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An Efficient Genocchi Wavelet Collocation Approach for Analyzing the Dynamics of a Human Liver Model

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Abstract:
Mathematical models play a significant role in capturing dynamics of the biological models which explains the non-linear phenomena in living organisms. In this article, we study mathematical model of human liver via a numerical approach called Genocchi wavelet collocation method. The primary objective of this study is explore and determine the results for system of ordinary differential equations arising in the considered mathematical model and to investigate the dynamical aspects model. This model consists of two system of equations that is Bromsulphthalein (BDP) content in blood (Z) and Bromsulphthalein (BDP) content in liver (W). The numerical results of the considered system is executed by proposed method and also compared with Euler method. The results are analysed using graphs and plots which shows the precise dynamics of the model. The proposed technique is highly effective, accurate, and takes less time to examine nonlinear difficulties in a variety of epidemical and biological models. Finally, the present work contributes to examining the wild class of models and their performance in the real world.

***Key Word**: Liver model; Collocation method; Mathematical Modeling; Numerical Simulation.*

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I. Introduction

Liver is a largest internal organ and central chemical processing plant of the human body which have major importance in metabolism and also responsible for filtration of blood and neutralization of toxins. Liver also helps in removal of toxins, alcohol, and drugs into safe waste products and also produces bile juice which helps to reduction of fats while digestion. It also has importance in building proteins, storing energy. The liver is a triangle organ located in the abdominal cavity below the diaphragm. The liver is one of the most active and complex organs with the most functions in the human body. Bromsulphthalein (BSP) a synthetic dye is used to measure the working capacity of the liver by injecting it into the blood. Then liver is the only organ to absorb (BSP) from blood and sends it with bile. Then after sometime liver must extract the dye from bloodstream and must send it to membranes but if it fails to actively absorb dye then liver cells have lost their capacity to absorb[1,2] Baleanu et al.[3] worked on mathematical model of liver via Caputo-Fabrizio fractional derivative. Calvetti et al.[4] studied spatially distributed two-compartment (blood and tissue) model for liver metabolism using fast adaptive Markov chain Monte Carlo (MCMC) sampling scheme. Chalhoub et al. [5] investigated carbohydrate transport and metabolism of the liver during rest and height intensity workout. Friedman and Hao[6] developed mathematical model of liver fibrosis by a system of partial differential equations. Bonfiglio et al.[7] developed a mathematical model of blood circulation in the liver lobule which determines the pressure and flux distributions within a liver lobule. Many other mathematical models are also developed to study the dynamics of liver[8,9].

Differential equations are those mathematical equations which consist of an unknown function together with one or more of its derivatives. These are the most important means for modelling systems where states depend continuously on time or space coordinates. They occur in numerous fields such as physics[10], nanotechnology[11], biology[12], biochemistry[13], fluids [14] and even economics[15]. The study of differential equations is nothing but the study of rates of change and relationships among the variables in the system. The differential equations are divided into ordinary differential equations[16] and partial differential equations[17] based on the number of independent variables that the differential equation contains.

At the end of the 17th century, Newton and Leibniz began discovering the calculus from their history of differential equations came into existence[18]. Newton used differential equations in order to develop laws of motion and gravitation, whereas Leibniz developed notation to make analysis of the thing (mathematical operations) easier. In the eighteenth and nineteenth centuries, differential equations were extensively used and developed by several mathematicians including Euler, Lagrange, Laplace, and Cauchy. Throughout history, differential equations became very important for research in science and engineering[19]. Differential equations are still of great significance for various branches of knowledge today.

Traditional numerical approaches such as finite differences and classic spectral techniques tend to be unable to achieve compromise between accurate global calculations and detailed local results while solving differential equations.[20] Wavelet theory provides a solution for this issue through the concept of multi-resolution analysis, which acts as a mathematical zooming approach to decomposing the solution into a series of nested levels containing local details. The process involves scaling and translating a base function called the mother wavelet to form an adjustable mathematical basis. Since wavelets have compact support, i.e., they are null outside a certain domain, they can capture localized discontinuities or singularities without interfering with the global matrix of computation. Moreover, the presence of vanishing moments ensures that the output matrices from the calculations are highly sparse. When solving differential equations, operators involving calculus are mapped to the bases using the operational matrix of differentiation.

Taking advantage of the above features, the Genocchi Wavelet Method (GWM) utilizes a very effective family of wavelets that have been developed based on Genocchi polynomials, but only over certain subintervals[21]. As opposed to classic wavelets such as Chebyshev or Legendre wavelets, the Genocchi polynomials only possess integer coefficients, thus preventing any premature truncation error caused by round-offs and the floating-point operations in the calculation process via computer systems. Moreover, they have relatively smaller structures, as fewer number of polynomial coefficients would be necessary to generate the same spatial details, making the most of CPU utilization. In order to solve a differential system directly using this technique without employing integrations, the solution functions along with their derivatives are assumed to consist of the linear combination of these Genocchi basis wavelets. Upon inserting this assumption in the original differential system alongside the collocation technique which forces the residuals of the error term to be zero at certain nodes an algebraic system is obtained.

II. Material And Methods

Preliminaries:

In this part, we briefly explain some essential definitions related to Genocchi Wavelets.

Definition 1. (Genocchi wavelets) The Genocchi wavelets in the interval [0,1) are defined[24, 25] as follows:

$$\psi_{n,m}(t)=\begin{cases} 2^{\frac{k-1}{2}}\,\tilde{G}_m(2^k t-\tilde{n}), & \dfrac{\tilde{n}}{2^{k-1}}\le t\le \dfrac{\tilde{n}+1}{2^{k-1}}, \\ 0, & Otherwise. \end{cases} \qquad (1)$$

with

$$\tilde{G}_m(2^k t-n+1)=\begin{cases} 1, & m=1, \\ \dfrac{1}{\sqrt{\dfrac{2(-1)^{m-1}(m!)^2}{(2m)!}g_{2m}}}\,G_m(2^k t-n+1), & m>1. \end{cases}$$

where $m=0,1,2,\ldots,M-1, n=1,2,\ldots,2^{k-1}. k$ is a positive integer and m is the order of Genocchi polynomial.

Remark 1. The convergence and error analysis of proposed Genocchi wavelets are examined in[22, 23].

Genocchi wavelet matrix of integration (GWMI):

The Genocchi wavelet basis when $k=1$ and $M=6$ is defined as follows[25]:

$$\psi_{1,0}(t)=1,$$

$$\psi_{1,1}(t)=\sqrt{3}(-1+2t),$$

$$\psi_{1,2}(t)=\sqrt{30}(-1+t)t,$$

$$\psi_{1,3}(t)=\sqrt{\frac{35}{17}}(1-6t^{2}+4t^{3}),$$

$$\psi_{1,4}(t)=3\sqrt{\frac{70}{31}}(t-2t^{3}+t^{4}),$$

$$\psi_{1,5}(t)=3\sqrt{\frac{154}{691}}(-1+2t)(1+t-t^{2})^{2},$$

$$\psi_{1,6}(t)=2\sqrt{\frac{3003}{5461}}t(-3+5t^{2}-3t^{4}+t^{5}),$$

$$\psi_{1,7}(t)=3\sqrt{\frac{715}{929569}}(17-84t^{2}+70t^{4}-28t^{6}+8t^{7}).$$

Now, integrating the first six wavelet bases concerning t from limits 0 to t, the linear combination of Genocchi wavelet bases can be expressed in following manner:

$$\int_{0}^{t}\psi_{1,0}(t)dt=\begin{bmatrix}\frac{1}{2} & \frac{1}{2\sqrt{3}} & 0 & 0 & 0 & 0\end{bmatrix}\psi_{6}(t)$$

$$\int_{0}^{t}\psi_{1,1}(t)dt=\begin{bmatrix}0 & 0 & \frac{1}{\sqrt{10}} & 0 & 0 & 0\end{bmatrix}\psi_{6}(t)$$

$$\int_{0}^{t}\psi_{1,2}(t)dt=\begin{bmatrix}-\frac{\sqrt{\frac{5}{6}}}{2} & 0 & 0 & \frac{\sqrt{\frac{17}{42}}}{2} & 0 & 0\end{bmatrix}\psi_{6}(t)$$

$$\int_{0}^{t}\psi_{1,3}(t)dt=\begin{bmatrix}0 & 0 & 0 & 0 & \frac{\sqrt{\frac{31}{34}}}{3} & 0\end{bmatrix}\psi_{6}(t)$$

$$\int_{0}^{t}\psi_{1,4}(t)dt=\begin{bmatrix}3\sqrt{\frac{7}{310}} & 0 & 0 & 0 & 0 & \frac{\sqrt{\frac{691}{1705}}}{2}\end{bmatrix}\psi_{6}(t)$$

$$\int_{0}^{t}\psi_{1,5}(t)dt=\begin{bmatrix}0 & 0 & \frac{1}{\sqrt{10}} & 0 & 0 & 0\end{bmatrix}\psi_{6}(t)$$

$$\int_{0}^{t}\psi(t)dt=P_{6\times 6}\psi_{6}(t)+\bar{\psi}_{6}(t) \qquad (2)$$

where

$$\psi_{6}(t)=\left[\psi_{1,0}(t),\psi_{1,1}(t),\psi_{1,2}(t),\psi_{1,3}(t),\psi_{1,4}(t),\psi_{1,5}(t)\right]^{T}$$

$$B_{6\times 6}=\begin{bmatrix} \frac{1}{2} & \frac{1}{2\sqrt{3}} & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{\sqrt{10}} & 0 & 0 & 0 \\ -\frac{\sqrt{5/6}}{2} & 0 & 0 & \frac{\sqrt{\frac{17}{42}}}{2} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\sqrt{\frac{31}{34}}}{2} & 0 \\ 3\sqrt{\frac{7}{310}} & 0 & 0 & 0 & 0 & \frac{\sqrt{\frac{691}{1705}}}{2} \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$\bar{\psi}_6(t)=\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ \sqrt{\frac{5461}{53898}}\psi_{1,6}(t) \end{bmatrix}.$$

The generalized form of n-wavelet basis of first integration at $k=1$ is demarcated as:

$$\int_0^t \psi(t)dt = P_{n\times n}\psi(t)+\bar{\psi}_n(t).$$

Mathematical Model of Human Liver:

The mathematical model of human liver consists of two system of equations, the amount of Bromsulphthalein (BDP) in the blood (Z) and the amount of Bromsulphthalein (BDP) in the liver (W). The considered model demonstrated as

$$\frac{dZ}{dt}=-aZ+bW$$

$$\frac{dW}{dt}=aZ-(b+d)W \qquad (3)$$

The constants a,b,d are transfer rates and are unknown. $Z(t)$ is the amount of Bromsulphthalein in the blood at time t, $W(t)$ amount of Bromsulphthalein in the liver at time t and the initial conditions are given as

$$Z(0)=Z_0$$

$$W(0)=W_0 \qquad (4)$$

where

$$A^T=\left[a_{1,0},a_{1,1},\ldots a_{1,M-1},a_{2,0},a_{2,1},\ldots a_{2,M-1},\ldots,\ldots a_{2^{k-1},0},a_{2^{k-1},1},\ldots a_{2^{k-1},M-1}\right]$$

$$B^T=\left[b_{1,0},b_{1,1},\ldots b_{1,M-1},b_{2,0},b_{2,1},\ldots b_{2,M-1},\ldots,\ldots b_{2^{k-1},0},b_{2^{k-1},1},\ldots b_{2^{k-1},M-1}\right]$$

where,

$\psi(t)=\left[\psi(t)_{1,0},\ldots\psi(t)_{1,M-1},\psi(t)_{2,0},\ldots\psi(t)_{2,M-1},\ldots\psi(t)_{2^{k-1},0},\ldots\psi(t)_{2^{k-1},M-1}\right].$

A,B are unknown coefficients which are to be determined and $\psi(t)$ is the Genocchi wavelets basis. Integrating the system in Eq. (4) with regard to variable t from 0 to t and interpreting the initial assumptions in terms of wavelet functions, we have

$$Z(t)=C^T\psi(t)+A^T\left[P\psi(t)+\bar{\psi}(t)\right]$$

$$W(t)=D^T\psi(t)+B^T\left[P\psi(t)+\bar{\psi}(t)\right] \qquad (5)$$

Here, C,D are known vectors.

Substitute these values obtained along with Eq. (4) in the model and collocating the system the above system with the following points $t_j=\dfrac{2j-1}{2^k M}$, $j=1,2,\ldots M$. Then, we have got the system of algebraic equations which are derived using collocation points and we extract the unknown coefficients with the aid of Newton-Raphson method. Substituting the unknown coefficients obtained in Eq. (4), we estimate the wavelet solution for the considered model (3).

III. Result

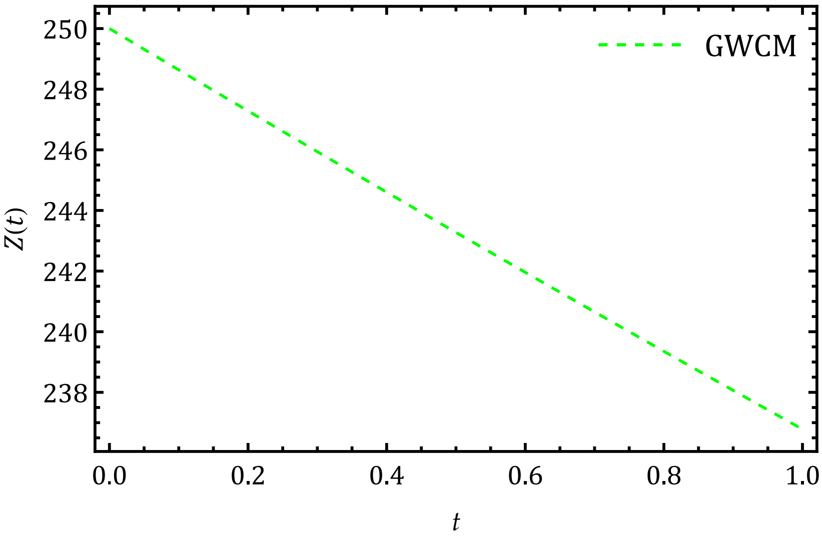

Figure 1: Behaviour of Z(t) for liver model using GWCM.

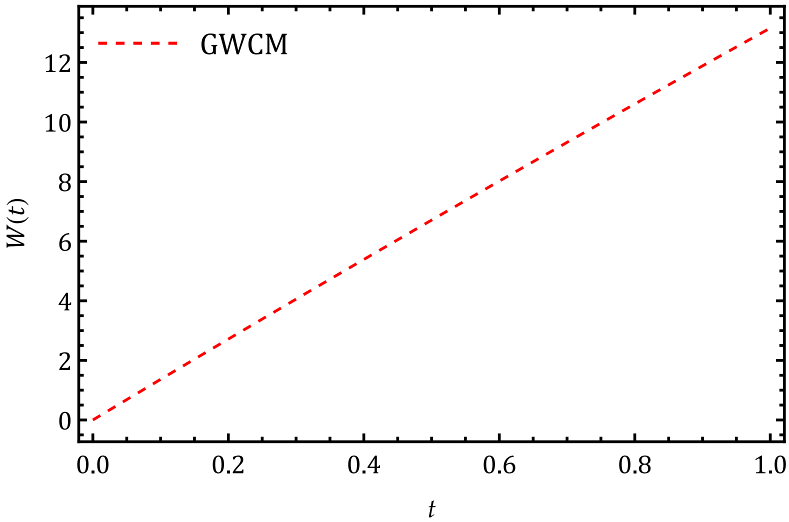

Figure 2: Behaviour of W(t) for liver model using GWCM.

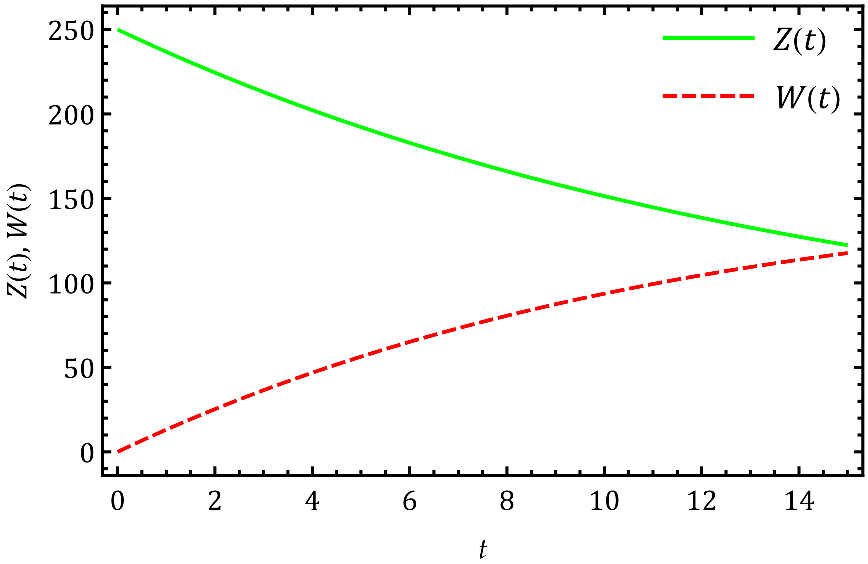

Figure 3: Behaviour of both Z(t) and W(t) for liver model over time t using GWCM.

Table 1: Numerical simulation of Z(t) and W(t) of liver model using proposed method.

t	GWCM Solution of Z(t)	GWCM Solution of W(t)
0	250.0000000000000	0.0
0.1	248.6363783542881	1.3629808381962405
0.2	247.2822676483007	2.7151758862895266
0.3	245.93759959963828	4.056663518340018
0.4	244.6023064175526	5.387521543424266
0.5	243.2763207994063	6.707827209704369
0.6	241.9595759271572	8.01765720846824
0.7	240.65200546386822	9.317087678140963
0.8	239.35354355024197	10.606194208267294
0.9	238.06412480118098	11.885051843465241
1.0	236.7836843023726	13.153735087350743

IV. Discussion

The mathematical model of the human liver presented by a coupled systems of ordinary differential equations are studied using the proposed Genocchi Wavelet Collocation Method (GWCM). The numerical simulation was carried out on interval $0 < t < 1$ using the initial conditions as $Z(0) = 250$ and $W(0) = 0$ .Numerical values obtained are given in Tables 1 and 2. From Table 1 and Figure 1 we can see that the concentration of Bromsulphthalein (BSP) in blood (Z(t)) monotonically decreases as time elapses. The initial amount of BSP in blood is 250 units and this is steadily decreasing to 236.7837 units at $t = 1$ The decrease in amount of BSP in blood can be attributed to the removal of BSP by the liver due to its absorption. As we can see from the graph in Figure 1., the numerical solution is smooth, indicating that the proposed wavelet-based approach is also stable and converges. In Figure 2., we obtain that the amount of BSP in the liver, denoted by $W(t)$, increases steadily from the beginning up to 13.1537 at $t = 1$ which is according to the physical significance, is the reciprocal interaction implying transferring BSP from the blood to the liver. The system of equations describing the uptake of Bromsulphthalein (BSP) by the liver was forced with a random input by assuming that the changing blood perfusion rate (BPR) is a stochastic process. The generalized Galerkin scheme based on the Genocchi wavelet collocation method (GWM) was employed for approximating the stochastic system of BSP bio-dynamics described by the deterministic partial differential equations (PDEs). In this paper, we presented a concise modeling framework for stochastic bio-dynamics using the continuous Genocchi wavelet collocation method. A linear combination of a finite Genocchi wavelet collocation basis series was considered as the candidate approximate solutions to describe time evolution of the involved state variables. This method has the advantage that it can be easily implemented and it can be applied for both linear and non-linear models. Another attractive characteristic of this method is that it does not require the explicit forms of the governing equations for constructing the approximate solutions. Thus, this smoothing method can help to solve the problem of modelling in the presence of random inputs without the knowledge of the functional forms of governing equations. In this study, the stochastic PDE was transformed into deterministic PDE. The deterministic PDE was then approximated with the Genocchi wavelet collocation method. Numerical results showed that the GWM-based approximations of the pathogen concentrations by means of the state variables was successful. The combined phase plot of $Z(t)$ and $W(t)$ is also plotted in Figure 3. to investigate the transport properties of BSP between blood and liver. Clearly $Z(t)$ is a decreasing function with time interval, and $W(t)$ is a monotonically increasing function. It is clear that the oscillatory and unstable behavior, which could not be justified in the biological context, is not observed, hence confirming the relevance and the reliability of our approach. It is also clear that the obtained solutions are smooth and highly reliable. The GWCM is able to provide good approximations at very little cost. Therefore, the GWCM can be considered an efficient and reliable computational tool for solving biological and physiological models governed by systems of differential equations. The obtained findings validate the effectiveness of the proposed approach and demonstrate its potential applicability to more complex biomedical and epidemiological models.

V. Conclusion

A mathematical model is a crucial tool for explaining the complexities, transmission in the real-world. In this study, we successfully implemented Genocchi wavelets to solve mathematical model of human liver and graphs are plotted via obtained numerical values. In the obtained graphs, it is detected that the amount of Bromsulphthalein (BSP) in the blood decreases with time and the amount of Bromsulphthalein (BSP) in the liver increases with time. The considered model's results are displayed through graphs and also carried out numerical simulations using suggested approach which shows the dynamics of the model. Also, we compared the obtained results with the Euler method, but the proposed method is very effective and precise. Compared to current methods, our suggested method offers quick algorithms, incredibly accurate values, no controllable parameters, and less computational effort. Moreover, it gives a more realistic way to analyse complex phenomena and aids in understanding the mathematical models. We conclude that contemporary research has expanded to include mathematical models from numerous scientific fields. Extending the model with real-world data and modifying parameters can enhance forecast accuracy and validate assumptions.

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