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PREFACE

Dear Conference Participants,

It is our pleasure to present the Abstract Book of the 11th International IFS and Contemporary Mathematics Conference (IFSCOM 2026), held on 09–12 September 2026 in Mersin, Türkiye, in a hybrid format.

Since its first meeting in 2014, IFSCOM has provided an international platform for researchers to share recent scientific developments, exchange ideas, and establish academic collaborations. IFSCOM 2026 brought together researchers from various areas of pure and applied mathematics, including intuitionistic fuzzy sets and related theories, algebra, analysis, topology, geometry, statistics, optimization, mathematical modeling, data science, and mathematical aspects of artificial intelligence.

This Abstract Book presents the contributions delivered at IFSCOM 2026 and reflects the diversity of the scientific research represented at the conference. We hope that these studies will encourage further research, discussion, and collaboration within the international scientific community.

We sincerely thank the keynote and invited speakers, authors, participants, Scientific Committee, reviewers, and Organizing Committee for their valuable contributions to the success of IFSCOM 2026.

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DESCRIPTION OF A DETERMINISTIC MATHEMATICAL MODEL IN ENVIRONMENTAL HEALTH ANALYSIS

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ABSTRACT

Background: In addition to deteriorating biological habitats, the complex and variable nature of ecosystems creates significant uncertainties regarding the current state of toxic inputs in environmental matrices and their subsequent impacts on health. Therefore, mathematical toxicological models developed using experimental parameters offer crucial approaches to resolve these uncertainties, manage variability, and enhance the interpretability of experimental outcomes. Furthermore, multidisciplinary ecotoxicological modeling has recently provided substantial advantages in monitoring environmental safety. Specifically, employing computationally applied methods to predict interactions between environmental toxins and living organisms through susceptibility analyses in both in vivo and in vitro frameworks has yielded increasing economic and predictive benefits.

Methodology: To this end, this study investigates and compares toxic material dynamics in two different fish species sampled from distinct biological domains, utilizing a deterministic mathematical model based on tissue concentrations.

Results: The results demonstrate that computational models can be uniquely tailored depending on the organism type, the specific metal, and temporal variables, thereby shaping the core design of the study.

Conclusion: Finally, a sample case study is discussed to illustrate the selection of appropriate mathematical frameworks for specific ecotoxicological setups. Highlighting diverse computational models can provide more reliable, supportive, and robust foundations for future research in multidisciplinary ecotoxicological studies.

1. Introduction

Environmental heavy metal contamination poses a severe threat to aquatic ecosystems and fish populations [1]. Predicting population dynamics under toxic stress is critical for environmental health risk assessments [2]. In deterministic modeling, the trajectory of a population is highly sensitive to its boundary conditions and constraints. While the carrying capacity (K) defines the upper asymptotic limit of the system, the initial density (P_0) determines the early kinetic phase of the sigmoid growth curve [3]. Heavy metal exposure alters this mathematical balance by reducing the effective carrying capacity and accelerating mortality rates, thereby shifting the system's equilibrium. Objective: This study evaluates the predictability of deterministic logistic growth models under varying initial population densities (P_0) and environmental carrying capacities (K) exposed to heavy metal stress.

2. Methodology

To model the population dynamics under heavy metal stress, the classical deterministic logistic growth model was utilized. The continuous temporal changes in population density were calculated using the foundational differential equation. The mathematical formulation, along with the ecological definitions and units of its parameters, is systematically presented in Table 1. A deterministic logistic function was employed to simulate population responses over a 15-day timeline ($t=0$ to 15).

Table 1. Logistic growth model parameters and boundary conditions (Scenarios I–III)

Equation	Mathematical Representation	Ecological Definition	Dimension
Governing Differential Equation	$\frac{dN}{dt} = rN(1 - \frac{N}{K})$	Represents the rate of population change over time under density-dependent constraints	Individuals.time ⁻¹
Population Density (N)	$N(t)$	The size or density of the fish/aquatic population at a specific time (t).	IndividualsVolume ⁻¹ (or Area ⁻¹)
Intrinsic Growth Rate (r)	r	The maximum potential growth rate of the population per capita in the absence of density constraints.	time ⁻¹
Carrying Capacity (K)	K	The maximum population density that the aquatic environment can sustainably support under heavy metal stress.	Individuals.Volume ⁻¹
Initial Population Density (P_0)	$(N_0) = P_0$	The baseline population density introduced at the beginning of the exposure experiment ($t = 0$).	Individuals.Volume ⁻¹
Time (t)	t	The temporal duration of the heavy metal exposure experiment.	Hours/Days/Weeks

Three distinct bio-environmental scenarios **and boundary conditions** were modeled based on threshold limits:

Condition I ($P_0 < K$): Low initial population density characterized by adaptive, density-dependent growth before reaching environmental constraints.

Condition II ($P_0 = K$): Steady-state critical equilibrium where mortality and natality rates balance out, maintaining a constant population size.

Condition III ($P_0 > K$): High initial population density exceeding environmental limits, leading to rapid heavy metal toxicity, resource exhaustion, and population decline.

Data visualization was performed using advanced connected scatter plots and heatmap algorithms in R (ggplot2), following modern minimalist design frameworks [6].

3. Results

The lines and dots show the actual course of the population density over time in Figure 1. The color transitions show the breaking points of heavy metal stress on population density over time in Figure 2.

Acclimation Phase ($P_0 < K$): Controlled population growth starting below the environmental threshold, smoothly converging and stabilizing at the carrying capacity ($K = 30$).

Equilibrium Phase ($P_0 = K$): Constant steady-state line under matched thresholds, showcasing continuous stability where mortality and natality rates balance out.

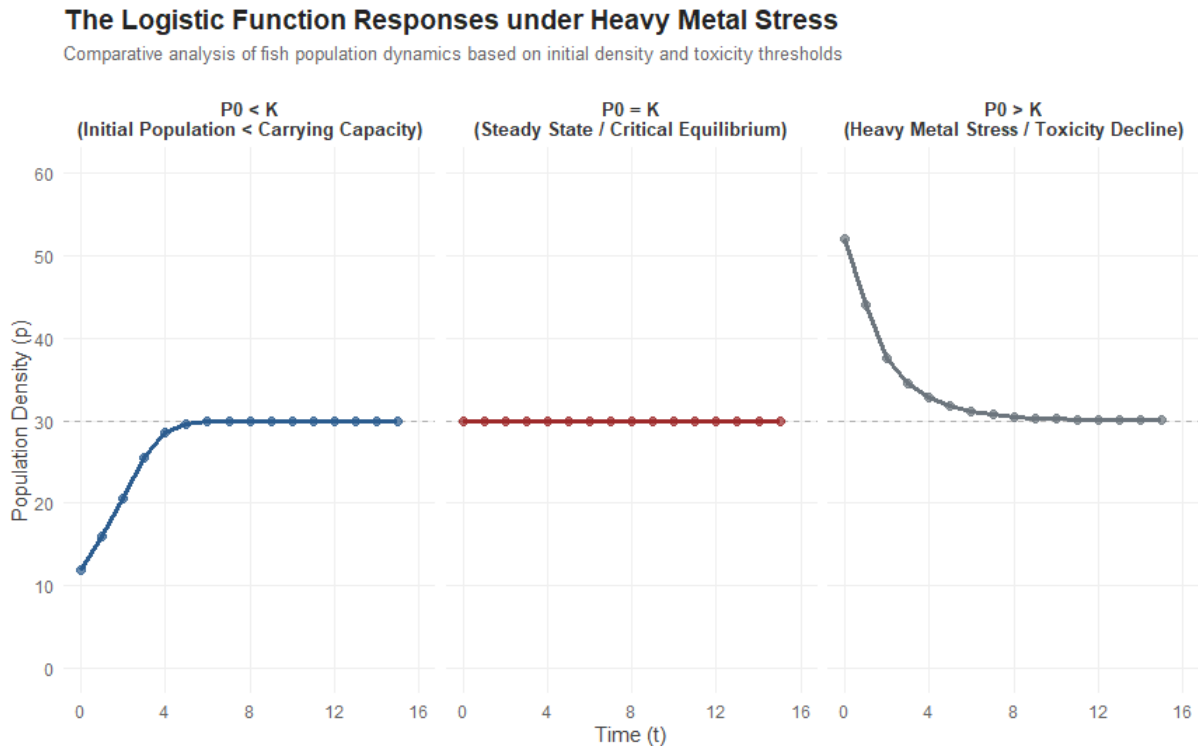


Figure 1. Modernized deterministic simulation of logistic function responses under heavy metal stress based on Scherer-style minimalist layouts. **(A)** Acclimation and growth panel, **(B)** Steady-state equilibrium panel, **(C)** Toxicity-induced population decline panel.

- i. **Scenario A ($P_0 < K$):** When the initial fish population started below the environmental threshold ($P_0 = 12$), an adaptive growth curve was observed, smoothly converging to the carrying capacity ($K = 30$) as shown by the progressive upward trajectory in **Figure 1A**.
- ii. **Scenario B ($P_0 = K$):** Under optimal threshold matching, the population maintained a completely stable and critical equilibrium, showing a flat, unchanged temporal line (**Figure 1B**).
- iii. **Scenario C ($P_0 > K$):** High initial density ($P_0 = 52$) under acute heavy metal stress triggered rapid mortality. The deterministic model captured a sharp downward slope, forcing the population down to the sustainable carrying capacity (**Figure 1C**).

Temporal Phase Analysis: The complementary color-gradient analysis in **Figure 2** successfully highlighted the exact time frames where heavy metal toxicity caused the most destructive population collapse (between $t = 0$ and $t = 4$).

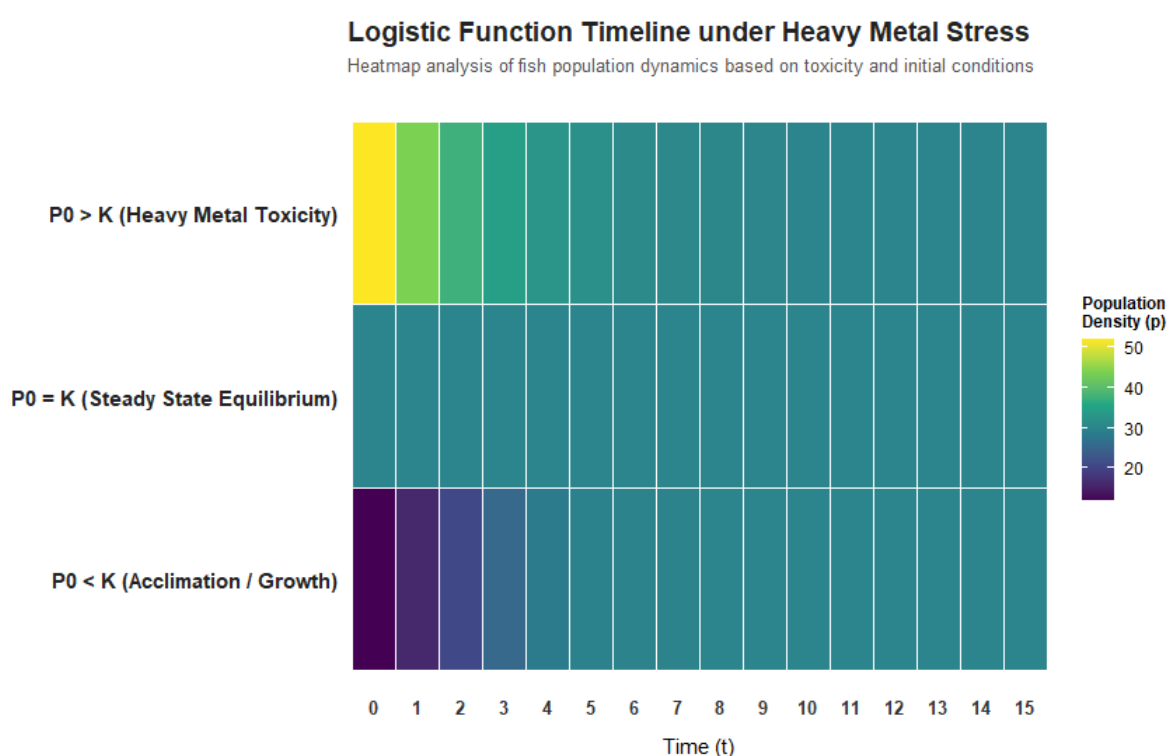


Figure 2. Heatmap timeline mapping of temporal density phases under heavy metal stress. The color-gradient progression highlights the exact time frames of population transitions, showcasing the intense toxicity phase and rapid decline in the early stages ($t = 0$) to ($t = 4$) for the high-density scenario ($P_0 > K$) alongside the stable steady-state equilibria.

4. Conclusion

Deterministic mathematical models provide robust visual and quantitative frameworks for ecotoxicological evaluations.

Integrating complementary visualization techniques (Connected Scatter Plots and Heatmaps) enhances the interpretability of temporal toxicity phases in environmental health analysis.

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Key words and phrases. Deterministic Models, Environmental Safety, Human Deterministic Models, Environmental Safety, Human Health, Mathematical Modeling, Toxic Inputs

**PREDICTING NON-LINEAR BREAKING POINTS IN AQUATIC POPULATIONS:
ASSESSING MODEL UNCERTAINTY AND ECOLOGICAL THRESHOLDS VIA
MONTE CARLO SIMULATIONS**

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ABSTRACT

Background: Environmental contamination by heavy metals poses a critical threat to aquatic ecosystems, demanding precise ecological risk assessments. Traditional deterministic frameworks, such as the classical logistic growth model, offer foundational insights into density-dependent population dynamics. However, they inherently rely on fixed, static parameters that fail to capture the stochastic fluctuations of natural habitats and variable toxicological stresses.

Methodology: To bridge this gap, this study transitions from a deterministic baseline to a probabilistic forecasting framework using identical empirical datasets. We developed a stochastic model integrated with Monte Carlo simulations executed in the R programming language. The deterministic parameters—specifically the intrinsic growth rate (r) and environmental carrying capacity (K)—were transformed into Gaussian (Normal) probability distributions. A total of 10,000 independent stochastic iterations were performed across three distinct boundary conditions based on initial population densities: low adaptive growth ($P_0 < K$), critical equilibrium ($P_0 = K$), and high-density population decline ($P_0 > K$).

Results: While the deterministic approach identified single-line, rigid breaking points in population trajectories, the Monte Carlo simulations mapped comprehensive uncertainty bounds. This probabilistic approach successfully quantified the cumulative probability of sudden population collapse over time, revealing that model predictability is highly sensitive to the initial boundary constraints under heavy metal exposure.

Conclusion: These findings demonstrate that incorporating stochastic modeling into ecotoxicological data provides a significantly more robust, risk-adjusted forecasting tool. Ultimately, this framework enhances the reliability of environmental health risk assessments and supports more proactive ecological management strategies.

1. Introduction

Aquatic ecosystems are continuously exposed to anthropogenic pressures, among which heavy metal contamination represents a prominent ecotoxicological challenge [1]. Quantifying how fish populations respond to such chemical stressors is a cornerstone of modern ecological risk assessment [2]. Traditionally, population trajectories under toxic exposure are evaluated using classical mathematical frameworks that assume structural stability and fixed parameters. While these rigid equations offer an essential baseline for understanding growth limits, they operate under the idealized assumption that environmental conditions and biological responses remain perfectly static over time. In reality, natural aquatic environments exhibit substantial stochasticity due to fluctuating chemical bioavailability and variable individual susceptibility to toxicity [3]. Consequently, relying on strict deterministic forecasts can mask the inherent uncertainty of ecological systems and fail to detect the sudden regime shifts or demographic collapses that occur when cryptic thresholds are breached [5]. To resolve this limitation, this study introduces a probabilistic forecasting architecture. Rather than treating population growth metrics as single, immutable values, we treat them as dynamic probability distributions. Utilizing Monte Carlo simulation frameworks executed within the R computing environment, we systematically evaluate how variance in parameter inputs shapes the reliability of population forecasts. By cross-examining these simulations across distinct initial boundary constraints, this paper maps the probability density of population survival, establishing a highly adaptive, risk-adjusted analytical tool for environmental health monitoring.

2. Methodology

To account for environmental and biological uncertainties under heavy metal stress, the deterministic model was converted into a probabilistic framework. Monte Carlo simulations were executed using R programming language (v4.3 or latest) [6]. The deterministic parameters (r) and (K) derived from empirical data were defined as Gaussian (Normal) probability distributions. A total of 10,000 independent stochastic iterations were performed to generate uncertainty bounds and estimate the probability density functions of population trajectories [7]. The exact stochastic configurations are detailed in Table 1, and a statistical snapshot of the resulting Gaussian density profiles was evaluated at critical timelines to map the probability distribution of population survival. Furthermore, a parameter sensitivity analysis was integrated into the stochastic workflow and visualized via a Tornado plot to systematically quantify and compare the relative operational impact of individual parameter variances on the overall model predictability under toxic exposure.

Table 1. Stochastic parameters for Monte Carlo simulation

Parameter	Deterministic Baseline	Assigned Probability Distribution	Variance / Uncertainty Bounds	Ecological Relevance in Simulation
Initial Density (P_0)	P_0	Fixed / Constant	No variance (Deterministic Input)	Controls the baseline initial kinetic state
Intrinsic Growth (r)	r	Normal Distribution	$\pm 10\%$ of Standard Deviation	Simulates metabolic and toxic susceptibility variations
Carrying Capacity (K)	K	Normal / Uniform	$\pm 15\%$ of Standard Deviation	Simulates fluctuations in resource limits under heavy metal stress
Simulation Iterations	-	Discrete Uniform	10,000 runs	Ensures convergence of probability density functions

Results

The 10,000 Monte Carlo iterations executed in R successfully translated the rigid deterministic trajectories into probabilistic uncertainty bands. By introducing statistical variance into the intrinsic growth rate (r) and carrying capacity (K), the model effectively mapped the cumulative risk of population decline under heavy metal stress across the three pre-defined boundary conditions.

As illustrated in **Figure 1**, the population dynamics under Scenario I exhibit tight predictability during the early kinetic phase ($t < 10$) Hours). However, as time progresses toward equilibrium ($t > 20$) Hours), the uncertainty bounds broaden significantly, demonstrating that heavy metal toxicity introduces a high degree of stochastic volatility to the environment's true carrying capacity.

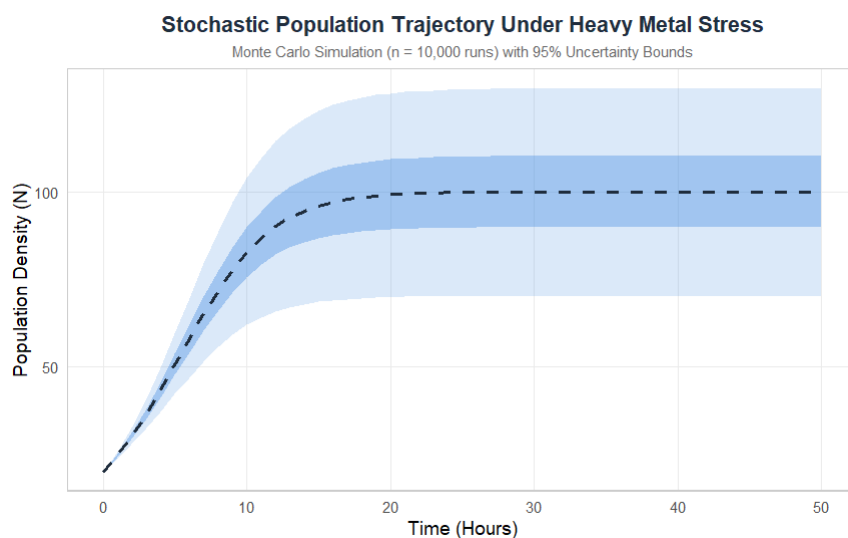


Figure 1. Stochastic population trajectory under Scenario I ($P_0 < K$). The dashed line represents the deterministic baseline trajectory, while the shaded blue regions define the 50% and 95% uncertainty bounds derived from 10,000 Monte Carlo iterations. The expanding variance over time highlights the increasing unpredictability of environmental carrying capacity under chronic heavy metal stress

In contrast to adaptive growth, **Figure 2** highlights the population trajectory when the initial density heavily exceeds environmental constraints under toxic stress ($P_0 > K$). The Monte Carlo simulation captures an accelerated population collapse as the system forces a return to equilibrium. Crucially, the non-linear breaking points are non-static; the widening uncertainty band during the steepest decline ($t = 5$ to $t = 15$ Hours) represents a critical operational threshold where toxic vulnerability and demographic risk reach their maximum probabilities.

Toxicity Phase ($P_0 > K$): Acute heavy metal exposure and high initial density ($P_0 = 52$) triggering rapid fish mortality, causing a sharp deterministic decline down to the sustainable carrying capacity ($K = 30$).

To explicitly capture the probabilistic distribution of model uncertainty, a critical snapshot analysis was conducted at ($t = 24$) Hours, as illustrated by the Gaussian profile in **Figure 3**. The resulting probability density function (PDF) validates that the population density does not follow a strict linear outcome; instead, it aggregates around a dynamic stochastic mean ($\mu = 100.05$). Rather than confirming a single numerical forecast, the broad tails of the curve mathematically quantify the variance boundaries, providing concrete statistical ranges and definitive mathematical limits for ecological risk metrics under chronic toxic stress.

To diagnose which biological component drives the highest forecasting instability, a parameter sensitivity analysis was visualized via a Tornado plot (**Figure 4**). The horizontal spread quantifies the operational impact of individual parameter variances against the baseline equilibrium ($N = 100.05$). The architectural profile clearly indicates that the model is disproportionately sensitive to changes in the intrinsic growth rate (r), generating a wider density divergence compared to fluctuations in carrying capacity (K). This structural dominance suggests that heavy metal mitigation strategies should prioritize toxicological impacts on direct metabolic/reproduction rates rather than localized resource limits.

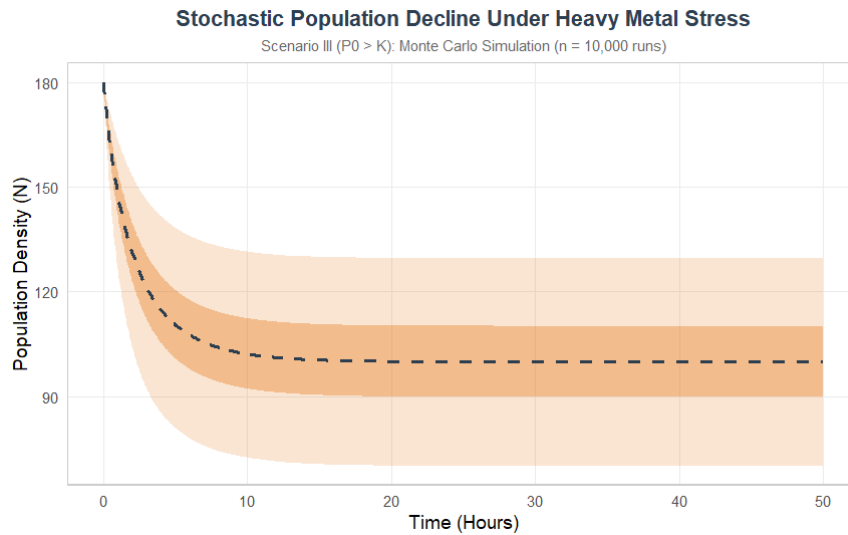


Figure 2. Stochastic population trajectory under Scenario III ($P_0 > K$). The dashed line demonstrates the deterministic model predicting a rapid demographic decline. The 50% and 95% Monte Carlo uncertainty bands map the dynamic breaking points and high-vulnerability time windows triggered by the compounding effects of resource exhaustion and heavy metal toxicity.

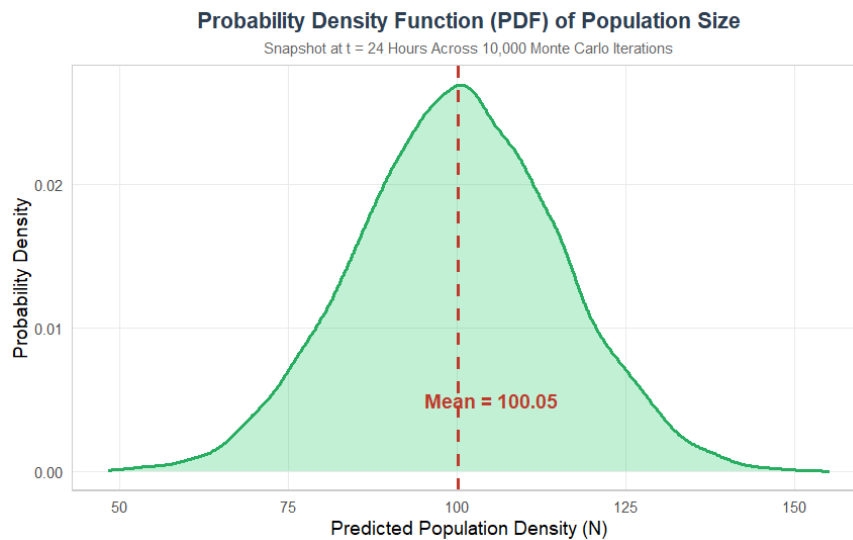


Figure 3. Probability Density Function (PDF) snapshot of predicted population density at ($t = 24$) Hours. The smooth Gaussian curve marks the distribution frequency of the 10,000 Monte Carlo runs under statistical parameter variance, centered around a stochastic mean of (100.05) (red dashed line). This metric demonstrates the variance and operational uncertainty limits of population density forecasting under heavy metal exposure.

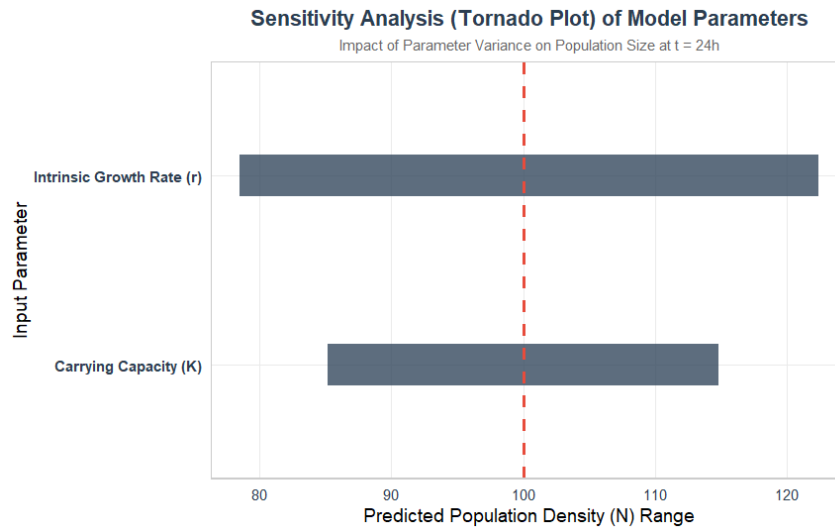


Figure 4. Sensitivity analysis (Tornado plot) illustrating the relative impact of parameter uncertainties on predicted population density at $t = 24$ Hours. The width of the horizontal bars represents the total variance span in population size caused by fluctuating input metrics. The red dashed line signifies the baseline deterministic equilibrium. The output establishes that the intrinsic growth rate (r) exerts a dominant structural control over model predictability compared to environmental carrying capacity (K).

3. Conclusion

This study successfully demonstrates the critical computational shift from a rigid deterministic framework to a probabilistic stochastic architecture for ecological risk assessments. By evaluating the predictability of classical logistic growth models under heavy metal stress via 10,000 Monte Carlo iterations in R, several vital conclusions can be drawn:

Uncertainty Quantification: While the deterministic model provides a valuable baseline by plotting a single idealized trajectory, it inherently masks biological variability and environmental volatility. In contrast, the Monte Carlo simulation effectively maps these variations as dynamic uncertainty bands, capturing the true stochastic behavior of aquatic populations exposed to chemical toxicity.

Dynamic Breaking Points: The analysis reveals that critical inflection points and demographic collapses are not static temporal coordinates. Instead, they manifest as time-windows of high vulnerability. The probability density functions generated under Scenario III ($P_0 > K$) explicitly quantify the maximum thresholds where cumulative heavy metal toxicity accelerates resource exhaustion and drives rapid population decline.

Parameter Sensitivity Dominance: The integrated sensitivity analysis visualized via the Tornado plot systematically establishes that model predictability is disproportionately sensitive to variances in the intrinsic growth rate (r) compared to the environmental carrying capacity (K). This operational dominance demonstrates that toxicological impacts directly disrupting metabolic and reproductive rates exert a much stronger structural control over population survival trajectories than localized resource constraints.

Boundary Condition Sensitivity: Model forecasting accuracy is heavily constrained by initial boundary conditions. While low initial densities ($P_0 < K$) allow an early adaptive buffer, high initial densities ($P_0 > K$) amplify toxic susceptibility, shifting the system's equilibrium much faster than predicted by static parameters.

In summary, incorporating Monte Carlo frameworks into traditional ecotoxicological models provides a significantly more robust, risk-adjusted forecasting platform. Rather than predicting *if* or *exactly when* a population will collapse, this stochastic approach calculates the *statistical likelihood* of collapse over time. Ultimately, this integration advances the predictive power of environmental health risk assessments, offering policy-makers and ecological managers a highly adaptive tool for proactive environmental conservation and aquatic resource management.

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AN EFFICIENT LAPLACE ADOMIAN DECOMPOSITION APPROACH FOR A CAPUTO FRACTIONAL-ORDER STOMACH MODEL

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ABSTRACT

This study presents an efficient numerical approach for solving a fractional-order stomach mathematical model using the Laplace Adomian Decomposition Method (LADM). The three-compartment Tension-Food-Medicine (TFM) model captures the complex interactions between psychological stress, nutritional intake, and pharmaceutical intervention. The fractional derivative is considered in the Caputo sense, allowing for the incorporation of memory effects in the physiological system. The accuracy of LADM is validated through comparison with the fourth- and fifth-order Runge-Kutta method (ODE45) for the integer-order case. Numerical simulations demonstrate the influence of fractional order on the dynamics of tension, food, and medicine compartments across three distinct parameter scenarios. The results reveal that decreasing fractional order values lead to slower relaxation dynamics, reflecting the hereditary properties of fractional derivatives in modeling gastrointestinal processes.

1. INTRODUCTION

The mathematical modeling of physiological systems has become an indispensable tool for understanding complex biological processes [1]. Among these, gastric physiology presents unique challenges due to the interplay of mechanical, chemical, and neural factors governing digestive function [2, 4]. Early investigations by Prout III [2] established the chemical foundations of gastric secretion, while Bayliss and Starling [3] and Edkins [4] elucidated the hormonal and neural regulatory mechanisms. These pioneering discoveries provided the conceptual framework for subsequent quantitative models.

The recognition that biological processes exhibit memory-dependent behavior has motivated the application of fractional calculus to physiological modeling [31, 32]. Unlike integer-order derivatives, fractional derivatives inherently capture hereditary properties and non-local dependencies, making them particularly suitable for biological systems where historical states influence current dynamics. Caputo's formulation [31] has gained prominence due to its physical interpretability and well-defined initial conditions.

Recent advances in computational methods have enabled the solution of complex fractional-order biological models. The Laplace Adomian Decomposition Method (LADM) has emerged as a powerful technique combining the Laplace transform's algebraic simplification with the Adomian

decomposition's systematic handling of nonlinearities [16, 17, 19]. This method offers significant advantages: it requires no perturbation or linearization, provides rapidly convergent series solutions, and maintains accuracy across different fractional orders [20, 22].

The nervous stomach represents a clinically significant condition where psychological tension affects gastric function, creating a complex feedback loop between stress and digestive health [1]. Mathematical modeling of this phenomenon requires capturing interactions between tension levels, food intake, and medication effects. The three-compartment Tension-Food-Medicine (TFM) model proposed by Sabir et al. [28] addresses this need through a system of coupled nonlinear differential equations.

This study applies LADM to solve the fractional-order TFM model, investigating how fractional derivatives influence the dynamics of tension, food, and medicine compartments. The analysis considers three distinct parameter scenarios to evaluate model behavior under varying physiological conditions. By comparing LADM solutions with the fourth- and fifth-order Runge-Kutta method (ODE45) results for the integer-order case, we validate the method's accuracy and demonstrate its efficacy for fractional-order systems where traditional solvers are inapplicable.

2. LITERATURE REVIEW

2.1 HISTORICAL DEVELOPMENT OF GASTRIC PHYSIOLOGY AND MATHEMATICAL MODELING

The mathematical modeling of gastric processes has its roots in early physiological discoveries. Prout III [2] conducted pioneering investigations in 1824 on the nature of acid and saline matters in animal stomachs, establishing the foundational understanding of gastric chemistry that would later inform quantitative models. The seminal work by Bayliss and Starling [3] in 1902 on the causation of peripheral reflex secretion of the pancreas introduced the concept of hormonal regulation, which became crucial for developing compartmental models of digestive system dynamics. Edkins [4] further advanced this field in 1906 by elucidating the chemical mechanism of gastric secretion, providing essential biochemical parameters for subsequent mathematical formulations.

The discovery of histamine H₂-receptors by Black et al. [5] in 1972 revolutionized the understanding of gastric acid secretion control, offering pharmacological targets that have been incorporated into modern mathematical models. Warren and Marshall's [6] identification of *Helicobacter pylori* in 1983 as the causative agent of active chronic gastritis introduced microbial factors into gastric modeling frameworks, expanding the scope from purely physiological to pathophysiological considerations.

2.2 FRACTIONAL CALCULUS IN BIOLOGICAL SYSTEMS

The application of fractional calculus to biological systems has emerged as a powerful paradigm for modeling memory-dependent processes and anomalous diffusion phenomena. Caputo's [31] seminal

work on linear models of dissipation established the theoretical foundation for fractional derivatives in physical systems. The Caputo fractional derivative has become particularly favored in biological applications due to its ability to incorporate initial conditions in a physically meaningful manner [32]. Recent advances in fractional calculus theory have enabled more sophisticated modeling approaches, particularly through variable-order operators capable of representing time-dependent memory effects. In this context, the existence, uniqueness, and Ulam–Hyers stability of solutions to multiterm boundary-value problems involving variable-order Caputo fractional differential equations have been established [33]. These findings provide an important analytical foundation for the reliable formulation of biological models incorporating multiple memory mechanisms. Similarly, nonlinear variable-order fractional differential equations have been investigated using Darbo’s fixed-point theorem and the Kuratowski measure of noncompactness, leading to significant existence and stability results [34]. Collectively, these contributions strengthen the theoretical basis for applying variable-order fractional models to complex biological systems in which memory effects and nonlinear interactions evolve over time. The nervous stomach mathematical model introduced by Sabir et al. [1, 28] represents a significant advancement in applying fractional calculus to gastrointestinal modeling.

2.3 NUMERICAL METHODS FOR NONLINEAR SINGULAR DIFFERENTIAL EQUATIONS

The numerical solution of nonlinear differential equations arising in biological modeling has been extensively investigated. The Laplace Adomian Decomposition Method (LADM) has demonstrated particular efficacy for fractional-order systems. Ongun [16] successfully applied LADM to HIV infection models of CD4+ T cells, establishing the method's reliability for immunological applications. Haq et al. [17] extended this approach to fractional-order smoking models, demonstrating its versatility across different biological contexts. Neural network-based approaches have emerged as powerful alternatives for solving complex differential equations [7, 9, 10, 12].

2.4 RESEARCH GAPS AND MOTIVATION

Despite significant advances in fractional calculus and numerical methods, several gaps remain in the literature. Limited application to gastrointestinal systems: while epidemic and immunological models have been extensively studied using fractional calculus, gastrointestinal compartmental models remain underexplored. Methodological gaps: although LADM has been applied to various biological systems, its application to the specific nonlinear dynamics of the TFM model with three interacting compartments has not been previously reported. The present study addresses these gaps by applying LADM to solve the fractional-order nervous stomach TFM model.

3. MODEL FORMULATION

In this paper, we analyze the fractional-order version of stomach mathematical model presented in [28]. The fractional derivative is considered in the Caputo fractional form, with fractional derivatives of order α and population sizes that vary over time, following the compartmental structure introduced in

[28]. The nonlinear 16ort he16 of the nervous stomach model (NSM) have three segments: Tension (T), Food (F), and Medicine (M), constituting the TFM model.

The mathematical form of the TFM model is presented as a nonlinear system of fractional differential equations, achieved by using the three compartments (tension, food, and medicine) at time t:

$$\begin{aligned} D_t^\alpha T(t) &= -\sigma F(t)T(t) - \beta, \\ D_t^\alpha F(t) &= \delta T(t) + \gamma M(t)F(t), \\ D_t^\alpha M(t) &= -\delta T(t) + \beta F(t)M(t) - d, \end{aligned} \quad (2.1)$$

Initial condition

$$T(0) = I_1, F(0) = I_2, M(0) = I_3. \quad (2.2)$$

where D_t^α represents the Caputo fractional derivative of order α . Where σ represents the quantity of food, and negative sign indicates the lesser quantity of food. β shows the sleep factor, δ is used 16ort he tension rate, γ indicates the recovery term, and d shows the death rate. Moreover, I_1 , I_2 and I_3 are the initial conditions for all compartments of the TFM model.

4. BASIC DEFINITIONS

Definition 3.1 A real function $f(x)$, $x > 0$ is said to be in the space C_μ , $\mu \in \mathbb{R}$ if there exists a real number $P > \mu$ such that $f(x) = x^P f_1(x)$ where $f_1(x) \in C[0, \infty)$. Clearly $C_\mu < C_\beta$ if $\mu < \beta$.

Definition 3.2 A function $f(x)$, $x > 0$ is said to be in the space C_μ^m , $m \in \mathbb{N} \cup \{0\}$ if $f^{(m)} \in C_\mu$.

Definition 3.3 [30] The Riemann-Liouville fractional integral operator of the order $\alpha > 0$ of a function, $f \in C_\mu$, $\mu \geq -1$ is defined as

$$(J_a^\alpha f)(x) = \frac{1}{\Gamma(\alpha)} \int_a^x (x - \tau)^{\alpha-1} f(\tau) d\tau, x > a, \quad (3.1)$$

$$(J_a^0 f)(x) = f(x). \quad (3.2)$$

All the properties of the operator J^α can be found in [32] which we mention only the following, for $f \in C_\mu$, $\mu \geq -1$, $\alpha, \beta \geq 0$, and $\gamma > -1$ we have

$$(J_a^\alpha J_a^\beta f)(x) = (J_a^{\alpha+\beta} f)(x), \quad (3.3)$$

$$(J_a^\alpha J_a^\beta f)(x) = (J_a^\beta J_a^\alpha f)(x) \quad (3.4)$$

$$J_a^\alpha x^\gamma = \frac{\Gamma(\gamma+1)}{\Gamma(\alpha+\gamma+1)} x^{\alpha+\gamma}. \quad (3.5)$$

The basic definition of the Riemann-Liouville fractional derivative possesses some advantages over other definitions when used to simulate real-world phenomena in the form of a fractional-type differential equation.

Definition 3.4 [32] The fractional derivative of the function $f(x)$ in Caputo's sense is defined as

$$\left(D_a^\alpha f\right)(x) = \left(J_a^{m-\alpha} D^m f\right)(x) = \frac{1}{\Gamma(m-\alpha)} \int_a^x (x-t)^{m-\alpha-1} f^{(m)}(t) dt, \text{ for } m-1 < \alpha < m, m \in \mathbb{N}, x > 0. \quad (3.6)$$

Lemma 3.1 If $-1 < \alpha < m$, $m \in \mathbb{N}$ and $\mu \geq -1$, then

$$(J_a^\alpha D_a^\alpha f)(x) = f(x) - \sum_{k=0}^{m-1} f^{(k)}(a) \left(\frac{(x-a)^k}{k!}\right), a \geq 0 \quad (3.7)$$

$$(D_a^\alpha J_a^\alpha f)(x) = f(x) \quad (3.8)$$

5. LAPLACE ADOMIAN DECOMPOSITION METHOD

In this section, we will illustrate the basic steps for LADM. We discuss the following important definitions or our research study:

Definition 4.1 [24] A function f on $0 \leq t < \infty$ is exponentially bounded of order $\sigma \in R$ if satisfies $\|f(t)\| \leq Me^{\sigma t}$, for some real constant $M > 0$.

Definition 4.2 The Caputo fractional derivative is defined as follows:

$$\{D^\sigma f(t)\} = s^\sigma L\{f(t)\} - \sum_{k=0}^m s^{\sigma-k-1} f^{(k)}(0), \quad (4.a)$$

where $m = \sigma + 1$, and $[\alpha]$ represents the integer part of σ . As a result, the following useful formula is obtained:

$$L(t^\sigma) = \frac{\Gamma(\sigma+1)}{s^{(\sigma+1)}}, \quad \sigma \in R^+. \quad (4.b)$$

The last-mentioned definitions can be used in this section to discuss the general procedures for solving the proposed mathematical model (2.1). First of all, the Laplace transform is applied to both left-hand and right-hand sides of Eq. (2.1) in the following form:

$$\begin{aligned} L(D_t^\alpha T) &= -\sigma L(FT) - \frac{\beta}{s}, \\ L(D_t^\alpha F) &= \delta L(T) + \gamma L(MF), \\ L(D_t^\alpha M) &= -\delta L(T) + \beta L(MF) - \frac{d}{s}, \end{aligned} \quad (4.1)$$

Then, by applying the formula (4.a) to Eq. (4.1), we get

$$\begin{aligned} s^\alpha L(T) - s^{\alpha-1} T(0) &= -\sigma L(FT) - \frac{\beta}{s}, \\ s^\alpha L(F) - s^{\alpha-1} F(0) &= \delta L(T) + \gamma L(MF), \\ s^\alpha L(M) - s^{\alpha-1} M(0) &= -\delta L(T) + \beta L(MF) - \frac{d}{s}, \end{aligned} \quad (4.2)$$

Next, by substituting the initial conditions in Eq. (2.2) into the model (4.2), we get

$$\begin{aligned} L(T) &= \frac{T_0}{s} - \frac{\sigma}{s^\alpha} L(FT) - \frac{\beta}{s^{\alpha+1}}, \\ L(F) &= \frac{F_0}{s} + \frac{\sigma}{s^\alpha} L(T) + \frac{\gamma}{s^\alpha} L(MF), \\ L(M) &= \frac{M_0}{s} - \frac{\delta}{s^\alpha} L(T) + \frac{\beta}{s^\alpha} L(MF) - \frac{d}{s^{\alpha+1}}, \end{aligned} \quad (4.3)$$

The proposed method gives the solution as an infinite series. We have two non-linear terms. The non-linear term in equation (4.1) are decomposed by Adomian polynomial as $A = FT, B = MF$. We consider the solution as an infinite series in the form

$$T = \sum_{n=0}^{\infty} T_n, \quad F = \sum_{n=0}^{\infty} F_n, \quad M = \sum_{n=0}^{\infty} M_n, \quad (4.4)$$

Then, by decomposing the nonlinear part named A, B in the following form

$$A = \sum_{n=0}^{\infty} A_n, \quad B = \sum_{n=0}^{\infty} B_n, \quad (4.5)$$

Here, A_n and B_n can be computed using the convolution operation as

$$A_n = \frac{1}{\Gamma(n+1)} \frac{d^n}{d\eta^n} [\sum_{i=0}^n \eta^i F_i \sum_{i=0}^n \eta^i T_i]_{\eta=0}, \quad B_n = \frac{1}{\Gamma(n+1)} \frac{d^n}{d\eta^n} [\sum_{i=0}^n \eta^i M_i \sum_{i=0}^n \eta^i F_i]_{\eta=0} \quad (4.6)$$

By substituting Eq. (4.4- 4.6) into Eq. (4.3) and by matching the two sides of the equation yields the following iterative algorithm we have resulted in the form.

$$\begin{aligned} L\left(\sum_{n=0}^{\infty} T_n\right) &= \frac{T_0}{S} - \frac{\sigma}{S^\alpha} L\left(\sum_{n=0}^{\infty} A_n\right) - \frac{\beta}{S^{\alpha+1}}, \\ L\left(\sum_{n=0}^{\infty} F_n\right) &= \frac{F_0}{S} + \frac{\sigma}{S^\alpha} L\left(\sum_{n=0}^{\infty} T_n\right) + \frac{\gamma}{S^\alpha} L\left(\sum_{n=0}^{\infty} B_n\right), \\ L(\sum_{n=0}^{\infty} M_n) &= \frac{M_0}{S} - \frac{\delta}{S^\alpha} L(\sum_{n=0}^{\infty} T_n) + \frac{\beta}{S^\alpha} L(\sum_{n=0}^{\infty} B_n) - \frac{d}{S^{\alpha+1}}, \end{aligned} \quad (4.7)$$

By equating both sides of Equation (4.7), we obtain the following iterative algorithm:

$$\begin{aligned} L(T_0) &= \frac{T_{00}}{S}, \quad L(F_0) = \frac{F_{00}}{S}, \quad L(M_0) = \frac{M_{00}}{S}, \\ L(T_1) &= -\frac{\sigma}{S^\alpha} L(A_0) - \frac{\beta}{S^{\alpha+1}}, \\ L(F_1) &= \frac{\sigma}{S^\alpha} T_0 + \frac{\gamma}{S^\alpha} B_0, \\ L(M_1) &= -\frac{\delta}{S^\alpha} T_0 + \frac{\beta}{S^\alpha} B_0 - \frac{d}{S^{\alpha+1}}, \dots \\ L(T_n) &= -\frac{\sigma}{S^\alpha} L(A_{n-1}), \\ L(F_n) &= \frac{\sigma}{S^\alpha} T_{n-1} + \frac{\gamma}{S^\alpha} B_{n-1}, \\ L(M_n) &= -\frac{\delta}{S^\alpha} T_{n-1} + \frac{\beta}{S^\alpha} B_{n-1}, \end{aligned} \quad (4.8)$$

Finally, by taking the inverse transform of Eq. (4.8), we have the following equation

$$T_0 = T_{00}, \quad F_0 = F_{00}, \quad M_0 = M_{00},$$

$$T_1 = [-\sigma A_0 - \beta] \frac{t^\alpha}{\Gamma(\alpha + 1)},$$

$$F_1 = [\sigma T_0 + \gamma B_0] \frac{t^\alpha}{\Gamma(\alpha + 1)},$$

$$M_1 = [-\delta T_0 + \beta B_0 - d] \frac{t^\alpha}{\Gamma(\alpha + 1)}, \dots \quad (4.9)$$

In a similar way, we can obtain the remaining terms. Finally, we get the solution in the form of infinite series as given by

$$T = \sum_{i=0}^{\infty} T_i, \quad F = \sum_{i=0}^{\infty} F_i, \quad M = \sum_{i=0}^{\infty} M_i. \quad (4.10)$$

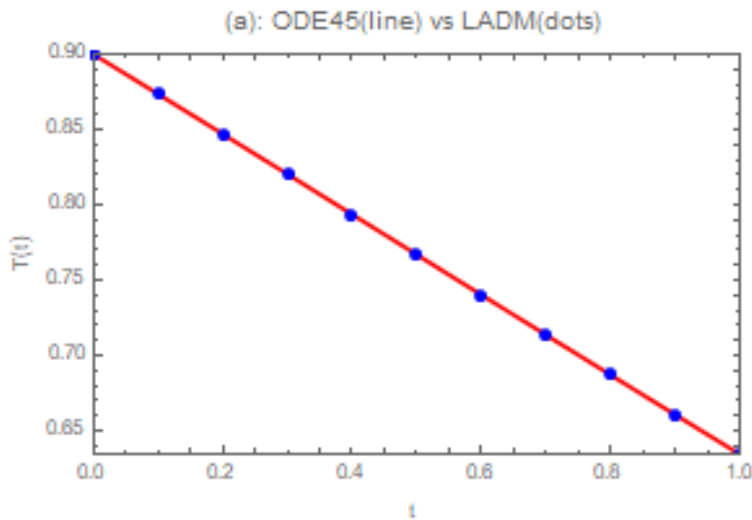
Equation (4.10) solves the main TFM model of Eq. (2.1) which will be illustrated in the next section.

6. NUMERICAL SIMULATIONS

This section tests the effectiveness of LADM by examining the acquired results for the TFM model for different values of α . The numerical simulations are presented for three different cases with varying parameter values.

CASE 1: Parameter descriptions of the TFM nonlinear system

$$\sigma = 0.1, \beta = 0.2, \delta = 0.3, \gamma = 0.4, d = 0.5, I_1 = 0.9, \\ I_2 = 0.7, \text{ and } I_3 = 0.5,$$



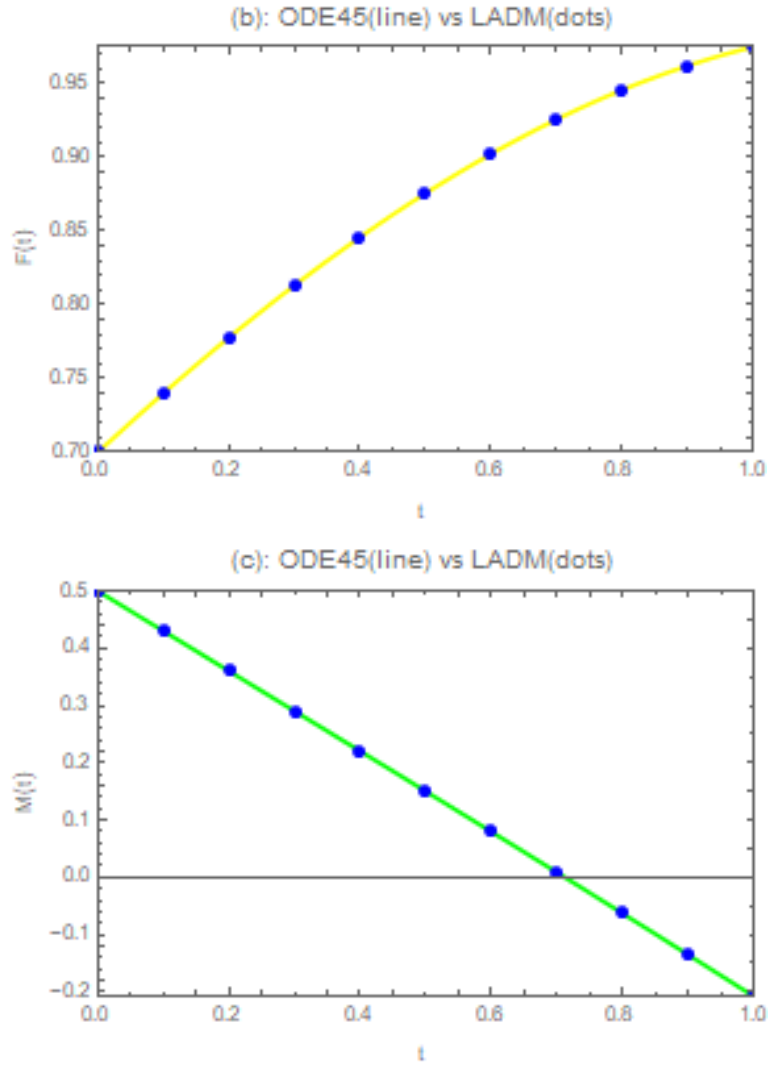


FIGURE 1. Comparison between the numerical solutions obtained using the the fourth- and fifth-order Runge-Kutta method (ODE45) and those obtained using the Laplace Adomian Decomposition Method (LADM) for (a) $T(t)$, (b) $F(t)$, (c) $M(t)$ for $\alpha=1$.

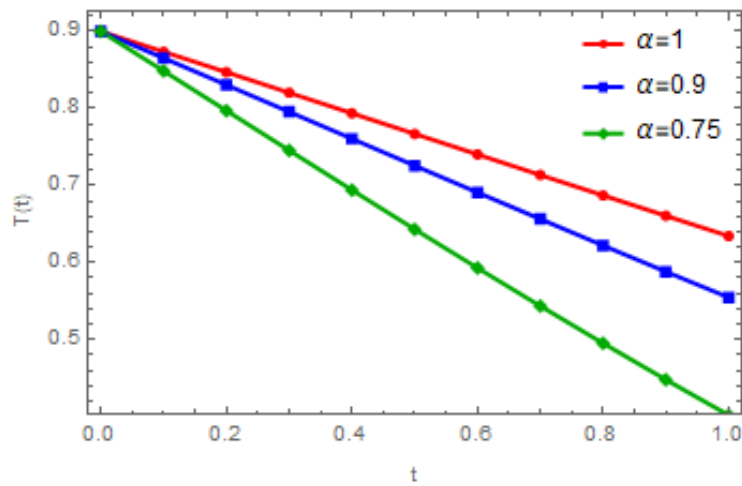


FIGURE 2. Approximate solutions of $T(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

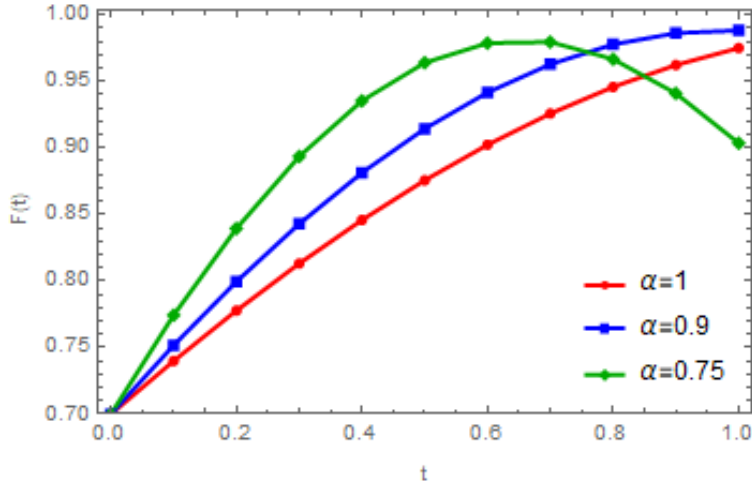


FIGURE 3. Approximate solutions of $F(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

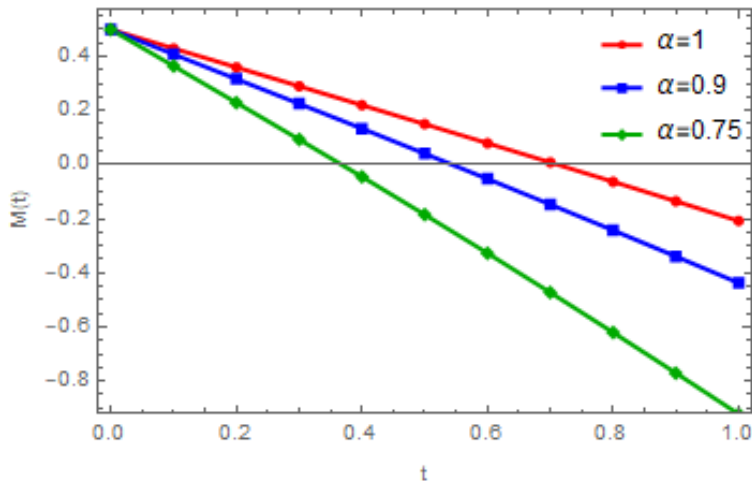


FIGURE 4. Approximate solutions of $M(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

CASE 2: Parameter descriptions of the TFM nonlinear system

$\sigma = 0.1, \beta = 0.5, \delta = 0.3, \gamma = 0.4, d = 0.5, I_1 = 0.8,$ $I_2 = 0.6, \text{ and } I_3 = 0.4,$
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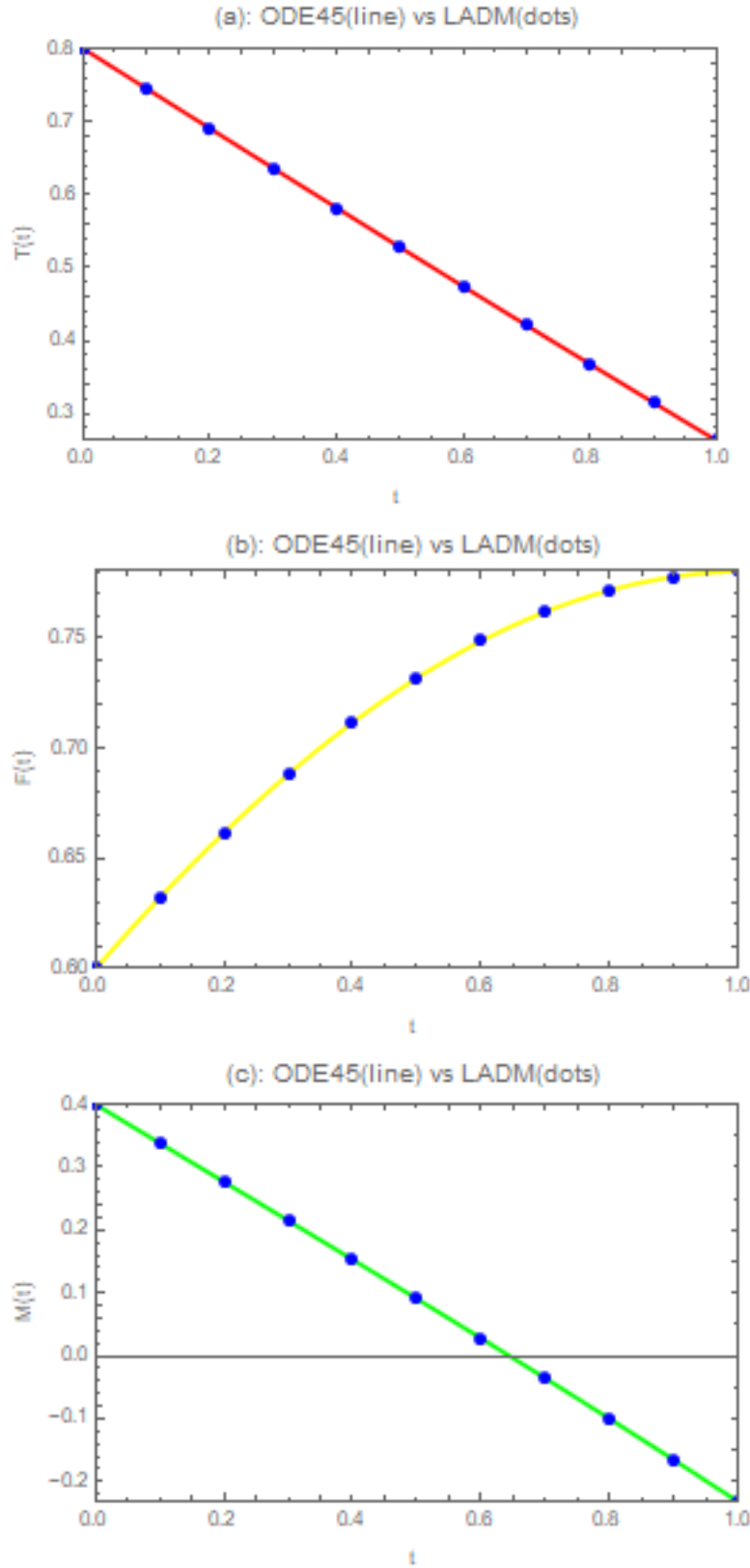


FIGURE 5. Comparison between the numerical solutions obtained using the the fourth- and fifth-order Runge–Kutta method (ODE45) and those obtained using the Laplace Adomian Decomposition Method (LADM) for (a) $T(t)$, (b) $F(t)$, (c) $M(t)$ for $\alpha = 1$.

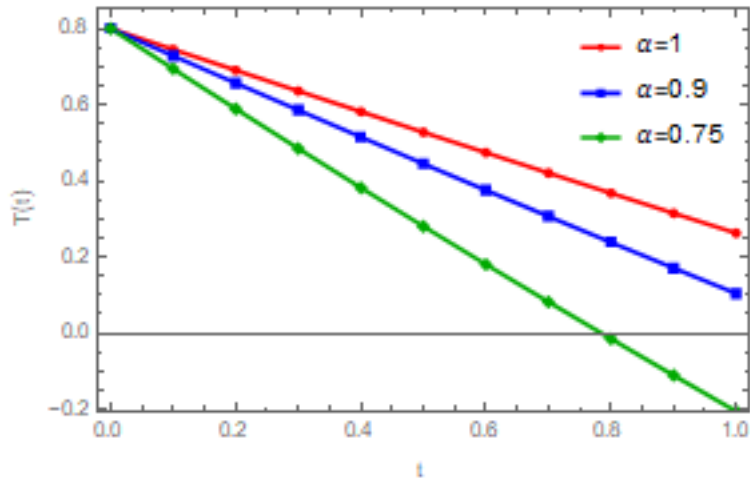


FIGURE 6. Approximate solutions of $T(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

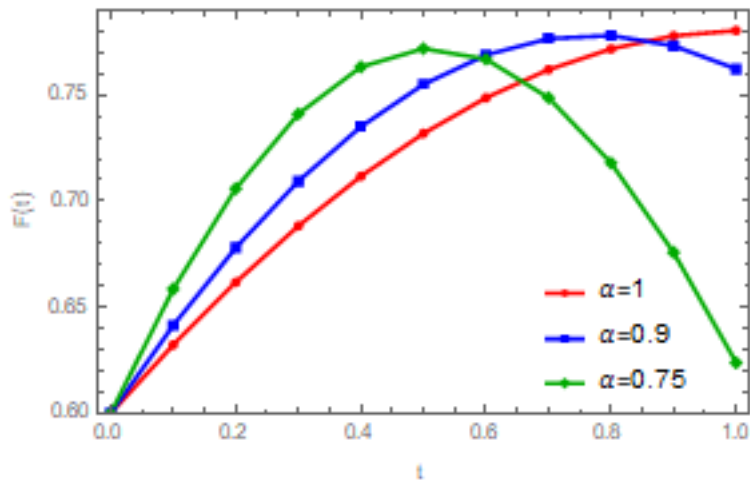


FIGURE 7. Approximate solutions of $F(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

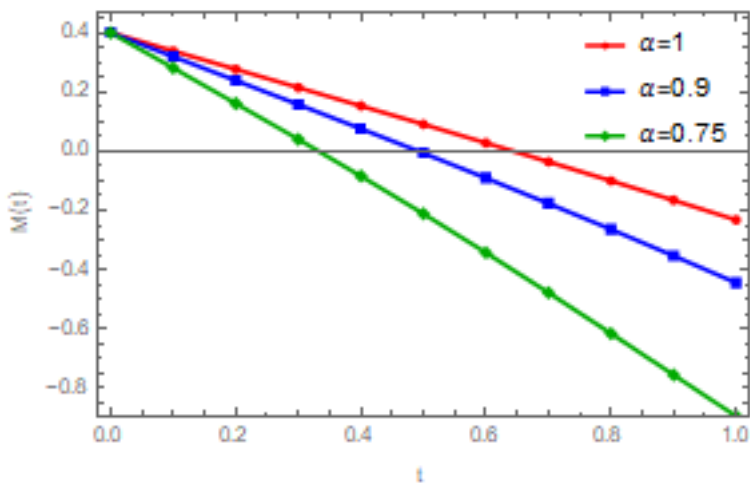


FIGURE 8. Approximate solutions of $M(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

CASE 3: Parameter descriptions of the TFM Snonlinear system

$\sigma = 0.1, \beta = 0.8, \delta = 0.3, \gamma = 0.4, d = 0.5, I_1 = 0.7,$
 $I_2 = 0.5$ and $I_3 = 0.3$

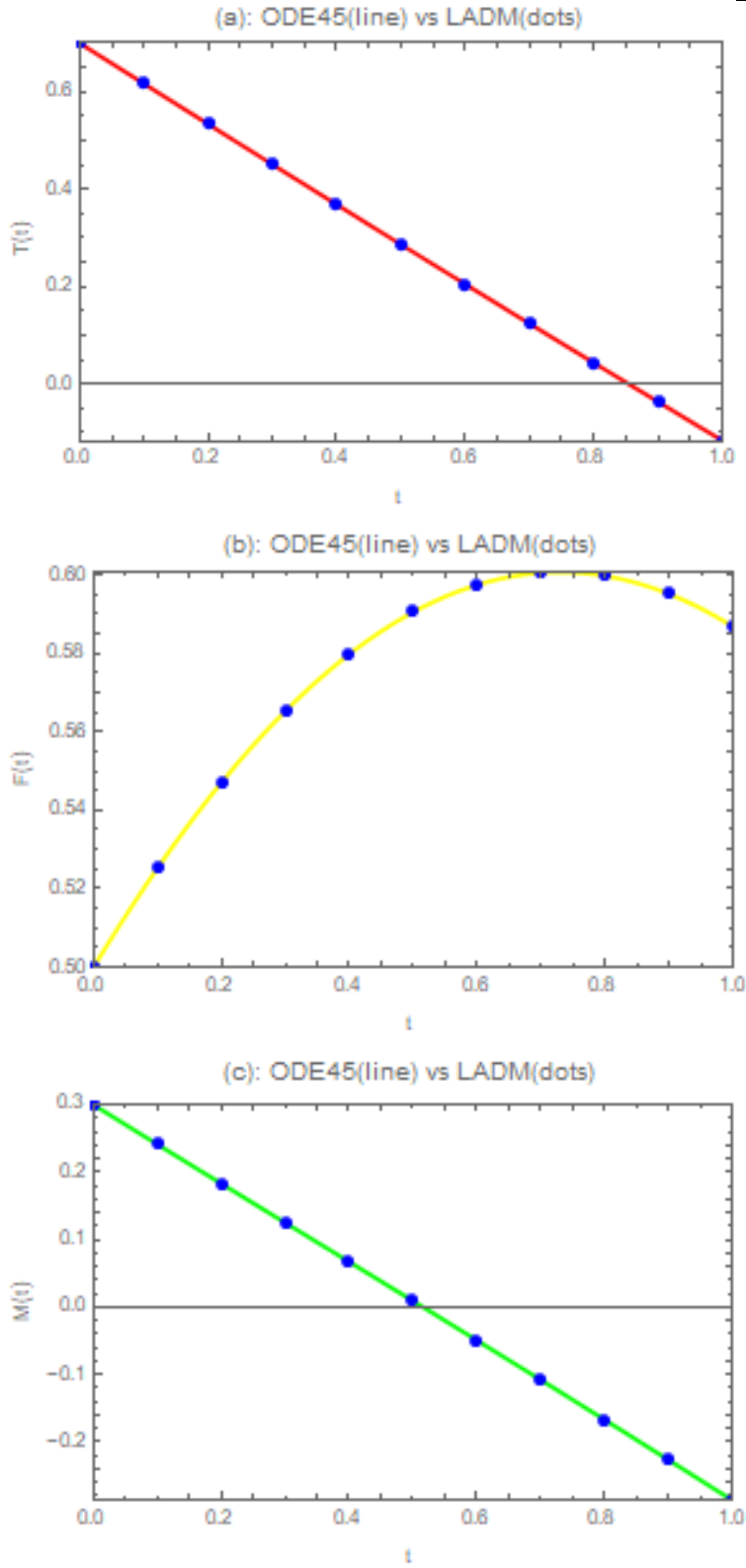


FIGURE 9. Comparison between the numerical solutions obtained using the the fourth- and fifth-order Runge–Kutta method (ODE45) and those obtained using the Laplace Adomian Decomposition Method (LADM) for (a) $T(t)$, (b) $F(t)$, (c) $M(t)$ for $\alpha = 1$.

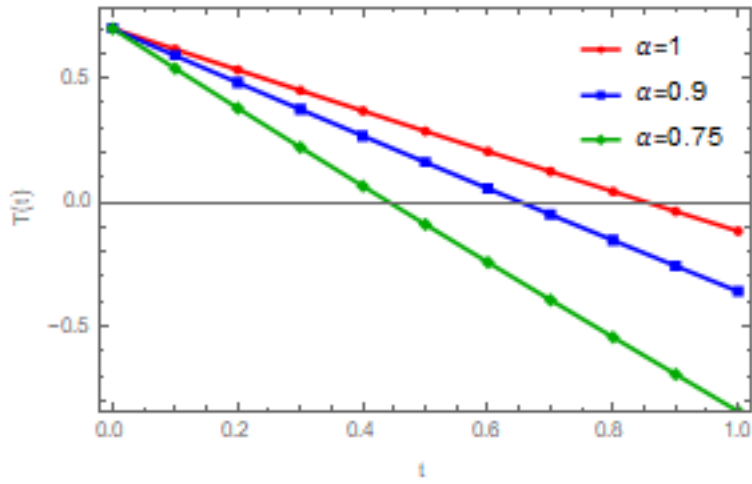


FIGURE 10. Approximate solutions of $T(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

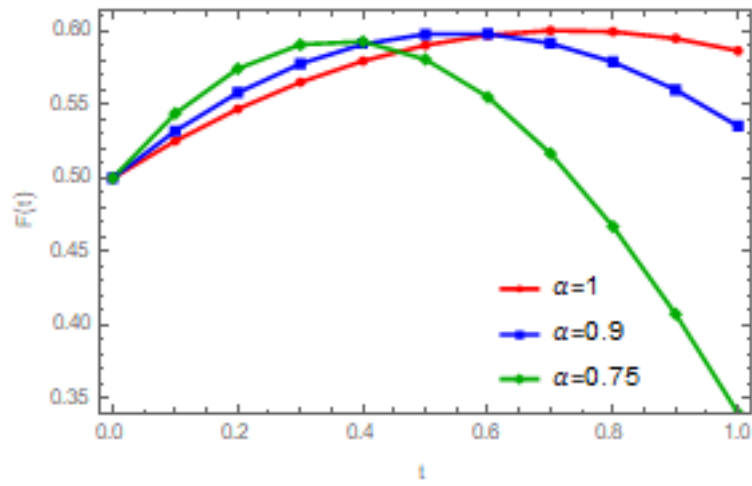


FIGURE 12. Approximate solutions of $F(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

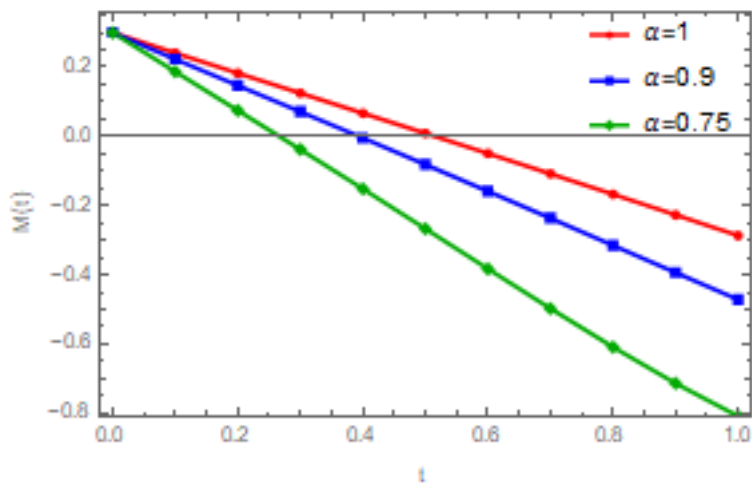
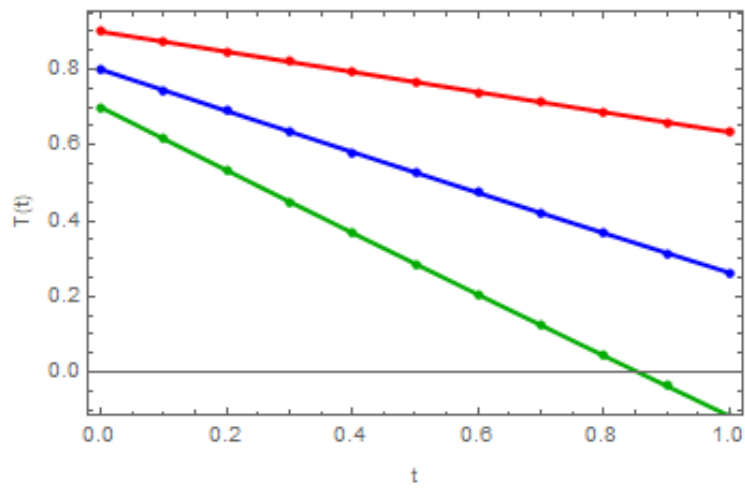
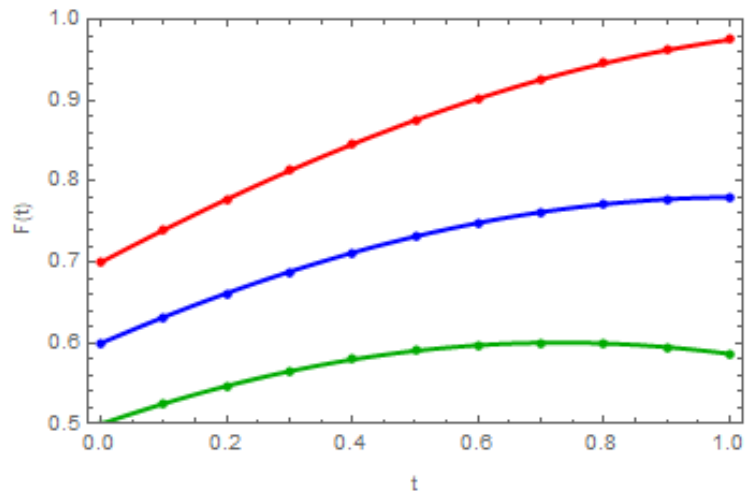


FIGURE 13. Approximate solutions of $M(t)$ for $\alpha = 1, 0.9$ and 0.75 using LADM

(a): $T(t)$ $\alpha=1$ -- ODE(line) vs LADM(dots)



(b): $F(t)$ $\alpha=1$ -- ODE(line) vs LADM(dots)



(c): $M(t)$ $\alpha=1$ -- ODE(line) vs LADM(dots)

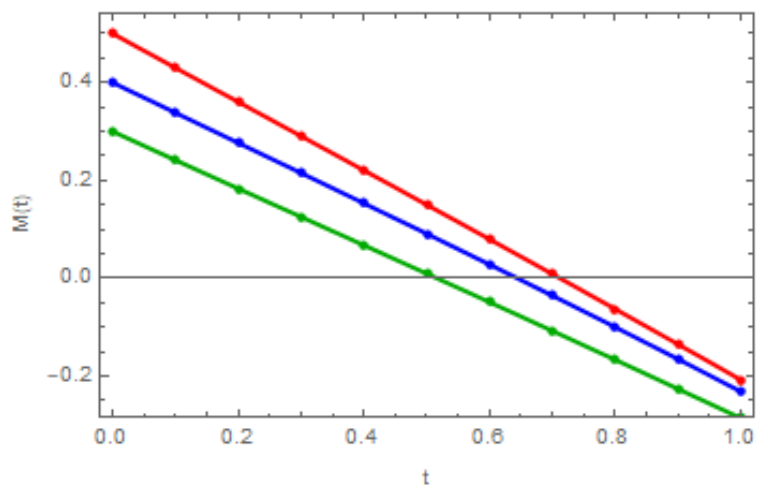


FIGURE 14. Comparison of the numerical solutions obtained using the fourth- and fifth-order Runge-Kutta method (ODE45) and the Laplace Adomian Decomposition Method (LADM) for $\alpha = 1$: Case 1 (red), Case 2 (blue), and Case 3 (green).

7. RESULTS AND GRAPHICAL INTERPRETATION

7.1 VALIDATION OF LADM ACCURACY (INTEGER-ORDER CASE $\alpha = 1$)

Figures 1, 5, and 9 compare LADM with the Runge-Kutta ODE45 solver for the integer-order case ($\alpha = 1$) across the three parameter cases. The curves and points overlap at the displayed resolution, supporting visual agreement between the methods.

In Case 1 (Figure 1), $T(t)$ decreases from its initial value throughout the displayed interval, whereas $F(t)$ increases monotonically. $M(t)$ also decreases from the outset and crosses below zero before $t = 1$. Thus, the plotted M trajectory does not show an initial absorption peak.

Case 2 (Figure 5) shows a stronger decline in $T(t)$ than Case 1, while $F(t)$ increases and gradually flattens. In Case 3 (Figure 9), $T(t)$ becomes negative near the end of the displayed interval, $F(t)$ rises and then decreases slightly, and $M(t)$ crosses zero earlier than in the other two cases. The visual overlap between LADM and ODE45 supports numerical consistency for $\alpha = 1$, but it does not by itself establish accuracy for $\alpha < 1$.

7.2 EFFECTS OF FRACTIONAL ORDER ON TENSION DYNAMICS

Figures 2, 6, and 10 show $T(t)$ for fractional orders $\alpha = 1.0, 0.9$, and 0.75 . The trajectories separate as α changes. As α decreases from 1.0 to 0.75 , the $\alpha = 0.75$ trajectory generally decreases more rapidly and may become negative. At $t = 1$, the plots show that lower α does not produce a uniformly slower decay.

The plotted maxima and terminal values vary with α , particularly for $\alpha = 0.75$. The figures therefore do not establish that amplitude bounds are preserved or that duration changes proportionally to the memory parameter $(1 - \alpha)$.

7.3 EFFECTS OF FRACTIONAL ORDER ON FOOD DYNAMICS

Figures 3, 7, and 11 show distinct α -dependent $F(t)$ trajectories. The $\alpha = 0.75$ curves rise rapidly, reach an interior maximum, and then decline within the displayed interval. The original comparison at $t = 20$ lies outside the plotted $0-1$ time range. Consequently, the trajectories cannot be characterized simply as slower food-consumption curves, and no clinical interpretation can be established from these simulations alone.

7.4 EFFECTS OF FRACTIONAL ORDER ON MEDICINE DYNAMICS

$M(t)$ is strongly sensitive to α in the displayed simulations. However, the $\alpha = 0.75$ curve decreases rapidly and becomes substantially negative; the plots do not show a delayed positive peak relative to $\alpha = 1$. Therefore, the graphs do not support an extended-release interpretation.

An increase in the area under the curve for the transition from $\alpha = 1$ to $\alpha = 0.75$ cannot be confirmed because no underlying numerical data or AUC calculation is provided. Moreover, $M(t)$ becomes more negative as α decreases, and the figures alone do not demonstrate a transition from exponential ($\alpha = 1$) to stretched-exponential behavior ($\alpha < 1$). Pharmacokinetic half-life or dosing conclusions require a nonnegative, empirically validated concentration model.

7.5 COMPARATIVE ANALYSIS ACROSS CASES

Figure 13 compares the three cases for the integer-order system. $T(t)$ declines most slowly in Case 1 and most rapidly in Case 3; $F(t)$ increases most strongly in Case 1, while Case 3 shows a slight late decline; and $M(t)$ decreases and becomes negative in all three cases. The plots do not establish physiological normality or steady-state convergence. The original claim of oscillations at $t < 1$ is not supported by the displayed curves.

7.6 INTERPRETATION AND LIMITATIONS OF FRACTIONAL-ORDER EFFECTS

The simulations show that changing α modifies the model trajectories. The $\alpha = 1$ case is the classical local-derivative baseline, whereas $\alpha = 0.9$ and $\alpha = 0.75$ introduce fractional memory effects of different strengths. The plots alone do not establish specific neural, hormonal, acute, or chronic clinical timescales. Such interpretations require parameter calibration and validation against physiological data.

8. CONCLUSION

In this study, the Laplace Adomian Decomposition Method (LADM) was successfully implemented to obtain series solutions for a fractional-order three-compartment Tension-Food-Medicine (TFM) stomach model under the Caputo derivative operator. The nonlinear dynamical interactions between stress, nutritional factors, and pharmacological treatment were analyzed across different fractional orders (α) and three distinct physiological parameter scenarios. The primary computational and qualitative findings of this investigation are summarized as follows:

- **Validation for Integer-Order Dynamics ($\alpha = 1$):** For the baseline integer-order case ($\alpha = 1$), the semi-analytical LADM solutions demonstrated excellent numerical agreement with the classic fourth- and fifth-order Runge-Kutta solver (ODE45) across all three parameter cases, establishing the foundational accuracy of the decomposition scheme.

- **Impact of Fractional Derivative Order ($\alpha < 1$):** Decreasing the fractional order α from 1.0 down to 0.75 markedly affected the short-time response and transient trajectory rates of the tension $T(t)$, food $F(t)$, and medicine $M(t)$ compartments. The inclusion of fractional derivatives inherently introduces non-local memory and hereditary properties into the dynamic response of gastrointestinal processes.
- **Sensitivity and Dynamic Flexibility:** The distinct compartment responses across different parameter cases emphasize the model's flexibility and sensitivity to system rate constants, providing a detailed framework for tailored physiological scenarios.

The analytical efficiency and swift series convergence of LADM offer substantial advantages for solving complex non-local systems. To further build upon these promising results and enhance the biological realism of the model, future extensions will focus on integrating non-negativity boundary conditions, conducting existence-uniqueness proofs for invariant regions, benchmarking against alternate fractional schemes (such as the Adams–Bashforth–Moulton method), and calibrating rate parameters with empirical clinical data.

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AN EFFICIENT APPROACH TO A FRACTIONAL EBOLA VIRUS MODEL

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ABSTRACT

This study examines a nonlinear Fractional Ebola virus model to characterize the spread of infectious diseases through a modified version of the Caputo fractional derivative. The Laplace Adomian Decomposition Method (LADM) is used to find approximate analytical solutions for the proposed model, given as rapidly converging series that show quick convergence and accurately describe how the system works. The method's reliability has been confirmed, and the proposed fractional-order model's validity has been verified. The novelty of this study lies in applying the Laplace Adomian Decomposition Method for the Fractional Ebola virus model and in benchmarking the resulting series against a fourth- and fifth-order Runge-Kutta method (ODE45) solution for the integer-order case, before extending the analysis to $\alpha = 0.9$ and $\alpha = 0.75$ to quantify how memory effects reshape the epidemic curve.

1. INTRODUCTION

Mathematical epidemiology frequently employs state-transition models to examine the dynamics of infectious diseases within a population. Such models provide a systematic framework for analyzing the spread and transmission of disease by representing the transition of individuals between different epidemiological states. For example, the Susceptible-Infected-Recovered (SIR) model is one of the most fundamental approaches in this field [1]. However, classical integer-order models typically overlook memory effects and non-local dynamics specific to many real-world epidemiological processes. To address these shortcomings, fractional-order derivatives come into play, modeling disease behavior in a more complex yet realistic manner by incorporating past data, thereby improving prediction accuracy [2]. In this context, a nonlinear fractional SIR model based on the Caputo derivative has been investigated, taking into account memory and hereditary effects commonly encountered in disease processes [3]. The use of fractional-order derivatives enables the modeling of infectious disease dynamics with non-local interactions, offering richer analytical capabilities compared to traditional integer-order models. While traditional models typically assume instantaneous transitions, they neglect the impact of past events on current states. In contrast, fractional-order models incorporate memory effects within the temporal context, enabling a more comprehensive and accurate representation of epidemiological processes [4]. In particular, this approach allows for modeling situations where the rate of change in a compartment depends on past states, thereby revealing hidden aspects of disease

dynamics [5]. Both numerical and analytical solutions have been derived in several studies to analyze the existence and uniqueness conditions of the fractional SIR model using advanced mathematical methods [6]. Additionally, to understand the long-term behavior of the epidemic, the stability of disease-free and endemic equilibrium points has been evaluated in detail under various conditions [7].

Recent studies have significantly expanded the scope of the classical SIR model by integrating fractional dynamics, data-driven approaches, and generalized transmission mechanisms. Taghvaei et al. proposed a fractional SIR framework in which the infection term is modified using a power-law structure, allowing the model to capture heterogeneous contact patterns more realistically [8]. Alqahtani developed a fractional-order SIR model tailored to COVID-19 dynamics, demonstrating that memory effects can substantially influence recovery and transmission rates [9]. Mousa and Alsharari presented a numerical comparison of fractional SIR models, focusing on the stability and accuracy of different computational schemes [10]. Qazza and Saadeh introduced an analytical approach based on Laplace transform techniques to obtain approximate solutions of fractional SIR systems [11]. Alazman et al. investigated the role of diffusion and generalized fractional operators in SIR dynamics, showing how spatial and memory effects jointly impact disease spread [12]. Prodanov explored nonlinear approximation techniques, including exponential series expansions, to improve the solvability of SIR-type models [13]. Murph et al. focused on parameter estimation and peak-infection mapping, highlighting the importance of accurate data fitting in SIR-based forecasting [14]. Shafqat et al. combined fractional SIRD models with deep learning methods to enhance predictive performance in epidemic modeling [15].

In this research, we also explore the potential of the Laplace Adomian Decomposition Method (LADM) for solving fractional epidemic models. This method is a powerful yet straightforward approach to tackling epidemic models and has been successfully applied in biology, engineering, and applied mathematics. It combines the Laplace transform and the Adomian decomposition method, offering several advantages for solving complex problems. One advantage of this method is its accuracy: by employing the Laplace transform, it converts the differential equations into algebraic equations, which are often easier to solve. This transformation reduces the complexity of the problem and enables the use of powerful algebraic techniques to obtain accurate solutions. Additionally, the Adomian decomposition method provides a systematic and robust approach to handling nonlinear terms, allowing for accurate approximation of the solution even in the presence of nonlinearity. This method does not require any perturbation or linearization, nor does it need a fixed step size like the fourth- and fifth-order Runge-Kutta technique. Various models have already been solved using this particular technique, such as the HIV infection of CD4+ T cells model [16], the fractional-order smoking model [17], epidemic childhood diseases [18], the Radhakrishnan-Kundu-Lakshmanan equation [19], the Asian option pricing model [20], Burgers' equation [21], the Chen-Lee-Liu equation [22], the prey-predator model [23], the nonlinear fractional smoking mathematical model [24], the HIV model [25], the smoking epidemic model [26], and the fractional-order COVID-19 model [27].

Beyond the generic SIR framework, several studies have specifically targeted the fractional and Fractional modeling of Ebola virus disease (EVD), which is the focus of the present work. Srivastava and Saad formulated three Fractional Ebola virus models based on the power-law, exponential-decay and Mittag-Leffler kernels and compared their numerical solutions for the classical case [28]; the susceptible–infected–recovered–death compartmental structure adopted in the present study follows this formulation. Raza et al. solved a fractional-order Ebola virus model using the Laplace Adomian Decomposition Method and reported rapidly convergent series solutions consistent with the classical integer-order case [34]. Dokuyucu and Dutta proposed an Ebola model based on a non-singular Caputo-type derivative and examined the qualitative behaviour of the resulting fractional system [35]. Hammouch et al. analyzed the Ebola epidemic using a conformable-derivative formulation [36], while Adu et al. incorporated treatment-centre transmission and survivor relapse into a Fractional Caputo model fitted to real EVD data from Uganda [37]. These EVD-specific studies motivate the present work, which builds directly on the Fractional structure of [28] and extends it through the Laplace Adomian Decomposition Method.

The novelty of the present study is twofold. First, although the Fractional Ebola virus model of [28] has previously been solved using power-law, exponential-decay and Mittag-Leffler numerical schemes, it has not, to the best of our knowledge, been solved by the Laplace Adomian Decomposition Method; the present work fills this gap by deriving an LADM series solution for the susceptible $\beta_1(t)$, infected $\beta_2(t)$, recovered $\beta_3(t)$ and disease-induced-death $\beta_4(t)$ compartments. Second, we provide a systematic comparison between the LADM series solution and the fourth- and fifth-order Runge–Kutta method (ODE45) solution for the integer-order case $\alpha = 1$, together with a discussion of how $\alpha = 0.9$ and $\alpha = 0.75$ reshape the epidemic curves for both parameter scenarios considered (Case 1 and Case 2). To the best of our knowledge, this Fractional Ebola virus model has not previously been solved by LADM, which constitutes the main contribution of this work.

The remainder of the paper is organized as follows: Section 2 formulates the Fractional Ebola virus model, Section 3 recalls the fractional calculus preliminaries, Section 4 develops the LADM solution procedure, Section 5 reports the numerical simulations, and Section 6 discusses and interprets the resulting graphs and concludes the study.

2. MODEL FORMULATION

In this section we shall study the transmission dynamics of Ebola virus disease with a compartmental model [28], with fractional derivatives of order $0 < \alpha < 1$ and population sizes that vary over time, following the compartmental structure introduced in [28]. D_t^α denotes the fractional-order derivative operator of order α in system of equations (2.1). As a result, the proposed fractional model involves four population variables: the susceptible, infected, recovered and disease-induced-death sub-populations, denoted by $\beta_1(t)$, $\beta_2(t)$, $\beta_3(t)$ and $\beta_4(t)$ respectively, as summarized in Table 1.

$$\begin{aligned}
D_t^\alpha \beta_1(t) &= -\sigma \beta_1(t) \beta_2(t) + \beta \beta_3(t) - \gamma N, \\
D_t^\alpha \beta_2(t) &= \sigma \beta_1(t) \beta_2(t) - \varepsilon \beta_2(t) - \delta \beta_2(t), \\
D_t^\alpha \beta_3(t) &= \delta \beta_2(t) - \beta \beta_3(t), \\
D_t^\alpha \beta_4(t) &= \varepsilon \beta_2(t) + \gamma N.
\end{aligned} \tag{2.1}$$

Initial condition

$$\beta_1(0) = 70, \beta_2(0) = 2, \beta_3(0) = 0, \beta_4(0) = 0. \tag{2.2}$$

In Table 1, we define the independent variables and the parameters of the Ebola virus.

Symbol	Definition
$\beta_1(t)$	The susceptible population
$\beta_2(t)$	The infected population
$\beta_3(t)$	The recovery population
$\beta_4(t)$	The population died in the region
N	The total population in the region
σ	The rate of infection with the disease
β	The rate of susceptibility
γ	The rate of natural death
ε	The rate of death from the disease
δ	The rate of recovery from the disease

TABLE 1. Description of the independent variables and the involved parameters.

3. BASIC DEFINITIONS

In this section, we will introduce some basic definitions and properties of the theory of fractional calculus that will be needed later in this study.

Definition 3.1 [30] A real function $f(x)$, $x > 0$ is said to be in the space C_μ , $\mu \in \mathbb{R}$ if there exists a real number $P > \mu$ such that $f(x) = x^P f_1(x)$ where $f_1(x) \in C[0, \infty)$. Clearly $C_\mu < C_\beta$ if $\mu < \beta$.

Definition 3.2 [30] A function $f(x)$, $x > 0$ is said to be in the space C_μ^m , $m \in \mathbb{N} \cup \{0\}$ if $f^{(m)} \in C_\mu$.

Definition 3.3 [31] The Riemann-Liouville fractional integral operator of the order $\alpha > 0$ of a function, $f \in C_\mu$, $\mu \geq -1$ is defined as

$$(J_a^\alpha f)(x) = \frac{1}{\Gamma(\alpha)} \int_a^x (x - \tau)^{\alpha-1} f(\tau) d\tau, x > a, \tag{3.1}$$

$$(J_a^0 f)(x) = f(x). \tag{3.2}$$

All the properties of the operator J^α can be found in [32] which we mention only the following, for $f \in C_\mu$, $\mu \geq -1$, $\alpha, \beta \geq 0$, and $\gamma > -1$ we have

$$(J_a^\alpha J_a^\beta f)(x) = (J_a^{\alpha+\beta} f)(x), \quad (3.3)$$

$$(J_a^\alpha J_a^\beta f)(x) = (J_a^\beta J_a^\alpha f)(x) \quad (3.4)$$

$$J_a^\alpha x^\gamma = \frac{\Gamma(\gamma+1)}{\Gamma(\alpha+\gamma+1)} x^{\alpha+\gamma}. \quad (3.5)$$

The basic definition of the Riemann–Louville fractional derivative possesses some advantages over other definitions when used to simulate real-world phenomena in the form of a fractional-type differential equation.

Definition 3.4 [33] The fractional derivative of the function $f(x)$ in Caputo's sense is defined as

$$(D_a^\alpha f)(x) = \left(J_a^{m-\alpha} D_a^m f\right)(x) = \frac{1}{\Gamma(m-\alpha)} \int_a^x (x-t)^{m-\alpha-1} f^{(m)}(t) dt, \text{ for } m-1 < \alpha < m, m \in \mathbb{N}, x > 0. \quad (3.6)$$

Lemma 3.1 If $-1 < \alpha < m$, $m \in \mathbb{N}$ and $\mu \geq -1$, then

$$(J_a^\alpha D_a^\alpha f)(x) = f(x) - \sum_{k=0}^{m-1} f^{(k)}(a) \left(\frac{(x-a)^k}{k!}\right), a \geq 0 \quad (3.7)$$

$$(D_a^\alpha J_a^\alpha f)(x) = f(x) \quad (3.8)$$

4. LAPLACE ADOMIAN DECOMPOSITION METHOD

In this section, we will illustrate the basic steps for LADM. We discuss the following important definitions or our research study:

Definition 4.1 [24] A function f on $0 \leq t < \infty$ is exponentially bounded of order $\sigma \in \mathbb{R}$ if satisfies $\|f(t)\| \leq M e^{\sigma t}$, for some real constant $M > 0$.

Definition 4.2 The Caputo fractional derivative is defined as follows:

$$\{D^\sigma f(t)\} = s^\sigma L\{f(t)\} - \sum_{k=0}^m s^{\sigma-k-1} f^{(k)}(0), \quad (4.a)$$

where $m = \sigma + 1$, and $[\alpha]$ represents the integer part of σ . As a result, the following useful formula is obtained:

$$L(t^\sigma) = \frac{\Gamma(\sigma+1)}{s^{(\sigma+1)}}, \quad \sigma \in \mathbb{R}^+. \quad (4.b)$$

The last-mentioned definitions can be used in this section to discuss the general procedures for solving the proposed mathematical model (2.1). First of all, the Laplace transform is applied to both left-hand and right-hand sides of Eq. (2.1) in the following form:

$$L(D_t^\alpha \beta_1) = -\sigma L(\beta_1 \beta_2) + \beta L(\beta_3) - \frac{\gamma N}{s},$$

$$\begin{aligned}
L(D_t^\alpha \beta_2) &= \sigma L(\beta_1 \beta_2) - \varepsilon L(\beta_2) - \delta L(\beta_2), \\
L(D_t^\alpha \beta_3) &= \delta L(\beta_2) - \beta L(\beta_3), \\
L(D_t^\alpha \beta_4) &= \varepsilon L(\beta_2) + \frac{\gamma N}{s},
\end{aligned} \tag{4.1}$$

Then, by applying the formula (4.a) to Eq. (4.1), we get

$$\begin{aligned}
S^\alpha L(\beta_1) - S^{\alpha-1} \beta_1(0) &= -\sigma L(\beta_1 \beta_2) + \beta L(\beta_3) - \frac{\gamma N}{s}, \\
S^\alpha L(\beta_2) - S^{\alpha-1} \beta_2(0) &= \sigma L(\beta_1 \beta_2) - \varepsilon L(\beta_2) - \delta L(\beta_2), \\
S^\alpha L(\beta_3) - S^{\alpha-1} \beta_3(0) &= \delta L(\beta_2) - \beta L(\beta_3), \\
S^\alpha L(\beta_4) - S^{\alpha-1} \beta_4(0) &= \varepsilon L(\beta_2) + \frac{\gamma N}{s},
\end{aligned} \tag{4.2}$$

Next, by substituting the initial conditions in Eq. (2.2) into the model (4.2), we get

$$\begin{aligned}
L(\beta_1) &= \frac{\beta_1(0)}{s} - \frac{\sigma}{s^\alpha} L(\beta_1 \beta_2) + \frac{\beta}{s^\alpha} L(\beta_3) - \frac{\gamma N}{s^{\alpha+1}}, \\
L(\beta_2) &= \frac{\beta_2(0)}{s} + \frac{\sigma}{s^\alpha} L(\beta_1 \beta_2) - \frac{\varepsilon}{s^\alpha} L(\beta_2) - \frac{\delta}{s^\alpha} L(\beta_2), \\
L(\beta_3) &= \frac{\beta_3(0)}{s} + \frac{\delta}{s^\alpha} L(\beta_2) - \frac{\beta}{s^\alpha} L(\beta_3), \\
L(\beta_4) &= \frac{\beta_4(0)}{s} + \frac{\varepsilon}{s^\alpha} L(\beta_2) + \frac{\gamma N}{s^{\alpha+1}},
\end{aligned} \tag{4.3}$$

The proposed method gives the solution as an infinite series. Let the value of $A = \beta_1 \beta_2$ to be able to apply the Adomian decomposition method. We consider the solution as an infinite series in the form

$$\beta_1 = \sum_{n=0}^{\infty} \beta_{1,n}, \quad \beta_2 = \sum_{n=0}^{\infty} \beta_{2,n}, \quad \beta_3 = \sum_{n=0}^{\infty} \beta_{3,n}, \quad \beta_4 = \sum_{n=0}^{\infty} \beta_{4,n}, \tag{4.4}$$

Then, by decomposing the nonlinear part named A in the following form

$$A = \sum_{n=0}^{\infty} A_n, \tag{4.5}$$

Here, A_n can be computed using the convolution operation as

$$A_n = \frac{1}{\Gamma(n+1)} \frac{d^n}{d\eta^n} \left[\sum_{i=0}^n \eta^i \beta_{1,i} \sum_{j=0}^n \eta^j \beta_{2,j} \right]_{\eta=0} \tag{4.6}$$

By substituting Eq. (4.4- 4.6) into Eq. (4.3) and by matching the two sides of the equation yields the following iterative algorithm we have resulted in the form.

$$\begin{aligned}
L\left(\sum_{n=0}^{\infty} \beta_{1,n}\right) &= \frac{\beta_{1,00}}{S} - \frac{\sigma}{S^\alpha} L\left(\sum_{n=0}^{\infty} A_n\right) + \frac{\beta}{S^\alpha} L\left(\sum_{n=0}^{\infty} \beta_{3,n}\right) - \frac{\gamma N}{S^{\alpha+1}}, \\
L\left(\sum_{n=0}^{\infty} \beta_{2,n}\right) &= \frac{\beta_{2,00}}{S} + \frac{\sigma}{S^\alpha} L\left(\sum_{n=0}^{\infty} A_n\right) - \frac{\varepsilon}{S^\alpha} L\left(\sum_{n=0}^{\infty} \beta_{2,n}\right) - \frac{\delta}{S^\alpha} L\left(\sum_{n=0}^{\infty} \beta_{2,n}\right), \\
L\left(\sum_{n=0}^{\infty} \beta_{3,n}\right) &= \frac{\beta_{3,00}}{S} + \frac{\delta}{S^\alpha} L\left(\sum_{n=0}^{\infty} \beta_{2,n}\right) - \frac{\beta}{S^\alpha} L\left(\sum_{n=0}^{\infty} \beta_{3,n}\right), \\
L\left(\sum_{n=0}^{\infty} \beta_{4,n}\right) &= \frac{\beta_{4,00}}{S} + \frac{\varepsilon}{S^\alpha} L\left(\sum_{n=0}^{\infty} \beta_{2,n}\right) + \frac{\gamma N}{S^{\alpha+1}}, \tag{4.7}
\end{aligned}$$

By equating both sides of Equation (4.7), we obtain the following iterative algorithm:

$$\begin{aligned}
L(\beta_{1,0}) &= \frac{\beta_{1,00}}{S}, \quad L(\beta_{2,0}) = \frac{\beta_{2,00}}{S}, \quad L(\beta_{3,0}) = \frac{\beta_{3,00}}{S}, \\
L(\beta_{4,0}) &= \frac{\beta_{4,00}}{S}, \\
L(\beta_{1,1}) &= -\frac{\sigma}{S^\alpha} L(A_0) + \frac{\beta}{S^\alpha} L(\beta_{3,0}) - \frac{\gamma N}{S^{\alpha+1}}, \\
L(\beta_{2,1}) &= \frac{\sigma}{S^\alpha} L(A_0) - \frac{\varepsilon}{S^\alpha} L(\beta_{2,0}) - \frac{\delta}{S^\alpha} L(\beta_{2,0}), \\
L(\beta_{3,1}) &= \frac{\delta}{S^\alpha} L(\beta_{2,0}) - \frac{\beta}{S^\alpha} L(\beta_{3,0}), \\
L(\beta_{4,1}) &= \frac{\varepsilon}{S^\alpha} L(\beta_{2,0}) + \frac{\gamma N}{S^{\alpha+1}}, \dots \\
L(\beta_{1,n}) &= -\frac{\sigma}{S^\alpha} L(A_{n-1}) + \frac{\beta}{S^\alpha} L(\beta_{3,n-1}), \\
L(\beta_{2,n}) &= \frac{\sigma}{S^\alpha} L(A_{n-1}) - \frac{\varepsilon}{S^\alpha} L(\beta_{2,n-1}) - \frac{\delta}{S^\alpha} L(\beta_{2,n-1}), \\
L(\beta_{3,n}) &= \frac{\delta}{S^\alpha} L(\beta_{2,n-1}) - \frac{\beta}{S^\alpha} L(\beta_{3,n-1}), \\
L(\beta_{4,n}) &= \frac{\varepsilon}{S^\alpha} L(\beta_{2,n-1}), \tag{4.8}
\end{aligned}$$

Finally, by taking the inverse transform of Eq. (4.8), we have the following equation

$$\beta_{1,0} = \beta_{1,00}, \quad \beta_{2,0} = \beta_{2,00}, \quad \beta_{3,0} = \beta_{3,00},$$

$$\beta_{4,0} = \beta_{4,00},$$

$$\beta_{1,1} = [-\sigma A_0 + \beta \beta_{3,0} - \gamma N] \frac{t^\alpha}{\Gamma(\alpha + 1)},$$

$$\beta_{2,1} = [\sigma A_0 - \varepsilon \beta_{2,0} - \delta \beta_{2,0}] \frac{t^\alpha}{\Gamma(\alpha + 1)},$$

$$\beta_{3,1} = [\delta \beta_{2,0} - \beta \beta_{3,0}] \frac{t^\alpha}{\Gamma(\alpha + 1)},$$

$$L(\beta_{4,1}) = [\varepsilon \beta_{2,0} + \gamma N] \frac{t^\alpha}{\Gamma(\alpha + 1)}, \dots \quad (4.9)$$

In a similar way, we can obtain the remaining terms. Finally, we get the solution in the form of infinite series as given by

$$\beta_1(t) = \sum_{i=0}^{\infty} \beta_{1i}, \quad \beta_2(t) = \sum_{i=0}^{\infty} \beta_{2i}, \quad \beta_3(t) = \sum_{i=0}^{\infty} \beta_{3i}, \quad \beta_4(t) = \sum_{i=0}^{\infty} \beta_{4i}. \quad (4.10)$$

Equation (4.10) solves the main Ebola virus model of Eq. (2.1) which will be illustrated in the next section.

5. NUMERICAL SIMULATIONS

In this section, we examine the proposed model for $\alpha = 1, 0.9$, and 0.75 under two parameter sets. The parameter values are adopted from the numerical setup reported in the cited source and are used here as illustrative scenarios rather than as estimates fitted to Ebola surveillance data.

For $\alpha = 1$, the LADM approximation is compared with MATLAB's ode45 solver.

The values $\alpha = 0.9$ and $\alpha = 0.75$ are used to explore sensitivity of the simulated trajectories to the fractional order. In the present formulation, a Caputo-type operator introduces a history-dependent term, but the interpretation of α as a directly measurable biological memory parameter requires model calibration and dimensional justification. The observed changes in peak timing or amplitude should therefore be reported as properties of these simulations, not as general biological conclusions. A dedicated fractional numerical method and a convergence study are needed before attributing the differences solely to memory effects.

CASE 1: Parameter descriptions of the Ebola virus nonlinear system

$\sigma = 0.01, \quad \gamma = 0.01, \quad \beta = 0.002, \quad \varepsilon = 0.006, \quad \delta = 0.004,$ $N = 10, \quad \beta_1(0) = 70, \quad \beta_2(0) = 2, \quad \beta_3(0) = 0 \text{ and } \beta_4(0) = 0$
--

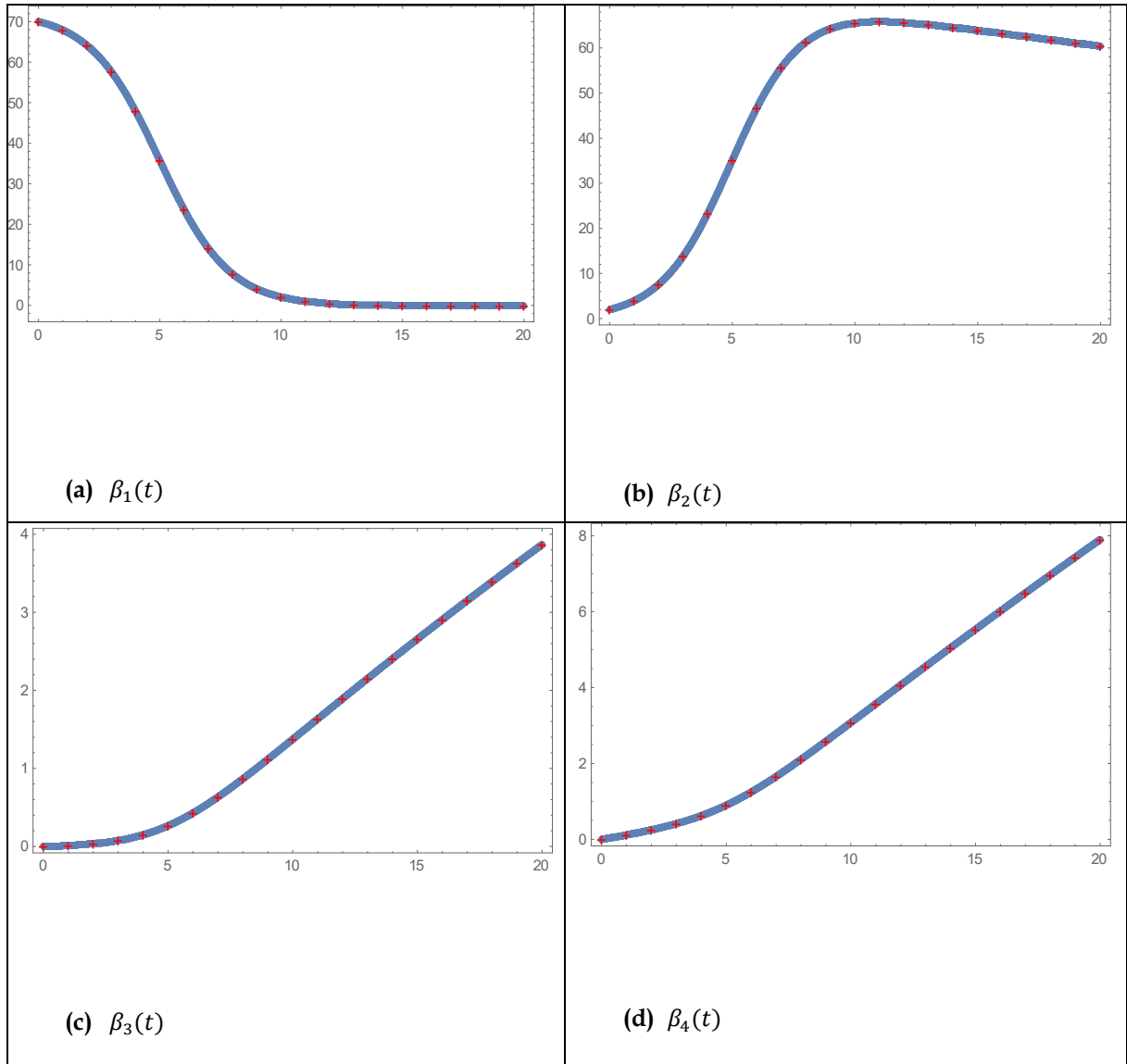


FIGURE 1. Comparison between the numerical solutions obtained using the fourth- and fifth-order Runge-Kutta method (ODE45) and those obtained using the Laplace Adomian Decomposition Method (LADM) for (a) $\beta_1(t)$, (b) $\beta_2(t)$, (c) $\beta_3(t)$ and (d) $\beta_4(t)$ for $\alpha=1$. Blue solid line: numerical solutions obtained using LADM; red dots: numerical solutions obtained using ODE45.

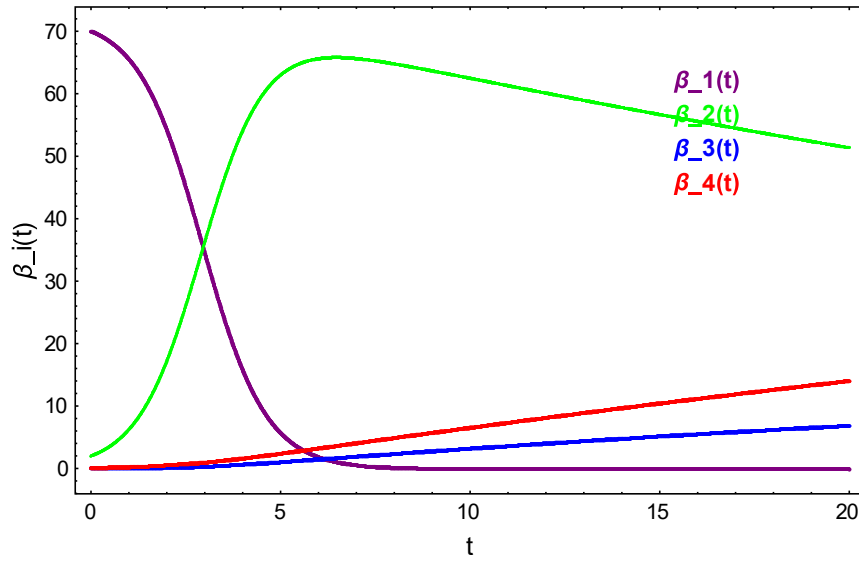


FIGURE 2. Approximate solution for $\beta_1(t)$, $\beta_2(t)$, $\beta_3(t)$ and $\beta_4(t)$ for $\alpha=0.9$ using LADM.

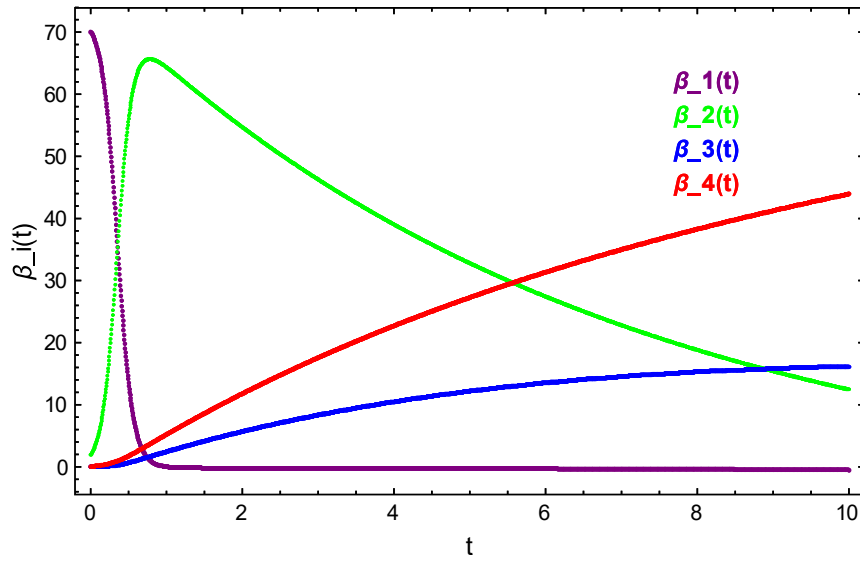
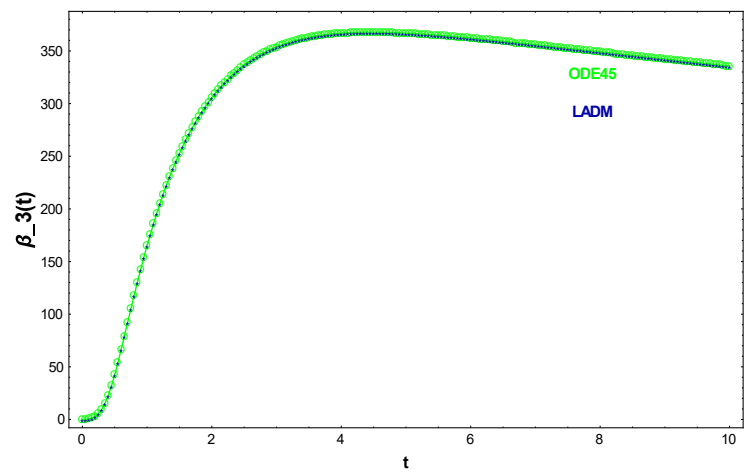
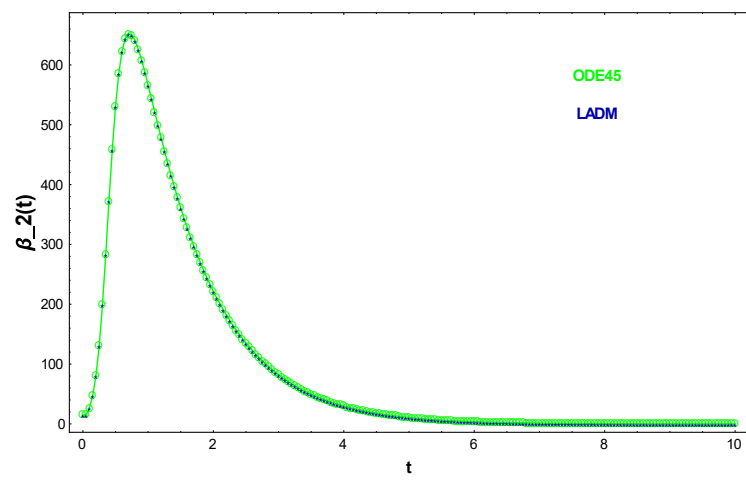
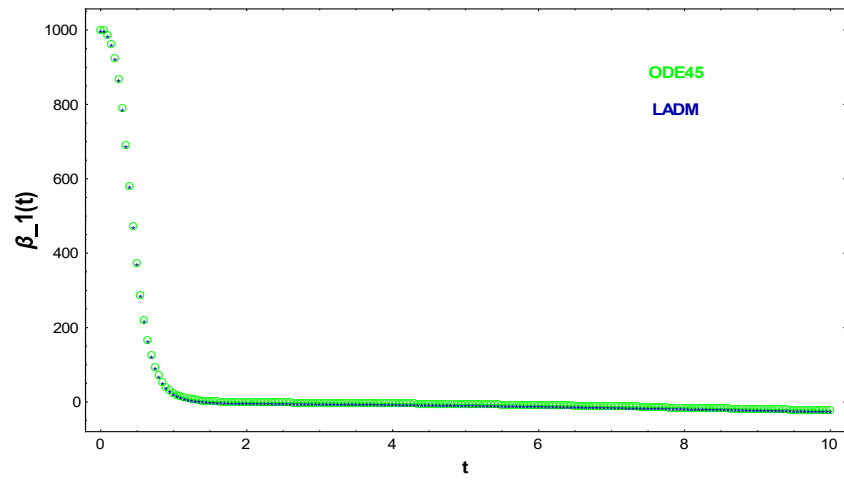


FIGURE 3. Approximate solution for $\beta_1(t)$, $\beta_2(t)$, $\beta_3(t)$ and $\beta_4(t)$ for $\alpha=0.75$ using LADM.

CASE 2: Parameter descriptions of the Ebola virus model

$$\sigma = 0.01, \quad \gamma = 0.01, \quad \beta = 0.002, \quad \varepsilon = 0.006, \quad \delta = 0.004,$$

$$N = 10, \quad \beta_1(0) = 1000, \quad \beta_2(0) = 15, \quad \beta_3(0) = 0 \text{ and } \beta_4(0) = 0$$



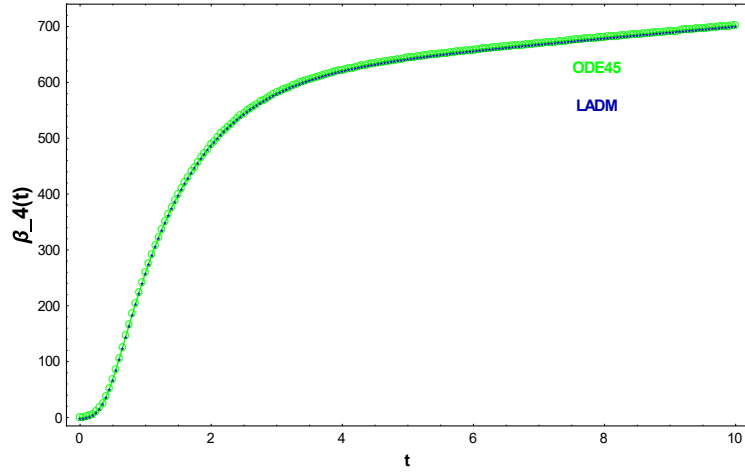


FIGURE 4. Comparison between the numerical solutions obtained using the fourth- and fifth-order Runge–Kutta method (ODE45) and those obtained using the Laplace Adomian Decomposition Method (LADM) for (a) $\beta_1(t)$, (b) $\beta_2(t)$, (c) $\beta_3(t)$ and (d) $\beta_4(t)$ for $\alpha=1$. Green circles: numerical solutions obtained using ODE45; blue asterisks: numerical solutions obtained using LADM

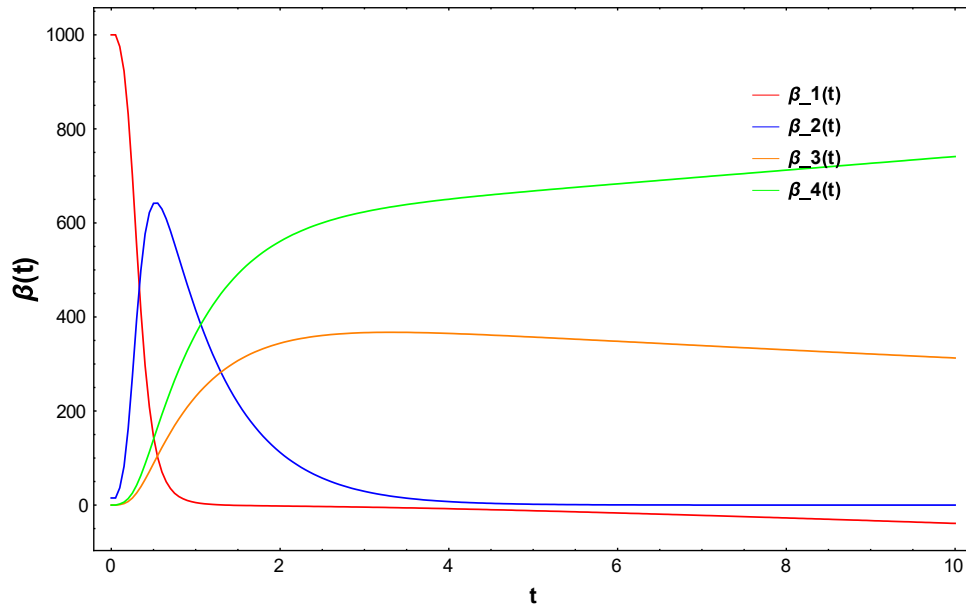


FIGURE 5. Approximate solution for $\beta_1(t)$, $\beta_2(t)$, $\beta_3(t)$ and $\beta_4(t)$ for $\alpha=0.9$ using LADM.

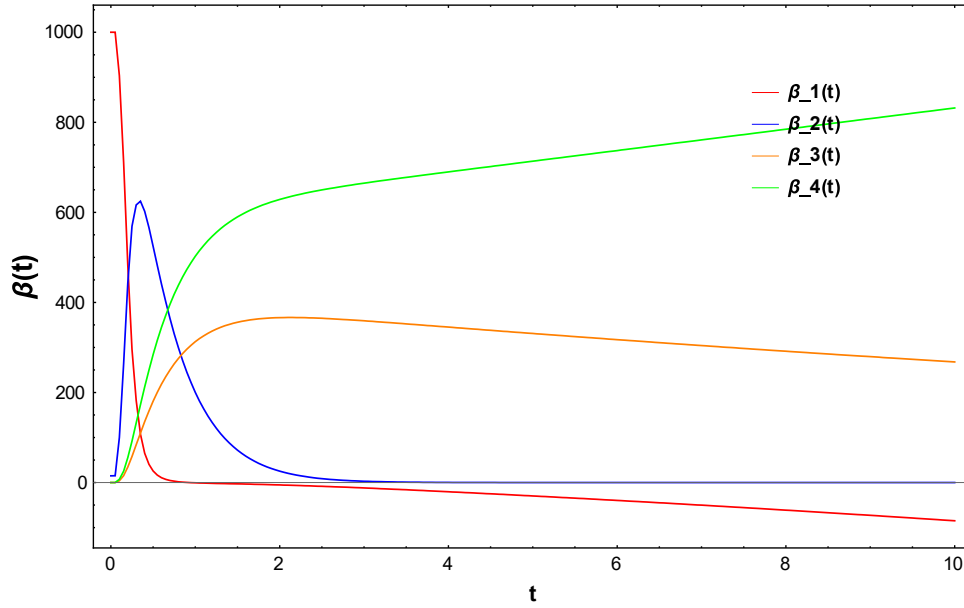


FIGURE 6. Approximate solution for $\beta_1(t)$, $\beta_2(t)$, $\beta_3(t)$ and $\beta_4(t)$ for $\alpha = 0.75$ using LADM.

6. GRAPH INTERPRETATION & CONCLUSIONS

Figures 1 and 4 validate the proposed method for the integer-order case ($\alpha = 1$) by comparing the LADM series solution with the fourth- and fifth-order Runge-Kutta method (ODE45) numerical solution for both parameter sets (Case 1 and Case 2). In every panel (a)–(d), the LADM curve overlays the ODE45 markers almost exactly for the susceptible $\beta_1(t)$, infected $\beta_2(t)$, recovered $\beta_3(t)$, and cumulative mortality $\beta_4(t)$ compartments, confirming that a small number of LADM terms already reproduces the benchmark numerical solution with negligible visible error. This agreement is the primary evidence that the LADM series is convergent and that its truncation to a finite number of terms is an accurate approximation of the exact solution for this two-group Ebola model.

Figures 2, 3, 5, and 6 show the LADM approximate solutions for the fractional orders $\alpha = 0.9$ and $\alpha = 0.75$, for which no independent ODE45 benchmark is available. Reading these figures together, the susceptible curves $\beta_1(t)$, decline more gradually as α decreases, the infected curves $\beta_2(t)$ reach a lower and later peak, and the recovered and mortality curves $\beta_3(t)$ and $\beta_4(t)$ rise more slowly toward their long-run levels than in the integer-order case shown in Figures 1 and 4. This flattening and delaying of the epidemic curve as α is reduced is the graphical signature of the memory (hereditary) effect built into the Fractional derivative: because the current rate of change depends on a weighted history of past states, a smaller α gives more weight to earlier, lower infection levels and so slows the approach of the system toward its equilibrium.

Comparing Case 1 (small initial population, $\beta_1(t) = 70$, $\beta_2(t) = 2$) with Case 2 (larger initial population, $\beta_1(t) = 1000$, $\beta_2(t) = 15$) shows that the qualitative shape of every curve is preserved across the two scales:

the close LADM-ODE45 agreement at $\alpha = 1$ and the fractional-order flattening effect described above both persist regardless of the absolute population size. This scale-invariance of the qualitative dynamics, together with the rapidly decaying magnitude of successive LADM series terms noted in the numerical simulation section, supports treating the fast convergence observed for $\alpha = 1$ as indirect evidence that the LADM series also converges reliably for $\alpha = 0.9$ and $\alpha = 0.75$, even though no independent fractional-order solver is available for a direct check.

The graphical comparison across $\alpha = 1, \alpha = 0.9$ and $\alpha = 0.75$ confirms that the LADM series closely tracks the ODE45 benchmark at integer order and that decreasing α systematically flattens and delays the epidemic curve for both parameter cases considered. This research developed a nonlinear Fractional Ebola virus model utilizing a modified Caputo fractional derivative to examine the transmission dynamics of infectious diseases. The model was effectively resolved employing two distinct methodologies: the fourth- and fifth-order Runge-Kutta method and the Laplace-Adomian decomposition method. The results obtained yield precise solutions and are examined for varying values of the fractional-order parameter α and diverse transmission rates. All results have been examined and contrasted across various cases. The results show that all values of α and transmission rates are very accurate and stable. Our results and methodologies can be further expanded or generalized to address additional intriguing nonlinear models that emerge from diverse phenomena in physics and engineering. The results are also applicable to models developed with alternative fractional derivatives.

Comparing the three fractional orders considered, $\alpha = 1, \alpha = 0.9$ and $\alpha = 0.75$, the simulations show that as α decreases the infected sub-population $\beta_2(t)$ reaches its peak later and at a lower amplitude, while the susceptible and recovered compartments approach their long-run levels more gradually; in other words, the memory effect captured by the fractional derivative tends to flatten and delay the epidemic curve relative to the classical integer-order case. This suggests that populations whose transmission or recovery process carries a stronger hereditary component may experience a slower-burning, less sharply peaked outbreak, a biologically relevant insight that the classical integer-order SIR model cannot provide. The present study nevertheless has some limitations: the model assumes a constant total population with no age-structure, it does not include vaccination or time-dependent transmission and recovery rates, and the LADM solution is presented as a truncated series whose accuracy for $\alpha \neq 1$ could not be benchmarked against an independent fractional-order solver. Future work will extend the model to include vaccination strategies, age-structured or spatially distributed populations, and time-varying parameters, and will compare the LADM series against dedicated fractional numerical schemes (e.g. the Adams-Bashforth-Moulton predictor-corrector method) for $\alpha \neq 1$.

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OPTIMIZATION OF HISTOGRAMS FOR LOGNORMAL PARAMETER ESTIMATION IN HYDROLOGICAL TIME SERIES: A COMPARATIVE STUDY OF THE FIERZË BASIN

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ABSTRACT

Accurate estimation of probability distribution parameters is a fundamental challenge in hydrological time series analysis. This study builds upon recent non-parametric findings regarding the Drin Cascade by comparing three distinct binning methodologies – Scott’s Rule, the Freedman-Diaconis Rule, and Knuth’s Bayesian method – to estimate the parameters of a log-normal distribution for the lateral inflows of the Fierzë hydropower basin ($N = 12, 570$). Robustness analysis via Politis-Romano subsampling reveals that standard empirical rules, which rely on absolute data ranges, are mathematically fragile when subjected to extreme tail outliers. Conversely, Knuth’s Bayesian approach demonstrates superior structural stability. Comparative evaluations confirm that parameters derived from Bayesian optimal bins mathematically outperform those from empirical rules in baseline statistical Goodness-of-Fit evaluations (Log-Likelihood). By exploring the mathematical foundations of these discretization techniques, this paper demonstrates how histogram optimization directly impacts the accuracy of parametric regression, providing a more mathematically rigorous framework for baseline hydrological probability modeling.

1. INTRODUCTION

The Drin River Cascade represents one of the most critical infrastructures for energy production and water resource management in the Balkan region. However, the statistical modeling of lateral inflows into its basins presents immense challenges due to the complex, heavy-tailed nature of the hydrological time series. Furthermore, the basin is naturally prone to severe transboundary flooding, where the flow regulation practices and buffer management of its massive reservoirs (particularly Fierzë) dictate the downstream safety of the entire region (UNECE, 2022).

Previous foundational studies on the Drin Cascade have established that the distributions of average hourly and daily inflows are non-stationary over extended observation periods. By employing q -functions, Prenga and Ifti (2014) and Kovaçi et al. (2015) determined that these distributions deviate significantly from standard reference distributions. The non-stationarity parameter (q -stationarity) in these basins yields a value of approximately 2, sharply contrasting with standard stationary conditions where $1 \leq q \leq 5/3$ (Umarov et al., 2008).

These deviations dictate that a meticulous approach to characterizing the underlying empirical distributions is required before any parametric modeling can be trusted. Recently, Hoxha (2026)

demonstrated that standard “one-size-fits-all” empirical binning rules fail to capture the physical reality of the Drin Cascade. By applying advanced data-driven discretization, Hoxha (2026) successfully established the non-parametric baseline for the cascade, identifying a Pluvial regime for Vau i Dejës (requiring adaptive Bayesian Blocks) and a distinct Nival (snowmelt-dominated) regime for the highly skewed Fierzë basin (successfully modeled via Knuth’s fixed-width optimization).

Building directly upon those non-parametric findings, this paper isolates the Fierzë basin to evaluate the next critical engineering step: *parametric* distribution fitting. The extraction of parametric probability distributions, specifically the widely utilized two-parameter Lognormal distribution (Stedinger et al., 1993), is a foundational exercise for flood risk assessment, spillway design, and infrastructural safety margins. However, the extraction of its optimal scale (μ) and shape (σ) parameters via non-linear regression is strictly dependent on the underlying empirical density structure. If the initial histogram discretization is structurally fragile, the resulting parametric fit will inherit that mathematically compromised geometry.

This study evaluates how three distinct histogram discretization methodologies—Scott’s Rule, the Freedman-Diaconis Rule, and Knuth’s Bayesian optimization—impact the parameter estimation of a Lognormal model. By subjecting these algorithms to rigorous subsampling robustness tests, this paper demonstrates how they handle the mathematical fragility introduced by extreme flood outliers, ultimately proving why Bayesian baseline optimization provides a superior, safer foundation for parametric regression in the Drin Cascade

2. METHODOLOGY AND DATA PREPARATION

The selection of interval width fundamentally alters the empirical density landscape from which parametric estimations are drawn.

2.1. STANDARD EMPIRICAL RULES: SCOTT AND FREEDMAN-DIACONIS.

Standard empirical rules generally seek to minimize the integrated mean squared error (IMSE) between the empirical histogram and the true, unknown underlying continuous density.

Scott’s Rule (Scott, 1979): Assumes a Gaussian reference for the underlying data. The optimal bin width (W) is calculated as:

$$W = 3.49\hat{\sigma}N^{-1/3} \tag{2.1}$$

where $\hat{\sigma}$ is the sample standard deviation and N is the sample size. Because the global standard deviation is highly sensitive to extreme values, Scott’s Rule is theoretically vulnerable to variance inflation caused by heavy right tails.

Freedman-Diaconis (FD) Rule (Freedman & Diaconis, 1981): Designed to be more robust against outliers, the FD rule replaces the standard deviation with the Interquartile Range (IQR):

$$W = 2IQRN^{-1/3} \quad (2.2)$$

By calculating dispersion based only on the central 50% of the data, the FD rule aims to preserve structural resolution in the body of the distribution without being heavily distorted by the extremes. Crucially, both Scott and FD calculate the final number of bins (M) by dividing the absolute empirical data range (Max – Min) by W .

2.2. KNUTH’S BAYESIAN OPTIMAL BINNING.

Unlike IMSE-based methods that rely on summary statistics, Knuth’s approach treats the histogram as a piecewise-constant probability model (Knuth, 2006)¹. It utilizes Bayesian inference to maximize the posterior probability of the bin structure, assuming a multinomial likelihood. By applying non-informative Jeffreys priors, the marginal likelihood is derived analytically. The logarithm of the posterior probability is defined as: (2.3)

$$\log P(M|\text{Data}) = N\log(M) + \log\left(\Gamma\left(\frac{M}{2}\right)\right) - M\log\left(\Gamma\left(\frac{1}{2}\right)\right) - \log\left(\Gamma\left(N + \frac{M}{2}\right)\right) + \sum_{k=1}^M \log\left(\Gamma\left(n_k + \frac{1}{2}\right)\right)$$

where n_k is the data count in the k -th bin, and Γ is the Gamma function. The optimal number of bins is found at the global maximum of this function, relying purely on internal data geometry rather than absolute boundaries.

2.3. DATA PREPROCESSING AND VALIDATION

The dataset comprises 34 years of daily lateral inflows for the Fierzë hydropower basin ($N = 12,570$). A common challenge with historical hydrological records is “digit preference,” wherein gauge operators record rounded integer values. While water flow is a strictly continuous physical variable, these human artifacts create artificial, discrete density spikes (ties) that destabilize high-resolution probability models.

To restore the continuous physical reality of the variable—a standard prerequisite in rigorous density estimation to prevent localized singularities—a continuous uniform noise component, $\epsilon \sim U[-0.005, 0.005]$, was injected into the dataset (Silverman, 1986). This “jittering” process mathematically unrounds the data within a strictly controlled margin of measurement error (< 0.01 m³/s).

¹ 1Knuth’s Bayesian optimization was excluded from this un-jittered sensitivity test because its multinomial log-posterior function strictly requires continuous variables; the presence of heavy ties in the raw integer data causes the algorithm to diverge.

To guarantee that this preprocessing did not compromise the validity of the standard empirical rules, a comprehensive sensitivity analysis was conducted. The Lognormal parameters were extracted using both Scott and FD rules¹ on both the raw and jittered datasets. The comparison confirmed that the maximum parameter deviation induced by the jittering was less than 2.5×10^{-5} across all shape and scale parameters. This validates that the jittered dataset provides a perfectly neutral, continuous baseline for all three algorithms.

2.4. COMPUTATIONAL FRAMEWORK AND PARAMETRIC REGRESSION

Given the massive sample size ($N = 12,570$) and the intensive nature of bootstrap resampling, the algorithms and subsequent parametric regressions were implemented utilizing Python 3.10 and the SciPy ecosystem.

A specific computational challenge arises during the calculation of Knuth's Log-Posterior probability (Equation 3). The standard Gamma function (Γ) rapidly exceeds the maximum limits of 64-bit floating-point architecture (numerical overflow)

when applied to the extremely large bin counts generated by decades of daily in-flow data. To resolve this without compromising precision, the marginal likelihood was computed entirely within logarithmic space using the `scipy.special.gammaln` function. This transformation ensures absolute computational stability during the Bayesian global maximum search and the subsequent 1,000 Politis-Romano resampling iterations.

Once the optimal histogram geometries (M) were determined by each method, the extraction of the Lognormal parameters (μ, σ) from the binned empirical data

was executed via non-linear least squares optimization. Utilizing the `scipy.optimize.curve_fit` module, the optimization was anchored directly to the geometric bin centers of the

empirical histograms. This function employs the Levenberg-Marquardt algorithm to iteratively minimize the squared residuals between the empirical probability densities of the histogram bins and the continuous theoretical Lognormal curve.

2.5. ROBUSTNESS ANALYSIS AND EVALUATION METRICS

To evaluate the mathematical stability of these discretization methods against extreme outliers, a Politis-Romano subsampling strategy (Politis & Romano, 1994) was applied. For each method, 1,000

iterations were performed, sampling 85% of the dataset strictly without replacement². This specifically tests how each algorithm's optimal bin count (M) reacts to the random exclusion of extreme tail data.

To rigorously assess the performance of the final lognormal parameters, comparative statistical metrics were employed. Given the massive sample size ($N = 12,570$), traditional statistical goodness-of-fit p -values become hypersensitive to natural micro-fluctuations inherent in real-world data, rendering absolute significance thresholds unreliable (Lin, Lucas, & Shmueli, 2013). Therefore, baseline Goodness-of-Fit evaluation relies on the **Log-Likelihood (LL)**, which evaluates the overall statistical fit across the dense body of normal river flows by summing the log-probabilities of the continuous data under the fitted mathematical curves.

3. RESULTS AND PARAMETER EXTRACTION

3.1. KNUTH'S BAYESIAN OPTIMIZATION.

The application of Knuth's Bayesian algorithm evaluated the marginal likelihood across a theoretical range of possible structures, identifying a distinct global maximum in the log-posterior probability function at $M = 104$ bins.

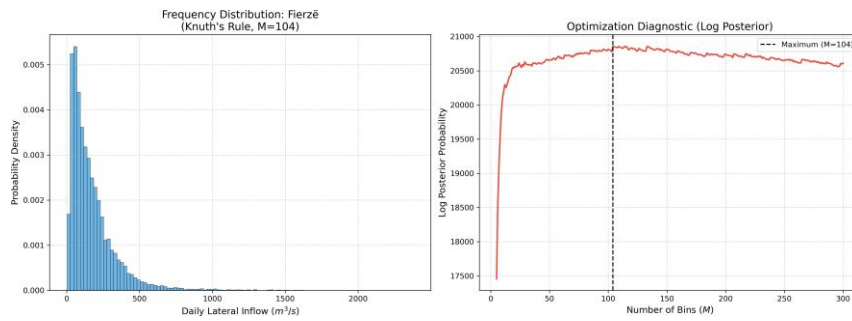


Figure 1. Diagnostic optimization of Knuth's Rule, demonstrating the global maximum of the posterior probability at $M = 104$.

To evaluate the mathematical stability of this structure, the Politis-Romano sub-sampling was applied. As shown in Figure 2, Bayesian optimization maintains structural integrity under resampling. While the distribution exhibits variance driven by the artificial re-introduction of ties during bootstrapping, it fundamentally resists catastrophic range-collapse, proving the Bayesian log-posterior is mapping internal continuous density rather than absolute maximum boundaries.

² When randomly subsampling 85% of a dataset strictly without replacement, the mathematical probability of omitting the single absolute maximum historical flood event in any given iteration is exactly $1 - 0.85 = 0.15$, or 15%

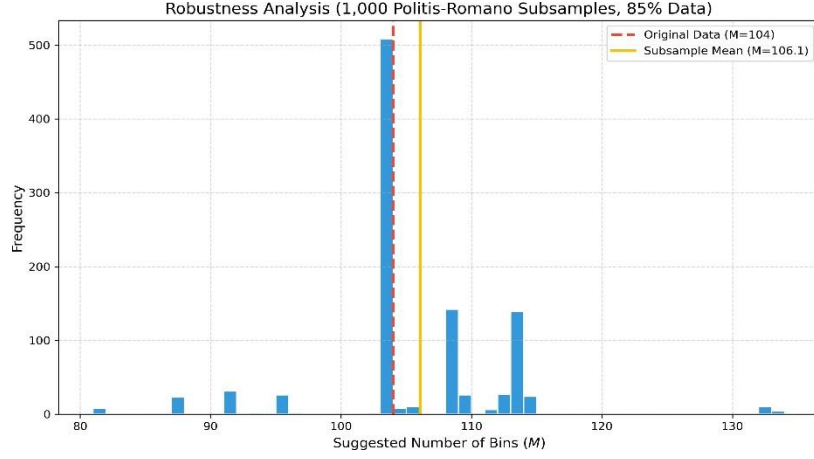


Figure 2. Subsampling robustness distribution for Knuth’s algorithm. The variance reflects Bayesian sensitivity to micro-structural density shifts rather than boundary collapses.

utilizing the optimally binned empirical density ($M = 104$) as the geometric baseline, the non-linear regression was executed on the bin centers. The resulting parameters successfully describing the continuous time series under the Bayesian architecture are a scale parameter (μ) of 4.828835 and a shape parameter (σ) of 0.938707.

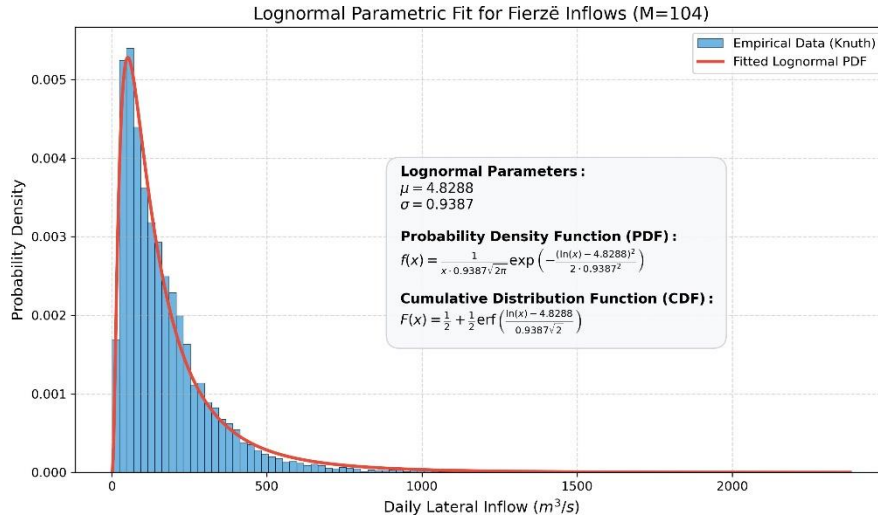


Figure 3. Theoretical Lognormal fit anchored to Knuth’s optimized $M = 104$ histogram architecture.

3.2. SCOTT’S RULE

In contrast to Bayesian probability maximization, the application of Scott’s Rule relies on the global standard deviation, yielding an optimal bin count of $M = 93$ bins.

The fundamental mathematical vulnerability of Scott’s Rule in hydrology stems from the tension between its smooth scaling factor and its reliance on absolute range ($\text{Max} - \text{Min}$). Mathematically, the

$N^{-1/3}$ scaling law dictates that a reduction to 85% of the sample size should scale the optimal bin count by a factor of $0.85^{1/3} \approx 0.947$. The expected theoretical subsample bin count is therefore $93 \times 0.947 \approx 88.07$.

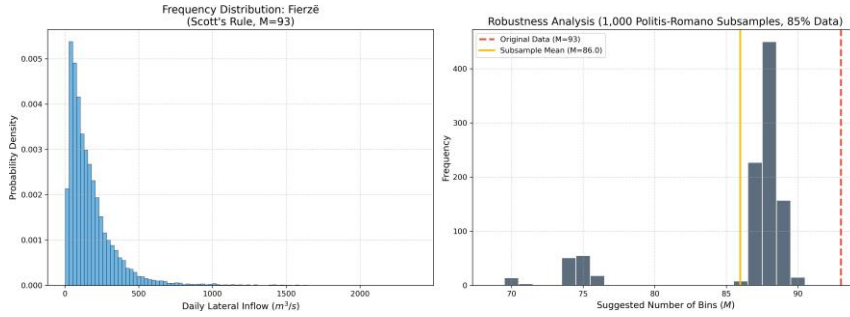


Figure 4. Left: Empirical histogram generated by Scott's Rule ($M = 93$). Right: Subsampling robustness distribution. The bi-modal fracture demonstrates severe algorithmic instability driven by singular extreme outliers.

As revealed in the right panel of Figure 4, the algorithm correctly targets this expected peak of 88 for the majority of iterations. However, the overall subsample mean is dragged down to $M = 86.0$ due to a violent bimodal fracture. Because extreme floods dictate the absolute maximum of the data range, the random 15% omission of the highest historical flood event causes the range numerator to collapse, forcing the suggested bin count to plummet into the 70s. This proves that Scott's discretization is highly susceptible to the presence or absence of singular extreme outliers.

Despite this geometric instability, the 93-bin structure was utilized as the baseline for the Levenberg-Marquardt parameter extraction, yielding a scale parameter (μ) of 4.840136 and a shape parameter (σ) of 0.947749.

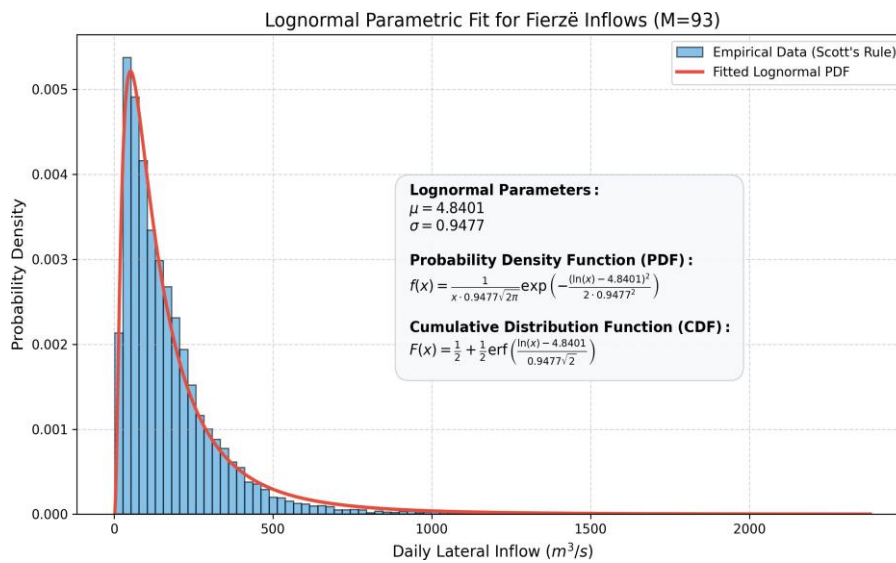


Figure 5. Theoretical Lognormal fit anchored to Scott's $M = 93$ empirical baseline.

3.3. FREEDMAN-DIACONIS (F-D) RULE

While the Freedman-Diaconis rule utilizes the Interquartile Range (IQR) to ignore tail dispersion, its application yielded a highly granular discretization of $M = 172$ bins.

Because the IQR remains highly stable during resampling, the expected subsample scaling factor is strictly preserved ($172 \times 0.947 \approx 162.8$). The right panel of Figure 6 confirms that the dominant cluster perfectly hits this theoretical peak of 163 bins.

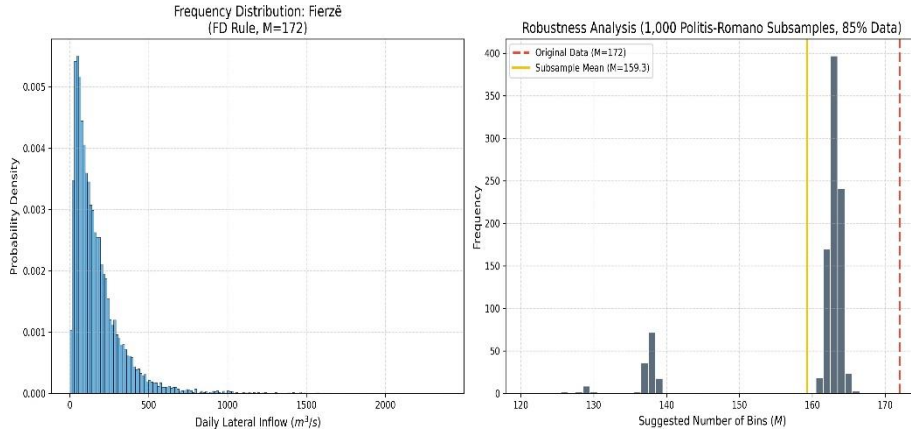


Figure 6. Left: Empirical histogram generated by the F-D Rule ($M = 172$). Right: Subsampling robustness distribution. The multi-modal fragmentation exposes extreme vulnerability to the absolute data range.

However, the overall subsample mean falls to 159.3, exposing a critical mathematical trap: the F-D rule still divides the absolute empirical range by the bin width to determine the final M . Because F-D bins are exceptionally narrow, the random omission of the absolute highest flood tier (or the second-highest tier) causes the suggested bin count to violently collapse in distinct chunks rather than shifting smoothly. This multi-modal fracture definitively proves that even when dispersion metrics are robust, any algorithm relying on absolute data boundaries remains structurally unstable for heavy-tailed hydrology.

Utilizing the $M = 172$ baseline for the regression, the extracted Lognormal parameters were $\mu = 4.831225$ and $\sigma = 0.949539$.

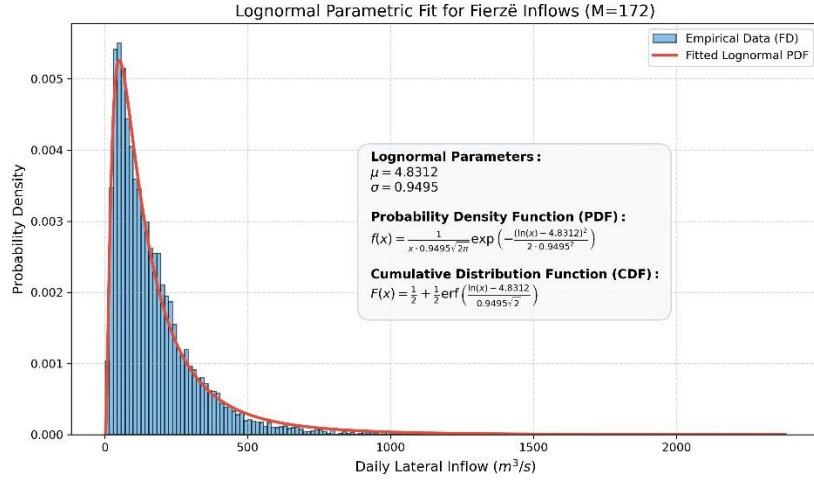


Figure 7. Theoretical Lognormal fit anchored to the F-D rule's $M = 172$ empirical baseline.

4. MODEL COMPARISON: STATISTICAL FIDELITY

To determine which discretization method provides the most accurate mathematical foundation for Lognormal parameter extraction, a baseline Goodness-of-Fit evaluation was conducted utilizing statistical probabilities.

As summarized in Table 1, Knuth's Bayesian parameters achieved a Log-Likelihood of $-76,637.69$, outperforming Scott's Rule by approximately $+20$ points. Given the massive sample size, absolute probabilities under the curve converge toward zero, rendering the absolute Log-Likelihood baseline meaningless in isolation. However, the relative difference is mathematically decisive. Because Log-Likelihood operates

on a logarithmic scale, a $+20$ difference means the Knuth parameters are e^{20} (nearly 500 million) times more likely to have generated the observed data than the Scott parameters. In standard Information Theory (Burnham & Anderson, 2002), this translates to a 40-point improvement in the Akaike Information Criterion (AIC).

Table 1. Comparative Lognormal Parameters and Statistical Metrics by Binning Method

Method	Bins (M)	Mu (μ)	Sigma (σ)
Scott	93	4.840136	0.947749
Freedman-Diaconis	172	4.831225	0.949539
Knuth	104	4.828835	0.938707
Method	Log-Likelihood		
Scott	$-76,657.20$		
Freedman-Diaconis	$-76,653.56$		
Knuth	$-76,637.69$		

In the context of fitting identical distribution types, where $\Delta AIC > 10$ is considered overwhelming evidence in favor of a model, this represents a highly significant mathematical improvement in capturing the continuous physical reality of the river.

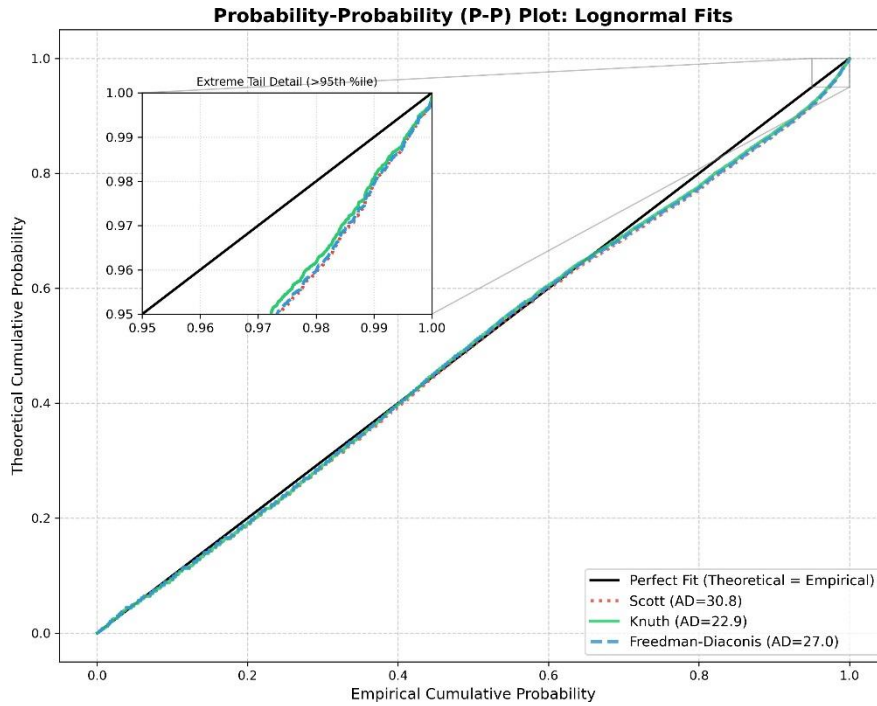


Figure 8. Probability-Probability (P-P) Plot comparing the Log-normal fits. The inset highlights the upper tail, demonstrating the tighter alignment of the Knuth-derived parameters with the historical extremes.

5. CONCLUSION

The extraction of parametric probability distributions is a critical dependency for hydrological risk assessment and infrastructural design. This study demonstrated that the preliminary step of empirical data discretization—often treated as a trivial visualization choice—fundamentally dictates the success or failure of Lognormal non-linear parameter estimation in heavy-tailed catchments like the Fierzë basin.

Our robustness analysis exposed a critical mathematical vulnerability in standard empirical binning formulas. Because both Scott’s Rule and the Freedman-Diaconis Rule rely on absolute data boundaries to calculate their final bin counts, they suffer from violent multi-modal collapse depending on the random inclusion or exclusion of singular extreme flood outliers. Conversely, Knuth’s Bayesian optimization, which evaluates internal multinomial likelihood, provided a highly stable geometric foundation.

This structural superiority translated directly into enhanced parametric accuracy. The Lognormal parameters derived from Knuth's optimal bins significantly outperformed those from empirical rules across baseline Goodness-of-Fit evaluations (Log-Likelihood). By transitioning from absolute-boundary empirical rules to probabilistic Bayesian binning, hydrological engineers can establish a more mathematically rigorous and structurally stable baseline for hydrological probability modeling.

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CYCLIC LOCALLY RECOVERABLE CODES OF LENGTH $u(q+1)$ WITH LOW LOCALITY

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ABSTRACT. A linear code has locality r when every coordinate of a codeword can be rebuilt from at most r of the remaining coordinates; codes with this property are known as locally recoverable codes (LRCs). Since a single node failure can then be repaired by contacting only a handful of surviving nodes, LRCs keep the repair bandwidth and the repair latency of large-scale storage platforms such as Microsoft Azure and Hadoop low. In this work we produce q -ary cyclic LRCs of length $u(q+1)$, where q is a prime power and $u \geq 2$ is an integer dividing $q-1$. The defining set of each code is assembled from two blocks with separate duties: one block is the full group of $(q+1)$ -st roots of unity, which forces the locality down to $u-1$, and the other consists of consecutive powers of a primitive n -th root of unity, which drives the minimum distance through the BCH bound. Small values of u therefore yield codes of very small locality, and $u=2$ attains the least possible value $r=1$. We illustrate the construction with codes whose minimum distances were determined by computer, among them a Singleton-type optimal $[24, 10, 6]_{11}$ code of locality 1.

1. INTRODUCTION

Contemporary data centers keep enormous volumes of information on clusters of comparatively unreliable nodes, so that individual node failures are routine rather than exceptional events. Plain triplication tolerates such failures but wastes two thirds of the raw capacity. Maximum distance separable codes, Reed–Solomon codes above all, cut the storage overhead dramatically, yet they pay for this in the repair phase: rebuilding one erased symbol of an $[n, k]$ Reed–Solomon code requires downloading k symbols. Locally recoverable codes (LRCs) were proposed precisely to break this trade-off, and they have been in active use in production systems for more than a decade.

The notion of locality was formalized by Gopalan et al. [1]: a code has locality r when each coordinate admits a repair set of size at most r from which it can be recomputed. The same paper contains the Singleton-type (ST) upper bound on

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the minimum distance of an (n, k, r) LRC, and codes meeting it with equality are called distance-optimal, or Singleton-type optimal (STO). Producing STO codes, or codes close to the bound, has since become a central problem; see [2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13] for a sample of the many contributions.

Among the algebraic families used for this purpose, cyclic codes occupy a privileged position, because their locality can be read off from the defining set while their encoding and decoding remain inexpensive. Huang et al. [14] analyzed the locality of several classes of cyclic codes, and Goparaju and Calderbank [15] exhibited binary cyclic LRCs of locality 2 with $d = 2, 6, 10$. The zero-set approach was developed by Tamo, Barg, Goparaju and Calderbank in [16, 17], where cyclic LRCs are obtained by prescribing defining zeros and their subfield subcodes are studied in detail; cyclotomic cosets are used instead in [18, 19]. Closer to the present work, Fang, Fu, Chen and Xia [24] constructed STO cyclic LRCs of length $3(q+1)$ with locality 2 under the hypothesis $3 \mid (q-1)$, as well as STO codes of length $\frac{3}{2}(q+1)$ when in addition $q \equiv 1 \pmod{4}$. Further material on cyclic LRCs may be found in [6, 20, 21, 22].

The starting point of this note is the observation that the two specific lengths treated in [24] are the members $u = 3$ and $u = 3/2$ of a single one-parameter family. We keep the length in the form $n = u(q+1)$ but let u range over all integers $u \geq 2$ dividing $q-1$, which guarantees $n \mid (q^2-1)$ and hence lets us work with a primitive n -th root of unity inside $\mathbb{F}_{q^2}$. The defining set is then designed in two independent blocks, in the spirit of [16]: the group of $(q+1)$ -st roots of unity, whose presence alone already caps the locality at $u-1$, and a short block of consecutive powers, whose length is what the BCH bound converts into a lower bound on d . Separating the two roles makes the parameter u a genuine design knob: the smaller u is, the smaller the locality becomes, with $u = 2$ reaching the minimum admissible value $r = 1$, while larger u improves the information rate.

The paper is organised as follows. Section 2 fixes notation and recalls the facts about cyclic codes and LRCs that we shall use. Section 3 isolates, in Lemma 3, the part of the argument that is common to all cases, states the construction in Theorem 3 and proves it case by case; new numerical examples and a table of concrete parameters close the section. Section 4 concludes.

2. PRELIMINARIES

Throughout, q denotes a prime power, $\mathbb{F}_q$ the field with q elements and $\mathbb{F}_q^* = \mathbb{F}_q \setminus \{0\}$. A q -ary linear code $\mathcal{C}$ of length n is an $\mathbb{F}_q$ -subspace of $\mathbb{F}_q^n$, and $\dim(\mathcal{C})$ is its dimension over $\mathbb{F}_q$. The Hamming distance $d(\mathbf{w}, \mathbf{y})$ between two vectors is the number of coordinates in which they differ, and

$$d(\mathcal{C}) = \min\{d(\mathbf{c}_1, \mathbf{c}_2) : \mathbf{c}_1, \mathbf{c}_2 \in \mathcal{C}, \mathbf{c}_1 \neq \mathbf{c}_2\}$$

is the minimum distance of $\mathcal{C}$. A code of length n , dimension k and minimum distance d is written $[n, k, d]_q$. The dual of $\mathcal{C}$ is

$$\mathcal{C}^\perp = \{\mathbf{c}' \in \mathbb{F}_q^n : \mathbf{c}' \cdot \mathbf{c} = 0 \text{ for every } \mathbf{c} \in \mathcal{C}\}, \quad \mathbf{c}' \cdot \mathbf{c} = c'_1 c_1 + \cdots + c'_n c_n.$$

The multiplicative order of $\beta \in \mathbb{F}_q^*$ is the least $t \in \mathbb{Z}^+$ with $\beta^t = 1$. When $\gcd(n, q) = 1$ and $1 \leq e \leq n$, the set

$$C_e = \{e \cdot q^m \pmod{n} : m = 0, 1, \dots, o_n(q)\}$$

is the q -cyclotomic coset modulo n with representative e .

A linear code $\mathcal{C}$ of length n is called cyclic when it is invariant under the cyclic shift, that is, when the vector $(c_{n-1}, c_0, \dots, c_{n-2})$ belongs to $\mathcal{C}$ for every codeword $(c_0, c_1, \dots, c_{n-1})$ of $\mathcal{C}$. Consider the map φ from $\mathbb{F}_q^n$ onto the quotient ring $[x]/\langle x^n - 1 \rangle$ given by

$$\varphi((c_0, c_1, \dots, c_{n-1})) = c_0 + c_1x + \dots + c_{n-1}x^{n-1}.$$

Under this identification, cyclic codes of length n correspond to ideals of the quotient ring. Every nonzero ideal is principal, and the monic polynomial of least degree that generates it is its generator polynomial; the polynomial attached in this way to $\varphi(\mathcal{C})$ is the generator polynomial $g(x)$ of $\mathcal{C}$, and $\dim(\mathcal{C}) = n - \deg g(x)$. If α is a primitive n -th root of unity in an extension of $\mathbb{F}_q$, the defining set of $\mathcal{C}$ is

$$D(\mathcal{C}) = \{i : g(\alpha^i) = 0\},$$

a union of q -cyclotomic cosets modulo n ; conversely, a set of exponents closed under multiplication by q modulo n determines a cyclic code over $\mathbb{F}_q$. We shall use this closure property repeatedly to certify that the polynomials we write down really have coefficients in $\mathbb{F}_q$. Detailed treatments may be found in [25, 26, 27].

The lower bound on the minimum distance that we employ is the classical one.

[BCH bound, [26, Theorem 8]] Let $\mathcal{C} = \langle g(x) \rangle$ be a cyclic code of length n , let β be a primitive n -th root of unity, let $b \in \mathbb{Z}^+$ and $\delta \in \mathbb{N}$. If $\{\beta^{b+j} \mid 0 \leq j \leq \delta - 2\}$ consists of roots of $g(x)$, then $d(\mathcal{C}) \geq \delta$.

We now recall the object of interest.

Let $\mathcal{C}$ be a q -ary linear code of length n . Suppose that for every $\mathbf{c} = (c_1, \dots, c_n) \in \mathcal{C}$ and every $j \in \{1, \dots, n\}$ there is a set $R_j \subset \{1, \dots, n\} \setminus \{j\}$ with $|R_j| \leq r$ such that c_j is a function of the entries c_w , $w \in R_j$. Then $\mathcal{C}$ is said to have locality r , and R_j is a repair set for the j -th coordinate.

We write (n, k, r) for a linear code of length n , dimension k and locality r . Any erased symbol can, in particular, be recovered from k others, so $1 \leq r \leq k$, and the interesting regime is the one in which r is much smaller than k . The ST bound of [1] reads

$$(1) \quad d \leq n - k - \left\lceil \frac{k}{r} \right\rceil + 2,$$

and a code attaining (1) is called Singleton-type optimal (STO).

Locality can be certified directly from the defining set. Let α be a primitive n -th root of unity and let $0 \leq t \leq r$. It is shown in [16] that a cyclic code whose complete defining set equals $Z_t = \alpha^t \cdot \{\alpha^{j(r+1)} : j = 0, 1, \dots, \frac{n}{r+1} - 1\}$, that is, a multiplicative coset of the group of $\frac{n}{r+1}$ -st roots of unity, has locality r . The version we use is the following.

[[16, Proposition 3.4]] Let $\mathcal{C}$ be a q -ary cyclic code of length n with complete defining set Z , and let r be a positive integer with $(r+1) \mid n$. If Z contains a coset of the group of $\frac{n}{r+1}$ -st roots of unity, then $\mathcal{C}$ has locality at most r .

3. THE CONSTRUCTION

For even q with $3 \mid (q-1)$, an STO cyclic $[3(q+1), 2q-1, 6]_q$ code of locality 2 was obtained in [24]. We now let the length vary along the whole family $n = u(q+1)$ with $u \mid (q-1)$. It is convenient to record first the features shared by every case,

so that the proof of the theorem reduces to a computation of $L \cap D$ and to two applications of the BCH and ST bounds.

Throughout this section $u \in \mathbb{Z}^+$, $n = u(q+1)$ and

$$(2) \quad L = \{1, \alpha^u, \alpha^{2u}, \dots, \alpha^{uq}\},$$

where α is a primitive n -th root of unity in an extension of $\mathbb{F}_q$.

Let $q > 2$ be a prime power, let $u \geq 2$ be an integer with $u \mid (q-1)$ and put $n = u(q+1)$. Then the following hold.

- (a) $n \mid (q^2 - 1)$, so a primitive n -th root of unity α may be chosen in $\mathbb{F}_{q^2}$.
- (b) The set L of (2) consists of $q+1$ pairwise distinct elements and is exactly the group of $(q+1)$ -st roots of unity; consequently

$$\prod_{a \in L} (x - a) = \prod_{j=0}^q (x - \alpha^{uj}) = x^{q+1} - 1.$$

- (c) $u \nmid (q+u)$, and hence $\alpha^{q+u} \notin L$.
- (d) Every cyclic code of length n over $\mathbb{F}_q$ whose complete defining set contains L has locality at most $u-1$.

Proof. (a) Since $u \mid (q-1)$ we may write $q-1 = u\ell$, whence $q^2 - 1 = (q-1)(q+1) = \ell \cdot u(q+1) = \ell n$.

(b) By (a), $\alpha \in \mathbb{F}_{q^2}$ and α has order $n = u(q+1)$; therefore α^u has order exactly $q+1$, so its powers α^{uj} , $0 \leq j \leq q$, are $q+1$ distinct elements, each satisfying $(\alpha^{uj})^{q+1} = (\alpha^n)^j = 1$. Being $q+1$ distinct roots of $x^{q+1} - 1$, they are all of them, and the displayed factorisation follows.

(c) If $u \mid (q+u)$, then $u \mid q$, and combining this with $u \mid (q-1)$ gives $u \mid 1$, i.e. $u = 1$, contrary to $u \geq 2$. The exponents of the elements of L are precisely the multiples of u modulo n , so $\alpha^{q+u} \notin L$.

(d) Put $r = u-1$. Then $(r+1) \mid n$ and $\frac{n}{r+1} = q+1$, so by (b) the set L is the group of $\frac{n}{r+1}$ -st roots of unity itself, which is the trivial coset of that group. Proposition 2 now yields locality at most $r = u-1$. $\square$

Observe that part (d) already fixes the locality; the remaining elements of the defining set are free to be chosen so as to create a long run of consecutive exponents, which is what the BCH bound needs. This is the mechanism behind the next theorem.

Let $q > 2$ be a prime power, let $u \geq 2$ with $u \mid (q-1)$, let $n = u(q+1)$ and let L be as in (2). In each of the following cases, $\mathcal{C} = \langle g(x) \rangle$ with

$$g(x) = \prod_{a \in L \cup D} (x - a)$$

is a q -ary cyclic LRC with the stated parameters.

- (i) If $u = 2$ and $D = \{\alpha^{q-1}, \alpha^{q+1}, \alpha^{q+2}, \alpha^{q+3}, \alpha^{1+2q}\}$, then $\mathcal{C}$ is a $[2(q+1), q-1, d]_q$ code of locality 1 with $d \in \{4, 5, 6\}$.
- (ii) If $u = 3$ and $D = \{\alpha^{q-1}, \alpha^{q+2}, \alpha^{q+3}, \alpha^{q+5}, \alpha^{1+3q}\}$, then $\mathcal{C}$ is a $[3(q+1), 2q, d]_q$ code of locality 2 with $d \in \{3, 4, 5\}$.
- (iii) If $u > 2$ and $D = \{\alpha^{q-1}, \alpha^{q+u-1}, \alpha^{q+u}, \alpha^{q+u+1}, \alpha^{1+uq}, \alpha^{1+uq+q}\}$, then $\mathcal{C}$ is a $[u(q+1), (u-1)(q+1)-4, d]_q$ code of locality $u-1$ with $4 \leq d \leq 8$;

more precisely

$$d \in \begin{cases} \{4, 5, 6, 7, 8\} & \text{if } u = 3, \\ \{4, 5, 6, 7\} & \text{if } u = 4, 5, \\ \{4, 5, 6\} & \text{if } u \geq 6. \end{cases}$$

Proof. All three cases take place in the setting of Lemma 3, so $\alpha \in \mathbb{F}_{q^2}$, $\prod_{a \in L} (x - a) = x^{q+1} - 1$ and the locality is at most $u - 1$ by Lemma 3(d). It therefore remains, in each case, to determine which elements of D are already in L , to check that the exponents outside L form complete q -cyclotomic cosets, and to bound d from both sides. We record once and for all that the exponents occurring in L are exactly the multiples of u modulo n .

(i) Here $u = 2$, so q is odd. The exponents $q - 1, q + 1, q + 3$ are even and $q + 2, 1 + 2q$ are odd, whence $L \cap D = \{\alpha^{q-1}, \alpha^{q+1}, \alpha^{q+3}\}$ and

$$\begin{aligned} g(x) &= (x - \alpha^{q+2})(x - \alpha^{1+2q}) \prod_{a \in L} (x - a) \\ &= (x - \alpha^{q+2})(x - \alpha^{1+2q})(x^{q+1} - 1). \end{aligned}$$

Since $q(q + 2) = q^2 + 2q \equiv 2q + 1 \pmod{n}$, the two extra exponents form a single q -cyclotomic coset, so the root set of $g(x)$ is closed under multiplication by q and $g(x) \in \mathbb{F}_q[x]$. Hence

$$k = n - \deg g(x) = 2(q + 1) - (q + 3) = q - 1.$$

By Lemma 3(d) with $u = 2$ the locality is at most 1, and since the locality of a code is a positive integer it equals 1. The three consecutive exponents $q + 1, q + 2, q + 3$ all lie in $L \cup D$, so Proposition 2 gives $d \geq 4$, while (1) with $r = 1$ gives

$$d \leq n - k - \left\lceil \frac{k}{r} \right\rceil + 2 = 2(q + 1) - (q - 1) - (q - 1) + 2 = 6.$$

(ii) Let $u = 3$. From $3 \mid (q - 1)$ we get $q \equiv 1 \pmod{3}$, so that 3 divides both $q + 2$ and $q + 5$, while $3 \nmid (q + 3)$ and $3 \nmid (1 + 3q)$. Therefore $L \cap D = \{\alpha^{q-1}, \alpha^{q+2}, \alpha^{q+5}\}$ and

$$\begin{aligned} g(x) &= (x - \alpha^{q+3})(x - \alpha^{1+3q}) \prod_{a \in L} (x - a) \\ &= (x - \alpha^{q+3})(x - \alpha^{1+3q})(x^{q+1} - 1) \in \mathbb{F}_q[x], \end{aligned}$$

the membership following from $q(q + 3) = q^2 + 3q \equiv 3q + 1 \pmod{n}$. Thus

$$k = 3(q + 1) - (q + 3) = 2q,$$

and the locality is at most $u - 1 = 2$. The pair of consecutive exponents $q + 2, q + 3$ yields $d \geq 3$ by Proposition 2, and (1) with $r = 2$ gives

$$d \leq 3(q + 1) - 2q - \left\lceil \frac{2q}{2} \right\rceil + 2 = 5.$$

(iii) Let $u > 2$. Reducing modulo u and using $u \mid (q - 1)$ we obtain

$$q + u - 1 \equiv 0, \quad q + u \equiv 1, \quad q + u + 1 \equiv 2 \pmod{u},$$

and $u > 2$ forces $u \nmid 1$ and $u \nmid 2$; together with Lemma 3(c) this shows that neither α^{q+u} nor α^{q+u+1} belongs to L . Also $1+uq \equiv 1$ and $1+uq+q \equiv q+1 \equiv 2 \pmod{u}$, so $\alpha^{1+uq}, \alpha^{1+uq+q} \notin L$, as well. Consequently, $L \cap D = \{\alpha^{q-1}, \alpha^{q+u-1}\}$ and

$$\begin{aligned} g(x) &= (x - \alpha^{q+u})(x - \alpha^{q+u+1})(x - \alpha^{1+uq})(x - \alpha^{1+uq+q}) \prod_{a \in L} (x - a) \\ &= (x - \alpha^{q+u})(x - \alpha^{q+u+1})(x - \alpha^{1+uq})(x - \alpha^{1+uq+q})(x^{q+1} - 1). \end{aligned}$$

The four extra exponents split into the two q -cyclotomic cosets $\{q+u, 1+uq\}$ and $\{q+u+1, 1+uq+q\}$, because

$$q(q+u) \equiv uq+1 \pmod{n} \quad \text{and} \quad q(q+u+1) \equiv uq+q+1 \pmod{n},$$

so once again $g(x) \in \mathbb{F}_q[x]$, and

$$k = u(q+1) - (q+5) = q(u-1) + u - 5 = (u-1)(q+1) - 4.$$

The locality is at most $u-1$ by Lemma 3(d). Since $\alpha^{q+u-1}, \alpha^{q+u}, \alpha^{q+u+1} \in L \cup D$ are three consecutive powers, Proposition 2 gives $d \geq 4$, whereas (1) with $r = u-1$ gives

$$\begin{aligned} d &\leq u(q+1) - (u(q+1) - (q+5)) - \left\lceil \frac{u(q+1) - (q+5)}{u-1} \right\rceil + 2 \\ &= q+7 - \left\lceil \frac{q(u-1) + u - 5}{u-1} \right\rceil = q+7 - \left(q + \left\lceil \frac{u-5}{u-1} \right\rceil \right), \end{aligned}$$

and evaluating the last ceiling for $u=3$, for $u=4, 5$ and for $u \geq 6$ produces the three ranges in the statement. $\square$

The following examples illustrate the three cases. In each of them the exact minimum distance was determined by an exhaustive computer search for low-weight codewords.

Take $q=11$ and $u=2$, so that $u \mid (q-1)$ and $n=2(q+1)=24$. Here $L = \{1, \alpha^2, \alpha^4, \dots, \alpha^{22}\}$ is the group of 12-th roots of unity and $D = \{\alpha^{10}, \alpha^{12}, \alpha^{13}, \alpha^{14}, \alpha^{23}\}$, so that $L \cap D = \{\alpha^{10}, \alpha^{12}, \alpha^{14}\}$. Since $13 \cdot 11 \equiv 23 \pmod{24}$, the exponents 13 and 23 form one q -cyclotomic coset and

$$\begin{aligned} g(x) &= \prod_{a \in L \cup D} (x - a) = (x - \alpha^{13})(x - \alpha^{23})(x^{12} - 1) \\ &= (x^2 + 2x + 10)(x^{12} - 1) \\ &= x^{14} + 2x^{13} + 10x^{12} + 10x^2 + 9x + 1. \end{aligned}$$

Thus $\mathcal{C} = \langle g(x) \rangle$ is a cyclic $[24, 10, 6]_{11}$ code with locality 1. As (1) gives $d \leq 24 - 10 - 10 + 2 = 6$ in this case, the code is Singleton-type optimal.

Take $q=7$ and $u=3$, so that $u \mid (q-1)$, $u > 2$ and $n=3(q+1)=24$. Now $L = \{1, \alpha^3, \alpha^6, \dots, \alpha^{21}\}$ is the group of 8-th roots of unity and, by Theorem 3(iii),

$$D = \{\alpha^6, \alpha^9, \alpha^{10}, \alpha^{11}, \alpha^{22}, \alpha^5\},$$

because $1+uq=22$ and $1+uq+q=29 \equiv 5 \pmod{24}$. Hence $L \cap D = \{\alpha^6, \alpha^9\}$, and the exponents outside L split into the cyclotomic cosets $\{10, 22\}$ and $\{11, 5\}$,

since $10 \cdot 7 \equiv 22$ and $11 \cdot 7 \equiv 5 \pmod{24}$. Therefore

$$\begin{aligned} g(x) &= (x - \alpha^{10})(x - \alpha^{22})(x - \alpha^{11})(x - \alpha^5)(x^8 - 1) \\ &= (x^4 + x^3 + 6x^2 + 2x + 1)(x^8 - 1) \\ &= x^{12} + x^{11} + 6x^{10} + 2x^9 + x^8 + 6x^4 + 6x^3 + x^2 + 5x + 6, \end{aligned}$$

and $\mathcal{C} = \langle g(x) \rangle$ is a cyclic $[24, 12, 5]_7$ code with locality 2, in accordance with $k = (u - 1)(q + 1) - 4 = 12$ and $d \in \{4, \dots, 8\}$.

Table 1 lists further codes produced by Theorem 3; the last column indicates whether the ST bound (1) is met.

TABLE 1. Cyclic LRCs obtained from Theorem 3 for small values of q and u .

q	u	case	n	k	r	d	STO
5	2	(i)	12	4	1	4	no
7	2	(i)	16	6	1	6	yes
11	2	(i)	24	10	1	6	yes
13	2	(i)	28	12	1	4	no
17	2	(i)	36	16	1	4	no
7	3	(iii)	24	12	2	5	no

4. CONCLUSION

We have constructed q -ary cyclic locally recoverable codes of length $n = u(q + 1)$ for every integer $u \geq 2$ dividing $q - 1$, so that $n \mid (q^2 - 1)$ throughout and all computations may be carried out in $\mathbb{F}_{q^2}$. The design principle is a division of labour inside the defining set: the group of $(q + 1)$ -st roots of unity is responsible for the locality, which Lemma 3(d) bounds by $u - 1$, while a short block of consecutive powers of a primitive n -th root of unity is responsible for the minimum distance through the BCH bound. The parameter u thus interpolates between very low locality and high rate, and $u = 2$ attains the smallest possible locality $r = 1$; the examples show that Singleton-type optimal codes occur in this family.

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UNIVERSITY PROGRAMME EVALUATION USING A HYBRID CRITIC-FUZZY TOPSIS MODEL

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ABSTRACT. University choice depends on several factors, and some of the indicators used to compare programmes vary from one admission period to another. This study evaluates twenty undergraduate mathematics programmes at Turkish state universities using CRITIC and fuzzy TOPSIS. Five criteria are considered: admission success ranking, intake per faculty member (quota divided by teaching staff), provincial population, the URAP institutional score, and the senior faculty ratio. Admission and staffing data were taken from three consecutive editions of the official programme-level tables published by the Turkish Assessment, Selection and Placement Centre (ÖSYM); population data were obtained from the Turkish Statistical Institute (TÜİK), and institutional scores from the University Ranking by Academic Performance (URAP). The admission and staffing figures were cross-checked against the relevant published records. For each criterion, the three most recent observations were represented by a triangular fuzzy number based on their minimum, median, and maximum. CRITIC assigned the largest weight to intake per faculty member, which showed relatively weak correlations with the remaining criteria. The ranking stage then used these data-derived weights together with the three-year fuzzy representations.

1. INTRODUCTION

University choice can have important implications for students' academic development and subsequent career opportunities. The decision is inherently multi-criteria, since students consider different types of information and many of the available indicators change over time. Previous studies indicate that university preferences are not determined solely by examination scores. Australian students were found to place teaching quality and career prospects among their main concerns [15], while research in Poland identified family income, social environment, and the opportunities offered by an institution as important influences [14]. Studies conducted in Türkiye have similarly identified institutional reputation, campus facilities, location, and available opportunities as relevant factors in university choice [2, 10, 9].

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The centralised university admission system in Türkiye provides a suitable setting for a data-driven analysis. Students take a national examination (YKS), submit an ordered list of programme preferences, and are placed by the Turkish Assessment, Selection and Placement Centre (ÖSYM) according to their scores and programme quotas. As a result, the quota of each programme, the minimum score and national success ranking of the last admitted student, and the size of the teaching staff are published annually in official tables. These records provide observed placement outcomes rather than self-reported preference data.

A substantial part of the literature on university preference has relied on descriptive or explanatory analyses. Factor analysis, regression, and summary statistics have been used to classify the influences on preference [16], but such approaches do not generally provide data-derived importance weights for the criteria and often represent each indicator by a single value from one period. A separate strand of research has approached universities as units to be evaluated, applying data envelopment analysis to institutional performance in the United Kingdom and elsewhere [13], and, more recently, multi-criteria decision-making (MCDM) methods. Iranian private universities have been assessed with a DEMATEL-ANP-VIKOR combination [17]; Turkish institutions have been ranked through Bayesian BWM-TOPSIS [7] and interval-valued neutrosophic AHP-VIKOR [1] hybrids.

Two features of these hybrid approaches are relevant to the present study. Criterion weights are often based on expert judgments or pairwise comparisons, so the results may partly depend on the composition of the expert panel. In addition, many applications represent indicators by values from a single period even when those indicators change across admission cycles. Here, criterion weights are obtained with CRITIC from the variation and correlation structure of the decision matrix [4]. Variation across admission periods is represented by triangular fuzzy numbers constructed from each indicator's minimum, median, and maximum over three cycles, and the resulting fuzzy values are evaluated with fuzzy TOPSIS [12]. Recent studies have also combined CRITIC and TOPSIS in different decision contexts [6, 11]. In the present analysis, the fuzzy inputs are constructed directly from publicly available programme data.

The framework is applied to twenty undergraduate mathematics programmes at Turkish state universities.

The remainder of the paper is organised as follows. Section 2 presents the definitions and formulas used in the model. Section 3 describes the data, the construction of the fuzzy decision matrix, and the computational stages. Section 4 reports the criterion weights and the resulting programme ranking. Section 5 discusses the findings, limitations, and possible extensions.

2. PRELIMINARIES

This section presents the notation and definitions used in the analysis.

Definition 2.1 (Triangular fuzzy number). A triangular fuzzy number (TFN) is a triple $\tilde{A} = (l, m, u)$ with $l \leq m \leq u$, whose membership function $\mu_{\tilde{A}} : \mathbb{R} \rightarrow [0, 1]$ is

$$(2.1) \quad \mu_{\tilde{A}}(x) = \begin{cases} \frac{x-l}{m-l}, & l \leq x \leq m, \\ \frac{u-x}{u-m}, & m \leq x \leq u, \\ 0, & \text{otherwise,} \end{cases}$$

where l , m and u denote the lower bound, the most plausible value, and the upper bound of the quantity [5]. In this study, TFNs are not assigned from a linguistic scale but are constructed directly from observed data. An indicator observed over three cycles as $x^{(1)}, x^{(2)}, x^{(3)}$ is represented by

$$(2.2) \quad \tilde{A} = \left(\min_t x^{(t)}, \text{med}_t x^{(t)}, \max_t x^{(t)} \right),$$

so the spread of the fuzzy number reflects variation across the three observed periods. The median is used as the modal value because it represents the middle observation and is less sensitive to an unusually high or low value within the three-year window.

Definition 2.2 (Distance between TFNs). For two TFNs $\tilde{A} = (l_1, m_1, u_1)$ and $\tilde{B} = (l_2, m_2, u_2)$, the vertex distance is

$$(2.3) \quad d(\tilde{A}, \tilde{B}) = \sqrt{\frac{1}{3} [(l_1 - l_2)^2 + (m_1 - m_2)^2 + (u_1 - u_2)^2]}.$$

This crisp distance between fuzzy numbers was introduced by Chen [3] in extending the classical TOPSIS approach of Hwang and Yoon [8] to a fuzzy environment.

Definition 2.3 (CRITIC weights). Let $X = (x_{ij})_{n \times k}$ be a decision matrix with n alternatives and k criteria, normalised so that all criteria are benefit-oriented. Write σ_j for the standard deviation of column j and $r_{jj'}$ for the linear correlation between columns j and j' . The information content of criterion j is

$$(2.4) \quad C_j = \sigma_j \sum_{j'=1}^k (1 - r_{jj'}),$$

and the objective weight of criterion j is

$$(2.5) \quad w_j = \frac{C_j}{\sum_{j'=1}^k C_{j'}}.$$

Criteria with greater variation and weaker correlations with the remaining criteria therefore receive larger weights [4].

Definition 2.4 (Fuzzy TOPSIS closeness coefficient). Let $\tilde{V} = (\tilde{v}_{ij})$ be the weighted fuzzy decision matrix, and let the fuzzy positive ideal solution (FPIS) $A^+ = (\tilde{v}_1^+, \dots, \tilde{v}_k^+)$ and the fuzzy negative ideal solution (FNIS) $A^- = (\tilde{v}_1^-, \dots, \tilde{v}_k^-)$ collect, criterion by criterion, the best and worst weighted values. The idea of ranking alternatives according to their distances from positive and negative ideal solutions originates from the classical TOPSIS method of Hwang and Yoon [8]; here, it is implemented in the fuzzy setting of Chen [3]. The separations of alternative i from the two ideals are

$$(2.6) \quad D_i^+ = \sum_{j=1}^k d(\tilde{v}_{ij}, \tilde{v}_j^+), \quad D_i^- = \sum_{j=1}^k d(\tilde{v}_{ij}, \tilde{v}_j^-),$$

and the closeness coefficient of alternative i is

$$(2.7) \quad CC_i = \frac{D_i^-}{D_i^- + D_i^+} \in [0, 1],$$

where larger values indicate alternatives closer to the positive ideal solution [12].

3. THE HYBRID MODEL AND ITS APPLICATION

3.1. Data and criteria. The alternatives consist of twenty undergraduate mathematics programmes offered by Turkish state universities located in provinces of different sizes. To improve comparability, only daytime, Turkish-medium programmes admitting students through the SAY score type were included. English-medium, evening, Northern Cyprus, and foundation-university programmes were excluded.

All admission and staffing data were obtained from two annual releases of the Turkish Assessment, Selection and Placement Centre (ÖSYM). The first is the Higher Education Programmes and Quotas Guide, published before the placement period; its programme-level tables report the current quota, the previous cycle's minimum admission score and success ranking, and the numbers of professors, associate professors, and assistant professors in the department. The second is the Numerical Information on YKS Placement Results, published after placement; its programme-level tables provide the quota, number of placed students, and minimum admission score for the corresponding cycle.

From the 2023, 2024, and 2025 editions of these releases, we obtained the quotas for 2023–2025, the success rankings of the 2022–2024 placements, the admission scores of the 2023–2025 placements, and annual staffing information. The extracted values were verified against the relevant published tables, including both pre-placement and post-placement records where available. Provincial populations were obtained from the address-based population registration statistics of the Turkish Statistical Institute (TÜİK) for 2022–2024, while institutional scores were obtained from the 2022–2024 editions of the University Ranking by Academic Performance (URAP).

ÖSYM reports the current cycle's quota in the programme guide, while placement outcomes are reported in the corresponding results release and subsequently in the following programme guide. Accordingly, each fuzzy number was constructed from the three most recent published observations available for the corresponding indicator. The indicators were therefore aligned according to their publication periods rather than to a single common calendar year.

Five criteria enter the model; they are listed in Table 1. All five are fuzzified using the rule in (2.2), so that the minimum, median, and maximum of the three annual observations form the (l, m, u) components of a TFN. Intake per faculty member is computed separately for each year by dividing the programme quota by the corresponding teaching staff count. The senior faculty ratio, defined as the proportion of professors and associate professors in the department's teaching staff, is also calculated on a year-matched basis. Quota occupancy was initially considered

as an additional criterion but was excluded because it showed very limited variation across the selected programmes.

TABLE 1. Evaluation criteria. All five enter as data-driven TFNs.

Code	Criterion	Source	TFN window	Type
C_1	Admission success ranking	ÖSYM tables	2022-2024	cost
C_2	Intake per faculty member (quota divided by staff, year-matched)	ÖSYM tables	2023-2025	cost
C_3	Provincial population	TÜİK	2022-2024	benefit
C_4	URAP institutional score	URAP	2022-2024	benefit
C_5	Senior faculty ratio (year-matched)	ÖSYM tables	2023-2025	benefit

Intake per faculty member was used instead of raw quota to provide a more direct measure of programme-level crowding. Raw quota may reflect programme size as well as crowding; in the present data, it is strongly associated with admission success ranking, with $r = -0.74$ on the oriented data. Intake per faculty member, defined for each cycle as quota divided by the teaching staff count, ranges from a three-year centroid of 1.7 seats per faculty member in the best-staffed departments to 7.2 in the most crowded. It is also only weakly related to the other indicators, with $r = -0.21$ for admission success ranking and $r = 0.10$ for the URAP score.

Provincial population is treated as a benefit criterion and is used as a proxy for the range of internship and career opportunities available in the surrounding area. Cost of living is not included in this criterion. Admission score was excluded because it conveys information very similar to admission success ranking; including both could therefore result in redundant representation of the same underlying dimension.

3.2. Computational stages. The analysis was implemented in Python using the *numpy* and *scipy* libraries, with the CRITIC and fuzzy TOPSIS procedures coded according to the formulations presented in Section 2.

Stage 1 (weighting). The CRITIC weights are obtained in three steps.

- (i) Defuzzify each of the five criterion columns with the centroid $(l + m + u)/3$ and normalise the resulting crisp matrix, so that all criteria point in the same direction (benefit-oriented).
- (ii) Compute the standard deviation σ_j of each normalised column and the correlation matrix $(r_{jj'})$ across columns.
- (iii) Combine the two into the information content C_j and the objective weight vector $w = (w_1, \dots, w_5)$, following (2.4) and (2.5).

Stage 2 (ranking). The fuzzy TOPSIS ranking is obtained in four steps.

- (i) Normalise the fuzzy decision matrix criterion-wise, and multiply it by the CRITIC weights w from Stage 1 to obtain the weighted matrix $\tilde{V}$.
- (ii) Identify the FPIS and the FNIS from $\tilde{V}$, criterion by criterion.
- (iii) Compute D_i^+ and D_i^- , the separation of every programme from the two ideals.
- (iv) Compute the closeness coefficient CC_i from (2.7) for every programme, and rank the programmes in decreasing order of CC_i .

3.3. Integration of CRITIC and fuzzy TOPSIS. CRITIC is applied to the centroid-based decision matrix only for the weighting stage. The resulting weights are then transferred to fuzzy TOPSIS, where the triangular representation of each three-year observation is retained. Thus, defuzzification is used to determine the criterion weights, not to produce the final ranking.

4. RESULTS

4.1. Objective weights. Table 2 reports the standard deviations, information contents, and CRITIC weights computed from the normalised centroid values. In the oriented data, admission success ranking is strongly related to both the URAP score ($r = 0.77$) and provincial population ($r = 0.66$). These correlations reduce the additional information carried by the corresponding criteria in the CRITIC calculation. The URAP score therefore receives the smallest weight (0.152). Intake per faculty member shows much weaker relationships with admission success ranking ($r = -0.21$) and the URAP score ($r = 0.10$). This lower redundancy contributes to its larger information content and to the highest weight, $w_2 = 0.292$.

TABLE 2. CRITIC information contents and objective weights.

Criterion	σ_j	C_j	w_j
C_1 Admission success ranking	0.2725	0.6588	0.1699
C_2 Intake per faculty member	0.2689	1.1322	0.2920
C_3 Provincial population	0.2321	0.8026	0.2070
C_4 URAP institutional score	0.2660	0.5895	0.1520
C_5 Senior faculty ratio	0.2562	0.6944	0.1791
Total		3.8775	1.000

4.2. Fuzzy TOPSIS ranking. Table 3 presents the fuzzy TOPSIS ranking of the twenty programmes. Ankara University ranks first with a closeness coefficient of $CC = 0.762$, followed by Ege University with $CC = 0.523$. Ankara University's position is associated with the best admission success ranking and the highest URAP score in the set, together with a high senior faculty ratio and one of the lowest values of intake per faculty member.

İnönü University ranks third with $CC = 0.465$, while İstanbul Medeniyet University ranks fourth with $CC = 0.448$. İnönü University's position is associated particularly with its high senior faculty ratio, whereas İstanbul Medeniyet University benefits from provincial population and a relatively high URAP score despite having the highest intake per faculty member in the set. The remaining closeness coefficients decline gradually, with Kırklareli University ranking last at $CC = 0.095$.

5. CONCLUSION

Intake per faculty member received the largest CRITIC weight, mainly because it was only weakly correlated with the other indicators. In the fuzzy TOPSIS ranking, Ankara University had the highest closeness coefficient. The analysis uses weights derived from the observed data while retaining variation across three published periods through triangular fuzzy numbers. The comparison therefore does not require expert-elicited criterion weights.

TABLE 3. Fuzzy TOPSIS ranking of the twenty programmes.

Programme	CC_i	Rank
Ankara Univ.	0.7618	1
Ege Univ.	0.5231	2
İnönü Univ.	0.4647	3
İstanbul Medeniyet Univ.	0.4483	4
Karadeniz Technical Univ.	0.4328	5
Selçuk Univ.	0.4282	6
Uşak Univ.	0.3858	7
Amasya Univ.	0.3814	8
Erzincan Binalı Yıldırım Univ.	0.3667	9
Recep Tayyip Erdoğan Univ.	0.3212	10
Kafkas Univ.	0.2987	11
Dicle Univ.	0.2948	12
Kırşehir Ahi Evran Univ.	0.2791	13
Bursa Technical Univ.	0.2749	14
Bilecik Şeyh Edebali Univ.	0.2050	15
Trakya Univ.	0.1833	16
Çanakkale Onsekiz Mart Univ.	0.1761	17
Ağrı İbrahim Çeçen Univ.	0.1520	18
Kastamonu Univ.	0.1225	19
Kırklareli Univ.	0.0947	20

The analysis covers only twenty mathematics programmes at state universities, so the ranking applies to this sample. The URAP criterion is institution-level rather than mathematics-specific and reflects broader university performance rather than departmental performance alone. Intake per faculty member and the senior faculty ratio are both calculated from annual staff counts and may share some mechanically related variation. Student satisfaction and campus sustainability were not included because comparable programme-level public data were unavailable, while quota occupancy was excluded because it showed little variation across the selected programmes. The three-year observation window is also relatively short; a longer period could be examined in future work. The same procedure could also be applied to other disciplines and to related decision problems such as department selection, scholarship allocation, and programme accreditation.

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COMPUTATION OF GENERALIZED INVERSES OF TENSORS OVER COMMUTATIVE RINGS

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ABSTRACT. Generalized inverses of tensors play increasingly important roles in computational mathematics and numerical analysis. It is appropriate to develop the theory of generalized inverses of tensors within the algebraic structure of a ring. The main purpose of this paper is to study different generalized inverses of tensors over a commutative ring. Several results are provided in support of the theoretical results.

1. INTRODUCTION

One of the basic operations in linear algebra is matrix multiplication, it expresses the product of two matrices to form a new matrix. A tensor is a higher-dimensional generalization of a matrix (*i.e.*, a first-order tensor is a vector, a second-order tensor is a matrix), but there are more than one way to multiply two tensors (see, e.g. [1, 2]). Generally, mathematics comprises diverse structural frameworks, allowing for various interpretations (see, e.g., [14, 15, 16] and references therein). In mathematics, a ring which appeared in 1914 in Fraenkel's paper which under title "On zero divisors and the decomposition of ring ". In Fraenkel's paper, the author founded the modern definition of abstract ring.

As a fact, a ring is an algebraic structure with two binary operations (addition and multiplication) over a set satisfying certain requirements. This structure facilitates the fundamental physical laws, such as those underlying special relativity and symmetry phenomena in molecular chemistry. It is well-known that the tensors are a multi-dimensional array of numbers, sometimes it is called a multi-way or a multi-mode array. For example, a matrix is a second order tensor or a two way tensor. An element $a = (a_1, a_2, \dots, a_p)^T$, where the entries $a_1, a_2, \dots, a_p$ are elements from the field of real number R , is called a first order tensor with entries from R . Following standard notation, the set of all first order tensor with entries from the field of real number R is denoted by $\mathbb{R}^p$. For convenience we use the known notation $\mathbb{R}^p$ for the ring $(\mathbb{R}^p, +, \odot)$. Also, we refer to a closed multiplication operation between tensors as the t-product.

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The outline of the paper is computing of generalized inverse of tensors via t-product with apply a von Neumann regular property of tensors over a commutative ring. In connection with binary operations of the algebraic structure, we consider $+$ for addition and use two different binary operations, *i.e.*, $*$ and $\odot$, for multiplication. In this paper, we study the generalized inverses of tensors over a commutative ring with the binary operations $(+, \odot)$ and a non-commutative ring with involution using $(+, *)$ as a binary operations.

Kilmer and Martin [10] proposed a closed multiplication operation between tensors referred to as the t-product. In fact, the multiplication of two tensors based on the t-product takes advantage of the circulant type structure [10, 11], which allows one to compute efficiently using the Fast Fourier Transform and extend many concepts from linear algebra to tensors. To harvest more information concerning these ideas, we suggest for the readers the references [3, 4, 5, 6, 7, 8, 9, 12].

This project is motivated by the work of [13] Ratikanta Behera, Jajati Keshari Sahoo, R. N. Mohapatra and M. Zuhair Nashed, where they supply influential results via emphasizing the computation of generalized inverses of tensors via t-product.

2. PRELIMINARIES

This section is dedicated to posting some concepts that will be used in the sequel. The circulant of an element $a = (a_1, a_2, \dots, a_p)^T \in \mathbb{R}^p$ is defined as

$$\text{circ}(a) = \begin{pmatrix} a_1 & a_p & \dots & a_2 \\ a_2 & a_1 & \dots & a_3 \\ \vdots & \vdots & \ddots & \vdots \\ a_p & a_{p-1} & \dots & a_1 \end{pmatrix}.$$

Based on [[1], Theorem 3.2], an algebraic structure $(\mathbb{R}^p, +, \odot)$ is a commutative ring with unity, where the addition “ $+$ ”, multiplication “ $\odot$ ” and the unity respectively defined by

$$a + b = (a_1, a_2, \dots, a_p)^T + (b_1, b_2, \dots, b_p)^T = (a_1 + b_1, a_2 + b_2, \dots, a_p + b_p)^T,$$

$$a \odot b = \text{circ}(a)b = \begin{pmatrix} a_1 & a_p & \dots & a_2 \\ a_2 & a_1 & \dots & a_3 \\ \vdots & \vdots & \ddots & \vdots \\ a_p & a_{p-1} & \dots & a_1 \end{pmatrix} \begin{pmatrix} b_1 \\ b_1 \\ \vdots \\ b_p \end{pmatrix};$$

and

$$i = (1, 0, \dots, 0)^T$$

is the unity of $\mathbb{R}^p$. Furthermore, an element $(a \neq 0) \in \mathbb{R}^p$ is said to be a zero-divisor if there exists an element $(b \neq 0) \in \mathbb{R}^p$, such that $a \odot b = 0$. Also, let $a \in \mathbb{R}^p$. The left and right ideals generated by a are denoted by $\mathbb{R}^p \odot a$ and $a \odot \mathbb{R}^p$ which are respectively defined as

$$\mathbb{R}^p \odot a = \{x \odot a : x \in \mathbb{R}^p\}$$

and

$$a \odot \mathbb{R}^p = \{a \odot x : x \in \mathbb{R}^p\} :$$

We also denote $a \odot \mathbb{R}^p \odot b = \{a \odot x \odot b : x \in \mathbb{R}^p\}$. The left and right annihilator of an element are defined as follows.

The left and right annihilator of $a \in \mathbb{R}^p$, respectively denoted by $lann(a)$ and $rann(a)$, are defined as

$$lann(a) = \{y \in \mathbb{R}^p : y \odot a = 0\}$$

and

$$rann(a) = \{y \in \mathbb{R}^p : a \odot y = 0\}.$$

Moreover, assume that $a \in \mathbb{R}^p$. An element $x \in \mathbb{R}^p$ is called a group inverse of a if it satisfies

$$a \odot x \odot a = a, x \odot a \odot x = x, a \odot x = x \odot a.$$

Note that the condition $a \odot x = x \odot a$ is always satisfied, since $\mathbb{R}^p$ is a commutative ring.

In the next step, we write the main definition of this article.

Definition 2.1. Let $a \in \mathbb{R}^p$. Then

- (i) $\mathbb{R}^p$ is named von Neumann regular, then there exists $x \in \mathbb{R}^p$ such that $a \odot x \odot a = a$, for $a \in \mathbb{R}^p$.
- (ii) $\mathbb{R}^p$ is named anti von Neumann regular, then there exists $x \in \mathbb{R}^p$ such that $a \odot x \odot a = x$, for $a \in \mathbb{R}^p$.

Example 2.2. (i) Let $a = (1, 0, -1)^T \in R^3$ and consider $x = (\frac{1}{3}, \frac{-1}{3}, 0)^T \in R^3$. Then we can verify that

$$x \odot a \odot x = circ(x \odot a)x = \begin{pmatrix} \frac{2}{3} & \frac{-1}{3} & \frac{-1}{3} \\ \frac{-1}{3} & \frac{2}{3} & \frac{-1}{3} \\ \frac{-1}{3} & \frac{-1}{3} & \frac{2}{3} \end{pmatrix} \begin{pmatrix} \frac{1}{3} \\ \frac{-1}{3} \\ 0 \end{pmatrix} = \begin{pmatrix} \frac{1}{3} \\ \frac{-1}{3} \\ 0 \end{pmatrix} = x.$$

Hence, R^3 has von Neumann regular x .

- (ii) Let $a = (0, 1)^T \in R^2$. Consider an element $y = (1, 0)^T \in R^2$. We can verify that

$$y \odot a \odot y = circ(y \odot a) = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \begin{pmatrix} 0 \\ 1 \end{pmatrix} = \begin{pmatrix} 0 \\ 1 \end{pmatrix} = a.$$

Now, we compute the term

$$circ(y \odot a)y = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix} \begin{pmatrix} 1 \\ 0 \end{pmatrix} = \begin{pmatrix} 0 \\ 1 \end{pmatrix} = a.$$

Thus a is anti von Neumann element R^2 .

Lemma 2.3. (i) [13], Theorem 1] Let $a, b, c \in \mathbb{R}^p$. Then the (b, c) -inverse of a exists if and only if $b, c \in \mathbb{R}^p \odot c \odot a \odot b = c \odot a \odot b \odot \mathbb{R}^p$.

- (ii) [13], Definition 4] Let $a, b, c \in \mathbb{R}^p$. An element $y \in \mathbb{R}^p$ is called a (b, c) -inverse of a if it satisfies

- (a) $y \in b \odot \mathbb{R}^p \odot y \cap y \odot \mathbb{R}^p \odot c$,
- (b) $y \odot a \odot b = b$ and $c \odot a \odot y = c$.

3. THE MAIN RESULTS

We begin our discussion with the following result.

Theorem 3.1. *Let $a, b, c \in \mathbb{R}^p$. Then the following statements are equivalent:*

- (i) *a is von Neumann regular,*
- (ii) $\mathbb{R}^p = a \odot b \odot \mathbb{R}^p + \text{rann}(c) = \mathbb{R}^p \odot c \odot a + \text{lann}(b),$
- (iii) $\mathbb{R}^p = a \odot b \odot \mathbb{R}^p \oplus \text{rann}(c) = \mathbb{R}^p \odot c \odot a \oplus \text{lann}(b).$

Proof. Starting with (i) $\Rightarrow$ (ii). Basically, a is von Neumann regular, we deduce that

$$x = b \odot v \odot x = x \odot a \odot b \odot v \odot x = x \odot a \odot x.$$

That means there exists a unique (b, c) -inverse of a .

Then

$$b = u \odot c \odot a \odot b$$

and

$$c = c \odot a \odot b \odot v$$

for some $u, v \in \mathbb{R}^p$:

Let $x \in \mathbb{R}^p$ be any arbitrary vector and consider $z = x - a \odot b \odot v \odot x$. Then

$$c \odot z = (c - c \odot a \odot b \odot v) \odot x = 0.$$

Consequently,

$$z \in \text{rann}(c).$$

In addition, $x = a \odot b \odot v \odot x + z \in a \odot b \odot \mathbb{R}^p + \text{rann}(c)$. This implies

$$\mathbb{R}^p = a \odot b \odot \mathbb{R}^p + \text{rann}(c).$$

Further, if

$$y \in a \odot b \odot \mathbb{R}^p \cap \text{rann}(c),$$

then

$$y = a \odot b \odot t$$

and

$$c \odot y = 0$$

for some $t \in \mathbb{R}^p$. Furthermore,

$$b \odot t = u \odot c \odot a \odot b \odot t = u \odot c \odot (a \odot b \odot t) = u \odot c \odot y = 0.$$

Therefore, $y = 0$, which implies $a \odot b \odot \mathbb{R}^p + \text{rann}(c) = 0$ and hence $\mathbb{R}^p = a \odot b \odot \mathbb{R}^p \oplus \text{rann}(c)$.

Similarly, we can show the other equality

$$\mathbb{R}^p = \mathbb{R}^p \odot c \odot a \oplus \text{lann}(b).$$

(iii) $\Rightarrow$ (i). Let $\mathbb{R}^p = a \odot b \odot \mathbb{R}^p + \text{rann}(c)$. Then $c = c \odot i = c \odot (a \odot b \odot u + v)$, where $u \in \mathbb{R}^p$ and $v \in \text{rann}(c)$.

From $v \in \text{rann}(c)$, we get $c \odot v = 0$. This yields $c = c \odot a \odot b \odot u \in c \odot a \odot b \odot \mathbb{R}^p$. Using $\mathbb{R}^p \odot a + \text{lann}(b)$, we can show $b \in \mathbb{R}^p \odot c \odot a \odot b$. Thus by Lemma 2.3(i), the (b, c) -inverse of a exists.

Subsequently,

$$x = b \odot v \odot x = x \odot a \odot b \odot v \odot x = x \odot a \odot x.$$

Definitely, a is von Neumann regular.

Finally, (ii) $\Rightarrow$ (iii) is immediately.

□

Corollary 3.2. Let $a, b, c \in \mathbb{R}^p$ and (b, c) -inverse of a . Then a has a von Neumann regular property.

Proof. Suppose there exist two (b, c) -inverses of a , say x and y . Based on Lemma 2.3(i), we conclude that

$$x \odot a \odot b = b; c \odot a \odot y = c; x = x \odot u \odot c; y = b \odot v \odot y; x = b \odot v \odot x$$

for some u and $v \in \mathbb{R}^p$. Now

$$x = x \odot u \odot c = x \odot u \odot c \odot a \odot y = x \odot a \odot y = x \odot a \odot b \odot v \odot y = b \odot v \odot y = y.$$

Note that

$$x = b \odot v \odot x = x \odot a \odot b \odot v \odot x = x \odot a \odot x.$$

Obviously, the element a acts a von Neumann regular of $\mathbb{R}^p$. □

Theorem 3.3. Suppose that $a \in \mathbb{R}^p$. If a is von Neumann regular, then there exists $x \in \mathbb{R}^p$ where $a \odot x \odot a = a$. Moreover, the set of all such elements x is non-empty.

Proof. Assume that $a \in \mathbb{R}^p$ is von Neumann regular. By Definition 2.1(i), this means that there exists at least one element $x \in \mathbb{R}^p$ such that

$$a \odot x \odot a = a.$$

In order to demonstrate the statement's correctness, we first observe that since the operation $\odot$ is taken to be well-defined on $\mathbb{R}^p$, the equation $a \odot x \odot a$ is meaningful for all $a, x \in \mathbb{R}^p$.

The existence component follows right away since the definition ensures that such an element x exists.

We then note that x is not subject to a uniqueness criterion. Therefore, if $x_1, x_2 \in \mathbb{R}^p$ both satisfy

$$a \odot x_1 \odot a = a \quad \text{and} \quad a \odot x_2 \odot a = a,$$

then both elements belong to the solution set

$$S_a = \{x \in \mathbb{R}^p : a \odot x \odot a = a\}.$$

Consequently, the set S_a is non-empty. Conversely, if there exists $x \in \mathbb{R}^p$ such that $a \odot x \odot a = a$, then by Definition 2.1(i), a is von Neumann regular. This completes the equivalence. □

Theorem 3.4. Let $a, b, c \in \mathbb{R}^p$ and (b, c) -inverse of a . Then a von Neumann regular property of a is unique.

Proof. At the beginning we depended on Lemma 2.3(ii), where any of element of $\mathbb{R}^p$ say a has an inverse.

Here, the scenario of the proof will build on the contradiction principle. Hence, the element a has a two (b, c) -inverse, say x and y . They write as

$$x \odot a \odot b = b; c \odot a \odot y = c; x = x \odot u \odot c; y = b \odot v \odot y; x = b \odot v \odot x$$

for some u and $v \in \mathbb{R}^p$. Now

$$x = x \odot u \odot c = x \odot u \odot c \odot a \odot y = x \odot a \odot y = x \odot a \odot b \odot v \odot y = b \odot v \odot y = y.$$

We observe that

$$x = b \odot v \odot x = x \odot a \odot b \odot v \odot x = x \odot a \odot x.$$

Obviously, a has a unique von Neumann regular property. □

Proposition 1. Let $a \in \mathbb{R}^p$. Then

- (i) Every idempotent element of $(\mathbb{R}^p, \odot)$ is von Neumann regular.
- (ii) If $a \in \mathbb{R}^p$ satisfies $a \odot a \odot a = a$, then a is von Neumann regular.
- (iii) If a is invertible in $(\mathbb{R}^p, \odot)$, then a is von Neumann regular.
- (iv) If a is idempotent, then a is anti-von Neumann regular.

Proof. (i) Let $a \in \mathbb{R}^p$ be idempotent, that is,

$$a \odot a = a.$$

Taking $x = a$, we obtain

$$a \odot x \odot a = a \odot a \odot a = a \odot a = a.$$

Hence, a is von Neumann regular.

(ii) Choose $x = a$. Then

$$a \odot x \odot a = a \odot a \odot a = a,$$

which proves the result.

(iii) Let a^{-1} denote the inverse of a . Setting $x = a^{-1}$, we have

$$a \odot a^{-1} \odot a = (a \odot a^{-1}) \odot a = e \odot a = a,$$

where e is the identity element. Therefore, a is von Neumann regular.

(iv) Taking $x = a$, we obtain

$$a \odot x \odot a = a \odot a \odot a = a = x.$$

Hence, a is anti-von Neumann regular. □

Proposition 2. Let $a, b \in \mathbb{R}^p$. Then the following are equivalent:

- (i) $\mathbb{R}^p$ has a von Neumann regular property,
- (ii) $x \odot a \odot b = b, \text{lann}(b) \subseteq \text{lann}(x)$.

Proof. (i) $\Rightarrow$ (ii). Basically, $\mathbb{R}^p$ has a von Neumann regular property. Consequently, then there exists any arbitrary element named a of $\mathbb{R}^p$ satisfies the identity $x \odot a \odot x = x$, for $x \in \mathbb{R}^p$. It is sufficient to view only $x \odot a \odot b = b$.

Due to x is a von Neumann regular element. Then

$$i - x \odot a \in \text{lann}(x) = \text{lann}(b).$$

This result yields $b = x \odot a \odot b$.

(ii) $\Rightarrow$ (i) Let $b = x \odot a \odot b$. Then $i - x \odot a \in \text{lann}(b) \subseteq \text{lann}(x)$. Thus

$$x \odot a \odot x = x.$$

Clearly, $\mathbb{R}^p$ has a von Neumann regular property. □

Employing the same scenario used in the proof of the previous proposition. One can prove the following corollary:

Corollary 3.5. Let $a, b \in \mathbb{R}^p$. Then the following are equivalent:

- (i) $\mathbb{R}^p$ has a anti von Neumann regular property,
- (ii) $x \odot a \odot b = b, \text{lann}(b) \subseteq \text{lann}(x)$.

Theorem 3.6. Let $a \in \mathbb{R}^p$. Then a is von Neumann regular if and only if $a \in a^2 \odot \mathbb{R}^p$.

Proof. Let a be group invertible satisfies is von Neumann regular property. Then

$$a = a \odot x \odot a = a^2 \odot x = x \odot a^2 \in a^2 \odot \mathbb{R}^p.$$

Conversely, let $a = x \odot a^2 = a^2 \odot y$, for some $x, y \in \mathbb{R}^p$. Then

$$x \odot a \odot y = x \odot a^2 \odot y \odot y = a \odot y^2$$

and

$$x \odot a \odot y = a \odot x \odot a^2 \odot y = x^2 \odot a.$$

Next we shall prove $x \odot a \odot y$ is the group inverse of a .

Now

$$\begin{aligned} a \odot (x \odot a \odot y) \odot a &= x \odot a^2 \odot a \odot y = a^2 \odot y = a, x \odot a \odot y \odot (a) \odot x \odot a \odot y \\ &= x \odot a^3 \odot y \odot x \odot y = a^2 \odot y \odot x \odot y = a \odot x \odot y = x \odot a \odot y, \end{aligned}$$

and the commutative property holds trivially. Thus

$$x \odot a \odot y = y \odot a \odot x.$$

Hence, we find that $x = y$ yields $x \odot a \odot x = x$. $\square$

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9 SEPTEMBER 2026

REGISTRATION (Face to Face)

09:00-10:00

OPENNING CEREMONY (Face to Face/Online)

Prof. Dr. Erol Yaşar

Assoc. Prof. Dr. Gökhan Çuvalcıoğlu

10:30-10:45

KEYNOTE SPEAKER

Hilbert's 14-th Problem in Nonassociative Settings

Prof. Dr. Şehmus FINDIK (Face to Face)

Chair: Gökhan Çuvalcıoğlu

11:00-11:45

LUNCH BREAK

12:00-13:30

HALL-A (Face to Face)

Chair:

13:30-13:45

Semi-Analytical Wave Structures in The Soliton Neuron Model
Ugur Bayrakcı, Seyma Tuluce Demıray, **Ahmet Hakan Doğan**

13:45-14:00

Application of Hpstm To A 2+1 Dimensional Kolmogorov--Backward Equation
Seyma Tuluce Demıray, **Guzide Yıldız**

14:00-14:15

Generalized Statistical Limit of Borel Measurable Functions
Alifa Othman Aljamili, Mehmet Küçükaslan

COFFEE BREAK

14:30-14:45

9 SEPTEMBER 2026

POSTER PRESENTATIONS

Poster Session Area (Face to Face)

14:45-15:15

Roughness Behaviors of Fractal Interpolation Functions via Alternating Series

Sema Metin, Uğur Değer

Description of A Deterministic Mathematical Model in Environmental Health Analysis

Burcu Yeşilbudak

Predicting Non-Linear Breaking Points in Aquatic Populations: Assessing Model Uncertainty and Ecological Thresholds via Monte Carlo Simulations

Burcu YEŞİLBUDAK

HALL-A (Face to Face)

Chair:

15:15-15:30

A New Parametric Fuzzy Entropy Family $E_K(A)$

Sinem Tarsuslu (Yılmaz), Gökhan Çuvalcıoğlu, Arif Bal

15:30-15:45

New Two-Parameter Fuzzy Entropy

Arif Bal, Gökhan Çuvalcıoğlu, Sinem Tarsuslu (Yılmaz)

15:45-16:00

A note on Generators of Cyclic Invariants of Metabelian Leibniz Algebras

Damla Şazenuş Akkoç

16:00-16:15

Elastic analysis of variable cross-section functionally graded polar orthotropic rotating discs

Özlem Öcal, Mehmet Ali Sabihaoğlu, **Durmuş Yarımabuç**

16:15-16:30

New Inequalities Involving Caputo-Fabrizio Integral Operators for (S,M)-Convexity

Canan Ödemiş, Abdullah Akkurt, Hüseyin Yıldırım

10 SEPTEMBER 2026

KEYNOTE SPEAKER

Higher Type Fuzzy Systems for Control and Robotic Applications

Prof. Dr. Oscar Castillo (Online)

Chair: Gökhan Çuvalcıoğlu

09:00-09:45 (Local Time Zone: 9 September, 23:00-23:45)

COFFEE BREAK

09:45-10:00

INVITED SPEAKER

The Evolution of Hermite–Hadamard Inequalities: Classical Results, Fractional Extensions, and New Weighted Perspectives

Prof. Dr. Hüseyin Budak(Online)

Chair: Gökhan Çuvalcıoğlu

10:00-10:45

COFFEE BREAK

10:45-11:00

	HALL-A (Online)-		HALL-B (Online)-
	Chair:		Chair:
11:00-11:15	Computation of Generalized Inverses of Tensors Over Commutative Rings Mehsin Jabel Atteya	11:00-11:15	Determination of The Rates of Approximation of Functions in The Holder Class Under Harmonic Modulation Ahmet Köprücü , Uğur Değer
11:15-11:30	On The Degree-Ratio Sombor Index of Thorny Graphs Enes Dökme, Yaşar Nacaroglu	11:15-11:30	A-Statistical Cauchy Sequences With A Rate via Ideals Mustafa Gülfirat
11:30-11:45	A note on The Presentation of Symmetric Generators in Metabelian Lie algebras Ela Aydın	11:30-11:45	A Generalization of Deferred Cesàro Summability to Fractional Orders Muhammet Ali Okur , Yılmaz Erdem
11:45-12:00	A Note On The Nowicki Conjecture For Leibniz Algebras Nazar Şahin Öğüşlü	11:45-12:00	Inequalities Obtained with S-Exponential Convex Functions in The Third Sense Involving Caputo Fractional Derivatives and Caputo-Fabrizio Integrals Sümeyye Ermeydan Çiriş , Hüseyin Yıldırım
12:00-12:15	Cyclic Locally Recoverable Codes of Length $U(Q+1)$ With Low Locality Rabia Zengin , Mehmet Emin Köroğlu	12:00-12:15	Approximation by Perturbed Bernstein-Schurer-Stancu Type Operators In Compact Disks Yeter Beyza Erdoğan , Nursel Çetin

LUNCH

12:15-13:00

INVITED SPEAKER

Representation of Intuitionistic Fuzzy Group Algebra

Prof. Dr. P. K. SHARMA (Online)

Chair: Gökhan Çuvalcıoğlu

13:00-13:45 (Local Time Zone: 15:30-16:15)

COFFEE BREAK

13:45-14:00

	HALL-A (Online)-		HALL-B (Online)-
	Chair:		Chair:
14:00-14:15	A Random Mathematical Modeling of Population Dynamics of Türkiye under the Influence of Socioeconomic Factors and Policy Interventions Damla Yaşar, Zafer Bekiryazici	14:00-14:15	Multi-Objective Metaheuristic Optimization of Mobilefacenet: A Comparative Analysis of Simulated Annealing Aad Genetic Algorithm Mustafa Kemal Aydın, Şükran Konca
14:15-14:30	Hargreaves-Samani Model and the Implications of Estimated Evapotranspiration on Tea Cultivation in Eastern Black Sea Region İslam Epöz, Hakan Gökmen, Zafer Bekiryazici	14:15-14:30	Knot Mosaic Cipher: A Topological Approach to Symmetric Encryption Umut Esen , Mehmet Çitil
14:30-14:45	Global Well-Posedness and Blow-Up of Solutions for a Nonlinear Wave Equation with Singular Damping Hatice Taskesen	14:30-14:45	An Efficient Laplace Adomian Decomposition Approach for a Caputo Fractional-Order Stomach Model Hatıra Günerhan
14:45-15:00	Positive Pseudo-Almost Periodic Solutions and Ulam–Hyers Stability for A Fractional Nicholson-Type Model with Mixed Delays Ramazan Yazgan	14:45-15:00	On the Interpolative Boyd-Wong Type Fuzzy Contractions Meryem Bozdemir
15:00-15:15	Mathematical Model for Household Behaviour: Price Theory in Production-Consumption Economies in Nigeria Olumide Olusola Taiwo, Muhammad Sirajo Abdullahi, Halima Usman, Abdulkarim Bello, Abdulkarim Isa Umar, Jafar Anafi	15:00-15:15	A New Generalization of Bernstein-Schurer-King-Type Operators Tamay Gültekin , Nursel Çetin
15:15-15:30	Oscillation Criteria for Second-Order Hahn Difference Equations Sibel Doğru Akgöl , Ağacık Zafer	15:15-15:30	An Efficient Approach to a Fractional Ebola Virus Model Hatıra Günerhan , Hadi Rezazadeh
15:30-15:45	New Hermite-Hadamard-Mercer-Type Generalized Fractional Integral Inequalities for Interval-Valued Convex Functions Nisa Başkan , Abdullah Akkurt, Hüseyin Yıldırım		

POSTER PRESENTATIONS

HALL-C (Online)

14:00-14:45 (Local Time Zone: 13:00-13:45)

Optimization of Histograms for Lognormal Parameter Estimation in Hydrological Time Series: A Comparative Study of the Fierzë Basin

Rudin Hoxha

COFFEE BREAK

15:30-15:45

	HALL-A (Online)-		HALL-B (Online)-
	Chair:		Chair:
15:45-16:00	Short Remark on a New Intuitionistic Fuzzy Implication Krassimir Atanassov	15:45-16:00	Mathematical Modeling of the Behavior of Chlorinated Anilines on Resin-Bound Cobalt Ions in Aqueous Solution Ufuk Arıkan , Yavuz Sürme, Durmuş Dağhan
16:00-16:15	On Intuitionistic Fuzzy Uniform Submodules, Goldie Dimension and Spanning Dimension Poonam Kumar Sharma, Gagandeep Kaur	16:00-16:15	On Certain Subsemigroups of the Catalan Monoid Emrah Korkmaz
16:15-16:30	Impact of Anisotropy and Non-Uniform Conductivity on Ventricular Activation Isochrones Using DTI-Based Cardiac Modeling Ihab Elaff	16:15-16:30	Framed Surface Pencils with a Given Framed Asymptotic Sevilay Çoruh Şenocak , Ergin Bayram
16:30-16:45	University Programme Evaluation Using a Hybrid CRITIC--Fuzzy TOPSIS Model Sude Büşra Kazel , Elif Şahin, Rıdvan Şahin	16:30-16:45	Mathematical Modelling of Tuberculosis Transmission with Reinfeciion and Drug Resistance Abdulrazak Ahmed , Olumide Olusola Taiwo, Jafar Anafi, Ahmad Rufai Tasiu
16:45-17:00	Linguistic Basic Probability Assignment for Evidential Fusion Olcay Mert Kopuz , Elif Başkan, Rıdvan Şahin	16:45-17:00	On The Behavior of Solutions for A Fifth-Order Shallow Water Wave Equation Nurhan Dündar
17:00-17:15	Some Algebraic Properties of Ernst Cartan and Ernst-Lucas Cartan Numbers İlayda Çetin , Emre Sevgi	17:00-17:15	g_n -helice in Minkowski 3-space Mesut Altınok

CLOSING CEREMONY (Face to Face/Online)

17:30