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COMPARATIVE ANALYSIS OF ORTHOGONAL POLYNOMIALS FOR SOLVING VOLTERRA INTEGRAL EQUATION MODEL OF BLOOD GLUCOSE DYNAMICS

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Abstract
In this study, we solve Volterra-type blood glucose concentration model by using collocation approaches which employ four various types of orthogonal polynomial bases such as Lucas polynomials, Modified Boubaker Polynomials, Gegenbauer polynomials, and Touchard polynomials. To achieve this aim, we investigate the effect of these polynomial families on the numerical solution of the model under two different types of collocation points which are uniform points and Chebyshev-Gauss-Lobatto points. The proposed numerical method converts the original Volterra-type model into a system of algebraic equations in terms of the approximate expansion of the unknown blood glucose concentration function via proper polynomial expansions. The efficiency and accuracy of the proposed numerical method are tested according to absolute error, relative error, percentage error, residual error, and CPU time. Moreover, the numerical results of the method using the four different polynomial bases are compared to the exact solution of the model. The comparison between the solutions provides us the effect of the selection of the appropriate polynomial and collocation points on the efficiency and accuracy of the numerical solution. The findings of this study are supposed to present an effective spectral collocation technique for solving Volterra-type blood glucose concentration models.

1 Introduction

Integral equations play an important role in applied mathematics and various scientific fields because they naturally describe memory, hereditary, and cumulative effects. An integral equation involves an unknown function under an integral sign and may generally be written as

$$u(x) = f(x) + \lambda \int_{\alpha(x)}^{\beta(x)} k(x,t)u(t)\,dt, \tag{1.1}$$

where the function $k(x,t)$ is the kernel, $f(x)$ is a known function, λ is the coupling parameter, and $u(x)$ is the unknown function. Based on the limits of integration, integral equations are commonly classified as Volterra and Fredholm equations. A Volterra integral equation has a variable upper limit,

$$u(x) = f(x) + \lambda \int_{a}^{x} k(x,t)u(t)\,dt, \tag{1.2}$$

whereas a Fredholm integral equation has fixed limits,

$$u(x) = f(x) + \lambda \int_{a}^{b} k(x,t)u(t)\,dt. \tag{1.3}$$

Volterra equations are particularly suitable for models in which the present state depends on previous states. They arise in population dynamics, biological systems, and other applications involving memory effects. In population biology, Volterra-type models can describe population evolution by incorporating reproduction, mortality, competition, environmental resistance, and historical effects [1–5]. Since exact solutions are often difficult to obtain for differential and integral equations, especially for practical problems, numerical and semi-analytical methods are essential and have been proposed by several researchers, such as [2, 6–10] and the references cited therein.

Polynomial approximation, collocation, and operational matrix methods have been widely used for the numerical solution of Volterra and related integral equations. Legendre polynomials have been successfully employed in collocation methods for Volterra integro-differential equations [10], while Boubaker polynomials have been applied to many differential and integral equations using operational matrices and collocation techniques [11]. Modified Boubaker Polynomials have also been developed and studied through their orthogonality, recurrence relations, Rodrigues formula, and Sturm–Liouville properties, providing a useful basis for numerical approximation [12]. Similarly, Lucas polynomials have been incorporated into operational matrix methods for Volterra-type equations and demonstrated promising numerical accuracy [13]. Other families, including Gegenbauer and Touchard polynomials, have also been considered in spectral and collocation-based numerical methods, see for example; [14-16]. The dynamics of blood glucose are affected by various physiological activities, and the current level of glucose depends on previous states and inputs. The historical nature of the system under consideration is one of the factors that make Volterra integral equations suitable for blood glucose dynamics modeling. This study presents such a system that enables comparison of various polynomials.

Although numerous numerical approaches have been developed for Volterra integral equations [8, 9, 17–21], most studies focus on a single polynomial family or a limited numerical framework. To the best of our knowledge, a systematic comparison of Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials for the same Volterra integral equation has received limited attention.

Motivated by this gap, the present study investigates and compares these four polynomial bases for the numerical solution of a Volterra integral equation arising from a blood glucose concentration model. A common collocation framework with uniform and Chebyshev–Gauss–Lobatto nodes is employed to ensure a consistent comparison. The performance of the polynomial bases is evaluated in terms of accuracy, convergence, numerical stability, and computational efficiency. The study aims to identify suitable combinations of polynomial bases and collocation points and to provide useful numerical guidelines for efficient modeling of glucose dynamics.

2 Material and Methods

The present study uses a numerical methodology to solve a linear Volterra integral equation that comes from a blood glucose concentration model. Four different polynomial families, namely Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials, are used to build approximations of the unknown glucose concentration. The same mathematical model and the same numerical framework are used for all four families so that the performance of each can be compared under consistent conditions.

The proposed procedure has several steps. First, the blood glucose model is written as a Volterra equation. Next, the solution is approximated with a finite polynomial expansion. Then, the needed bases are generated. After that, the coefficients are obtained by using collocation, and finally, the solutions are evaluated according to the error measures and computational time. Both uniform collocation points and Chebyshev–Gauss–Lobatto collocation points are tested to see how each

affects the accuracy of the numerical approximations. Finally, the resulting solutions are compared with the exact solution of the blood glucose model.

2.1 Mathematical Model

The mathematical model used in this study describes the blood glucose concentration $C(t)$ of a patient during continuous intravenous glucose infusion. As discussed in [22], it is written as the following linear Volterra integral equation:

$$C(t) = C_i + \frac{\alpha}{V}t - k\int_0^t C(x)\,dx, \qquad t \in [0,T]. \quad (2.1)$$

Here, $C(t)$ represents the blood glucose concentration at time t measured in mg/dL, C_i denotes the initial glucose concentration (mg/dL), α is the rate of glucose infusion (mg/min), V represents the glucose distribution volume in dL, and k is the constant rate of glucose elimination measured in min^{-1}. The presence of the integral term shows that the concentration at a given time depends on the previous values of the concentration, which gives the model its Volterra structure.
The goal is to get a numerical approximation of $C(t)$ and to study the performance of the four chosen orthogonal polynomial families in solving the model given in (2.1).

2.2 Polynomial Approximation

The unknown function $C(t)$ is approximated by a polynomial expansion of degree N in the form as follows:

$$C_N(t) = \sum_{i=0}^{N} a_i\,\Phi_i(t), \quad (2.2)$$

where $\Phi_i(t)$ is the chosen polynomial basis, a_i are the unknown coefficients, and N is the degree of approximation.
The basis $\Phi_i(t)$ is selected one after another from the Lucas, Modified Boubaker, Gegenbauer, and Touchard orthogonal polynomial families. Substituting the approximation into the Volterra integral equation (2.1) gives the following form:

$$\sum_{i=0}^{N} a_i\,\Phi_i(t) = C_i + \frac{\alpha}{V}t - k\int_0^t \sum_{i=0}^{N} a_i\,\Phi_i(x)\,dx. \quad (2.3)$$

Because the summation has a finite number of terms, the equation can be written as

$$\sum_{i=0}^{N} a_i\,\Phi_i(t) = C_i + \frac{\alpha}{V}t - k\sum_{i=0}^{N} a_i\int_0^t \Phi_i(x)\,dx. \quad (2.4)$$

This expression is then evaluated at the selected collocation points to determine the unknown coefficients.

2.3 Orthogonal Polynomial Bases

In this study, four orthogonal polynomial families are examined. The definitions and recurrence relations for each family are used to construct the basis functions needed for the approximation.

2.3.1 Lucas Polynomials

Lucas polynomials $L_n(t)$, as explained in [13], are defined by the recurrence relation

$$L_n(t) = tL_n - 1(t) + L_{n-2}(t), \qquad n \geq 2, \quad (2.5)$$

with initial conditions

$$L_0(t) = 2, \qquad L_1(t) = t. \quad (2.6)$$

The approximate solution based on the Lucas polynomial family is written as follows:

$$C_N^{(L)}(t) = \sum_{i=0}^{N} a_i\,L_i(t), \quad (2.7)$$

where the parameters a_i are the unknown Lucas coefficients.

2.3.2 Modified Boubaker Polynomials

The Modified Boubaker family, as proposed in [12], is denoted by $M_n(t)$. The corresponding recurrence relation is given by

$$M_n(\boldsymbol{t}) = B_n(\boldsymbol{t}) - \sum_{i=0}^{n-1} \frac{\langle B_n(\boldsymbol{t}), M_i(\boldsymbol{t})\rangle}{\langle M_i(\boldsymbol{t}), M_i(\boldsymbol{t})\rangle} M_i(\boldsymbol{t}), \quad (2.8)$$

where

$$B_n(t) = \sum_{p=0}^{\lfloor n/2 \rfloor} \frac{n-4p}{n-p} \binom{n-p}{p} (-1)^p t^{n-2p}. \quad (2.9)$$

with initial polynomials to be as follows:

$$P_0(t) = 1, \qquad P_1(t) = t - 1. \quad (2.10)$$

Using these polynomials as the basis functions, the approximate solution is represented in the following form:

$$C_N(t) = \sum_{n=0}^{N} a_n M_n(t), \quad (2.11)$$

where $a_n, n = 0,1, \dots, N$, are unknown Modified Boubaker coefficients. The Modified Boubaker basis is first generated up to the required degree and then incorporated into the same collocation procedure used for the other polynomial families.

2.3.3 Gegenbauer Polynomials

Gegenbauer polynomials $C_n^{(\alpha)}(t)$, as discuused in [14], satisfy the recurrence relation

$$C_n^{(\alpha)}(t) = 1/n[2t(n + \alpha - 1)tC_{n-1}^{(\alpha)}(t) - (n + 2\alpha - 2)C_{n-1}^{(\alpha)}(t)], \quad (2.12)$$

with initial conditions

$$C_0^{(\alpha)}(t) = 1, \qquad C_1^{(\alpha)}(t) = 2\alpha t. \quad (2.13)$$

For the present study, the parameter α is selected as:

$$\alpha = 0.5. \quad (2.14)$$

The corresponding approximate solution is therefore as follows and is given by:

$$C_N^{(G)}(t) = \sum_{i=0}^{N} a_i C_i^{(0.5)}(t), \quad (2.15)$$

where the parameters c_i are the unknown coefficients.

2.3.4 Touchard Polynomials

The Touchard polynomials $T_n(t)$, as mentioned in [15], are defined in terms of the Stirling numbers of the second kind as

$$T_n(t) = \sum_{k=0}^{n} S(n,k) t^k, \quad (2.16)$$

where $S(n,k)$ denotes the Stirling number of the second kind. They can also be generated using the recurrence.

$$T_{n+1}(t) = t\left(T_n(t) + \frac{d}{dt} T_n(t)\right), \quad (2.17)$$

with

$$T_0(t) = 1. \quad (2.18)$$

The approximate solution using the Touchard polynomial basis is given by

$$C_N^{(T)}(t) = \sum_{i=0}^{N} d_i T_i(t), \quad (2.19)$$

Where the parameters d_i are the unknown Touchard coefficients.

2.4 Collocation Method

The collocation method is used to determine the unknown coefficients of each polynomial approximation. When a chosen polynomial approximation is substituted into the Volterra integral equation, the resulting equation should satisfy the governing equation at several discrete collocation points.

In this study, two types of collocation points are considered: uniform and Chebyshev–Gauss–Lobatto.

2.4.1 Uniform Collocation Points

The uniform collocation points for the interval $[0, T]$ are given as

$$t_j = \frac{jT}{K}, \qquad j = 0,1, \dots, K. \quad (2.20)$$

Here, the computational interval is divided evenly.

2.4.2 Chebyshev–Gauss–Lobatto Collocation Points

The Chebyshev–Gauss–Lobatto collocation points are defined as

$$t_j = \frac{T}{2}\left(1 + \cos\frac{j\pi}{K}\right), \qquad j = 0,1,\dots,K. \tag{2.21}$$

The two distributions of collocation points are applied to each polynomial family to investigate their effect on the numerical approximation.

2.5 Determination of the Polynomial Coefficients

For the general approximation

$$C_N(t) = \sum_{i=0}^{N} a_i\, \Phi_i(t), \tag{2.22}$$

Substituting this expression into the integral equation and evaluating at a collocation point t_j gives the following result.

$$\sum_{i=0}^{N} a_i \left[\Phi_i(t_j) + k\int_0^{t_j} \Phi_i(x)\,dx\right] = C_i + \frac{\alpha}{V} t_j. \tag{2.23}$$

Applying the above equation at

$$t_j, \qquad j = 0,1,\dots,N,$$

produces a system of $N+1$ linear algebraic equations for the $N+1$ unknown coefficients.

The resulting system can be represented in matrix form as

$$A\boldsymbol{a} = \boldsymbol{b}, \tag{2.24}$$

where A is the coefficient matrix, $\boldsymbol{a}$ is the vector of unknown polynomial coefficients, and $\boldsymbol{b}$ is the vector on the right-hand side.

The coefficient vector $\boldsymbol{a}$ is obtained by solving this linear system. The resulting coefficients are then substituted into the corresponding polynomial expansion to construct the numerical approximation of the blood glucose concentration. This procedure is done independently for the Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomial bases.

2.6 Procedure for Numerical Simulations

The numerical procedure used in this study begins by formulating the blood glucose concentration model as a linear Volterra integral equation. To solve the integral equation numerically, an accurate degree N of a polynomial is first selected. Then four different polynomial families, namely the Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials, are generated up to polynomial degree N. The unknown blood glucose concentration is approximated by a finite expansion in terms of the selected polynomial basis.

The resulting polynomial approximation is substituted into the Volterra integral equation. To reduce the continuous problem into a system of algebraic equations, the governing equation is evaluated at collocation points within the computational interval. Two sets of collocation points, namely Chebyshev–Gauss–Lobatto points and uniformly distributed points, are considered to investigate the influence of point selection on the numerical performance of the problem.

Evaluation of the governing equation at the collocation points leads to a linear algebraic system whose unknowns are the polynomial coefficients. The linear system is then solved to get the polynomial coefficients and construct the polynomial approximation $C_N(t)$. Comparison is made between the numerical approximation obtained using the four polynomial bases and their corresponding analytical solutions. To evaluate the accuracy and reliability of the proposed numerical schemes, several error measures are computed, including absolute error, relative error, percentage error, and residual error. In addition, the computational efficiency of each method is assessed by investigating the required computational time. A comprehensive comparison is finally performed among the four polynomial families under both uniform and Chebyshev–Gauss–Lobatto collocation-point distributions. This comparative analysis shows the influence of the polynomial basis and collocation

methods on the accuracy, convergence behavior, and computational efficiency of the numerical solution of the blood glucose concentration model.

2.7 Error Analysis

The precision of each numerical approximation is computed by comparing the numerical solution $C_N(t)$ with the exact solution $C(t)$. The following error measures are considered:

2.7.1 Absolute Error

The absolute error is defined as

$$E_{\text{abs}}(t) = |C(t) - C_N(t)|.$$

2.7.2 Relative Error

The relative error is given by

$$E_{\text{rel}}(t) = \frac{|C(t) - C_N(t)|}{|C(t)|}.$$

2.7.3 Percentage Error

The percentage error is calculated as

$$E_{\text{perc}}(t) = \frac{|C(t) - C_N(t)|}{|C(t)|} \times 100\%.$$

2.7.4 Residual Error

The residual error is used to calculate how closely the numerical approximation satisfies the original Volterra integral equation. It is defined as

$$R_N(t) = C_N(t) - \left[C_i + \frac{\alpha}{V}t - k\int_0^t C_N(x)\,dx\right].$$

A smaller residual shows that the numerical approximation satisfies the governing integral equation closely.

2.8 Computational Efficiency

In addition to the error measures, we also recorded the time required by each polynomial method in seconds. The CPU time indicates how much computational effort is needed to construct and test the numerical approximation.

We recorded the time under the same conditions for all four polynomial families and for both collocation-point distributions. This allows us to compare the methods in terms of both numerical accuracy and computational efficiency.

2.9 Comparative Evaluation

The final stage of the methodology entails carrying out a comparison of the numerical results generated using the four types of polynomials. This comparison will be carried out at different degrees of polynomials in order to determine how the increased degree of approximation changes the accuracy of the numerical result. This will be done by considering the polynomial methods in terms of absolute error, relative error, percentage error, residual error, CPU time, and degree of polynomial. Also, the impact of the two different collocation point distributions will be considered. The numerical solutions that will be generated using Lucas, modified Boubaker, Gegenbauer, and Touchard polynomials will be compared to the exact solution. All the comparisons will be done using the same mathematical method and under similar computational conditions. In this way, the impact of using different polynomials on the accuracy and computational efficiency of the numerical solutions will be assessed.

3 Numerical Experiments with Results and Discussion

This section presents the numerical experiments performed to investigate the accuracy and computational performance of the proposed collocation methods based on Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomial bases. The four polynomial families are applied to the same Volterra integral equation so that their numerical behavior can be compared under identical model parameters and computational conditions.

Problem 1. ***The blood glucose concentration model is as follows:***

$$C(t) = C_i + \frac{\alpha}{V}t - k\int_0^t C(x), dx, 0 \le t \le 1.$$

where $C_i = 30,\quad \alpha = 20,\quad V = 41,\quad k = 0.0058,$ *In the present experiment given in Problem 1, the collocation system is formed using uniform collocation points with* $M = 5$ *. The approximate and exact solutions are subsequently evaluated at* $t = 0.5$.

The results for Problem 1 presented in Table 1 and Figure 1 demonstrate that all four polynomial methods provide highly accurate approximations. The Modified Boubaker Method (MBM) achieves zero absolute, relative, and percentile errors at $t = 0.5$, while the Lucas Method (LM) and Gegenbauer Method (GM) produce absolute errors of 3.55×10^{-15} and the Touchard Method (TM) gives 7.11×10^{-15}. The residual error is identical for all methods at 2.27×10^{-4}. In terms of computational efficiency, MBM requires the least CPU time (5.87×10^{-5} s), followed closely by GM, whereas TM requires the highest computational time. Figure 1 further shows that the absolute-error curves are very close to each other, confirming the comparable accuracy of the four approaches.

3.1 Experimental Setup

The numerical experiments are carried out for the blood glucose concentration model

$$C(t) = C_i + \frac{\alpha}{V}t - k\int_0^t C(x), dx, \quad 0 \le t \le 1.$$

where the exact solution is given by

$$C(t) = C_i e^{-kt} + \frac{\alpha}{Vk}\left(1 - e^{-kt}\right).$$

The numerical approximations are constructed using polynomial expansions based on the Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomial families.

Table 1. Error metrics obtained using the four polynomial methods at $t = 0.5$ ***and*** $M = 5$ ***with uniform collocation points for Problem 1.***

Method	AE	RE	PE	Residual	CPU Time
LM	3.55×10^{-15}	1.18×10^{-16}	1.18×10^{-14}	2.27×10^{-4}	6.11×10^{-5}
MBM	0	0	0	2.27×10^{-4}	5.87×10^{-5}
GM	3.55×10^{-15}	1.18×10^{-16}	1.18×10^{-14}	2.27×10^{-4}	5.88×10^{-5}
TM	7.11×10^{-15}	2.36×10^{-16}	2.36×10^{-14}	2.27×10^{-4}	8.58×10^{-5}

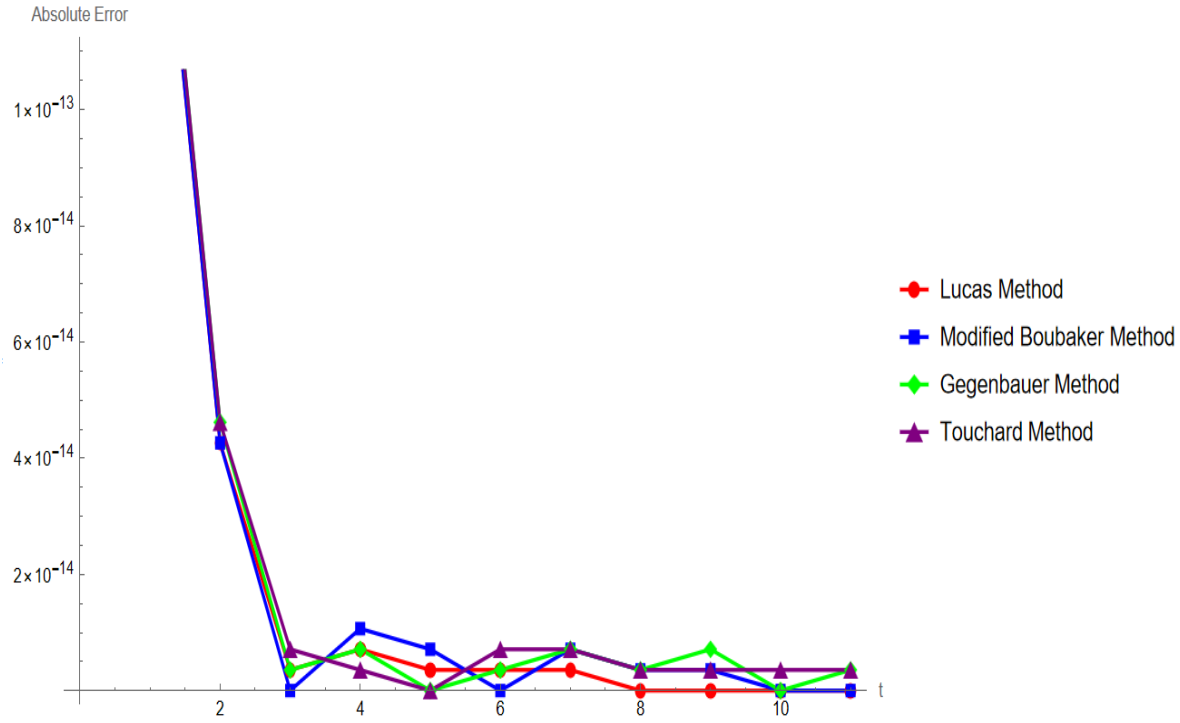

Figure 1. The comparison of the absolute errors obtained from the four polynomial methods for Problem 1 is carried out using uniform collocation points with $M = 5$.

Problem 2. ***The blood glucose concentration model is as follows:***

$$C(t) = C_i + \frac{\alpha}{V}t - k\int_0^t C(x), dx, \quad 0 \le t \le 1.$$

where $C_i = 46, \quad \alpha = 25, \quad V = 34, \quad k = 0.0487,$

In the present experiment given in Problem 2, the collocation system is formed using four different polynomial methods, namely Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials, with uniform collocation points with $M = 5$. *The approximate and exact solutions are subsequently evaluated at* $t = 0.5$.

For Problem 2, Table 2 shows that all four polynomial methods produce identical error measures to the reported precision, with an absolute error of 2.30×10^{-11}, relative error of 5.07×10^{-13}, and percentile error of 5.07×10^{-11}. The residual error is also identical for all methods, equal to 9.01×10^{-3}. However, a considerable difference is observed in CPU time: the Modified Boubaker Method is the fastest (4.36×10^{-5} s), closely followed by the Touchard Method (4.39×10^{-5} s), whereas the Lucas Method requires substantially higher computational time. Figure 2 shows that the absolute-error profiles of the four methods are nearly coincident, indicating essentially equivalent numerical accuracy for this problem.

Table 2. Error metrics obtained using the four polynomial methods at $t = 0.5$ *and* $M = 5$ *with uniform collocation points for Problem 2.*

Method	AE	RE	PE	Residual	CPU Time
LM	2.30×10^{-11}	5.07×10^{-13}	5.07×10^{-11}	9.01×10^{-3}	2.69×10^{-2}
MBM	2.30×10^{-11}	5.07×10^{-13}	5.07×10^{-11}	9.01×10^{-3}	4.36×10^{-5}
GM	2.30×10^{-11}	5.07×10^{-13}	5.07×10^{-11}	9.01×10^{-3}	7.45×10^{-5}
TM	2.30×10^{-11}	5.07×10^{-13}	5.07×10^{-11}	9.01×10^{-3}	4.39×10^{-5}

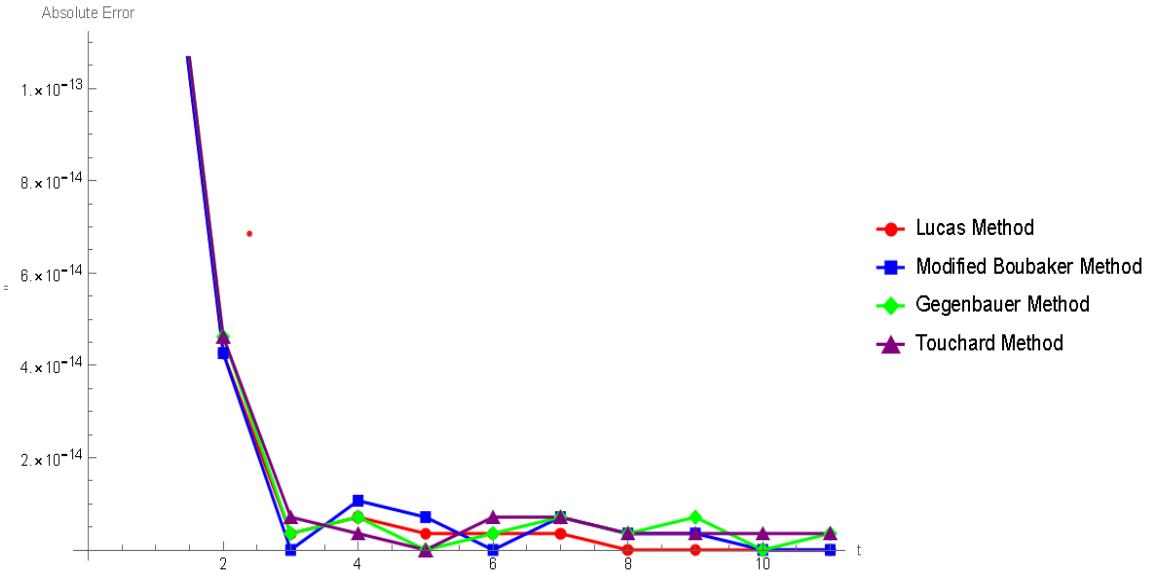

Figure 2. The comparison of absolute errors produced by each method under consideration for Problem 2 using uniform collocation points with $M = 5$.

Problem 3. ***The blood glucose concentration model is as follows:***

$$C(t) = C_i + \frac{\alpha}{V}t - k\int_0^t C(x), dx, \quad 0 \le t \le 1.$$

where $C_i = 23, \quad \alpha = 19, \quad V = 11, \quad k = 0.0865,$ *In the present experiment given in Problem 3, the collocation system is formed using four different polynomial bases, namely Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials, with uniform collocation points using* $M = 5$. *The approximate and exact solutions are subsequently evaluated at* $t = 0.5$.

For Problem 3, the results in Table 3 indicate that the four polynomial methods yield exactly the same error measures to the reported precision. Each method produces an absolute error of 2.89×10^{-11}, relative error of 1.26×10^{-12}, percentile error of 1.26×10^{-10}, and residual error of 2.75×10^{-3}. The main difference is observed in computational cost, where MBM requires the lowest CPU time (4.37×10^{-5} s), followed by GM (4.71×10^{-5} s), while LM requires considerably more computational time. As illustrated in Figure 3, the error curves corresponding to all four polynomial bases almost completely overlap, confirming their comparable accuracy for the considered problem.

Table 3. Error metrics obtained using the four polynomial methods at $t = 0.5$ and $M = 5$ with uniform collocation points for Problem 3.

Method	AE	RE	PE	Residual	CPU Time
LM	2.89×10^{-11}	1.26×10^{-12}	1.26×10^{-10}	2.75×10^{-3}	1.29×10^{-2}
MBM	2.89×10^{-11}	1.26×10^{-12}	1.26×10^{-10}	2.75×10^{-3}	4.37×10^{-5}
GM	2.89×10^{-11}	1.26×10^{-12}	1.26×10^{-10}	2.75×10^{-3}	4.71×10^{-5}
TM	2.89×10^{-11}	1.26×10^{-12}	1.26×10^{-10}	2.75×10^{-3}	5.16×10^{-5}

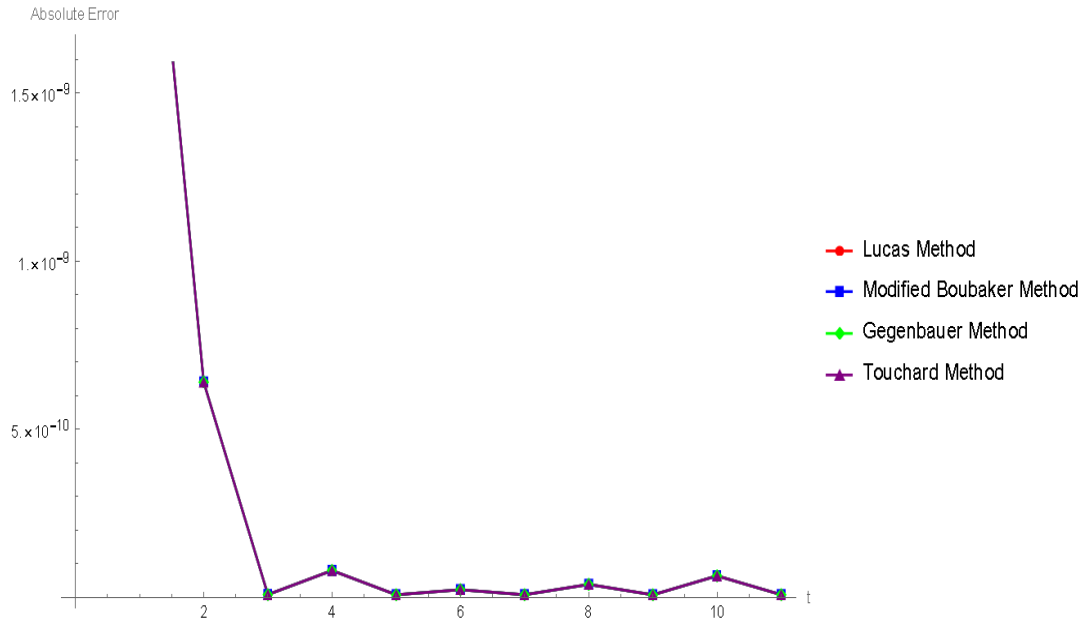

Figure 3. Comparison of absolute errors produced by each method under consideration for Problem 3 taking uniform collocation points with $M = 5$.

Problem 4. ***The blood glucose concentration model is as follows:***

$C(t) = C_i + \frac{\alpha}{V}t - k\int_0^t C(x), dx, \quad 0 \le t \le 1.$

where $C_i = 45, \quad \alpha = 23, \quad V = 37, \quad k = 0.0055,$ *In the present experiment given in Problem 4, the collocation system is formed using four different polynomial bases, namely Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials, with Chebyshev Gauss–Lobatto collocation points using* $M = 3$. *The approximate and exact solutions are subsequently evaluated at* $t = 0.5$.

For Problem 4, Table 4 demonstrates that all four polynomial methods produce identical numerical errors, with an absolute error of 7.11×10^{-15}, relative error of 1.57×10^{-16}, percentile error of 1.57×10^{-14}, and residual error of 2.57×10^{-4}. The CPU times are also relatively close, although GM records the lowest computational time (5.80×10^{-5} s), followed by TM and MBM, while LM requires the highest time. Figure 4 confirms that the absolute-error curves obtained from the four methods are virtually indistinguishable, demonstrating that all four polynomial bases provide highly consistent approximations for this problem.

Table 4. Error metrics obtained using the four polynomial methods at $t = 0.5$ and $M = 3$ with Chebyshev Gauss–Lobatto collocation points for Problem 4.

Method	AE	RE	PE	Residual	CPU Time
LM	7.11×10^{-15}	1.57×10^{-16}	1.57×10^{-14}	2.57×10^{-4}	1.01×10^{-4}
MBM	7.11×10^{-15}	1.57×10^{-16}	1.57×10^{-14}	2.57×10^{-4}	7.41×10^{-5}
GM	7.11×10^{-15}	1.57×10^{-16}	1.57×10^{-14}	2.57×10^{-4}	5.8×10^{-5}
TM	7.11×10^{-15}	1.57×10^{-16}	1.57×10^{-14}	2.57×10^{-4}	6.81×10^{-5}

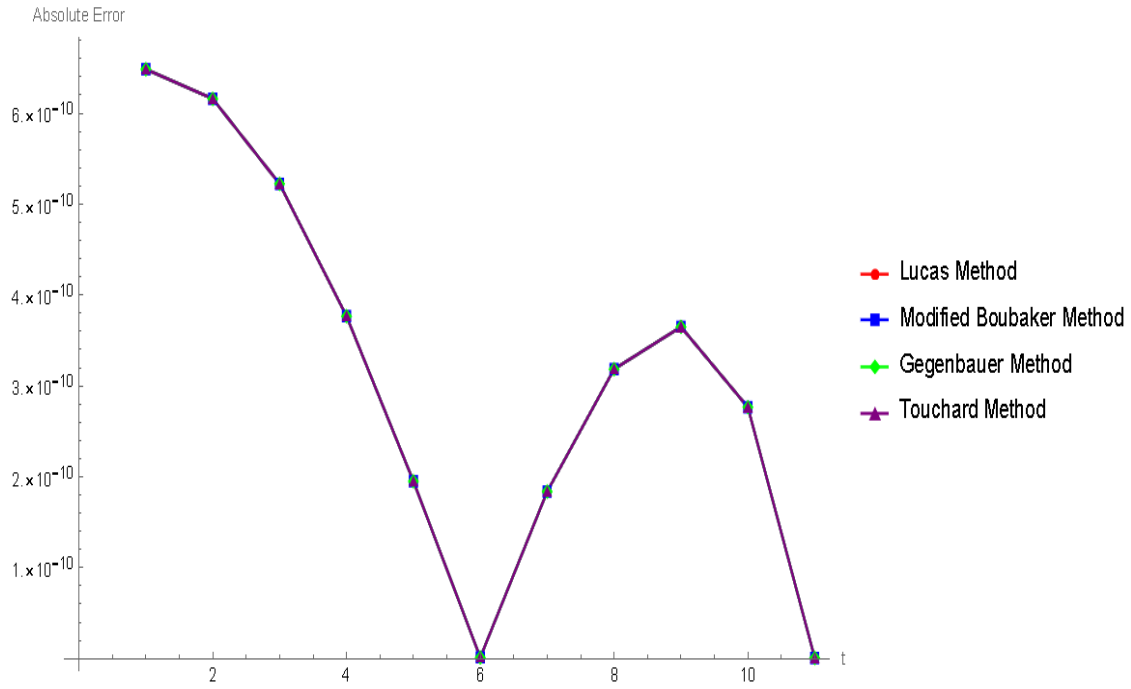

Figure 4. The comparison of absolute errors produced by each method under consideration for Problem 4 using Chebyshev Gauss–Lobatto collocation points with $M = 3$.

Problem 5. ***The blood glucose concentration model is as follows:***

$$C(t) = C_i + \frac{\alpha}{V}t - k\int_0^t C\,(x), dx, \quad 0 \le t \le 1.$$

where $C_i = 52, \quad \alpha = 34, \quad V = 25, \quad k = 0.0084,$

In the present experiment given in Problem 5, the collocation system is formed using four different polynomial bases, namely Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials, with Chebyshev Gauss–Lobatto collocation points using $M = 3$.

The comparative results for Problem 5, given in Table 5, show that all four polynomial methods achieve identical error measures to the reported precision. The absolute error is 1.51×10^{-11}, the relative error is 2.88×10^{-13}, the percentile error is 2.88×10^{-11}, and the residual error is 9.67×10^{-4} for each method. Regarding computational efficiency, GM provides the lowest CPU time (3.87×10^{-5} s), followed by TM, LM, and MBM. Figure 5 shows an almost complete overlap of the absolute-error curves, further confirming that the four polynomial bases exhibit essentially the same numerical accuracy for the considered problem.

Table 5. Error metrics obtained using the four polynomial methods at $t = 0.5$ and $M = 3$ with Chebyshev Gauss–Lobatto collocation points for Problem 5.

Method	AE	RE	PE	Residual	CPU Time
LM	1.51×10^{-11}	2.88×10^{-13}	2.88×10^{-11}	9.67×10^{-4}	4.44×10^{-5}
MBM	1.51×10^{-11}	2.88×10^{-13}	2.88×10^{-11}	9.67×10^{-4}	4.54×10^{-5}
GM	1.51×10^{-11}	2.88×10^{-13}	2.88×10^{-11}	9.67×10^{-4}	3.87×10^{-5}
TM	1.51×10^{-11}	2.88×10^{-13}	2.88×10^{-11}	9.67×10^{-4}	4.4×10^{-5}

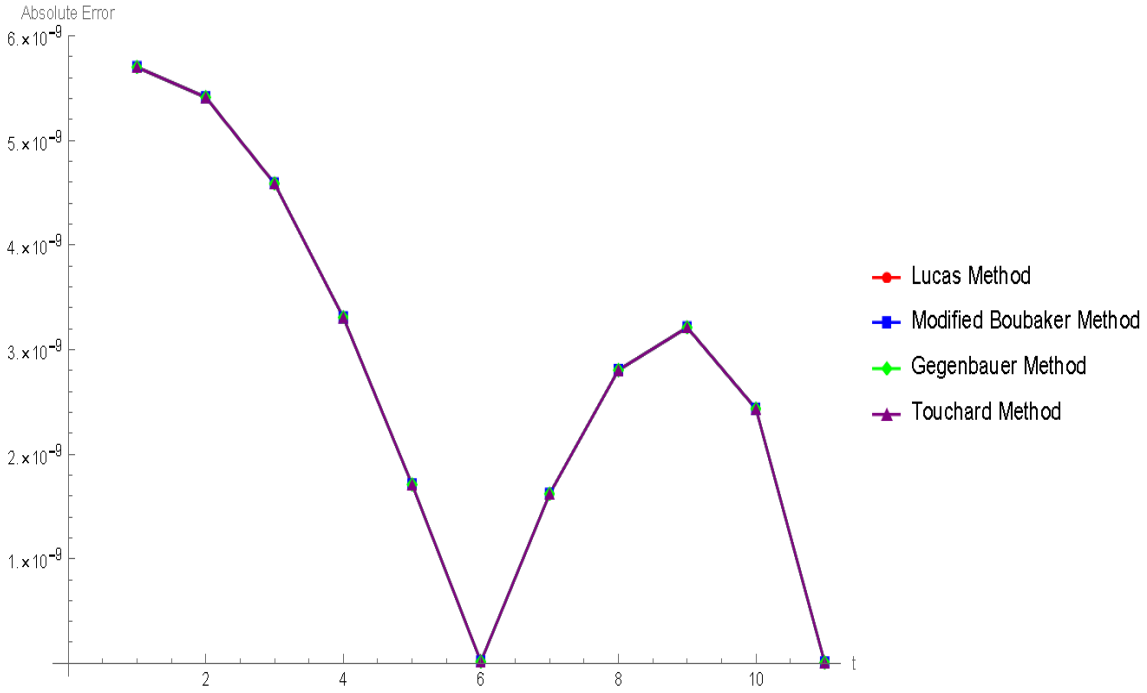

Figure 5. The comparison of absolute errors produced by each method under consideration for Problem 5 using Chebyshev Gauss–Lobatto collocation points with $M = 3$.

Across the five numerical problems, the comparative analysis demonstrates that the Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomial methods provide highly accurate and consistent approximations to the considered Volterra-type blood glucose concentration model. The reported absolute errors in Tables 1–5 range from approximately 10^{-15} to 10^{-11}, while the error curves in Figures 1–5 are almost completely coincident, indicating no substantial difference in accuracy among the polynomial bases for the test cases considered. In contrast, noticeable variations are observed in computational efficiency, with the Modified Boubaker method generally performing efficiently for uniform collocation points, while the Gegenbauer method exhibits comparatively lower CPU times for the Chebyshev–Gauss–Lobatto cases. Overall, the results indicate that the choice of polynomial basis has little effect on accuracy for these smooth test problems but can influence the computational cost of the numerical procedure.

4 Concluding Remarks with Future Directions

In this study, a Volterra-type blood glucose concentration model was solved using a spectral collocation approach based on four polynomial bases, namely Lucas, Modified Boubaker, Gegenbauer, and Touchard polynomials. Both uniformly distributed and Chebyshev–Gauss–Lobatto collocation points were considered, and the numerical performance was assessed through absolute, relative, percentage, and residual errors, together with CPU time. The numerical results show that all four polynomial methods provide highly accurate approximations to the exact solution for the considered parameter sets, with errors reaching orders as small as 10^{-15}–10^{-11}. The corresponding error plots also demonstrate that the numerical solutions obtained from the four bases are nearly indistinguishable. Although the four methods exhibit comparable accuracy, noticeable differences are observed in computational efficiency. For the uniform collocation cases, the Modified Boubaker method

generally requires less CPU time among the methods considered, whereas the Gegenbauer method provides the lowest CPU time in the reported Chebyshev–Gauss–Lobatto cases. The results obtained above indicate that in the smooth case of blood glucose model, which is used in the current investigation, the choice of the polynomial basis affects more the computation time compared to its impact on approximation error. Thus, the suggested polynomial-based collocation approach represents an effective and accurate numerical method for the solution of the investigated Volterra-type model of blood glucose concentration. In the future, the introduced methodology may be developed to be applied to non-linear and fractional Volterra models, glucose-insulin models and multi-dimensional biomedical models.

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