frac{a + b}{2} - \text{sign}(b-a)(|b - \frac{a + b}{2} + \text{sign}(b-a)|) = \frac{a + b}{2} + (-b + \frac{a + b}{2} + \varepsilon) = a + \varepsilon
  \]
  
  \[
  \lim_{|f(a)|^p \to 0} d = a + \varepsilon.
  \]

- If \( |f(b)|^p = |f(a)|^p \) so

  \[
  \lim_{|f(a)|^p \to 0} d = \frac{a + b}{2}.
  \]

\[ \square \]

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.
**Algorithm 1: GA-Kansa method**

1. Initial random feasible population: $pop \leftarrow \{c_1, c_2, \ldots, c_N\}$

2. **WHILE** (iteration condition)

3. Kansa method computes ASN2R (or ARE) for population

4. $\text{Fitness} \leftarrow \exp\left(\frac{1}{1 + \text{ASN2R(OR ARE)}}\right)$

5. Sorting the population: $\forall c_i, c_j \in pop, i < j \iff \text{Fitness}(c_i) > \text{Fitness}(c_j)$

6. Elitism: $pop' \leftarrow \{c_1, c_2, \ldots, c_{\text{elit}}\}$

7. **FOR** $i = \text{elit} + 1$ to $N$

8. $[p_1, p_2] \leftarrow \text{ParentalSelection}(pop)$

9. $c_i' \leftarrow \text{PCF}(p_1, p_2)$

10. $c_i'' \leftarrow \text{Mutation}(c_i')$

11. $pop' \leftarrow pop' \cup \{c_i''\}$

12. **END FOR**

13. $pop \leftarrow pop'$

14. **END WHILE**

---

Figure 3: Plots of $T(t)$, $I(t)$, $V(t)$ for $N = 20$
Figure 4: Plots of residual $T(t), I(t), V(t)$ for $N = 20$
Table 6: Numerical results for $T(t)$

| $t$  | BCM  | RKM  | HDM  | LWM  | Present method for $N = 20$ |
|------|------|------|------|------|----------------------------|
| 0.2  | 0.2038616561 | 0.2088080833 | 0.2088072731 | 0.2088073215 | 0.2088080843 |
| 0.4  | 0.4062405393 | 0.4061052625 | 0.4061245634 | 0.4062405427 |
| 0.6  | 0.69423890 | 0.7641476415 | 0.764238985 |
| 0.8  | 1.4140468310 | 1.377746217 | 1.4140468518 |
| 1.0  | 2.5915948020 | 2.329197610 | 2.5915948516 |

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

| $t$  | BCM  | Runge-Kutta | HDM  | LWM  | Present method for $N = 20$ |
|------|------|-------------|------|------|----------------------------|
| 0.2  | 0.6247872e-5 | 0.6032704e-5 | 0.6032704e-5 | 0.6032704e-5 |
| 0.4  | 0.1315834e-4 | 0.1315834e-4 | 0.1315834e-4 | 0.1315834e-4 |
| 0.6  | 0.2122378e-4 | 0.2122378e-4 | 0.2122378e-4 | 0.2122378e-4 |
| 0.8  | 0.3017742e-4 | 0.3017742e-4 | 0.3017742e-4 | 0.3017742e-4 |
| 1.0  | 0.4003781e-4 | 0.4003781e-4 | 0.4003781e-4 | 0.4003781e-4 |

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

| $t$  | BCM  | Runge-Kutta | HDM  | LWM  | Present method for $N = 20$ |
|------|------|-------------|------|------|----------------------------|
| 0.2  | 0.0618799185 | 0.0618798433 | 0.0618799076 | 0.0618798432 |
| 0.4  | 0.0382948878 | 0.0383234157 | 0.0382948877 |
| 0.6  | 0.0237045500 | 0.0238109873 | 0.0237045500 |
| 0.8  | 0.0146803636 | 0.0162138976 | 0.0146803636 |
| 1.0  | 0.0091008449 | 0.0160504423 | 0.0091008449 |

Figures (5,6) 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 $(0.1 , 5) \rightarrow (0.15 , 0.45)$
- 10 collocation points $(0.1 , 5) \rightarrow (0.3 , 0.59)$
- 15 collocation points $(0.1 , 5) \rightarrow (0.45 , 0.75)$
- 20 collocation points $(0.1 , 5) \rightarrow (0.74 , 0.95)$.

Figure(7) shows the condition of ASN2R based on the SP in the domain $(0.1, 5)$. The $\epsilon$-optimum SP for 5 collocation points is in the domain $(0.12, 0.35)$ and for 15 collocation points is in the domain $(0.2, 0.8)$. 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. (8) and Fig. (9) display the average of value population (A VP) and the average of the residual population (ARP). After a number of steps, the A VP 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 case, we transformed the non-linear system (2) to an iterative linear system using Quasi-linearization method (QLM) [41]. The obtained linear system is:

$$
\frac{d}{dt} S_{n+1} + \rho S_{n+1} + \beta I_{n+1} S_{n+1} = \mu + \gamma C_{n},
$$

$$
\frac{d}{dt} I_{n+1} - \beta S_{n+1} I_{n+1} - \sigma \beta C_{n+1} I_{n+1} + (\mu + \theta) I_{n+1} = 0,
$$

$$
\frac{d}{dt} R_{n+1} + (\mu + \phi) R_{n+1} = (1 - \sigma) \beta C_{n+1} I_{n} + \phi I_{n},
$$

$$
\frac{d}{dt} C_{n+1} + \beta I_{n} + C_{n+1} + (\mu + \gamma) C_{n+1} = \delta R_{n}.
$$

11
Table 9: Numerical comparison for N = 5, 10, 15, 20 in best SP

| t  | N=5      | Res  | c=0.21635819 | N=10      | Res  | c=0.33489998 | N=15      | Res  | c=0.51637831 | N=20      | Res  | c=0.77428513 |
|----|----------|------|--------------|----------|------|--------------|----------|------|--------------|----------|------|--------------|
| 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 | 0.4062423618 | 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 |

| t  | N=5      | Res  | c=0.21635819 | N=10      | Res  | c=0.33489998 | N=15      | Res  | c=0.51637831 | N=20      | Res  | c=0.77428513 |
|----|----------|------|--------------|----------|------|--------------|----------|------|--------------|----------|------|--------------|
| 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-03 | 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 |

| t  | N=5      | Res  | c=0.21635819 | N=10      | Res  | c=0.33489998 | N=15      | Res  | c=0.51637831 | N=20      | Res  | c=0.77428513 |
|----|----------|------|--------------|----------|------|--------------|----------|------|--------------|----------|------|--------------|
| 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| 0.024215096 | 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-03 | 0.0091008467 | 2.11e-08 | 0.0091008449 | 6.50e-08 | 0.0091008449 | 4.10e-79 |
Figure 6: Total population for SP domain in latest iteration

(a) $N=5$

(b) $N=10$

(c) $N=15$

(d) $N=20$

Figure 7: ASN2R condition based on Shape parameter

(a) $N = 5$

(b) $N = 15$
Figure 8: Average of population value in iterations

(a) N=5

(b) N=10

(c) N=15

(d) N=20
(a) $N=5$
(b) $N=10$
(c) $N=15$
(d) $N=20$

Figure 9: Average of population fitness in iterations
We used Matlab 2010 to solve this problem and applied the function \( \psi = \exp(-\eta r^2) \) for solving the model with a minor change in the Gaussian radial function:

\[
\psi = \exp(-\eta r^2) \quad \eta = \sqrt{c^2},
\]

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. Four target functions have been obtained from 60 collocation points whose plots are shown in Fig. (10). In addition, in Fig. (11), treatment of functions for 20, 40 and 60 collocation points are considered. Initial and total population are presented in Fig. (12) and Fig. (13).

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. (15). Figure (14) shows the condition of ARE based on the SP selected from the domain (1, 200). For 20 collocation points, the optimum SP is in the 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.

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 optimum Shape parameters in method. Additionally we tested ASN2R for HIV and ARE for SIRC model in fitness function and a new crossover formula called Pseudo-combination defined for using the considered GA. Finally, we showed that our approach is applicable and suitable for the solving system of the differential equations such as differential biological systems.

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Figure 11: Gained plots for $N = 20, 40, 60$
Figure 12: Initial population for SP domain

(a) $N = 60$

(b) $N = 40$

(c) $N = 20$
Figure 13: Total population for SP domain

(a) $N = 60$

(b) $N = 40$

(c) $N = 20$

Figure 14: ARE condition based on Shape parameter

(a) $N = 20$

(b) $N = 40$
Figure 15: Average of population value in iterations

(a) $N = 60$

(b) $N = 40$

(c) $N = 20$
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         | 0.449962534          | 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   | 9.85557e-10  | -3.67796e-07         | -2.23659e-09         | -1.066306e-09        | 2.051861e-09      |
| 1.0   | -7.72143e-10 | -2.21603e-05         | -1.42839e-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         | 1.139696e-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  | 0.9098003610         | 0.0990852949         | 0.0975773248         | 8.472540e-05      |
| 0.4   | 0.1718730376  | 0.1556924837         | 0.1741092475         | 0.1717627291         | 1.103685e-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      |
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