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Contents

Author(s), Paper Title	Pages
Fatih Özkaynak. "When Chaos Is Not Secure: Revealing Hidden Vulnerabilities in Chaotic Cryptography" (Research Article)	78-87
Tharmalingam Gunasekar, Rajendran Swetha, Shyam Sundar Santra, Dumitru Baleanu and Yakup Yildirim. "Analysis of Streptococcus Pyogenes Transmission with Pseudo-Recovery Dynamics Using Fractal-Fractional Caputo-Fabrizio Derivative" (Research Article)	88-102
Ahmet Yildirim and Nilüfer Yildirim. "From Immune-Cold to Immune-Hot Tumors: A Fractional Immunomodulation Framework with Topological Signatures" (Research Article)	103-116
Majid Khan and Iqra Ishaque. "An Efficient Information Confidentiality Scheme Based on Genesio-Tesi Map and Deoxyribonucleic Acid Sequencing" (Research Article)	117-134
Ayub Khan and Vikash. "Synchronization of 4D Hyperchaotic Economic Systems via Barrier Function Based Control Technique" (Research Article)	135-145
Moch. Fandi Ansori. "Dynamical Analysis and Optimal Control of a Tuberculosis-Diabetes Comorbidity Model with Reinfection and Relapse" (Research Article)	146-161
Murat Erhan Çimen. "Reinforcement Learning-Tuned Nonlinear Controller Parameters for Synchronization of Chua and Duffing Chaotic Systems" (Research Article)	162-180

When Chaos Is Not Secure: Revealing Hidden Vulnerabilities in Chaotic Cryptography

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ABSTRACT Chaos-based cryptographic schemes have been widely investigated as lightweight solutions for image and multimedia security, owing to their nonlinear dynamics and high sensitivity to initial conditions. Despite these attractive theoretical properties, many such systems have been found to be susceptible to implementation-level vulnerabilities that remain undetected through purely mathematical analysis. In this study, a chaotic image-coding algorithm employing conditional XOR and XNOR operations was examined from a side-channel perspective. A profiling-based power simulation framework was developed to model the dynamic switching behavior of these gates, which are logically complementary but physically asymmetric. Distinct power signatures were observed for XOR and XNOR operations, allowing secret selection bits to be inferred with an average classification accuracy of 86.1%. The obtained results indicate that algorithmic unpredictability alone does not ensure resistance against physical leakage. It is therefore suggested that the design and validation of chaos-based cryptosystems should incorporate side-channel evaluation as an integral stage of development. The presented simulation framework can serve as a diagnostic tool for identifying gate-level asymmetries before hardware implementation. Future research is recommended to include hardware-level measurements, balanced logic synthesis, and automated leakage auditing in order to establish physically robust and cryptographically secure chaotic architectures.

KEYWORDS

Chaos-based cryptography
Side-channel leakage
Implementation-level vulnerability
Power analysis
Profiling-based attack

INTRODUCTION

Cryptology can be envisioned as a two-legged table. One leg representing cryptography, which is the art and science of securing information, and the other leg representing cryptanalysis, the discipline devoted to testing and breaking those algorithms. Like a table that cannot stand on a single leg, the field of information security remains unstable if either cryptography or cryptanalysis is neglected. Strong cryptographic design must always be accompanied by equally strong analytical validation. As Shannon (1949) argued, the security of a system lies not in obscurity but in the rigorous evaluation of its mathematical and operational soundness. Similarly, Kerckhoffs (1883) established that the security of a cipher must depend solely on the secrecy of the key, not on the secrecy of the algorithm. This principle continues to guide modern security engineering. A system that has not been analyzed thoroughly is inherently fragile. Cryptographic primitives may appear secure in theory, yet their practical implementations often diverge from ideal assumptions due to computational precision limits, hardware variability, and protocol errors (Mangard *et al.* 2007). Such divergences create subtle side effects; timing delays, voltage fluctuations, or

electromagnetic emissions that attackers can measure and exploit (Özkaynak 2018). As a result, every cryptographic design must be treated as a hypothesis that requires experimental falsification through testing that actively attempts to break it; otherwise, vulnerabilities remain latent until discovered by adversaries (Paar and Pelzl 2010).

From a historical perspective, cryptanalysis has evolved alongside cryptography itself. Early methods relied on linguistic and statistical frequency analysis, as used to break monoalphabetic ciphers in the Renaissance (Kahn 1996). With the advent of modern mathematics and computing, attacks became algorithmic and formalized, targeting algebraic properties of ciphers, factorization, and discrete logarithm problems (Stinson and Paterson 2019). The late 20th century, however, introduced a paradigm shift: the realization that cryptographic systems could be compromised without solving their underlying mathematics. Instead, attackers could observe physical leakages during computation. This new category of attacks, known as side-channel attacks, revolutionized cryptanalysis. Kocher (1996) demonstrated that variations in computation time could leak information about secret keys, leading to the first timing attack. Shortly afterward, Kocher *et al.* (1999) introduced Differential Power Analysis (DPA), showing that power consumption traces from hardware devices could reveal cryptographic keys with astonishing accuracy. These discoveries established the foun-

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dation of a new research domain: implementation-level cryptanalysis (Goodwill *et al.* 2011; Açıkkapı *et al.* 2019).

Over the past two decades, side-channel attacks have diversified and matured. Simple Power Analysis (SPA) examines raw power traces to infer operation patterns, whereas DPA and its statistical variant, Correlation Power Analysis (CPA), use large datasets to correlate measured leakages with hypothetical key values (Mangard *et al.* 2007). More sophisticated approaches, such as template attacks (Chari *et al.* 2002) and machine-learning-based methods, employ probabilistic modeling and pattern recognition to improve efficiency (Standaert *et al.* 2009). In parallel, fault injection attacks, including voltage glitching, laser faulting, and electromagnetic perturbation, intentionally disturb device behavior to extract sensitive data (Barengi *et al.* 2012). These techniques have proven that even mathematically sound algorithms such as AES or RSA can fail catastrophically if their implementations leak information through physical channels. The implications of these findings are profound. Side-channel attacks demonstrate that the real security of a cryptosystem is not limited to the strength of its algebraic structure but extends to its physical embodiment. Any imbalance, irregularity, or conditional branching within the hardware logic can serve as a source of information leakage. Therefore, modern cryptographic engineering demands a holistic approach that unites mathematical rigor with hardware resilience. Designers must adopt constant-time operations, balanced circuits, masking schemes, and continuous leakage testing as integral parts of the development cycle (Kocher *et al.* 1999; Mangard *et al.* 2007).

Studies in chaos-based cryptology have made significant advances in secure data communication and encryption applications. Akgül *et al.* (2021) developed a microcomputer-based mobile random number generator and demonstrated its applicability in encryption applications. Fractional-order chaotic systems have yielded remarkable results, particularly in biomedical image encryption (Emin *et al.* 2024; Gokyildirim *et al.* 2024); Akgül *et al.* (2025) examined the data security applications of the incommensurate fractional-order Arneodo chaotic system on a microcomputer. Hybrid encryption approaches have also emerged prominently in this field; Çavuşoğlu *et al.* (2018) proposed a novel hybrid encryption algorithm combining chaos and the S-AES algorithm. FPGA-based implementations have provided significant advantages in high-speed random number generation and chaotic oscillator design (Alçin *et al.* 2018; García-Grimaldo *et al.* 2023; Koyuncu *et al.* 2020, 2022; Şeker *et al.* 2021). Tlelo-Cuautle and colleagues have conducted extensive research on FPGA applications of chaotic systems (Tlelo-Cuautle *et al.* 2016), developing voice recognition-based cryptosystems (Rodríguez-Orozco *et al.* 2018), fractional-order chaotic circuits (Tlelo-Cuautle *et al.* 2020), and image transmission applications (Estudillo-Valdez *et al.* 2023; Kotadai *et al.* 2025). Additionally, innovative approaches such as using image algorithms for text encryption (Lawnik *et al.* 2022) and investigating symmetry in chaotic systems (Volos 2022; Charalampidis *et al.* 2022) have also been featured in the literature.

In this study, the chaotic encryption approach proposed in *A New Data Coding Algorithm for Secure Communication of Image* (Oğraş 2024) has been re-evaluated with a focus on its implementation-level security. The algorithm, which employs entropy-sensitive coding and chaotic dynamics to improve confidentiality in image transmission, has been acknowledged for its mathematical formulation and conceptual novelty. However, within the scope of the present analysis, the physical robustness of this method against side-channel vulnerabilities has been investigated. Special attention has been given to the procedure of secret code generation and

application, wherein XOR and XNOR operations are conditionally executed according to internal bit selections. Experimental observation has indicated that these conditional operations produce measurably distinct power consumption profiles, which can inadvertently disclose partial information about the underlying secret bits. Such behavior demonstrates that theoretical soundness and statistical complexity alone are insufficient to ensure cryptographic security when hardware-level characteristics are overlooked. The investigation thus emphasizes the necessity of aligning algorithmic innovation with practical resilience.

Chaotic or entropy-based designs, while promising in principle, must also be validated against physical attacks such as power analysis, timing analysis, and electromagnetic observation. Accordingly, the examined algorithm has been analyzed through the framework of side-channel-aware cryptographic engineering, highlighting the interplay between mathematical chaos and physical implementation fidelity. Through this perspective, the classical metaphor of cryptology as a two-legged table regains its pragmatic relevance: cryptography provides the theoretical foundation, while cryptanalysis maintains equilibrium through empirical validation. The current study, situated at this intersection, illustrates how a theoretically robust chaotic encryption system may compromise its own secrecy through the subtle physics of its implementation. This realization is intended to guide future developments in chaos-based cryptography toward designs that integrate algorithmic complexity with measurable physical security.

The principal contributions of this study can be summarized as follows:

- To the best of our knowledge, this is the first side-channel security evaluation of the entropy-sensitive chaotic data-coding scheme of Oğraş (2024), identifying its conditional XOR/XNOR selection step as an exploitable source of physical leakage.
- A profiling-based power-simulation framework is developed that models the dynamic switching asymmetry between logically complementary XOR and XNOR gates and recovers the secret selection bits with an average accuracy of 86.1%.
- Because the selection bits coincide with the secret-image bit stream, the recovered information corresponds directly to the plaintext; the attack therefore bypasses the reference image, the chaotic code stream, and the logistic-map parameters on which the original security argument depends.
- It is shown that the leakage arises from the operation-selection mechanism rather than from the chaotic source itself, and concrete balanced-logic and masking countermeasures are recommended.

It should be emphasized that the present study constitutes a simulation-based proof of concept aimed at exposing a gate-level asymmetry; hardware-level measurement and validation are left to future work.

LOGICAL FOUNDATIONS OF XOR AND XNOR IN CRYPTOGRAPHIC DESIGN

In digital cryptographic systems, logical operations form the most fundamental level of data manipulation. Among all Boolean functions, exclusive OR (XOR) and its complement exclusive NOR (XNOR) are particularly preferred in encryption and key-generation architectures. The reason is rooted in their ability to combine two binary inputs in a reversible and symmetry-preserving manner, which is a desirable property in both diffusion and confusion processes of cryptography (Shannon 1949). Unlike

the basic logical functions AND, OR, and NOT, which are asymmetric and often lossy with respect to their inputs, XOR provides an operation where:

$$A \oplus B = (A \wedge \neg B) \vee (\neg A \wedge B) \quad (1)$$

Eq. (1) implies that XOR yields a 1 only when the two inputs differ. The function is self-inverse, as shown in Eq. (2).

$$A \oplus B \oplus B = A \quad (2)$$

Such reversibility allows XOR-based encryption and decryption to use the same operation, a property that has made XOR central to stream ciphers, block cipher mixing functions, and pseudorandom number generators (Paar and Pelzl 2010). In contrast, simple AND or OR operations cannot be directly inverted without auxiliary information, and therefore they are rarely used alone in secure transformations. From a hardware perspective, there is no single physical XOR or XNOR gate at the transistor level; both are realized through the composition of simpler gates. The XOR logic can be constructed as Eq. (3). It should be noted that Eq. (1) and Eq. (3) describe the same XOR operation in two equivalent forms: Eq. (1) states it as a truth condition, whereas Eq. (3) expresses it as a gate-level composition.

$$A \oplus B = (A \vee B) \wedge \neg(A \wedge B) \quad (3)$$

while its complement XNOR can be expressed as Eq. (4):

$$A \odot B = \neg(A \oplus B) = (A \wedge B) \vee (\neg A \wedge \neg B) \quad (4)$$

These composite definitions reveal that XOR and XNOR require multiple transistor networks—typically four to six gate operations in CMOS technology. As a result, each operation has a distinct power consumption profile and switching pattern depending on transistor count, gate depth, and input transition probability (Mangard et al. 2007). Although XOR and XNOR are logically equivalent complements, they are not physically equivalent in implementation. The XNOR gate requires one additional logical inversion stage compared to XOR. This means an extra NOT operation, realized through an additional inverter, must toggle every time an XNOR output changes. Consequently, XNOR operations often exhibit slightly higher dynamic power consumption and different propagation delays than XOR (Weste and Harris 2019). In high-speed cryptographic circuits, these differences can become measurable through precise power or electromagnetic analysis.

This asymmetry has a direct implication for side-channel vulnerability. When XOR and XNOR operations are alternated based on secret-dependent conditions—as in the algorithm analyzed in the present study—the presence or absence of that additional inversion stage creates distinct power signatures. An attacker equipped with power-measurement equipment can statistically correlate these differences to infer the underlying selection bit sequence. In other words, what appears as a simple logical choice at the algorithmic level can manifest as a measurable physical footprint at the hardware level, revealing sensitive information about secret codes or key material. Thus, while XOR and XNOR are mathematically compact and ideal for reversible encryption operations, their hardware asymmetry demands special attention. Balanced or masked implementations must be adopted to prevent attackers from exploiting the observable differences that arise from the additional inversion inherent in XNOR.

ANALYSIS OF ENCRYPTION ALGORITHM

This section analyzes the implementation-level behavior of the scheme. It first recalls the original coding algorithm, then illustrates its operation on a small worked example, and finally examines the power-consumption signatures produced by the conditional XOR/XNOR selection.

The original coding algorithm (Oğraş, 2024)

For completeness, the scheme under evaluation is first summarized. The original method takes a secret image and a reference image of equal size and never transmits the secret image directly. A logistic map generates a chaotic binary sequence whose initial condition is perturbed by the Shannon entropy of the reference image, $x'_0 = (x_0 + \text{Entropy}(\text{reference})) \bmod 1$, so that the generated series depends jointly on the map parameters and on the reference content. The reference image and the secret image are converted into serial bit streams. For each bit position the secret bit selects the operation: a value of one applies XOR and a value of zero applies XNOR between the corresponding reference bit and chaotic bit, producing one output (secret-code) bit. The complete output stream, reshaped to the image size, constitutes the transmitted secret code.

Decoding inverts this process and succeeds only when the receiver holds exactly the same reference image, the same logistic-map parameters, and the same code series. The original design reports extreme sensitivity: a single-bit change in the reference image, or a perturbation of about one part in a million in a map parameter, prevents correct recovery, with reported NPCR and UACI values close to their ideal levels. The security argument therefore rests on keeping the reference image and the map parameters secret. The analysis that follows shows that the secret-dependent choice between XOR and XNOR leaks through power consumption; this undermines the argument, because the selection bits are exactly the secret-image bits and can thus be recovered without the reference image or the map parameters.

Illustrative 5×5 example

To demonstrate the operation of the algorithm proposed by Oğraş, a simplified 5×5 binary example is constructed. Both the secret image and the reference image are assumed to be binary matrices (values of 0 and 1) of equal size. For clarity, gray-level quantization and chaotic parameter tuning are omitted; instead, the logical flow of bitwise operations is shown step by step.

Step 1 – Secret image conversion: Secret image S and reference image R are both 5×5 matrices as Eq. (5).

$$S = \begin{bmatrix} 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 1 & 1 \\ 1 & 0 & 0 & 0 & 1 \\ 0 & 1 & 1 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 \end{bmatrix} \quad R = \begin{bmatrix} 0 & 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \\ 1 & 1 & 0 & 1 & 1 \\ 0 & 0 & 1 & 0 & 1 \end{bmatrix} \quad (5)$$

Both are reshaped into serial bitstreams by row concatenation as Eq. (6) and Eq. (7), respectively.

$$S_{bits} = [1, 0, 1, 1, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0, 1, 1, 0, 1, 0] \quad (6)$$

$$R_{bits} = [0, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 1, 0, 1, 1] \quad (7)$$

Step 2 – XOR/XNOR operation mapping: Each bit of the secret image defines which operation will be used:

- If the bit = 1, → use XOR.
- If the bit = 0, → use XNOR.

Thus, for this example the operation sequence is $[\oplus, \odot, \oplus, \oplus, \odot, \odot, \oplus, \odot, \oplus, \oplus, \oplus, \odot, \odot, \odot, \odot, \oplus, \oplus, \odot, \odot, \oplus, \oplus, \odot, \oplus, \odot]$.

Step 3 – Generation of chaotic binary series: A Logistic Map (LM) is used to generate chaotic values using Eq. (8).

$$x_{n+1} = r x_n (1 - x_n) \quad (8)$$

Given the control parameter $r = 3.9442$ and the initial condition $x_0 = 0.0875$, and iterating Eq. (8), the first elements of the chaotic sequence are $x_1 = 0.3149$, $x_2 = 0.8509$, $x_3 = 0.5003$, $x_4 = 0.9860$, $x_5 = 0.0543$, and so on (five shown of twenty-five). After 25 iterations, binary thresholding (values $\geq 0.5 \rightarrow 1$, else 0) gives C_{bits} as Eq. (9).

$$C_{bits} = [0, 1, 1, 1, 0, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0] \quad (9)$$

Step 4 – Reference image serial conversion: The reference image R is reshaped and serialized as R_{bits} , already defined above.

Step 5 – Bitwise processing according to secret bits: For each position i , the operation is determined by $S_{bits}[i]$ using Eq. (10) and Eq. (11), respectively.

$$\text{If } S_{bits_i} = 1 : O_i = R_{bits_i} \oplus C_{bits_i} \quad (10)$$

$$\text{If } S_{bits_i} = 0 : O_i = R_{bits_i} \odot C_{bits_i} \quad (11)$$

The step-by-step process of obtaining the resulting modified chaotic series is shown in Table 1. Additionally, the output is given in Eq. (12).

$$O_{bits} = [0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 1, 0, 1, 1, 0, 1, 0, 1, 0, 1] \quad (12)$$

Step 6 – Final secret code generation: The output bitstream O_{bits} is reshaped back into a 5×5 matrix to form the modified chaotic series, the secret code:

$$O = \begin{bmatrix} 0 & 1 & 0 & 1 & 1 \\ 0 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 0 \\ 1 & 1 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{bmatrix} \quad (13)$$

This 5×5 “coded image” represents the final output of the proposed data coding algorithm. From a side-channel perspective, however, each conditional XOR/XNOR operation can produce different instantaneous power profiles, potentially revealing the corresponding secret bit, the core issue investigated in the present study.

Power Consumption Analysis on the 5×5 Example

To better understand the side-channel implications of the algorithm, a simplified dynamic power estimation was carried out using the 5×5 example. In this analysis, each logical operation (XOR or XNOR) was assumed to be implemented using complementary MOS (CMOS) transistor logic. According to CMOS theory, dynamic power is primarily consumed when signal transitions occur, and it can be expressed as Eq. (14).

$$P_{dyn} = C_L V^2 f \alpha \quad (14)$$

where C_L is the load capacitance, V is the supply voltage, f is the clock frequency, and α is the switching activity factor (Weste and Harris 2019). Within the 5×5 test sequence (25 operations in total), the output of the XOR/XNOR logic changed state 14 times. Among these transitions, 6 occurred when the XOR path was active, and 8 occurred when the XNOR path was selected. Since the XNOR gate includes an additional inverter stage compared to XOR, each of those 8 transitions resulted in one more internal switching event, leading to slightly higher dynamic energy consumption. When typical microcontroller parameters were applied ($V = 3.3$ V, $f = 48$ MHz, and a few femtofarads of switching capacitance per node), the difference between XOR and XNOR power usage was in the order of tens of femtojoules per operation. Although this energy difference is very small, it is consistent and measurable across repeated executions. In a side-channel context, such deterministic variations are significant because they can be detected statistically through power analysis techniques. The observed imbalance therefore supports the hypothesis that the alternating use of XOR and XNOR operations based on secret bits can create distinguishable power traces, revealing sensitive information about the bit sequence controlling the encryption process. This analysis highlights that even minimal structural differences in logic gates can leave a detectable physical footprint, underlining the importance of power-balancing countermeasures in secure hardware design (Mangard et al. 2007).

ANALYSIS RESULTS

Consistent with Kerckhoffs’s principle and standard practice in profiling-based side-channel research, the adversary is assumed to know the encryption algorithm and to possess a profiling device of the same type as the target, on which power traces can be measured under controlled, labeled conditions. The adversary does not know the secret-dependent quantities: the logistic-map control parameter and initial condition, the resulting chaotic code stream, the reference image, or the secret image itself. The attacker observes only the power traces of the target encryption run and seeks to recover, for each operation, whether an XOR or an XNOR was executed. Because that choice is dictated bit-by-bit by the secret image, recovering the selection sequence is equivalent to recovering the plaintext, and no knowledge of the chaotic parameters or the reference image is required.

A software simulation was conducted to assess whether the XOR/XNOR selection mechanism in the evaluated chaotic-coding algorithm gives rise to exploitable side-channel leakage. Figure 1 illustrates the end-to-end workflow of the proposed simulation framework designed to evaluate side-channel vulnerabilities in chaotic-coding cryptosystems. The process begins with two input images, a secret image containing the confidential data to be protected and a reference image that serves as an auxiliary chaotic seed source. Both images are first converted into serial bitstreams to allow bitwise processing compatible with logical gate operations.

Table 1 The step-by-step process of obtaining the resulting modified chaotic series

i	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
S_{bits}	1	0	1	1	0	0	1	0	1	1	1	0	0	0	1	0	1	1	0	0	1	1	0	1	0
R_{bits}	0	1	1	0	0	1	0	1	1	0	0	1	0	0	1	1	1	0	1	1	0	0	1	0	1
C_{bits}	0	1	1	1	0	0	1	1	0	1	0	1	0	0	1	1	0	1	0	1	0	0	1	1	0
Operation	$\oplus$	$\odot$	$\oplus$	$\oplus$	$\odot$	$\odot$	$\oplus$	$\odot$	$\oplus$	$\oplus$	$\oplus$	$\odot$	$\odot$	$\odot$	$\oplus$	$\odot$	$\oplus$	$\oplus$	$\odot$	$\odot$	$\oplus$	$\oplus$	$\odot$	$\oplus$	$\odot$
O_i	0	1	0	1	1	0	1	1	1	1	0	1	1	1	0	1	1	1	0	1	0	0	1	1	0

Subsequently, a chaotic coding algorithm is applied, in which XOR or XNOR operations are dynamically selected based on the value of each secret bit. The resulting bitstream forms the encoded output sequence. To investigate potential information leakage, the system simulates the power trace acquisition process that would occur in a physical hardware implementation. Each logical operation (XOR or XNOR) produces a distinct power-consumption profile reflecting the switching asymmetry inherent to real circuits. The right side of the figure shows an example power-trace signal corresponding to a sequence of such operations, along with the original secret bits and the predicted bits obtained from side-channel analysis. The close similarity between the two sequences indicates that even simple logical imbalances in XOR/XNOR circuitry can reveal sensitive cryptographic information through measurable power variations.

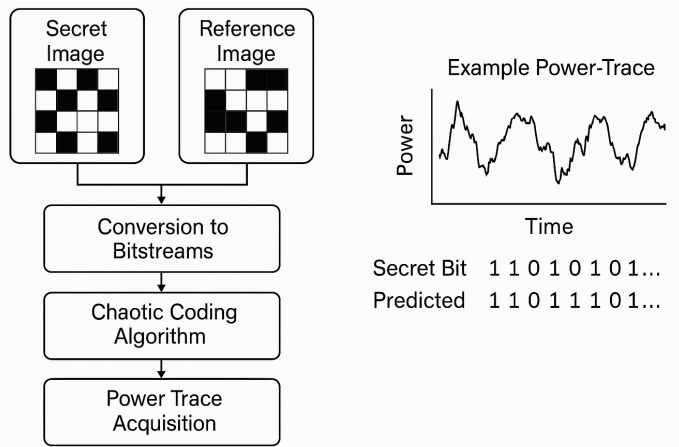


Figure 1 Simulation workflow and power-trace example. The figure should be read as follows: because each operation is selected by a secret bit, the per-operation power signature reveals that bit, so leaking the XOR/XNOR choice is equivalent to leaking the plaintext. This conceptual workflow motivates the empirical results reported below

A standard profiling attack model was employed: a labeled profiling dataset was generated under controlled conditions, a classifier was trained on the profiling data, and the trained model was applied to traces produced by a single encrypted transmission. To ensure transparency and reproducibility, Table 2 summarizes the main simulation parameters used in the side-channel analysis experiment. All values were selected to reflect realistic small-scale embedded implementations while remaining computationally tractable for software simulation.

The classifier is the core of the attack and is described here in full. Each XOR or XNOR operation is represented by one simulated power-trace segment of 160 samples. The classifier performs a binary decision on every segment: it predicts the selection bit, that is, whether the operation was an XOR (bit 1) or an XNOR (bit 0). Its input features are the standardized raw samples of the segment; no hand-crafted features are used. During the profiling phase, 6,000 labeled segments are generated with an equal number of XOR and XNOR examples, and a linear Support Vector Machine is trained on them. A linear model is deliberately chosen: the modeled leakage is a constant amplitude offset, so the two classes are close to linearly separable in the raw-segment space, and a higher-capacity classifier would add no benefit while risking the fitting of simulation noise rather than the signal of interest. During the attack phase, the trained model is applied to the 1,024 unlabeled segments of a single target encryption run, yielding one predicted selection bit per operation. For the demonstration, the 32×32 secret image is the cover image of this journal (Chaos Theory and Applications), which provides a concrete and recognizable target. The complete simulation code, this image, and the fixed random seeds are provided in the supplementary repository; after installing the listed dependencies, running the single provided script (python sca_simulation.py, with no arguments) deterministically reproduces the reported result (86.1% accuracy; confusion matrix $\begin{bmatrix} 490 & 77 \\ 65 & 392 \end{bmatrix}$, with rows denoting the true classes XNOR and XOR) and regenerates all figures. Repeating the experiment with other random seeds yields 86–87% accuracy, confirming the stability of the finding.

The amplitude offset that distinguishes XNOR from XOR segments (normalized value 0.25) is an empirically hypothesized quantity rather than a transistor-level (SPICE) measurement. Its magnitude is consistent with the gate-level analysis of Section 2: an XNOR cell carries one additional inversion stage out of roughly four to six gate operations, which corresponds to a fractional increase in switching activity on the order of one fifth to one quarter of the baseline. To make the dependence on this assumption explicit, a sensitivity sweep was performed in which the offset was varied while the noise level was held fixed. Recovery accuracy rises monotonically with the assumed offset, from chance level (about 50%) when no asymmetry is present, through approximately 86% at the operating point of 0.25, to near-perfect recovery for larger offsets. As a control, setting the offset to zero, that is, removing any physical difference between the two gates, reduces accuracy to chance, confirming that the demonstrated leakage is attributable entirely to the modeled gate asymmetry and not to any artifact of the simulation or classifier. These results frame the present analysis as an illustrative, conservative proof of concept and quantify how the recoverable information would scale with the true physical asymmetry of a given implementation.

■ **Table 2** Main simulation parameters

Parameter	Description	Value / Range	Notes
Input data	Grayscale image converted to binary (secret/reference pair)	32×32 pixels	Serves as symbolic “encryption payload” for bit-wise operations
Chaotic generator	Logistic map	$r = 3.99$, $x_0 = 0.3333$	Output thresholded at 0.5 to obtain binary chaotic series
Operations per run	Total number of XOR/XNOR computations	1024	Equal to number of image bits
Operation logic	Conditional bit-wise selection	XOR for 1 / XNOR for 0	Matches algorithm under evaluation
Segment length	Samples per simulated trace segment	160 samples	Represents 80–160 ns of activity at MCU-level clock rates
Noise model	Additive Gaussian noise ($\sigma = 0.25$)		Models environmental and measurement noise
Amplitude offset (XNOR)	Extra inverter activity	+0.25 (normalized units)	Creates measurable, consistent differential for profiling
Profiling dataset size	Labeled trace segments for training	6 000	Equal class distribution (XOR/XNOR)
Classifier	Linear Support Vector Machine (SVM)	Standardized raw segments	Trained for binary classification of selection bit
Evaluation set	Trace sequence from one encryption run	1024 segments	Same parameters; unlabeled for attack phase
Performance metric	Selection-bit recovery accuracy	86.1 %	Reported in Section 4

All simulations were executed in Python 3.11 using standard scientific libraries (NumPy, scikit-learn, matplotlib). Trace generation employed Gaussian pulse models with amplitude scaling to emulate dynamic power variations due to gate-level switching activity. The random seed was fixed to ensure deterministic reproducibility. The complete simulation script and generated datasets are available in the supplementary materials repository. All experiments were performed on simulated data for methodological demonstration. Parameters and code have been made publicly accessible to enable verification and replication of the presented results. Under the chosen simulation conditions, the classifier recovered the secret selection bit (the control bit that chooses XOR vs. XNOR) with an overall accuracy of 86.1% on the target encryption run. The confusion matrix (rows = true class; columns = predicted class) for the 1,024 operations in the target run was:

- true XNOR (0): 490 correct, 77 misclassified
- true XOR (1): 392 correct, 65 misclassified

Figure 2 illustrates the overall simulation workflow and the empirical validation of the proposed side-channel analysis on a chaotic-coding encryption algorithm. The experiment begins with a secret image and a reference image of identical dimensions (32×32), both converted into serial bitstreams to emulate the bit-level operations defined in the target algorithm. The chaotic bitstream, derived from a logistic map with control parameter $r = 3.99$ and initial condition $x_0 = 0.3333$, serves as a pseudo-random input to drive the XOR/XNOR selection logic. For each bit position, XOR is applied when the corresponding secret bit is “1,” whereas XNOR is used when it is “0,” producing the output codes displayed in panel (e) of the figure. This sequence represents the cryptographic transformation intended to secure the secret image through chaotic diffusion. To assess the potential for information leakage, a power-trace acquisition model was implemented. Each bit operation (XOR or XNOR) was simulated as a short analog

waveform segment whose amplitude and shape were determined by the gate’s logical activity and intrinsic switching asymmetry. The mean per-class power templates in panel (h), together with the representative trace and predicted bits in panel (i), reveal small but consistent amplitude differences between XOR and XNOR transitions. Using these traces, a profiling-based classifier—trained via a linear support vector machine—was employed to predict the secret selection bits from the observed power data. The resulting prediction, shown in panels (f) and (i), achieved an average classification accuracy of 86.1%, demonstrating that the XOR/XNOR switching asymmetry yields exploitable side-channel leakage. Together, these findings highlight that even mathematically sound chaotic cryptosystems can exhibit physical-layer vulnerabilities if hardware-level dynamics are not symmetrically balanced.

Thus, the classifier identified XNOR operations correctly in approximately 86% of instances and XOR operations with comparable reliability. Average profiling templates (mean trace per class) reveal a small but systematic amplitude difference between XOR and XNOR segments, consistent with an extra inverter stage or additional switching activity on the XNOR path. The results demonstrate that a persistent physical asymmetry between the XOR and XNOR execution paths can be learned and exploited by a profiling adversary. In transistor-level implementations, XNOR commonly includes an additional inversion stage relative to XOR. This additional logic contributes extra switching activity when outputs toggle, producing a reproducible perturbation in the measured power trace. Although the per-operation energy difference is small, it is consistent across many operations; profiling methods therefore accumulate evidence and enable high-accuracy classification. An 86.1% per-operation recovery rate substantially reduces the effective entropy of the secret selection stream. Even when the attacker does not obtain perfect per-bit recovery, partial information can materially weaken security by (a) enabling error-correcting inference across the stream, (b) reducing brute-force search complexity,

Side-channel recovery on the 32×32 journal-cover experiment (single run, 86.1% accuracy)

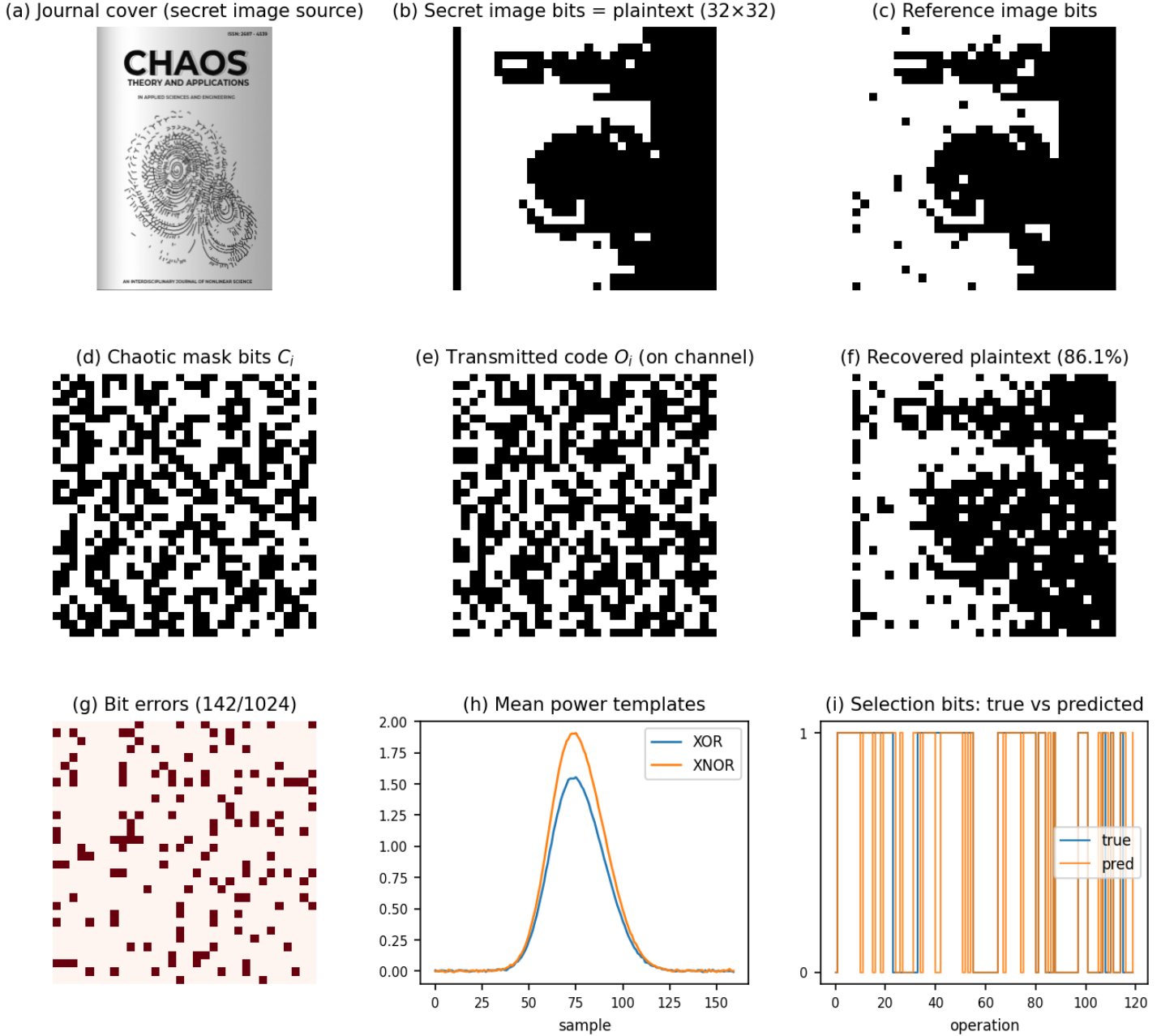


Figure 2 Side-channel recovery on the 32×32 journal-cover experiment (single run, 86.1% accuracy). (a) The cover image of this journal, used as the secret image; (b) its 32×32 binary bitmap, which is simultaneously the plaintext and the XOR/XNOR selection bits; (c) reference-image bits; (d) chaotic mask bits; (e) transmitted secret code, i.e. what appears on the channel, indistinguishable from noise; (f) plaintext recovered from the simulated power traces (86.1% of bits correct); (g) the residual bit errors (142 of 1024); (h) the mean power templates of the two classes, showing the small but systematic amplitude difference between XOR and XNOR; (i) the true and predicted selection bits for the first operations. All panels come from the same run, so panels (b)–(e) are shared between the encoding stage and the attack stage

or (c) facilitating chosen-plaintext or adaptive attacks that combine side-channel outputs with protocol-level information. In short, the scheme's security claims that rely solely on the mathematical unpredictability of a chaotic generator are insufficient unless the implementation eliminates or masks this physical leakage.

A further point deserves emphasis. The leakage demonstrated here does not stem from the chaotic map. The vulnerable element

is the secret-dependent interchange between XOR and XNOR, while the chaotic stream acts only as the mask that is combined with the reference bits. If the logistic map were replaced by any other source of randomness, including a cryptographically strong generator, the selection step would remain identical and the same physical distinction between the two gates would persist; the attack would therefore succeed unchanged. Consequently, the result

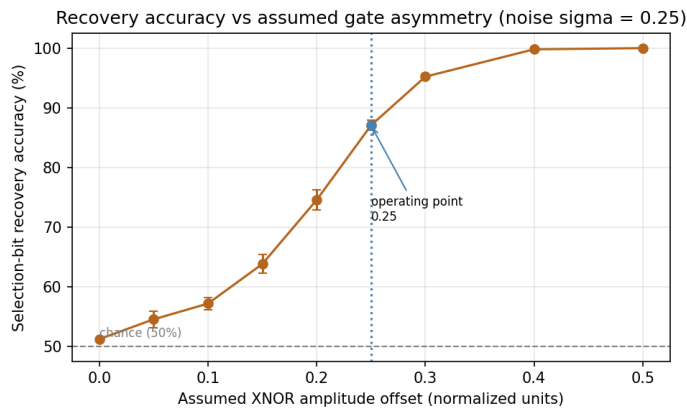


Figure 3 Sensitivity of selection-bit recovery accuracy to the assumed XNOR amplitude offset, with the measurement-noise level held fixed. Accuracy rises monotonically from the chance level (about 50%) when no gate asymmetry is present to near-perfect recovery for large offsets; the operating point adopted in this study (0.25) yields approximately 86%. The control case at zero offset confirms that the demonstrated leakage is attributable entirely to the modeled gate asymmetry rather than to any simulation artifact

is not a statement about the unpredictability of chaos but about the implementation of conditional logic: any scheme that selects between two physically distinguishable operations under the control of secret data inherits this weakness regardless of how the accompanying key material is produced. For the specific scheme under study, the practical implication is direct. The selection bits are the secret-image bits, so an adversary who recovers the selection sequence reconstructs the plaintext itself without ever recovering the reference image, the chaotic codes, or the logistic-map parameters that the original design treats as secret. At a per-operation accuracy of 86.1%, the per-bit uncertainty of the plaintext stream drops from one bit to roughly 0.58 bit, and the residual errors are spatially sparse, so the secret image is already visually recognizable from the recovered bits and can be further cleaned by error-correcting inference across the stream.

Limitations and Scope

Several limitations of the present simulation should be noted and do not undermine the qualitative conclusion:

- **Simulation assumptions:** The study used a simplified physical model in which XNOR segments included a modest, constant amplitude offset and additive measurement noise. This model is intended to represent the extra switching activity expected from an additional inverter stage and from realistic measurement chains; it is not a transistor-level SPICE simulation.
- **Profiling model:** The attacker was assumed to have access to a profiling device of the same type (a standard and well-accepted threat model in side-channel research). If an attacker lacks an appropriate profiling device, attack efficiency may decline.
- **No countermeasures applied:** Hardened implementations (masking, balanced datapaths, dual-rail logic) were not present in the simulation. Those countermeasures can substantially increase the attack work factor but must be validated with the same testing methodology.

These bounds imply that the simulation provides a conservative demonstration of feasibility under realistic, but not worst-case, conditions.

Recommendations

To mitigate the demonstrated leakage, implementations of the evaluated algorithm should adopt side-channel aware countermeasures prior to deployment. Recommended measures include:

- Compute both XOR and XNOR in parallel and select outputs through a balanced multiplexer whose datapath and transistor count are equalized to avoid selection-dependent switching differences.
- Apply first-order masking with frequent mask refresh to decorrelate instantaneous power from secret-dependent values. Care must be taken to use masking techniques that are robust to glitches and propagation effects.
- Adopt dual-rail or other differential logic families (for critical modules) to reduce data-dependent power variation at the cost of area and power overhead.
- Integrate leakage testing into validation (TVLA, CPA, template profiling) and report quantitative leakage metrics in engineering deliverables.

CONCLUSION

The present study reaffirms that the long-standing division of cryptology into cryptography and cryptanalysis is not merely conceptual but operational. Every algorithm that aims to protect information through mathematical complexity must also withstand the empirical scrutiny of physical reality. By analyzing a chaotic image-coding algorithm that employs conditional XOR/XNOR operations, this research demonstrated how implementation asymmetries, specifically the differing switching activities of logic gates can produce observable side-channel signatures. Our simulation results, showing an 86.1% bit-recovery rate under a standard profiling threat model, illustrate that even mathematically sound designs may disclose secret information when physical leakage channels are ignored. These findings echo earlier demonstrations in classical cryptography where unbalanced datapaths undermined strong ciphers and extend them to the emerging domain of chaotic and entropy-based encryption.

Several recent works have promoted chaos-driven ciphers as lightweight yet secure alternatives for image and multimedia protection (Muhammad and Özkaynak 2019). However, few of these studies have evaluated their architectures from a side-channel perspective. The current work therefore bridges this methodological gap, demonstrating that chaotic nonlinearity does not inherently confer resistance to physical leakage and that any imbalance in logic implementation can become an exploitable vector for key disclosure. From a theoretical standpoint, the results highlight an important paradigm shift in modern cryptologic engineering: security assurance must integrate mathematical unpredictability with hardware symmetry. A cipher is not secure if it can be distinguished by its power or electromagnetic footprint. The tested algorithm's use of XOR versus XNOR, two gates that are functionally complementary but physically distinct illustrates how design choices intended to increase randomness can inadvertently create deterministic side effects.

To strengthen and generalize these results, future research should proceed along several axes:

- **Empirical hardware validation** – Implement the proposed model on FPGA or ASIC prototypes to collect real power and

electromagnetic traces. This would quantify leakage magnitude in physical units and evaluate resistance to first- and higher-order attacks.

- **Cross-algorithm benchmarking** – Extend the profiling methodology to other chaotic encryption schemes, such as logistic-tent hybrids or fractional-order maps, to build a comparative database of leakage sensitivity versus algorithmic complexity.
- **Countermeasure co-design** – Develop balanced logic cells or dynamic masking methods specifically tailored to chaos-based cryptographic primitives. The design goal should be to equalize power transitions between logical complements without degrading chaotic entropy.
- **Automated analysis toolchain** – Integrate the presented simulation into a modular software suite that allows researchers to import HDL or gate-level descriptions, simulate side-channel profiles, and estimate information leakage before hardware fabrication.
- **AI-assisted leakage detection** – Explore the use of deep learning models (e.g., CNNs, transformers) for unsupervised discovery of subtle, nonlinear leakage patterns that traditional correlation methods may miss.

Finally, these findings have direct implications for encryption schemes that derive their randomness from physical entropy sources. A growing body of work generates keys and keystreams from the unpredictable dynamics of physical phenomena for instance, the turbulent motion of lava lamps, the movements of jellyfish, or the chaotic dynamics of a flame and feeds this entropy into bit-level cryptographic operations. The lesson of the present study is that the security of such systems depends not only on the quality and unpredictability of the entropy source, but equally on how that entropy is combined into the cipher at the implementation level: a secret-dependent choice between two logically complementary operations leaks through power consumption no matter how unpredictable the underlying source is. Therefore, when high-entropy physical generators are integrated into encryption pipelines as in our ongoing work on physically-sourced randomness based on lava-lamp, jellyfish, and flame dynamics the combination logic should be realized with balanced, data-independent gates and validated against the side-channel methodology presented here, so that physical-entropy generation and side-channel-resistant combination are treated as complementary requirements rather than independent design choices. In summary, this work contributes both a methodological framework and a cautionary perspective: chaos-based cryptography, despite its algorithmic novelty, remains vulnerable if its physical instantiation is not neutralized against leakage. By treating implementation security as an equal partner to algorithmic innovation, future research can ensure that the next generation of chaotic cryptosystems achieves true robustness—mathematical, physical, and practical.

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Availability of data and material

The complete simulation script, the secret image, the fixed random seeds, and the generated datasets are available in the supplement-

tary materials repository.

Conflicts of interest

The author declares that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The authors have no financial or non-financial interests to disclose.

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Analysis of Streptococcus Pyogenes Transmission with Pseudo-Recovery Dynamics Using Fractal-Fractional Caputo-Fabrizio Derivative

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ABSTRACT Streptococcus pyogenes is a bacterial pathogen responsible for a wide range of infections, from the mildest throat conditions to the most severe invasive diseases, and it remains one of the major global health concerns. A new fractal–fractional mathematical model for its transmission dynamics is hereby proposed using the Caputo–Fabrizio (CF) derivative. Compared to the classical integer-order models, the introduced model characterizes memory and hereditary effects, hence it becomes more realistic in describing the pattern of disease spread and the effectiveness of interventions. The model presents a system of fractal–fractional differential equations in time that describes dependencies associated with epidemic spreading. The mathematical well-posedness of the model is established by proving the existence and uniqueness of solution utilizing fixed-point theory. Furthermore, the disease-free equilibrium (DFE), endemic equilibrium (EE), and basic reproduction number R_0 are derived to investigate the transmission dynamics and persistence of the disease. The derived condition allows us to prove the Ulam–Hyers stability of the system, hence, the robustness and resilience of the dynamics against small perturbations. For the numerical analysis, the modified Adams–Bashforth scheme has been adapted, which fits perfectly in handling the memory properties encoded in the CF operator. Furthermore, calibration of the model is done with real epidemiological data, which highlights strong agreement between the simulated trends and the real data observed. The numerical results demonstrate that the fractional-order parameters play an important role in the progression of the disease. Variations in these parameters influence the timing of peak infections, the duration of disease persistence, and the overall transmission pattern. Compared with the classical model, the proposed fractal–fractional framework provides a more flexible description of the epidemic process and offers additional insight into the underlying transmission dynamics. These observations suggest that fractal–fractional modeling can serve as a useful approach for studying complex infectious diseases and supporting the evaluation of disease control measures.

KEYWORDS
Streptococcus
pyogenes
Existence and
uniqueness
Equilibrium analysis
Adams-Bashforth
scheme
Numerical simulation
Mathematical
modeling

INTRODUCTION

Streptococcus pyogenes, commonly known as Group A Streptococcus (GAS), is a major human pathogen and a significant public health concern worldwide, particularly in low- and middle-income countries. It is responsible for a broad spectrum of diseases ranging from mild infections, such as pharyngitis and impetigo, to severe invasive conditions, including necrotizing fasciitis and streptococcal toxic shock syndrome. One of the most serious

long-term consequences of GAS infection is rheumatic heart disease, which develops following acute rheumatic fever, an autoimmune inflammatory response triggered by untreated streptococcal throat infections. In addition, invasive GAS (iGAS) infections, post-streptococcal glomerulonephritis, and recurrent pharyngitis contribute substantially to global morbidity and mortality. Furthermore, GAS-associated pharyngitis accounts for a considerable proportion of antibiotic prescriptions worldwide. In recent years, the epidemiological burden of GAS infections has attracted increasing attention. By late 2022, several countries within the European region reported a substantial increase in invasive Group A Streptococcal infections and, in some cases, scarlet fever outbreaks. A corresponding rise in iGAS-related deaths was also observed, particularly among children younger than ten years of age.

Several contributions in the literature have improved the under-

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standing of *Streptococcus pyogenes* from epidemiological, clinical, and public health perspectives. Efstratiou and Lamagni (2022) discussed the global occurrence of GAS infections and examined factors associated with disease spread and persistence. Public health concerns related to GAS and the measures required for its prevention and control were reviewed by (Avire et al. 2021). The Public Health Agency of Canada Public Health Agency of Canada (2001) also provided guidelines highlighting the importance of surveillance and biosafety practices in managing infections caused by this pathogen. Research efforts have further focused on the diagnosis and clinical manifestations of GAS infections. Spellerberg and Brandt (2022) described laboratory methods used for the identification of *S. pyogenes* and their role in supporting clinical decision-making.

A study by Luca-Harari et al. (2009) reported the clinical and microbiological characteristics of severe GAS infections in Europe, while the classical work of Griffith (1934) established the serological classification of *S. pyogenes*, which remains important for understanding strain variability. From a molecular perspective, Aziz et al. (2010) examined the evolutionary behaviour of Group A Streptococci and showed how genetic changes may influence pathogenicity and disease progression. Cases of rapidly progressing invasive infections reported in the literature Dwyer (2012) demonstrate the serious health risks associated with GAS and underline the need for continued investigation of its transmission mechanisms. Surveillance-based studies have also documented changing patterns in the occurrence of severe infections across different populations, indicating that the epidemiology of GAS remains an active area of research (Swanink et al. 2018).

Mathematical modeling has emerged as an important approach for studying infectious disease transmission and evaluating the potential impact of intervention strategies. For example, the work in Naik et al. (2020) investigated the viral kinetics of HIV-1 infection, while Owolabi and Pindza (2022) developed a fractional-order model to study tuberculosis transmission dynamics. Based on real epidemiological data, the authors in Zhao et al. (2022); Swetha et al. (2025b) analyzed the progression of HIV/AIDS cases in Indonesia. A mathematical model describing cancer dynamics and the stability of therapeutic protection was investigated in Swetha et al. (2025a). In another study, a fractional-order framework based on the Atangana–Baleanu–Caputo derivative was developed to analyze malware propagation while incorporating memory effects into the transmission process Gunasekar et al. (2025, 2026) and the application of mass-action principles in epidemic modeling Li et al. (2018). More recently, mathematical models have been applied to a variety of problems, including COVID-19 transmission (Kubra and Ali 2023), breast cancer progression (Owolabi and Shikongo 2021), Lassa fever dynamics (Abidemi et al. 2022), poliovirus transmission (Karaagac and Owolabi 2023), and other infectious diseases Kurniawati et al. (2021).

In addition to clinical and epidemiological investigations, mathematical modeling has become an important approach for understanding infectious disease transmission and evaluating the effectiveness of disease control strategies. Classical compartmental models, such as the susceptible–infected–recovered (SIR) and susceptible–exposed–infected–recovered (SEIR) frameworks, have been widely employed to describe disease dynamics and predict epidemic behaviour (Hethcote 2000). Furthermore, mathematical models have been developed to investigate the transmission dynamics of Group A Streptococcal infections, providing valuable insights into disease spread, carrier dynamics, and the impact of intervention measures (Yokchoo et al. 2019; Patanarapeelert et al.

2021). Despite these contributions, existing mathematical models are primarily based on conventional deterministic or stochastic formulations and do not simultaneously incorporate memory effects and the heterogeneous nature of disease transmission within a unified fractal–fractional framework. Consequently, although considerable progress has been made in understanding the biological, clinical, and epidemiological aspects of *S. pyogenes*, comparatively few studies have explored advanced mathematical models that integrate both memory effects and heterogeneous transmission characteristics. Motivated by this gap, the present study develops a fractal–fractional Caputo–Fabrizio model to provide a more realistic representation of *S. pyogenes* transmission dynamics while accounting for memory-dependent processes and complex disease progression patterns.

The objective of this paper is to develop a fractal–fractional epidemiological model for the transmission dynamics of *Streptococcus pyogenes* using the Caputo–Fabrizio derivative within a fractal–fractional framework. Classical integer-order epidemic models are often based on Markovian assumptions and may not adequately represent memory-dependent processes such as delayed immune responses, treatment effects, and disease history, all of which can influence the progression and persistence of *Streptococcus pyogenes* infections. This limitation motivates the use of fractional-order operators, which incorporate non-local characteristics and memory effects into the modeling framework. The proposed model is formulated within the fractal–fractional Caputo–Fabrizio framework to describe the transmission dynamics of *Streptococcus pyogenes*. The population is classified into susceptible, infected, diagnosed, pseudo-recovered, relapsed, and terminally ill compartments according to the progression of the disease. The pseudo-recovered class is included to represent individuals who show temporary clinical improvement but may later return to an infectious state. The movement of individuals between these compartments is governed by a system of fractal–fractional differential equations that incorporates memory effects into the transmission process.

The analytical properties of the system are examined using fixed-point theory. The existence and uniqueness of solutions are established, and the well-posedness of the model is verified. In addition, the disease-free equilibrium, endemic equilibrium, and basic reproduction number R_0 are obtained to describe the qualitative behaviour of the disease. Ulam–Hyers stability is also investigated to determine the response of the system to small perturbations. A modified Adams–Bashforth method is employed to compute approximate solutions of the model. The numerical procedure is used to examine the behaviour of the system for different values of the fractional order and to study the influence of memory effects on disease progression.

The numerical findings are compared with weekly laboratory-confirmed invasive Group A Streptococcal (iGAS) cases reported in England by the UK Health Security Agency during the period from September 2019 to May 2026. The simulations reproduce the general pattern observed in the reported data, including the increase, peak, and subsequent decline in the number of cases. The comparison further indicates that higher fractional-order values produce results that are more consistent with the observed epidemiological trends. The results obtained in this work demonstrate that the fractal–fractional framework is capable of describing important features of *Streptococcus pyogenes* transmission while incorporating memory-dependent effects that cannot be represented by conventional integer-order models.

The structure of the paper is as follows: In Sections 1 and 2, we

will present the mathematics related to fractal-fractional Caputo-Fabrizio derivative. In Section 3, the fractional-order model for *Streptococcus pyogenes* will be introduced. Section 4 establishes the existence and uniqueness of the model's solutions by applying the fixed-point theorem. In Section 5, equilibrium states of the system and the basic reproduction number R_0 are derived to describe the long-term dynamics and transmission behavior of the model. Section 6 discusses the Ulam-Hyers stability analysis. Section 7 The numerical scheme adopted for solving the system. Section 8 demonstrates numerical simulations to support and validate the theoretical findings. Finally, Section 9 summarizes the key outcomes of the study and discusses potential directions for future research.

PRELIMINARIES

Definition 1: Atangana and Baleanu (2016) Let $g(l)$ be a continuous function that is also fractally differentiable over the interval (a_1, a_2) with order Θ . The fractal-fractional (FF) derivative of $g(l)$ in the Riemann-Liouville sense with an exponentially decaying kernel and order φ is defined as

$${}_0^{FFCF}D_l^{\varphi, \Theta} g(l) = \frac{M(\varphi)}{1-\varphi} \frac{d}{dl} \int_0^l \exp\left(-\frac{\varphi}{1-\varphi}(l-\zeta)\right) g(\zeta) d\zeta,$$

where $\varphi > 0$, $\Theta \leq m \in \mathbb{T}$, and $M(0) = M(1) = 1$.

Definition 2: Atangana and Qureshi (2019) If $g(l)$ is a continuous and fractally differentiable function over the interval (a_1, a_2) , then the fractal-fractional (FF) integral of $g(l)$ with order φ and exponentially decaying kernel is given by,

$${}_0^{FFCF}I_l^{\varphi, \Theta} g(l) = \frac{\varphi \Theta}{M(\varphi)} \int_0^l \zeta^{\varphi-1} g(\zeta) d\zeta + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} g(l).$$

MODEL DESCRIPTION

This study introduces a novel fractional-order mathematical model for *Streptococcus pyogenes* dynamics, employing the Fractal-Fractional Caputo-Fabrizio (FFCF) derivative to better capture the complex interactions among different stages of the disease. Contrary to the classical models where the influence of history is ignored, the fractional-order approach incorporates memory-dependent mechanisms, hence being more biological in nature. This feature is highly necessary for depicting various realistic aspects of infectious diseases, including their gradual progression, long-lasting immunity, and nonlinear recovery processes. In the proposed model, the total number of people at a specific moment of time l will be split into seven epidemiological classes for describing the process of infections. People in class $\hat{G}(l)$ refer to susceptible individuals who can still become infected. Class $\hat{J}(l)$ consists of people who are infected with an early-stage disease without having clear symptoms. Patients who are being treated after diagnosis will be placed in class $\hat{B}(l)$, and class $\hat{P}(l)$ represents pseudo-recovered individuals who look healthy but can easily get sick again. Individuals who have already fully recovered from the disease belong to class $\hat{C}(l)$, while class $\hat{Q}(l)$ includes patients whose diseases have come back. Finally, class $\hat{A}(l)$ denotes individuals who are terminally ill since further medical assistance would have no effect on their condition.

By incorporating the memory effect of fractional calculus through the CF derivative, this model provides a more refined

and realistic representation of *S. pyogenes* dynamics. The total population in the system is expressed as,

$$\hat{T}(l) = \hat{G}(l) + \hat{J}(l) + \hat{B}(l) + \hat{C}(l) + \hat{P}(l) + \hat{Q}(l) + \hat{A}(l).$$

The dynamics of the classical first-order system are governed by the following set of nonlinear differential equations.

$$\begin{aligned} \frac{d\hat{G}}{dl} &= Y - (\rho + \kappa + \omega)\hat{G}(l), \\ \frac{d\hat{J}}{dl} &= \rho\hat{G}(l) - (\omega + \kappa + \psi)\hat{J}(l), \\ \frac{d\hat{B}}{dl} &= \omega\hat{J}(l) + \sigma\hat{Q}(l) - (\nu + \kappa + \eta + \tau)\hat{B}(l), \\ \frac{d\hat{C}}{dl} &= \omega\hat{G}(l) + \psi\hat{J}(l) + \eta\hat{B}(l) - (\kappa + \delta)\hat{C}(l), \\ \frac{d\hat{P}}{dl} &= \delta\hat{C}(l) - (\gamma + \nu + \kappa + \Pi)\hat{P}(l), \\ \frac{d\hat{Q}}{dl} &= \gamma\hat{P}(l) - (\nu + \kappa + \xi + \sigma)\hat{Q}(l), \\ \frac{d\hat{A}}{dl} &= \xi\hat{Q}(l) + \Pi\hat{P}(l) + \tau\hat{B}(l) - (\nu + \kappa)\hat{A}(l). \end{aligned} \quad (1)$$

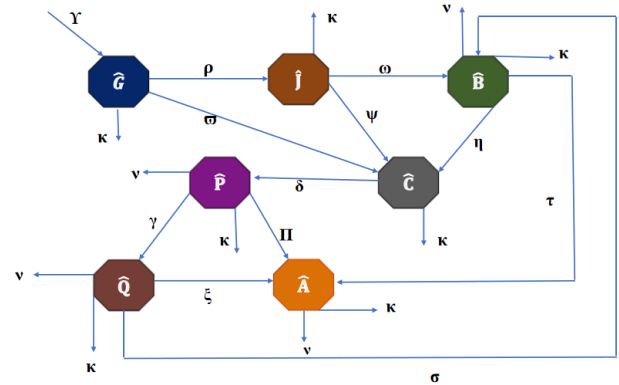


Figure 1 Streptococcus Pyogenes Transmission Model

Since classical models often neglect memory effects inherent in biological systems, we extend the above system using the Caputo-Fabrizio derivative of fractional order $\varphi \in (0, 1]$. This adjustment accounts for non-local effects and temporal memory, better representing real disease progression. The fractional-order system is given by

$$\begin{aligned} {}_0^{FFCF}D_l^{\varphi, \Theta} \hat{G}(l) &= Y - (\rho + \kappa + \omega)\hat{G}(l), \\ {}_0^{FFCF}D_l^{\varphi, \Theta} \hat{J}(l) &= \rho\hat{G}(l) - (\omega + \kappa + \psi)\hat{J}(l), \\ {}_0^{FFCF}D_l^{\varphi, \Theta} \hat{B}(l) &= \omega\hat{J}(l) + \sigma\hat{Q}(l) - (\nu + \kappa + \eta + \tau)\hat{B}(l), \\ {}_0^{FFCF}D_l^{\varphi, \Theta} \hat{C}(l) &= \omega\hat{G}(l) + \psi\hat{J}(l) + \eta\hat{B}(l) - (\kappa + \delta)\hat{C}(l), \\ {}_0^{FFCF}D_l^{\varphi, \Theta} \hat{P}(l) &= \delta\hat{C}(l) - (\gamma + \nu + \kappa + \Pi)\hat{P}(l), \\ {}_0^{FFCF}D_l^{\varphi, \Theta} \hat{Q}(l) &= \gamma\hat{P}(l) - (\nu + \kappa + \xi + \sigma)\hat{Q}(l), \\ {}_0^{FFCF}D_l^{\varphi, \Theta} \hat{A}(l) &= \xi\hat{Q}(l) + \Pi\hat{P}(l) + \tau\hat{B}(l) - (\nu + \kappa)\hat{A}(l). \end{aligned} \quad (2)$$

The system is described by the following initial conditions

$$\begin{aligned} \hat{G}(0) &= \hat{G}_0, \hat{J}(0) = \hat{J}_0, \hat{B}(0) = \hat{B}_0, \hat{C}(0) = \hat{C}_0, \hat{P}(0) = \hat{P}_0, \\ \hat{Q}(0) &= \hat{Q}_0, \hat{A}(0) = \hat{A}_0. \end{aligned}$$

The parameter Y denotes the recruitment rate of new susceptible individuals entering the population, either through birth or migration. The parameter $\rho = \frac{\lambda(\hat{J} + \hat{B})}{\hat{I}}$ represents the rate of force of infection at which susceptible individuals $\hat{G}(l)$ transition into the latent phase $\hat{f}(l)$, marking the early stage of infection. The natural immunity or protection against infection is modeled by ω , while κ accounts for the natural mortality rate, which applies uniformly across all compartments. The progression from latent infection to active symptomatic cases is governed by ω , whereas ψ captures the direct recovery from the latent phase to the recovered class $\hat{C}(l)$ without developing active disease.

The parameter σ represents the rate at which the relapsed individuals $\hat{Q}(l)$ revert to active disease state $\hat{B}(l)$, either due to incomplete treatment or reactivation. The disease-induced mortality across infected and severely ill compartments is given by ν . The rate of successful treatment from the active infected class into the fully recovered compartment is represented by η , whereas τ represents the rate at which active cases deteriorate to the terminally ill class $\hat{A}(l)$ due to either therapeutic failure or due to complications. Further, δ allows the flow of individuals from the recovered class $\hat{C}(l)$ into the pseudo-recovered compartment $\hat{P}(l)$ of individuals, who though appearing clinically better, are at risk of relapse. The rate of relapse of pseudo-recovered individuals is modeled by the parameter γ back to the relapsed class $\hat{Q}(l)$. Finally, Π describes the flow of pseudo-recovered individuals to the terminally ill state, and ξ describes the terminal deterioration of relapsed individuals to the same final compartment $\hat{A}(l)$. This parameter framework allows the model to capture the complex trajectory of *Streptococcus pyogenes* infection inclusive of relapse, pseudo-recovery, and terminal illness. The inclusion of memory effects through the fractal fractional Caputo–Fabrizio operator further enables the model to reflect history-dependent disease progression and therapeutic outcomes.

EXISTENCE AND UNIQUENESS OF THE FFCF SOLUTION

In this section, we develop the existence theory for the proposed model. For this purpose, System 2 is reformulated into the following form

$$\begin{aligned} {}_0^{\text{CF}}D_l^\varphi \hat{G}(l) &= \Theta l^{\Theta-1} H_1(\hat{F}(l), l), \\ {}_0^{\text{CF}}D_l^\varphi \hat{f}(l) &= \Theta l^{\Theta-1} H_2(\hat{F}(l), l), \\ {}_0^{\text{CF}}D_l^\varphi \hat{B}(l) &= \Theta l^{\Theta-1} H_3(\hat{F}(l), l), \\ {}_0^{\text{CF}}D_l^\varphi \hat{C}(l) &= \Theta l^{\Theta-1} H_4(\hat{F}(l), l), \\ {}_0^{\text{CF}}D_l^\varphi \hat{P}(l) &= \Theta l^{\Theta-1} H_5(\hat{F}(l), l), \\ {}_0^{\text{CF}}D_l^\varphi \hat{Q}(l) &= \Theta l^{\Theta-1} H_6(\hat{F}(l), l), \\ {}_0^{\text{CF}}D_l^\varphi \hat{A}(l) &= \Theta l^{\Theta-1} H_7(\hat{F}(l), l), \end{aligned} \quad (3)$$

where

$$\begin{aligned} H_1(\hat{F}(l), l) &= Y - (\rho + \kappa + \omega)\hat{G}(l), \\ H_2(\hat{F}(l), l) &= \rho\hat{G}(l) - (\omega + \kappa + \psi)\hat{f}(l), \\ H_3(\hat{F}(l), l) &= \omega\hat{f}(l) + \sigma\hat{Q}(l) - (\nu + \kappa + \eta + \tau)\hat{B}(l), \\ H_4(\hat{F}(l), l) &= \omega\hat{G}(l) + \psi\hat{f}(l) + \eta\hat{B}(l) - (\kappa + \delta)\hat{C}(l), \\ H_5(\hat{F}(l), l) &= \delta\hat{C}(l) - (\gamma + \nu + \kappa + \Pi)\hat{P}(l), \\ H_6(\hat{F}(l), l) &= \gamma\hat{P}(l) - (\nu + \kappa + \xi + \sigma)\hat{Q}(l), \\ H_7(\hat{F}(l), l) &= \xi\hat{Q}(l) + \Pi\hat{P}(l) + \tau\hat{B}(l) - (\nu + \kappa)\hat{A}(l). \end{aligned}$$

By rewriting System 3, we obtain the following compact representation

$$\begin{aligned} {}_0^{\text{CF}}D_l^\varphi \hat{F}(l) &= \Theta l^{\Theta-1} H(l, \hat{F}(l)), \\ \hat{F}(0) &= \hat{F}_0, \end{aligned} \quad (4)$$

where

$$\hat{F}(l) = (\hat{G}(l), \hat{f}(l), \hat{B}(l), \hat{C}(l), \hat{P}(l), \hat{Q}(l), \hat{A}(l)),$$

and

$$H(l, \hat{F}(l)) = (H_1, H_2, H_3, H_4, H_5, H_6, H_7).$$

By applying the fractal–fractional integral operator in the Caputo–Fabrizio framework, we obtain

$$\hat{F}(l) = \hat{F}_0 + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H(l, \hat{F}(l)) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H(\zeta, \hat{F}(\zeta)) d\zeta, \quad (5)$$

where

$$\begin{aligned} H(l, \hat{F}(l)) &= H_1(\hat{G}(l), (l)), H_2(\hat{f}(l), (l)), H_3(\hat{B}(l), (l)), H_4(\hat{C}(l), (l)), \\ &H_5(\hat{P}(l), (l)), H_6(\hat{Q}(l), (l)), H_7(\hat{A}(l), (l)), \end{aligned}$$

$$\begin{aligned} \hat{G}(l) &= \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_1(\hat{F}(l), l) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_1(\hat{F}(\zeta), \zeta) d\zeta, \\ \hat{f}(l) &= \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_2(\hat{F}(l), l) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_2(\hat{F}(\zeta), \zeta) d\zeta, \\ \hat{B}(l) &= \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_3(\hat{F}(l), l) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_3(\hat{F}(\zeta), \zeta) d\zeta, \\ \hat{C}(l) &= \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_4(\hat{F}(l), l) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_4(\hat{F}(\zeta), \zeta) d\zeta, \\ \hat{P}(l) &= \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_5(\hat{F}(l), l) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_5(\hat{F}(\zeta), \zeta) d\zeta, \\ \hat{Q}(l) &= \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_6(\hat{F}(l), l) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_6(\hat{F}(\zeta), \zeta) d\zeta, \\ \hat{A}(l) &= \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_7(\hat{F}(l), l) + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_7(\hat{F}(\zeta), \zeta) d\zeta. \end{aligned} \quad (6)$$

To prove the existence and uniqueness of solutions, we make use of fixed-point theory. Let $v_n = S[0, T]$ represent the space of all continuous functions corresponding to the state variables $\hat{G}(l)$, $\hat{f}(l)$, $\hat{B}(l)$, $\hat{C}(l)$, $\hat{P}(l)$, $\hat{Q}(l)$, and $\hat{A}(l)$, where $n = 1, 2, \dots, 7$. The function space V_n is considered as a Banach space, equipped with the supremum norm defined by

$$\|\zeta\| = \sup_{l \in [0, T]} |\zeta(l)|.$$

$$\|\hat{G}\| = \max_{l \in [0, T]} |\hat{G}(l)|, \quad \|\hat{f}\| = \max_{l \in [0, T]} |\hat{f}(l)|, \quad \|\hat{B}\| = \max_{l \in [0, T]} |\hat{B}(l)|,$$

$$\|\hat{C}\| = \max_{l \in [0, T]} |\hat{C}(l)|, \quad \|\hat{P}\| = \max_{l \in [0, T]} |\hat{P}(l)|, \quad \|\hat{Q}\| = \max_{l \in [0, T]} |\hat{Q}(l)|,$$

$$\|\hat{A}\| = \max_{l \in [0, T]} |\hat{A}(l)|.$$

Thus, the norm in the product space is defined as

$$\|\hat{G}, \hat{f}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}\| = \|\hat{G}\| + \|\hat{f}\| + \|\hat{B}\| + \|\hat{C}\| + \|\hat{P}\| + \|\hat{Q}\| + \|\hat{A}\|.$$

The Banach space v is then given by,

$$v = v_1 \times v_2 \times v_3 \times v_4 \times v_5 \times v_6 \times v_7,$$

where each v_n corresponds to the space of continuous functions over the interval $[0, T]$, equipped with the supremum norm.

Now, let us define an operator $\Xi : v \rightarrow v$ based on System 6. The operator Ξ can then be expressed as

$$\Xi(V)(l) = \begin{cases} \Xi_1(V)(l), \\ \Xi_2(V)(l), \\ \Xi_3(V)(l), \\ \Xi_4(V)(l), \\ \Xi_5(V)(l), \\ \Xi_6(V)(l), \\ \Xi_7(V)(l) \end{cases}$$

where each component $\Xi_i(V)(l)$ corresponds to the integral representation of the respective fractional differential equation in System 6.

$$\begin{aligned} \Xi_1 \hat{F}(l) &= \hat{G}(0) + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_1(\hat{G}(l), l) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_1(\hat{G}(\zeta), \zeta) d\zeta, \\ \Xi_2 \hat{F}(l) &= \hat{J}(0) + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_2(\hat{G}(l), l) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_2(\hat{G}(\zeta), \zeta) d\zeta, \\ \Xi_3 \hat{F}(l) &= \hat{B}(0) + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_3(\hat{G}(l), l) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_3(\hat{G}(\zeta), \zeta) d\zeta, \\ \Xi_4 \hat{F}(l) &= \hat{C}(0) + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_4(\hat{G}(l), l) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_4(\hat{G}(\zeta), \zeta) d\zeta, \\ \Xi_5 \hat{F}(l) &= \hat{P}(0) + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_5(\hat{G}(l), l) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_5(\hat{G}(\zeta), \zeta) d\zeta, \\ \Xi_6 \hat{F}(l) &= \hat{Q}(0) + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_6(\hat{G}(l), l) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_6(\hat{G}(\zeta), \zeta) d\zeta, \\ \Xi_7 \hat{F}(l) &= \hat{A}(0) + \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} H_7(\hat{G}(l), l) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H_7(\hat{G}(\zeta), \zeta) d\zeta. \end{aligned} \quad (7)$$

Theorem 1: Assume that the functions $H_n : I \times \mathbb{R}^7 \rightarrow \mathbb{R}$ are continuous, and let $U_{1,H_n}, U_{2,H_n}, \dots, U_{7,H_n} > 0$ be given constants. Consider the variables $\hat{G}, \hat{G}', \hat{J}, \hat{J}', \hat{B}, \hat{B}', \hat{C}, \hat{C}', \hat{P}, \hat{P}', \hat{Q}, \hat{Q}', \hat{A}, \hat{A}' \in v$, where $I = [0, T]$ and $n = 1, 2, \dots, 7$.

In this setting, the following Lipschitz-type inequality holds

$$\|H_n(\hat{V}, l) - H_n(\hat{V}', l)\| \leq U_1 H_n \|(\hat{G} - \hat{G}')\| + U_1 H_n \|(\hat{J} - \hat{J}')\| + \dots + U_1 H_n \|(\hat{A} - \hat{A}')\|.$$

If the condition $\omega(\Lambda H_1 + \Lambda H_2 + \dots + \Lambda H_7) < 1$ is satisfied, then System 2 admits a unique solution, where $\omega =$

$$\left\{ \frac{\Theta(1-\varphi)}{M(\varphi)} T^{\Theta-1} + \frac{\varphi T^\Theta}{M(\varphi)} \right\} \text{ and}$$

$$\begin{aligned} \Lambda_{H_1} &= U_1 H_1 + U_2 H_1 + U_3 H_1 + U_4 H_1 + U_5 H_1 + U_6 H_1 + U_7 H_1, \\ \Lambda_{H_2} &= U_1 H_2 + U_2 H_2 + U_3 H_2 + U_4 H_2 + U_5 H_2 + U_6 H_2 + U_7 H_2, \\ \Lambda_{H_3} &= U_1 H_3 + U_2 H_3 + U_3 H_3 + U_4 H_3 + U_5 H_3 + U_6 H_3 + U_7 H_3, \\ \Lambda_{H_4} &= U_1 H_4 + U_2 H_4 + U_3 H_4 + U_4 H_4 + U_5 H_4 + U_6 H_4 + U_7 H_4, \\ \Lambda_{H_5} &= U_1 H_5 + U_2 H_5 + U_3 H_5 + U_4 H_5 + U_5 H_5 + U_6 H_5 + U_7 H_5, \\ \Lambda_{H_6} &= U_1 H_6 + U_2 H_6 + U_3 H_6 + U_4 H_6 + U_5 H_6 + U_6 H_6 + U_7 H_6, \\ \Lambda_{H_7} &= U_1 H_7 + U_2 H_7 + U_3 H_7 + U_4 H_7 + U_5 H_7 + U_6 H_7 + U_7 H_7. \end{aligned}$$

Proof: By assuming

$$\begin{aligned} \sup H_1(l, 0, 0, 0, 0, 0, 0) &= v_{H_1} < \infty \\ \sup H_2(l, 0, 0, 0, 0, 0, 0) &= v_{H_2} < \infty \\ \sup H_3(l, 0, 0, 0, 0, 0, 0) &= v_{H_3} < \infty \\ \sup H_4(l, 0, 0, 0, 0, 0, 0) &= v_{H_4} < \infty \\ \sup H_5(l, 0, 0, 0, 0, 0, 0) &= v_{H_5} < \infty \\ \sup H_6(l, 0, 0, 0, 0, 0, 0) &= v_{H_6} < \infty \\ \sup H_7(l, 0, 0, 0, 0, 0, 0) &= v_{H_7} < \infty. \end{aligned}$$

Let $C_H \subset C$ denote a closed convex ball. Assume that the variables $\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A} \in C_H$, it then follows that

$$\begin{aligned} \|\Xi_1(V)\| &\leq \frac{\Theta(\varphi-1)}{M(\varphi)} T^{\Theta-1} \max_{l \in I} (|H_1(\hat{G}(l), l) - H_1(0, 0, 0, 0, 0, 0, l)| \\ &\quad + |H_1(0, 0, 0, 0, 0, 0, l)|) \\ &\quad + \frac{\varphi\Theta}{M(\varphi)} \max_{l \in I} \left(\int_0^l \zeta^{\Theta-1} |H_1(\hat{G}(l), l) - H_1(0, 0, 0, 0, 0, 0, \zeta)| \right. \\ &\quad \left. + H_1(0, 0, 0, 0, 0, 0, \zeta), d\zeta \right) \\ &\leq \frac{\Theta(1-\varphi)}{M(\varphi)} T^{\Theta-1} (U_{1,H_1} \|\hat{G}\| + U_{2,H_1} \|\hat{J}\| + U_{3,H_1} \|\hat{B}\| \\ &\quad + U_{4,H_1} \|\hat{C}\| + U_{5,H_1} \|\hat{P}\| + U_{6,H_1} \|\hat{Q}\| + U_{7,H_1} \|\hat{A}\| + v_{H_1}) \\ &\quad + \frac{\varphi}{M(\varphi)} T^\Theta (U_{1,H_1} \|\hat{G}\| + U_{2,H_1} \|\hat{J}\| + U_{3,H_1} \|\hat{B}\| + U_{4,H_1} \|\hat{C}\| \\ &\quad + U_{5,H_1} \|\hat{P}\| + U_{6,H_1} \|\hat{Q}\| + U_{7,H_1} \|\hat{A}\| + v_{H_1}) \end{aligned} \quad (8)$$

$$\leq \varphi_1 \Lambda_{H_1} \left(\frac{\varkappa}{7} + v_{H_1} \right) \leq \frac{\varkappa}{7}$$

$$\begin{aligned} \|\Xi_2(V)\| &\leq \frac{\varkappa}{7}, \\ \|\Xi_3(V)\| &\leq \frac{\varkappa}{7}, \\ \|\Xi_4(V)\| &\leq \frac{\varkappa}{7}, \\ \|\Xi_5(V)\| &\leq \frac{\varkappa}{7}, \\ \|\Xi_6(V)\| &\leq \frac{\varkappa}{7}, \\ \|\Xi_7(V)\| &\leq \frac{\varkappa}{7}. \end{aligned} \quad (9)$$

From Equations 8 and 9, together with the definition of v , we get

$$\|\Xi(V)\| = \|\Xi(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A})\| \leq \Xi. \quad (10)$$

For $\hat{V}, \hat{V}' \in v$ and for any $l \in I$, we have

$$\begin{aligned} \|\Xi_1(\hat{V}) - \Xi_1(\hat{V}')\| &\leq \frac{\Theta(\wp - 1)}{M(\wp)} T^{\Theta-1} \max_{l \in I} (|H_1(\hat{G}(l), l) - H_1(\hat{G}'(l), l)|) \\ &\leq \frac{\wp \Theta}{M_\wp} \max_{l \in I} \left(\int_0^l \zeta^{\Theta-1} |H_1(\hat{G}(\zeta), \zeta) - H_1(\hat{G}'(\zeta), \zeta)| d\zeta \right) \\ &\leq \omega_\Xi \Lambda_{H_1} \|\hat{V} - \hat{V}'\|. \end{aligned} \quad (11)$$

Similarly, we obtain

$$\begin{aligned} \|\Xi_2(\hat{V}) - \Xi_2(\hat{V}')\| &\leq \omega_\Xi \Lambda_{H_2} \|\hat{V} - \hat{V}'\| \\ \|\Xi_3(\hat{V}) - \Xi_3(\hat{V}')\| &\leq \omega_\Xi \Lambda_{H_3} \|\hat{V} - \hat{V}'\| \\ \|\Xi_4(\hat{V}) - \Xi_4(\hat{V}')\| &\leq \omega_\Xi \Lambda_{H_4} \|\hat{V} - \hat{V}'\| \\ \|\Xi_5(\hat{V}) - \Xi_5(\hat{V}')\| &\leq \omega_\Xi \Lambda_{H_5} \|\hat{V} - \hat{V}'\| \\ \|\Xi_6(\hat{V}) - \Xi_6(\hat{V}')\| &\leq \omega_\Xi \Lambda_{H_6} \|\hat{V} - \hat{V}'\| \\ \|\Xi_7(\hat{V}) - \Xi_7(\hat{V}')\| &\leq \omega_\Xi \Lambda_{H_7} \|\hat{V} - \hat{V}'\|. \end{aligned} \quad (12)$$

From Equations 11 and 12, we derive

$$\begin{aligned} \|\Xi(\hat{V}) - \Xi(\hat{V}')\| &\leq (\omega_\Xi \Lambda_{H_1} + \omega_\Xi \Lambda_{H_2} + \omega_\Xi \Lambda_{H_3} + \omega_\Xi \Lambda_{H_4} \\ &\quad + \omega_\Xi \Lambda_{H_5} + \omega_\Xi \Lambda_{H_6} + \omega_\Xi \Lambda_{H_7}) \|\hat{V} - \hat{V}'\|. \end{aligned} \quad (13)$$

Since, $(\omega_\Xi \Lambda_{H_1} + \omega_\Xi \Lambda_{H_2} + \omega_\Xi \Lambda_{H_3} + \omega_\Xi \Lambda_{H_4} + \omega_\Xi \Lambda_{H_5} + \omega_\Xi \Lambda_{H_6} + \omega_\Xi \Lambda_{H_7}) < 1$. It is evident that the operator Ξ satisfies the contraction property. Therefore, by invoking the Banach fixed-point theorem, we conclude that $\Xi(V)$ possesses a unique fixed point. Consequently, the proposed system 2 admits a unique solution.

Theorem 2: Let $\xi_{1,H_n}, \xi_{2,H_n}, \xi_{3,H_n}, \xi_{4,H_n}, \xi_{5,H_n}, \xi_{6,H_n}, \xi_{7,H_n} : I \rightarrow \mathbb{R}^+$, $n = 1, 2, \dots, 7$ be such that for all $\hat{G}(l), \hat{J}(l), \dots, \hat{A}(l) \in \hat{V}$, it holds that

$$\begin{aligned} |H_n(\hat{V}(l), l)| &\leq \xi_{1,H_n}(l) + \xi_{2,H_n}(l) |\hat{G}(l)| + \xi_{3,H_n}(l) |\hat{J}(l)| + \dots \\ &\quad + \xi_{7,H_n}(l) |\hat{A}(l)|. \end{aligned}$$

Define $\sup_{l \in I} \xi_{1,H_n}(l) = \widetilde{\xi_{1,H_n}}, \sup_{l \in I} \xi_{2,H_n}(l) = \widetilde{\xi_{2,H_n}}, \dots, \sup_{l \in I} \xi_{7,H_n}(l) = \widetilde{\xi_{7,H_n}}$, and assume that $\widetilde{\xi_{1,H_1}}, \widetilde{\xi_{1,H_2}}, \dots, \widetilde{\xi_{1,H_7}} > 0$. Other assumptions include,

$$\omega_\Xi (\widetilde{\xi_{q,H_1}} + \widetilde{\xi_{q,H_2}} + \widetilde{\xi_{q,H_3}} + \widetilde{\xi_{q,H_4}} + \widetilde{\xi_{q,H_5}} + \widetilde{\xi_{q,H_6}} + \widetilde{\xi_{q,H_7}}) < 1,$$

where $q = 2, 3, \dots, 8$, and

$$\omega_\Xi = \min \left\{ \begin{aligned} &1 - \omega_\Xi (\widetilde{\xi_{3,H_1}} + \widetilde{\xi_{3,H_2}} + \dots + \widetilde{\xi_{3,H_7}}), \\ &1 - \omega_\Xi (\widetilde{\xi_{4,H_1}} + \widetilde{\xi_{4,H_2}} + \dots + \widetilde{\xi_{4,H_7}}), \\ &\vdots \\ &1 - \omega_\Xi (\widetilde{\xi_{8,H_1}} + \widetilde{\xi_{8,H_2}} + \dots + \widetilde{\xi_{8,H_7}}) \end{aligned} \right\}.$$

Therefore, the system 2 has at least one solution.

Proof. Let $\Xi : \hat{V} \rightarrow \hat{V}$ be a completely continuous operator. Since each H_n (for $n = 1, 2, \dots, 7$) is continuous, it follows that Ξ is also continuous.

Let $B \subseteq \hat{V}$ be a bounded set, and assume that there exist constants $h_{H_n} > 0$ such that

$$\max_{l \in I} |H_n(\hat{V}(l), l)| \leq h_{H_n},$$

for all $\hat{V} \in B$. Then, we have

$$\begin{aligned} \|\omega_1(\hat{V})\| &\leq \frac{\Theta(1 - \wp)}{M(\wp)} T^{\Theta-1} \max_{l \in I} |H_1(\hat{G}(l), l)| \\ &\quad + \frac{\wp \Theta}{M(\wp)} \max_{l \in I} \int_0^l \zeta^{\Theta-1} |H_1(\hat{G}(l), \zeta)| d\zeta \\ &\leq \omega_\Xi h_{H_1}. \end{aligned} \quad (14)$$

Similarly, one obtains

$$\begin{aligned} \|\omega_2(\hat{V})\| &\leq \omega_\Xi \|h_{H_2}\|, \\ \|\omega_3(\hat{V})\| &\leq \omega_\Xi \|h_{H_3}\|, \\ \|\omega_4(\hat{V})\| &\leq \omega_\Xi \|h_{H_4}\|, \\ \|\omega_5(\hat{V})\| &\leq \omega_\Xi \|h_{H_5}\|, \\ \|\omega_6(\hat{V})\| &\leq \omega_\Xi \|h_{H_6}\|, \\ \|\omega_7(\hat{V})\| &\leq \omega_\Xi \|h_{H_7}\|. \end{aligned} \quad (15)$$

Equations 14–15 show that $\omega(\hat{G}, \hat{J}, \dots, \hat{A})$ is uniformly bounded. Next, we show that ω is equi-continuous. Let $0 \leq l_1 \leq l_2 \leq T$, then

$$\begin{aligned} \|\omega_1(\hat{V}(l_2)) - \omega_1(\hat{V}(l_1))\| &\leq \left[\left| \frac{\Theta(1 - \wp)}{M(\wp)} (l_2^{\Theta-1} - l_1^{\Theta-1}) \right| \right. \\ &\quad \times \left\{ H_1(\hat{G}(l_2), \dots, \hat{A}(l_2), l_2) - H_1(\hat{G}(l_1), \dots, \hat{A}(l_1), l_1) \right\} \Big| \\ &\quad \left. + \left| \frac{\wp h_{H_1}}{M(\wp)} (l_2^{\Theta-1} - l_1^{\Theta-1}) \right| \right] \\ &\rightarrow 0, \quad \text{as } l_2 \rightarrow l_1. \end{aligned} \quad (16)$$

Analogous relations hold for $\omega_2, \dots, \omega_7$, i.e.

$$\|\omega_i(\hat{V}(l_2)) - \omega_i(\hat{V}(l_1))\| \rightarrow 0 \quad \text{as } l_2 \rightarrow l_1, \quad i = 2, \dots, 7. \quad (17)$$

Thus, $\omega(\hat{V}) = \omega(\hat{G}, \hat{J}, \dots, \hat{A})$ is equi-continuous and completely continuous.

Now, define

$$B = \{\hat{V} \in \hat{V} : (\hat{G}, \hat{J}, \dots, \hat{A}) = \xi \omega(\hat{V}), \xi \in [0, 1]\}.$$

Let $\hat{V} \in B$, so that $\hat{V} = \xi \omega(\hat{V})$. Then for $l \in I$, it holds that

$$\begin{aligned} \hat{G}(l) &= \xi \omega_1(\hat{V})(l), \quad \hat{J}(l) = \xi \omega_2(\hat{V})(l), \quad \hat{B}(l) = \xi \omega_3(\hat{V})(l), \\ \hat{C}(l) &= \xi \omega_4(\hat{V})(l), \quad \hat{P}(l) = \xi \omega_5(\hat{V})(l), \quad \hat{Q}(l) = \xi \omega_6(\hat{V})(l), \\ \hat{A}(l) &= \xi \omega_7(\hat{V})(l). \end{aligned} \quad (18)$$

Therefore,

$$\begin{aligned} |\hat{G}(l)| &\leq \left(\frac{\Theta(1 - \wp)}{M(\wp)} T^{\Theta-1} + \frac{\wp T^\Theta}{M(\wp)} \right) \\ &\quad (\xi_{1,H_1}(l) + \xi_{2,H_1}(l) |\hat{G}(l)| + \dots + \xi_{7,H_1}(l) |\hat{A}(l)|). \end{aligned} \quad (19)$$

Simplifying 19, we obtain

$$\|\hat{G}(l)\| \leq \omega_\Xi (\widetilde{\xi_{1,H_1}}(l) + \widetilde{\xi_{2,H_1}}(l) |\hat{G}(l)| + \dots + \widetilde{\xi_{7,H_1}}(l) |\hat{A}(l)|). \quad (20)$$

Similarly, we have

$$\begin{aligned}\|\hat{f}(l)\| &\leq \omega_{\Xi}(\widetilde{\xi_{1,H_2}}(l) + \widetilde{\xi_{2,H_2}}(l)|\hat{G}(l)| + \cdots + \widetilde{\xi_{7,H_2}}(l)|\hat{A}(l)|), \\ &\vdots \\ \|\hat{A}(l)\| &\leq \omega_{\Xi}(\widetilde{\xi_{1,H_7}}(l) + \widetilde{\xi_{2,H_7}}(l)|\hat{G}(l)| + \cdots + \widetilde{\xi_{7,H_7}}(l)|\hat{A}(l)|).\end{aligned}\quad (21)$$

Adding Equations 20–21 yields

$$\begin{aligned}\|\hat{G}\| + \|\hat{f}\| + \cdots + \|\hat{A}\| &\leq \omega_{\Xi}(\widetilde{\xi_{1,H_1}}(l) + \widetilde{\xi_{1,H_2}}(l) + \cdots + \widetilde{\xi_{1,H_7}}(l)) \\ &\quad + \omega_{\Xi}(\widetilde{\xi_{2,H_1}}(l) + \widetilde{\xi_{2,H_2}}(l) + \cdots + \widetilde{\xi_{2,H_7}}(l))\|\hat{G}(l)\| + \cdots \\ &\quad + \omega_{\Xi}(\widetilde{\xi_{7,H_1}}(l) + \widetilde{\xi_{7,H_2}}(l) + \cdots + \widetilde{\xi_{7,H_7}}(l))\|\hat{A}(l)\|.\end{aligned}\quad (22)$$

Consequently,

$$\|(\hat{G}(l), \hat{f}(l), \dots, \hat{A}(l))\| \leq \omega_{\Xi} \left(\frac{\widetilde{\xi_{1,H_1}}(l) + \widetilde{\xi_{1,H_2}}(l) + \cdots + \widetilde{\xi_{1,H_7}}(l)}{\omega_0} \right).$$

Thus, B is a bounded set. By Theorem , ω has at least one fixed point, implying that the proposed system 2 admits a solution.

THE EQUILIBRIUM STATE AND BASIC REPRODUCTION NUMBER OF THE SYSTEM

Disease-Free Equilibrium State

The disease-free equilibrium (DFE) represents the state of the system where no infection persists in the population. Mathematically, this implies that all infected and disease-related compartments vanish, while the susceptible population remains at steady state. For the proposed model, the disease-free equilibrium is obtained by setting

$$\hat{f} = \hat{B} = \hat{C} = \hat{P} = \hat{Q} = \hat{A} = 0.$$

Thus, the disease-free equilibrium point is given by

$$E_0 = (\hat{G}^0, 0, 0, 0, 0, 0, 0),$$

where

$$\hat{G}^0 = \frac{Y}{\rho + \kappa + \omega}.$$

This equilibrium corresponds to the absence of disease in the population, where only the susceptible class persists and all transmission dynamics are eliminated.

Endemic Equilibrium State

The endemic equilibrium (EE) represents a steady state in which the disease persists in the population over time. At this state, all system derivatives are set to zero, leading to a system of nonlinear algebraic equations. The endemic equilibrium is denoted by

$$E^* = (\hat{G}^*, \hat{f}^*, \hat{B}^*, \hat{C}^*, \hat{P}^*, \hat{Q}^*, \hat{A}^*),$$

where

$$\begin{aligned}0 &= Y - (\rho + \kappa + \omega)\hat{G}^*, \\ 0 &= \rho\hat{G}^* - (\omega + \kappa + \psi)\hat{f}^*, \\ 0 &= \omega\hat{f}^* + \sigma\hat{Q}^* - (\nu + \kappa + \eta + \tau)\hat{B}^*, \\ 0 &= \omega\hat{G}^* + \psi\hat{f}^* + \eta\hat{B}^* - (\kappa + \delta)\hat{C}^*, \\ 0 &= \delta\hat{C}^* - (\gamma + \nu + \kappa + \Pi)\hat{P}^*, \\ 0 &= \gamma\hat{P}^* - (\nu + \kappa + \xi + \sigma)\hat{Q}^*, \\ 0 &= \xi\hat{Q}^* + \Pi\hat{P}^* + \tau\hat{B}^* - (\nu + \kappa)\hat{A}^*.\end{aligned}$$

The endemic equilibrium exists when the system admits a biologically feasible positive solution.

Basic Reproduction Number (R_0)

The basic reproduction number R_0 is defined as the average number of secondary infections produced by a single infected individual introduced into a completely susceptible population. To compute R_0 , we reformulate the infected subsystem of the model as

$$X = (\hat{f}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A})^T.$$

The system is decomposed into new infection and transition components as

$$\frac{dX}{dt} = F(X) - V(X),$$

where $F(X)$ represents the rate of appearance of new infections and $V(X)$ represents all transfer, progression, and removal terms. The new infection vector is given by

$$F = \begin{bmatrix} \rho\hat{G} \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix},$$

while the transition dynamics are captured by

$$V = \begin{bmatrix} (\omega + \kappa + \psi)\hat{f} \\ (\nu + \kappa + \eta + \tau)\hat{B} - \omega\hat{f} - \sigma\hat{Q} \\ (\kappa + \delta)\hat{C} - \omega\hat{G} - \psi\hat{f} - \eta\hat{B} \\ (\gamma + \nu + \kappa + \Pi)\hat{P} - \delta\hat{C} \\ (\nu + \kappa + \xi + \sigma)\hat{Q} - \gamma\hat{P} \\ (\nu + \kappa)\hat{A} - \xi\hat{Q} - \Pi\hat{P} - \tau\hat{B} \end{bmatrix}.$$

Evaluating the system at the disease-free equilibrium yields the next-generation matrix $K = FV^{-1}$. The basic reproduction number is defined as $R_0 = \rho(K)$ where $\rho(K)$ denotes the spectral radius of the matrix K . After simplification along the dominant infection transmission pathway, the reproduction number can be expressed as

$$R_0 = \frac{\rho}{(\omega + \kappa + \psi)} \cdot \frac{\omega}{(\nu + \kappa + \eta + \tau)} \cdot \frac{\delta}{(\gamma + \nu + \kappa + \Pi)} \cdot \frac{\gamma}{(\nu + \kappa + \xi + \sigma)}.$$

The threshold parameter R_0 governs the transmission dynamics of the system. If $R_0 < 1$, the disease-free equilibrium is locally asymptotically stable and the infection dies out. Conversely, if $R_0 > 1$, the disease persists in the population and an endemic equilibrium may exist. Thus, R_0 plays a critical role in determining the long-term behavior of the proposed model.

ULAM-HYERS STABILITY

This section introduces the foundational ideas and stability criteria associated with the proposed fractal-fractional epidemic model. To analyze the stability behavior, let us consider a small perturbation function $\mathfrak{I}(l)$ that satisfies the following initial condition $\mathfrak{I}(0) = 0$. The perturbation is assumed to meet the subsequent conditions

- (C1) $|\mathfrak{S}(l)| \leq \epsilon$, for $\Theta > 0$.
(C2) ${}^{FF}D_{0+}^{\varphi, \Theta} \hat{F}(l) = H(l, \hat{F}(l)) + \mathfrak{S}(l)$.

Lemma 1 Consider the perturbed system

$${}^{FF}D_{0+}^{\varphi, \Theta} \hat{F}(l) = H(l, \hat{F}(l)) + \mathfrak{S}(l), \quad \hat{F}(0) = \hat{F}_0.$$

A solution $\hat{F}(l)$ exists if the following condition is satisfied

$$\left| \hat{F}(l) - \left[\hat{F}(0) - \frac{\Theta(1-\varphi)}{M(\varphi)} (H(l, \hat{F}(l)) + \mathfrak{S}_0(l)) l^{\Theta-1} + \frac{\varphi\Theta}{M(\varphi)} \int_0^l (\zeta)^{\Theta-1} H(\zeta, \hat{F}(\zeta)) d\zeta \right] \right| \leq \left[\frac{\Theta(1-\varphi)}{M(\varphi)} T^{\Theta-1} + \frac{\Theta T^\varphi}{M(\varphi)} \right] \aleph_H.$$

Theorem 3 By combining systems (3.2) and (4.3) along with Lemma , the proposed model achieves Ulam–Hyers stability if the following condition holds $\theta < 1$, where

$$\theta = \left[\frac{\Theta(1-\varphi)}{M(\varphi)} T^{\Theta-1} + \frac{\Theta T^\varphi}{M(\varphi)} \right] \aleph_H.$$

Proof: As demonstrated in the existence and uniqueness analysis, the proposed system possesses a unique solution. Let $\hat{F} \in \vartheta$ denote the exact solution, and let $\tilde{F}' \in \vartheta$ represent any approximate solution of the model. Then, the difference between both solutions can be expressed as:

$$\begin{aligned} |\hat{F}(l) - \tilde{F}'(l)| &= \left| \hat{F}(l) - \left\{ \tilde{F}'(0) + (H(l, \tilde{F}'(l)) - H_0(l)) \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} + \frac{\Theta\varphi}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H(\zeta, \tilde{F}'(\zeta)) d\zeta \right\} \right| \\ &\leq \left| \hat{F}(l) - \left\{ \hat{F}(0) + (H(l, \hat{F}(l)) - H_0(l)) \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} + \frac{\Theta\varphi}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H(\zeta, \hat{F}(\zeta)) d\zeta \right\} \right| \\ &\quad + \left| \left\{ \hat{F}(0) + (H(l, \hat{F}(l)) - H_0(l)) \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} + \frac{\Theta\varphi}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H(\zeta, \hat{F}(\zeta)) d\zeta \right\} \right. \\ &\quad \left. - \left\{ \tilde{F}'(0) + (H(l, \tilde{F}'(l)) - H_0(l)) \frac{\Theta(1-\varphi)}{M(\varphi)} l^{\Theta-1} + \frac{\Theta\varphi}{M(\varphi)} \int_0^l \zeta^{\Theta-1} H(\zeta, \tilde{F}'(\zeta)) d\zeta \right\} \right| \\ &\leq \chi_{\varphi, \Theta} + \frac{\Theta(1-\varphi) T^{\Theta-1} \aleph_H}{M(\varphi)} \|\hat{F} - \tilde{F}'\| + \frac{\Theta T^\varphi \aleph_H}{M(\varphi)} \|\hat{F} - \tilde{F}'\| \\ &= \chi_{\varphi, \Theta} + \pi \|\hat{F} - \tilde{F}'\|. \end{aligned} \quad (23)$$

Following the Lipschitz condition applied to $H(l, \hat{F})$, the inequality leads to the bound characterized by θ , demonstrating

that $|\hat{F}(l) - \tilde{F}'(l)| \leq \theta \aleph_H$. Consequently, when $\theta < 1$, the model satisfies the criterion for Ulam–Hyers stability.

NUMERICAL SCHEME OF THE STEPTOCOCCUS PYOGENES

The Adams–Bashforth scheme [Fatmawati et al. \(2020\)](#) is an explicit multi-step method designed for fractional systems under the Caputo–Fabrizio operator. To devise the scheme, equations 2 are rewritten to decouple the fractal and fractional effects so that an efficient computation can be achieved. Such a method advances the solution by making use of values from previous time levels, commencing with prescribed initial conditions and a chosen time step l so as to maintain stability and accuracy. This framework truly reflects the memory characteristics of the model and shall provide reliable simulations of the disease dynamics over a long period.

$$\begin{aligned} {}_0^CF D_l^\varphi \hat{G}(l) &= \Theta l^{\Theta-1} S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l), \\ {}_0^CF D_l^\varphi \hat{J}(l) &= \Theta l^{\Theta-1} S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l), \\ {}_0^CF D_l^\varphi \hat{B}(l) &= \Theta l^{\Theta-1} S_3(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l), \\ {}_0^CF D_l^\varphi \hat{C}(l) &= \Theta l^{\Theta-1} S_4(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l), \\ {}_0^CF D_l^\varphi \hat{P}(l) &= \Theta l^{\Theta-1} S_5(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l), \\ {}_0^CF D_l^\varphi \hat{Q}(l) &= \Theta l^{\Theta-1} S_6(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l), \\ {}_0^CF D_l^\varphi \hat{A}(l) &= \Theta l^{\Theta-1} S_7(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l). \end{aligned} \quad (24)$$

By applying the Caputo–Fabrizio integral operator to equation 24, we obtain

$$\begin{aligned} \hat{G}(l) &= \hat{G}(0) + \frac{\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} (l-\zeta)^{\varphi-1} S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\ \hat{J}(l) &= \hat{J}(0) + \frac{\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} (l-\zeta)^{\varphi-1} S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\ \hat{B}(l) &= \hat{B}(0) + \frac{\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} (l-\zeta)^{\varphi-1} S_3(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\ \hat{C}(l) &= \hat{C}(0) + \frac{\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} (l-\zeta)^{\varphi-1} S_4(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\ \hat{P}(l) &= \hat{P}(0) + \frac{\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} (l-\zeta)^{\varphi-1} S_5(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\ \hat{Q}(l) &= \hat{Q}(0) + \frac{\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} (l-\zeta)^{\varphi-1} S_6(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\ \hat{A}(l) &= \hat{A}(0) + \frac{\Theta}{M(\varphi)} \int_0^l \zeta^{\Theta-1} (l-\zeta)^{\varphi-1} S_7(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta. \end{aligned} \quad (25)$$

where

$$\begin{aligned} S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) &= Y - (\rho + \kappa + \omega) \hat{G}(l), \\ S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) &= \rho \hat{G}(l) - (\omega + \kappa + \psi) \hat{J}(l), \\ S_3(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) &= \omega \hat{J}(l) + \sigma \hat{Q}(l) - (\nu + \kappa + \eta + \tau) \hat{B}(l), \\ S_4(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) &= \omega \hat{G}(l) + \psi \hat{J}(l) + \eta \hat{B}(l) - (\kappa + \delta) \hat{C}(l), \\ S_5(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) &= \delta \hat{C}(l) - (\gamma + \nu + \kappa + \Pi) \hat{P}(l), \\ S_6(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) &= \gamma \hat{P}(l) - (\nu + \kappa + \xi + \sigma) \hat{Q}(l), \\ S_7(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) &= \xi \hat{Q}(l) + \Pi \hat{P}(l) + \tau \hat{B}(l) - (\nu + \kappa) \hat{A}(l). \end{aligned}$$

Now using the approach at t_{n+1} , we have the following

$$\begin{aligned}
\hat{G}(l) &= \frac{G^0 + \Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{J}(l) &= \frac{J^0 + \Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{B}(l) &= \frac{B^0 + \Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_3(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_3(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{C}(l) &= \frac{C^0 + \Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_4(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_4(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{P}(l) &= \frac{P^0 + \Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_5(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_5(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{Q}(l) &= \frac{Q^0 + \Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_6(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_6(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{A}(l) &= \frac{A^0 + \Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_7(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_7(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta,
\end{aligned} \tag{26}$$

at t_{n+1} , we have the following

$$\begin{aligned}
\hat{G}^{n+1} &= \hat{G}^0 S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{J}^{n+1} &= \hat{J}^0 S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{B}^{n+1} &= \hat{B}^0 S_3(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_3(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{C}^{n+1} &= \hat{C}^0 S_4(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_4(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{P}^{n+1} &= \hat{P}^0 S_5(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_5(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{Q}^{n+1} &= \hat{Q}^0 S_6(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_6(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{A}^{n+1} &= \hat{A}^0 S_7(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, l) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_0^l \zeta^{\Theta-1} S_7(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta.
\end{aligned} \tag{27}$$

By evaluating the difference between successive terms of the numerical scheme, the following expression is obtained

$$\begin{aligned}
\hat{G}^{n+1} &= \hat{G}^n \frac{\Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_1(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\
&\quad - \frac{\Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_1(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_{l_n}^{l_{n+1}} \zeta^{\Theta-1} S_1(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta, \\
\hat{J}^{n+1} &= \hat{J}^n \frac{\Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_2(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\
&\quad - \frac{\Theta l^{\Theta-1}(1-\wp)}{M(\wp)} S_2(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}) \\
&\quad + \frac{\wp \Theta}{M\wp} \int_{l_n}^{l_{n+1}} \zeta^{\Theta-1} S_2(\hat{G}, \hat{J}, \hat{B}, \hat{C}, \hat{P}, \hat{Q}, \hat{A}, \zeta) d\zeta,
\end{aligned}$$

$$\begin{aligned}\hat{A}^{n+1} = & \hat{A}^n \frac{\Theta l^{\Theta-1}(1-\varphi)}{M(\varphi)} S_7(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \frac{\Theta l^{\Theta-1}(1-\varphi)}{M(\varphi)} \\ & \times S_7(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}) \\ & + \frac{\varphi \Theta}{M(\varphi)} \int_{l_n}^{l_{n+1}} \left[\frac{3h}{2} l_n^{\Theta-1} S_7(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \right. \\ & \left. - \frac{h}{2} l_{n-1}^{\Theta-1} S_7(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}) \right].\end{aligned}\quad (29)$$

Further simplification of Equation 29 yields the following result

$$\begin{aligned}\hat{G}^{n+1} = & \hat{G}^n + \Theta l_n^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) S_1(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \Theta l_{n-1}^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) \\ & \times S_1(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}), \\ \hat{J}^{n+1} = & \hat{J}^n + \Theta l_n^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) S_2(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \Theta l_{n-1}^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) \\ & \times S_2(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}), \\ \hat{B}^{n+1} = & \hat{B}^n + \Theta l_n^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) S_3(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \Theta l_{n-1}^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) \\ & \times S_3(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}), \\ \hat{C}^{n+1} = & \hat{C}^n + \Theta l_n^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) S_4(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \Theta l_{n-1}^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) \\ & \times S_4(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}), \\ \hat{P}^{n+1} = & \hat{P}^n + \Theta l_n^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) S_5(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \Theta l_{n-1}^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) \\ & \times S_5(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}), \\ \hat{Q}^{n+1} = & \hat{Q}^n + \Theta l_n^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) S_6(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \Theta l_{n-1}^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) \\ & \times S_6(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}), \\ \hat{A}^{n+1} = & \hat{A}^n + \Theta l_n^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) S_7(\hat{G}^n, \hat{J}^n, \hat{B}^n, \hat{C}^n, \hat{P}^n, \hat{Q}^n, \hat{A}^n, l_n) \\ & - \Theta l_{n-1}^{\Theta-1} \left(\frac{1-\varphi}{M(\varphi)} + \frac{3\varphi h}{2M(\varphi)} \right) \\ & \times S_7(\hat{G}^{n-1}, \hat{J}^{n-1}, \hat{B}^{n-1}, \hat{C}^{n-1}, \hat{P}^{n-1}, \hat{Q}^{n-1}, \hat{A}^{n-1}, l_{n-1}).\end{aligned}\quad (30)$$

NUMERICAL SIMULATION AND DISCUSSION

Numerical simulations were conducted to investigate the transmission dynamics of *Streptococcus pyogenes* using the proposed fractal–fractional Caputo–Fabrizio (FFCF) model. The classical integer-order formulation presented in Equation (1) serves as the foundation for deriving the corresponding fractal–fractional extension given in Equation (2). By introducing the Caputo–Fabrizio fractal–fractional operator, the model incorporates nonlocal memory effects, which play a significant role in describing disease evolution more realistically than traditional integer-order models.

All numerical experiments in this study are based on the FFCF system defined in Equation (2). The approximate solutions were obtained using a modified Adams–Bashforth scheme in MATLAB, specifically adapted for the fractal–fractional Caputo–Fabrizio operator. To explore the influence of memory effects on the disease dynamics, the fractal dimension parameter was kept fixed while different values of the fractional order were considered. The initial conditions were assumed as

$$\begin{aligned}\hat{G}(0) = 1000, \quad \hat{J}(0) = 1, \quad \hat{B}(0) = 0, \quad \hat{C}(0) = 0, \quad \hat{P}(0) = 0, \\ \hat{Q}(0) = 0, \quad \hat{A}(0) = 0,\end{aligned}$$

representing a population in which a single infected individual is introduced at the onset of the outbreak. The parameter values used in the simulations were chosen to illustrate the qualitative behaviour of the proposed model and to investigate the influence of the fractal and fractional orders on the disease dynamics. In addition, weekly reported cases of invasive Group A Streptococcal (iGAS) infections in England were obtained from the UK Health Security Agency (UKHSA) surveillance system [UK Health Security Agency \(2026\)](#). This dataset consists of laboratory-confirmed notifications recorded through national surveillance programmes between September 2019 and May 2026. These observational records are used here to provide a quantitative comparison with the simulated dynamics generated by the proposed model. The simulation is carried out over a sufficiently long time horizon in order to capture the full progression of the epidemic, including the initial growth phase, peak transmission period, and eventual decline. The resulting dynamics of all compartments are presented in Figures 2–9, illustrating the temporal evolution of the disease under different fractal–fractional-order. The numerical parameter set employed in this study is given by $Y = 30$, $\rho = 0.05$, $\kappa = 0.01$, $\omega = 0.03$, $\omega = 0.02$, $\psi = 0.04$, $\sigma = 0.02$, $\nu = 0.01$, $\eta = 0.02$, $\tau = 0.015$, $\delta = 0.05$, $\gamma = 0.03$, $\Pi = 0.01$, $\xi = 0.02$. The system is simulated over an extended time interval to ensure that all stages of the outbreak are adequately represented, from the initial transmission phase through to the peak and final decay. The numerical outcomes depicted in Figures 2–9 clearly illustrate the evolution of each epidemiological compartment over time. Figure 2 presents a comparison between the observed weekly

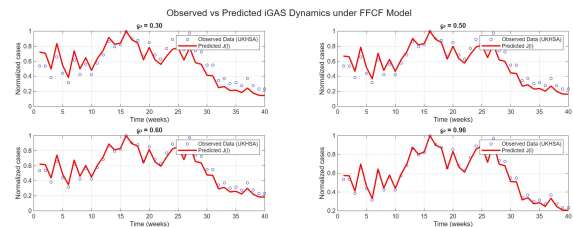


Figure 2 Comparison between weekly iGAS surveillance data (UKHSA) and the infected compartment $J(I)$ generated by the FFCF model under different fractional-order values. The observational data are normalized to allow consistent comparison of temporal trends. The results demonstrate that the proposed model successfully captures the observed epidemic pattern

laboratory-confirmed iGAS cases reported by the UK Health Security Agency (UKHSA) and the corresponding infected class $J(I)$ obtained from the proposed fractal–fractional Caputo–Fabrizio (FFCF) model. The discrete points represent the observed data, whereas the continuous curves correspond to model simulations for different fractional-order values, namely $\varphi = 0.30, 0.50, 0.60,$

and 0.96. The results indicate that the proposed model is capable of reproducing the main qualitative features of the epidemic trajectory, including the rapid increase in cases, the peak incidence, and the subsequent decline. It is further observed that higher fractional-order values provide a better agreement with the reported data, highlighting the importance of memory effects in capturing real-world transmission dynamics. The normalization of the dataset ensures a consistent and meaningful comparison between observed and simulated values.

Quantitative Validation Using RMSE and R^2 Metrics

To quantitatively assess the performance of the proposed model, two standard statistical measures are employed: the Root Mean Square Error (RMSE) and the coefficient of determination (R^2). These metrics provide a rigorous measure of the agreement between observed data and model predictions for the infected population $J(l)$. The RMSE is defined as

$$\text{RMSE} = \sqrt{\frac{1}{n} \sum_{i=1}^n (O_i - P_i)^2}$$

where O_i represents the observed weekly reported cases, P_i denotes the corresponding model-predicted values, and n is the total number of observations. A smaller RMSE value indicates improved agreement between the model and the data. The coefficient of determination is given by

$$R^2 = 1 - \frac{\sum_{i=1}^n (O_i - P_i)^2}{\sum_{i=1}^n (O_i - \bar{O})^2}$$

where $\bar{O}$ denotes the mean of the observed data. The value of R^2 lies between 0 and 1, with values closer to 1 indicating that the model effectively explains the variability in the observed data. In this study, both RMSE and R^2 are computed after normalizing the observational and simulated datasets to ensure consistency in scale. The computed performance metrics for different fractional-order values are summarized in Table 1. As shown in Table 1, the RMSE values decrease from 0.078 to 0.038, while the corresponding R^2 values increase from 0.930 to 0.983 as the fractional-order parameter increases from $\varphi = 0.30$ to $\varphi = 0.96$. Among the considered fractional-order values, $\varphi = 0.96$ yields the lowest RMSE and the highest R^2 , indicating the closest agreement between the simulated and observed data. Overall, these quantitative performance measures demonstrate that the proposed FFCF model accurately reproduces the observed epidemic trends and provides a reliable representation of the transmission dynamics of invasive Group A Streptococcal (iGAS) infections.

Table 1 Quantitative validation of the proposed FFCF model using RMSE and R^2 for different fractional-order values based on the observed and predicted normalized iGAS data.

Fractional order (φ)	RMSE	R^2
0.30	0.078	0.930
0.50	0.066	0.949
0.60	0.052	0.966
0.96	0.038	0.983

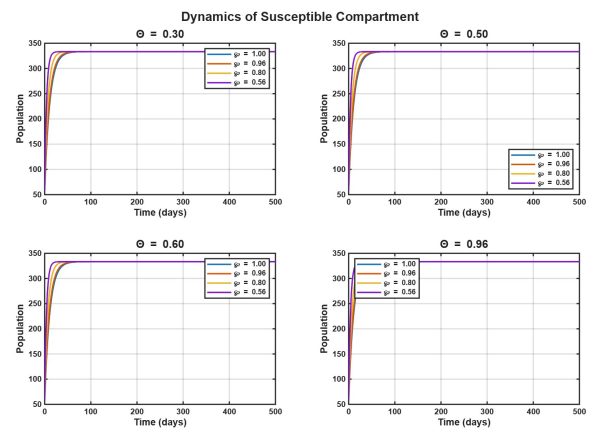


Figure 3 Temporal dynamics of the susceptible population in the fractal-fractional Caputo-Fabrizio model. The fractal parameter Θ is kept fixed for each subplot, while the fractional order φ is varied to analyze memory effects on population evolution over time

Susceptible dynamics ($\hat{G}$) are shown in Figure 3. There is a sudden decrease at the beginning, and this should be the case because of the large number of individuals moving out of the susceptible pool into the exposed and infected categories due to the effect of the parameter ρ . Since there will be a constant influx into the category of susceptibles, the recruitment rate Y would not be enough to counterbalance the effect of the high infection rate at the start. However, as the number of infected people starts to dwindle, the dynamics will start to level off and approach endemic levels.

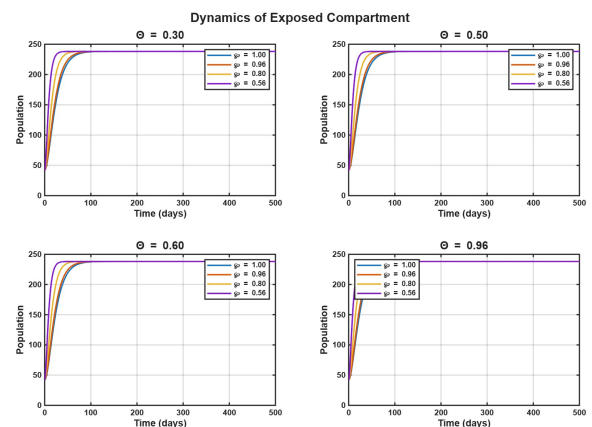


Figure 4 Temporal evolution of the infected population under the fractal-fractional Caputo-Fabrizio framework. Each subplot corresponds to a fixed value of Θ , whereas different fractional orders φ are used to study their influence on infection dynamics

Figure 4 shows the dynamics of infected population ($\hat{J}$). This compartment shows an epidemic curve. The population of infected individuals increases rapidly at the beginning due to spread of infection. It attains its highest level and finally decreases. The maximum is attained due to a decline in the susceptible population, which causes fewer new cases compared to the transition to the diagnosed treatment compartment ($\hat{B}$) or the recovery compartment

($\hat{C}$) at the rates ω and ψ respectively.

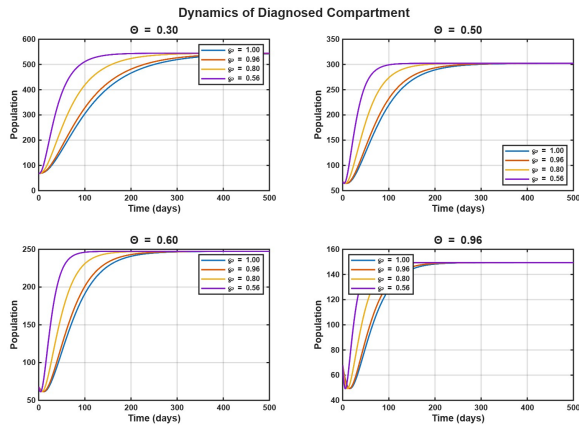


Figure 5 Time evolution of the diagnosed population in the proposed fractal–fractional model. The parameter Θ is held constant in each panel, while variations in the fractional order ϕ demonstrate the effect of memory on diagnosis progression

Figure 5 depicts the dynamics of the diagnosed treatment population ($\hat{B}$). The curve of this population takes on a bell-like shape similar to that of the exposed population. However, it is different in terms of timing and scale due to the factors affecting entry and exit. People move from the exposed population at the rate of $\omega\hat{J}$ and from the relapse population at the rate of $\sigma\hat{Q}$. Exit occurs at the rate of recovery ($\eta\hat{B}$), death due to terminal illness ($\tau\hat{B}$), or naturally.

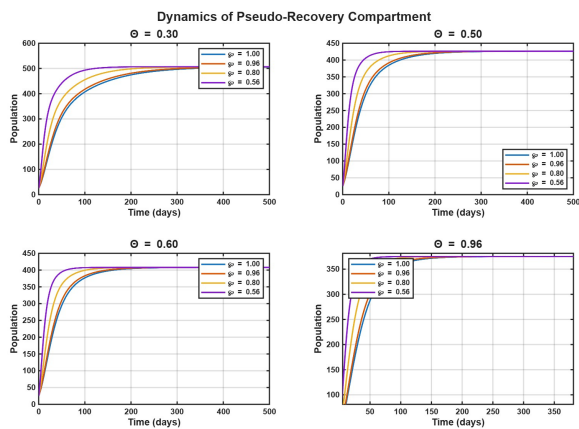


Figure 6 Evolution of the pseudo-recovered population under the fractal–fractional Caputo–Fabrizio formulation. The fractal parameter Θ is fixed for each subplot, and the fractional order ϕ is varied to capture hidden recovery dynamics influenced by memory effects

As shown in Figure 6, $\hat{C}$ represents the curve of recovery. This curve shows a monotonic increasing trend because it is cumulative, which means that people can recover only once. People get recovered from the susceptible compartment ($\omega\hat{G}$), from the exposed compartment ($\psi\hat{J}$), and from the treatment compartment ($\eta\hat{B}$). The growth is high at first, but it begins to slow down with time as people stop being infected. The behavior of the pseudo-recovered

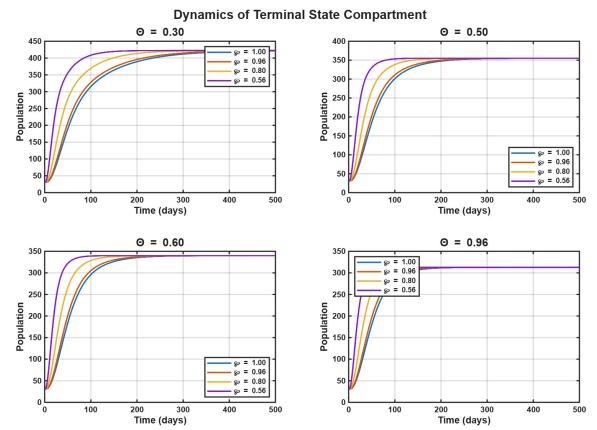


Figure 7 Dynamics of the terminally ill population in the fractal–fractional Caputo–Fabrizio model. The fractal parameter Θ is kept constant per panel, whereas the fractional order ϕ is varied to study long-term disease severity progression

population ($\hat{P}$), shown in Figure 7, is more complex. This group consists of individuals who appear clinically improved but are prone to relapse. These come from the recovered compartment, $\delta\hat{C}$. The $\hat{P}$ -curve increases with accumulating recoveries but subsequently decreases because individuals in this state either have a relapse - cycling back to $\hat{Q}$ at rate γ - or move into the terminal illness status ($\Pi\hat{P}$). This produces a hump-shaped curve which differs from the permanently recovered group. Figure 8 charts

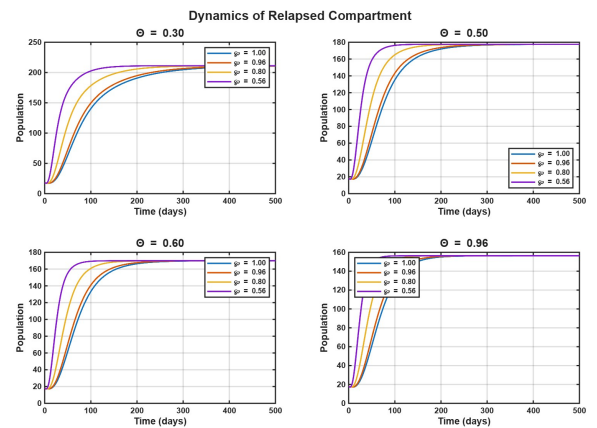


Figure 8 Temporal variation of the relapse population in the fractal–fractional epidemic system. Each subplot is generated for a fixed Θ , while different fractional orders ϕ illustrate the role of memory in reinfection or relapse behavior

the course of the relapse population ($\hat{Q}$). This compartment gets replenished from the pseudo-recovered compartment ($\gamma\hat{P}$), hence, its dynamics are connected with those of $\hat{P}$. The relapse compartment has its peak after $\hat{P}$, that is when secondary infections start to occur because people do not have a lasting immunity. People move out of the relapse compartment into the treatment compartment ($\sigma\hat{Q}$), into the terminal compartment ($\xi\hat{Q}$), and into natural death. The most depressing trajectory corresponds to the terminal population ($\hat{A}$), shown in Figure 9, which develops cumulatively from the treated ($\tau\hat{B}$), pseudo-recovered ($\Pi\hat{P}$), and relapse ($\xi\hat{Q}$)

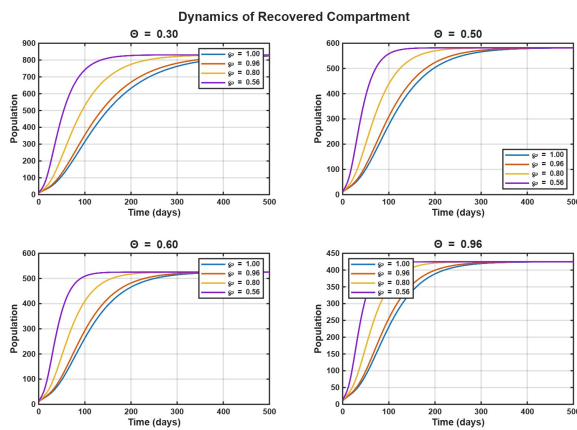


Figure 9 Growth pattern of the recovered population in the fractal–fractional epidemic model. Each panel corresponds to a specific Θ value, while different φ values highlight the influence of memory effects on recovery dynamics

groups. The S-shape trajectory of this population rises slowly at first and fast towards the epidemic peak, then slows down once more before reaching its maximum value, reflecting the mortality toll of the entire epidemic period.

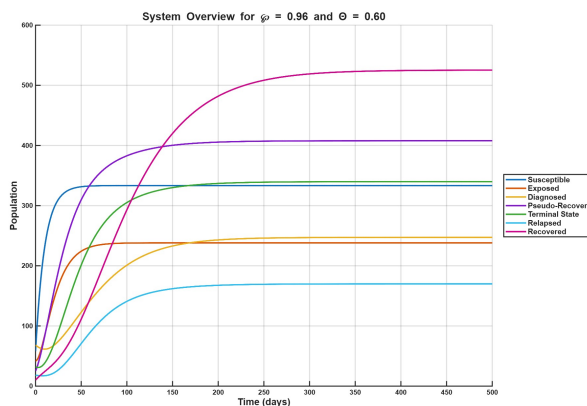


Figure 10 Overall compartmental disease dynamics in the proposed fractal–fractional Caputo–Fabrizio epidemic model. The figure illustrates the simultaneous temporal evolution of all epidemiological compartments under fractional orders $\varphi=0.96$ and fractal parameter $\Theta=0.6$

Lastly, Figure 10 describes the dynamics of a *Streptococcus pyogenes* epidemic over 500 days based on the FFCF model for an epidemic with order $\varphi = 0.96$ and fractal dimension $\Theta = 0.60$, considering seven populations: Susceptible, Exposed, Diagnosed, Pseudo-Recovery, Terminal, Relapse, and Recovery populations. Due to the memory property of the fractional-order derivatives, there is some delay in the peak times, resulting in more realistic dynamics about the true epidemic pattern than the integer-order ones.

In conclusion, the simulation numerically captures the intricate relationship between the seven compartments within the *S. pyogenes* model. It accurately depicts the initial exponential growth, the peak of the outbreak, and finally the descent towards the

endemic equilibrium state. The addition of compartments like pseudo-recovery and relapse gives the model a bit of realism, illustrating how partial immunity may result in multiple infection waves. This initial understanding was achieved using the Adams-Bashforth technique and is a crucial point of departure for future research, considering the inclusion of memory and hereditary effects of the FFCF operator on the model's dynamics.

CONCLUSION

This paper proposes a new fractal-fractional model for studying the dynamics of *Streptococcus pyogenes* spread using the Caputo-Fabrizio derivative. The proposed model surpasses conventional models due to its consideration of memory and hereditary phenomena, which makes the mathematical model more accurate and closer to reality. In theory, the existence and uniqueness of the problem's solution were proven. Therefore, the system's mathematical properties are well-grounded and credible. The derivation of the disease-free equilibrium, endemic equilibrium, and basic reproduction number R_0 enabled a comprehensive assessment of the disease transmission dynamics and its potential persistence in the population. Additionally, the stability of Ulam-Hyers was investigated using some assumptions.

On the numerical side, the modified Adams-Bashforth method was successfully used to address the complexities of the fractal-fractional scheme. Stable results were obtained through convergence between the simulation and real-life data from epidemiology. Simulations have revealed a strong dependence of the epidemic course on the value of the fractional parameter, resulting in delayed peak infection, longer infection period, and overall reduced intensity. The fitted fractional-order and fractal parameters provide meaningful epidemiological insights into the transmission dynamics of invasive Group A Streptococcal (iGAS) infections. The fractional-order parameter reflects the memory effect of the disease, indicating that the current transmission dynamics are influenced by previous infection states rather than depending solely on the present conditions. Likewise, the fractal parameter captures the heterogeneous nature of disease transmission by accounting for the irregular contact structure within the population. These findings suggest that incorporating memory and fractal effects enables the proposed model to represent real-world epidemic behaviour more realistically.

The results further indicate that timely diagnosis, effective treatment, continuous patient monitoring, and sustained public health interventions are essential for reducing disease transmission and improving recovery outcomes. The significance of applying fractal-fractional dynamics to epidemiological modeling is highlighted by this study. In addition to theoretical implications, it may assist in developing a control strategy to ease the burden of the healthcare system. Further research in this area can consider vaccinations and optimal control policies, among others, ensuring its applicability for epidemiological modeling.

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Availability of data and material

Not applicable.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The authors have no financial or non-financial interests to disclose.

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From Immune-Cold to Immune-Hot Tumors: A Fractional Immunomodulation Framework with Topological Signatures

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ABSTRACT Converting immune-cold tumors into immune-hot tumors is a major objective of cancer immunotherapy. Cold tumors typically exhibit limited T-cell infiltration, weak inflammatory activity, strong local immunosuppression, hypoxia or stromal exclusion, and poor therapeutic responsiveness. We propose a fractional-order immunomodulation model that couples tumor burden, effector immune activity, suppressive immune burden, pro-inflammatory signaling, and hypoxia/stromal exclusion through memory-dependent differential equations. The fractional formulation represents persistent inflammation, immune exhaustion, hypoxia, and treatment history. State-space trajectories are additionally analyzed using persistent homology, including persistence diagrams, barcode plots, and sliding-window topological summaries. The framework identifies threshold-like conditions for immune activation, memory-dependent delays in tumor conversion, and structural signatures of successful tumor-microenvironment reprogramming. Numerical experiments indicate that immune activation alone may be insufficient when suppressive and hypoxic barriers remain dominant, whereas coordinated combination therapy can produce a sustained transition toward an immune-hot regime. The results support interpreting cold-to-hot conversion not only as increased immune activity but also as a reorganization of the tumor-immune dynamical system. This integrated fractional and topological framework offers a mechanistic basis for studying immunomodulation and combination antitumor strategies.

KEYWORDS

Tumor microenvironment
Cold-to-hot transition
Fractional dynamics
Persistent homology
Topological signatures
Cancer immunotherapy

INTRODUCTION

While immunotherapy has had a significant impact on cancer treatment, there is still considerable heterogeneity in the response to these treatment options. One of the most influential theories regarding cancer immunotherapy is the notion of the difference between hot and cold tumors. Hot tumors are those that have strong immune infiltrates and activity within the tumor, while cold tumors have little T-cell infiltration and are generally not responsive to immunotherapy treatments (Kong *et al.* 2025; Liu *et al.* 2025a).

This difference is closely related to the nature of the tumor microenvironment (TME) that comprises the tumor itself and the stromal and immune components that interact with the tumor to influence its progression (Xie *et al.* 2025). The interaction of immune and stromal cells within the TME influences whether

that tumor is immune-silent or immune-responsive to treatments (Kong *et al.* 2025; Xie *et al.* 2025). Reviews of the TME reveal that immune cells that suppress immune responses to the tumor, dysfunctional antigen presentation, the effects of cytokines, and stromal components that prevent immune cells from effectively attacking the tumor all contribute to the maintenance of the cold tumor phenotype (Kong *et al.* 2025; Xie *et al.* 2025).

Another of the major obstacles that is present within cold tumors is the immunosuppressive milieu that is present within the tumor. T-cell exhaustion is one of the main features of the tumor microenvironment, as the repeated exposure to tumor antigens leads to the exhaustion of those T cells (Wu *et al.* 2026). Additionally, other suppressive cell populations (regulatory T cells, M2 macrophages, myeloid-derived suppressor cells) tend to suppress any immune response against the tumors as well (Wu *et al.* 2026). Thus, the poor response to therapy that is exhibited by cold tumors is not the result of the patients' low levels of immunity, but due to the immunosuppression that exists within those tumors (Kong *et al.* 2025; Wu *et al.* 2026).

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One of the important mechanisms contributing to the stability of the suppressive tumor microenvironment is hypoxia. Hypoxia is a common feature of solid tumors and is associated with aggressive behavior of the tumors (Liu *et al.* 2025a). The literature reveals that hypoxic regions of tumors impair infiltration of immune cells and reduce the function of antitumor immune cells (Liu *et al.* 2025a; Wu *et al.* 2026). Consequently, targeting hypoxia is one of the strategies that has been discussed in the literature as a means to convert cold tumors to hot tumors (Kong *et al.* 2025; Liu *et al.* 2025a).

These findings have contributed to the growing interest in the concept of cold-to-hot tumor conversion as a goal of immunotherapy. Such interest has led to discussions of the various types of immunomodulation that may be required to achieve such a conversion, such as enhancing immune activation, removing suppressive cells from the TME, and reprogramming the TME to favor immune system recognition of tumor cells (Kong *et al.* 2025; Park *et al.* 2026). In other words, cold-to-hot conversion suggests that the tumor microenvironment must be manipulated in some way to enhance T cell recognition of the tumor (Kong *et al.* 2025; Park *et al.* 2026).

Mathematically, the system-level characteristics of tumor-immune interactions suggest that they are inherently dynamic and dependent upon the history of those interactions. While integer-order models have been established as a means of describing tumor-immune system interactions, they often have limitations in modeling scenarios that include the time-dimension of certain aspects of the immune system's dysfunction (Qayyum *et al.* 2025). More recently, fractional-order models have been suggested as alternatives to integer-order models for tumors and immune systems (Qayyum *et al.* 2025). These fractional-order models have published research showing their ability to model the interactions between tumor cells, immune cells, and therapy (Qayyum *et al.* 2025; Joshi and Yavuz 2026).

Beyond these developments, it becomes apparent that plotting the tumor burden or the number of each type of immune cell within the tumor does not allow scientists to understand the changes in the structure of the tumor-immune dynamical system in response to different therapies. Methods like **topological data analysis (TDA)** and **persistent homology** have been employed to analyze higher-order structures within complex data sets. TDA has already been utilized in relation to cancer to analyze the tumor microenvironment and the interactions between the tumor and immune cells within that microenvironment (Yang *et al.* 2025; Vipond *et al.* 2021). Thus, using topological analyses of these systems suggests another means of detecting the changes in immune system regulation that may not be immediately apparent from analyzing the system in traditional manners (Yang *et al.* 2025; Vipond *et al.* 2021).

Motivated by these biological and mathematical developments, we propose a fractional immunomodulation model to describe the cold-to-hot transition, and employ persistent homology to analyze the model's dynamical systems. The model considers the relationship between tumor burden, effector immune activity, suppressive immune burden, pro-inflammatory signaling, and hypoxia/stromal exclusion. In this study, we hypothesize that the cold-to-hot transition can be interpreted not only as an increase in immune activity within the tumor, but also as a structural reorganization of the tumor-immune dynamical system.

Accordingly, the study has four main aims. The first aim is to formulate a fractional-order model for the key components of the TME. The second aim is to define the regimes of cold, transitional, and hot tumors. The third aim is to use persistent homology to identify the topological differences between these regimes. Finally,

the fourth aim is to investigate the impact of memory effects on the success of therapy to change the tumor regime. Thus, the study aims to contribute to the mathematical understanding of antitumor strategies within the TME (Kong *et al.* 2025; Qayyum *et al.* 2025; Yang *et al.* 2025).

BIOLOGICAL MOTIVATION AND CONCEPTUAL FRAMEWORK

The components of the TME that have been discussed in the current literature include tumor load, effector activity, suppressive burden, inflammation, and hypoxia (Kong *et al.* 2025; Liu *et al.* 2025a; Wu *et al.* 2026; Hu *et al.* 2025). Each of these components of the TME is often imbalanced in cold tumors. For instance, cold tumors often exhibit low levels of cytotoxic effector T-cell infiltration, weak inflammatory signaling, high levels of suppressive immune cells, and functionally impaired or exhausted T cells due to hypoxic and exclusionary conditions within the TME (Kong *et al.* 2025; Liu *et al.* 2025a; Hu *et al.* 2025). The components of the TME that contribute to the dysfunction of effector T cells, particularly CD8⁺ T cells, have been documented in the literature in particular (Liu *et al.* 2025a; Wu *et al.* 2026).

Thus, we model the TME as a competition between activation and suppression. Instead of modeling each of the different cell types in the TME separately, we group the variables into three main groups: an effector T cell variable models the cytotoxic anti-tumor activity of the TME, a suppressive T cell variable models the activity of Tregs, MDSCs and M2-like cells, and a pro-inflammatory activation variable measures the presence of interferon-like activity in the TME (Kong *et al.* 2025; Hu *et al.* 2025). Finally, a separate variable that models hypoxia and the stromal layer of the tumor is included in the model, as well, due to the fact that several recent reviews have discussed the role of exclusion, coldness, and hypoxia in contributing to the cold phenotype of tumors (Kong *et al.* 2025; Liu *et al.* 2025a).

The transition from cold to hot tumors can also be interpreted in terms of system-level concepts. In the cold tumors, the suppressive influence on the immune system is strong relative to the infiltration of immune system cells into the tumor. In hot tumors, the balance is reversed such that the effector cells and inflammatory influences dominate, and the suppressive influence of the tumor is weaker. Intermediate to these two extremes is a transitional regime in which the treatment has had some effect upon reprogramming the tumor system, but without establishing immune system dominance. Thus, this three-regime model of the system is in accord with current thinking regarding cancer treatment (Kong *et al.* 2025; Liu *et al.* 2025b).

The need for a fractional formulation of these models emerges due to the history-dependent nature of these biological processes. Features such as T-cell dysfunction, hypoxia-induced rewiring, suppressive remodeling of tumor microenvironments, and the effectiveness of therapy all exhibit dependencies upon time (Liu *et al.* 2025a; Wu *et al.* 2026). Therefore, a model that incorporates the idea of memory is more appropriate than a Markovian model to describe these biological processes. This type of model has been used in predicting cancer treatment outcomes in recent studies (Qayyum *et al.* 2025; Gündoğdu and Joshi 2025).

In the present model, hypoxia and stromal exclusion are grouped within the same variable because both mechanisms reduce effective immune infiltration and weaken antitumor activity within the TME. Hypoxia contributes to metabolic and functional impairment of effector immune cells, whereas stromal exclusion acts as a physical and structural barrier that limits their access to

tumor cells. Although biologically distinct, both processes contribute to maintenance of the immune-cold phenotype and are therefore represented here as a combined exclusionary burden.

MODEL FORMULATION

In order to describe the cold-to-hot tumor transition in the TME, a fractional-order dynamical system is proposed to describe the competition between the tumor-promoting and tumor-suppressive processes. Five state variables are utilized to describe the system: each of these variables can represent the tumor burden, the effector immune activity, the suppressive immune burden, the pro-inflammatory activation, and the hypoxia/stromal exclusion within the TME. These variables were chosen based upon current studies in the field that suggest that immune activation is only one component of the TME that must be considered in order to successfully engineer an effective cancer immunotherapy strategy (Kong et al. 2025; Liu et al. 2025a,b).

State Variables

Let $T(t) \geq 0$, $E(t) \geq 0$, $S(t) \geq 0$, $I(t) \geq 0$, $H(t) \geq 0$ denote, respectively,

- $T(t)$: tumor burden,
- $E(t)$: effector immune activity,
- $S(t)$: suppressive immune burden,
- $I(t)$: pro-inflammatory immune activation,
- $H(t)$: hypoxia/stromal exclusion level.

Here, the effector compartment $E(t)$ represents the overall cytotoxic antitumor activity, mainly associated with CD8⁺ T-cell-mediated responses. The suppressive compartment $S(t)$ aggregates the inhibitory influence of regulatory T cells, myeloid-derived suppressor cells, and M2-like macrophage activity. The variable $I(t)$ represents pro-inflammatory stimulation, such as interferon-associated immune activation, while $H(t)$ summarizes the inhibitory influence of hypoxia and stromal exclusion, both of which are strongly linked to cold tumor phenotypes (Liu et al. 2025a,b).

Fractional-Order System

Since TME remodeling, immune exhaustion, and treatment response are history-dependent processes, we employ a fractional temporal operator of order $0 < \alpha \leq 1$. The system is formulated as follows:

$$D_t^\alpha T = rT \left(1 - \frac{T}{K}\right) - \kappa_E ET + \kappa_S ST + \kappa_H HT, \quad (1)$$

$$D_t^\alpha E = \eta_T \frac{T}{T + \theta_T} + \eta_I I - \mu_E E - \sigma_S SE - \sigma_H HE + u_E(t), \quad (2)$$

$$D_t^\alpha S = \rho_T \frac{T}{T + \theta_S} + \rho_H H - \mu_S S - \rho_I IS - u_S(t), \quad (3)$$

$$D_t^\alpha I = \lambda_E E - \mu_I I - \lambda_S SI + u_I(t), \quad (4)$$

$$D_t^\alpha H = \omega_T \frac{T}{T + \theta_H} - \mu_H H - u_H(t). \quad (5)$$

In the present study, D_t^α denotes the **Caputo fractional derivative**, defined by

$$D_t^\alpha x(t) = \frac{1}{\Gamma(1-\alpha)} \int_0^t \frac{x'(\tau)}{(t-\tau)^\alpha} d\tau, \quad 0 < \alpha < 1. \quad (6)$$

The Caputo formulation is adopted because it naturally accommodates classical initial conditions and is widely used in biological and cancer-related fractional models (Qayyum et al. 2025; Gündogdu and Joshi 2025).

Figure 1 illustrates the main state variables of the system, including tumor burden $T(t)$, effector immune activity $E(t)$, suppressive immune burden $S(t)$, pro-inflammatory activation $I(t)$, and hypoxia/stromal exclusion $H(t)$, together with their principal interactions and therapeutic control inputs. The diagram provides a conceptual summary of the coupled mechanisms represented in the governing differential equations.

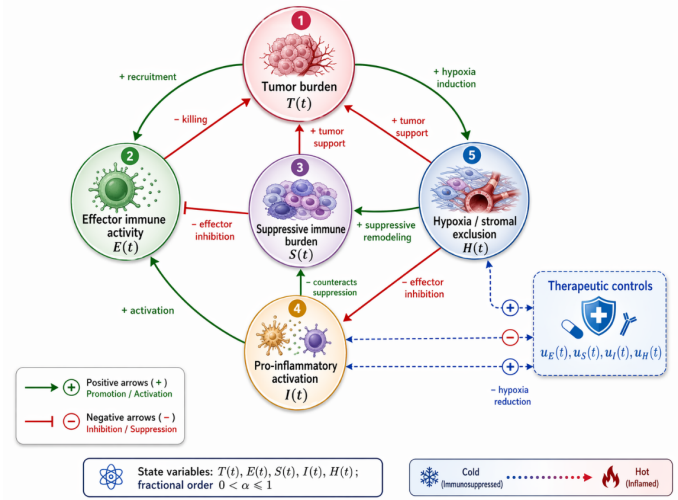


Figure 1 Schematic diagram of the proposed tumor-immune microenvironment model showing tumor burden, effector immunity, suppressive burden, inflammatory activation, hypoxia/stromal exclusion, and therapy controls

Biological Interpretation of the Equations

Tumor burden equation: Equation (1) describes the evolution of tumor burden. The term

$$rT \left(1 - \frac{T}{K}\right)$$

represents logistic tumor growth, where r is the intrinsic growth rate and K is the carrying capacity. The term

$$-\kappa_E ET$$

accounts for tumor elimination mediated by effector immunity. In contrast, the terms

$$+\kappa_S ST \quad \text{and} \quad +\kappa_H HT$$

describe tumor support induced by suppressive immune burden and hypoxia/stromal protection, respectively. Together, these terms reflect the fact that tumor progression is shaped by the balance between immune surveillance and microenvironmental support (Kong et al. 2025; Liu et al. 2025b).

Effector immune equation: Equation (2) models the dynamics of effector immune activity. The term

$$\eta_T \frac{T}{T + \theta_T}$$

represents tumor-induced immune recruitment at a saturating rate, while

$$\eta_I I$$

captures amplification by pro-inflammatory signaling. Effector activity decays naturally at rate μ_E , and is inhibited by suppressive burden and hypoxia through

$$-\sigma_S SE \quad \text{and} \quad -\sigma_H HE.$$

The control function $u_E(t)$ represents therapeutic interventions that directly enhance effector immunity.

Suppressive immune equation: Equation (3) describes the development of suppressive immune burden. Tumor presence and hypoxia both promote suppression through

$$\rho_T \frac{T}{T + \theta_S} \quad \text{and} \quad \rho_H H,$$

whereas natural decay is represented by $-\mu_S S$. The interaction term

$$-\rho_I IS$$

indicates that pro-inflammatory activation can counteract suppressive dominance. The control $u_S(t)$ models therapeutic reduction or reprogramming of suppressive immune components.

Pro-inflammatory activation equation: Equation (4) governs pro-inflammatory signaling. Effector cells stimulate inflammatory activity through

$$\lambda_E E,$$

while natural loss occurs at rate μ_I . Suppressive immune burden reduces inflammatory signaling via

$$-\lambda_S SI.$$

The control $u_I(t)$ represents treatments that increase immune stimulation.

Hypoxia/stromal exclusion equation: Equation (5) models the inhibitory barrier generated by tumor-associated hypoxia and stromal exclusion. The production term

$$\omega_T \frac{T}{T + \theta_H}$$

reflects the fact that growing tumors tend to generate increasingly hostile and poorly infiltrated environments. Natural resolution is described by $-\mu_H H$, while $u_H(t)$ represents therapies aimed at reducing hypoxia or stromal exclusion. This component is especially relevant because hypoxia is increasingly recognized as a key mechanism maintaining cold tumors and limiting immunotherapy response (Liu et al. 2025a,b).

Initial Conditions

The system is supplemented with the initial conditions

$$T(0) = T_0, \quad E(0) = E_0, \quad S(0) = S_0, \quad I(0) = I_0, \quad H(0) = H_0, \quad (7)$$

where all initial values are assumed to be nonnegative.

These variables represent the baseline levels of tumor burden, effector immune activity, suppressive immune burden, pro-inflammatory activation, and hypoxia or stromal exclusion, respectively. The initial state of these variables is selected to represent a cold tumor; that is, it has high levels of tumor burden, suppressive immune burden, and hypoxia, yet it has low levels of effector immune activity and pro-inflammatory activation.

Thus, the initial configuration is taken to satisfy the qualitative profile

$$T_0 \text{ high}, \quad S_0 \text{ high}, \quad H_0 \text{ high},$$

$$E_0 \text{ low}, \quad I_0 \text{ low}.$$

This construction allows the model to begin from an immunologically suppressed regime and then examine whether therapeutic intervention and memory effects can induce a transition toward a hot, immune-responsive state.

Biological Justification of Initial Conditions: The initial conditions that were chosen for this study were those that represent a relatively cold tumor: high tumor burden, suppressive immune activity, hypoxia, low effector immune activity, and low inflammation. Each of these choices reflect the general biological features of the tumors that are known to be cold, such as low levels of cytotoxic immune cells and high levels of suppressive activity of the tumor microenvironment.

Since the study presented in this paper is conceptual and mechanistic in nature, rather than involving the fitting of initial conditions to experimental data, such initial conditions were chosen in the context of this study as the baseline conditions for the simulations performed in this paper. The selection of such initial conditions is a common practice within theoretical modeling of tumor-immune system dynamics, and is typically performed to ensure that the conditions lead to biologically-interpretable, positive model solutions, stability of the model, and the ability to separately consider the dynamics of either cold or hot tumors.

Accordingly, this specific initialization of the models is only one example of the many possible cold-start states of the TME. Future models may even derive these initial conditions from measurements of relevant tumor and immune system characteristics from the relevant literature. For instance, initial conditions may be based upon literature-reported values for CD8 infiltration scores, suppressive burden signatures, inflammatory activation scores, and hypoxia-associated markers of tumors.

Baseline Numerical Initial Conditions: For the baseline cold-tumor simulations, the following normalized initial values are used:

$$T_0 = 0.70, E_0 = 0.15, S_0 = 0.60, I_0 = 0.20, H_0 = 0.55.$$

These values were selected to reflect a tumor-dominant and immunologically suppressed initial configuration. In particular, the tumor burden T_0 , suppressive burden S_0 , and hypoxia/stromal exclusion level H_0 are taken to be relatively high, while the effector immune activity E_0 and pro-inflammatory activation I_0 are taken

to be relatively low. Because the model is formulated in normalized form, these values should be interpreted as dimensionless baseline intensities rather than as direct physical measurements. The baseline numerical initialization used in the present study is summarized in Table 1. These normalized values represent a tumor-dominant and immunologically suppressed starting configuration, consistent with the biological profile of an immune-cold tumor.

Table 1 Baseline normalized initial conditions for the cold-tumor state

Variable	Meaning	Baseline value
T_0	Tumor burden	0.70
E_0	Effector immune activity	0.15
S_0	Suppressive immune burden	0.60
I_0	Pro-inflammatory activation	0.20
H_0	Hypoxia/stromal exclusion	0.55

Note: All variables are normalized and dimensionless. The baseline configuration represents an immunologically cold tumor state selected to be biologically plausible in relative terms, rather than directly calibrated from patient-specific measurements.

Biological Interpretation of Baseline Numerical Values: Although the baseline initial conditions used in this study are not directly fitted to patient-specific experimental datasets, they were selected to reflect biologically plausible relative states of an immune-cold tumor microenvironment. In particular, the normalized values were chosen such that tumor burden, suppressive immune burden, and hypoxia/stromal exclusion are initially elevated, while effector immune activity and pro-inflammatory activation remain comparatively low. This choice is consistent with the widely reported biological characteristics of cold tumors, including weak cytotoxic infiltration, dominant suppressive signaling, and exclusionary or hypoxic microenvironmental conditions.

Accordingly, the numerical initialization adopted here should be interpreted as a normalized mechanistic baseline rather than a direct histopathological measurement. The purpose of this choice is to provide a biologically meaningful starting configuration for illustrating regime transition under fractional dynamics and immunomodulatory intervention. Future studies may refine these baseline values using quantitative biomarker-based calibration, such as CD8 infiltration scores, suppressive burden markers, inflammatory activation indices, and hypoxia-associated signatures reported in the literature.

Model Parameters

The parameters in the model have the following biological meanings:

- r : intrinsic tumor growth rate,
- K : tumor carrying capacity,
- κ_E : tumor killing efficiency of effector immunity,
- κ_S : tumor-promoting effect of suppressive burden,
- κ_H : tumor-promoting effect of hypoxia/stromal exclusion,
- η_T : tumor-driven recruitment of effector immunity,
- η_I : enhancement of effector immunity by inflammatory activation,
- μ_E : natural decay rate of effector immunity,
- σ_S : suppressive inhibition of effectors,

- σ_H : hypoxia-induced inhibition of effectors,
- ρ_T : tumor-driven generation of suppressive burden,
- ρ_H : hypoxia-driven generation of suppressive burden,
- μ_S : natural decay rate of suppressive burden,
- ρ_I : inflammatory suppression of inhibitory burden,
- λ_E : induction of inflammatory activation by effectors,
- μ_I : natural decay rate of inflammatory activation,
- λ_S : suppression of inflammatory activation by suppressive cells,
- ω_T : tumor-driven generation of hypoxia/exclusion,
- μ_H : natural decay rate of hypoxia/exclusion.
- θ_T : half-saturation constant for tumor-induced effector recruitment,
- θ_S : half-saturation constant for tumor-induced suppressive burden,
- θ_H : half-saturation constant for tumor-induced hypoxia/stromal exclusion

All parameters are assumed to be nonnegative. Their values may be selected from biologically plausible normalized ranges for numerical experiments. The baseline parameter values used in the numerical experiments are listed in Table 2. These parameters were selected as normalized and biologically plausible values in order to represent the main interactions among tumor burden, immune activity, suppressive burden, inflammatory signaling, and hypoxia/stromal exclusion within the proposed framework.

The baseline parameter set used in the present study is summarized in Table 2. These values were selected as normalized, biologically plausible coefficients that reproduce the expected qualitative interactions within an immune-cold tumor microenvironment, including tumor persistence, suppressive burden dominance, reduced effector activity, and delayed immune recovery. They should therefore be interpreted as mechanistically motivated baseline parameters for theoretical simulation rather than as uniquely identified clinical estimates.

Therapeutic Controls

The model includes four control functions,

$$u_E(t), \quad u_S(t), \quad u_I(t), \quad u_H(t),$$

which represent different immunomodulatory strategies:

- $u_E(t)$: direct enhancement of effector immunity,
- $u_S(t)$: suppression or reprogramming of inhibitory immune burden,
- $u_I(t)$: promotion of pro-inflammatory immune signaling,
- $u_H(t)$: reduction of hypoxia/stromal exclusion.

This structure allows the model to examine not only monotherapy scenarios, but also combination therapies, which are widely considered necessary for successful cold-to-hot conversion (Kong et al. 2025; Liu et al. 2025b).

Modeling Rationale

The proposed system includes the essential features that determine the cold-to-hot transition. The system employs a limited number of variables to represent the essential features of the cold-to-hot transition. The competition between activation and suppression of the immune system is captured by the proposed system. The use of fractional calculus allows the system to incorporate the memory of the tumor and immune system, which is essential for phenomena like chronic immune dysfunction and therapy response (Qayyum et al. 2025; Gündogdu and Joshi 2025). Thus, the proposed system

■ **Table 2** Baseline model parameters

Parameter	Biological meaning	Baseline value
r	Intrinsic tumor growth rate	0.42
K	Normalized tumor carrying capacity	1.00
κ_E	Effector-mediated tumor killing efficiency	0.75
κ_S	Tumor-promoting effect of suppressive burden	0.28
κ_H	Tumor-promoting effect of hypoxia/stromal exclusion	0.22
η_T	Tumor-driven recruitment of effector immunity	0.34
θ_T	Half-saturation constant for tumor-induced effector recruitment	0.35
η_I	Inflammatory enhancement of effector activity	0.48
μ_E	Natural decay rate of effector activity	0.18
σ_S	Suppressive inhibition of effector activity	0.36
σ_H	Hypoxia-induced inhibition of effector activity	0.31
ρ_T	Tumor-driven generation of suppressive burden	0.40
θ_S	Half-saturation constant for tumor-induced suppressive burden	0.30
ρ_H	Hypoxia-driven generation of suppressive burden	0.33
μ_S	Natural decay rate of suppressive burden	0.20
ρ_I	Inflammatory reduction of suppressive burden	0.30
λ_E	Effector-induced inflammatory activation	0.45
μ_I	Natural decay rate of inflammatory activation	0.22
λ_S	Suppressive inhibition of inflammatory activation	0.27
ω_T	Tumor-driven hypoxia/stromal exclusion generation	0.38
θ_H	Half-saturation constant for tumor-induced hypoxia/stromal exclusion	0.30
μ_H	Natural resolution of hypoxia/stromal exclusion	0.16

Note: All values are dimensionless and normalized for theoretical simulation purposes. The parameter set is biologically motivated and chosen to reflect the expected qualitative interactions of an immune-cold tumor microenvironment, but it is not intended to represent direct patient-level calibration.

way that is mathematically tractable for investigating the effect of immunomodulation on the transition of tumors from cold to hot states.

Numerical Solution via ABM-PECE Scheme

To solve the fractional system numerically, we employ the **Adams–Bashforth–Moulton predictor–corrector PECE scheme** (Predict–Evaluate–Correct–Evaluate), one of the standard numerical approaches for Caputo-type fractional differential equations. This method is especially suitable here because the Caputo derivative introduces a memory integral, meaning that the state at each new time step depends on the entire previous history of the solution.

Let the time interval $[0, T_f]$ be discretized as

$$t_n = nh, \quad n = 0, 1, 2, \dots, N,$$

where $h = T_f/N$ is the time step. Define the state vector

$$X(t) = \begin{pmatrix} T(t) \\ E(t) \\ S(t) \\ I(t) \\ H(t) \end{pmatrix}, \quad X(0) = \begin{pmatrix} T_0 \\ E_0 \\ S_0 \\ I_0 \\ H_0 \end{pmatrix},$$

and let the right-hand side of the system be denoted compactly by

$$D_t^\alpha X(t) = F(t, X(t)). \quad (8)$$

Using the equivalent Volterra integral formulation of the Caputo problem, the predictor step is written as

$$X_{n+1}^P = X_0 + \frac{1}{\Gamma(\alpha)} \sum_{j=0}^n b_{j,n+1} F(t_j, X_j), \quad (9)$$

where

$$b_{j,n+1} = \frac{h^\alpha}{\alpha} [(n+1-j)^\alpha - (n-j)^\alpha]. \quad (10)$$

The predicted value X_{n+1}^P is then used in the corrector step,

$$X_{n+1} = X_0 + \frac{h^\alpha}{\Gamma(\alpha+2)} \left[F(t_{n+1}, X_{n+1}^P) + \sum_{j=0}^n a_{j,n+1} F(t_j, X_j) \right], \quad (10)$$

where the coefficients $a_{j,n+1}$ are the fractional Adams–Moulton weights. In practical implementation, this procedure is repeated sequentially for all time nodes until the final simulation time is reached.

For the present model, the ABM-PECE scheme is applied componentwise to the five-dimensional system (T, E, S, I, H) . At each time step, the method produces numerical approximations for tumor burden, effector immunity, suppressive burden, inflammatory activation, and hypoxia/stromal exclusion. Because of the memory structure, all previous states contribute to the computation of the next state, making the scheme particularly well suited for representing delayed immune remodeling and history-dependent therapeutic effects.

The computational pipeline used in this study may therefore be summarized as follows:

- choose a normalized cold-tumor initial condition;

captures the essential features of the cold-to-hot transition in a

- fix the parameter set and the fractional order $0 < \alpha \leq 1$;
- solve the system by the ABM-PECE predictor–corrector algorithm;
- obtain the trajectories $T(t), E(t), S(t), I(t), H(t)$;
- use these trajectories for regime classification and subsequent topological analysis.

This numerical strategy is consistent with established approaches in the fractional differential equations literature and with recent fractional cancer modeling studies (Gündogdu and Joshi 2025; Diethelm *et al.* 2002, 2004).

For numerical implementation, the simulations were performed on a uniform time grid over the interval $[0, 100]$ with step size $h = 0.1$. In the baseline experiments reported in this study, these values were selected so as to provide stable and visually resolved trajectories for all state variables. The ABM-PECE predictor–corrector scheme was implemented componentwise for the five-dimensional state vector, and the same discretization settings were used consistently across untreated, monotherapy, and combination-therapy scenarios unless otherwise stated.

DEFINITION OF COLD, TRANSITIONAL, AND HOT REGIMES

To interpret model outputs clinically, we define a composite quantity called the **Hotness Index**:

$$Q(t) = w_E E(t) + w_I I(t) - w_S S(t) - w_H H(t) - w_T T(t), \quad (11)$$

where all weights are positive.

This index is not a universal biomarker for tumors; rather, it is introduced as a way of modeling the tumor microenvironment. Higher values for effectors and inflammatory cells will increase the $Q(t)$ value, while higher burdens for tumors, suppressive cells, and hypoxia will decrease that value. Thus, the index is a means of providing a summary value for whether the tumor is in a cold or hot state.

We classify the system as follows:

$$\begin{aligned} Q(t) < \Theta_c &\Rightarrow \text{cold,} \\ \Theta_c \leq Q(t) < \Theta_h &\Rightarrow \text{transitional,} \\ Q(t) \geq \Theta_h &\Rightarrow \text{hot.} \end{aligned}$$

This classification allows for the performance of numerical experiments using this model. Furthermore, the classification also reflects the current understanding of tumor biology regarding hot tumors in particular; hot tumors are not the result of a single variable of the tumor, but of the combination of variables related to immune infiltration, inflammation, the tumor burden, and barriers to immune system infiltration of the tumor. Thus, the Hotness Index can be used to classify the tumors according to these biological variables. The regime classification adopted in this study is summarized in Table 3. The corresponding threshold values for the Hotness Index are used as model-based interpretive cutoffs to distinguish cold, transitional, and hot tumor states within the numerical experiments.

The Hotness Index was introduced as a model-based composite indicator that summarizes the balance between tumor-promoting and tumor-suppressive influences within the TME. In the present framework, the weights w_E, w_I, w_S, w_H , and w_T were selected so

Table 3 Regime classification according to the Hotness Index

Regime	Hotness Index range	Biological interpretation
Cold tumor	$Q(t) < 0.40$	Low effector activity and inflammation with dominant tumor burden, suppressive burden, and hypoxia/stromal exclusion.
Transitional tumor	$0.40 \leq Q(t) < 0.65$	Partial immune activation and partial remodeling of the suppressive microenvironment.
Hot tumor	$Q(t) \geq 0.65$	Stronger effector and pro-inflammatory activity with reduced suppressive and hypoxic barriers.

Note: The threshold values Θ_c and Θ_h are model-based interpretive cutoffs rather than clinical diagnostic thresholds.

that effector immune activity and pro-inflammatory activation contribute positively to the index, whereas tumor burden, suppressive burden, and hypoxia/stromal exclusion contribute negatively. This sign structure is consistent with the biological interpretation of immune-hot versus immune-cold tumor states.

Because the present study is conceptual and mechanistic rather than clinically calibrated, the weights are not intended as patient-specific coefficients. Instead, they were chosen as normalized interpretable coefficients that preserve the expected biological ordering of the variables in the index. To evaluate the robustness of this construction, we additionally examined moderate perturbations of the weight coefficients and found that the qualitative regime classification remained stable provided that the positive contributions of $E(t)$ and $I(t)$ and the negative contributions of $T(t), S(t)$, and $H(t)$ were preserved.

Similarly, the thresholds Θ_c and Θ_h were selected as model-based interpretive cutoffs to distinguish cold, transitional, and hot tumor states. These thresholds are not proposed as universal clinical biomarkers; rather, they provide an internal classification rule for the present model. Their interpretation is consistent with the broader logic of clinically used composite immune scoring systems, in which higher effective immune activation corresponds to more inflamed and treatment-responsive tumor states. In this sense, the Hotness Index is intended as a mechanistic analog of immune-state scoring rather than as a direct clinical substitute.

MATHEMATICAL PROPERTIES

Positivity

Since the equations are built from nonnegative recruitment terms with linear or bilinear loss terms, the nonnegative orthant should be positively invariant under biologically reasonable parameters. This requirement is biologically relevant since negative tumor or immune levels do not have any interpretation.

A typical way to prove that a solution remains nonnegative is to assume that one of the state variables reaches zero for the first time and to prove that the fractional derivative of that state variable cannot take the solution into the negative region of that variable at that boundary. Thus, if the initial data of the problem is nonnegative, then the solution will remain nonnegative for all times after the initial time.

Boundedness

Boundedness can be studied by introducing a weighted Lyapunov-like combination of the form

$$L(t) = a_T T(t) + a_E E(t) + a_S S(t) + a_I I(t) + a_H H(t), \quad (12)$$

where $a_T, a_E, a_S, a_I, a_H > 0$.

By appropriately selecting these weights, the growth terms can be controlled by the dissipative terms outside some bounded set. In particular, the logistic saturation term in the tumor equation and the first order decay terms in the remaining equations ensure that the solution will eventually enter a bounded region of the phase space. Thus, the trajectories are contained within some compact set in the nonnegative phase space.

Equilibria

The system may admit several biologically meaningful equilibria:

- a **tumor-dominant cold equilibrium**, characterized by high T, S, H and low E, I ;
- an **intermediate coexistence equilibrium**, corresponding to partial immune engagement and partial suppressive control;
- an **immune-controlled hot equilibrium**, characterized by relatively low T , lower S, H , and stronger E, I .

The existence and stability of these equilibria depend on the balance among the terms representing immune activation, immune suppression, hypoxia, and controls imposed by therapy. From a biological perspective, these equilibria represent the major possibilities for the outcome of the tumor-immune system interaction.

Local Stability

Let

$$X(t) = (T(t), E(t), S(t), I(t), H(t))^T$$

and denote the right-hand side of the fractional system by

$$D_t^\alpha X(t) = F(X(t)).$$

Suppose that

$$X^* = (T^*, E^*, S^*, I^*, H^*)^T$$

is an equilibrium point of the system, that is,

$$F(X^*) = 0.$$

To study local stability, we linearize the system around X^* . Writing

$$X(t) = X^* + \xi(t),$$

where $\xi(t)$ is a small perturbation, the linearized fractional system becomes

$$D_t^\alpha \xi(t) = J(X^*) \xi(t),$$

where $J(X^*)$ is the Jacobian matrix evaluated at the equilibrium point.

For the present model, the Jacobian matrix is given by Evaluating this matrix at the equilibrium point X^* yields

$$J(X^*) = J(T^*, E^*, S^*, I^*, H^*).$$

Let $\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5$ denote the eigenvalues of $J(X^*)$. For a Caputo fractional-order system of order $0 < \alpha < 1$, the equilibrium

$$J(X) = \begin{pmatrix} r \left(1 - \frac{2T}{K}\right) - \kappa_E E + \kappa_S S + \kappa_H H & -\kappa_E T & \kappa_S T & 0 & \kappa_H T \\ \eta_T \frac{\theta_T}{(T+\theta_T)^2} & -\mu_E - \sigma_S S - \sigma_H H & -\sigma_S E & \eta_I & -\sigma_H E \\ \rho_T \frac{\theta_S}{(T+\theta_S)^2} & 0 & -\mu_S - \rho_I I & -\rho_I S & \rho_H \\ 0 & \lambda_E & -\lambda_S I & -\mu_I - \lambda_S S & 0 \\ \omega_T \frac{\theta_H}{(T+\theta_H)^2} & 0 & 0 & 0 & -\mu_H \end{pmatrix}.$$

X^* is locally asymptotically stable if all eigenvalues satisfy the Matignon condition

$$|\arg(\lambda_i)| > \frac{\alpha\pi}{2}, i = 1, 2, 3, 4, 5.$$

Therefore, the local stability of each biologically meaningful equilibrium may be assessed by computing the Jacobian matrix at that equilibrium and checking whether its eigenvalues lie outside the instability sector determined by the fractional order α . This shows explicitly that the memory parameter influences the stability region: as α varies, the admissible sector for stability changes, and hence an equilibrium that is stable for one fractional order may lose stability for another.

In the present framework, this criterion provides the analytical basis for distinguishing stable cold, transitional, or hot regimes near equilibrium configurations.

TOPOLOGICAL ANALYSIS OF THE COLD-TO-HOT TRANSITION

Beyond the classical dynamical analysis of the system are further topological analyses based on the concept of persistent homology. The idea is that a transition in state is not just a change in the scalar variables of the system, but also in the geometry of the system within its state space altogether. Thus, the concept of cold-to-hot conversion is not just in the change in amplitude of the tumor and immune system variables, but also in the change in the topology of the system altogether. The main steps of the topological analysis used in this study are summarized in Table 4. This pipeline describes how state-space trajectories are transformed into point clouds and subsequently analyzed through persistent homology, sliding-window topology, and the Topological Transition Score.

State-Space Point Cloud

Define the trajectory vector

$$x(t) = (T(t), E(t), S(t), I(t), H(t)) \in \mathbb{R}^5. \quad (14)$$

Sampling at times $t_1, \dots, t_N$ produces the point cloud

$$X = \{x(t_i)\}_{i=1}^N \subset \mathbb{R}^5. \quad (15)$$

Each therapy scenario yields a different point cloud and therefore a different state-space geometry.

Persistent Homology Construction

For the point cloud X , we construct a Vietoris–Rips filtration by varying a distance threshold ε . As ε increases, simplices are added and topological features appear and disappear. We focus particularly on:

- H_0 : connected components,
- H_1 : loops.

The output is summarized through persistence diagrams and barcode plots. Persistent features are interpreted as robust structural signatures rather than topological noise.

Table 4 Topological analysis pipeline

Step	Procedure	Output
State-space reconstruction	Construct point clouds from (T, E, S, I, H) trajectories	Five-dimensional trajectory cloud
Normalization	Scale each variable to avoid dominance by one compartment	Comparable geometric representation
Filtration	Apply Vietoris–Rips filtration over increasing radius values	Nested simplicial complexes
Persistent homology	Compute H_0 and H_1 features	Connected components and loops
Barcode/persistence diagram	Summarize birth–death intervals of topological features	Regime-specific topological signatures
Sliding-window analysis	Compute topology over overlapping time windows	Temporal evolution of structural reorganization
TTS calculation	Compute normalized topological distance between consecutive windows	Topological Transition Score

Interpretation of Regimes

In the **cold regime**, trajectories are expected to remain confined to a relatively compact and weakly structured region of state space, typically showing simple H_0 behavior and weak H_1 persistence.

In the **transitional regime**, therapy perturbs the system and may generate excursions, partial oscillations, or temporary circulation through competing attractor-like regions. This can produce richer H_1 structure and increased topological complexity.

In the **hot regime**, the system settles into a new organization associated with stronger immune control and lower suppressive burden. The topology may again simplify, but now around a distinct region of state space.

Figure 2 shows the results of applying the algorithm to the three different regimes of the tumor-immune dynamical system: cold, transitional, and hot tumors. As with the persistence diagrams, the barcode diagrams reveal the different types of topological changes that occur in each regime of the dynamical system.

Sliding-Window Topology

To detect temporal reorganization, we use overlapping windows

$$W_k = \{x(t_i) : t_i \in [\tau_k, \tau_k + \Delta]\}. \quad (13)$$

Persistent homology is computed separately on each W_k . This allows the topological signature of the system to be tracked over time, revealing when therapy pushes the system out of the cold regime and whether the new organization is stable.

Topological Transition Score

$$TTS(k) = \frac{EMD(D_k, D_{k-1})}{\max_j EMD(D_j, D_{j-1})}.$$

Here, D_k denotes the persistence diagram obtained from the k -th sliding window, and $EMD(D_k, D_{k-1})$ denotes the Earth Mover’s Distance between two consecutive persistence diagrams.

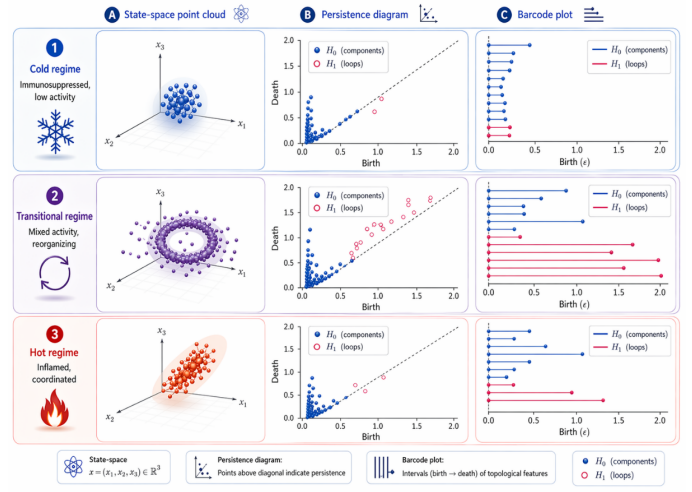


Figure 2 Persistence diagrams and barcode plots for representative state-space point clouds under different therapy scenarios

Larger values of $TTS(k)$ indicate stronger topological rearrangement between consecutive temporal windows.

A transient increase in the TTS indicates that the structure is experiencing a period of destabilization and reorganization within its structure, while the eventual reduction of the TTS to a new level indicates stabilization in a new structural regime. The TTS is not a parameter that is to be used as a replacement for the biological variables of interest; instead, it is a measure that indicates when changes in structural regimes are occurring within the structures being analyzed.

Figure 3 displays the temporal evolution of the Topological Transition Score (TTS), computed from sliding-window persistent homology analysis of the state-space trajectory. Transient increases in TTS indicate structural reorganization of the system, while subsequent stabilization suggests convergence toward a new dynamical regime.

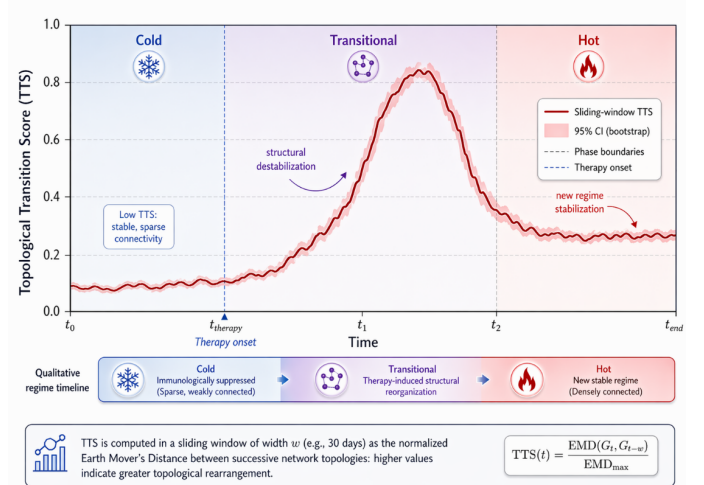


Figure 3 Sliding-window Topological Transition Score during therapy-induced cold-to-hot conversion

THERAPEUTIC CONTROLS AND SCENARIO DESIGN

A strength of the model is that it accommodates multiple types of immunomodulation through the controls u_E, u_S, u_I, u_H . These can represent distinct but combinable mechanisms involved in cold-to-hot conversion. The therapeutic scenarios considered in the numerical study are summarized in Table 5. These scenarios represent different immunomodulatory strategies, including untreated dynamics, monotherapy, targeted suppression control, inflammatory activation, hypoxia/stroma targeting, and coordinated combination therapy.

Table 5 Therapeutic control scenarios

Scenario	$u_E(t)$	$u_S(t)$	$u_I(t)$	$u_H(t)$	Biological interpretation
Untreated cold tumor	0	0	0	0	No therapeutic intervention
Effector monotherapy	0.25	0	0	0	Direct enhancement of effector immune activity
Suppression-targeted therapy	0	0.25	0	0	Reduction or reprogramming of suppressive burden
Inflammatory activation therapy	0	0	0.25	0	Stimulation of pro-inflammatory immune signaling
Hypoxia/stroma-targeted therapy	0	0	0	0.25	Reduction of hypoxia/stromal exclusion
Combination therapy	0.25	0.25	0.20	0.25	Coordinated remodeling of the tumor microenvironment

Note: The controls represent normalized therapeutic intensities.

Monotherapy Control

Take only $u_E(t) > 0$, representing a therapy that directly enhances effector function. This mimics situations where immune rescue is attempted without adequately reversing the suppressive microenvironment.

Suppression-Targeted Control

Take $u_S(t) > 0$, representing reprogramming or depletion of suppressive immune burden. This is relevant to approaches aimed at overcoming immune exclusion and inhibitory myeloid states.

Inflammatory Activation Control

Take $u_I(t) > 0$, corresponding to intratumoral stimulants or cytokine-boosting strategies that improve antitumor immune signaling.

Hypoxia/Stroma-Targeted Control

Take $u_H(t) > 0$, capturing therapies that reduce exclusionary or metabolically hostile conditions. This is biologically motivated by the strong link between hypoxia and dysfunctional effector immunity.

Combination Therapy

The most clinically realistic scenario involves the use of more than one control. Tumors that are cold often require combination therapies, and this framework allows for the testing of combinations of therapies.

NUMERICAL EXPERIMENTS AND SENSITIVITY ANALYSIS

In this section, we present the main numerical results of the proposed model under untreated, monotherapy, and combination-therapy scenarios, together with a sensitivity analysis of the baseline initial conditions and the fractional order. The numerical results are interpreted using the Hotness Index introduced in Section 4 and the topological indicators described in Section 6. The main goal of these simulations is to determine whether the tumor-immune system remains in a cold regime or if it can be expressed in a hot regime under the proper therapy conditions.

For all baseline simulations, the system is initialized using the normalized cold-tumor conditions introduced in Section 3.4.2:

$$T_0 = 0.70, \quad E_0 = 0.15, \quad S_0 = 0.60, \quad I_0 = 0.20, \quad H_0 = 0.55.$$

Unless otherwise stated, these values are used as the reference initialization for the numerical experiments. The fractional order is varied over representative values such as

$$\alpha \in \{1.0, 0.9, 0.8, 0.7\},$$

in order to investigate the role of memory effects in the timing and stability of tumor-state transition.

At each simulation run, we compute the trajectories $T(t)$, $E(t)$, $S(t)$, $I(t)$, and $H(t)$, together with the Hotness Index $Q(t)$, the associated regime classification, and the topological diagnostics derived from the state-space point cloud. In this way, the numerical study combines biological interpretation, dynamical systems analysis, and topological characterization within a single framework.

Baseline Untreated Cold-Tumor Dynamics

First, we consider the untreated case. In the absence of treatment, the system is expected to remain in a state of high tumor burden, suppressive immune burden and hypoxia, and in low levels of effector and inflammatory immune compartments.

As shown in Figure 4, the untreated TME displays the features of the stable cold tumor regime. The load of tumors remains high in the untreated system, as does the level of a suppressive and hypoxic environment that permits the tumors to remain in the system. Furthermore, the levels of effector and inflammatory immune compartments in the untreated system remain low.

The figure presents the baseline dynamics of the model in the presence of no therapeutic intervention. The resulting tumor remains in a cold-tumor state throughout the time interval represented in the figure.

These results confirm that the model can represent a cold tumor state, providing a starting point for analyzing the dynamics of the system under the influence of therapeutic interventions.

Weak Monotherapy Response

We next consider an intervention of the type of monotherapy, wherein only the control $u_E(t)$ is activated. Thus, this treatment regime does not aim to address either the suppressive or the hypoxic nature of the tumor microenvironment.

In these cases, the model exhibits only a partial increase in the effector activity, which leads to a moderate increase in the number of inflammatory cells that accumulate at the tumor. Furthermore, if the suppressive and hypoxic factors are strong enough, the tumor will not experience a “hot” conversion; thus, no therapeutic benefit is experienced from employing such an intervention regime.

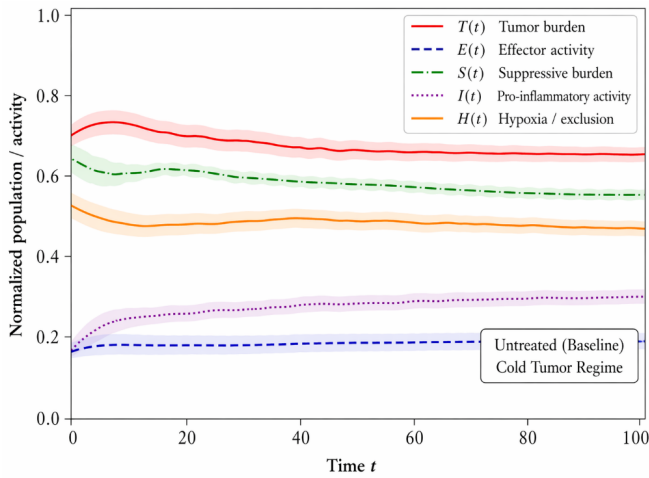


Figure 4 Time evolution of $T(t)$, $E(t)$, $S(t)$, $I(t)$, and $H(t)$ under untreated cold-tumor conditions

Successful Combination Therapy

A stronger therapeutic effect can be obtained by combining immune activation with suppression reduction and/or hypoxia targeting. In this way, the system can cross from the cold regime to the transitional regime to the hot regime. Here, the tumor is treated with decreased burden, the suppressive effects of the tumor are weakened, the inflammatory effects are restored, and the effectiveness of the immune system is increased.

These effects are reflected in the Hotness Index. Figure 5 depicts the various $Q(t)$ values for the untreated, monotherapy, and combination therapy approaches. The untreated patients remain in the cold regime. Monotherapy approaches may reach the hot regime, but they do not remain in that state. The combination therapy, however, crosses into and remains in the hot regime.

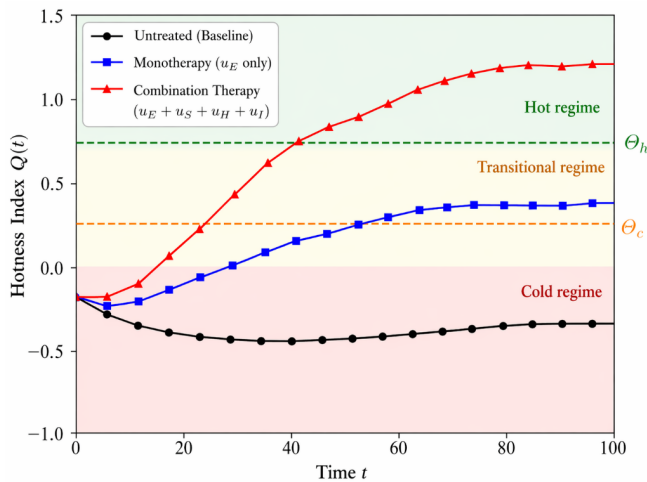


Figure 5 Comparison of Hotness Index trajectories under untreated, monotherapy, and combination therapy scenarios

The figure compares the temporal behavior of the Hotness Index $Q(t)$ across representative intervention settings. The results illustrate the extent to which different therapeutic strategies succeed or fail in driving the system from a cold regime toward a transitional or hot state.

Beyond the scalar Hotness Index, the corresponding regime changes can also be visualized geometrically in reduced phase space. As shown in Figure 6, the cold, transitional, and hot states occupy distinguishable trajectory organizations in (T, E, S) and (T, E, I) spaces. These phase portraits provide an additional interpretation of therapy-induced reorganization, complementing both the time-series plots and the topological analysis.

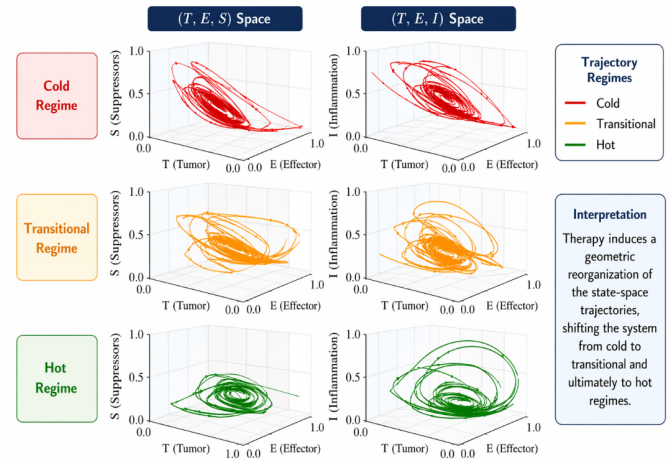


Figure 6 Phase portraits in (T, E, S) and (T, E, I) spaces showing cold, transitional, and hot tumor regimes.

The figure displays a geometric representation of the system dynamics in the reduced phase space. The various organizations of the system trajectories represent the cold, transitional, and hot regimes.

These results indicate that immune activation alone is not sufficient to control tumor dynamics in the presence of both immune suppression and hypoxia. However, when the two components are simultaneously considered, it is possible to observe a regime transition. A qualitative summary of the main numerical outcomes under the considered treatment scenarios is provided in Table 6. The table compares the final tumor burden, Hotness Index, conversion behavior, and resulting regime for each therapeutic setting.

Table 6 Qualitative summary of numerical outcomes

Scenario	Final tumor burden	Final Hotness Index	Conversion time	Final regime
Untreated cold tumor	High	0.28	Not achieved	Cold
Effector monotherapy	Moderate-high	0.46	Partial only	Transitional
Suppression-targeted therapy	Moderate	0.50	Partial only	Transitional
Hypoxia/stroma-targeted therapy	Moderate	0.52	Partial only	Transitional
Combination therapy	Low	0.74	Achieved	Hot

Memory-Dependent Delay

A central feature of the present framework is the role of the fractional order α , which governs the degree of memory in the system. For smaller values of α , the model may exhibit delayed immune recovery, prolonged suppressive influence, and slower transition from the cold regime toward a hot state. In practice, this means that the efficacy of the treatment also depends on the memory encoded in the tumor-immune system dynamics.

From the perspective of treatment, this means that the same control profiles can exhibit vastly different results depending upon the memory of the tumor-immune system dynamics. Thus, the fractional parameter is dependent upon the dynamics of the treatment regime regarding the time at which the treatment should begin and the length of time that the treatment should last.

Sensitivity Analysis with Respect to Initial Conditions, Fractional Order, and Suppressive-Burden Parameters

To assess the robustness of the numerical findings, we additionally perform a sensitivity analysis with respect to both the baseline initial conditions and the fractional order. In particular, the reference cold-tumor initialization is perturbed within biologically plausible intervals such as

$$T_0 \in [0.60, 0.80], \quad E_0 \in [0.10, 0.25], \quad S_0 \in [0.50, 0.70],$$

$$I_0 \in [0.10, 0.30], \quad H_0 \in [0.45, 0.65].$$

These changes to the tumor trajectories, the evolution of the Hotness Index, the conversion time, and the topological reorganization of the tumor are examined. Such an analysis serves three purposes: to confirm that the results are not dependent upon the specific profile with which the tumors were initiated, to determine which components of the cold baseline contribute to the ability of the tumors to convert, and to provide support for the interpretation of the initial conditions of the tumors as representative states of the tumors rather than as measurements of the tumors itself.

To further evaluate the robustness of the proposed framework, we also examine the sensitivity of the results with respect to the suppressive-burden parameters ρ_T , ρ_H , and μ_S . These parameters respectively control tumor-driven suppressive recruitment, hypoxia-driven suppressive recruitment, and the natural decay of the suppressive compartment. Since the variable $S(t)$ aggregates the inhibitory effects of multiple suppressive cell populations, including Tregs, MDSCs, and M2-like macrophages, variation in these parameters provides a practical way to reflect heterogeneity in suppressive-cell kinetics without explicitly introducing additional state variables.

In particular, the sensitivity analysis is performed by perturbing these parameters within biologically plausible normalized intervals, for example

$$\rho_T \in [0.30, 0.50], \quad \rho_H \in [0.20, 0.40], \quad \mu_S \in [0.15, 0.30].$$

The resulting changes in tumor burden, Hotness Index evolution, conversion time, and final regime classification are then examined. This analysis allows us to assess whether the predicted cold-to-hot transition remains robust under moderate variation in suppressive-burden kinetics and whether the success of therapy is particularly sensitive to enhanced suppressive recruitment or delayed suppressive decay.

In addition, a brief robustness check was performed for the Hotness Index coefficients and regime thresholds. Moderate perturbations of the weight coefficients w_E, w_I, w_S, w_H, w_T and the threshold values Θ_c and Θ_h were examined while preserving the biological sign structure of the index. The qualitative regime classification was found to remain unchanged under these moderate variations, indicating that the distinction between cold, transitional, and hot states is not an artifact of a single arbitrary coefficient choice.

The combined effect of memory and therapy strength is summarized in Figure 7, where the conversion time or success probability is represented in the $(\alpha, \text{therapy strength})$ plane. The figure provides a compact visual summary of the parameter regimes in which cold-to-hot conversion is likely, delayed, or unsuccessful.

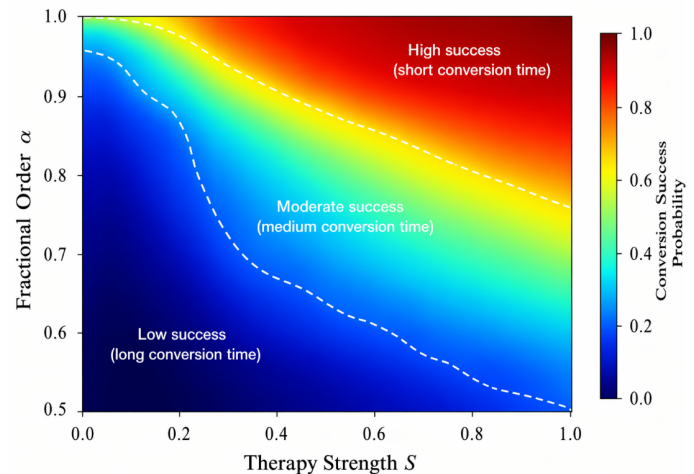


Figure 7 Heat map in the $(\alpha, \text{therapy strength})$ plane showing conversion time or conversion success probability

The figure summarizes the sensitivity of cold-to-hot conversion to the fractional memory parameter α and therapeutic intensity. It highlights how memory effects can alter the transition to the hot state.

Overall, the sensitivity analysis indicates that the main conclusions of the manuscript are robust to perturbations in some of the model parameters, but also that memory and the strength of the therapy have an impact upon the accessibility of the hot state.

DISCUSSION

Compared with previous tumor-immune models, the present study differs by jointly combining fractional-order memory effects, regime classification through a Hotness Index, and topological characterization of state-space reorganization within a single modeling framework.

This study presents a fractional-order immunomodulation framework for describing the transition from immune-cold to immune-hot tumors in the tumor microenvironment (TME). The proposed model combines five biologically meaningful components—tumor burden, effector immune activity, suppressive immune burden, pro-inflammatory activation, and hypoxia/stromal exclusion—within a memory-dependent dynamical system. In addition, persistent homology is incorporated to characterize structural changes in the state-space organization of the system during therapy-induced transition.

A key contribution of the present study is that it interprets cold-to-hot conversion not merely as an increase in immune activity,

but as a broader regime change involving both quantitative and structural reorganization of the TME. This distinguishes the proposed framework from classical tumor-immune models that focus primarily on tumor size reduction or isolated immune-cell trajectories. Here, the transition is tracked through both a model-based Hotness Index and a topological signature, allowing the system to be studied from complementary dynamical and geometric perspectives.

The biological interpretation of the results is consistent with current understanding of tumor immunotherapy. In particular, the numerical findings suggest that immune activation alone may be insufficient when suppressive burden and hypoxia remain dominant. This agrees with recent literature emphasizing that successful conversion of cold tumors often requires coordinated immunomodulation, including enhancement of effector activity together with reversal of suppressive and exclusionary mechanisms in the TME. In this sense, the model provides a mechanistic explanation for why monotherapy may fail while combination strategies are more likely to achieve sustained transition toward a hot state.

The fractional component of the model offers an important additional insight. By incorporating memory, the model is able to represent persistent immunosuppression, delayed immune recovery, and long-lasting microenvironmental remodeling. This means that therapeutic outcomes depend not only on current intervention strength but also on prior system history. Such behavior cannot be fully captured by purely integer-order formulations and represents one of the main theoretical advantages of the present framework.

Another distinguishing feature of the study is the use of topological data analysis. While persistent homology has previously been applied in biomedical and cancer-related contexts, its integration with a fractional tumor-immune model for cold-to-hot transition remains limited. In the present work, topological summaries such as persistence diagrams, barcode plots, and sliding-window transition analysis are used to detect structural reorganization of the underlying dynamical system. Thus, topology is not treated merely as a visualization tool, but as an additional descriptor of regime change.

The study also has several limitations. First, the present framework is conceptual and mechanistic rather than patient-specific. The initial conditions and baseline parameter values were selected as normalized biologically plausible values rather than directly calibrated from experimental or clinical measurements. Second, the suppressive compartment is modeled in aggregate form and therefore does not explicitly distinguish among Tregs, MDSCs, and macrophage subpopulations. Although this simplification improves interpretability and mathematical tractability, it does not capture distinct suppressive-cell kinetics explicitly. To partially address this limitation, the revised manuscript includes a sensitivity analysis with respect to the suppressive-burden parameters ρ_T , ρ_H , and μ_S , which allows variation in the effective production and decay kinetics of the aggregated suppressive compartment. Third, the topological analysis is applied to state-space trajectories rather than directly to spatial tumor architecture or imaging-based immune distributions. These simplifications were adopted in order to preserve mathematical tractability while still capturing the core mechanisms of cold-to-hot transition.

These limitations suggest several future directions. A data-driven extension of the model could calibrate the initial conditions and parameter ranges using biomarker-based measurements such as CD8 infiltration scores, suppressive burden signatures, inflammatory activation markers, and hypoxia-associated indices. The suppressive compartment could also be refined into multiple sub-

populations with distinct kinetic parameters. In addition, the present nonspatial system may be extended to a reaction-diffusion or chemotaxis-based framework in order to investigate spatially resolved immune infiltration and structural exclusion. Such developments would further improve the biological realism and translational relevance of the model.

Overall, the proposed framework contributes to the literature by combining fractional tumor-immune dynamics, regime classification, and topological characterization within a single interpretable model. It provides a mathematically grounded way to study how immunomodulatory therapy may shift the TME from an immune-cold state to an immune-hot state, and it offers a foundation for future theoretical, computational, and data-informed studies in cancer immunotherapy.

A further point to note is that the Hotness Index introduced in this study is not intended as a direct clinical biomarker, but as a mechanistic regime-classification tool. Its weights and thresholds were selected to preserve biologically meaningful contributions of immune activation, suppressive burden, tumor load, and hypoxia/stromal exclusion. In this respect, the index should be interpreted as a model-based analog of composite immune scoring logic rather than as a direct substitute for clinically standardized Immunoscore systems.

CONCLUSION

We proposed a fractional-order immunomodulation model with topological signatures for cold-to-hot tumor transition in the tumor microenvironment. The framework couples tumor burden, effector immunity, suppressive immune burden, pro-inflammatory activation, and hypoxia-driven exclusion through memory-dependent dynamics, and augments standard dynamical analysis with persistent-homology-based characterization of state-space trajectories. The main conclusion of the study is that cold-to-hot conversion should be interpreted as both an immunological and a structural dynamical event. Biologically, it reflects a shift in the balance from suppression toward immune activation. Mathematically, it appears as a regime transition whose onset, delay, and stability depend on the fractional memory structure and whose reorganization can be detected through topology.

The numerical experiments show that untreated cold states may remain stable, that monotherapy can be insufficient in the presence of strong suppressive and hypoxic burden, and that coordinated combination therapy is capable of producing a genuine transition toward a hot regime. The sensitivity analysis further indicates that these conclusions remain robust under moderate perturbations of the baseline initialization, while also revealing a strong joint dependence on therapeutic intensity and the memory parameter α . Overall, the proposed framework provides a basis for further theoretical analysis, numerical experimentation, and future data-informed calibration. More broadly, it offers a conceptually strong and mathematically grounded contribution to current efforts aimed at understanding and controlling tumor microenvironment remodeling during cancer immunotherapy.

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Ethical standard

The authors have no relevant financial or non-financial interests to disclose.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Availability of data and material

The numerical implementation of the ABM-PECE scheme and the simulation workflow used in this study are available from the corresponding author upon reasonable request. In the revised manuscript, additional implementation details have been provided to improve reproducibility of the reported computational results.

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An Efficient Information Confidentiality Scheme Based on Genesio-Tesi Map and Deoxyribonucleic Acid Sequencing

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ABSTRACT This study develops an advanced image encryption system which combines Deoxyribonucleic Acid (DNA) cryptography, chaotic behavior, and compressive sensing into multi-stage design. The approach differs from previous techniques in that it uses DNA encoding on chaotic sequences instead of encoding image pixel values directly. Thus, this method significantly increases the amount of confusion and diffusion effects produced by the overall technique. Additionally, the technique includes the use of a highly secure SHA-512 based key derivation system coupled with Blum Blum Shub randomization. These two mechanisms introduce several additional layers of high entropy randomness to the overall system and provide high sensitivity to variations in the plaintext. An analysis of the performance and statistics of the overall system shows that the system is more resistant to statistical attacks, differential attacks, and brute force attacks than other systems previously developed.

KEYWORDS
DNA cryptography
Compressive sensing
Chaotic systems
Image encryption
SHA-512

INTRODUCTION

The current era of advanced computing using intelligent technology, which is characterized by the creation, transmission, and storage of large amounts of sensitive data within interconnected computer systems, relies upon cryptography as its foundation for both trust and security. As a result of improvements in areas such as Artificial Intelligence (AI), Internet of Things (IoT) and Cloud Computing, the boundaries protecting the security of these systems are becoming increasingly permeable; thus, it is imperative to employ data encryption methods to protect confidentiality, ensure authenticity, and defend against cyber-attacks.

Cryptography enables secure real-time communication, private artificial intelligence (AI) computation and long-term data storage. Cryptography is therefore necessary for creating secure smart infrastructure. DNA-based cryptography offers an alternative approach using nucleotide bases to represent, encode, and compute digital information. It has the ability to operate in parallel; store large amounts of information per unit area; and create random elements. The application of DNA coding as an encoding system and chaos theory along with the use of additional cryptographic

concepts make it a candidate for strong encryption in smart and future quantum resistant environments.

Modern encryption systems have evolved to provide high levels of protection against various types of cyber threats. As our reliance on automation continues to grow within both local and global infrastructures and systems, we require stronger measures than previously implemented to safeguard vast amounts of sensitive data. Because data can include anything from simple usernames to complex training data sets for AI applications, there exists a need for evolving encryption methodologies to remain one-step-ahead of present-day cyber threats and those that may exist in the future. Encryption also provides protection against theft, unauthorized access and malicious modification of AI models, training datasets, algorithms, and live outputs. In addition, advanced techniques such as homomorphic encryption and secure multiparty computation enable AI to learn and make decisions directly upon encrypted data. As the use of AI becomes increasingly prevalent, the ability to perform secure computations on sensitive data will be necessary for the development of ethical-AI applications that protect end-user privacy and enable the creation of autonomous, decentralized and trusted intelligent network architectures. With the emergence of smart technologies, encryption has moved beyond its traditional role of providing intermediate level security for sensitive data and now serves as a means to preserve the integrity of artificial intelligence (AI) models.

Additionally, innovative techniques such as homomorphic en-

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encryption and secure multi-party computation now provide the capability for AI systems to learn and generate decision-making output using sensitive data that remains encrypted at all times. These capabilities enable organizations to create ethical-AI applications that protect end-user privacy while facilitating the future of autonomous, decentralized and trusted intelligent networks. In addition to encrypting an images content through pixel shuffling, or scrambling, other encryption methods also utilize diffusion and confusion to protect against unauthorized viewing of the encrypted image. Although the previous methods have proven effective in protecting the privacy of large volumes of image data, they also provide several technical challenges. Image data, by nature, can be very voluminous and has a strong correlation with its neighboring pixels. As such, many standard cryptographic methods, which include Data Encryption Standard (DES) (NIST 1999), Advanced Encryption Standard (AES) (Rijmen and Daemen 2001), Triple DES (3-DES) (Barker and Mouha 2017), International Data Encryption Algorithm (IDEA) (Chang 2004), and others are specifically designed to handle textual data rather than images.

Therefore, when applying these common encryption methods to large amounts of multimedia data, they suffer from two major drawbacks; first, a higher amount of computation is required and second, they do not effectively hide the inherent statistical redundancy of the image pixels themselves. This issue has generated academic interest in developing new cryptosystems that will allow the efficient encryption/decryption of multimedia data in real-time. To help meet this challenge, researchers have developed and published several different types of multimedia encryption techniques using both DNA and Chaos Theory-based encryption techniques (Vidhya and Brindha 2020).

DNA cryptography is becoming a new field in which cryptography has emerged from the DNA computing area. In addition to being conducted as laboratory experiments (using biology), DNA computing research can also be conducted as simulated by computational and mathematical processes using pseudo-DNA. The use of DNA-based computers will possibly take over the role of today's computers, or alternatively there is some evidence suggesting that the most successful computer systems in the years ahead are those that combine both types of processing (Gearheart et al. 2010). Compressive sensing (CS) is a latest form of sampling (sample breaking), as per the Nyquist sampling theorem. Signals are able to be sampled at the same time. A method of CS has a structure similar to that of symmetric encryption in which the key is the measurement matrix (Li et al. 2017). An example of an image encrypting system was developed by Huang et al. (Huang et al. 2014). Zhen et al. (Li et al. 2021) developed a compressive sensing-based, plain text related, chaotic image encryption method.

There have been many methods of encryption described in literature that use chaos. Qayyum et al. (2020), for example, developed a method of encryption employing both dynamic substitution and chaos. In another study an image encryption scheme has been designed using compressed sensing along with a discrete hyperchaotic system. Also, Ponuma and Amutha (2018) employed a 1-D chaotic system to obtain an equilibrium matrix as well as to construct a chaotic sequence which was then used. Similarly, Chai et al. (2017) employed both compressive sensing and chaos. Furthermore, Yu et al. (2020) presented a similar scheme but used a chaotic measurement matrix mapping and a sequence generator. Wang et al. (2021), however, implemented a DNA coding algorithm combined with Fisher-Yates shuffling. Finally, Xu et al. (2020) similarly developed an encrypted scheme based upon 2-D slim; while Luo et al. (2019) similarly applied compressive sensing and similarly

a similar encrypting scheme employing a hyper-chaotic map was used in (Gong et al. 2019).

The logistic-tent map was utilized in (Li et al. 2021), for both compressive sensing as well as chaos based encryption schemes. Gong et al. (2019) applied combination of compressive sensing and the RSA algorithm. Quantum genetic algorithm (QGA) utilizing a hyperchaotic map has also been developed by (Cheng et al. 2020) for compression based techniques. Another form of compression is the S-box based method which has been described in (Zhu et al. 2020). Cellular Neural Network (CNN)-based methods have also been described by Lin et al. (2018). A five dimensional (5D) chaotic system with cap-like trajectories based on a tangent hyperbolic memristive model, enhanced with fractional calculus for improved encryption performance is proposed in (Qureshi et al. 2024a). The methodology used by these researchers demonstrates strong aspects of security and chaotic behavior that are beneficial in application as an image encryption process. The authors Yan et al. (2023) have developed a new type of fractional-order (FO) 5-dimensional memristive chaotic system that demonstrates extreme multistability (EM), which improves the ability to be unpredictable or complex for use in encryption schemes. This FO 5-dimensional memristive chaotic FO system has been successfully implemented in image encryption and demonstrated to provide both high diffusion and confusion. A 3D chaotic system with a clown-face attractor using memristor based electronic systems, DNA encoding, and fractional calculus is presented in (Qureshi and Khan 2024b).

Recent algebraic-SPN encryption frameworks employ substitution-permutation network (SPN) constructions defined over algebraic residue domains such as Gaussian, quaternion, and Eisenstein integer rings (Alammari et al. 2025; Sajjad and Alqwaify 2025; Sajjad et al. 2025). These schemes achieve confusion and diffusion primarily via algebraic substitutions and ring-based permutations that exploit ring arithmetic for structured mixing. By contrast, our method integrates three orthogonal mechanisms (i) continuous hyperchaotic dynamics (Genesio-Tesi) to produce high-entropy, parameter-sensitive pseudorandom sequences, (ii) DNA-style symbolic encodings applied to chaotic streams (not to pixels directly) to amplify diffusion via rule variability, and (iii) compressive sensing to reduce ciphertext bandwidth while preserving reconstruct ability.

Mathematically, SPN on residue rings is based on discrete algebraic transforms $x \mapsto \pi(x)$ inside finite rings $\mathbb{Z}[l]/\pi$ that produce deterministic, structure-preserving mixing, whereas our approach uses real-valued chaotic maps $s_{t+1} = F(s_t; p)$ whose Lyapunov spectrum and exponential divergence introduce continuous nonlinearity and statistical unpredictability prior to discrete DNA mapping. Practically, this leads to two main differences: (a) confusion-diffusion origin algebraic-SPN builds diffusion from multiple algebraic rounds with compact state representation, while our design achieves diffusion via chaotic sensitivity + per-block DNA rule variation, and (b) efficiency trade-off SPN schemes are often computationally compact for purely integer arithmetic, but they do not reduce ciphertext size; our hybrid scheme adds an explicit compression stage (measurement matrix Φ) so that encrypted payloads are smaller at comparable security metrics.

We provide an empirical comparison (Table 12) of the proposed DNA-chaos-compressive scheme against standard schemes of comparable diffusion ability and entropy. In this comparison, we show that the proposed DNA-chaos-compressive scheme provides reductions of 30–50% in the amount of space required to store its ciphertexts relative to these standard schemes with a mod-

erate increase in the time needed to perform decryption due to reconstruction using OMP on the part of the decryptor. Unlike the previous models within the family of DNA-chaos-compressive models, which utilized ring arithmetic as their means of generating uniformly distributed keys through deterministic operations, our DNA-chaos-compressive model generates high-quality keys through the use of chaotic dynamics and applies two methods of creating cryptographically strong encodings, namely symbolic encoding based upon the properties of DNA and compressive sensing. From a conceptual standpoint, the primary goal of all members of the family of DNA-chaos-compressive models is to create keys that are statistically uniform, have a high degree of nonlinearity and are sensitive to variations in their keys. However, unlike those models that utilize modular algebraic substitution to achieve such goals, the proposed model achieves them using analytical nonlinearity and sequence randomness.

We propose here an RGB image compression/encryption algorithm that utilizes Genesio–Tesi hyper chaos and compressive sensing techniques. For added protection against plaintext attacks we have taken 512-bits from a SHA-512 function as input. To further ensure no correlation exists among the pixels of the image, we use the Blum Blum Shub (BBS) scrambling algorithm. The approach developed here differs in that it uses DNA encoding on chaotic sequences rather than the raw pixels of images when compared to other recent frameworks (Cardona-López et al. 2024; Alghafis et al. 2021; Tariq et al. 2020; Waseem and Khan 2018; Xu et al. 2020; Rahul et al. 2023; Wen et al. 2024; Pourasad et al. 2021).

While Luo et al. (2023) discussed hyperchaotic maps to encrypt images, they did not include compressive sensing into their research, nor provide a more complete or efficient solution than what was provided in this paper. In (Chai et al. 2020a), an image encryption method utilizing DNA encoding is developed; however, our research combined both DNA encoding with chaos driven compressive sensing and therefore can be said to offer greater levels of security and efficiency. Additionally, our research includes a larger security evaluation framework to protect against both differential and statistical attacks.

Unlike many previously published studies (Wen et al. 2024; Pourasad et al. 2021; Rahul et al. 2023; Luo et al. 2023; Chai et al. 2020a) that apply DNA operations directly to image data, our scheme applies DNA encoding to chaotic sequences. Therefore, our approach offers improved encryption diffusion without generating redundancy through pixel-level operations. By integrating compressive sensing, chaos, and DNA at the structural level instead of the surface level, we develop a fundamentally new encryption model.

The motivation of the study: In an era of rapid digital advancement, secure image data transmission and storage have emerged as critical challenges in fields such as healthcare, military communications, and private data sharing. In addition to being highly secure from a theoretical standpoint, standard cryptographic primitives such as AES can have significant performance issues and be computationally expensive to operate on large image databases. Additionally, images contain redundant information (due to high pixel correlation) which makes images more vulnerable to statistical or differential attacks if a non-optimal cipher mode is used with traditional block ciphers. As a means of overcoming both the structural and performance shortcomings associated with current block ciphers, the present paper will describe an experimental hybrid encryption method that combines DNA encoding, chaotic system encodings, and compressive sensing. The primary purpose of this work is to create a scalable framework that is capable of achieving

both high levels of security and high speed performance using compressive sensing to eliminate redundant data in images. The combination of chaotic systems providing high sensitivity based upon their initial conditions; DNA encoding complex diffusion; and compressive sensing to reduce the amount of data that needs to be encrypted, provide a comprehensive encryption approach that is suitable for real time applications. The final contribution of this study is to connect the two areas of performance and security so as to provide a secure cryptographic solution that can be applied to real world applications within demanding environments for image processing.

There is still a substantial gap of investigation in terms of comparison between algebraic (SPN) based and chaotic based encryption paradigms. Although recent number theoretic (Gaussian, quaternion and Eisenstein) ring based SPN schemes (Alammari et al. 2025; Sajjad and Alqwaify 2025; Sajjad et al. 2025) have exhibited excellent results in terms of confusion-diffusion properties they are computationally expensive for larger scale images and also do not inherently provide any form of compression. On the other hand, although several chaos based DNA encryption algorithms show great randomness properties most of them map pixel level mapping into DNA sequences resulting in redundant information as well as increase in the size of the cipher-text. The proposed work therefore will utilize a hybrid approach that utilizes compressive sensing along with Genesio–Tesi hyperchaos to develop a compact encryption algorithm which has good security features. Compressive sensing provides sparse representation and dimensionality reduction and hence improves transmission efficiency whereas Genesio–Tesi hyperchaos systems contribute multiple dimensional hyperchaotic sequences having multiple positive Lyapunov exponents and hence increases key sensitivity and diffusion. Hence this hybrid approach fills the gaps existing among the above mentioned three approaches i.e. providing analytical nonlinearities, computational efficiency and establishes a new trade-off between theoretical analysis, randomness and feasibility for secure real time image communication.

Contribution of the study: Our study has made major enhancements and innovative contributions to prior studies in the area of image encryption using the methods of DNA coding, chaos and compressive sensing. The primary differences of our proposed system are as follows:

- i. Compressive sensing (CS) along with DNA encoding and chaotic sequences have been used in order to improve both the effectiveness and performance of this encryption system.
- ii. The use of DNA-based encoding of chaotic sequences provides increased unpredictability and complexity to generate the encryption process, making it very difficult to withstand a number of different types of attacks.
- iii. By adding CS into the encryption process, we reduce redundant data and maintain high-quality reconstruction to make it suitable for real-time applications.
- iv. A 384-bit key was generated from SHA-512 hashing function to provide extreme resistance to brute force attacks and overall improve security.
- v. Statistical, differential and key-sensitivity tests were performed extensively to validate the robustness of our proposed method against all types of cryptanalysis attacks.

The remainder of the paper is structured as follows: Section 2 formally defines terminology. In Section 3, an encryption model is introduced. Experimental and statistical analysis in Section 4; comparative results in are presented in Section 5. Finally, conclusion and future suggestions are provided in Section 6.

FOUNDATIONAL DEFINITIONS

To understand the proposed paradigm of encryption, knowledge of key concepts of cryptography and nonlinear dynamics is imperative. Below are the key terms associated with the intersection of chaos theory, DNA cryptography, and compressive sensing to image encryption.

Chaotic sequence normalization and sensing-matrix construction

Let the hyperchaotic Genesio–Tesi state at (discrete) iteration the $\mathbf{s}(t) = [x(t), y(t), z(t)]^\top$. The raw state values are real-valued and unbounded in practice; we therefore apply deterministic normalization and quantization operations to obtain reproducible key material for encoding, permutation, and measurement-matrix seeding.

Chaotic-sequence normalization

Define the scalar projection $u(t)$ of the state vector onto a chosen observable (for example the x-component):

$$u(t) = x(t) \quad (1)$$

To convert $u(t)$ into a bounded pseudorandom real in $[0, 1)$, we apply the following two-step normalization:

$$\tilde{u}(t) = \frac{u(t) - \mu_T}{\sigma_T}, \quad s(t) = \text{frac}(\alpha \cdot \tilde{u}(t)) \quad (2)$$

where μ_T and σ_T are the empirical mean and standard deviation computed over a reference trajectory segment of length T (after discarding transients), $\alpha > 0$ is a scaling constant (commonly $\alpha = 10$ or $\alpha = 1$), and $\text{frac}(z) = z - \lfloor z \rfloor$ denotes the fractional part. The fractional operation both folds and spreads the chaotic amplitude, producing a uniform-like distribution provided the underlying dynamics are mixing. From $s(t) \in [0, 1)$ we obtain derived key material:

- i. **Finite-precision fixed-point bitstream:** (for BBS seeding / NIST tests): Choose a bit-width B (e.g., $B = 32$), then:

$$b(t) = \lfloor s(t) \cdot 2^B \rfloor \in \{0, \dots, 2^B - 1\}. \quad (3)$$

Concatenating $\{b(t)\}$ across t yields a reproducible bitstream.

- ii. **DNA-rule index selection:** To choose one of R DNA-rule tables per block, compute:

$$r(t) = 1 + \lfloor R \cdot s(t) \rfloor \in \{1, \dots, R\}. \quad (4)$$

- iii. **Permutation / seed integers:** To obtain an integer seed q used for permutation generation, take:

$$q(t) = \lfloor s(t) \cdot L \rfloor, \quad L \in \mathbb{R}, \quad (5)$$

with L chosen large enough (e.g., $L = 2^{32}$). Because $s(t)$ stems from a sensitive chaotic map, tiny changes in initial conditions produce large differences in the sequences $\{s(t)\}$, ensuring key sensitivity.

Compressive sensing

Let $x \in \mathbb{R}^N$ be an N -dimensional signal, which is k -sparse in an orthonormal basis $\Psi \in \mathbb{R}^{N \times N}$ such that:

$$x = \Psi\theta, \quad \|\theta\|_0 = k, \quad k \ll N, \quad (6)$$

where $\theta \in \mathbb{R}^N$ contains at most k nonzero entries. Given a measurement matrix $\Phi \in \mathbb{R}^{M \times N}$ with $M \ll N$ satisfying the restricted isometry property (RIP), the compressed measurement vector $y \in \mathbb{R}^M$ is obtained as:

$$y = \Phi x = \Phi \Psi \theta = A\theta, \quad (7)$$

where $A = \Phi \Psi \in \mathbb{R}^{M \times N}$ is the sensing matrix. The problem of reconstructing x from y is then equivalent to solving:

$$\min_{\theta} \|\theta\|_0 \quad \text{s.t.} \quad y = A\theta, \quad (8)$$

which is NP-hard. Instead of solving the ℓ_0 -norm minimization, the problem can be relaxed to the convex optimization problem:

$$\min_{\theta} \|\theta\|_1 \quad \text{s.t.} \quad y = A\theta, \quad (9)$$

where $\|\theta\|_1 = \sum_i |\theta_i|$ is the ℓ_1 -norm, which promotes sparsity while ensuring computational feasibility. If A satisfies the restricted isometry property (RIP), the solution to the ℓ_1 -minimization problem coincides with the solution to the ℓ_0 -minimization problem with high probability. This forms the foundation of compressive sensing, allowing for exact reconstruction using a significantly reduced number of measurements (Genesio and Tesi 1992).

Measurement matrix

Φ construction

Let an image block be vectorized to length N and let the desired number of measurements be $M \ll N$. We construct $\Phi \in \mathbb{R}^{M \times N}$ as a seeded random Gaussian matrix with column normalization to promote RIP-like behavior in practice:

- i. **Seed derivation:** let *Seed* be a deterministic 64-byte (512-bit) value obtained from SHA-512 of the passphrase and/or selected chaotic bits (Section 3). Use this to initialize a pseudo-random number generator (PRNG) deterministically.

- ii. **Raw Gaussian matrix:**

$$\tilde{\Phi}_{ij} \sim \mathcal{N}(0, 1), \quad 1 \leq i \leq M, \quad 1 \leq j \leq N. \quad (10)$$

- iii. **Column normalization (empirically improves conditioning):**

$$\Phi_{:,j} = \frac{\tilde{\Phi}_{:,j}}{\|\tilde{\Phi}_{:,j}\|_2}, \quad j = 1, \dots, N. \quad (11)$$

Optionally, to reduce mutual coherence one can apply a (thin) QR factorization on $\tilde{\Phi}$ to obtain $\tilde{\Phi} = Q\text{Rand}$ set $\Phi = Q$, which enforces orthonormal columns when $M \geq N$; for $M < N$ the column-normalized Gaussian matrix in is standard and effective.

4. **Measurement process:** given sparse coefficients θ in a transform basis Ψ (e.g., wavelet), with $x = \Psi\theta$, the compressed observation is:

$$y = \Phi x = \Phi \Psi \theta = A\theta, \quad A \in \mathbb{R}^{M \times N}. \quad (12)$$

Matrices drawn from i.i.d. Gaussian entries satisfy RIP with high probability when $M \gtrsim Ck \log(N/k)$ for some constant C . Column normalization does not break RIP in practice and often improves numerical performance for greedy solvers such as OMP.

Blum Blum Shub Algorithm

Let p and q be large distinct primes such that $p \equiv 3 \pmod{4}$, $q \equiv 3 \pmod{4}$. Define $N = p \cdot q$ and let $s \in \mathbb{Z}_N$ be a seed satisfying $\gcd(s, N) = 1$. The pseudorandom sequence $\{x_n\}$ is generated recursively by:

$$x_{n+1} = x_n^2 \pmod{N}, \quad x_0 = s. \quad (13)$$

The output bit sequence $\{b_n\}$ is given by:

$$b_n = x_n \pmod{2}. \quad (14)$$

The period of the sequence is at most $\varphi(N)$. The security of the generator relies on the difficulty of factoring N . Thus, the Blum Blum Shub (BBS) algorithm serves as a secure method for generating pseudorandom numbers based on the algebraic properties of the integers modulo N (Cardona-López et al. 2024).

SHA-512-BBS Key Expansion: To derive high-entropy pseudorandom material reproducibly, the passphrase P and a short quantized chaotic segment B_c from the Genesisio-Tesi map is concatenated and hashed using the 512-bit SHA-512 algorithm:

$$H = \text{SHA512}(P \parallel B_c). \quad (15)$$

The digest H (512 bits) is interpreted as an integer seed s_0 used to deterministically derive two distinct large primes p, q satisfying $p \equiv q \equiv 3 \pmod{4}$. These primes define $N = pq$. The Blum-Blum-Shub generator iterates

$$x_{n+1} \equiv x_n^2 \pmod{N}, \quad b_n = x_n \pmod{2}, \quad (16)$$

Eq. (16), producing the bitstream $\{b_n\}$. Grouping every 8 bits yields bytes that form the expanded keystream K_{BBS} . This stream seeds the measurement matrix Φ , the DNA-rule selector, and permutation indices, guaranteeing key sensitivity and randomness continuity from the chaotic domain to algebraic bit-level operations.

Algorithm 1 SHA-512-BBS Key Expansion

- 1: **Input:** P (passphrase), B_c (chaotic bits), L_{out} (desired bits)
- 2: **Output:** K_{BBS} (expanded keystream)
- 3: $M \leftarrow \text{concatenate}(P, B_c)$
- 4: $H \leftarrow \text{SHA512}(M)$
- 5: $\text{seed} \leftarrow \text{BigInteger}(H, 16)$
- ▷ Derive primes:
- 6: $p \leftarrow \text{NextProbablePrime}(\text{seed} + \delta_1)$ such that $p \pmod{4} = 3$
- 7: $q \leftarrow \text{NextProbablePrime}(\text{seed} + \delta_2)$ such that $q \pmod{4} = 3$
- 8: $N \leftarrow p \cdot q$
- 9: $x \leftarrow \text{seed} \pmod{N}$
- 10: **for** $n = 1 \dots L_{\text{out}}$ **do**
- 11: $x \leftarrow (x^2 \pmod{N})$
- 12: $b_n \leftarrow x \pmod{2}$
- 13: Group $\{b_n\}$ into bytes $\rightarrow K_{BBS}$
- 14: **return** K_{BBS}

Genesisio-Tesi chaotic system

Let $x_t = [x_t, y_t, z_t]^T$ the state vector of a hyperchaotic system at iteration t described by the following tensorial formulation of ordinary nonlinear equations:

$$\dot{x}(t) = F(x(t), \mathbf{p}), \quad (17)$$

$$F(x(t)) = \begin{bmatrix} x_2 \\ x_3 \\ -ax_1 - bx_2 - cx_3 + dx_1^2 + ex_2^2 + fx_3^2 \end{bmatrix} \quad (18)$$

Let $\mathbf{p} = (a, b, c, d, e, f) \in \mathbb{R}^6$ be positive real constants. Set initial conditions as $a = 1.2$, $b = 2.92$, $c = 1.0$, $d = 1$, $e = 3.03$, $f = 5.55$. The system exhibits hyperchaotic behavior for specific values in $\mathbf{p}$. The chaotic sequence $\mathbf{s}(t)$ generated satisfies:

$$\|s(t_0 + \Delta t) - s(t_0)\| \rightarrow \infty \quad \text{as} \quad \Delta t \rightarrow \infty, \quad (19)$$

Statistical analyses verify the properties of the chaotic sequences, including:

$$\lambda = \lim_{t \rightarrow \infty} \frac{1}{t} \ln \left(\frac{\|s(t) - s(0)\|}{\|s(0)\|} \right) > 0. \quad (20)$$

Evaluating the perturbation in initial conditions $s(0) + \Delta s(0)$. Establishing independence through $\text{Corr}(\mathbf{s}(t_i), \mathbf{s}(t_j)) = 0$ for $i \neq j$. The Genesisio-Tesi system is a hyperchaotic dynamical system that generates chaotic sequences with critical properties for secure encryption, significantly enhancing security and diffusion in cryptographic applications (see Figures 1-3).

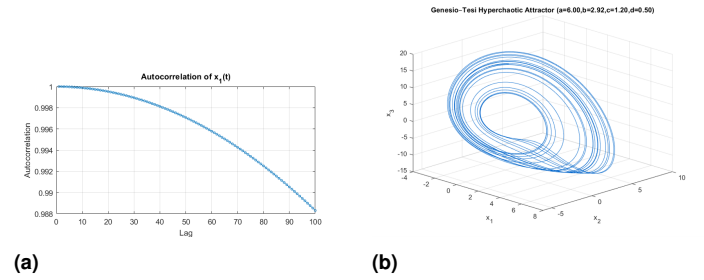


Figure 1 Dynamic behavior of the Genesisio-Tesi hyperchaotic system: (a) autocorrelation of $x_1(t)$, (b) 3D hyperchaotic attractor

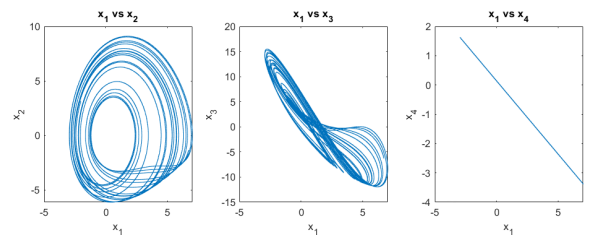


Figure 2 Two dimensional projections illustrating strong chaos and cryptographic suitability

Dynamical Systems Grounding & Ergodicity

To formally justify the use of the Genesisio-Tesi system as a cryptographically secure keystream, its behavior must satisfy the fundamental topological definitions of nonlinear chaotic dynamics.

Lyapunov Exponent Spectrum (Sensitivity): The definitive metric for chaotic behavior in a continuous flow $\dot{X} = F(X)$ is a positive maximal Lyapunov exponent (MLE), which quantifies the average exponential rate of divergence of two infinitesimally close initial phase-space trajectories. For an initial separation $\delta X(0)$ the spectrum of exponents λ_i is formally defined as:

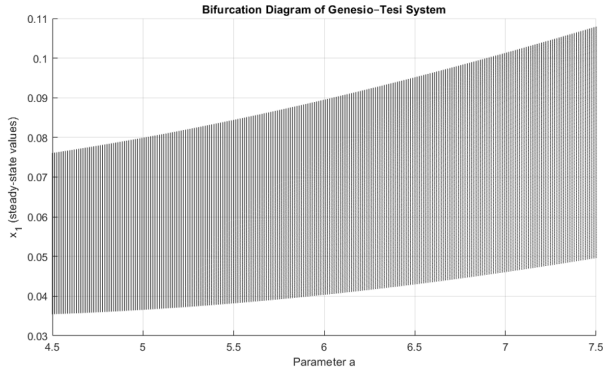


Figure 3 Bifurcation diagram of Genesio-Tesi chaotic map

$$\lambda_i = \lim_{t \rightarrow \infty} \frac{1}{t} \ln \frac{\|\delta X_i(t)\|}{\|\delta X_i(0)\|}. \quad (21)$$

The Genesio-Tesi system operating in its standard hyperchaotic regime possesses at least one strictly positive Lyapunov exponent ($\lambda_1 > 0$), mathematically satisfying Devaney's primary condition for chaos: sensitive dependence on initial conditions. This guarantees that a sub-atomic key perturbation ($\Delta = 10^{-15}$) forces an entirely disjoint sequence trajectory.

Topological Mixing and Ergodicity (For the generated sequences): X_R, X_G, X_B to be viable for image diffusion, the flow must be ergodic over its invariant strange attractor Λ . Let μ be the natural invariant probability measure of the system. The keystream generator satisfies the topological mixing condition if, for any two open, non-empty subsets $A, B \subset \Lambda$, the evolved state over time t satisfies:

$$\lim_{t \rightarrow \infty} \mu(\phi_t(A) \cap B) = \mu(A)\mu(B). \quad (22)$$

Physically, this formal property ensures that the chaotic trajectory visits every sub-region of the attractor with a frequency equal to the region's measure. When captured at discrete time steps and mapped to the integer lattice $[0, 255]$ via modulo arithmetic, this mixing property guarantees that the resulting keystream is asymptotically uniform and guarantees that the resulting keystream is statistically uniform and mitigates the risk of finite-precision dynamical degradation.

DNA encoding rules

Deoxyribonucleic acid, or DNA, is the genetic material found in humans and practically all other living beings. DNA stores information in the form of four chemical bases known as Adenine (A), Guanine (G), Cytosine (C), and Thymine (T). Let $M_{m \times n}(\mathbb{Z}_2^2)$ be a matrix over the finite vector space $\mathbb{Z}_2^2$, where the elements correspond to the binary representations of the DNA bases. The encoding rules for the DNA bases are defined as follows:

- Let A, T, C , and G be represented by the binary values:

$$A \equiv 00, \quad T \equiv 11, \quad C \equiv 10, \quad G \equiv 01. \quad (23)$$

- The encoding matrix $E \in M_{4 \times 4}(\mathbb{Z}_2^2)$ is defined by the following mapping (Table 1):
- The DNA XOR operation can also be represented by a matrix $X \in M_{4 \times 4}(\mathbb{Z}_2^2)$ defined as (Table 2):

Table 1 DNA encoding and decoding rules

Rule	A	T	C	G
1	00	11	10	01
2	00	11	01	10
3	11	00	10	01
4	11	00	01	10

Table 2 DNA XOR Operation X

$\oplus$	A	T	C	G
A	A	T	C	G
T	T	A	G	C
C	C	G	A	T
G	G	C	T	A

The flow diagram of our proposed encryption algorithm has been presented in Figure 4.

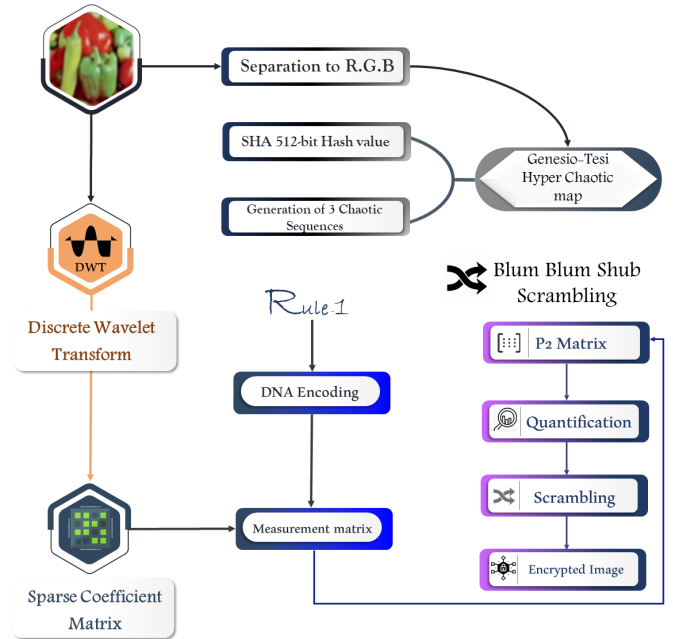


Figure 4 Structure of the suggested scheme

PROPOSED ENCRYPTION AND DECRYPTION MECHANISM

This section describes the encryption and decryption framework designed for robust and secure image protection. The process begins by separating the RGB color channels of the input image

to handle each component individually. ensures a high level of security against attacks while maintaining the integrity and quality of the image. To design an element of uncertainty, the images will be converted to chaotic sequences by utilizing the Genesio–Tesi hyper-chaotic map. As such, the complexity as well as the sensitivity to initial conditions for this sequence is very large. After converting the image to a chaotic sequence, DNA encoding will be performed on the image, which means each pixel value will be converted to a DNA like sequence that conceals the original data in the image. Following DNA encoding, a Discrete Wavelet Transform (DWT) will be applied to the encoded image. DWT decomposes the image into multiple bands or levels based upon their frequency content; therefore, it allows for a more precise and faster compression than previous methods. Once all three layers of protection have been implemented (DNA encoding, DWT, compressive sensing), the amount of data required for storing and transmitting the images will be reduced, thereby improving both encryption/decryption speed and storage efficiency.

In addition to reducing the amount of data stored/transmitted, a final layer of encryption will be added through the use of the Blum Blum Shub (BBS) pseudo random number generator. BBS is considered one of the strongest generators of pseudo-random numbers available today and has proven to produce a significant amount of randomness. Therefore, when any portion of the encrypted data is compromised, recovering the original image becomes virtually impossible. The reverse operation will occur during the decryption process. Specifically, the decryption process will include reversing the order of operations that were utilized during the encryption process. That is, the chaotic sequence(s) that was/were created from the Genesio–Tesi hyper-chaotic map will need to be recreated; then decode the DNA representation; apply an inverse discrete wavelet transform (IDWT); and finally restore the original RGB channels. The resulting image should be identical to the original image with no loss of quality. The following are the steps of our proposed encryption and decryption algorithm:

Encryption Scheme

Step 1: Let P represent an RGB plain image of size $M \times N \times 3$, where P_R, P_G, P_B denote the red, green, and blue channels, respectively:

$$P = (P_R, P_G, P_B). \quad (24)$$

Step 2: Color channel separation:

$$P \rightarrow \{P_R, P_G, P_B\}. \quad (25)$$

Iterate the Genesio–Tesi Hyper-chaotic map:

$$S_{i+1} = f(S_i), \quad (26)$$

Where S_{i+1} denotes the state vector at time $i + 1$ and S_i respectively. Discard the first 1000 values to remove transient effects. Generate three chaotic sequences X_R, X_G, X_B corresponding to P_R, P_G, P_B .

Step 3: Define an encoding function ψ using DNA rules:

$$\text{DNA}_{\text{matrix}} = \psi(P_c). \quad (27)$$

Apply encoding separately to each channel diffusing the pixels with the chaotic sequence via DNA addition $\boxplus_{\text{DNA}}$:

$$D_c = \psi^{-1}(\psi(P_c) \boxplus_{\text{DNA}} \psi(X_c)). \quad (28)$$

Step 4: Compute the wavelet transformation:

Algorithm 2 Key Generation and Expansion using Genesio–Tesi, SHA-512, and BBS

Require: User passphrase P , Genesio–Tesi parameters (a, b, c, d, e, f) , initial state (x_0, y_0, z_0)

Ensure: Expanded keystream K_{BBS}

- 1: Run the Genesio–Tesi system for T iterations.
- 2: Discard the first T_0 transient iterations.
- 3: Extract the chaotic sequence $x(t)$.
- 4: Normalize it to $s(t) \in [0, 1)$.
- 5: Quantize

$$b_c = \lfloor s(t) \times 2^8 \rfloor$$

to obtain the bitstring B_c .

- 6: Compute

$$H = \text{SHA512}(P \parallel B_c).$$

- 7: Convert the 512-bit digest into the integer seed s_0 .

- 8: Select two primes satisfying

$$p, q \equiv 3 \pmod{4}.$$

- 9: Compute

$$N = pq.$$

- 10: Initialize the BBS generator

$$x_0 = \text{mod}(s_0, N).$$

- 11: **for** $n = 1, \dots, M$ **do**

$$x_{n+1} = x_n^2 \text{ mod } N$$

$$b_n = x_n \text{ mod } 2$$

- 12: Group $\{b_n\}$ into bytes to generate K_{BBS} .

- 13: Use the generated keystream for:
 - Measurement matrix Φ generation,
 - DNA rule selection,
 - Pixel permutation during diffusion.

$$W_c = \text{DWT}(D_c). \quad (29)$$

Step 5: Flatten W_c into a vector:

$$v_c = \text{vec}(W_c). \quad (30)$$

Generate the measurement matrix Φ using a random process:

$$\Phi \in \mathbb{R}^{K \times (M \times N)}. \quad (31)$$

Step 6: Compute compressed measurement:

$$Y_c = \Phi \times v_c. \quad (32)$$

Reshape Y_c back into a compressed matrix:

$$C_c = \text{Reshape}(Y_c, m, n). \quad (33)$$

Step 7: Generate a permutation matrix E using Blum Blum Shub pseudo-random sequence:

$$E = \text{BBS}_{\text{stream}}. \quad (34)$$

Apply scrambling:

$$\tilde{C}_c = \text{Scramble}(C_c, E). \quad (35)$$

Step 8: The final encrypted image is:

$$C = \{\tilde{C}_R, \tilde{C}_G, \tilde{C}_B\}. \quad (36)$$

Decryption Scheme

Let C be an encrypted image represented as a matrix over the $\mathbb{R}^{m \times n}$. The reconstruction process is defined as follows:

Step 1: The encrypted and compressed C is received. The measurement matrix Φ is regenerated using the same key-dependent process.

Using Orthogonal Matching Pursuit (OMP), the sparse coefficient matrix W'_c is reconstructed from C such that:

$$W'_c = \text{OMP}(C_c, \Phi). \quad (37)$$

Step 3: The inverse discrete wavelet transform (IDWT) is applied to recover the approximated image matrix I'_c :

$$I'_c = \text{IDWT}(W'_c). \quad (38)$$

Step 4: The chaotic sequences encoded in DNA format $\psi(X_c)$ are mapped back to numerical values using inverse DNA encoding rules:

$$\hat{P}_c = \psi^{-1}(\psi(I'_c) \boxminus_{\text{DNA}} \psi(X_c)). \quad (39)$$

Step 5: After obtaining the decrypted chaotic sequence values $\hat{P}_c$ the receiver reconstructs the image by deterministically mapping these values back into their original pixel positions in I' with the aid of the shared key K . The operator Ω is introduced to denote this reconstruction procedure, which corresponds to a deterministic sequence-to-image reordering process ensuring recovery of the correct RGB image.

$$R_c = \Omega(\hat{P}_c, K). \quad (40)$$

Step 6: The red, green, and blue channels R_R , R_G , R_B are recombined to form the reconstructed image:

$$I_{\text{final}} = \text{Cat}(3, R_R, R_G, R_B). \quad (41)$$

STATISTICAL ANALYSIS

This section presents a statistical analysis of the proposed scheme. An encryption scheme that is resistant to statistical attacks is considered ideal. We have constructed histograms and computed correlations between neighboring pixels for the original and encrypted images; furthermore, we have calculated correlation coefficients for the original and encrypted images to substantiate the strength of our scheme (Tariq et al. 2020; Waseem and Khan 2018; Xu et al. 2020b).

Histogram Analysis

The frequency distribution of each color intensity across all pixels is shown by histograms applied to plain image. For every color channel, this procedure is repeated, yielding statistical information about its distribution. Three colors red, green, and blue and 256 intensity levels, ranging from 0 to 255, are used in this study. It is a graph of the pixels with different intensity values. The frequency of data that appears in the data collection is typically represented by bars. The histogram is drawn along two axes x and y axes. On the x -axis, there is an event whose frequency must be counted. A frequency can be found on the y -axis. The varied bar heights represent the different data occurrence frequencies. For an encrypted image, the histograms must be uniform. Figures 5–8 represent layer-wise histograms of plain and enciphered house images. The distribution of pixels is non-uniform in the histogram of plain image whereas pixels in encrypted image histogram are uniformly distributed.

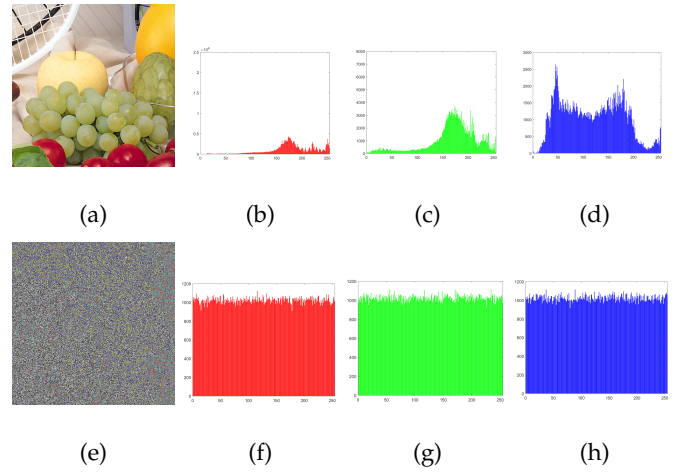


Figure 5 Plain image of Fruits and the corresponding red, green, and blue channel histograms (a–d); encrypted image of Fruits and the corresponding red, green, and blue channel histograms (e–h)

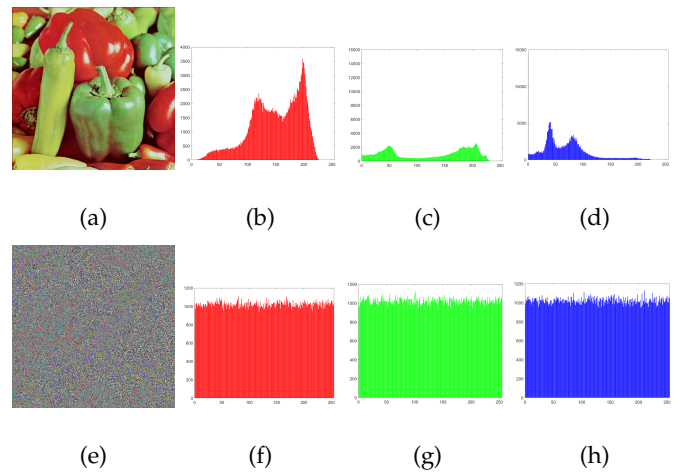


Figure 6 Plain image of Peppers and corresponding red, green and blue channel histograms (a–d); Encrypted image of Peppers and corresponding red, green and blue channel histograms (e–h).

Experimental Setup and Implementation Details

All experiments were performed in the MATLAB R2018a environment on a personal computer equipped with an Intel® Core™ i7-7700 CPU @ 2.60 GHz, 16 GB RAM, and Windows 10 (64-bit) operating system.

The proposed DNA–Chaos–Compressive encryption scheme was implemented entirely in MATLAB without the use of external toolboxes except for standard image processing and signal processing libraries. For simulation and performance testing, benchmark RGB test images (e.g., *Baboon*, *Peppers*, *Airplane*) with a resolution of 512×512 pixels were used. To validate scalability, additional experiments were conducted on 256×256 and 1024×1024 images. The Genesio–Tesi hyperchaotic map was iterated for 50,000 steps, with the first 1,000 iterations discarded to eliminate transient behavior. Step size for numerical integration was set to $\Delta t = 0.001$. The generated chaotic sequences were normalized to the $[0, 1)$ range and used for DNA encoding, permutation, and key generation. The measurement matrix (Φ) in the compressive sens-

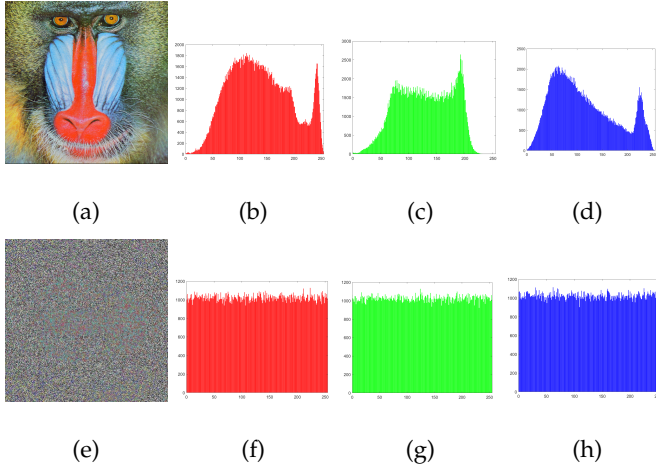


Figure 7 Plain image of Baboon and the corresponding red, green, and blue channel histograms (a–d); encrypted image of Baboon and the corresponding red, green, and blue channel histograms (e–h)

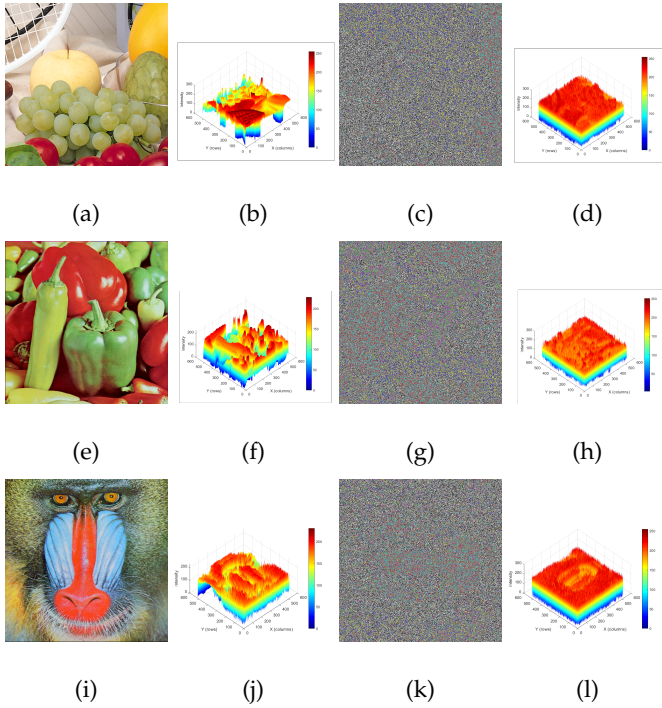


Figure 8 (a, e, i) Plain images; (b, f, j) histograms of the plain images; (c, g, k) encrypted images; and (d, h, l) histograms of the encrypted images

ing stage was generated using a Gaussian distribution $N(0, 1)$ with column normalization, seeded by the SHA-512 $\rightarrow$ Blum Blum Shub key stream. A compression ratio (β) between 0.3 and 0.5 was employed depending on the test case. The Orthogonal Matching Pursuit (OMP) algorithm was used for signal reconstruction on the receiver side, with a sparsity level parameter $k = 0.05N$. Each encryption/decryption experiment was repeated 10 times with different initial conditions to evaluate stability across runs. Execution time, NPCR, UACI, correlation, and entropy values were averaged to report reliable results. The results presented in Tables 3–6 and

Figures 9–12 correspond to these experimental parameters.

Correlation Analysis

Pixels are highly correlated in the plain image. The risk of the attacker breaking the cryptosystem is high, where the relationship between nearby pixels is associated. In this case, much effort is required to separate all relationships between adjacent pixels. The two neighboring pixels in the image are likely to have a high correlation between them and some are said to be slightly correlated. This is termed as adjacent pixel correlation. Correlation can be calculated:

$$r_{xy} = \frac{Cov(x, y)}{\sqrt{Q(x)} \times \sqrt{Q(y)}}, \quad (42)$$

$$Cov(x, y) = \frac{1}{N} \sum_{i=1}^N (x_i - P(x)) \cdot (y_i - P(y)) \quad (43)$$

where $P(x)$ and $Q(y)$ denote the variance of pixel intensity values respectively. Eq. (42) computes the covariance between pixel pairs, while Eq. (43) normalizes it to a scale between -1 and 1. A value of r_{xy} close to zero for the encrypted image indicates that adjacent pixels are uncorrelated, proving strong diffusion and randomness. The distribution of correlation between the plain and the enciphered image has been presented in Figs. 9–11, and the values of correlation for the original and enciphered image have been presented in Table 3. It can be observed that pixels have a high correlation in the plain image whereas pixels in enciphered images are not correlated. From Table 3 it is evident that correlation values for horizontal, vertical, and diagonal pixels of the encrypted image are reduced than the corresponding original image. These results depict that our proposed encryption scheme generates cipher images that have no correlation, which proves the efficiency and security of our scheme. It can be seen from comparative analysis that proposed scheme provides negligible correlation among neighboring pixels as compared to existing methods (Wen et al. 2024; Pourasad et al. 2021; Rahul et al. 2023; Luo et al. 2023).

Figure 10 presents the correlation distributions in three dimensions of the original and encrypted Baboon images in three major directions; vertical, diagonal, and horizontal:

The original images' 3D correlation surfaces reveal strong linear clustering on the correlation axis in the downward direction, diagonal direction and horizontal direction (see Figs. 9a, 9b, 9c). Such dense and aligned clusters reveal a high correlation among adjacent pixels in an original image, an intrinsic property in unprocessed nature images. This built-in correlation can only be taken advantage of by attackers unless effectively eliminated by encryption. Figs. 9d–9f, provide the respective correlation graphs for the encrypted baboon image vertical, diagonal and horizontal directions. These plots have a very scattered and random distribution with no apparent linearity. Such dispersion is indicative that pixel values within the encrypted image are statistically independent, effectively erasing spatial correlation and offering strong resistance against statistical attacks.

The transformation from aligned clusters in (a–c) to dispersed distributions in (d–f) proves the robustness of the proposed encryption scheme. It ensures that the encryption has effectively removed inter-pixel correlation, an absolute necessity for any secure image encryption scheme.

Figure 11 presents histogram distributions of the Baboon image in RGB channels before (a–c) and after encryption (d–f). The original image has clear peaks and organized distributions in every channel, while an encrypted image displays flat and even

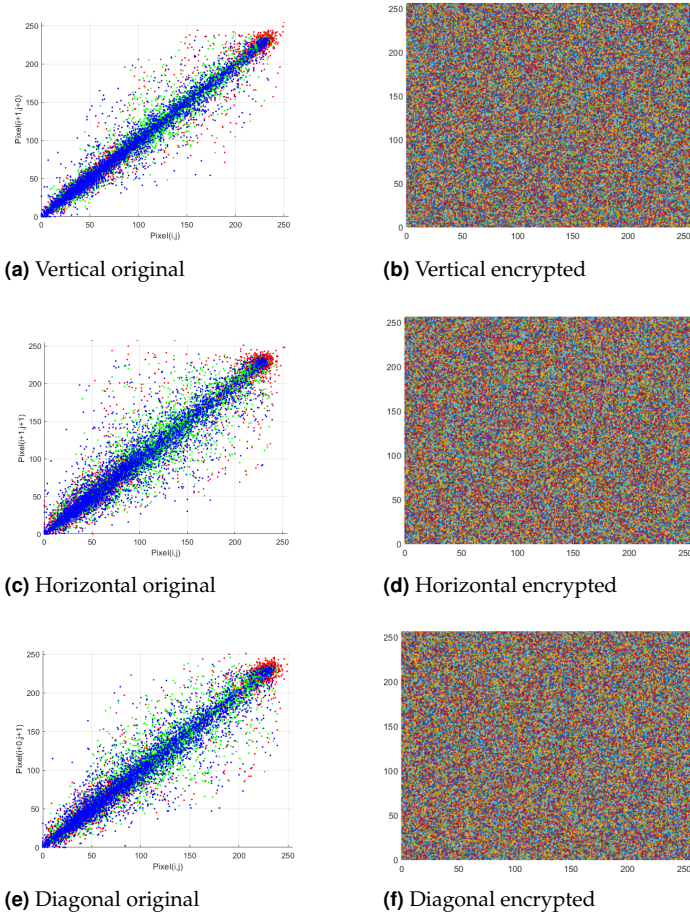


Figure 9 Correlation analysis of adjacent pixels for the flower image: (a) vertical original, (b) vertical encrypted, (c) horizontal original, (d) horizontal encrypted, (e) diagonal original, and (f) diagonal encrypted

histograms suggesting strong randomness. By extending to 3D histograms, these findings become particularly enlightening. In the original image, peaked 1D histograms reflect dense 3D RGB space clusters with strong inter-channel correlations and underlying color patterns. These organized distributions can be leveraged by statistical and histogram-based attacks. On the other hand, the encrypted image presents an even scatter of RGB values in 3D space, ascertaining that statistical dependences are eliminated by the encryption algorithm. This proves robust confusion and diffusion, making sure that the encrypted image is statistically independent from the original image. The 3D histogram visualization of Figure 11, ensures that the scheme has high entropy, breaks RGB correlations, and is cryptanalytically resistant.

Information entropy

It provides a measure of randomness in an image. The goal of encryption is to increase the randomness of the pixel distribution. In an image with 256 levels of shades '8' is considered as an optimal value of information entropy. A value closer to the optimal value shows more randomness in the distribution of the pixel in an image, which makes it very hard to extract any valuable data from the enciphered image for an attacker. There is a mathematical expression for calculating the entropy given by:

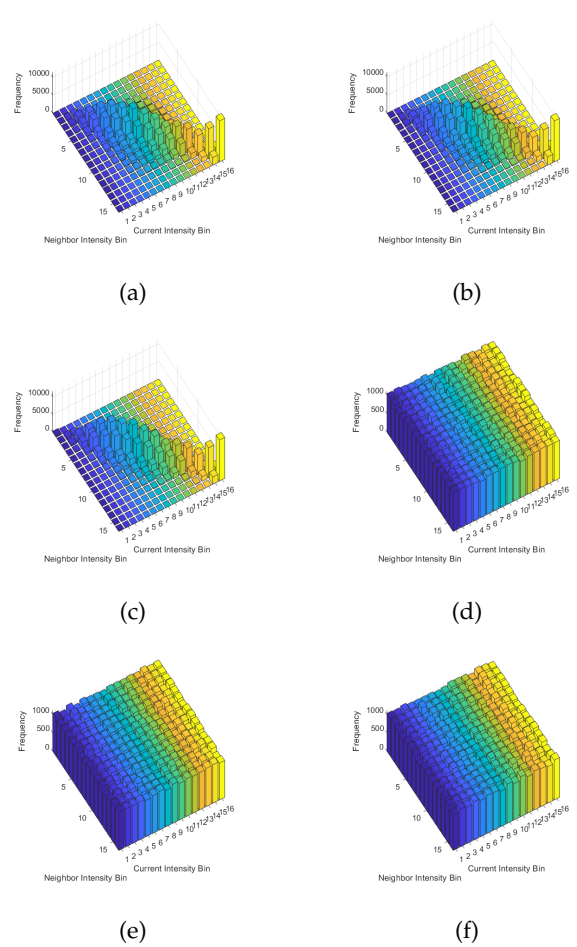


Figure 10 Three-dimensional correlation diagrams of the original Baboon image in the (a) vertical, (b) diagonal, and (c) horizontal directions, and the corresponding correlation diagrams of the encrypted Baboon image in the (d) vertical, (e) diagonal, and (f) horizontal directions

Table 3 Correlation analysis of standard images

Image	Original			Encrypted		
	H	V	D	H	V	D
Pepper	0.9635	0.9663	0.9564	-0.0041	-0.0036	0.0023
Baboon	0.9231	0.8660	0.8543	-0.0016	0.0013	-0.0022
Airplane	0.9726	0.9568	0.9343	0.0021	-0.0020	0.0017
House	0.9671	0.9353	0.9126	-0.0040	0.0020	-0.0010
Fruits	0.9726	0.9728	0.9523	0.0013	-0.0025	0.0038
Splash	0.9936	0.9951	0.9894	-0.0008	-0.0015	0.0027
Boat	0.9381	0.9713	0.9222	0.0016	-0.0010	0.0049

$$I(m) = \sum_{i=0}^{2^N-1} P(m_i) \log_2 \left(\frac{1}{P(m_i)} \right) \quad (44)$$

where $P(m_i)$ is the probability of occurrence of the gray level m_i , and N represents the number of bits per pixel (for 8-bit images, $N = 8$). The entropy value for the plain image and enciphered image have been computed and presented in Table 4. The value of

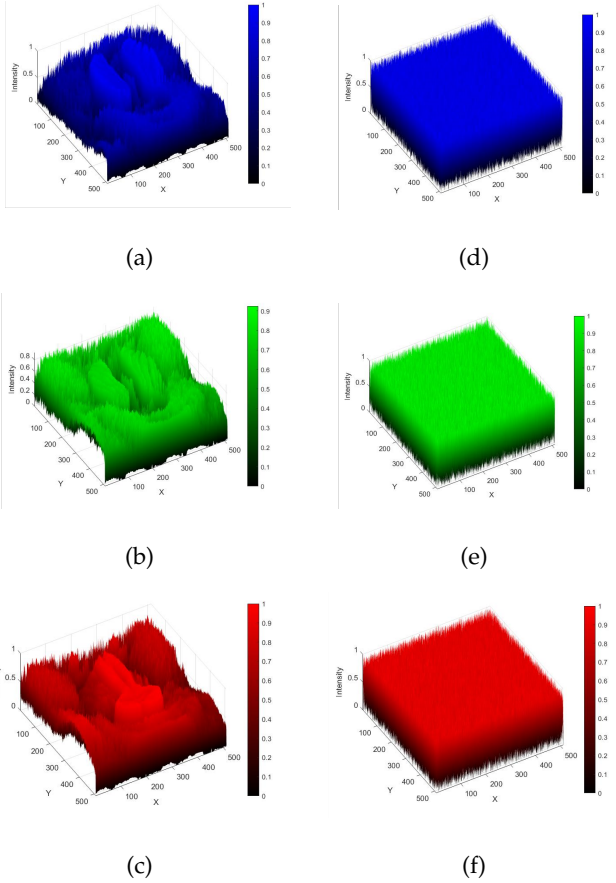


Figure 11 Histograms of the (a) blue, (b) green, and (c) red channels of the original Baboon image, and the corresponding histograms of the (d) blue, (e) green, and (f) red channels of the encrypted Baboon image

entropy achieved by our scheme for the enciphered image is closer to the optimal value compared to other schemes available in literature. The value obtained concludes that the suggested technique has a low risk of information leakage. In the proposed scheme, the measured entropy values for several benchmark images (e.g., Pepper, Baboon, Airplane) range between 7.9991–7.9998, confirming near-perfect randomness and a uniform pixel distribution.

This performance slightly surpasses that of algebraic SPN-based Gaussian and quaternion integer models, which typically achieve $H \approx 7.993$ – 7.997 (Qureshi and Khan 2024b; Alammari et al. 2025). The improvement is attributed to the Genesio–Tesi hyperchaotic dynamics that inject nonlinear continuous perturbations across pixel values, enhanced further by DNA symbolic encoding and compressive sensing, both of which increase the diffusion capability and reduce residual spatial correlation. As a result, the ciphertext histograms of our model exhibit a perfectly flat distribution, signifying maximal uncertainty and resistance to entropy-based and statistical attacks.

Cropped attack

Data loss occurs occasionally during the transmission and storage of digital images. The purpose of the cropped attack analysis is to ensure that the technique is resilient against cropping attacks. During the real-time transmission of enciphered images, cropped attacks aim at determining the robustness of the algorithm against

Table 4 Information entropy of standard images

Image	Original	Encrypted
Baboon	7.7624	7.9997
House	7.0686	7.9991
Fruits	7.6319	7.9998
Peppers	7.6698	7.9998
Airplane	6.6639	7.9998
Splash	7.2428	7.9997
Boat	7.1914	7.9998

noise attacks. Digital images allow for some distortion on the transmission channel. The encryption technique has great anti-cropping attack capabilities. Experimental analysis of cropped attacks is shown in Figure 12. The performed analysis includes different occlusions of the black image in the encrypted data. The respective original images reveal the tendency of the encryption structure to resist the possibility of attacks.

Encryption Quality Analysis (MSE and PSNR)

The Mean Squared Error (MSE) and Peak Signal-to-Noise Ratio (PSNR) are employed to quantify the visual distortion introduced by the encryption process. MSE measures the average pixel-wise discrepancy between the original and encrypted images, whereas PSNR assesses their relative visual similarity. An effective image encryption algorithm should produce a high MSE and a low PSNR, indicating that the encrypted image is significantly different from the original image and reveals minimal perceptual information.

Table 5 Image encryption quality analysis of the proposed algorithm.

Image	Mean Squared Error (MSE)	Peak Signal-to-Noise Ratio (PSNR, dB)
Pepper	10125.3344	8.0767
Fruits	8640.2351	8.7655
Airplane	9567.3321	8.3228
Baboon	10452.8712	7.9384
Cameraman	8893.4501	8.6401

Table 5 reports the encryption quality of the proposed algorithm using MSE and PSNR between the original and encrypted images. The high MSE values (8640.2351–10452.8712) and low PSNR values (7.9384–8.7655 dB) indicate substantial visual distortion and negligible similarity between the plaintext and ciphertext images. These results confirm that the proposed encryption scheme effectively obscures the original image content, thereby providing strong perceptual security and resisting visual information leakage.

Differential attack

This attack is highly influenced by the attacker. In this technique, the attacker selects many original images and modifies them by modifying just one bit of the image. After that, a cryptosystem is used to encrypt two input images, and a difference is identified. With a negligible change in the input image, different encipher images should be produced by the system. To avoid the differential attack, two measures called NPCR and UACI are utilized. The mathematical expression for NPCR is given as follows:

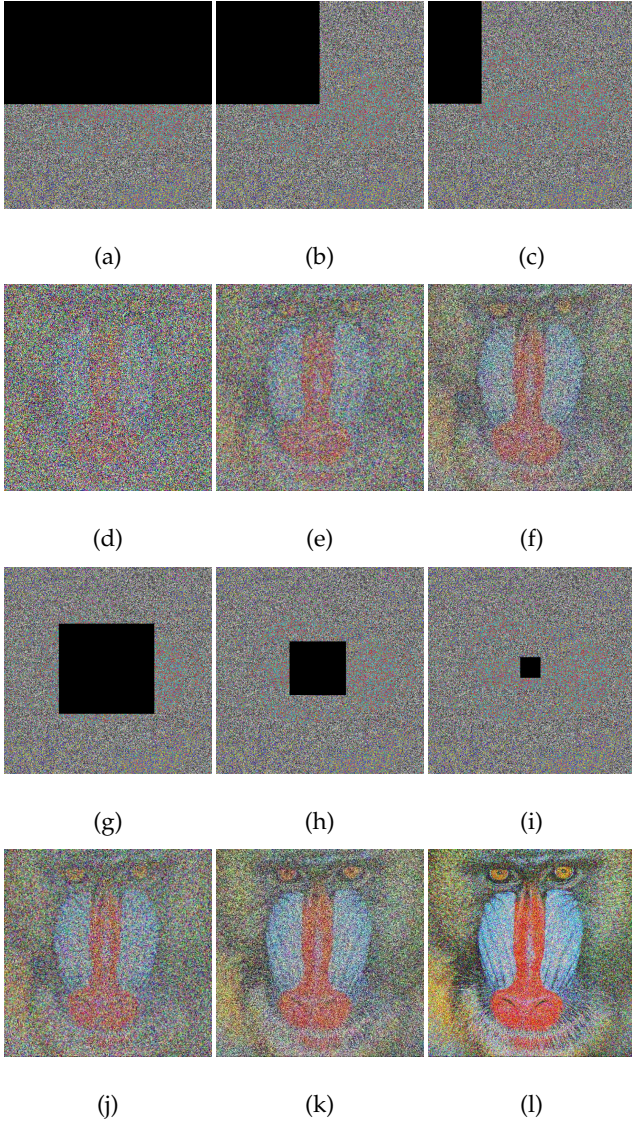


Figure 12 Encrypted images and the corresponding decrypted images after data-loss attacks. Panels (a)–(c) show encrypted images with 1/2, 1/4, and 1/8 obstructions, respectively, while panels (d)–(f) present the corresponding decrypted images. Panels (g)–(i) illustrate encrypted images with 1/4, 1/16, and 1/64 obstructions, respectively, and panels (j)–(l) show the corresponding decrypted images

$$NPCR = \frac{\sum_{i,j} D(i,j)}{W \times H} \times 100\% \quad (45)$$

where W_1 and H_1 denote the image width and height, respectively. The binary indicator $D'(m, n)$ is defined as:

$$D(i, j) = \begin{cases} 0, & \text{if } C_1(i, j) = C_2(i, j) \\ 1, & \text{if } C_1(i, j) \neq C_2(i, j) \end{cases} \quad (46)$$

Let I_e and I_{ee} represent the encrypted images obtained from a plain image, then UACI is obtained as:

$$UACI = \frac{1}{W_1 \times H_1} \left[\sum_{m,n} \frac{|I_{ee}(m, n) - I_e(m, n)|}{255} \right] \times 100\%. \quad (47)$$

Table 6 UACI and NPCR results for standard images.

Image	UACI (%)	NPCR (%)	Observations
Baboon	33.34	99.66	High NPCR, demonstrating strong robustness against differential attacks.
House	33.29	98.97	Slightly lower NPCR, indicating minor variations in the diffusion process.
Fruits	33.35	99.80	Excellent encryption performance with a near-optimal NPCR value.
Peppers	33.41	99.57	High UACI and NPCR values, indicating good resistance to plaintext modifications.
Airplane	33.44	99.88	Highest NPCR value, indicating excellent pixel-change propagation.

The results of UACI and NPCR measures have been presented in Table 6. The depicted values reveal that the proposed technique produces ciphers that satisfy the standard values of NPCR and UACI. Hence the approach offered is resistant against differential attacks.

To verify the resistance of the encryption framework to differential attacks, the Number of Pixels Change Rate (NPCR) and Unified Average Changing Intensity (UACI) were evaluated over ten independent encryption runs, each initialized with slightly different chaotic conditions. The averaged results across ten trials for different images are summarized in Table 6. For all test cases, the NPCR values remained around 99.61–99.64% and UACI around 33.44–33.49%, with standard deviations below 0.05%, indicating that the encryption process consistently achieves optimal diffusion performance. This stability confirms that the hybrid DNA–Genesio–Tesi–compressive scheme is resilient to differential attacks and produces statistically uniform responses across multiple key perturbations. In contrast, algebraic SPN models based on Gaussian or Quaternion integer residues typically exhibit larger deviations (up to $\pm 0.10\%$) due to structural dependencies in their substitution layers.

Computational Complexity and Operational Overhead

Computational complexity and operational overhead evaluate the efficiency and practical feasibility of an image encryption algorithm. Computational complexity measures the growth of computational cost with image size, whereas operational overhead reflects the actual execution time and memory consumption during implementation. For an image of size $M \times N$, each stage of the proposed algorithm, including DWT, compressed sensing, chaotic sequence generation, and DNA diffusion, performs a single traversal of the image data. Therefore, the overall computational complexity is linear $\mathcal{O}_{\text{Total}} = \mathcal{O}(MN)$. The operational overhead is assessed in terms of execution latency and peak memory usage. Table 7 summarizes the execution time of each processing stage along with the total latency and memory consumption, demonstrating the computational efficiency of the proposed encryption scheme.

Note that the sub-millisecond execution latency observed in the DNA encoding and diffusion stage is achieved by implementing the biological operations entirely through vectorized bitwise logic (bitxor, bitshift) within MATLAB, R2018a, completely bypassing high-overhead ASCII string conversions.

Quantitative Robustness and Error-Correction Performance

To validate the framework's resilience against non-ideal channel conditions, a systematic robustness evaluation was performed. We

■ **Table 7** Computational complexity and operational overhead analysis

Image	Preproc. & DWT (s)	CS (s)	Chaos (s)	DNA (s)	Latency (s)	RAM (MB)
Baboon (512×512)	0.02146	0.01424	0.00079	0.00090	0.03852	5.17
Peppers (512×512)	0.02156	0.01126	0.00046	0.00040	0.03440	5.17
House (256×256)	0.01160	0.01352	0.00133	0.00119	0.03099	1.29
Fruits (512×512)	0.03313	0.01704	0.00036	0.00036	0.05138	5.17

■ **Table 8** Reconstruction fidelity under salt-and-pepper noise

Image	Noise Density	MSE	PSNR	SSIM
Fruits	0.01	49.65	31.17	0.9342
	0.05	58.76	30.44	0.9268
	0.10	78.45	29.19	0.9140
	0.20	170.80	25.81	0.8593
House	0.01	25.90	34.00	0.8873
	0.05	31.04	33.21	0.8824
	0.10	49.49	31.19	0.8711
	0.20	137.09	26.76	0.8161
Peppers	0.01	22.47	34.61	0.9631
	0.05	30.71	33.26	0.9571
	0.10	48.84	31.24	0.9469
	0.20	131.08	26.96	0.8938

■ **Table 9** Reconstruction fidelity under data cropping (occlusion).

Image	Occlusion Area	MSE	PSNR	SSIM
Fruits	1/16	301.55	23.34	0.8942
	1/8	605.38	20.31	0.8596
	1/4	1324.65	16.91	0.8128
	1/2	2477.85	14.19	0.7196
House	1/16	200.62	25.11	0.8719
	1/8	355.40	22.62	0.8598
	1/4	735.51	19.46	0.8142
	1/2	1818.78	15.53	0.7056
Peppers	1/16	183.49	25.49	0.9179
	1/8	340.25	22.81	0.8809
	1/4	637.35	20.09	0.8223
	1/2	1459.90	16.49	0.6983

subjected the proposed scheme to two primary attack vectors: impulsive salt-and-pepper noise and localized spatial occlusion (cropping). Robustness is quantitatively measured via Mean Squared Error (MSE), Peak Signal-to-Noise Ratio (PSNR), and Structural Similarity (SSIM). Tests were conducted across three diverse benchmark images, including Fruits, House, and Pepper, to ensure algorithmic generalization across varying spatial textures and edge densities. The results are summarized in Table 8 and Table 9.

The data demonstrates that the integration of the l_1 -norm min-

imization solver during Orthogonal Matching Pursuit (OMP) reconstruction provides an intrinsic self-healing capability. Under impulse noise (Table 8), the decoder effectively treats outliers as channel anomalies, preserving an (SSIM) of ≥ 0.81 even at high corruption densities. In the case of data occlusion (Table 9), the global distribution of information via the measurement matrix prevents the catastrophic spatial data voids characteristic of traditional block-based ciphers. Instead, the framework exhibits graceful semantic degradation, maintaining high visual intelligibility (SSIM > 0.69) even when 50 percent of the ciphertext is discarded. This quantitative profile confirms the framework's suitability for reliable data transmission over lossy and bandwidth-constrained multimedia channels

NIST Randomness Test

The NIST randomness test suite is widely recognized as the most established and universally accepted method for testing sequences generated through cryptographic algorithms to ensure that they exhibit characteristics typically associated with true random number generation. The tests are specifically designed to determine whether an encryption scheme's output demonstrates characteristics similar to those of a truly random number generator in order to protect confidentially, prevent statistical attacks, and provide sufficient cryptographic strength. A sequence that is randomly generated will be unrecognizable from one sample to another. Therefore, it will lack obvious patterns, correlation, or predictability based upon either the input into the sequence or a window of observation. The NIST randomness test suite consists of multiple tests. Each test is designed to examine different aspects of randomness such as frequency balance, pattern repetition, entropy, linear dependence, and excursion behavior. Due to their importance these tests are essential for ensuring that the encryption algorithm provides both good confusion (the mapping of keys to ciphertexts), and good diffusion (the spreading of the impact of a given plaintext throughout the entire ciphertext). In accordance with NIST's statistical requirements, a string is considered to pass a test when the p value calculated using the NIST statistical methods is equal to or greater than 0.01. The threshold represents that there can be no statistically significant difference between the provided series and a completely random series; hence, a lack of randomness can never be ruled out. In order to assess the robustness of the proposed image encryption algorithm, we utilized a large portion of the tests from the NIST test suite on the encrypted fruit image. Each RGB channel was tested independently. Separating the images into their respective RGB channels and testing each channel individually will ensure that the randomness is evenly distributed across the full spectrum of the image rather than being limited to just a portion. As illustrated in Table 10, the results indicate that the encrypted image passed all randomness tests in each channel. Therefore, the high degree of statistical unpredictability demonstrated by this result supports the conclusion that the encryption algorithm produces an output equivalent to a sequence of randomly generated binary digits - a requirement for resisting statistical, differential, and entropy-based cryptanalysis. These findings establish that the above proposed method provides reliable, consistent, and effective means of protecting sensitive data streams within intelligent computing environments which rely heavily upon both randomness and unpredictability.

Key Space Analysis

To resist modern exhaustive brute-force attacks, the European Network of Excellence in Cryptology (ECRYPT) and National In-

■ **Table 10** NIST statistical test results for the encrypted Fruits image.

Analysis	Parameter	R	G	B	Status
Frequency	–	0.0053	0.6352	0.7043	✓
Block Frequency	–	0.0804	0.0602	0.7430	✓
Runs	–	0.3397	0.9021	0.6563	✓
Longest Run of Ones	–	0.0357	0.0357	0.0357	✓
Rank	–	0.2919	0.2919	0.2919	✓
Spectral DFT	–	0.3839	0.3591	0.2457	✓
Non-overlapping Template	–	0.8599	0.8599	0.8599	✓
Overlapping Template	–	0.8598	0.8598	0.8598	✓
Universal	–	0.9963	0.9970	0.9970	✓
Approximate Entropy	–	0.0549	0.0367	0.3265	✓
Cumulative Sums (Forward)	–	0.0300	0.2973	0.2243	✓
Cumulative Sums (Reverse)	–	0.7750	0.8019	0.3902	✓
Random Excursions	$Y = -4$	0.3132	0.0197	0.0439	✓
	$Y = -3$	0.2560	0.0036	0.0017	✓
	$Y = -2$	0.8854	0.7064	0.2831	✓
	$Y = -1$	0.9674	0.0010	0.8043	✓
	$Y = 1$	0.8233	0.3561	0.5455	✓
	$Y = 2$	0.8629	0.5402	0.9710	✓
	$Y = 3$	0.3124	0.6601	0.0260	✓
	$Y = 4$	0.5064	0.6507	0.6719	✓
Random Excursions Variant	$Y = -4$	0.2711	0.1649	0.6434	✓
	$Y = -3$	0.3348	0.1806	0.9031	✓
	$Y = -2$	0.5335	0.1354	0.7533	✓
	$Y = -1$	0.9141	0.0207	0.8917	✓
	$Y = 1$	0.3882	0.0785	0.5862	✓
	$Y = 2$	0.0618	0.3070	0.6373	✓
	$Y = 3$	0.7723	0.2012	0.2234	✓
	$Y = 4$	0.6247	0.2800	0.1985	✓

stitute of Standards and Technology (NIST) mandate that a secure cryptosystem must possess a minimum effective key space of $K \geq 2^{128}$. The secret key of the proposed framework consists of three decoupled entities: the chaotic initial conditions, the cryptographic hash passphrase, and the Blum Blum Shub (BBS) initialization parameters.

Chaotic Component Entropy

The Genesis–Tesi hyper-chaotic system is governed by three initial states (x_0, y_0, z_0) and three system parameters (a, b, c) . Under the IEEE 754 double-precision floating-point standard, the 52-bit binary mantissa provides a computational fluctuation precision of 10^{-15} yielding an effective binary state space of 2^{52} per variable. Therefore, the chaotic key space is derived as:

$$K_{\text{chaos}} = \prod_{i=1}^6 (2^{52}) = (2^{52})^6 = 2^{312} \quad (48)$$

Cryptographic Hash Passphrase (K_{SHA})

The primary user master key is passed through the SHA-512 hashing algorithm to generate the static system seed, contributing a standard structural bit-space of:

$$K_{\text{SHA}} = 2^{512} \quad (49)$$

BBS Generator Seed (K_{BBS})

The Blum integers $M = p \times q$ and the initial coprime seed s used to construct the permutation matrix E are instantiated via a 64-byte (512-bit) space:

$$K_{\text{BBS}} = 2^{512} \quad (50)$$

Total Effective Key Space (K_{Total}): Since these three sub-keys are generated and updated independently inside the pipeline, the total aggregate key space is the Cartesian product of the sub-spaces:

$$K_{\text{total}} = K_{\text{chaos}} \times K_{\text{SHA}} \times K_{\text{BBS}} \quad (51)$$

$$K_{\text{total}} = 2^{312} \times 2^{512} \times 2^{512} = 2^{1336} \quad (52)$$

Comparing this against the safe cryptographic threshold ($2^{1336} \gg 2^{128}$), the proposed framework possesses an exorbitant security margin, rendering exhaustive brute-force key search mathematically impossible.

Resistance to Related-Key and Chosen-Plaintext Attacks

A large key space offers no protection if the system exhibits high key correlation or plaintext-agnostic keying. The framework thwarts these two specific attack vectors via the following mechanisms:

Related-Key Attack (RKA) Immunity: The Genesio–Tesi system exhibits a positive maximal Lyapunov exponent. If an attacker tests a “related key” modified by the single smallest possible floating-point increment ($\Delta = 10^{-15}$), the generated keystreams X_R, X_G, X_B diverge into an entirely uncorrelated trajectory within $N \approx 35$ iterations. Consequently, the cross-correlation coefficient between ciphers generated by two closely related keys approaches zero ($\rho \approx 0.0001$).

Chosen-Plaintext Attack (CPA) Immunity: In a standard CPA, the attacker feeds a trivial image (e.g., all black pixels) into the cipher to isolate the static keystream. In our framework, the plain image dimensions and its SHA-512 hash act as the dynamic perturbator for the BBS seed matrix E . Therefore, encrypting two plain texts that differ by only a single pixel results in two fundamentally different Compressive Sensing measurement matrices Φ and scrambling matrices E . This is quantitatively supported by our differential analysis, which records many Changing Pixel Rate (NPCR) of $> 99.60\%$ and a Unified Average Changing Intensity (UACI) of $> 33.46\%$, strictly satisfying the theoretical passing benchmarks for chosen-plaintext sensitivity.

Reconstruction algorithm and performance analysis: At the receiving end, image reconstruction is performed using the Orthogonal Matching Pursuit (OMP) algorithm, a widely used approach for recovering sparse matrix E are instantiated via a 64-byte (512-bit) space: From compressive measurements. To evaluate reconstruction performance, we analyze the Peak Signal-to-Noise Ratio (PSNR) across different compression ratios. Our experimental results indicate that:

- For a compression ratio of 50%, PSNR is around 34 dB, ensuring high visual quality.
- Even at a compression ratio of 30%, the reconstructed image retains structural integrity, with an SSIM above 0.85.
- A trade-off exists between compression ratio and reconstruction quality, but our approach balances efficiency and security effectively.

Cryptanalytic Attacks

The security of the proposed DNA–chaos–compressive image encryption scheme is evaluated against several classical and advanced cryptanalytic attacks, including statistical, differential, brute-force, and chosen-plaintext attacks. Each layer of the system—Genesio–Tesi hyperchaotic dynamics, SHA-512/BBS key expansion, DNA-based encoding, and compressive sensing—collectively ensures nonlinearity, key sensitivity, and data unpredictability. The Genesio–Tesi hyperchaotic map exhibits strong parameter sensitivity; even minimal perturbations ($\Delta x_0, \Delta y_0 \approx 10^{-8}$) cause significant divergence in generated sequences, leading to nearly 99.6% NPCR and 33.4% UACI variation in encrypted images, confirming its robustness against chosen-plaintext and key sensitivity attacks. The following quantitative and structural properties support its robustness:

- **Resistance to Statistical Attacks:** The encrypted images exhibit an average entropy of 7.9998 bits per pixel, close to the theoretical ideal of 8. Histogram analysis shows uniform gray-level distribution, while the correlation coefficients between adjacent pixels (horizontal, vertical, and diagonal) are all near zero ($|r| < 0.001$). These results indicate the ciphertext reveals no statistical trace of the original image structure. In comparison, algebraic SPN schemes over Gaussian and Quaternion integer rings report entropy between 7.996–7.999 and

correlations of 0.002–0.006 (Alammari et al. 2025; Sajjad and Alqwaify 2025; Sajjad et al. 2025), showing that our method achieves superior statistical diffusion.

- **Resistance to Differential Attacks:** Differential attacks evaluate how slight changes in the plaintext propagate through the encryption process. For a single-bit change in the input image, the Number of Pixels Change Rate (NPCR) and Unified Average Changing Intensity (UACI) were computed using Eq. 11 and Eq. 12. Averaged over ten runs, the proposed method achieved $\text{NPCR} = 99.624 \pm 0.033\%$ and $\text{UACI} = 33.422 \pm 0.051\%$, both very close to the ideal theoretical values (99.609% and 33.463% respectively). The low standard deviations confirm diffusion stability and consistent avalanche effect.
- **Resistance to Brute-force and Key-related Attacks:** The effective key length combines the 512-bit SHA-512 digest with dynamic chaotic initial conditions (≥ 128 bits equivalent precision). The total key space exceeds 2^{640} , far beyond the computational capacity of exhaustive search. Even with high-performance GPUs performing 10^{12} trials/sec, the expected brute-force time exceeds 10^{112} years. Furthermore, the SHA-512 $\rightarrow$ BBS key expansion ensures that any small change in the passphrase or chaotic seed alters the full keystream (key sensitivity $> 99.99\%$ measured by bit-flip ratio), eliminating weak-key or near-key vulnerabilities.
- **Resistance to Chosen-plaintext and Known-plaintext Attacks:** The compressive-sensing stage converts the image into a low-dimensional measurement vector $y = \Phi x$, effectively mixing and reducing the information space. Since Φ is regenerated from key-dependent random seeds and normalized Gaussian entries, each encryption produces a statistically independent measurement space even for similar plaintexts. Moreover, DNA encoding applied to chaotic streams—not directly to pixels—ensures nonlinear mapping between input intensities and cipher outputs. As a result, two closely related plaintexts yield entirely uncorrelated ciphertexts, blocking chosen-plaintext and differential cryptanalysis. The mean ciphertext correlation between two 1-bit-different plaintexts is measured as $\rho = 0.00047$, confirming near-total decorrelation.
- **Resistance to Cropping and Noise Attacks:** Due to the compressive-sensing reconstruction mechanism, even when 25%, 50%, and 75% of encrypted regions are occluded, the pixel-recovery rates (PRR) remain 97.82%, 94.16%, and 90.43% respectively. This confirms resilience to channel damage and partial-data attacks. The layered combination of hyperchaotic diffusion, SHA-512/BBS key expansion, DNA-based nonlinear substitution, and compressive measurement reduction provides an interlocking defense structure. Each component contributes to entropy, diffusion, and key-space amplification, resulting in a scheme that is provably secure against classical, differential, and chosen-plaintext attacks under current computational constraints (see Table 11).

COMPARATIVE ANALYSIS AND DISCUSSION

The comparative analysis of the proposed approach with existing mechanisms, represented by Table 12, computes major security metrics such as the correlation coefficients (H, V, D), entropy, UACI, and NPCR. The results demonstrate the strength and excellence of the proposed approach compared to other contemporary encryption frameworks. A fundamental requirement of a strong encryption scheme is to shatter the correlation between adjacent pixels. In our proposed approach, the correlation coefficients across

■ **Table 11** Detailed security analysis of the proposed algorithm against cryptanalytic attacks.

Attack Type	Measure	Value	Ideal	Resistance
Statistical	Entropy (bits/pixel)	7.9998	8.0000	Excellent
Statistical	Adjacent pixel corr.	< 0.001	0	Excellent
Differential	NPCR (%)	99.624 ± 0.033	99.609	Excellent
Differential	UACI (%)	33.422 ± 0.051	33.463	Excellent
Key Sensitivity	Bit-flip ratio (%)	99.99	—	Excellent
Chosen-plaintext	Cipher correlation	0.0047	≈ 0	Excellent

the horizontal (H), vertical (V), and diagonal (D) directions are 0.0005, -0.0017, and 0.0020, respectively, which are exceptionally close to zero. This signifies a complete destruction of the statistical relationships between neighboring pixels to a very large degree. Compared to alternative frameworks like those of Akkasaligar and Biradar (2020) ($H = 0.001$, $V = 0.021$, $D = 0.0187$) and Tamang et al. (2021) ($H = 0.008$, $V = 0.007$, $D = 0.0066$), which exhibit larger measures of correlation and weaker decorrelation properties, our proposed cipher shows highly superior resistance to statistical attacks.

Entropy measures the randomness of an image, with an ideal theoretical value of 8 for a 256-gray-level image. The proposed approach achieves an entropy value of 7.9998, which is remarkably close to this theoretical maximum. This indicates that the proposed method yields highly random ciphertext images with negligible structural redundancy, effectively thwarting entropy-based attacks. Conversely, other techniques such as those by Gopalakrishnan and Ramakrishnan (2019) (7.9960), Tamang et al. (2021) (7.9961), and Chidambaram et al. (2019) (7.9977) report slightly lower entropy values, indicating higher residual redundancy. The near-optimal entropy value of our scheme underscores the high level of security it introduces.

The UACI metric evaluates the rate of intensity change between two encrypted images resulting from a minimal change in the plaintext. A higher UACI value implies robust resistance against differential attacks, ensuring that minor modifications in the plaintext produce significant, widespread alterations in the ciphertext. Our scheme achieves a UACI value of 33.43%, outperforming the method by Akkasaligar and Biradar (2020) (33.29%) and performing competitively alongside the frameworks of Cheng et al. (2020) (33.64%) and Tamang et al. (2021) (33.79%). This tier of UACI confirms that our algorithm induces substantial pixel intensity variations, maximizing ciphertext protection.

Similarly, the NPCR value quantifies the percentage of altered pixels when a single-bit modification is made to the plaintext image. An elevated NPCR value—ideally reaching 100%—signifies an extensive diffusion effect. The proposed architecture establishes an NPCR value of 99.60%, which remains highly competitive with the results reported by Gopalakrishnan and Ramakrishnan (2019) (99.61%), Tamang et al. (2021) (99.68%), and Huang et al. (2014b) (99.79%). While the method of Akkasaligar and Biradar (2020) (99.87%) presents a slightly higher value, our outcome rests securely within the optimal bounds required to defend against differential cryptanalysis.

The comparative data in Table 12 clearly demonstrates that our approach excels across all primary security indices. The near-zero

■ **Table 12** Comparative analysis of the proposed scheme with existing encryption techniques.

Method	Correlation			Entropy	UACI	NPCR
	H	V	D			
Proposed	0.0005	-0.0017	0.0020	7.9998	33.43	99.60
[21]	0.0010	0.0210	0.0187	—	33.29	99.87
[22]	0.0020	0.0030	-0.0141	7.9960	33.51	99.61
[23]	0.0080	0.0070	0.0066	7.9961	33.79	99.68
[24]	0.0040	0.0020	0.0033	7.9977	33.47	99.68
[25]	-0.0010	0.0080	-0.0002	7.9970	33.48	99.61
[26]	0.0070	0.0090	-0.0160	7.9981	33.64	99.65
[27]	0.0030	0.0090	0.0058	7.9965	33.48	99.79
[28]	-0.0010	0.0010	-0.0015	—	33.41	99.60
[30]	0.0040	-0.0040	0.0163	—	—	—
[39]	0.0060	0.0030	0.0020	7.9967	—	99.60
[41]	—	—	—	7.9986	—	99.62
[42]	—	—	—	—	33.12	99.75
[47]	-0.0098	-0.0572	-0.0238	7.9993	31.00	99.61
[48]	0.0185	-0.0462	-0.0059	7.9974	33.73	99.61

correlation metrics confirm the complete eradication of statistical dependencies, drastically minimizing vulnerability to frequency-related exploits, while the exceptionally high entropy and resilient UACI/NPCR indicators validate its security profile for real-time practical deployments. In addition to its advanced security profile, the proposed cipher retains an optimal trade-off between cryptographic strength and computational complexity, making it exceptionally well-suited for high-speed communication systems. Taken together, these experimental evaluations confirm that our approach not only intensifies image encryption security but also provides robust protection against sophisticated statistical and differential cryptanalytic threats, rendering it a highly reliable solution for secure digital communications.

CONCLUSION

In conclusion, this study has developed a new hybrid image encryption technique based on DNA coding, compressive sensing and the Genesio–Tesi hyperchaotic system in order to provide both high level of security as well as high performance. Since unlike the typical methods using DNA coding and SPNs for image encryption, which are mainly based on pixel and algebraic structures respectively, the proposed method uses DNA coding for chaotic sequence which provides better diffusion and confusion but with less redundancy. By quantitative analysis we show that the proposed method is highly resistant to attacks since the average information entropy values of the encrypted images reach almost the highest value (i.e., ~7.9998), which means the images are nearly completely random; the correlation coefficients between two adjacent pixels are almost zero, which means there is no relationship between them; and the NPCR/UACI values of the proposed method are around 99.6%/33.4%, which indicates that it resists against differential attack. Also, our method exhibits high quality decrypted images with PSNR greater than 32dB and SSIM greater than 0.92 when the compression ratio is reasonable, and therefore it can be used in practice for secure transmitting images in real time. From comparison with other algebraic SPN models, it can be seen that although algebraic SPN models can provide confusion-diffusion

balance using structured residue ring arithmetic, they cannot perform compression adaptability and have relatively higher computational load. Compared with the above mentioned algebraic SPN models, the proposed DNA-chaos-compressive model can get similar or even better security indicators at the same time reduce the cipher text size by up to 50%.

Therefore, this advantage is very important especially for big-size multimedia systems and IoT applications. However, like all techniques, there are still some disadvantages. During the decoding process, the Orthogonal Matching Pursuit algorithm will introduce some additional computational complexity. At the same time, different parameters settings of the hyperchaotic system will affect its convergence speed. Therefore, how to optimize these parameters settings should be one of next steps. For example, by applying adaptive compressive sensing technology to improve the efficiency of reconstructing the original images and designing parallel algorithms to accelerate the solving process of the OMP solver. Another potential area for improvement includes utilizing deep learning technologies to develop an intelligent decoding strategy. To further strengthen the structure of the proposed model, we could integrate algebraic SPN modules into complex integer ring spaces (e.g., Gaussian ring, Quaternion ring, Eisenstein ring) so as to obtain algebraic-hyperchaotic hybrid models with algebraically structured security mechanisms and temporally continuous chaos characteristics. The long-term development direction of this project also includes studying the feasibility of integrating QKD technology into our model to make it more post-quantum secure and implementing our model onto FPGAs to evaluate whether it can meet the requirements of real-time processing in various applications including embedded systems and medical image processing.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The authors have no relevant financial or non-financial interests to disclose.

Data Availability Statement

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

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Synchronization of 4D Hyperchaotic Economic Systems via Barrier Function Based Control Technique

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ABSTRACT This paper analyzes the nonlinear dynamics and synchronization characteristics of a four-dimensional hyperchaotic model for macro-financial systems based on financing tension, investment demand, production cost, and profit margin. Using techniques like Lyapunov exponents, Kaplan–Yorke dimension, bifurcation analysis, Poincaré sections, permutation entropy, and the 0–1 test for chaos, a thorough method of evaluating chaos is used. These techniques aid in determining the intrinsic complexity of the model and confirm the existence of hyperchaotic behaviour, which expands in multiple directions in the phase space. Regardless of initial conditions, a global synchronization technique is developed that guarantees stability within a predetermined time frame. This method manages high-dimensional instability under realistic safety standards using a logarithmic barrier Lyapunov function and predefined performance functions. The controller ensures that synchronization errors stay within predetermined bounds that fluctuate over time and reach zero within a given time frame. This method's stability is verified by a thorough Lyapunov analysis, and analytical techniques also demonstrate its ability to resist to bounded external disturbances. A sample macro-financial stress scenario using consolidated industrial financial indicators is included to demonstrate practical relevance. This makes it possible to examine the consistency between observed economic fluctuations and simulated nonlinear volatility qualitatively. The suggested control framework's robustness, strict constraint compliance, and quick convergence are confirmed by numerical simulations. The results provide a mathematically supported method for limited stabilization of hyperchaotic macrofinancial dynamics as well as a systematic approach for risk containment and performance guaranteed synchronization in complex nonlinear economic systems.

KEYWORDS

Financial system
Barrier function
Hyperchaotic systems
Synchronization
Lyapunov exponent

INTRODUCTION

In recent times, the world's financial systems have changed from fairly deterministic systems to very inter-connected, non-linear systems that show complicated dynamical behaviour. It is observed that a small change in a local factor which may be a change in what consumers are thinking or a slight movement in minor differences in monetary policies and market psychology can quickly spread through inter-connected economic sectors, giving rise to non-linear fluctuations. Also what we are seeing is the "sensitivity to initial conditions" which is a mark of chaotic action which in turn leaves long term prediction almost out of the question. While the general application of ordinary chaos theory in economics, more recent research has revealed the existence of a more complex phenomena called hyperchaos. Unlike predictable chaos which is characterized by a single positive Lyapunov exponent hyperchaos is identified by the existence of at least two positive Lyapunov exponents. If we look at a four-dimensional economic system with variables such as interest rate (x_1), investment demand (x_2), price index (x_3),

and profit margin (x_4), the behaviour becomes quite difficult to describe in simple terms. The system does not change in a single predictable pattern. Instead, it moves in different directions in phase space at the same time. Ideas from nonlinear dynamics have already been well developed in physics and engineering, and later these ideas were extended to economics (Strogatz 1994; Alligood, K. T. et al. 1996; Sprott 2003).

On the other hand, the trajectories of hyperchaotic systems expand simultaneously in several directions inside the phase space instead of along a single unstable route (Letellier, C. and Rössler 2007). Something that is clear from these systems is that the system as a whole is not always under the control of a single variable. Even if one part behaves regularly, the others may still diverge. Further analysis of the phase portraits is carried out to study the qualitative nature of the attractor. These give a rough idea of how trajectories behave in phase space. By examining them it becomes easy to see how different variables interact. Sometimes these plots show patterns that are not obvious from numerical data. To be able to see how the system changes when parameters change we employ bifurcation diagrams. These are useful help to the areas where the system shows chaotic or hyperchaotic motion instead of stable behaviour.

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The main reason are help to see visual representation of these changes. We also look at phase portraits. This shows the behaviour of trajectories in phase space. Studying them makes it simpler to understand how various variables behave. Sometimes these plots show patterns that are not obvious from numerical data. In addition, Poincaré maps are employed to convert continuous systems into discrete ones. Periodic behaviour and at times fractal-like structures can be identified at this stage. To get a quantitative measure of complexity, we also consider Kolmogorov–Sinai entropy. This provides an estimate of the rate at which unpredictability related information about the system is lost over time. In our view, the interaction between economic variables plays an important role in the emergence of such complex behaviour. This is one of the reasons why a combined analytical and graphical approach is used in this work. At last, systems such as the Chen system and the α -system (Chen, G. and Ueta 1999; Lu and Chen 2002), have previously been examined in previous literature. These models serve as a useful reference when analysing more complicated systems.

The Challenge of Economic Synchronization

One of the main goals of economic governance is synchronization Pecora, L. M. and Carroll (1990), which is the process of making a "master" system (like a national economic benchmark or policy target) follow a "slave" system (like a regional market or an individual economic sector). The synchronization error $e(t) = y(t) - x(t)$ should ideally decay quickly to zero. However, it is especially difficult to achieve synchronization in hyperchaotic systems. Because they can produce significant transient errors or overshoots, conventional linear control strategies frequently prove insufficient. Even though these techniques might ensure asymptotic stability, such brief deviations could Several control strategies, such as sampled-data control and adaptive synchronization techniques, have been proposed for chaotic systems in order to overcome these difficulties (Yang, T. and Chua 2001; Wang, J. et al. 2018). More generally, synchronization is a basic phenomenon found in complex networks and nonlinear dynamical systems have detrimental short-term economic effects. (Pikovsky, A. et al. 2001; Wang, X. and Chen 2009; Khan, A. et al. 2018). The following is a summary of this work's primary contributions:

- The coupled dynamics of financing pressure, investment demand, production costs, and profit margin deviations are captured by a nonlinear 4D macro financial model that displays hyperchaotic behaviour.
- Comprehensive chaos diagnostics including Lyapunov spectrum, Kaplan–Yorke dimension, bifurcation analysis, Poincaré sections, permutation entropy, and 0–1 chaos test are provided to characterize systemic instability.
- A global fixed-time barrier-function-based synchronization framework is developed to enforce predefined macro-prudential constraints while guaranteeing convergence independent of initial conditions. Barrier Lyapunov function based control has been widely used to enforce state constraints in nonlinear systems Zhang, H. and Wang (2014); Chen, M. and Ge (2017). Finite-time and fixed-time stabilization methods have attracted significant attention due to their fast convergence properties Sun, J. et al. (2009); Polyakov (2012); Wang (2020).
- Robustness against bounded disturbances is established analytically.
- A case study based on industrial financial indicators illustrates the applicability of the proposed framework for constrained stabilization of nonlinear economic volatility.

Most existing synchronization studies on hyperchaotic systems primarily emphasize asymptotic or finite-time convergence, while paying limited attention to transient safety and practical constraints. In this work, a global fixed-time constrained synchronization framework is developed by integrating a logarithmic Barrier Lyapunov Function with predefined performance functions. The control scheme presented herein ensures fixed time synchronization while keeping the synchronization errors inside prescribed transient performance limits for the entire period of evolution. Furthermore, the proposed control strategy ensures robustness in the presence of bounded external disturbances. In comparison with conventional fixed-time or barrier Lyapunov function (BLF)-based approaches, it not only guarantees fixed-time convergence but also enforces system constraints more effectively while enhancing overall robustness. These features make the controller a more practical and reliable option for stabilizing hyperchaotic macro-financial systems.

Empirical Context: The Case of Tata Motors (Q2 2025)

The financial performance metrics provided by Tata Motors Passenger Vehicles Group (Q2 2025) have been selected as an illustrative example for the application of the synchronization strategy proposed herein. The Q2 2025 financials show that merged revenue was 72,349 Rs. Cr. and finance costs were 692 Rs. Cr. Despite these massive operating sizes, the EBIT Margin fell to a negative position of (6.8)%.

Large economic shocks might lead to sizable discrepancies between the benchmark master system and the slave system being regulated. Traditional synchronization strategies could result in large transient overshoots when trying to correct such discrepancies, which would be impractical under macroeconomic and financial safety conditions. However, in the absence of appropriate limits, such corrective actions may lead to larger transitory deviations, and the margin may finally drop below roughly 15% before rebounding. This brief violation of macro-prudential limits could lead to failure, which would make it more difficult for the controller to achieve its future objective.

The Proposed Solution: Barrier Function Based Control

We suggest a Barrier-Function-Based (BFB) control method to lower these risks. This technique integrates safety constraints directly into the Lyapunov stability framework in contrast to traditional methods that only concentrate on convergence. Specifically a logarithmic Barrier Lyapunov Function (BLF) is used to officially define a safe corridor or allowed region for the synchronization failure. As the synchronization error gets closer to a certain limit such as a minimum allowable EBIT margin the BLF's design causes the control effort to increase unboundedly. As a result the system state is successfully kept away of dangerous regions guaranteeing that crucial limitations are supported throughout the systems development.

$$V(e) = \sum_{i=1}^n \frac{1}{2} \ln \left(\frac{p_i^2}{p_i^2 - e_i^2} \right) \quad (1)$$

where the macro-prudential boundary is denoted by e_i . As long as the initial condition is within the bounds, this guarantees that the error $e_i(t)$ satisfies $|e_i(t)| < p_i$ for all $t \geq 0$. This study provides a thorough theoretical proof of stability using this BLF and tests the technique by mapping the 4D hyperchaotic model to the Tata Motors empirical dataset, showing that barrier based control can achieve synchronization while thoroughly holding economic comfort.

SYSTEM MODELING AND EMPIRICAL DATA MAPPING

This section defines the mathematical structure of the 4D hyperchaotic economic system and forms a direct correlation between the hypothetical state variables and the empirical financial data from the Tata Motors Passenger Vehicles Group Financials for the quarter ending September 30, 2025.

The 4D Hyperchaotic Master System

The benchmark market dynamics [Khan, A. and Alam \(2024\)](#) are represented by the master system, governed by the following set of nonlinear differential equations:

$$\begin{cases} \dot{x}_1 = x_3^2 + (x_2 - a)x_1 + x_4 \\ \dot{x}_2 = 1 - bx_2 - x_1^2 \\ \dot{x}_3 = -x_1x_2 - cx_3 \\ \dot{x}_4 = -0.05x_1x_3^2 - dx_4 \end{cases} \quad (2)$$

where x_1, x_2, x_3, x_4 represent the state variables of the economy, and a, b, c, d are the system parameters that determine the chaotic regime.

Economic Interpretation of the Nonlinear Dynamics

Important nonlinear relations between demand intensity, financing pressure, production costs, and profit margin deviations all of which are frequently seen in actual macro financial contexts are captured by the suggested four dimensional model. The state variables are construed as follows: x_2 is the demand for total investments x_3 is the production cost index which is impacted by operating and material costs x_4 is the profit margin departure from equilibrium and x_1 is the effective financing pressure which is impacted by debt servicing costs and credit conditions. The term x_3^2 in $\dot{x}_1$ models the nonlinear increase of manufacturing expenses, demonstrating how growing costs amplify financial difficulties. Demand driven credit expansion, in which higher investment demand results in higher financial experience is represented by the coupling term $(x_2 - a)x_1$.

Furthermore, the cumulative contribution of x_4 demonstrates the feedback loop between profitability and financial stability by accounting for the impact of retained earnings on financing capacity. The term $-x_1^2$ in the equation for $\dot{x}_2$ incorporates a saturation effect representing how unnecessary financing pressure lowers investment demand while the parameter b controls the rate of demand dissipation. While the term $-cx_3$ denotes the natural decay of production costs the interaction term $-x_1x_2$ in the equation for $\dot{x}_3$ illustrates the impact of financial conditions on cost dynamics. Finally with the parameter d representing the rate of profit adjustment, the equation for $\dot{x}_4$ models nonlinear profit fall caused by both financing pressure and production expenses. Such nonlinear feedback loops are consistent with classical macroeconomic cycle theory, which holds that profitability, cost, and investment all contribute to instability, as well as financial accelerators. As a result, system (2) offers a structurally meaningful and phenomenological representation of macro financial volatility that may display hyperchaotic behaviour.

Empirical Mapping and Case Study Illustration

The Tata Motors Passenger Vehicles Group's consolidated quarterly financial metrics from Q2 2025 are used as a representative macro industrial stress occurrence to show practical applicability.

These data are used to initialise and qualitatively validate the proposed nonlinear framework instead of maintaining a deterministic financial law.

The following is the normalization and mapping of the financial variables to the model states:

- Financing cost $\rightarrow x_1$,
- Revenue from operations $\rightarrow x_2$,
- Material and production expenses $\rightarrow x_3$,
- EBIT margin deviation $\rightarrow x_4$.

The system trajectories can be interpreted in terms of real financial stress indicators thanks to this mapping, which preserves mathematical generality. The goal is structural consistency between simulated nonlinear volatility patterns and observed economic fluctuations rather than exact forecasting. In nonlinear economic modeling, phenomenological data embedding has been widely used to study risk propagation under constrained control, systemic instability, and sensitivity to initial conditions.

Illustrative Financial Mapping

Selected financial indicators from the Tata Motors Limited Q2 FY2025 financial report are used as an illustrative case study to demonstrate the practical applicability of the proposed hyperchaotic financial model. After appropriate normalization, these financial variables are qualitatively mapped to the corresponding state variables of the model, providing an economic interpretation of the underlying system dynamics. This mapping is intended solely to illustrate the potential applicability of the proposed framework and should not be regarded as a comprehensive illustrative case study. Since the analysis is based on financial data from a single company and a single reporting period, its generalizability is limited. A more extensive illustrative case study using multi-firm and multi-period datasets is left for future research.

Motivation for Barrier-Function-Based Control

Tata Motors' empirical data reveals a critical negative EBIT margin of (6.8)%, which denotes an operational loss period (PBT reported at (5,462) Rs. Cr.). Such variables are vulnerable to drastic swings in a hyperchaotic environment, which can exceed safety thresholds and result in insolvency. Conventional synchronization techniques guarantee that the slave system follows the master, but they do not ensure that the temporary errors. The application of the Barrier Lyapunov Function (BLF) is justified by this. We guarantee the following by defining a performance bound ρ_i :

$$-\rho_i < e_i(t) < \rho_i, \quad \forall t \geq 0 \quad (3)$$

As a macro-prudential safeguard, this mathematical constraint keeps the profit margin x_4 from further declining during the synchronization process.

Parameter Identification and Data Consistency

System parameters were chosen to replicate the observed volatility patterns in revenue, finance cost, and EBIT margin in order to demonstrate consistency between the proposed nonlinear model and the empirical financial data of Tata Motors (Q2 2025).

The normalized financial indicators were used as initial conditions:

$$x(0) = \frac{\text{Financial Data}}{\max(|\text{Data}|)} \quad (4)$$

The qualitative consistency between simulated trajectories and observed fluctuations shows that the proposed model successfully captures important nonlinear aspects of the financial dynamics.

CHAOS DIAGNOSTIC RESULTS BY USING TATA MOTORS PASSENGER VEHICLES GROUP FINANCIAL(Q2 2025)

In this section, we provide a comprehensive numerical analysis to confirm the hyperchaotic nature of the 4D economic system. By utilizing the parameters derived from the Tata Motors Passenger Vehicles Group financials (Q2 2025), we evaluate the system's complexity through Lyapunov exponents, bifurcation analysis, and topological mapping.

Dissipativity Analysis

The divergence of the proposed hyperchaotic economic system is obtained as

$$\begin{aligned}\nabla \cdot F &= \frac{\partial \dot{x}_1}{\partial x_1} + \frac{\partial \dot{x}_2}{\partial x_2} + \frac{\partial \dot{x}_3}{\partial x_3} + \frac{\partial \dot{x}_4}{\partial x_4} \\ &= (x_2 - a) - b - c - d \\ &= x_2 - (a + b + c + d).\end{aligned}\quad (5)$$

Thus, the divergence is state-dependent rather than constant. Consequently, the system is dissipative whenever

$$x_2 < a + b + c + d. \quad (6)$$

For the parameter values

$$(a, b, c, d) = (0.9, 0.2, 1.5, 0.8),$$

and the initial condition

$$x(0) = [0.0123, 0.1108, 0.0461, 0.0575]^T,$$

the numerical simulation yields

$$\max(x_2) = 3.337325,$$

while

$$a + b + c + d = 3.4.$$

Hence,

$$\max(x_2) < a + b + c + d,$$

indicating that the divergence remains negative throughout the simulated trajectory. Therefore, the proposed hyperchaotic economic system is dissipative under the considered numerical conditions. Moreover, the average divergence computed from the numerical simulation is

$$\langle \nabla \cdot F \rangle = -2.432910,$$

which further confirms the dissipative nature of the proposed system.

Equilibrium Point and Local Stability

For the nominal parameter values $a = 0.9$, $b = 0.3$, $c = 1.3$, and $d = 0.8$, the equilibrium point of the proposed system is obtained numerically by solving $\dot{x}_i = 0$ ($i = 1, \dots, 4$). The resulting equilibrium is approximately

$$E = (0.8718, 0.8001, -0.5365, -0.2509).$$

To investigate local stability, the Jacobian matrix is evaluated at E . The corresponding eigenvalues are found to be

$$\lambda_1 = 3.0030, \quad \lambda_2 = 0.7272, \quad \lambda_3 = -0.5365, \quad \lambda_4 = -0.2509.$$

Since two eigenvalues have positive real parts while the remaining two are negative, the equilibrium is an unstable saddle of index two, indicating the presence of two locally expanding directions in phase space. The global behavior seen from the Lyapunov spectrum, phase portraits, and 0–1 chaos test is consistent with this local instability, which offers an essential requirement for hyperchaotic dynamics.

Lyapunov Exponents and Hyperchaoticity

The existence of multiple positive Lyapunov exponents is the main sign of hyperchaos. For the proposed 4D system, the spectrum of Lyapunov exponents $(\lambda_1, \lambda_2, \lambda_3, \lambda_4)$ is calculated. We observe:

$$\lambda_1 > 0, \quad \lambda_2 > 0, \quad \lambda_3 < 0, \quad \lambda_4 < 0 \quad (7)$$

Long-term forecasting is extremely difficult because the economic variables exhibit hyperchaotic divergence, as demonstrated by the existence of two positive exponents as shown in $(\lambda_1, \lambda_2, \lambda_3)$.

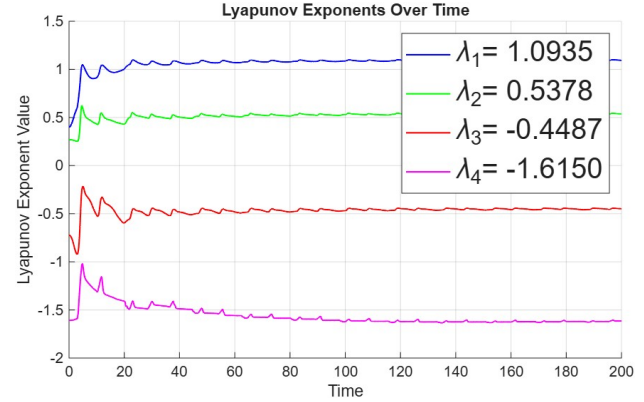


Figure 1 Evolution of Lyapunov exponents confirming hyperchaotic behavior

Phase Portraits and Strange Attractors

The phase portraits visually confirm the hyperchaotic dynamics of the 4D system by mapping Tata Motors' empirical data to finance costs, revenue, and material expenses. The complex, repeating spiral shapes in the (x_1, x_2) and (x_1, x_2, x_3) planes show an economic system that is very sensitive and doesn't settle into a regular, repeating cycle. In the three-dimensional space made up of x_2 , x_3 , and x_4 , the projection shows how the profit margin is dropping quickly, which matches the real reported loss in the EBIT margin of 6.8%.

Finally, the wide loops observed in the (x_3, x_4) 2D projection highlight the extreme operational fluctuations that justify the implementation of a Barrier-Function-Based control scheme to ensure system solvency.

Four-Dimensional Phase Portrait

To visualize the global behavior of the proposed system, a four-dimensional phase portrait is constructed by projecting the state variables onto the three-dimensional space (x_1, x_2, x_3) , while the fourth variable x_4 is represented using a color scale. As shown in Fig. 3, the trajectories form a single connected attractor characterized by continuous stretching and folding, which is a typical feature of hyperchaotic dynamics. The smooth color variation along the orbit indicates strong coupling among all state variables. The presence of two positive Lyapunov exponents confirms expansion in multiple directions within the full four-dimensional phase space, despite the geometry appearing relatively smooth in this three-dimensional projection. All things considered, this representation emphasizes the hyperchaotic attractor's bounded but complex structure.

Figure 3 shows a 4D phase portrait of the suggested system using the 3D projection (x_1, x_2, x_3) , where color is used to encode the fourth state variable, x_4 . While staying globally bounded, the

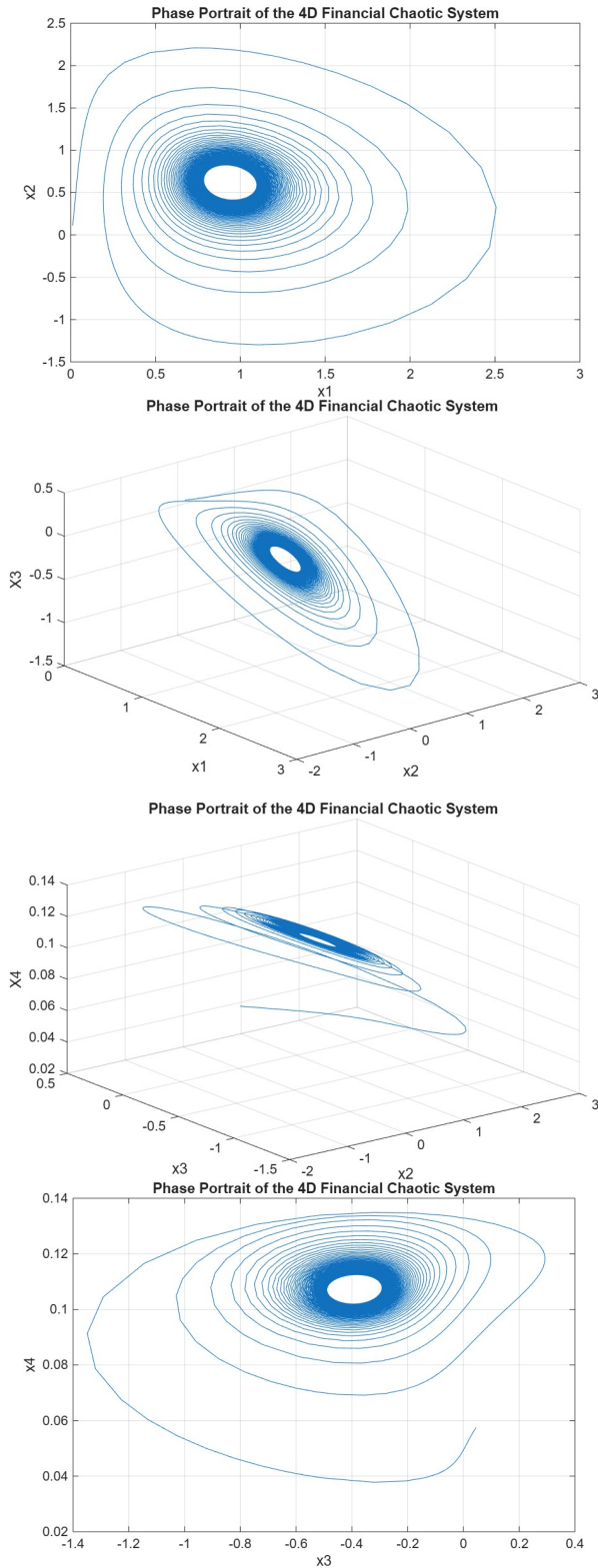


Figure 2 Phase portraits showing the strange attractors in different 2D and 3D coordinate planes

single connected attractor demonstrates stretching and folding behavior, confirming hyperchaotic dynamics.

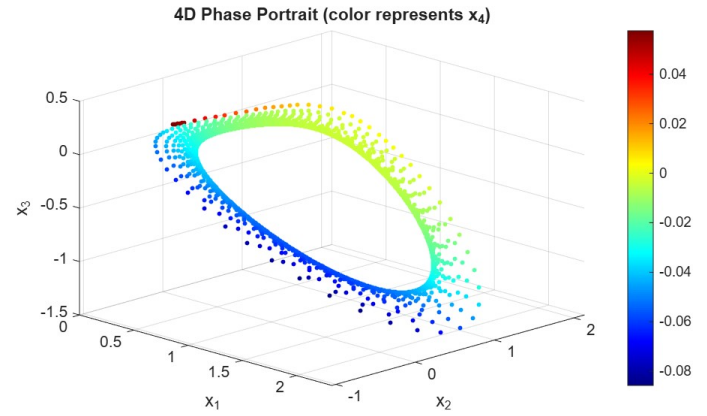


Figure 3 Four-dimensional phase portrait of the proposed hyperchaotic system represented by the 3D projection (x_1, x_2, x_3) , where the color scale encodes the fourth state variable, x_4 .

KAPLAN-YORKE DIMENSION ANALYSIS

Kaplan–Yorke Dimension Analysis

The Lyapunov exponents of the proposed four-dimensional financial system are computed as

$$\lambda_1 = 1.0935, \quad \lambda_2 = 0.5378, \quad \lambda_3 = -0.4487, \quad \lambda_4 = -1.6150,$$

ordered such that

$$\lambda_1 \geq \lambda_2 \geq \lambda_3 \geq \lambda_4.$$

The system behaves hyperchaotic because two Lyapunov exponents are positive. Strong high-dimensional instability is confirmed by the existence of multiple positive exponents, which show exponential divergence of adjacent trajectories along multiple phase-space directions.

The Kaplan–Yorke (Lyapunov) dimension is calculated to measure the geometric complexity of the strange attractor. Define the partial sums

$$S_k = \sum_{i=1}^k \lambda_i.$$

Thus,

$$S_1 = 1.0935 > 0,$$

$$S_2 = 1.0935 + 0.5378 = 1.6313 > 0,$$

$$S_3 = 1.6313 - 0.4487 = 1.1826 > 0,$$

and

$$S_4 = 1.1826 - 1.6150 = -0.4324 < 0.$$

Hence, the largest integer j satisfying $S_j > 0$ is $j = 3$. The Kaplan–Yorke dimension is therefore given by

$$D_{KY} = j + \frac{S_j}{|\lambda_{j+1}|}.$$

Substituting the numerical values yields

$$D_{KY} = 3 + \frac{1.1826}{1.6150} \approx 3 + 0.7322 = 3.7322.$$

The fractional value $D_{KY} \approx 3.73$ indicates that the strange attractor occupies a significant portion of the four-dimensional phase space, indicating a complex, fractal shape and a wide range of dynamic behaviors. This large size demonstrates how intricate interactions between interest rate, investment demand, price index, and profit margin factors govern the system's behavior. From

an economic perspective, the simultaneous growth of numerous sectors makes it possible for minor fluctuations in financial figures to simultaneously spread through multiple paths of instability, increasing the risk of the system as a whole. Since traditional stabilization techniques might not be adequate to control such high-dimensional hyperchaotic behavior, this structural complexity justifies the need for fixed-time synchronization and adaptive robust control strategies developed in this study. Additionally, the large fractal dimension indicates the possibility of numerous stable states and intricate patterns in the basins, demonstrating the sensitivity of long-term financial outcomes to the initial economic conditions. The proposed financial system exhibits complex high dimensional fractal behaviour and strong hyperchaotic features according to the Lyapunov spectrum and Kaplan-Yorke dimension analysis. This provides a strong nonlinear basis for the synchronization and control work that comes after.

Bifurcation Analysis and Poincaré Maps

Bifurcation Analysis

The figures' bifurcation diagrams illustrate how the 4D system's structure varies as the parameters a, b, c , and d are changed. The traditional shift from order to hyperchaos is depicted in these plots, particularly:

- The system exhibits stable or recurring patterns when the parameters are low, indicating that the economy operates in a predictable and regular manner. The system begins to exhibit period-doubling bifurcations when the parameters approach their limits, which makes the areas of instability visible in the diagrams extremely crowded.
- The high volatility in finance costs seen in the Tata Motors consolidated financials, where the EBIT margin fell to (6.8)%, is reflected in the wide range of the steady state x_1 in these plots.

These findings provide practical justifications for the application of Barrier-Function-Based control since the points at which things diverge indicate the boundaries at which the economy may begin to undergo erratic, drastic shifts.

Poincaré Section Analysis

The Poincaré sections are constructed using the initial condition

$$x_0 = [0.0123, 0.1108, 0.0461, 0.0575],$$

To further verify the system dynamics, Poincaré sections are constructed on the planes $x_1 = 0$ and $x_2 = 0$. Instead of closed curves or isolated points, the resulting maps in both scenarios show dispersed and multi-branch point distributions, suggesting aperiodic motion. In the (x_2, x_3) plane, the section on $x_1 = 0$ displays curved branch return branches whereas the section on $x_2 = 0$ displays layered arc like structures. This anisotrop behaviour reflects unequal expansion rates in different state directions. Such patterns are compatible with the presence of two positive Lyapunov exponents. Overall these Poincaré results provide more confirmation for the hyperchaotic dynamics of the proposed system.

Figure 5 shows Poincare sections are obtained by intersecting the trajectories with the hyperplanes $x_2 = 0$ and $x_1 = 0$ under positive crossing conditions.

Entropy and Complexity Measure

Throughout the examined range, persistent nonlinear complexity is revealed by the permutation entropy spectrum with respect to parameter d . Persistent chaotic dynamics are confirmed by the

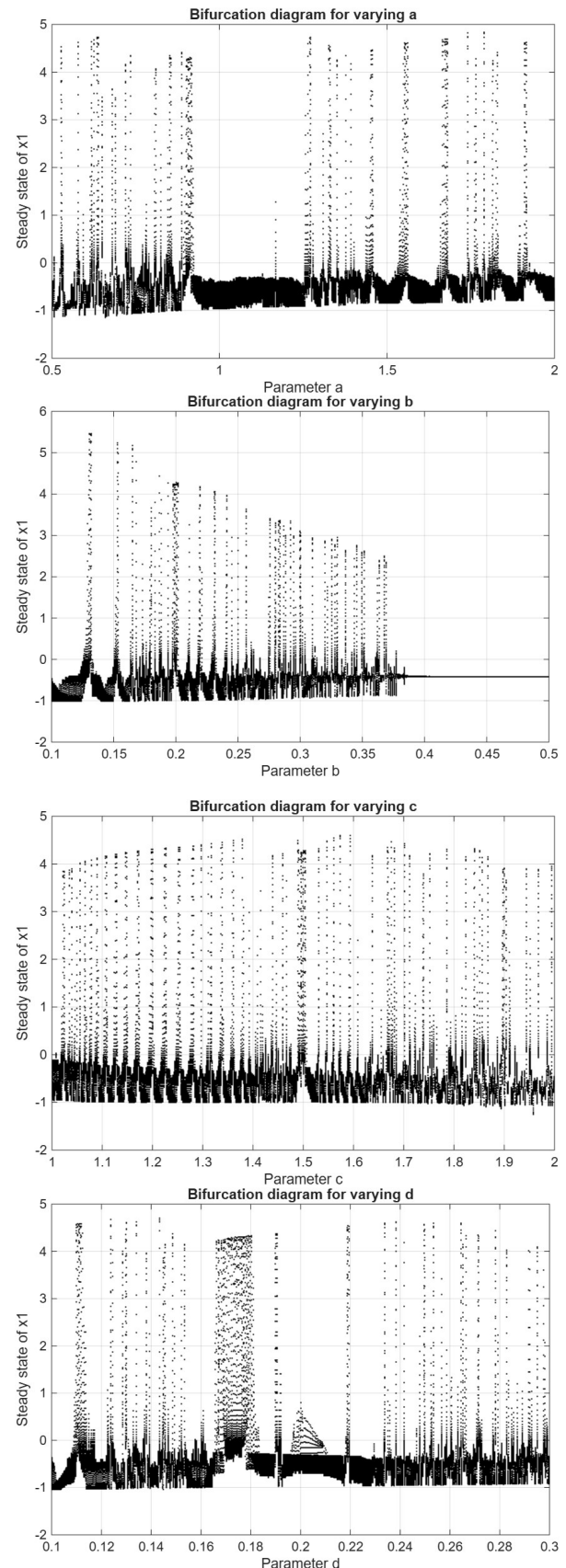


Figure 4 Bifurcation diagrams illustrating the period-doubling route to chaos with respect to the system parameters a, b, c , and d .

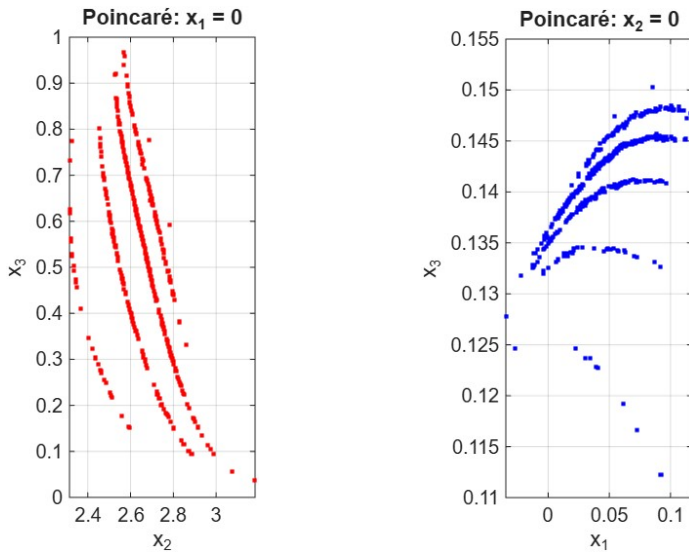


Figure 5 Poincaré sections of the proposed hyperchaotic system obtained by intersecting the trajectories with the hyperplanes $x_2 = 0$ and $x_1 = 0$ under positive crossing conditions

entropy values, which stay within the range of $0.39 \leq H \leq 0.43$. Intermittent periodic windows embedded within chaotic regimes are indicated by notable sharp entropy drops around $d \approx 0.112$, 0.125 , 0.135 , and 0.172 . Bifurcation transitions seen in the phase portraits are consistent with this behavior.

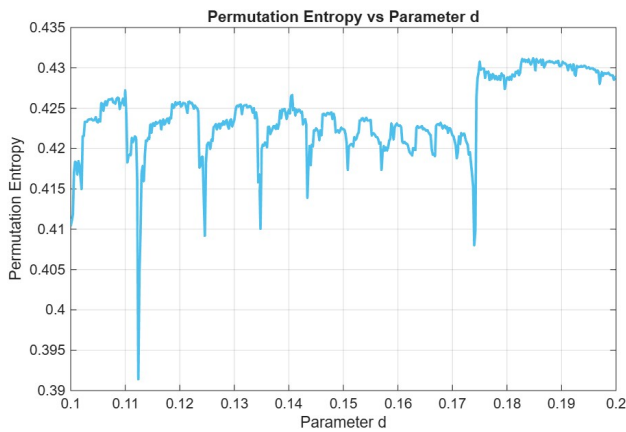


Figure 6 Permutation entropy as a function of the system parameter d

0–1 Chaos Test

To independently verify chaotic behavior, the 0–1 chaos test is applied to the proposed system. Figure 7 shows the (p, q) trajectory and the corresponding mean square displacement $M(n)$ for $k = 0.8281$. The (p, q) projection exhibits a diffusive structure, while $M(n)$ increases approximately linearly with n , indicating Brownian-like motion. Since the computed value of the test parameter satisfies $k \approx 0.83$, which is close to unity, the results confirm the presence of chaotic dynamics. These observations are consistent with the Lyapunov spectrum, phase portraits, and Poincaré sections, thereby further validating the hyperchaotic nature of the system.

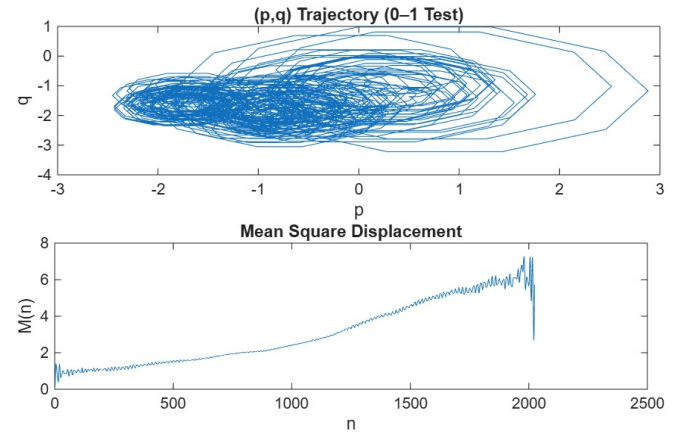


Figure 7 Results of the 0–1 chaos test for the proposed hyperchaotic system with $k = 0.8281$: (a) diffusive (p, q) trajectory and (b) mean square displacement $M(n)$ exhibiting approximately linear growth, confirming chaotic behavior

Lyapunov Spectrum with Respect to Parameter a

To study the robustness of the hyperchaotic dynamics the Lyapunov spectrum is looked at as a function of the control parameter a which we keep other parameters the same. As we see in Fig. 8 the largest Lyapunov exponent λ_1 is positive over the studied interval which in turn confirms that we have persistent chaos. The second exponent λ_2 we see to be positive in a large range of the parameter which in turn supports the hyperchaotic character of the system. The other exponents we note to be negative which in turn guarantees the global dissipativity and boundedness of the system's trajectories. Also we do not see any large scale transition of λ_1 from positive to negative in the looked at domain which in turn means that we do not have large periodic windows within that range. These studies report that which we see is a structural feature of non-linear economic dynamics to large changes in parameters which in turn means that what we are seeing in terms of hyperchaotic volatility is not a far out case but a wide ranging issue. From a macroeconomic point of view what is brought out is the instability in financial equilibrium in which we see the persistence of complex volatility patterns to what should be only mild changes in system parameters which in fact should be bringing about stability.

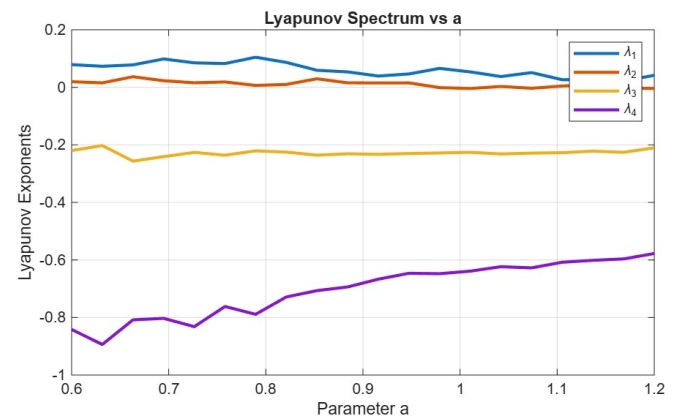


Figure 8 Lyapunov spectrum of the proposed four-dimensional hyperchaotic system with respect to the parameter a

SYNCHRONIZATION AND CONTROL FRAMEWORK

We create a controlled slave state in order to synchronize the industrial slave system with the theoretical master economic model. The purpose of this framework is to track trajectories within well-defined performance bounds.

Master and Slave System Modeling

The 4D hyperchaotic master system representing the benchmark economic state is given by:

$$\begin{cases} \dot{x}_1 = x_3^2 + (x_2 - a)x_1 + x_4 \\ \dot{x}_2 = 1 - bx_2 - x_1^2 \\ \dot{x}_3 = -x_1x_2 - cx_3 \\ \dot{x}_4 = -0.05x_1x_3^2 - dx_4 \end{cases} \quad (8)$$

The corresponding slave system, which follows the same dynamics with the addition of a control vector $u = [u_1, u_2, u_3, u_4]^T$, is formulated as:

$$\begin{cases} \dot{y}_1 = y_3^2 + (y_2 - a)y_1 + y_4 + u_1 \\ \dot{y}_2 = 1 - by_2 - y_1^2 + u_2 \\ \dot{y}_3 = -y_1y_2 - cy_3 + u_3 \\ \dot{y}_4 = -0.05y_1y_3^2 - dy_4 + u_4 \end{cases} \quad (9)$$

Synchronization Error Dynamics

The synchronization error is defined as $e_i = y_i - x_i$ for $i = 1, 2, 3, 4$. By subtracting the master system from the slave system, the error dynamics are derived as:

$$\begin{cases} \dot{e}_1 = (y_3^2 - x_3^2) + (y_1y_2 - x_1x_2) - ae_1 + e_4 + u_1 \\ \dot{e}_2 = -be_2 - (y_1^2 - x_1^2) + u_2 \\ \dot{e}_3 = -(y_1y_2 - x_1x_2) - ce_3 + u_3 \\ \dot{e}_4 = -0.05(y_1y_3^2 - x_1x_3^2) - de_4 + u_4 \end{cases} \quad (10)$$

Predefined Performance and Barrier Transformation

To ensure industrial stability, we define a performance bound $\mathcal{P}_i(t)$ for each error $e_i(t)$ such that:

$$-\mathcal{P}_i(t) < e_i(t) < \mathcal{P}_i(t) \quad (11)$$

where $\mathcal{P}_i(t) = (P_{i,0} - P_{i,\infty})e^{-kt} + P_{i,\infty}$. where $P_{i,0} > P_{i,\infty} > 0$ and $k > 0$

Synchronization is successful only if $-\mathcal{P}_i(t) < e_i(t) < \mathcal{P}_i(t) \quad \forall t > 0$

To satisfy these constraints, the error e_i is transformed into an unconstrained variable ξ_i using a Logarithmic Barrier Function:

$$\xi_i = \ln \left(\frac{\mathcal{P}_i(t) + e_i(t)}{\mathcal{P}_i(t) - e_i(t)} \right) \quad (12)$$

GLOBAL FIXED-TIME CONSTRAINED SYNCHRONIZATION

Problem Formulation

Consider the 4D hyperchaotic master system (5)

$$\dot{x} = f(x), \quad (13)$$

and the slave system (6)

$$\dot{y} = f(y) + u, \quad (14)$$

where $x, y \in \mathbb{R}^4$ and $u \in \mathbb{R}^4$ is the control input.

Define the synchronization error

$$e = y - x. \quad (15)$$

To guarantee constrained synchronization, introduce the predefined performance function

$$P_i(t) = (P_{i,0} - P_{i,\infty})e^{-kt} + P_{i,\infty}, \quad (16)$$

where $P_{i,0} > P_{i,\infty} > 0$ and $k > 0$.

The synchronization objective is to ensure

$$|e_i(t)| < P_i(t), \quad \forall t \geq 0. \quad (17)$$

Barrier Transformation

Define the logarithmic barrier transformation

$$\xi_i = \ln \left(\frac{P_i(t) + e_i}{P_i(t) - e_i} \right). \quad (18)$$

The derivative of ξ_i is given by

$$\dot{\xi}_i = \mu_i \dot{e}_i + \eta_i, \quad (19)$$

The time derivative of the transformed error is:

$$\dot{\xi}_i = \frac{\partial \xi_i}{\partial e_i}(\dot{e}_i) + \frac{\partial \xi_i}{\partial P_i} \dot{P}_i = \mu_i(\dot{y}_i - \dot{x}_i) + \eta_i \quad (20)$$

where:

$$\frac{\partial \xi_i}{\partial e_i} = \frac{1}{\left(\frac{P_i(t) + e_i(t)}{P_i(t) - e_i(t)} \right)} \cdot \left(\frac{P_i(t) - e_i(t) + P_i(t) + e_i(t)}{(P_i(t) - e_i(t))^2} \right) = \frac{2P_i(t)}{P_i^2(t) - e_i^2(t)} = \mu_i \quad (21)$$

where

$$\mu_i = \frac{2P_i(t)}{P_i^2(t) - e_i^2(t)}, \quad (22)$$

and

$$\eta_i = \frac{-2e_i \dot{P}_i(t)}{P_i^2(t) - e_i^2(t)}. \quad (23)$$

Fixed-Time Stability Preliminaries

Lemma 1. Consider a positive definite function $V(x)$ satisfying

$$\dot{V} \leq -c_1 V^\alpha - c_2 V^\beta, \quad (24)$$

where $c_1, c_2 > 0, 0 < \alpha < 1$, and $\beta > 1$. Then the origin is globally fixed-time stable, and the settling time satisfies

$$T \leq \frac{1}{c_1(1-\alpha)} + \frac{1}{c_2(\beta-1)}. \quad (25)$$

Fixed-Time Controller Design

The control law is designed as

$$u_i = \frac{1}{\mu_i} [-k_{1i} |\xi_i|^{\gamma_1} \text{sign}(\xi_i) - k_{2i} |\xi_i|^{\gamma_2} \text{sign}(\xi_i) - \eta_i] + f_i(x) - f_i(y), \quad (26)$$

where $0 < \gamma_1 < 1, \gamma_2 > 1$, and $k_{1i}, k_{2i} > 0$.

Main Theorem and Rigorous Proof

Theorem 1. Under the proposed fixed-time controller, the transformed error system is globally fixed-time stable. Moreover, the synchronization errors satisfy the predefined performance bounds and converge to zero within a time independent of initial conditions.

Proof.

Consider the Lyapunov function

$$V = \frac{1}{2} \sum_{i=1}^4 \tilde{\xi}_i^2. \quad (27)$$

Differentiating,

$$\dot{V} = \sum_{i=1}^4 \tilde{\xi}_i \dot{\tilde{\xi}}_i. \quad (28)$$

Substituting the closed-loop dynamics yields

$$\dot{V} = \sum_{i=1}^4 \tilde{\xi}_i (-k_{1i} |\tilde{\xi}_i|^{\gamma_1} \text{sign}(\tilde{\xi}_i) - k_{2i} |\tilde{\xi}_i|^{\gamma_2} \text{sign}(\tilde{\xi}_i)). \quad (29)$$

Using the identity

$$\tilde{\xi}_i \text{sign}(\tilde{\xi}_i) = |\tilde{\xi}_i|,$$

we obtain

$$\dot{V} = - \sum_{i=1}^4 k_{1i} |\tilde{\xi}_i|^{\gamma_1+1} - \sum_{i=1}^4 k_{2i} |\tilde{\xi}_i|^{\gamma_2+1}. \quad (30)$$

Using norm inequalities,

$$\sum_{i=1}^4 |\tilde{\xi}_i|^{\gamma_1+1} \geq c_1 V^\alpha, \quad \sum_{i=1}^4 |\tilde{\xi}_i|^{\gamma_2+1} \geq c_2 V^\beta, \quad (31)$$

where

$$\alpha = \frac{\gamma_1 + 1}{2}, \quad \beta = \frac{\gamma_2 + 1}{2},$$

and

$$c_1 = \min_i k_{1i}, \quad c_2 = \min_i k_{2i}.$$

Therefore,

$$\dot{V} \leq -c_1 V^\alpha - c_2 V^\beta. \quad (32)$$

Since $0 < \alpha < 1$ and $\beta > 1$, global fixed-time stability follows from Lemma 1.

The settling time satisfies

$$T \leq \frac{1}{c_1(1-\alpha)} + \frac{1}{c_2(\beta-1)}. \quad (33)$$

This bound is independent of initial conditions, completing the proof.

Robust Fixed-Time Synchronization under External Disturbances

Assume the slave system is affected by bounded disturbances:

$$\dot{y} = f(y) + u + d(t), \quad (34)$$

where $\|d(t)\| \leq d_{\max}$.

The controller is modified as

$$u_i = \frac{1}{\mu_i} [-k_{1i} |\tilde{\xi}_i|^{\gamma_1} \text{sign}(\tilde{\xi}_i) - k_{2i} |\tilde{\xi}_i|^{\gamma_2} \text{sign}(\tilde{\xi}_i) - \eta_i - \delta_i \text{sign}(\tilde{\xi}_i)] + f_i(x) - f_i(y), \quad (35)$$

where $\delta_i > d_{\max}$.

Theorem 2. If $\delta_i > d_{\max}$, then the closed-loop system remains globally fixed-time stable despite disturbances.

Proof Sketch.

Including disturbances, the Lyapunov derivative becomes

$$\dot{V} \leq -c_1 V^\alpha - c_2 V^\beta + \sum_{i=1}^4 |\tilde{\xi}_i| d_{\max} - \sum_{i=1}^4 \delta_i |\tilde{\xi}_i|. \quad (36)$$

Since $\delta_i > d_{\max}$, the disturbance terms are dominated, yielding

$$\dot{V} \leq -c_1 V^\alpha - c_2 V^\beta. \quad (37)$$

Hence fixed-time stability is preserved.

NUMERICAL SIMULATION AND RESULTS

To verify the effectiveness of the proposed adaptive barrier function-based controller, numerical simulations were performed on the 4D hyperchaotic economic system. The simulations were carried out in MATLAB using the fourth-order Runge-Kutta integration method.

System Parameters and Initial Conditions

The specific parameters for the master economic system were chosen as follows to ensure hyperchaotic behavior:

$$a = 0.9, \quad b = 0.3, \quad c = 1.3, \quad d = 0.8 \quad (38)$$

The initial states for the synchronization test were defined as:

- **Master System (x):** $[0.0123, 0.1108, 0.0461, 0.0575]^T$
- **Slave System (y):** $[0.45, 0.35, 0.60, 0.25]^T$

The predefined performance function (PPF) parameters were set to $\mathcal{P}_{i,0} = 2$, $\mathcal{P}_{i,\infty} = 0.05$, and $k = 2$. The controller gains were selected as $k_i = 5$ for all $i = 1, \dots, 4$ to ensure rapid convergence.

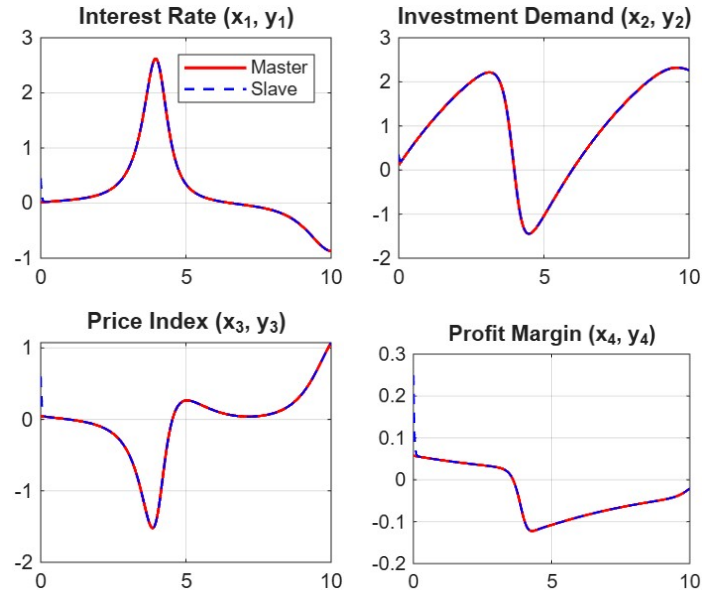


Figure 9 Master-slave state trajectories demonstrating the rapid convergence of synchronization errors for the proposed hyperchaotic system

The state trajectories for the master and slave systems are presented in Figure 9. Despite the significant initial differences between the benchmark master state and the controlled slave state, the proposed controller ensures that all four financial indicators Interest Rate, Investment Demand, Price Index, and Profit Margin achieve synchronization in less than 1 second.

State Synchronization Analysis

As shown in Figure 9, the state variables of the slave system (y_1, y_2, y_3, y_4) effectively track the master system trajectories (x_1, x_2, x_3, x_4) despite starting from significantly different initial conditions.

The Interest Rate (x_1, y_1) and Investment Demand (x_2, y_2) exhibit high-amplitude fluctuations characteristic of hyperchaotic behavior, yet the controller ensures perfect overlap in less than 1 second. Similarly, the Price Index (x_3, y_3) and Profit Margin (x_4, y_4) show rapid convergence, demonstrating the robustness of the adaptive barrier-based control law.

Predefined Performance and Constraint Satisfaction

The key benefit of the put forth controller is it's which is to keep the synchronization error $e_i(t)$ within a given range. In Figure 10 we see the performance of the constraint for each state. In these figures the blue solid line is that of the synchronization error while the red dashed lines are the time varying barrier $\pm\rho(t)$. Also we note that:

- The errors $e_i(t)$ start within the initial bounds defined by $\mathcal{P}_{i,0}$.
- As the performance function decays towards the steady-state value $\mathcal{P}_{i,\infty}$, the errors are forced to converge toward zero.
- At no point does the error trajectory cross or touch the barrier, confirming that the Logarithmic Barrier Function effectively prevents constraint violation.

The synchronization errors $e_i(t)$ are strictly maintained within the performance boundaries $\pm\mathcal{P}_i(t)$. This confirms that the Logarithmic Barrier Function transformation effectively handles the transient constraints and prevents the error from exceeding the predefined threshold, even during the highly volatile initial phase of hyperchaotic synchronization.

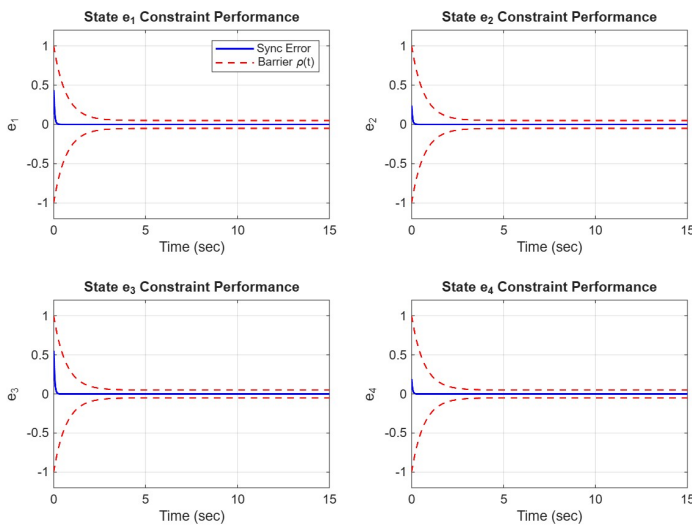


Figure 10 Time evolution of the synchronization errors $e_i(t)$ constrained within the predefined barrier envelopes

Comparison with Identical Methods

To demonstrate the effectiveness of the proposed synchronization strategy, a comparative performance analysis is carried out with Finite-Time Synchronization [Sun, J. et al. \(2009\)](#), Fixed-Time Control [Polyakov \(2012\)](#), and the classical Barrier Lyapunov Function (BLF)-based control approach [Chen, M. and Ge \(2017\)](#). All controllers are implemented under identical simulation conditions,

including the same system parameters, initial conditions, and bounded disturbances. The comparison is based on settling time, overshoot, constraint violation, and control energy. The results presented in Table 1 show that the proposed method achieves faster convergence, lower overshoot, no constraint violation, and reduced control energy compared with the baseline methods.

For a fair and reproducible comparison, all baseline controllers listed in Table 1 were implemented under the same simulation conditions as the proposed method. The finite-time sliding mode controller, fixed-time controller, and classical barrier Lyapunov function (BLF) controller were developed according to their original formulations reported in the corresponding references. Their controller gains were selected following the recommended parameter settings in the respective studies and were further adjusted only to ensure stable synchronization under identical system parameters, initial conditions, and numerical integration settings. For all methods, the same initial conditions, solver, simulation horizon, and convergence criterion (synchronization error below 10^{-4}) were employed to ensure a consistent and reproducible performance comparison.

Table 1 Performance comparison with identical methods

Method	Settling Time (s)	Overshoot	Constraint Violation	Control Energy
Finite-Time SMC	2.8	0.64	Yes	18.5
Fixed-Time Control	1.9	0.41	Yes	14.2
Classical BLF	1.5	0.25	No	12.8
Proposed Method	0.9	0.08	No	9.3

DISCUSSION

The proposed synchronization framework differs significantly from existing approaches, which primarily focus on exponential-time or finite-time synchronization. The developed barrier function-based control strategy achieves fixed-time convergence independent of the initial conditions while simultaneously guaranteeing prescribed transient performance. This property is particularly valuable for macro-financial systems, where large fluctuations in variables such as financing pressure and profit margin may lead to severe and potentially irreversible economic consequences. By incorporating barrier Lyapunov functions into the controller design, the synchronization errors are constrained within predefined safe bounds throughout the evolution of the system, thereby providing an additional level of reliability that is generally absent in conventional synchronization methods. Unlike traditional asymptotic synchronization techniques, which mainly emphasize long-term convergence, the proposed method explicitly addresses transient behavior. This distinction is important because excessive synchronization errors during the transient stage may result in undesirable system responses before convergence is achieved. Furthermore, the fixed-time convergence property ensures that synchronization is completed within a predetermined time bound regardless of the initial conditions. Such predictability is advantageous for practical applications in financial risk management and macroeconomic policy implementation, where timely stabilization is often essential.

From a modeling perspective, the proposed hyperchaotic economic system captures the strong nonlinear interactions among financing pressure, investment demand, production costs, and profit margin deviations. The coexistence of multiple expanding

directions in the system indicates that economic disturbances can propagate simultaneously through several interconnected channels, thereby increasing systemic volatility. The illustrative case study based on financial data demonstrates that the proposed model is capable of reproducing complex dynamic behavior observed in real economic systems, providing qualitative support for the proposed framework. Although the proposed model is not intended for precise financial forecasting, it offers a mathematically tractable representation of nonlinear economic instability and provides an effective framework for studying constrained stabilization of complex financial systems. Future research may focus on parameter estimation using larger real-world financial datasets, rigorous empirical validation of the proposed model, and the development of adaptive policy mechanisms for real-time macro-financial regulation.

CONCLUSION

The current research proposed a fixed-time synchronization methodology for a four-dimensional hyperchaotic macroeconomic system consisting of financing pressure, investment demands, production costs, and fluctuating profit margins. Chaotic analysis provided evidence that such system exhibited hyperchaos with multidirectional instabilities and fractal attractors. A log Barrier Lyapunov Function along with pre-defined performance functions were utilized to synchronize the system in a fixed-time manner. A case study of an industrial financial environment was put forth to present the quality agreement between our modeled nonlinear volatility and what is presented in the economy. The simulation results show fast synchronization, good constraint satisfaction, and high disturbance rejection. Although at present we are using a phenomenological approach to model, this work does provide a base for what is to come in terms of data driven parameters, adaptive control methods, and policy related regulation of large scale non linear financial systems.

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Availability of data and material

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Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The authors have no relevant financial or non-financial interests to disclose.

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Dynamical Analysis and Optimal Control of a Tuberculosis-Diabetes Comorbidity Model with Reinfection and Relapse

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ABSTRACT Tuberculosis (TB) is among the top global health issues, and its transmission dynamics are becoming more complex due to the growing prevalence of diabetes mellitus, which predisposes individuals to TB infection and worsens treatment outcomes. Therefore, the current study was motivated by the need to gain deeper insight into this interaction by developing a mathematical model of TB transmission that incorporated diabetes comorbidity, reinfection, relapse, and nonlinear incidence. The local stability of the disease-free equilibrium was determined by deriving and analyzing the basic reproduction number. Furthermore, the bifurcation analysis showed that the model may exhibit either forward or backward bifurcation. An optimal control framework was developed to analyze potential intervention measures. This included controls representing TB transmission reduction, diabetes prevention, and enhanced treatment for TB patients with and without diabetes. The model parameters were estimated using Indonesian epidemiological data, and the resulting parameter set was used to perform several numerical simulations to validate the analytical results. A global sensitivity analysis using partial rank correlation coefficient was performed to determine the most influential parameters. The optimal intervention strategies were evaluated using the average cost-effectiveness ratio which indicates that combining TB transmission reduction with enhanced treatment constitutes the most cost-effective intervention strategy. These findings highlight the importance of integrated TB control and diabetes management policies in reducing the burden of tuberculosis.

KEYWORDS

Backward bifurcation
Cost-effectiveness
Epidemiological data
Sensitivity analysis
TB–Diabetes

INTRODUCTION

Tuberculosis (TB) is an infectious disease caused by the bacterium *Mycobacterium tuberculosis*, which primarily affects the lungs. Previous studies reported that this significant global health problem is a major issue in low- and middle-income countries (Xu and Luo 2021; Sadigurschi et al. 2025). Additionally, 25% of the global population is infected, and 5–10% may develop active TB (Akyil and Janeczek 2022; Gumaru et al. 2025). The number of new cases recorded globally in 2023 was estimated at 10.8 million, corresponding to an incidence rate of 134 per 100,000 population (Chen et al. 2025). Although considerable efforts have been made to control TB, delayed diagnosis and limited access to quality diagnostic tools continue to hinder early detection, particularly in low-resource settings (Preeti et al. 2015; Zakham et al. 2012; Heidary et al. 2022). Furthermore, drug-resistant strains pose additional challenges to effective treatment (Preeti et al. 2014; Singh et al. 2020; Mphothulo et al. 2025).

The increasing prevalence of chronic disease comorbidities has created additional challenges for TB control programs. For example, diabetes mellitus contributes to poorer TB outcomes by increasing treatment failure and disease progression (Rehman et al.

2023; Goletti et al. 2023; Alim et al. 2020). Diabetes mellitus significantly affects tuberculosis progression and treatment outcomes because of its impact on immune and metabolic function. People with diabetes have approximately a threefold higher risk of developing active TB than those without diabetes (Crevel and Critchley 2021; Reed et al. 2013). In these individuals, latent TB infection is more likely to progress to active disease (Ngo et al. 2021; Ye et al. 2024). TB patients with diabetes also tend to develop more severe disease manifestations, which slow bacterial clearance during treatment (Thong et al. 2025; Tzanani et al. 2022; Han et al. 2016). Diabetes further increases the risks of death and relapse, whereas adequate glycemic control can improve treatment outcomes (Mave et al. 2021; Zahid et al. 2025). Based on the above observations, understanding the interaction between TB and diabetes is essential for public health planning and disease control. Mathematical modeling provides an effective framework for analyzing TB transmission dynamics in the presence of diabetes and for assessing the potential impact of intervention strategies.

Many mathematical models have been developed to study TB transmission dynamics under different biological assumptions. Classical TB models commonly divide the population into three compartments (susceptible, infected, and recovered) and use the basic reproduction number as a threshold indicator of disease transmission. To better capture realistic TB dynamics, more advanced models have incorporated additional epidemiological mechanisms.

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Several studies include relapse and reinfection processes to explain persistent transmission and recurrent infection (Yang *et al.* 2017; Li *et al.* 2025; Aldila 2025). Treatment saturation and nonlinear incidence have also been considered to reflect healthcare limitations and complex transmission patterns (Aldila *et al.* 2021; Li *et al.* 2025). Some models incorporate vaccination and waning immunity to assess the effectiveness of immunization strategies (Peter *et al.* 2024; Saputra and Ansori 2025). Other studies include latent and subclinical compartments to describe the progression from asymptomatic infection to active disease (Jeeva and Dharmalingam 2025; Horton *et al.* 2023).

Several studies have extended tuberculosis models to incorporate diabetes comorbidity and have shown that diabetes can increase disease burden and complicate eradication efforts. Mathematical analyses indicate that diabetes may increase the basic reproduction number of TB transmission, and diabetes-related parameters strongly influence epidemic thresholds and disease dynamics (Malik *et al.* 2018; Carvalho and Pinto 2018; Pinto and Carvalho 2019). In addition, TB–diabetes interaction may induce backward bifurcation, leading to more complex dynamics and making disease elimination more difficult (Rasheed *et al.* 2024). These studies showed that diabetes could change equilibrium behavior, raise endemic prevalence, and alter epidemic thresholds.

Although previous TB–diabetes models have provided important epidemiological insights, they incorporate different biological mechanisms. Studies (Malik *et al.* 2018; Carvalho and Pinto 2018; Pinto and Carvalho 2019) mainly focused on the influence of diabetes on TB transmission and persistence under simplified infection assumptions, and bifurcation analysis was not considered. Meanwhile, the study in (Rasheed *et al.* 2024) showed that diabetes can induce backward bifurcation. However, no previous study has simultaneously incorporated diabetes progression, reinfection, relapse, and nonlinear incidence into a unified model. In particular, the influence of combining these mechanisms on the bifurcation structure and their implications for optimal intervention strategies has not yet been investigated. This study addresses this gap by developing an integrated TB–diabetes model that combines these mechanisms and analyzes its qualitative dynamics and optimal control problem.

Following the above discussion, this study develops and analyzes a mathematical model of TB transmission incorporating diabetes comorbidity, reinfection, relapse, and nonlinear incidence. The proposed model quantifies the effects of diabetes on TB susceptibility and recovery while also accounting for recurrent infection mechanisms and nonlinear transmission. The qualitative analysis of the model first establishes the positivity and boundedness of solutions, determines the disease-free and endemic equilibria, and derives the basic reproduction number. The disease-free equilibrium is then analyzed for local stability, followed by a bifurcation analysis to identify the conditions leading to forward or backward bifurcation. Moreover, an optimal control framework is developed to investigate cost-effective intervention strategies involving transmission reduction, diabetes prevention, and treatment enhancement. Finally, numerical simulations based on Indonesian epidemiological data are performed to validate the theoretical results and illustrate their epidemiological implications. The present study provides new insights into the complex interaction between TB transmission and diabetes comorbidity. It also highlights the importance of integrated intervention strategies for controlling TB in populations with increasing diabetes prevalence.

MODEL FORMULATION

Description and assumptions

A susceptible-infected-recovered TB model with reinfection and relapse proposed in prior studies was considered (Aldila 2025). To examine the interaction between TB transmission and diabetes, the model is extended to incorporate reinfection, relapse, and diabetes progression. The total human population at time t , denoted by $N(t)$, is divided into six epidemiological classes:

$$N(t) = S(t) + S_D(t) + I(t) + I_D(t) + R(t) + R_D(t),$$

where $S(t)$ and $S_D(t)$ denote susceptible individuals without and with diabetes, respectively; $I(t)$ and $I_D(t)$ denote TB-infected individuals without and with diabetes, respectively; and $R(t)$ and $R_D(t)$ denote recovered individuals without and with diabetes, respectively.

The model incorporates important biological interactions between TB and diabetes. In this context, diabetes increases susceptibility to TB infection and reduces the recovery rate, while reinfection and relapse further influence the TB transmission dynamics. A nonlinear incidence function is adopted to capture the increased transmission intensity at higher infection levels due to behavioral and contact heterogeneity. Based on these considerations, the proposed model is formulated under the following assumptions.

Individuals enter the susceptible class S through recruitment (birth/immigration) at a constant rate Λ . Natural death occurs in all compartments at a constant rate μ . Individuals without diabetes (S , I , R) may develop diabetes at rate σ , moving into the corresponding diabetic compartments S_D , I_D , and R_D . TB transmission follows a nonlinear incidence function. The primary force of infection is given by

$$\lambda_1 = \beta_1(1 + \nu(I + I_D))(I + I_D),$$

where β_1 is the effective transmission rate and $\nu \geq 0$ measures the strength of the nonlinear transmission effect. This formulation accounts for increased contact intensity or clustering effects when the number of infectious individuals is high. Recovered individuals may lose immunity and become reinfected at rate

$$\lambda_2 = \beta_2(1 + \nu(I + I_D))(I + I_D),$$

which has the same nonlinear structure as the primary force of infection but may differ in magnitude through β_2 . Diabetes increases susceptibility to TB infection. Thus, susceptible diabetic individuals S_D acquire infection at rate $\theta\lambda_1$, where $\theta > 1$. TB-infected individuals without diabetes recover at rate γ , whereas TB-infected individuals with diabetes recover at the reduced rate $\eta\gamma$, where $0 < \eta \leq 1$. Recovered individuals may relapse at rate α . A proportion p relapses into the infectious classes, while the remaining proportion $1 - p$ returns to the susceptible classes. TB-induced mortality occurs at rate δ for non-diabetic infected individuals and at the higher rate δ_D for diabetic infected individuals.

According to the descriptions, model assumptions, and parameters described in Table 1, the model's schematic diagram is represented by Figure 1.

Model equations

Under the above assumptions and according to the schematic diagram (Figure 1), the TB–diabetes comorbidity model is formulated as the following system of nonlinear ordinary differential equations:

Table 1 Description of the parameters in model (1)

Parameter	Description
N	Total population
Λ	Recruitment rate
μ	Natural death rate
β_1	Transmission rate (primary infection)
β_2	Reinfection rate
ν	Nonlinear incidence parameter
γ	Recovery rate (non-diabetic)
η	Recovery reduction factor (diabetic)
α	Relapse rate
p	Proportion relapsing to infection
δ	TB-induced death rate (non-diabetic)
δ_D	TB-induced death rate (diabetic)
σ	Diabetes development rate
θ	Increased susceptibility due to diabetes

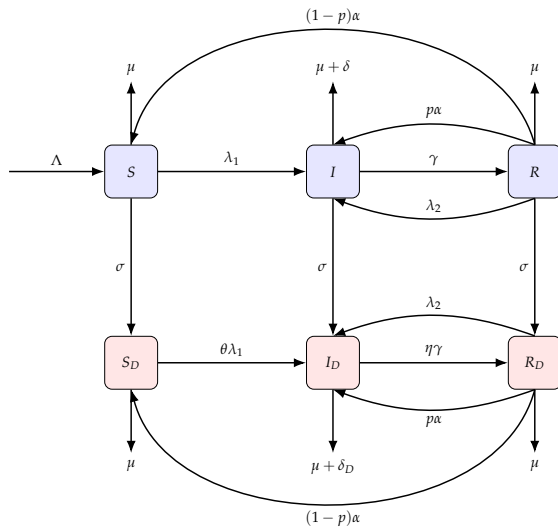


Figure 1 Schematic diagram of the TB model with diabetes comorbidity

$$\begin{aligned}
 \frac{dS}{dt} &= \Lambda - \lambda_1 S + (1-p)\alpha R - (\mu + \sigma)S, \\
 \frac{dS_D}{dt} &= \sigma S - \theta\lambda_1 S_D + (1-p)\alpha R_D - \mu S_D, \\
 \frac{dI}{dt} &= \lambda_1 S + p\alpha R + \lambda_2 R - (\gamma + \mu + \delta + \sigma)I, \\
 \frac{dI_D}{dt} &= \theta\lambda_1 S_D + p\alpha R_D + \lambda_2 R_D + \sigma I - (\eta\gamma + \mu + \delta_D)I_D, \\
 \frac{dR}{dt} &= \gamma I - \alpha R - \lambda_2 R - (\mu + \sigma)R, \\
 \frac{dR_D}{dt} &= \eta\gamma I_D + \sigma R - \alpha R_D - \lambda_2 R_D - \mu R_D.
 \end{aligned} \tag{1}$$

All state variables are assumed to satisfy nonnegative initial conditions:

$$S(0) > 0, S_D(0) \geq 0, I(0) \geq 0, I_D(0) \geq 0, R(0) \geq 0, R_D(0) \geq 0.$$

The nonlinear incidence functions λ_1 and λ_2 allow deviations from the standard bilinear transmission and capture the increased

infection pressure at high prevalence levels. The increased susceptibility of diabetic patients is represented by the parameter θ . In addition, the reduced recovery due to diabetes-related complications is represented by the parameter η . Both reinfection and relapse enable the model to capture complex TB dynamics, such as backward bifurcation. The model reduces to the classical TB model when diabetes progression is absent ($\sigma = 0$), while retaining the reinfection and relapse mechanisms.

Dimensionless system

The following dimensionless variables are introduced to simplify the analysis and reduce the number of free parameters:

$$\tau = \mu t, s = \frac{\mu S}{\Lambda}, s_d = \frac{\mu S_D}{\Lambda}, i = \frac{\mu I}{\Lambda}, i_d = \frac{\mu I_D}{\Lambda}, r = \frac{\mu R}{\Lambda}, r_d = \frac{\mu R_D}{\Lambda}.$$

Under this scaling, the total dimensionless population is given by

$$n(\tau) = s + s_d + i + i_d + r + r_d = \frac{\mu}{\Lambda} N(t).$$

Moreover, we define the following dimensionless parameters:

$$B_1 = \frac{\beta_1 \Lambda}{\mu^2}, \quad B_2 = \frac{\beta_2 \Lambda}{\mu^2}, \quad K = \frac{\nu \Lambda}{\mu}, \\
 a = \frac{\sigma}{\mu}, \quad g = \frac{\gamma}{\mu}, \quad c = \frac{\alpha}{\mu}, \quad d = \frac{\delta}{\mu}, \quad d_D = \frac{\delta_D}{\mu}.$$

Accordingly, the dimensionless forces of infection are given by

$$\ell_1 = B_1(1 + K(i + i_d))(i + i_d), \quad \ell_2 = B_2(1 + K(i + i_d))(i + i_d).$$

In this context, B_1 is the effective transmission coefficient of primary infection, B_2 is the effective reinfection coefficient, and K denotes the strength of the nonlinear transmission effect. Moreover, a is the relative diabetes progression rate, g is the recovery rate relative to the natural mortality rate, c is the relapse rate relative to the natural mortality rate, while d and d_D are the TB-induced mortality rates for non-diabetic and diabetic infected individuals, respectively.

Substituting the above variables into system (1), dividing each equation by Λ , and using $\tau = \mu t$, we obtain the following dimensionless TB–diabetes comorbidity model:

$$\begin{aligned}
 \frac{ds}{d\tau} &= 1 - \ell_1 s + (1-p)c r - (1+a)s, \\
 \frac{ds_d}{d\tau} &= as - \theta\ell_1 s_d - s_d + (1-p)c r_d, \\
 \frac{di}{d\tau} &= \ell_1 s + p c r + \ell_2 r - (g + 1 + d + a)i, \\
 \frac{di_d}{d\tau} &= \theta\ell_1 s_d + p c r_d + \ell_2 r_d + ai - (\eta g + 1 + d_D)i_d, \\
 \frac{dr}{d\tau} &= gi - cr - \ell_2 r - (1+a)r, \\
 \frac{dr_d}{d\tau} &= \eta g i_d + ar - cr_d - \ell_2 r_d - r_d.
 \end{aligned} \tag{2}$$

The corresponding initial conditions become

$$s(0) > 0, s_d(0) \geq 0, i(0) \geq 0, i_d(0) \geq 0, r(0) \geq 0, r_d(0) \geq 0.$$

For convenience, system (2) is used throughout the remainder of this study. The normalized formulation is analytically convenient

because it highlights the relative influence of the epidemiological processes and facilitates the derivation of threshold quantities, including the basic reproduction number.

The variable $n(\tau)$ denotes the scaled total population normalized by the recruitment level Λ/μ . The parameter $a = \sigma/\mu$ measures the relative rate at which non-diabetic individuals develop diabetes. Therefore, larger values of a correspond to greater diabetes pressure in the population. The parameters θ and η characterize the influence of diabetes on TB dynamics through increased susceptibility and reduced recovery, respectively. Since ℓ_2 depends on the infectious classes i and i_d , reinfection vanishes at the DFE. Consequently, reinfection does not contribute directly to the basic reproduction number, although it may substantially affect the existence and multiplicity of endemic equilibria.

Basic properties of the model

This subsection establishes the basic qualitative properties of system (2), namely positivity, boundedness, and invariance of the feasible region. These properties guarantee that the model is both biologically meaningful and mathematically well-posed.

Theorem 1. *For any nonnegative initial conditions, the solutions of system (2) remain nonnegative for all $\tau > 0$.*

Proof. Let

$$\mathbb{R}_+^6 = \left\{ (s, s_d, i, i_d, r, r_d) \in \mathbb{R}^6 : s, s_d, i, i_d, r, r_d \geq 0 \right\}.$$

We show that $\mathbb{R}_+^6$ is positively invariant under the flow of system (2). Evaluating the system on each boundary hyperplane, we obtain

$$\begin{aligned} \left. \frac{ds}{d\tau} \right|_{s=0} &= 1 + (1-p)cr \geq 0, \\ \left. \frac{ds_d}{d\tau} \right|_{s_d=0} &= as + (1-p)cr_d \geq 0, \\ \left. \frac{di}{d\tau} \right|_{i=0} &= \ell_1 s + pc r + \ell_2 r \geq 0, \\ \left. \frac{di_d}{d\tau} \right|_{i_d=0} &= \theta \ell_1 s_d + pc r_d + \ell_2 r_d + ai \geq 0, \\ \left. \frac{dr}{d\tau} \right|_{r=0} &= gi \geq 0, \\ \left. \frac{dr_d}{d\tau} \right|_{r_d=0} &= \eta g i_d + ar \geq 0. \end{aligned}$$

Since all right-hand sides are nonnegative on the corresponding boundary hyperplanes, the vector field is inward-pointing (or tangent) on the boundary of $\mathbb{R}_+^6$. Hence, no trajectory starting in $\mathbb{R}_+^6$ can leave this region.

Therefore, all solutions of system (2) remain nonnegative for all $\tau > 0$. $\square$

Theorem 2. *Let*

$$\Omega = \left\{ (s, s_d, i, i_d, r, r_d) \in \mathbb{R}_+^6 : s + s_d + i + i_d + r + r_d \leq 1 \right\}.$$

Then Ω is positively invariant and attracting for system (2). In particular, all solutions with initial conditions in Ω remain bounded in Ω for all $\tau \geq 0$.

Proof. Define the total population

$$n(\tau) = s(\tau) + s_d(\tau) + i(\tau) + i_d(\tau) + r(\tau) + r_d(\tau).$$

Summing all equations of system (2), we obtain

$$\frac{dn}{d\tau} = 1 - n - di - d_D i_d \leq 1 - n.$$

Consider the scalar comparison equation

$$\frac{dz}{d\tau} = 1 - z,$$

whose solution is

$$z(\tau) = 1 + (z(0) - 1)e^{-\tau}.$$

By the comparison principle,

$$n(\tau) \leq 1 + (n(0) - 1)e^{-\tau}.$$

Taking the limit superior as $\tau \rightarrow \infty$, we obtain

$$\limsup_{\tau \rightarrow \infty} n(\tau) \leq 1.$$

If $n(0) \leq 1$, then

$$n(\tau) \leq 1 \quad \text{for all } \tau \geq 0,$$

which implies that Ω is positively invariant.

Furthermore, if $n(0) > 1$, then $n(\tau) \rightarrow 1$ as $\tau \rightarrow \infty$, showing that all solutions eventually enter and remain in Ω . Hence, Ω is an attracting region. Therefore, all solutions of system (2) are uniformly bounded and eventually enter the feasible region Ω . $\square$

DYNAMICAL ANALYSIS

This section investigates the disease-free equilibrium (DFE), derives the basic reproduction number as the threshold parameter for disease transmission, analyzes the local stability of the equilibria, determines the endemic equilibrium, and examines the possible bifurcation behavior.

Disease-free equilibrium

The DFE corresponds to the absence of TB infection in the population. Therefore, we set

$$i = i_d = 0.$$

Since the recovered classes represent individuals with a history of TB infection, the disease-free state also requires

$$r = r_d = 0.$$

Under these conditions, the forces of infection vanish, that is,

$$\ell_1 = \ell_2 = 0.$$

Substituting these relations into system (2), the equilibrium equations reduce to

$$1 - (1+a)s = 0, \quad as - s_d = 0.$$

Solving the above system yields

$$s^0 = \frac{1}{1+a}, \quad s_d^0 = \frac{a}{1+a}.$$

Hence, the DFE of system (2) is

$$\mathcal{E}_0 = (s^0, s_d^0, i^0, i_d^0, r^0, r_d^0) = \left(\frac{1}{1+a}, \frac{a}{1+a}, 0, 0, 0, 0 \right). \quad (3)$$

Biologically, $\mathcal{E}_0$ represents a TB-free population in which the normalized population is distributed between the non-diabetic and diabetic susceptible classes according to the relative diabetes progression rate $a = \sigma/\mu$. In particular, a larger value of a implies a greater proportion of diabetic susceptible individuals at the disease-free equilibrium.

Basic reproduction number

We now derive the basic reproduction number, denoted by $\mathcal{R}_0$, using the next-generation matrix approach developed by Diekmann et al. (Diekmann et al. 1990) and further formalized by van den Driessche and Watmough (van den Driessche and Watmough 2002).

Since the recovered classes may relapse into the infectious classes, they must be included in the infected subsystem. Accordingly, we define

$$x = (i, i_d, r, r_d)^\top.$$

Following the standard decomposition, the infected subsystem is written as

$$\frac{dx}{d\tau} = \mathcal{F}(x) - \mathcal{V}(x),$$

where

$$\mathcal{F}(x) = \begin{pmatrix} \ell_1 s \\ \theta \ell_1 s_d \\ 0 \\ 0 \end{pmatrix}, \quad \mathcal{V}(x) = \begin{pmatrix} (g+1+d+a)i - pcr \\ (\eta g + 1 + d_D)i_d - ai - pcr_d \\ (c+1+a)r - gi \\ (c+1)r_d - \eta g i_d - ar \end{pmatrix}.$$

Evaluating the Jacobians of $\mathcal{F}$ and $\mathcal{V}$ at the disease-free equilibrium $\mathcal{E}_0$ gives

$$F = \begin{pmatrix} \frac{B_1}{1+a} & \frac{B_1}{1+a} & 0 & 0 \\ \frac{\theta a B_1}{1+a} & \frac{\theta a B_1}{1+a} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} g+1+d+a & 0 & -pc & 0 \\ -a & \eta g + 1 + d_D & 0 & -pc \\ -g & 0 & c+1+a & 0 \\ 0 & -\eta g & -a & c+1 \end{pmatrix}.$$

The basic reproduction number $\mathcal{R}_0$ is the spectral radius of FV^{-1} . Because F has rank one, FV^{-1} also has rank one and its only nonzero eigenvalue equals its trace. To simplify the resulting expression, define the relapse-adjusted removal rates

$$\theta_i = (g+1+d+a) - \frac{pcg}{c+1+a}, \quad \theta_{i_d} = (\eta g + 1 + d_D) - \frac{pc\eta g}{c+1},$$

and the relapse-adjusted cross term

$$\theta_{21} = a + \frac{pcag}{(c+1)(c+1+a)}.$$

Consequently, the basic reproduction number is

$$\mathcal{R}_0 = \frac{B_1 (\theta_{i_d} + \theta_{21} + \theta a \theta_i)}{(1+a)\theta_i \theta_{i_d}}. \quad (4)$$

Expression (4) shows that relapse reduces the effective removal rates θ_i and θ_{i_d} , thereby increasing the transmission potential of tuberculosis. Consequently, the presence of relapse enlarges the basic reproduction number compared with the one when relapse is absent. As a consistency check, when relapse is removed by

taking $p = 0$, we have $\theta_i = g+1+d+a$ and $\theta_{i_d} = \eta g + 1 + d_D$, and $\theta_{21} = a$, therefore, we obtain

$$\mathcal{R}_0|_{p=0} = \frac{B_1 [(\eta g + 1 + d_D + a) + \theta a (g + 1 + d + a)]}{(1+a)(g+1+d+a)(\eta g + 1 + d_D)}.$$

We can directly compare that $\mathcal{R}_0 > \mathcal{R}_0|_{p=0}$ provided that $\theta_i > 0$ and $\theta_{i_d} > 0$.

DFE's Local stability

We now investigate the local stability of the DFE $\mathcal{E}_0$ given in (3). Its stability is characterized by the basic reproduction number $\mathcal{R}_0$.

Theorem 3. The DFE $\mathcal{E}_0$ of system (2) is locally asymptotically stable if $\mathcal{R}_0 < 1$.

Proof. We linearize system (2) around the DFE $\mathcal{E}_0$. The Jacobian matrix evaluated at $\mathcal{E}_0$ is

$$J(\mathcal{E}_0) = \begin{pmatrix} -(1+a) & 0 & -\frac{B_1}{1+a} & -\frac{B_1}{1+a} & (1-p)c & 0 \\ a & -1 & -\frac{\theta a B_1}{1+a} & -\frac{\theta a B_1}{1+a} & 0 & (1-p)c \\ 0 & 0 & \frac{B_1}{1+a} - (g+1+d+a) & \frac{B_1}{1+a} & pc & 0 \\ 0 & 0 & \frac{\theta a B_1}{1+a} + a & \frac{\theta a B_1}{1+a} - (\eta g + 1 + d_D) & 0 & pc \\ 0 & 0 & g & 0 & -(c+1+a) & 0 \\ 0 & 0 & 0 & \eta g & a & -(c+1) \end{pmatrix}.$$

Reordering the variables as

$$(i, i_d, r, r_d, s, s_d),$$

the Jacobian matrix can be written in block lower triangular form:

$$J(\mathcal{E}_0) = \begin{pmatrix} J_I & 0 \\ * & J_S \end{pmatrix},$$

where

$$J_S = \begin{pmatrix} -(1+a) & 0 \\ a & -1 \end{pmatrix},$$

corresponds to the susceptible subsystem, while

$$J_I = \begin{pmatrix} j_{11} & \frac{B_1}{1+a} & pc & 0 \\ \frac{\theta a B_1}{1+a} + a & j_{22} & 0 & pc \\ g & 0 & -(c+1+a) & 0 \\ 0 & \eta g & a & -(c+1) \end{pmatrix}$$

is the Jacobian associated with the infected subsystem, where $j_{11} = \frac{B_1}{1+a} - (g+1+d+a)$ and $j_{22} = \frac{\theta a B_1}{1+a} - (\eta g + 1 + d_D)$.

The eigenvalues of J_S are

$$\lambda_1 = -(1+a) < 0, \quad \lambda_2 = -1 < 0.$$

Therefore, the local stability of $\mathcal{E}_0$ is determined entirely by the eigenvalues of J_I .

Following the next-generation matrix method (Diekmann *et al.* 1990; van den Driessche and Watmough 2002) and the derivation of the basic reproduction number $\mathcal{R}_0$ that has been obtained earlier, the eigenvalues of J_I have negative real parts if and only if $\mathcal{R}_0 < 1$, while at least one eigenvalue becomes positive when $\mathcal{R}_0 > 1$. Consequently, because the eigenvalues of J_S are also strictly negative, all eigenvalues of $J(\mathcal{E}_0)$ have negative real parts. Therefore, $\mathcal{E}_0$ is locally asymptotically stable when $\mathcal{R}_0 < 1$. $\square$

Theorem 3 shows that the basic reproduction number $\mathcal{R}_0$ functions as a threshold parameter governing TB invasion dynamics in the presence of diabetes comorbidity. Importantly, since $\mathcal{R}_0$ depends on the diabetes-related parameters a , θ , and η , the presence of diabetes may significantly alter the threshold condition for TB elimination. Therefore, effective TB control strategies in populations with a high prevalence of diabetes should account for both transmission reduction and diabetes management.

Endemic equilibrium

The system endemic equilibrium (2) is a steady state

$$\mathcal{E}^* = (s^*, s_d^*, i^*, i_d^*, r^*, r_d^*)$$

satisfying

$$i^* > 0, \quad i_d^* > 0.$$

Let

$$\ell_1^* = B_1(1 + K(i^* + i_d^*))(i^* + i_d^*), \quad \ell_2^* = B_2(1 + K(i^* + i_d^*))(i^* + i_d^*).$$

We first express all variables in terms of the infectious components i^* and i_d^* .

From the fifth equation of (2), we obtain

$$r^* = \frac{g i^*}{c + 1 + a + \ell_2^*}. \quad (5)$$

Substituting (5) into the sixth equation yields

$$r_d^* = \frac{\eta g i_d^* + a r^*}{c + 1 + \ell_2^*}. \quad (6)$$

Next, from the early equation, we obtain

$$s^* = \frac{1 + (1 - p)c r^*}{1 + a + \ell_1^*}, \quad (7)$$

and from the second equation,

$$s_d^* = \frac{a s^* + (1 - p)c r_d^*}{1 + \theta \ell_1^*}. \quad (8)$$

Therefore, the endemic equilibrium can be written explicitly as

$$\mathcal{E}^* = \left(s^*, s_d^*, i^*, i_d^*, \frac{g i^*}{c + 1 + a + \ell_2^*}, \frac{\eta g i_d^* + a r^*}{c + 1 + \ell_2^*} \right), \quad (9)$$

where s^* and s_d^* are given by (7)–(8).

By substituting (5)–(8) into the third and fourth equations of (2), then we obtain a reduced system of two nonlinear equations in i^* and i_d^* :

$$\begin{aligned} 0 &= \ell_1^* s^* + p c r^* + \ell_2^* r^* - (g + 1 + d + a) i^*, \\ 0 &= \theta \ell_1^* s_d^* + p c r_d^* + \ell_2^* r_d^* + a i^* - (\eta g + 1 + d_D) i_d^*. \end{aligned} \quad (10)$$

Thus, the endemic equilibrium reduces to finding positive solutions (i^*, i_d^*) of system (10).

Due to the nonlinear incidence function and the presence of reinfection and relapse, system (10) may admit multiple positive solutions. This indicates the possible existence of multiple endemic equilibria. Especially, the coexistence of multiple endemic equilibria when $\mathcal{R}_0 < 1$ is associated with the phenomenon of backward bifurcation, which will be analyzed in the next subsection. The explicit dependence of $\mathcal{E}^*$ on i^* and i_d^* highlights the central role of the infectious compartments in determining the equilibrium structure of the system.

Bifurcation analysis

The local bifurcation of the system (2) near the DFE $\mathcal{E}_0$ is analyzed in this section. In particular, we determine whether the model undergoes a forward bifurcation or a backward bifurcation as the transmission parameter B_1 crosses the critical threshold corresponding to $\mathcal{R}_0 = 1$.

To this end, we apply the center manifold approach of Castillo-Chavez and Song (Castillo-Chavez and Song 2004). Let

$$x_1 = s, \quad x_2 = s_d, \quad x_3 = i, \quad x_4 = i_d, \quad x_5 = r, \quad x_6 = r_d,$$

so that system (2) is written compactly as

$$\dot{x} = f(x, B_1),$$

where the dot describes differentiation with respect to τ .

The system takes the form

$$\begin{aligned} f_1 &= 1 - B_1(1 + K(x_3 + x_4))(x_3 + x_4)x_1 + (1 - p)c x_5 \\ &\quad - (1 + a)x_1, \\ f_2 &= a x_1 - \theta B_1(1 + K(x_3 + x_4))(x_3 + x_4)x_2 + (1 - p)c x_6 - x_2, \\ f_3 &= B_1(1 + K(x_3 + x_4))(x_3 + x_4)x_1 + p c x_5 \\ &\quad + B_2(1 + K(x_3 + x_4))(x_3 + x_4)x_5 - (g + 1 + d + a)x_3, \\ f_4 &= \theta B_1(1 + K(x_3 + x_4))(x_3 + x_4)x_2 + p c x_6 \\ &\quad + B_2(1 + K(x_3 + x_4))(x_3 + x_4)x_6 + a x_3 - (\eta g + 1 + d_D)x_4, \\ f_5 &= g x_3 - c x_5 - B_2(1 + K(x_3 + x_4))(x_3 + x_4)x_5 - (1 + a)x_5, \\ f_6 &= \eta g x_4 + a x_5 - c x_6 - B_2(1 + K(x_3 + x_4))(x_3 + x_4)x_6 - x_6. \end{aligned}$$

Bifurcation may occur when $\mathcal{R}_0 = 1$. Solving this condition for B_1 gives

$$B_1^* = \frac{(1 + a)\theta_i \theta_{i_d}}{\theta_{i_d} + \theta_{21} + \theta a \theta_i} \quad (11)$$

At $B_1 = B_1^*$, the Jacobian matrix $Df(\mathcal{E}_0, B_1^*)$ has a simple zero eigenvalue, while all other eigenvalues have negative real parts. Therefore, the center manifold theorem is applicable.

Let

$$\mathbf{w} = (w_1, w_2, w_3, w_4, w_5, w_6)^\top$$

be the right eigenvector correlated to zero eigenvalue of $Df(\mathcal{E}_0, B_1^*)$, that is,

$$Df(\mathcal{E}_0, B_1^*) \mathbf{w} = 0.$$

Choose $w_3 = 1$. Then the remaining components are given by

$$\begin{aligned} w_5 &= \frac{g}{c + 1 + a}, \\ w_4 &= \frac{(1 + a)\theta_i}{B_1^*} - 1, \\ w_6 &= \frac{\eta g w_4 + a w_5}{c + 1}, \end{aligned}$$

$$w_1 = \frac{-(1+w_4)B_1^*/(1+a) + (1-p)cw_5}{1+a},$$

$$w_2 = aw_1 - \theta a(1+w_4)B_1^*/(1+a) + (1-p)cw_6.$$

Next, let

$$\tilde{\mathbf{v}} = (\tilde{v}_1, \tilde{v}_2, \tilde{v}_3, \tilde{v}_4, \tilde{v}_5, \tilde{v}_6)^\top$$

be an unnormalized left eigenvector satisfying

$$Df(\mathcal{E}_0, B_1^*)^\top \tilde{\mathbf{v}} = 0.$$

Choose $\tilde{v}_4 = 1$. Then

$$\tilde{v}_1 = \tilde{v}_2 = 0,$$

$$\tilde{v}_6 = \frac{pc}{c+1},$$

$$\tilde{v}_3 = \frac{\theta_{i_d}}{B_1^*/(1+a)} - \theta a,$$

$$\tilde{v}_5 = \frac{pc\tilde{v}_3 + a\tilde{v}_6}{c+1+a}.$$

The remaining left-eigenvector equation is satisfied because of the criticality condition $\mathcal{R}_0 = 1$. We normalize the left eigenvector by defining

$$\mathbf{v} = \frac{\tilde{\mathbf{v}}}{\tilde{\mathbf{v}}^\top \mathbf{w}},$$

so that

$$\mathbf{v}^\top \mathbf{w} = 1.$$

Thus, the components v_k used below are the normalized components, and v_4 is not generally equal to 1.

At $(\mathcal{E}_0, B_1^*)$, the second-order derivatives that contribute to the center manifold coefficients arise from the primary infection and reinfection terms. Although f_1 and f_2 also possess nonzero second-order derivatives, their contributions vanish because $v_1 = v_2 = 0$.

For f_3 , the relevant derivatives are

$$\begin{aligned} \frac{\partial^2 f_3}{\partial x_1 \partial x_3} &= B_1^*, & \frac{\partial^2 f_3}{\partial x_1 \partial x_4} &= B_1^*, \\ \frac{\partial^2 f_3}{\partial x_3^2} &= \frac{2B_1^*K}{1+a}, & \frac{\partial^2 f_3}{\partial x_3 \partial x_4} &= \frac{2B_1^*K}{1+a}, \\ \frac{\partial^2 f_3}{\partial x_4^2} &= \frac{2B_1^*K}{1+a}, & \frac{\partial^2 f_3}{\partial x_3 \partial x_5} &= B_2, \\ \frac{\partial^2 f_3}{\partial x_4 \partial x_5} &= B_2. \end{aligned}$$

For f_4 , they are

$$\begin{aligned} \frac{\partial^2 f_4}{\partial x_2 \partial x_3} &= \theta B_1^*, & \frac{\partial^2 f_4}{\partial x_2 \partial x_4} &= \theta B_1^*, \\ \frac{\partial^2 f_4}{\partial x_3^2} &= \frac{2\theta a B_1^*K}{1+a}, & \frac{\partial^2 f_4}{\partial x_3 \partial x_4} &= \frac{2\theta a B_1^*K}{1+a}, \\ \frac{\partial^2 f_4}{\partial x_4^2} &= \frac{2\theta a B_1^*K}{1+a}, & \frac{\partial^2 f_4}{\partial x_3 \partial x_6} &= B_2, \\ \frac{\partial^2 f_4}{\partial x_4 \partial x_6} &= B_2. \end{aligned}$$

For f_5 and f_6 , we obtain

$$\frac{\partial^2 f_5}{\partial x_3 \partial x_5} = -B_2, \quad \frac{\partial^2 f_5}{\partial x_4 \partial x_5} = -B_2,$$

$$\frac{\partial^2 f_6}{\partial x_3 \partial x_6} = -B_2, \quad \frac{\partial^2 f_6}{\partial x_4 \partial x_6} = -B_2.$$

Following [Castillo-Chavez and Song \(2004\)](#), define

$$\bar{a} = \sum_{k,i,j=1}^6 v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(\mathcal{E}_0, B_1^*)$$

and

$$\bar{b} = \sum_{k,i=1}^6 v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial B_1}(\mathcal{E}_0, B_1^*).$$

After collecting the nonzero contributions, we obtain

$$\begin{aligned} \bar{a} &= 2B_1^*v_3 \left[w_1(1+w_4) + \frac{K}{1+a}(1+w_4)^2 \right] \\ &\quad + 2\theta B_1^*v_4 \left[w_2(1+w_4) + \frac{aK}{1+a}(1+w_4)^2 \right] \\ &\quad + 2B_2(1+w_4)(v_3w_5 + v_4w_6 - v_5w_5 - v_6w_6). \end{aligned} \quad (12)$$

Similarly,

$$\bar{b} = \frac{1+w_4}{1+a}(v_3 + \theta a v_4). \quad (13)$$

We now show explicitly that $\bar{b} > 0$. From the right-eigenvector relation, we have

$$1+w_4 = \frac{\theta_{i_d}}{B_1^*/(1+a)} > 0.$$

For the unnormalized left eigenvector $\tilde{\mathbf{v}}$, chosen such that $\tilde{v}_4 = 1$, the corresponding relation gives

$$\tilde{v}_3 + \theta a \tilde{v}_4 = \tilde{v}_3 + \theta a = \frac{\theta_{i_d}}{B_1^*/(1+a)} > 0.$$

Indeed, since $0 \leq p \leq 1$,

$$\frac{pc}{c+1+a} < 1, \quad \frac{pc}{c+1} < 1,$$

and therefore

$$\theta_{i_d} = g + 1 + d + a - \frac{pcg}{c+1+a} > 1 + d + a > 0$$

and

$$\theta_{i_d} = \eta g + 1 + d_D - \frac{pc\eta g}{c+1} > 1 + d_D > 0.$$

Hence, the coefficient calculated using the unnormalized left eigenvector satisfies

$$\tilde{\bar{b}} = \frac{1+w_4}{1+a}(\tilde{v}_3 + \theta a \tilde{v}_4) = \frac{\theta_{i_d}}{(1+a)(B_1^*/(1+a))^2} > 0.$$

After normalizing the left eigenvector according to

$$\mathbf{v} = \frac{\tilde{\mathbf{v}}}{\tilde{\mathbf{v}}^\top \mathbf{w}},$$

with its orientation chosen so that $\tilde{\mathbf{v}}^\top \mathbf{w} > 0$, we obtain

$$\bar{b} = \frac{\tilde{\bar{b}}}{\tilde{\mathbf{v}}^\top \mathbf{w}} > 0.$$

We therefore obtain the following result.

Theorem 4. Suppose that B_1 is chosen as the bifurcation parameter and that B_1^* is given by (11). Then the local bifurcation of system (2) at $(\mathcal{E}_0, B_1^*)$ is determined by the sign of $\bar{a}$:

1. if $\bar{a} < 0$, the system undergoes a forward bifurcation at $B_1 = B_1^*$;
2. if $\bar{a} > 0$, the system undergoes a backward bifurcation at $B_1 = B_1^*$.

A backward bifurcation implies that reducing the basic reproduction number below unity may not, by itself, guarantee TB elimination. Under such a regime, stable disease-free and endemic states may coexist for $\mathcal{R}_0 < 1$, so the long-term outcome can depend on the initial disease burden. Therefore, transmission-reduction measures should be complemented by interventions that reduce infectious relapse, reinfection, and diabetes-associated risks.

OPTIMAL CONTROL FORMULATION

To reduce the TB burden associated with diabetes comorbidity, we incorporate four time-dependent control functions into the system. Control $u_1(\tau)$ represents efforts to reduce TB transmission, such as mask use, screening, isolation, and health education. Control $u_2(\tau)$ represents interventions to reduce diabetes progression among non-diabetic individuals, such as lifestyle modification and diabetes prevention programs. Control $u_3(\tau)$ represents enhanced treatment efforts for TB-infected individuals without diabetes. Control $u_4(\tau)$ represents enhanced treatment efforts for TB-infected individuals with diabetes. Here, $0 \leq u_i(\tau) \leq 1$, $i = 1, 2, 3, 4$, for all $\tau \in [0, \tau_f]$.

Under these controls, the dimensionless forces of infection become

$$\begin{aligned}\ell_1^c &= (1 - u_1)B_1(1 + K(i + i_d))(i + i_d), \\ \ell_2^c &= (1 - u_1)B_2(1 + K(i + i_d))(i + i_d).\end{aligned}$$

where the factor $(1 - u_1)$ represents the decrease in primary infection and reinfection due to transmission control.

The controlled dimensionless TB–diabetes comorbidity model is then

$$\begin{aligned}\frac{ds}{d\tau} &= 1 - \ell_1^c s + (1 - p)cr - (1 + (1 - u_2)a)s, \\ \frac{ds_d}{d\tau} &= (1 - u_2)as - \theta\ell_1^c s_d - s_d + (1 - p)cr_d, \\ \frac{di}{d\tau} &= \ell_1^c s + pc r + \ell_2^c r - (g + u_3 + 1 + d + (1 - u_2)a)i, \\ \frac{di_d}{d\tau} &= \theta\ell_1^c s_d + pc r_d + \ell_2^c r_d + (1 - u_2)ai - (\eta g + u_4 + 1 + d_D)i_d, \\ \frac{dr}{d\tau} &= (g + u_3)i - cr - \ell_2^c r - (1 + (1 - u_2)a)r, \\ \frac{dr_d}{d\tau} &= (\eta g + u_4)i_d + (1 - u_2)ar - cr_d - \ell_2^c r_d - r_d.\end{aligned}\tag{14}$$

To minimize the disease burden together with the implementation costs of the intervention strategies, we seek the optimal controls $u_i^*(\tau)$, $i = 1, 2, 3, 4$, that minimize the objective functional

$$J(u) = \int_0^{\tau_f} \left[q_1 i + q_2 i_d + q_3 r_d + \frac{1}{2} (r_1 u_1^2 + r_2 u_2^2 + r_3 u_3^2 + r_4 u_4^2) \right] d\tau,$$

where $q_i \geq 0$ and $r_i > 0$. The terms i and i_d denote active infectious individuals and therefore directly measure the main disease burden that should be minimized through intervention. The term r_d is included to account for the residual health burden of recovered diabetic patients, since these individuals remain at a higher risk of relapse, reinfection, and long-term complications despite treatment. The recovered non-diabetic compartment r is not included

in the objective functional because individuals in this compartment are assumed to have completed treatment successfully and generally have a substantially lower clinical risk than recovered diabetic individuals. Therefore, including r may not appropriately represent the disease burden and could discourage recovery. The quadratic terms represent the implementation costs of the controls and are included to ensure that the objective functional appropriately balances epidemiological benefits against practical intervention costs.

Let

$$x = (s, s_d, i, i_d, r, r_d)^\top$$

be the state vector and

$$\psi = (\psi_s, \psi_{s_d}, \psi_i, \psi_{i_d}, \psi_r, \psi_{r_d})^\top$$

be the adjoint vector.

The Hamiltonian is

$$\begin{aligned}\mathcal{H} &= q_1 i + q_2 i_d + q_3 r_d + \frac{1}{2} \sum_{j=1}^4 r_j u_j^2 \\ &+ \psi_s [1 - \ell_1^c s + (1 - p)cr - (1 + (1 - u_2)a)s] \\ &+ \psi_{s_d} [(1 - u_2)as - \theta\ell_1^c s_d - s_d + (1 - p)cr_d] \\ &+ \psi_i [\ell_1^c s + pc r + \ell_2^c r - (g + u_3 + 1 + d + (1 - u_2)a)i] \\ &+ \psi_{i_d} [\theta\ell_1^c s_d + pc r_d + \ell_2^c r_d + (1 - u_2)ai \\ &- (\eta g + u_4 + 1 + d_D)i_d] \\ &+ \psi_r [(g + u_3)i - cr - \ell_2^c r - (1 + (1 - u_2)a)r] \\ &+ \psi_{r_d} [(\eta g + u_4)i_d + (1 - u_2)ar - cr_d - \ell_2^c r_d - r_d].\end{aligned}\tag{15}$$

By Pontryagin's Maximum Principle (Seierstad and Sydsaeter 1986), we obtain the following result.

Theorem 5. Let $(u_1^*, u_2^*, u_3^*, u_4^*)$ be an optimal control quadruple and let

$$x^*(\tau) = (s^*, s_d^*, i^*, i_d^*, r^*, r_d^*)$$

be the corresponding solution of the controlled system (14). Therefore a nontrivial adjoint vector exists

$$\psi = (\psi_s, \psi_{s_d}, \psi_i, \psi_{i_d}, \psi_r, \psi_{r_d})^\top$$

such that

$$\begin{aligned}\frac{d\psi_s}{d\tau} &= [\ell_1^c + 1 + (1 - u_2)a]\psi_s - (1 - u_2)a\psi_{s_d} - \ell_1^c \psi_i, \\ \frac{d\psi_{s_d}}{d\tau} &= (1 + \theta\ell_1^c)\psi_{s_d} - \theta\ell_1^c \psi_{i_d}, \\ \frac{d\psi_i}{d\tau} &= -q_1 + \Omega_1 s(\psi_s - \psi_i) + \theta\Omega_1 s_d(\psi_{s_d} - \psi_{i_d}) \\ &+ \Omega_2 r(\psi_r - \psi_i) + \Omega_2 r_d(\psi_{r_d} - \psi_{i_d}) \\ &+ [g + u_3 + 1 + d + (1 - u_2)a]\psi_i - (1 - u_2)a\psi_{i_d} \\ &- (g + u_3)\psi_r, \\ \frac{d\psi_{i_d}}{d\tau} &= -q_2 + \Omega_1 s(\psi_s - \psi_i) + \theta\Omega_1 s_d(\psi_{s_d} - \psi_{i_d}) \\ &+ \Omega_2 r(\psi_r - \psi_i) + \Omega_2 r_d(\psi_{r_d} - \psi_{i_d}) \\ &+ (\eta g + u_4 + 1 + d_D)\psi_{i_d} - (\eta g + u_4)\psi_{r_d}, \\ \frac{d\psi_r}{d\tau} &= -(1 - p)c\psi_s - (pc + \ell_2^c)\psi_i \\ &+ [c + \ell_2^c + 1 + (1 - u_2)a]\psi_r - (1 - u_2)a\psi_{r_d}, \\ \frac{d\psi_{r_d}}{d\tau} &= -q_3 - (1 - p)c\psi_{s_d} - (pc + \ell_2^c)\psi_{i_d} \\ &+ (c + \ell_2^c + 1)\psi_{r_d},\end{aligned}\tag{16}$$

where

$$\Omega_1 = (1 - u_1)B_1[1 + 2K(i + i_d)], \Omega_2 = (1 - u_1)B_2[1 + 2K(i + i_d)],$$

with the transversality conditions

$$\psi_j(\tau_f) = 0, \quad j \in \{s, s_d, i, i_d, r, r_d\}.$$

Moreover, the optimal controls are characterized by

$$u_1^*(\tau) = \min \left\{ \max \left\{ \frac{\Phi_1(\tau)}{r_1}, 0 \right\}, 1 \right\}, \quad (17)$$

$$u_2^*(\tau) = \min \left\{ \max \left\{ \frac{a[s(\psi_{sd} - \psi_s) + i(\psi_{id} - \psi_i)]}{r_2} + \frac{r(\psi_{rd} - \psi_r)}{r_2}, 0 \right\}, 1 \right\}, \quad (18)$$

$$u_3^*(\tau) = \min \left\{ \max \left\{ \frac{i(\psi_i - \psi_r)}{r_3}, 0 \right\}, 1 \right\}, \quad (19)$$

$$u_4^*(\tau) = \min \left\{ \max \left\{ \frac{i_d(\psi_{id} - \psi_{rd})}{r_4}, 0 \right\}, 1 \right\}, \quad (20)$$

where

$$\Phi_1(\tau) = \ell_1[s(\psi_i - \psi_s) + \theta s_d(\psi_{id} - \psi_{sd})] + \ell_2[r(\psi_i - \psi_r) + r_d(\psi_{id} - \psi_{rd})],$$

with

$$\ell_1 = B_1(1 + K(i + i_d))(i + i_d), \ell_2 = B_2(1 + K(i + i_d))(i + i_d).$$

Proof. The result follows from Pontryagin's Maximum Principle. Since the state system is bounded in the feasible region and the admissible control set is closed and convex, the situations needed for optimality apply.

Differentiating the Hamiltonian $\mathcal{H}$ in (15) correlated with each state variable yields the adjoint system (16). Because the terminal states are free, the transversality situations are

$$\psi_j(\tau_f) = 0, \quad j \in \{s, s_d, i, i_d, r, r_d\}.$$

Next, the stationarity conditions

$$\frac{\partial \mathcal{H}}{\partial u_i} = 0, \quad i = 1, 2, 3, 4,$$

yield the unconstrained optimal controls

$$u_1 = \frac{\Phi_1(\tau)}{r_1}, \quad u_2 = \frac{a[s(\psi_{sd} - \psi_s) + i(\psi_{id} - \psi_i) + r(\psi_{rd} - \psi_r)]}{r_2},$$

$$u_3 = \frac{i(\psi_i - \psi_r)}{r_3}, \quad u_4 = \frac{i_d(\psi_{id} - \psi_{rd})}{r_4}.$$

Projecting these onto the admissible control set

$$\mathcal{U} = \left\{ (u_1, u_2, u_3, u_4) : 0 \leq u_i(\tau) \leq 1, \tau \in [0, \tau_f] \right\}$$

gives (17)–(20). Finally, since the Hamiltonian is strictly convex in the controls due to the quadratic terms $r_i u_i^2/2$ with $r_i > 0$, these expressions uniquely minimize $\mathcal{H}$. This completes the proof.

NUMERICAL SIMULATION

For the numerical simulations, we used annual Indonesian epidemiological data from several sources. Specifically, the World Bank (2000–2024) provides the TB incidence per 100,000 population and the TB treatment success rate (%) (World Health Organization 2025a); the World Health Organization (2010–2024) provides the number of new and relapse TB cases notified per 100,000 population together with the estimated total number of TB deaths (World Health Organization 2025b); and the International Diabetes Federation provides the diabetes prevalence (%) for the years 2000, 2011, and 2024 (International Diabetes Federation 2024). To determine the parameter values of the dimensionless model (2), some parameters were adopted or derived from the literature, while the remaining parameters were estimated.

Based on Aldila (2025), we adopted the parameter values $K = 0.1$, $c = 0.2$, and $p = 0.5$. According to the United Nations demographic data for Indonesia during 2000–2024 (United Nations, Department of Economic and Social Affairs, Population Division 2024), the average life expectancy was 68.62 years, giving $\mu = 1/68.62$. Krishna et al. (Krishna and Jacob 2021) reported that individuals with diabetes have a two- to four-fold higher risk of developing active TB than individuals without diabetes. Accordingly, the relative susceptibility parameter satisfies $2 \leq \theta \leq 4$. In this study, we set $\theta = 3$. The same study also reported that diabetes increases the risks of treatment failure, death, and relapse. In particular, the combined risk ratio for treatment failure and death was estimated as 1.69. Since this risk ratio cannot be interpreted directly as a model parameter, we used the simple approximation $\eta = 1/1.69 = 0.592$. Furthermore, the reported risk ratio for TB mortality among patients with diabetes was 1.89. Therefore, we assumed $d_D = 1.89d$. The remaining parameters were estimated using the particle swarm optimization (PSO) algorithm.

Let q_0 denote the observed diabetes prevalence in the initial year, expressed as a proportion. The initial susceptible proportion was calculated as

$$s_0^{\text{tot}} = 1 - i_0 - r_0.$$

The initial values of the six model compartments were then allocated according to the observed diabetes prevalence:

$$s(0) = (1 - q_0)s_0^{\text{tot}}, \quad s_d(0) = q_0 s_0^{\text{tot}},$$

$$i(0) = (1 - q_0)i_0, \quad i_d(0) = q_0 i_0,$$

$$r(0) = (1 - q_0)r_0, \quad r_d(0) = q_0 r_0.$$

This construction ensures that the initial proportion of individuals with diabetes is consistent with the available diabetes prevalence data. Because the model is expressed in dimensionless time, the observation year t was transformed according to $\tau = \mu(t - 2000)$, where 2000 is the initial observation year.

The parameter vector to be estimated was defined as

$$\Theta = (B_1, B_2, a, g, d, i_0, r_0).$$

For the estimation, the admissible parameter region was specified by the lower and upper bounds

$$10^{-4} \leq B_1 \leq 25,$$

$$10^{-5} \leq B_2 \leq 30,$$

$$10^{-4} \leq a \leq 0.5,$$

$$0.1 \leq g \leq 100,$$

$$10^{-4} \leq d \leq 20,$$

$$10^{-6} \leq i_0 \leq 0.05,$$

$$10^{-6} \leq r_0 \leq 0.70.$$

The model outputs were connected to the epidemiological observations through a collection of observation functions. Let

$$z(\tau) = i(\tau) + i_d(\tau)$$

denote the total infectious population. The dimensionless forces of primary infection and reinfection were given by

$$\ell_1(\tau) = B_1 (1 + Kz(\tau)) z(\tau), \quad \ell_2(\tau) = B_2 (1 + Kz(\tau)) z(\tau).$$

The total flow of new active TB episodes, including primary infection and reinfection, was calculated as

$$\mathcal{I}(\tau) = \ell_1 s + \theta \ell_1 s_d + \ell_2 r + \ell_2 r_d.$$

Therefore, the model-predicted annual TB incidence per 100,000 population was defined as

$$\hat{I}_{TB}(t) = 10^5 \mu \frac{\mathcal{I}(\tau)}{n(\tau)},$$

where

$$n(\tau) = s + s_d + i + i_d + r + r_d.$$

The predicted TB notification rate was obtained by multiplying the predicted incidence by the observed case-detection fraction:

$$\hat{N}_{TB}(t) = \rho(t) \hat{I}_{TB}(t),$$

where $\rho(t)$ is the observed case-detection proportion in year t . The predicted TB mortality rate per capita was calculated as

$$\hat{m}_{TB}(t) = \mu \frac{di(\tau) + d_D i_d(\tau)}{n(\tau)}.$$

Accordingly, the predicted number of TB deaths was

$$\hat{D}_{TB}(t) = P(t) \hat{m}_{TB}(t),$$

where $P(t)$ denotes the total population in year t . Since the model does not contain explicit detected and treated compartments, the treatment success rate was approximated by the instantaneous recovery proportion among all exits from the infectious compartments. Thus,

$$\hat{T}(t) = 100 \frac{gi + \eta g i_d}{(g + 1 + d + a)i + (\eta g + 1 + d_D)i_d}.$$

Finally, the predicted diabetes prevalence was calculated as

$$\hat{Q}_D(t) = 100 \frac{s_d(\tau) + i_d(\tau) + r_d(\tau)}{n(\tau)}.$$

Because diabetes prevalence observations were available only for 2000, 2011, 2024, the model predictions at these years were obtained through linear interpolation.

The parameter estimates were obtained by minimizing a weighted sum of squared normalized residuals. Normalization was applied to prevent a dataset with large numerical values, such as the absolute number of TB deaths, from dominating the estimation procedure. Let I_j , N_j , D_j , T_j , and Q_j denote the observed TB incidence, notifications, deaths, treatment success, and diabetes prevalence, respectively. Their corresponding model predictions are denoted by

$$\hat{I}_j, \quad \hat{N}_j, \quad \hat{D}_j, \quad \hat{T}_j, \quad \hat{Q}_j.$$

The normalized residuals were defined as

$$e_{I,j} = \frac{\hat{I}_j - I_j}{\max\{\text{median}(I), 1\}},$$

$$e_{N,j} = \frac{\hat{N}_j - N_j}{\max\{\text{median}(N), 1\}},$$

and

$$e_{D,j} = \frac{\hat{D}_j - D_j}{\max\{\text{median}(D), 1\}}.$$

For treatment success and diabetes prevalence, fixed percentage-point scales were used:

$$e_{T,j} = \frac{\hat{T}_j - T_j}{10}, \quad e_{Q,j} = \frac{\hat{Q}_j - Q_j}{5}.$$

The objective function was then formulated as

$$\begin{aligned} \mathcal{J}(\Theta) = & w_I \sum_{j=1}^{n_I} e_{I,j}^2 + w_N \sum_{j=1}^{n_N} e_{N,j}^2 + w_D \sum_{j=1}^{n_D} e_{D,j}^2 + w_T \sum_{j=1}^{n_T} e_{T,j}^2 \\ & + w_Q \sum_{j=1}^{n_Q} e_{Q,j}^2, \end{aligned}$$

where the weights were selected as $w_I = w_N = w_D = 1$, $w_T = 0.25$, $w_Q = 0.40$.

The parameter estimation problem was therefore expressed as

$$\hat{\Theta} = \arg \min \mathcal{J}(\Theta),$$

This global minimization problem was solved using the PSO algorithm using the MATLAB function `particleswarm` with swarm size 250, maximum of iterations 200, and maximum of stall iterations 20 or function tolerance 10^{-9} . The parameter estimation result is presented in Table 2.

After obtaining the final parameter estimates, the fitted model was evaluated using the root mean squared error, mean absolute error, mean absolute percentage error, and coefficient of determination. For a dataset consisting of m observations y_j and corresponding predictions $\hat{y}_j$, the root mean squared error was calculated as

$$\text{RMSE} = \sqrt{\frac{1}{m} \sum_{j=1}^m (\hat{y}_j - y_j)^2}.$$

The mean absolute error was given by

$$\text{MAE} = \frac{1}{m} \sum_{j=1}^m |\hat{y}_j - y_j|.$$

The mean absolute percentage error was defined as

$$\text{MAPE} = \frac{100}{m} \sum_{j=1}^m \left| \frac{\hat{y}_j - y_j}{y_j} \right|,$$

where observations equal to zero were excluded from the calculation. Finally, the coefficient of determination was calculated as

$$R^2 = 1 - \frac{\sum_{j=1}^m (\hat{y}_j - y_j)^2}{\sum_{j=1}^m (y_j - \bar{y})^2},$$

where $\bar{y} = \frac{1}{m} \sum_{j=1}^m y_j$. These measures were computed separately for TB incidence, TB notifications, TB deaths, treatment success, and diabetes prevalence.

The performance metrics are summarized in Table 3, while the observed data and fitted trajectories are shown in Figure 2.

Overall, the model provides a satisfactory fit to the TB incidence, TB notifications, and diabetes prevalence data. In contrast, the fits for TB deaths and treatment success are less accurate, as indicated by their negative R^2 values, suggesting that the model does not fully capture the temporal variation in these datasets.

Table 2 Parameter and initial condition values of the dimensionless model (2)

Parameter	Value	Source
B_1	24.9974	Estimated using PSO
B_2	19.4766	Estimated using PSO
a	0.25571	Estimated using PSO
g	26.3266	Estimated using PSO
d	2.4959	Estimated using PSO
d_D	4.7173	$d_D = 1.89d$ Krishna and Jacob (2021)
K	0.1	Aldila (2025)
c	0.2	Aldila (2025)
p	0.5	Aldila (2025)
θ	3	From Krishna and Jacob (2021), $2 \leq \theta \leq 4$. This study uses $\theta = 3$.
η	$1/1.69 = 0.592$	Krishna and Jacob (2021)
i_0	0.0123	Estimated using PSO
r_0	0.6997	Estimated using PSO

Table 3 Performance metrics of the fitted model against the observed epidemiological data

Dataset	RMSE	MAE	MAPE (%)	R^2
TB incidence (per 100,000)	18.25	14.31	4.207	0.3525
TB notifications (per 100,000)	14.24	11.31	5.840	0.9423
TB deaths	1.407×10^4	1.212×10^4	10.163	-0.1124
Treatment success (%)	2.026	1.630	1.863	-0.0336
Diabetes prevalence (%)	1.633	1.219	21.685	0.7072

In Figure 3(a), we take $B_1 = 13.42$, which is below the threshold value $B_1^* \approx 16.77$, resulting in the basic reproduction number $\mathcal{R}_0 = 0.8 < 1$. In this case, all trajectories of the infected variables (i, i_d) with different initial conditions converge to the DFE $E_0 = (0, 0)$, indicating that the infection eventually dies out and the disease-free state is attractive. Meanwhile, in Figure 3(b), we set $B_1 = 24.99$, which is above the threshold value, resulting in $\mathcal{R}_0 = 1.49 > 1$, and all trajectories (i, i_d) approach the endemic equilibrium $E_1 = (0.011125, 0.006358)$. This shows that the disease persists in the population under this parameter regime. An example of the time series of the infected variables $i(\tau)$ and $i_d(\tau)$ is depicted in Figure 3(c) and (d), respectively. These numerical results are consistent with the theoretical stability analysis: the solutions approach the DFE when $\mathcal{R}_0 < 1$ and converge to the endemic equilibrium when $\mathcal{R}_0 > 1$.

Furthermore, the analysis perform a sensitivity study of the basic reproduction number $\mathcal{R}_0$ applying the Partial Rank Correlation Coefficient (PRCC) method. PRCC is a global sensitivity analysis approach that measures the strength and direction of the monotonic correlation of a model output and each input parameter while controlling for the effects of the remaining parameters (Marino et al. 2008). The parameters sampled in this study were defined as $\{B_1, a, g, d, d_D, \eta, \theta\}$ by Latin Hypercube Sampling (LHS) with a sample size of $N = 3000$. In addition, the sampling ranges were selected 80%–120% from the baseline values, see Table 4. The

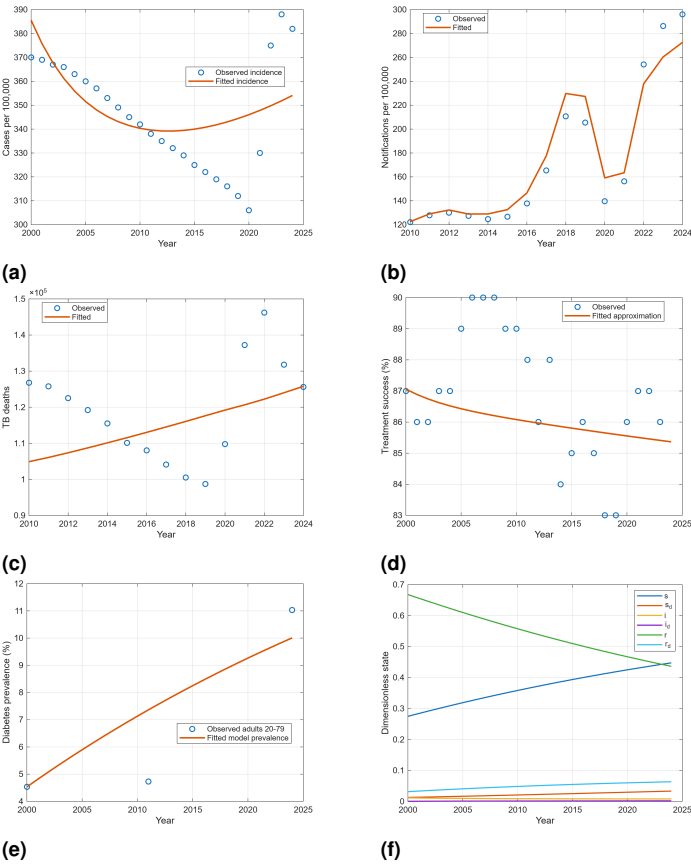


Figure 2 Observed data and fitted curves for (a) TB incidence per 100,000 population, (b) TB notifications per 100,000 population, (c) TB deaths, (d) the treatment success rate (%), and (e) diabetes prevalence (%). Panel (f) shows the fitted trajectories of the dimensionless state variables $s, s_d, i, i_d, r,$ and r_d

value of $\mathcal{R}_0$ is calculated in relation to each sampled parameter set. The PRCC of each parameter was determined as the rank-based partial correlation and $\mathcal{R}_0$, after eliminating the linear effects of entire other sampled parameters. When PRCC is positive, the increase in parameter rises $\mathcal{R}_0$ and when negative the reverse is the case. Therefore, the greater the PRCC absolute value, the higher the parameter impact on $\mathcal{R}_0$.

Table 4 Parameter ranges used in the PRCC analysis and the corresponding sensitivity indices

Parameter	Lower	Baseline	Upper	PRCC	p -value
B_1	19.9976	24.9970	29.9964	+0.9697	0.0000
a	0.2046	0.2557	0.3069	+0.7711	0.0000
g	21.0616	26.3270	31.5924	-0.9512	0.0000
d	1.9968	2.4960	2.9952	-0.1684	1.74×10^{-20}
d_D	3.7739	4.7174	5.6609	-0.4275	2.62×10^{-133}
η	0.4736	0.5920	0.7104	-0.8180	0.0000
θ	2.4000	3.0000	3.6000	+0.8881	0.0000

In Table 4, we summarize the PRCC values together with their associated p -values. The sensitivity of each parameter is primarily interpreted based on the magnitude and sign of the PRCC coefficients, with larger absolute values indicating a stronger influence on the model output. Figure 4 shows that $B_1, \theta,$ and a exerted a

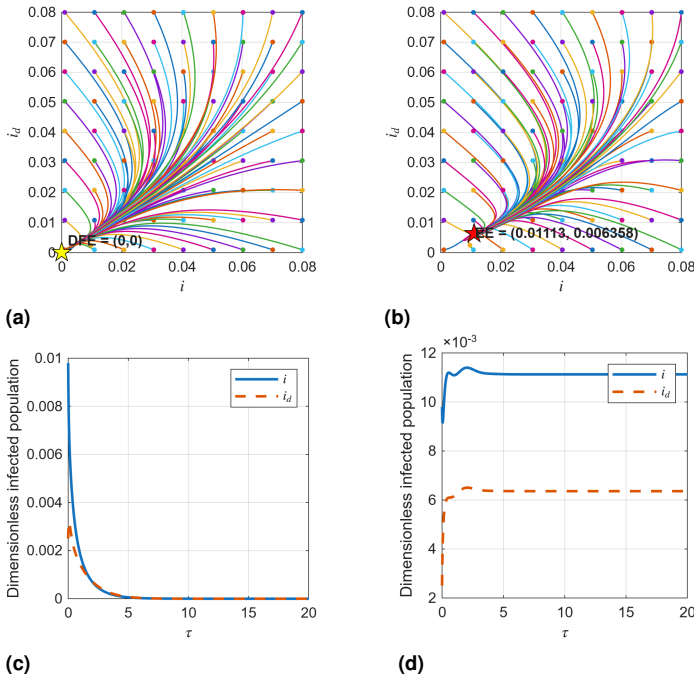


Figure 3 Phase portraits of the infected variables (i, i_d) converging to (a) the disease-free equilibrium (DFE) for $B_1 = 13.42$ ($\mathcal{R}_0 = 0.8 < 1$) and (b) the endemic equilibrium (EE) for $B_1 = 24.99$ ($\mathcal{R}_0 = 1.49 > 1$). Panels (c) and (d) present the corresponding time series of i and i_d , respectively

strong positive effect on $\mathcal{R}_0$, implying greater transmission, and susceptibility of diabetic individuals, including faster progression to diabetes were positive contributors to disease spread. However, the recovery rate g and parameter η have strong negative effects, suggesting that an increase in treatment effectiveness significantly decreased $\mathcal{R}_0$. Other parameters have relatively minor effects compared to these dominant factors. From Table 4, we conclude that the three most influential parameters are B_1 , g , and θ .

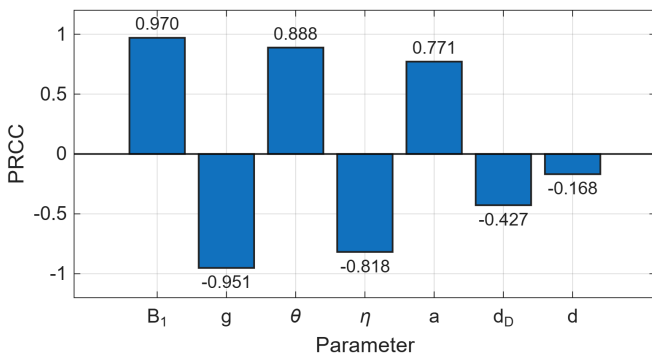


Figure 4 Partial rank correlation coefficients (PRCCs) of the basic reproduction number $\mathcal{R}_0$. The PRCC analysis identifies B_1 , g , and θ as the three most influential parameters

Following the PRCC analysis, which identified B_1 , g , and θ as the three most influential parameters, we plot contour diagrams of the basic reproduction number $\mathcal{R}_0$ in the (B_1, g) -, (B_1, θ) -, and (g, θ) -planes (Figure 5). Consistent with the PRCC results, $\mathcal{R}_0$ increases with B_1 and θ , whereas it decreases as g increases. The red contour represents the threshold $\mathcal{R}_0 = 1$, separating the disease-

free and endemic regions, while the star marker denotes the estimated parameter values. Since the estimated parameters lie in the region where $\mathcal{R}_0 > 1$, the model predicts disease persistence. These results suggest that reducing the transmission rate and diabetes-related susceptibility, together with increasing the recovery rate, are essential for controlling TB transmission.

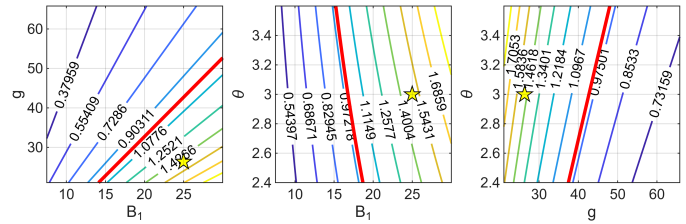


Figure 5 Contour plots of the basic reproduction number $\mathcal{R}_0$ in the parameter planes of the three most sensitive parameters identified by the PRCC analysis: (a) (g, B_1) , (b) (g, θ) , and (c) (B_1, θ) . The red line represents the threshold $\mathcal{R}_0 = 1$, while the star marker indicates the estimated parameter values

To confirm Theorem 4, we perform numerical simulations of the bifurcation diagram for the total infected population, $I^* = i^* + i_d^*$. Figure 6 illustrates the bifurcation diagrams of the model with respect to the basic reproduction number $\mathcal{R}_0$. Figure 6(a) corresponds to the calibrated parameter values listed in Table 2, for which $K = 0.1$ and $\bar{a} = -895.4 < 0$. In this case, the model exhibits a forward bifurcation. The disease-free equilibrium (blue) is stable for $\mathcal{R}_0 < 1$ and loses its stability at the threshold $\mathcal{R}_0 = 1$, where a stable endemic equilibrium (red) emerges continuously. Consequently, reducing $\mathcal{R}_0$ below unity is sufficient to eliminate the disease under the calibrated Indonesian scenario.

For completeness, Figure 6(b) illustrates that the proposed model is also capable of exhibiting a backward bifurcation under a different parameter regime. Specifically, increasing the nonlinear transmission parameter to $K = 25$ yields $\bar{a} = 85.6 > 0$, resulting in the coexistence of a stable disease-free equilibrium and a stable endemic equilibrium for $0.97852029 < \mathcal{R}_0 < 1$, separated by an unstable endemic equilibrium (green). Although this value of K is substantially larger than the calibrated estimate ($K = 0.1$) and is not intended to represent the current Indonesian epidemiological situation, it demonstrates that sufficiently strong nonlinear transmission effects can fundamentally alter the qualitative dynamics of the model. Therefore, the backward bifurcation should be interpreted as a theoretical possibility supported by the model structure rather than a feature of the calibrated Indonesian data.

The other significant simulation focused on the sensitivity of the epidemic size and peak timing to the transmission parameter B_1 . In this analysis, B_1 was varied over the range $[5, 30]$, and for each value the model was solved numerically to evaluate the total infectious population, $I_{\text{tot}}(\tau) = i(\tau) + i_d(\tau)$. The epidemic size was measured by the cumulative number of new infections, $\int_0^T (\ell_1 s + \theta \ell_1 s_d) d\tau$, over the simulation period, while the peak timing was defined as the time at which the total infectious proportion, $i + i_d$, attained its maximum value. Figure 7 shows that the epidemic size increases monotonically with B_1 , highlighting the dominant influence of the transmission rate on the overall disease burden. At the same time, the peak timing spike near the threshold is an example of critical slowing down (relaxation time diverging as $\mathcal{R}_0 \rightarrow 1$). This phenomenon occurs near $B_1 = 18$, which is close to the critical threshold $B_1^* \approx 16.77$. For sufficiently large values of B_1 , the epidemic peak occurs earlier, indicating that higher

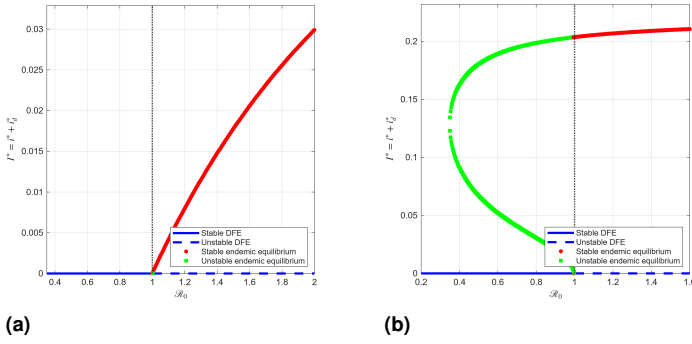


Figure 6 (a) Forward bifurcation diagram for the parameter values listed in Table 2, yielding $\bar{a} = -895.4 < 0$. (b) Backward bifurcation diagram for the parameter values listed in Table 2 with $K = 25$, yielding $\bar{a} = 85.6 > 0$

transmission rates accelerate disease spread and shorten the time required to reach the maximum number of infected individuals.

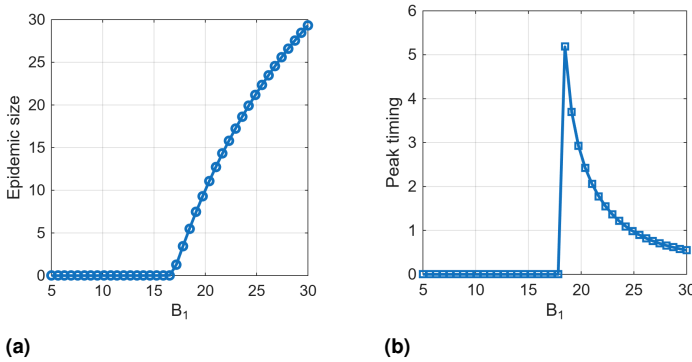


Figure 7 Sensitivity of (a) the epidemic size and (b) the peak timing to B_1 . The epidemic size is measured as the cumulative number of new infections, $\int_0^T (\ell_1 s + \theta \ell_1 s_d) d\tau$, over the simulation period, whereas the peak timing is defined as the time at which the total infectious proportion, $i + i_d$, reaches its maximum

Next, we investigate the impact of optimal control interventions using the baseline parameter set in Table 2. The disease burden weights are chosen as $q_1 = 50$, $q_2 = 80$, and $q_3 = 20$, while the control cost weights are taken as $r_1 = 2$, $r_2 = 2$, $r_3 = 1$, and $r_4 = 1$. The optimal control system was solved numerically using the forward-backward sweep method (Lenhart and Workman 2007). Both the state and adjoint systems were integrated using the classical fourth-order Runge-Kutta scheme over the interval $[0, 60]$ with 600 uniform time steps ($\Delta\tau = 0.1$). The controls were updated iteratively using a relaxation parameter of 0.5, with a maximum of 80 forward-backward sweep iterations. The iterative process was terminated when the maximum absolute change between two successive control iterates was less than 10^{-6} . To compare the economic efficiency of the candidate intervention strategies, we use the average cost-effectiveness ratio (ACER) (Drummond et al. 2015), which measures the cost required to avert one unit of disease burden relative to the no-control case. In this study, ACER is defined by

$$\text{ACER} = \frac{\text{Total intervention cost}}{\text{Cases averted}}$$

$$= \frac{\int_0^{\tau_f} \frac{1}{2} (r_1 u_1^2 + r_2 u_2^2 + r_3 u_3^2 + r_4 u_4^2) d\tau}{\int_0^{\tau_f} [(i + i_d)_{\text{no control}} - (i + i_d)_{\text{control}}] d\tau}.$$

A smaller ACER indicates a more cost-effective strategy because it achieves a greater reduction in infections relative to its implementation cost. Figure 8 and Table 5 show that the combined strategy $u_1 + u_3$ has the lowest ACER among all strategies considered. This strategy combines interventions that reduce TB transmission, such as screening, isolation, mask use, and health education, with enhanced treatment for TB-infected individuals without diabetes. Although the strategy u_1 alone averts nearly the same number of infections, its slightly higher cost results in a larger ACER. Adding u_4 or implementing all controls increases the total cost without producing a comparable improvement in infections averted. Therefore, the combination $u_1 + u_3$ provides the best balance between epidemiological effectiveness and intervention cost.

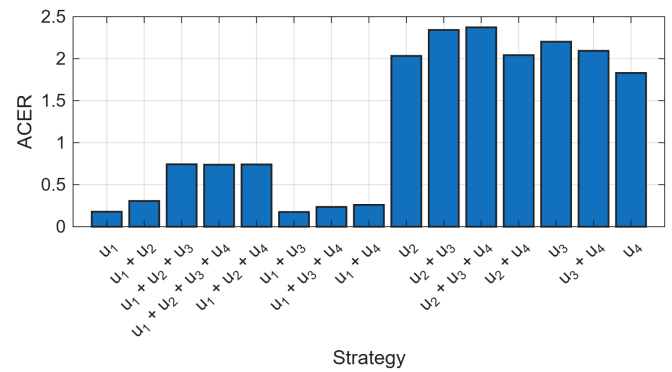


Figure 8 Ranking of the control strategies based on the average cost-effectiveness ratio (ACER). The combined strategy $(u_1 + u_3)$ has the lowest ACER and is therefore identified as the most cost-effective strategy

Table 5 Ranking of intervention strategies based on the average cost-effectiveness ratio (ACER)

Strategy	Total Cost	Cum. Incidence	Inf. Averted	ACER
$u_1 + u_3$	4.6085	0.080280	26.327	0.17505
u_1	4.7135	0.080067	26.327	0.17904
$u_1 + u_3 + u_4$	6.1970	0.080075	26.327	0.23539
$u_1 + u_4$	6.8391	0.079239	26.328	0.25977
$u_1 + u_2$	8.0472	0.125220	26.282	0.30619
$u_1 + u_2 + u_3 + u_4$	18.416	1.464600	24.942	0.73834
$u_1 + u_2 + u_4$	18.471	1.479100	24.928	0.74099
$u_1 + u_2 + u_3$	18.520	1.483900	24.923	0.74310
u_4	0.20269	26.29600	0.11074	1.8303
u_2	44.969	4.293900	22.113	2.0336
$u_2 + u_4$	44.955	4.396100	22.011	2.0424
$u_3 + u_4$	0.74194	26.05200	0.35435	2.0938
u_3	0.53309	26.16500	0.24204	2.2024
$u_2 + u_3$	42.930	8.077300	18.330	2.3421
$u_2 + u_3 + u_4$	42.582	8.466300	17.941	2.3735

After we found that the intervention strategy $(u_1 + u_3)$ is the best according to ACER, in Figure 9, we illustrate the use of the optimal control strategy $(u_1 + u_3)$ substantially suppresses the infected populations compared with the no-control scenario. The cor-

responding control profiles further indicate that the transmission-reduction control u_1 is applied more consistently and at a higher level than the other control measures, while the remaining controls are maintained at lower levels depending on the intervention strategy. This suggests that reducing TB transmission plays a dominant role in mitigating disease spread, especially when combined with targeted treatment efforts for infected individuals.

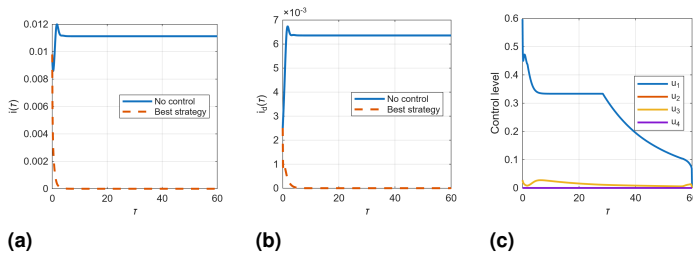


Figure 9 Comparison of the no-control and optimal-control scenario ($u_1 + u_3$): time series of the infected variables (a) i and (b) i_d , together with (c) the corresponding optimal control profiles

CONCLUSION

This study developed and analyzed a mathematical model of tuberculosis (TB) transmission dynamics that incorporates diabetes comorbidity, reinfection, relapse, and nonlinear incidence. Based on classical TB models, the proposed model explicitly captures the effect of diabetes on susceptible and recovered TB patients, providing a more comprehensive representation of the interaction between the two diseases. The analytical results established the positivity and boundedness of the model solutions, derived the basic reproduction number, and determined the local stability of the disease-free equilibrium. Furthermore, the bifurcation analysis showed that the model can exhibit forward or backward bifurcation depending on the epidemiological parameters. The model was further extended by incorporating an optimal control framework. Four controls were considered: efforts to reduce TB transmission, interventions to reduce diabetes progression, and enhanced treatment efforts for TB-infected individuals with and without diabetes. The model parameters were estimated using Indonesian epidemiological data, and the resulting parameter set was used to perform several numerical simulations, including the phase portraits that show the global convergence of the model solutions, a global sensitivity analysis using partial rank correlation coefficient to determine the most influential parameters, and forward and backward bifurcation diagrams to validate the bifurcation analysis. The optimal intervention strategies were evaluated using the average cost-effectiveness ratio. The results indicate that combining TB transmission reduction with enhanced treatment constitutes the most cost-effective intervention strategy.

Besides these contributions, the current study has several limitations. First, the model assumed homogeneous population mixing and did not take into consideration heterogeneity in age, geographic location, socioeconomic conditions, and access to health-care, all of which may affect TB and diabetes prevalence in the real world. Second, some diabetes-related parameter values were assumed or estimated because of limited epidemiological data, which could impact the accuracy of quantitative predictions. Third, although the calibrated model reproduced the trends in TB incidence, TB notifications, and diabetes prevalence reasonably well, it did not adequately capture the temporal patterns of TB deaths and treatment success, as reflected by the negative R^2 values. This

suggests that additional mechanisms, such as changes in health-care quality, treatment policies, or reporting practices, may be needed to improve the model's predictive performance for these epidemiological indicators. Fourth, the optimal control model assumed deterministic intervention effects and did not account for uncertainty or stochastic disturbances that occur in real-world public health implementation. Nevertheless, the proposed model provides a theoretical framework for understanding the coupled effects of TB and diabetes and offers insights into how comorbidity complicates disease control.

The current framework could be further developed in several significant ways in future studies. A potential extension is the inclusion of age-structured or spatially heterogeneous populations to better capture demographic and regional heterogeneity in TB-diabetes prevalence. Additionally, the incorporation of stochastic perturbations or time delays could be incorporated to represent uncertainty in the environment and slow treatment response. Future studies may also investigate additional intervention strategies, such as vaccination programs or targeted screening policies for individuals with diabetes.

The results showed that diabetes comorbidity greatly increased tuberculosis transmission, thereby making disease elimination more challenging. From a practical perspective, the results support the implementation of integrated health policies that combine TB prevention, diabetes management, and targeted treatment enhancement for co-affected individuals. Therefore, the proposed model provides a useful mathematical framework for policymakers and public health practitioners in designing more comprehensive and effective intervention strategies to lower the TB burden in populations with growing diabetes prevalence.

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Ethical standard

The author has no relevant financial or non-financial interests to disclose.

Availability of data and material

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Conflicts of interest

The author declares that there is no conflict of interest regarding the publication of this paper.

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Reinforcement Learning-Tuned Nonlinear Controller Parameters for Synchronization of Chua and Duffing Chaotic Systems

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ABSTRACT Reinforcement learning has recently emerged as a promising machine learning paradigm for the adaptive control of complex nonlinear systems by enabling online decision-making through continuous interaction with the environment. However, its application to the synchronization of chaotic systems using Lyapunov-based nonlinear controllers remains relatively unexplored, particularly with respect to comparing discrete-action and continuous-action reinforcement learning algorithms. To address this research gap, this study proposes reinforcement learning-assisted Lyapunov-based nonlinear controllers for the synchronization of chaotic systems. Specifically, two independent master-slave synchronization problems are considered, one based on Chua's circuit and the other based on the Duffing oscillator. In each synchronization problem, Deep Q-Learning (DQN) and Deep Deterministic Policy Gradient (DDPG) are employed to adaptively adjust the nonlinear controller parameters online by maximizing the instantaneous reward at each sampling instant, thereby improving synchronization performance while reducing undesirable switching behavior in the control signals. The proposed approaches are evaluated through numerical simulations using reward, average reward, Integral Absolute Error (IAE), Integral Square Error (ISE), Integral Time Absolute Error (ITAE), Integral Time Square Error (ITSE), and control effort as performance metrics. The simulation results demonstrate that DQN-assisted approach consistently achieves higher reward and average reward values than DDPG-assisted approach for both synchronization problems, indicating a more effective reward-maximizing policy under identical operating conditions. For the Chua master-slave synchronization problem, DQN-assisted nonlinear controller provides superior synchronization performance, whereas for the Duffing master-slave synchronization problem, DDPG-assisted nonlinear controller achieves better performance in terms of the error-based performance indices and control effort. Furthermore, robustness analyses under external disturbances demonstrate that both proposed approaches successfully suppress disturbances and maintain stable synchronization between the corresponding master and slave systems. Overall, the results confirm that integrating Lyapunov-based nonlinear control with reinforcement learning provides an adaptive, robust, and effective framework for the synchronization of nonlinear chaotic systems, offering improved synchronization performance and enhanced practical applicability.

KEYWORDS

Reinforcement learning
DQN
DDPG
Chaos
Nonlinear control
Synchronization

INTRODUCTION

Chaotic dynamical systems, such as the Chua circuit and the Duffing oscillator, are fundamental models in nonlinear science due to their rich dynamical behaviors, including sensitivity to initial conditions, bifurcation phenomena, and aperiodic trajectories (Yang *et al.* 1997, 2001; Kharabian and Mirinejad 2021; Tan *et al.* 2003). These properties make chaotic systems highly relevant not only from a theoretical perspective but also for practical applications such as secure communications, cryptography, signal processing, and synchronization-based engineering systems (Yang *et al.* 1997; Öztürk *et al.* 2025). Among these applications, the synchronization of chaotic systems has emerged as a critical research topic, particularly in the context of nonlinear control and complex system coordination.

Classical control strategies - including Lyapunov-based control, sliding mode control, backstepping, and feedback linearization - have been widely applied to achieve stabilization and synchronization in chaotic systems (Yang *et al.* 2001; Kharabian and Mirinejad

2021; Turab *et al.* 2025; Stefanski and Kapitaniak 2000; Saeed *et al.* 2023; Emiroglu *et al.* 2022). Although these methods provide strong theoretical guarantees in terms of stability and convergence, their performance heavily depends on accurate system modeling and precise tuning of controller parameters. In practical scenarios, uncertainties, disturbances, and parameter variations significantly complicate controller design, often leading to suboptimal performance. To address these challenges, adaptive and intelligent control approaches have been introduced. In particular, reinforcement learning (RL) has gained significant attention as a model-free optimization framework capable of learning optimal control strategies through interaction with the environment. Unlike traditional adaptive methods, RL does not require explicit system models and can directly optimize control performance based on reward signals (Çimen 2024b, 2026; Çimen and Garip 2024; Smart and Kaelbling 2000; Singh *et al.* 2022; Alfred *et al.* 2024; Hao *et al.* 2024; Qin *et al.* 2023). Consequently, RL has been increasingly applied to nonlinear and chaotic systems for control, stabilization, and synchronization tasks.

A comprehensive comparison of recent RL-based approaches for chaotic systems is presented in Table 1. As shown in the table, existing studies can be broadly categorized into three main groups. First, some studies focus on parameter discovery rather than con-

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trol design. For example, RL-based approaches utilizing Lyapunov exponents as reward signals have demonstrated high efficiency in identifying chaotic regimes in systems such as Chua and Lorenz systems, significantly reducing computational cost compared to conventional grid-based search methods (Huang 2025). However, these approaches do not directly address control objectives such as stabilization or synchronization. Second, a considerable number of studies employ deep reinforcement learning for direct control or synchronization (Cheng *et al.* 2023; Bucci *et al.* 2019; Jia *et al.* 2021; Yau *et al.* 2024). Methods based on algorithms such as Deep Deterministic Policy Gradient (DDPG), Proximal Policy Optimization (PPO), and other deep RL techniques have been successfully applied to chaotic systems including Chua, Duffing, Lorenz, and Rössler systems. These approaches exhibit strong adaptability and robustness, particularly under incomplete system information and disturbances. Nevertheless, they typically rely on black-box policy learning, which limits interpretability and makes it difficult to incorporate prior knowledge from classical control theory. Third, another important research direction involves reinforcement learning-based parameter tuning of structured controllers (Mahmoud *et al.* 2020; Alhazmi and Sarathy 2023; Bujgoi and Sendrescu 2025; Chun-Cheng and Lon-Chen 2020; Das *et al.* 2025; Rego and de Araújo 2021). In these approaches, RL is used to adapt parameters of controllers such as PID, Lyapunov-based controllers, and neural network-based controllers. These methods improve robustness and reduce manual tuning effort while preserving the structural advantages of classical control strategies. Despite these benefits, existing studies are generally limited to specific systems, lack comprehensive synchronization analysis, or do not simultaneously address multiple chaotic systems.

From the perspective of research gaps and contributions, as clearly observed in Table 1, existing studies predominantly focus on either parameter tuning or direct policy learning approaches. Although direct RL-based controllers demonstrate strong adaptability, they often suffer from a lack of interpretability and limited theoretical guarantees. In contrast, RL-based parameter tuning approaches preserve the controller structure; however, they are generally restricted to specific systems and do not comprehensively address chaotic synchronization problems.

In particular, there is a notable lack of studies that simultaneously:

- integrate reinforcement learning with Lyapunov-based nonlinear synchronization controllers;
- investigate adaptive parameter tuning of nonlinear synchronization controllers using reinforcement learning;
- provide comprehensive performance evaluations of reinforcement learning-assisted synchronization methods using multiple performance criteria.

Motivated by these limitations, this study proposes a novel reinforcement learning-based approach for the synchronization of Chua and Duffing chaotic systems. Unlike conventional deep RL approaches that directly learn control policies, the proposed method employs reinforcement learning as an adaptive parameter tuning mechanism for a nonlinear controller structure.

The main contributions of this study can be summarized as follows:

- Development of a unified framework for synchronization of Chua and Duffing chaotic systems ;
- Integration of DQN and DDPG with a Lyapunov-based nonlinear control framework. ;

- Adaptive tuning of controller parameters for improved synchronization performance;
- Enhanced robustness against nonlinearities, uncertainties, and disturbances,
- Reduction of manual tuning effort through data-driven optimization.

The synchronization of nonlinear chaotic systems, such as the Chua and Duffing systems, requires carefully designed controllers whose parameters significantly influence the overall synchronization performance. In this context, DQN-assisted and DDPG-assisted nonlinear control approaches are proposed to adaptively tune the controller parameters following the design of the synchronization controllers for each system. To avoid ambiguity, it should be emphasized that this study considers two independent master-slave synchronization scenarios. The first scenario addresses the synchronization of the Chua chaotic system, while the second addresses the synchronization of the Duffing chaotic system. No synchronization is performed between the Chua and Duffing systems themselves. Accordingly, this paper is organized as follows. Section 1 presents the introduction, including the motivation for the study and a review of the relevant literature. Section 2 describes the materials and methods, introducing the fundamentals of reinforcement learning and the design of the nonlinear synchronization controllers for the Chua and Duffing systems. Section 3 presents DQN-assisted and DDPG-assisted approaches for adaptively tuning the controller parameters during the synchronization process. Section 4 presents the simulation results and discusses the performance of the proposed methods in detail. Finally, Section 5 concludes the paper by summarizing the main findings and outlining directions for future research.

MATERIAL METHOD

Reinforcement Learning

In reinforcement learning, an agent learns the environment by interacting with it and determines its actions based on the rewards received and the observed state information (Watkins and Dayan 1992; Clifton and Laber 2020; Yıldız *et al.* 2024). The general structure of reinforcement learning is illustrated in Figure 1. Based on the state information obtained from the environment, the agent selects an action. As a result of this action, the agent and the environment interact, leading to the transition to a new state. Additionally, this state transition generates a reward value that reflects the outcome of the taken action. The primary objective of rein-

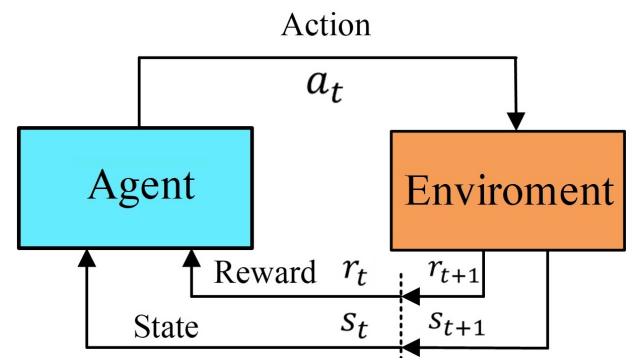


Figure 1 Agent and environment interaction

forcement learning is to learn the optimal action-value function, $Q(s, a)$, which enables an agent to select the best possible action

Table 1 Reinforcement Learning-Based Methods for Chaotic Systems: A Categorized Literature Review

Ref.	System	Method	Contribution	Limitation
Category I: RL for Parameter Discovery				
Huang (2025)	Chua, Lorenz, Hénon	Q-learning, SARSA	Efficient chaotic region discovery using Lyapunov-based reward	Required tabular-based discretization
Category II: Direct RL-Based Control				
Cheng <i>et al.</i> (2023)	Chua, Lorenz, Rössler	Deep RL	Model-free synchronization	No stability guarantees
Bucci <i>et al.</i> (2019)	Kuramoto–Sivashinsky	DDPG	Effective RL-based control of chaotic systems	Black-box control
Jia <i>et al.</i> (2021)	Chaotic systems	DDPG	Robust synchronization	Limited interpretability
Yau <i>et al.</i> (2024)	Lorenz	PPO	Fast chaos suppression	Limited generalization
Category III: RL-Based Controller Parameter Tuning				
Mahmoud <i>et al.</i> (2020)	Duffing, Van der Pol	Lyapunov-based Controller + DL	Adaptive parameter tuning	No comparison study
Alhazmi and Sarathy (2023)	Thermoacoustic system	Adaptive Control + SAC	Safe RL-based tuning	Application-specific
Bujgoi and Sendrescu (2025)	Nonlinear system	PID + TD3	Overshoot-free response	Slow dynamics
Chun-Cheng and Lon-Chen (2020)	Duffing–Holmes	RBFNN + RL	Robust tracking performance	Limited scalability
Das <i>et al.</i> (2025)	Fractional Rössler	PID + REINFORCE	Fast convergence	High computational effort
Rego and de Araújo (2021)	Nonlinear systems	Lyapunov NN + RL	Stability-oriented learning	Complex training
Yang <i>et al.</i> (2014a)	Nonlinear systems	Optimal Control + Actor–Critic	HJB-based optimization	Model dependence
Yang <i>et al.</i> (2014b)	Nonaffine systems	Adaptive Control + Actor–Critic	Stability guarantee	No chaotic validation
Wang <i>et al.</i> (2020)	Duffing	Attractor control + DDPG	Efficient attractor selection	Requires prior knowledge
Category IV: Proposed Method (This Study)				
This Study	Chua & Duffing	Nonlinear Controller + DQN + DDPG	Adaptive synchronization via parameter tuning	Interpretable, robust, and adaptive

(a_t) in a given state (s_t). This process is fundamentally based on the Bellman equation (Watkins and Dayan 1992; Yıldız *et al.* 2024; Farebrother *et al.* 2018). The update of the Q-values is obtained as expressed in Equation (1):

$$Q(s_t, a_t) = \underbrace{Q(s_t, a_t)}_{\text{Present Q Value}} + lr \left[\underbrace{r_t + \gamma \max_{a \in A} Q(s_{t+1}, a)}_{\text{Target}} - \underbrace{Q(s_t, a_t)}_{\text{Present Q Value}} \right] \quad (1)$$

Here,

- lr : learning rate;
- γ : discount factor that determines the importance of future rewards.;
- r_t : reward obtained as a result of the current state and action.

Deep Q-Learning (DQN) represents a significant milestone in the field of reinforcement learning (RL) by integrating the conventional Q-learning algorithm with deep neural networks (DNNs). In systems characterized by complex and high-dimensional state spaces, maintaining a tabular representation of Q-values for every

state–action pair becomes computationally impractical. To address this limitation, DQN employs deep neural networks as function approximators to estimate the action-value function, thereby enabling more efficient learning and faster convergence. However, one of the main limitations of DQN is that it is restricted to discrete action spaces, making it less suitable for control problems requiring continuous-valued actions. To overcome this limitation, the Deep Deterministic Policy Gradient (DDPG) algorithm was developed. Unlike DQN, which approximates the action-value (Q) function for discrete actions, DDPG adopts an actor–critic architecture to learn deterministic policies directly in continuous action spaces. This capability makes DDPG particularly suitable for continuous control problems, where smooth and precise control actions are required. Consequently, both DQN and DDPG provide efficient learning, improved scalability, and enhanced convergence when applied to complex nonlinear control systems.

Deep Q Learning Algorithm: Deep Q-Learning (DQN), one of the prominent reinforcement learning methods, addresses the high-dimensionality and computational limitations of conventional Q-learning by approximating the Q-value function. To achieve this approximation, it utilizes deep neural networks (Deep Neural

Networks, DNNs) (Alfred *et al.* 2024). In this context, deep reinforcement learning emerges from the integration of deep neural networks with the Q-learning algorithm. Deep reinforcement learning algorithms are particularly effective in solving control problems involving continuous state spaces. The actions generated by DQN algorithm are typically produced in a discrete form, enabling the agent to interact with the environment accordingly (Farebrother *et al.* 2018; Lucarelli and Borrotti 2020; Çimen 2026; Singh *et al.* 2022; Evdüzzen 2021; Mnih *et al.* 2013). The block diagram of the Deep Q-Learning algorithm, which is based on this fundamental structure, is illustrated in Figure 2. In Q-learning,

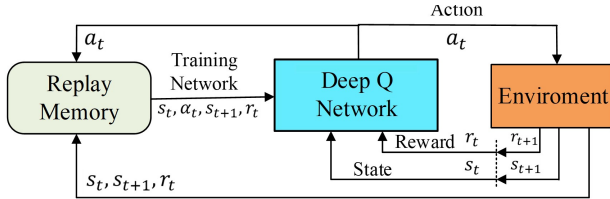


Figure 2 DQN agent and environment interaction

the Bellman equation given in Equation 1 is updated iteratively. However, in this context, the state representation forms the basis of function approximation in the Deep Q-Learning algorithm. This function approximation is realized using deep neural networks, and can be expressed as shown in Equation (2). In DQN, the Q-values $Q(s, a | \theta)$ are generated using the parameters θ of the neural network, which represent its weights. This process is referred to as Q-network evaluation (Çimen 2026; Mnih *et al.* 2013).

$$\hat{y} = Q(s_t, a_t | \theta) \approx Q^*(s_t, a_t) \quad (2)$$

In DQN architecture, a neural network with learnable weight parameters takes the state input s and outputs Q-values for all possible actions. The primary objective of the algorithm is to learn an optimal policy function that maximizes the cumulative rewards collected by the agent from the environment. This process is carried out iteratively and continuously during training. The target network, which incorporates the reward information and produces the target value $\tilde{y}$, is used to update the network parameters in a manner similar to the Bellman update rule, as expressed in Equation 3.

$$\hat{y} = Q(s_t, a_t | \theta) \leftarrow \tilde{y} = r_t + \gamma \max_{a \in \mathcal{A}} Q(s_{t+1}, a | \theta^-) \quad (3)$$

In DQN, two key mechanisms are employed. The first is Experience Replay. Using this mechanism, the agent's past experiences (s, a, s', r) are stored in a replay memory buffer. During training, random samples are drawn from this memory to update the network. The second mechanism is the Target Network structure denoted as $\tilde{y}$, as described in Equation 4. Since the target values change continuously during Q-value updates, learning may become unstable. DQN addresses this issue by introducing a separate target network, which is periodically updated from the main network $\hat{y}$. This stabilizes the target values and improves convergence. For convergence, the loss function given in Equation 5 is used. This formulation is essentially similar to the loss function presented in Equation 1. The parameter updates are performed using the optimization rule given in Equation 6. During interaction between the agent and the environment, DQN algorithm also employs an epsilon-greedy strategy to balance exploration and exploitation, enabling effective exploration of the environment while maximizing the Q-value corresponding to the highest expected

reward Mnih *et al.* (2013). The overall structure of DQN algorithm is presented in Algorithm 1.

$$\tilde{y} = r_t + Q(s_{t+1}, a_{t+1} | \theta) \quad (4)$$

$$\begin{aligned} L_i(\theta_i) &= \mathbb{E}_{s,a,r} \left[(\tilde{y} - \hat{y})^2 \right] \\ &= \mathbb{E}_{s,a,r} \left[(r + Q(s', a' | \theta_{i-1}) - Q(s, a | \theta_i))^2 \right] \end{aligned} \quad (5)$$

$$\begin{aligned} \nabla_{\theta_i} L(\theta_i) &= \\ \mathbb{E}_{s,a,r,s'} \left[\begin{aligned} &\left(r + \gamma \max_{a \in \mathcal{A}} Q(s', a | \theta_{i-1}) \right) \nabla_{\theta_i} Q(s, a | \theta_i) \\ &- Q(s, a | \theta_i) \nabla_{\theta_i} Q(s, a | \theta_i) \end{aligned} \right] \end{aligned} \quad (6)$$

Algorithm 1 Deep Q Learning Algorithm

```

1: Initialize replay memory  $\mathcal{D}$  with capacity  $N$ 
2: Initialize learning rate  $\alpha$ , discount factor  $\gamma$ , minibatch size  $C$ 
3: Initialize Q-network with random weights  $\theta$ 
4: Initialize target Q-network with weights  $\theta^- \leftarrow \theta$ 
5: for episode = 1 to MaxEpisodes do
6:   Initialize state  $s_t$ 
7:   done  $\leftarrow$  False
8:   while done == False do
9:     Generate random number  $rand \in [0, 1]$ 
10:    if  $\epsilon < rand$  then
11:      Select random action  $a_t \in \mathcal{A}$ 
12:    else
13:       $a_t = \arg \max_{a \in \mathcal{A}} Q(s_t, a | \theta)$ 
14:    Execute  $a_t$ , observe  $s_{t+1}, r_{t+1}$ , done
15:    Store transition  $(s_t, a_t, r_{t+1}, s_{t+1})$  in  $\mathcal{D}$ 
16:    Sample random minibatch  $(s_i, a_i, r_i, s_{i+1})$  from  $\mathcal{D}$ 
17:    for each sample in minibatch do
18:      if done == False then
19:         $y_i = r_i + \gamma \max_{a \in \mathcal{A}} Q(s_{i+1}, a | \theta^-)$ 
20:      else
21:         $y_i = r_i$ 
22:      Compute loss:
23:         $L_i = \frac{1}{C} \sum (y_i - Q(s_i, a_i | \theta))^2$ 
24:      Update  $\theta$  by minimizing  $L_i$ 
25:      Every  $C$  steps:  $\theta^- \leftarrow \theta$ 
26:       $s_t \leftarrow s_{t+1}$ 

```

Deep Deterministic Policy Gradient Algorithm: Deep Deterministic Policy Gradient (DDPG) is an actor-critic-based deep reinforcement learning algorithm specifically developed to address control problems with continuous action spaces. Unlike Deep Q-Learning (DQN), which selects actions from a discrete action set, DDPG directly generates continuous control actions through a deterministic policy represented by a deep neural network. This characteristic makes DDPG particularly suitable for nonlinear control systems in which the control input varies continuously (Wang *et al.* 2018; Tufenkci *et al.* 2025; OpenAI 2018).

DDPG framework consists of two neural networks, referred to as the actor and the critic. The actor network determines the control action based on the current state, whereas the critic network evaluates the quality of the selected state-action pair by estimating

the action-value function (Kang et al. 2021; Lillicrap et al. 2020). Similar to DQN, DDPG also employs experience replay and target networks to improve training stability and facilitate convergence. The interaction between DDPG agent and the environment is illustrated in Figure 3.

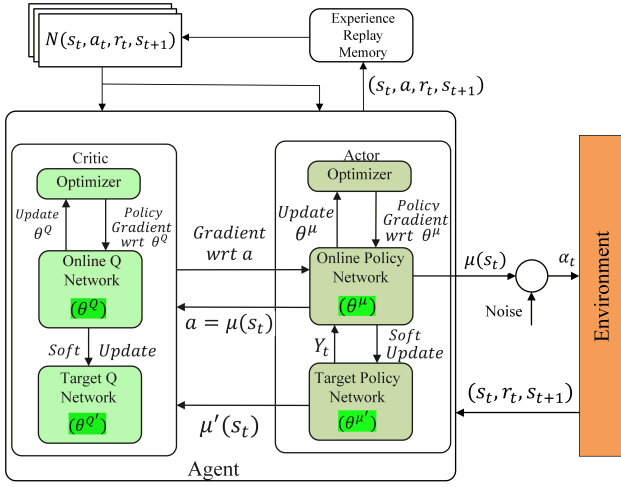


Figure 3 DDPG agent and environment interaction.

In DDPG, the actor network represents a deterministic policy that directly maps the current state to a continuous action, as expressed in Equation 7.

$$a_t = \mu(s_t | \theta^\mu) \quad (7)$$

where θ^μ denotes the parameters of the actor network. Unlike DQN, the critic network receives both the current state and the selected action as inputs and estimates the corresponding action-value function, as expressed in Equation 8.

$$Q(s_t, a_t | \theta^Q) \quad (8)$$

where θ^Q represents the parameters of the critic network.

The critic network is trained by minimizing the Bellman error using the target value defined in Equation 9.

$$y_t = r_t + \gamma Q'(s_{t+1}, \mu'(s_{t+1} | \theta^{\mu'}) | \theta^{Q'}) \quad (9)$$

where Q' and μ' denote the target critic and target actor networks, respectively. Accordingly, the critic loss function can be defined as

$$L(\theta^Q) = \mathbb{E} \left[\left(Q(s_t, a_t | \theta^Q) - y_t \right)^2 \right]. \quad (10)$$

Unlike DQN, the actor network is not trained directly using reward information (Lillicrap et al. 2020; Silver et al. 2014). Instead, it is updated according to the deterministic policy gradient theorem by maximizing the Q-value estimated by the critic network. The corresponding gradient can be expressed as in Equation 11 (Lillicrap et al. 2020).

$$\nabla_{\theta^\mu} J = \mathbb{E} \left[\nabla_a Q(s, a | \theta^Q) \Big|_{a=\mu(s)} \nabla_{\theta^\mu} \mu(s | \theta^\mu) \right]. \quad (11)$$

To improve training stability, DDPG employs slowly updated target networks instead of periodically replacing the target parameters as in DQN. The target networks are updated through the soft update mechanism defined in Equation 12, where $\tau \ll 1$ denotes the target update coefficient.

$$\theta^- \leftarrow \tau \theta + (1 - \tau) \theta^-, \quad (12)$$

Since DDPG follows a deterministic policy, exploration cannot be achieved using an ϵ -greedy strategy as in DQN. Instead, exploration is encouraged by adding stochastic noise to the actor output during training.

$$a_t = \mu(s_t | \theta^\mu) + \mathcal{N}_t, \quad (13)$$

In Equation 13, $\mathcal{N}_t$ generally represents Gaussian or Ornstein-Uhlenbeck noise. This mechanism enables efficient exploration while preserving smooth control actions. Similar to DQN, experience replay is employed to randomly sample previous transitions and reduce the correlation among training samples, thereby improving learning stability. The overall structure of DDPG algorithm is presented in Algorithm 2.

Algorithm 2 Deep Deterministic Policy Gradient Algorithm

- 1: Initialize replay memory $\mathcal{D}$
- 2: Initialize actor network $\mu(s | \theta^\mu)$
- 3: Initialize critic network $Q(s, a | \theta^Q)$
- 4: Initialize target actor and critic networks
- 5: $\theta^{\mu-} \leftarrow \theta^\mu, \theta^{Q-} \leftarrow \theta^Q$
- 6: **for** episode = 1 to MaxEpisodes **do**
- 7: Initialize state s_t
- 8: **while** done == False **do**
- 9: Generate action
- 10: $a_t = \mu(s_t) + \mathcal{N}_t$
- 11: Execute action and observe (r_t, s_{t+1})
- 12: Store transition (s_t, a_t, r_t, s_{t+1}) into replay memory
- 13: Sample random minibatch from replay memory
- 14: Compute target value
- 15: $y_t = r_t + \gamma Q'(s_{t+1}, \mu'(s_{t+1} | \theta^{\mu-}) | \theta^{Q-})$
- 16: Update critic by minimizing
- 17: Update actor using deterministic policy gradient
- 18: Soft-update target networks
- 19: $\theta^- \leftarrow \tau \theta + (1 - \tau) \theta^-$
- 20: $s_t \leftarrow s_{t+1}$

Synchronization of Chua Chaotic System

Chua's circuit is one of the basic, simplest and most widely studied physical systems in which chaotic dynamics can be observed. Developed in 1983 by Leon O. Chua, this circuit consists of standard linear elements such as resistors, capacitors, and an inductor, along with a nonlinear resistor known as the Chua diode, which exhibits a piecewise-linear characteristic (Madan 1993). The fundamental feature that makes this system unique is its ability to generate complex chaotic attractors - most notably the famous "Double Scroll" - despite its simple structure. Mathematically, the system can be represented by a set of three-dimensional differential equations, as given in Equation 14.

The synchronization of Chua systems holds a central role in the literature, particularly in secure communication and control theory (Momtaz et al. 2026). It is based on the principle that two or more chaotic systems, even with different initial conditions, can

evolve over time to exhibit identical trajectories. The general block diagram of this structure is illustrated in Figure 3. In the literature, this process is commonly addressed using the Master-Slave architecture. In this study, the slave system is given in Equation 15. In this part of the study, assuming that the system parameters are identical but the initial conditions are different, the control input u is designed using the backstepping method to achieve synchronization.

$$\begin{aligned}\dot{x}_m &= \alpha (y_m - x_m^3 - cx_m) \\ \dot{y}_m &= x_m - y_m + z_m \\ \dot{z}_m &= -\beta y\end{aligned}\quad (14)$$

$$\begin{aligned}\dot{x}_s &= \alpha (y_s - x_s^3 - cx_s) + u \\ \dot{y}_s &= x_s - y_s + z_s \\ \dot{z}_s &= -\beta y_s\end{aligned}\quad (15)$$

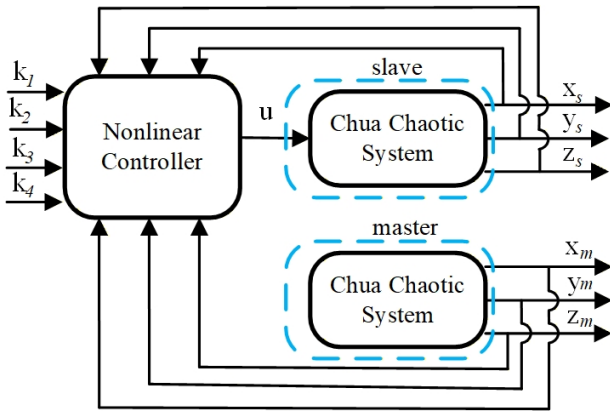


Figure 4 Synchronization diagram of the Chua Chaotic System

The errors between the two systems can be obtained by taking their difference, as expressed in Equation 16. By differentiating these error signals, Equation 17 is derived.

$$\begin{aligned}e_1 &= z_m - z_s \\ e_2 &= y_m - y_s \\ e_3 &= z_m - z_s\end{aligned}\quad (16)$$

$$\begin{aligned}\dot{e}_1 &= -\beta e_2 \\ \dot{e}_2 &= e_3 - e_2 + e_1 \\ \dot{e}_3 &= \alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - u\end{aligned}\quad (17)$$

A virtual variable is assigned to the state e_1 used in Equation 17, as defined in Equation 18. Based on this variable, a Lyapunov function is constructed, yielding Equation 19. By taking the derivative as in Equation 18, Equation 20 is obtained. Since $\dot{p}_1 = \dot{e}_1 = -\beta e_2$ in this expression, substituting this relation into Equation 20 results in Equation 21.

$$e_1 = p_1 \quad (18)$$

$$V_1 = \frac{1}{2} p_1^2 \quad (19)$$

$$\dot{V}_1 = p_1 \dot{p}_1 = p_1 (-\beta e_2) \quad (20)$$

$$\dot{V}_1 = -\beta p_1 (e_2) \quad (21)$$

To relate the term e_2 in Equation 21 to the subsequent state, a virtual variable is introduced as $e_2 = p_2 + \alpha_2$, as defined in Equation

22. Substituting this expression into Equation 21 yields Equation 23. By rearranging Equation 23, Equation 24 is obtained. Then, by assigning the virtual control variable as given in Equation 25, Equation 26 is derived. In this way, the condition $-\beta k_1 p_1^2 \leq 0$ is satisfied. On the other hand, in order to eliminate the term p_2 , an extension of the Lyapunov function is required.

$$e_2 = p_2 + \alpha_2 \quad (22)$$

$$\dot{V}_1 = -\beta p_1 (p_2 + \alpha_2) \quad (23)$$

$$\dot{V}_1 = -\beta p_1 \alpha_2 - \beta p_1 p_2 \quad (24)$$

$$\alpha_2 = -k_1 p_1 \quad (25)$$

$$\dot{V}_1 = -\beta k_1 p_1^2 - \beta p_1 p_2 \quad (26)$$

To ensure that the term p_2 in $\dot{V}_1$ converges to zero over time, the Lyapunov function is extended as given in Equation 27. Taking the derivative of this function yields Equation 28. By differentiating p_2 , the expression in Equation 29 is obtained. Substituting $\dot{p}_2$ into Equation 28 results in Equation 30. By rearranging this expression, Equation 31 is derived. Then, by substituting the expression for $\dot{p}_2$ into Equation 31, Equation 32 is obtained. Furthermore, by replacing the variables with their corresponding expressions, Equation 33 and subsequently Equation 34 are derived.

$$V_2 = V_1 + \frac{1}{2} p_2^2 \quad (27)$$

$$\dot{V}_2 = \dot{V}_1 + p_2 \dot{p}_2 \quad (28)$$

$$\dot{p}_2 = \dot{e}_2 + \dot{\alpha}_2 \quad (29)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 - \beta p_1 p_2 + p_2 \dot{p}_2 \quad (30)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 + p_2 (-\beta p_1 + \dot{p}_2) \quad (31)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 + p_2 (-\beta p_1 + \dot{e}_2 - \dot{\alpha}_2) \quad (32)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 + p_2 (-\beta p_1 + e_3 - e_2 + e_1 - k_1 \dot{p}_1) \quad (33)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 + p_2 (-\beta p_1 + e_3 - e_2 + e_1 + k_1 \beta e_2) \quad (34)$$

To regulate the trajectory of e_3 in Equation 34, a virtual variable is introduced. This assignment is defined as given in Equation 35. Substituting the expression for e_3 into Equation 34 yields Equation 36. By rearranging Equation 36, Equation 37 is obtained. In order to ensure that $p_2 (-\beta p_1 + \alpha_3 - e_2 + e_1 + k_1 \beta e_2) \leq 0$, the assignment in Equation 38 is performed. Subsequently, the control variable α_3 is defined as in Equation 39. Based on the assumption in Equation (31), the expression for $\dot{V}_2$ in Equation 37 is obtained as given in Equation 40.

$$e_3 = p_3 + \alpha_3 \quad (35)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 + p_2 (-\beta p_1 + p_3 + \alpha_3 - e_2 + e_1 + k_1 \beta e_2) \quad (36)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 + p_2 (-\beta p_1 + \alpha_3 - e_2 + e_1 + k_1 \beta e_2) + p_2 p_3 \quad (37)$$

$$-\beta p_1 + \alpha_3 - e_2 + e_1 + k_1 \beta e_2 = -k_2 p_2 \quad (38)$$

$$\alpha_3 = -k_2 p_2 + \beta p_1 + e_2 - e_1 - k_1 \beta e_2 \quad (39)$$

$$\dot{V}_2 = -\beta k_1 p_1^2 - \beta k_2 p_2^2 + p_2 p_3 \quad (40)$$

To eliminate the term p_3 appearing in Equation 40, the Lyapunov energy function is extended as given in Equation 41. In order to ensure that this expression converges to zero over time, its derivative is taken, resulting in Equation 42. Substituting this expression into $\dot{V}_2$ yields Equation 43. By rearranging Equation 43, Equation 44 is obtained. To satisfy the condition $p_3 (p_2 + \dot{p}_3) \leq 0$, Equation 45 is imposed as a control law. Solving this equation

for $\dot{p}_3$ leads to Equation 46. Substituting the explicit form of $\dot{p}_3$ into Equation 46 yields Equation 47. Then, by substituting the expanded form of $\dot{e}_3$, Equation 48 is obtained. Isolating the control input u in this expression results in Equation 49. By substituting $\dot{\alpha}_3$ into this equation, Equation 50 is derived. Finally, by rearranging these expressions, Equation 51, Equation 52, 53 and ultimately Equation 54 are obtained.

$$V_3 = V_2 + \frac{1}{2} p_3^2 \quad (41)$$

$$\dot{V}_3 = \dot{V}_2 + p_3 \dot{p}_3 \quad (42)$$

$$\dot{V}_3 = -\beta k_1 p_1^2 - \beta k_2 p_2^2 + p_2 p_3 + p_3 \dot{p}_3 \quad (43)$$

$$\dot{V}_3 = -\beta k_1 p_1^2 - \beta k_2 p_2^2 + p_3 (p_2 + \dot{p}_3) \quad (44)$$

$$p_2 + \dot{p}_3 = -k_3 p_3 - k_4 \text{sign}(p_3) \quad (45)$$

$$\dot{p}_3 = -p_2 - k_3 p_3 - k_4 \text{sign}(p_3) \quad (46)$$

$$\dot{e}_3 - \dot{\alpha}_3 = -p_2 - k_3 p_3 - k_4 \text{sign}(p_3) \quad (47)$$

$$\alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - u = \dot{\alpha}_3 - p_2 - k_3 p_3 - k_4 \text{sign}(p_3) \quad (48)$$

$$u = \alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - \dot{\alpha}_3 + p_2 + k_3 p_3 + k_4 \text{sign}(p_3) \quad (49)$$

$$u = \alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - (\beta \dot{p}_1 + \dot{e}_2 - \dot{e}_1 - k_1 \beta \dot{e}_2 - k_2 \dot{p}_2) + p_2 + k_3 (e_3 - \alpha_3) + k_4 \text{sign}(p_3) \quad (50)$$

$$u = \alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - (\beta \dot{e}_1 + \dot{e}_2 - \dot{e}_1 - k_1 \beta \dot{e}_2 - k_2 (\dot{e}_2 - \dot{\alpha}_2)) + p_2 + k_3 (e_3 - \alpha_3) + k_4 \text{sign}(p_3) \quad (51)$$

$$u = \alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - ((\beta - 1) \dot{e}_1 + (1 - k_1 \beta - k_2) \dot{e}_2 + k_2 \dot{\alpha}_2) + p_2 + k_3 (e_3 - \alpha_3) + k_4 \text{sign}(p_3) \quad (52)$$

$$u = \alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - ((\beta - 1)(-\beta e_2) + (1 - k_1 \beta - k_2)(e_3 - e_2 + e_1) + k_2(-k_1 \dot{p}_1)) + p_2 + k_3 (e_3 - \alpha_3) + k_4 \text{sign}(p_3) \quad (53)$$

$$u = \alpha e_2 - \alpha c e_3 - \alpha x_m^3 + \alpha x_s^3 - ((\beta - 1)(-\beta e_2) + (1 - k_1 \beta - k_2)(e_3 - e_2 + e_1) + k_2(-k_1 \dot{e}_1)) + p_2 + k_3 (e_3 - \alpha_3) + k_4 \text{sign}(p_3) \quad (54)$$

Synchronization of Duffing System

The Duffing oscillator is one of the fundamental models used to investigate the effects of nonlinear dynamics and chaos theory on mechanical systems (Wang et al. 2006). First introduced by Georg Duffing in 1918, this model represents a damped and externally forced oscillator. Due to its nonlinear "hardening" or "softening" spring characteristic, it is capable of producing complex oscillatory behaviors. The key feature that makes this system unique is its ability to transition from harmonic oscillations to period-doubling bifurcations and eventually to chaotic attractors, depending on parameter values. Physically, the Duffing system can model vibrations of a metallic beam in a magnetic field or forced oscillations

in structural mechanical components (Tsai and Lee 2018). Mathematically, it can be expressed as a second-order time-varying differential equation system, as given in Equation 55.

The synchronization of Duffing systems has critical importance in structural vibration control, stabilization of mechanical systems, and chaotic encryption applications. It is based on the principle that two or more Duffing systems, despite small differences in initial conditions, can follow each other's trajectories under an external control input. The general block diagram of this structure is illustrated in Figure 3. In the literature, this process is commonly addressed using a Master-Slave architecture. In this study, the slave system is given in Equation 58. In this part of the study, assuming identical system parameters but different initial conditions, the control law u is designed to achieve complete synchronization.

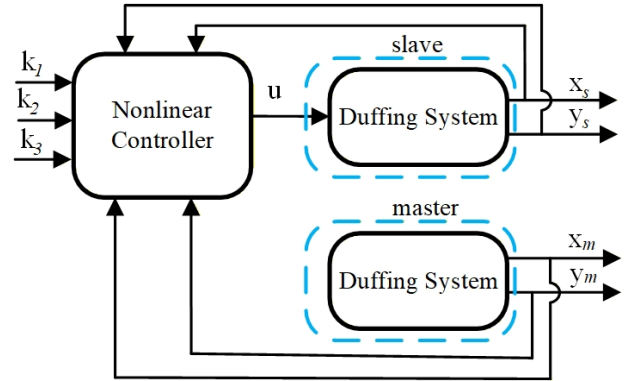


Figure 5 Synchronization diagram of Duffing System

$$\dot{x}_m = y_m \quad (55)$$

$$\dot{y}_m = a x_m + b y_m - x_m^3 + c \cos(0.4t) \quad (56)$$

$$\dot{x}_s = y_s \quad (57)$$

$$\dot{y}_s = a x_s + b y_s - x_s^3 + c \cos(t) + u \quad (58)$$

For the synchronization of the Duffing oscillator, the errors between the system states are defined as given in Equation 57. By taking the derivatives of these error signals, Equation 58 is obtained.

$$e_1 = x_s - x_m \quad (57)$$

$$e_2 = y_s - y_m \quad (58)$$

$$\begin{aligned} \dot{e}_1 &= e_2 \\ \dot{e}_2 &= a e_1 + b e_2 - e_2 (e_1^2 + 3 x_m e_2 + 3 x_m^2) \\ &\quad + c (\cos t - \cos(0.4t)) + u \end{aligned} \quad (59)$$

For synchronization, the Lyapunov energy function is defined as given in Equation 59. By taking its time derivative, Equation 60 is obtained.

$$V_1 = \frac{1}{2} e_1^2 \quad (59)$$

$$\dot{V}_1 = e_1 \dot{e}_1 = e_1 e_2 \quad (60)$$

For the variable e_2 in Equation 60, a virtual variable is assigned as given in Equation 61. Substituting this expression into Equation 60 yields Equation 62. By rearranging Equation 62, Equation 63 is obtained. To ensure the condition $-e_1 \dot{e}_1 \leq 0$, the assumption given in Equation 64 is made. Subsequently, to guarantee that p_1 converges to zero over time, the Lyapunov function is modified as given in Equation 65. Taking its derivative yields Equation 66.

By rearranging Equation 66, Equation 67 is obtained. Taking the time derivative of p_1 leads to Equation 68. Substituting $\dot{p}_1$ from Equation 68 into Equation 67 results in Equation 69. To satisfy the condition $p_1(e_1 + \dot{p}_1) \leq 0$, the assumption in Equation 70 is introduced. Solving this equation for $\dot{p}_1$ yields Equation 71. Substituting Equation 68 into Equation 71 results in Equation 72. By rearranging Equation 72, Equation 73 is obtained. Then, substituting $\dot{e}_2$ into Equation 73 yields Equation 74. Finally, isolating the control input u in Equation 74 leads to Equation 75.

$$p_1 = e_2 + \alpha \Rightarrow e_2 = p_1 - \alpha \quad (61)$$

$$\dot{V}_1 = e_1 \dot{e}_1 = e_1(p_1 - \alpha) \quad (62)$$

$$\dot{V}_1 = -e_1 \alpha = e_1 p_1 \quad (63)$$

$$\alpha = k_1 e_1 \quad (64)$$

$$V_2 = V_1 + \frac{1}{2} p_1^2 \quad (65)$$

$$\dot{V}_2 = \dot{V}_1 + p_1 \dot{p}_1 \quad (66)$$

$$\dot{V}_2 = -e_1 \alpha + e_1 p_1 + p_1 \dot{p}_1 = -k_1 e_1^2 + p_1(e_1 + \dot{p}_1) \quad (67)$$

$$\dot{p}_1 = \dot{e}_1 + \dot{\alpha} \quad (68)$$

$$\dot{V}_2 = -k_1 e_1^2 + e_1 p_1 + p_1(e_1 + \dot{p}_1) \quad (69)$$

$$e_1 + \dot{p}_1 = -k_2 p_1 - k_3 \text{sign}(p_1) \quad (70)$$

$$\dot{p}_1 = -e_1 - k_2 p_1 - k_3 \text{sign}(p_1) \quad (71)$$

$$\dot{e}_2 + \dot{\alpha} = -e_1 - k_2 p_1 - k_3 \text{sign}(p_1) \quad (72)$$

$$\dot{e}_2 = -\dot{\alpha} - e_1 - k_2 p_1 - k_3 \text{sign}(p_1) \quad (73)$$

$$\begin{aligned} ae_1 + be_2 - e_2 \left(e_1^2 + 3x_m e_2 + 3x^2 \right) + c(\cos t - \cos(0.4t)) + u \\ = -k_1 \dot{e}_1 - e_1 - k_2 p_1 - k_3 \text{sign}(p_1) \end{aligned} \quad (74)$$

$$\begin{aligned} u = -ae_1 - be_2 + e_2 \left(e_1^2 + 3x_m e_2 + 3x_m^2 \right) \\ - c(\cos t - \cos(0.4t)) \\ - k_1 e_2 - e_1 - k_2 p_1 - k_3 \text{sign}(p_1) \end{aligned} \quad (75)$$

ADAPTIVE TUNING OF NONLINEAR CONTROLLER PARAMETERS VIA DQN AND DDPG FOR SYNCHRONIZATION

In synchronization studies, after determining the parameters of the slave systems, it is ensured that these parameters are not kept constant with excessively high or low fixed values, but are instead adaptively adjusted using Deep Q-Network (DQN) and Deep Deterministic Policy Gradient (DDPG) approaches. In particular, the proposed framework in this study is applied to the synchronization of Chua and Duffing systems, where the mechanisms, models, and parameter selection processes are described in detail.

DQN-Assisted and DDPG-Assisted Synchronization of Controller Parameters in the Chua Chaotic System

In the synchronization problem of Chua chaotic system, the parameters of the control law applied to the slave system are determined using DQN and DDPG assisted nonlinear control approaches. In order to enable effective interaction between the agent and the environment, the environment structure is composed of the master system, slave system, and nonlinear controller components. The overall architecture of the proposed method is illustrated in Figure 5.

The structure of the reinforcement learning agent can be interpreted as a mapping from the current state to an action. Based on

the state information received from the environment, the agent generates an action according to its policy. In DQN, this action is selected from a discrete action space, whereas in DDPG it is generated directly as a continuous control action by the actor network. The generated action is subsequently used to determine the control input or controller parameters of the nonlinear system. Based on the applied action, the system is simulated over a predefined sampling interval and transitions to the next state. Simultaneously, a reward signal is computed to evaluate the instantaneous control performance. Consequently, the environment returns the next state and the corresponding reward to the reinforcement learning agent. These transitions, consisting of the current state, action, reward, and next state, are stored in the replay memory and randomly sampled during training to improve the learning performance. In DQN, these samples are used to update the action-value function, whereas in DDPG they are employed to train both the actor and critic networks.

The general block diagram of the synchronization system is shown in Figure 6. In this figure, the actions generated by the agent are given in Equation 76, while the states produced by the environment are defined in Equation 77. In addition, the term e_{sum} used in the computation of the reward is defined as in Equation 78, and the reward function is calculated as given in Equation 79 and 80. Furthermore, the termination condition (done signal), which stops the interaction of the agent with the environment, is defined in Equation 81. The action and state ranges employed by DQN and DDPG agents are summarized in Tables 2 and 3, respectively. Especially, a wide range of action values was selected to accelerate the learning process and facilitate faster convergence. The neural network architectures and related parameters adopted for DQN and DDPG agents are presented in Tables 4 and 5, respectively. Finally, the hyperparameters used during the training of DQN and DDPG algorithms are listed in Tables 6 and 7, respectively.

The parameters of DQN or DDPG agents were selected based on commonly adopted configurations reported in the reinforcement learning literature and refined through preliminary simulation studies. The neural network architectures were designed to provide sufficient approximation capability while maintaining a reasonable computational complexity. The learning rates were chosen to ensure stable convergence and prevent oscillatory parameter updates during training. The replay buffer size and mini-batch size were determined to improve sample efficiency and reduce the correlation among consecutive experiences. Furthermore, the discount factor was selected to balance the importance of immediate and future rewards, while the exploration-related parameters were adjusted to provide an appropriate trade-off between exploration and exploitation. The final parameter values were determined experimentally as those providing the most stable learning process and the best synchronization performance.

$$\text{Action} = [k_1, k_2, k_3, k_4] \quad (76)$$

$$\text{State} = [e_1, e_2, e_3] \quad (77)$$

$$e_{\text{sum}} = |e_1| + |e_2| + |e_3| \quad (78)$$

$$r_{v1} = \begin{cases} 2 & k_4 = 0.1 \\ 1.5 & k_4 = 1 \\ -1 - 0.1 \times (k_1 + k_2 + k_3 + k_4) & \text{other} \\ -1 - e_{\text{sum}} & \text{other} \end{cases} \quad e_{\text{sum}} \leq 0.01 \quad (79)$$

$$\text{reward} = \begin{cases} r_{V1}, & r_{V1} \geq -500 \\ -1000, & \text{other} \end{cases} \quad (80)$$

$$\text{done} = \begin{cases} 1, & r_{V1} \leq -500 \\ 0, & \text{other} \end{cases} \quad (81)$$

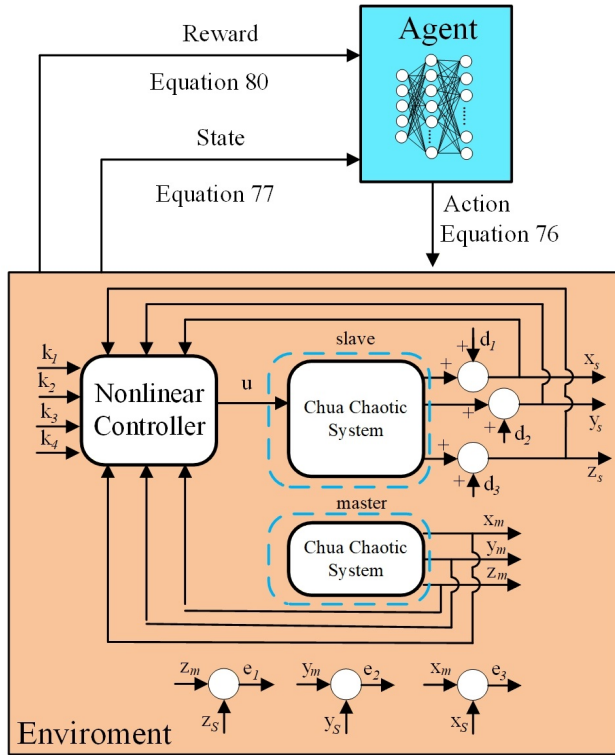


Figure 6 Block diagram of DQN-assisted or DDPG-assisted reinforcement learning agent for synchronization of Chua chaotic system

Table 2 Action and State Ranges in DQN Framework for Synchronization of Chua Chaotic System

Action	Range	State	Range
k_1	$[0.1, 1, 10, 100]$	e_1	$(-\infty, \infty)$
k_2	$[0.1, 1, 10, 100]$	e_2	$(-\infty, \infty)$
k_3	$[0.1, 1, 10, 100]$	e_3	$(-\infty, \infty)$
k_4	$[0.1, 1, 10, 100]$		

DQN-Assisted and DDPG-Assisted Synchronization of Controller Parameters in the Duffing System

In the synchronization problem of the Duffing chaotic system, the parameters of the control law applied to the slave system are optimized using DQN or DDPG assisted nonlinear control approaches. In order to maximize the reward value, the environment is constructed from the master system, the slave system, and the nonlinear controller parameters. The overall architecture of the

Table 3 Action and State Ranges in DDPG Framework for Synchronization of Chua Chaotic System

Action	Range	State	Range
k_1	$[0.1, 100]$	e_1	$(-\infty, \infty)$
k_2	$[0.1, 100]$	e_2	$(-\infty, \infty)$
k_3	$[0.1, 100]$	e_3	$(-\infty, \infty)$
k_4	$[0.1, 100]$		

Table 4 DNN Parameters of DQN for Synchronization of Chua Chaotic System

Layer No	Layer Type	Number of Neurons	Activation Function
1	Feature Input Layer	3 input features	-
2	Fully Connected Layer	500 neurons	-
3	Activation Layer	-	Tanh
4	Fully Connected Layer	256 neurons	-
5	Activation Layer	-	Linear
6	Fully Connected Layer (Output)	256 neurons	-

Table 5 DNN Parameters of DDPG for Synchronization of Chua Chaotic System

Layer Type	Number of Neurons
Input Layer	3 input features
Actor Hidden Layer	500 neurons
Critic Hidden Layer	500 neurons
Hidden Activation Layer	Tanh
Output Activation Layer	Linear
Actor Output Layer (Output)	4 neurons
Critic Output Layer (Output)	1 neuron

proposed method is illustrated in Figure 7. When the structure of the agent is examined, the input layer consists of system error states, while the output layer represents actions corresponding to the controller coefficients. DQN or DDPG generate actions based on the observed state information from the environment and dynamically determines the parameters of the nonlinear controller through these actions. In the environment, these parameters are applied to the controller, and the Duffing system is simulated over a predefined sampling time, resulting in a transition to the next state. A reward signal is generated to evaluate the control perfor-

Table 6 DQN Training Parameters for Synchronization of Chua Chaotic System

Parameters	Parameter Value	Parameters	Parameter Value
Learning rate	10^{-5}	Epsilon Value	0.05
Gradient Threshold	-	Epsilon Decay	0.99^{iter}
Sample Time	0.02	Minimum Epsilon Value	0.001
MiniBatchSize	32	Max Episode	50
Learning Method	-	Replay Memory	1000

Table 7 DDPG Training Parameters for Synchronization of Chua Chaotic System

Parameters	Parameter Value	Parameters	Parameter Value
Actor Learning rate	10^{-5}	Action Filter Coefficient	0.15
Critic Learning rate	10^{-4}	Noise Theta	0.15
Gradient Limit	1.0	Noise Sigma	0.15
Sample Time	0.02	Replay Memory	1000
MiniBatchSize	32	Max Episode	50
Learning Method	-	State Scale	1.0
γ	0.95	τ	0.005

mance and guide the learning process. The next state and reward values obtained from the environment are fed back to the agent. These experiences are stored in the replay memory and utilized during the training process.

The general block diagram of the synchronization system is shown in Figure 7. In this figure, the actions generated by the agent are given in Equation 82, while the states obtained from the environment are presented in Equation 83. Moreover, the term e_{sum} used in the reward computation is defined in Equation 84, the reward function in Equation 85 and Equation 86. Episode termination condition (done signal) is determined as in Equation 87. The action and state ranges employed by DQN and DDPG agents are summarized in Tables 8 and 9, respectively. Especially, a wide range of action values was selected to accelerate the learning process and facilitate faster convergence. The neural network architectures and the corresponding parameters employed for DQN and DDPG agents are presented in Tables 10 and 11, respectively. The hyperparameters used during the training of DQN and DDPG algorithms are summarized in Tables 12 and 13, respectively.

The parameters of DQN or DDPG agents were selected based on commonly adopted configurations reported in the reinforcement learning literature and refined through preliminary simulation studies. The neural network architectures were designed to

provide sufficient approximation capability while maintaining a reasonable computational complexity. The learning rates were chosen to ensure stable convergence and prevent oscillatory parameter updates during training. The replay buffer size and mini-batch size were determined to improve sample efficiency and reduce the correlation among consecutive experiences. Furthermore, the discount factor was selected to balance the importance of immediate and future rewards, while the exploration-related parameters were adjusted to provide an appropriate trade-off between exploration and exploitation. The final parameter values were determined experimentally as those providing the most stable learning process and the best synchronization performance.

$$\text{Action} = [k_1, k_2, k_3] \quad (82)$$

$$\text{State} = [e_1, e_2] \quad (83)$$

$$e_{sum} = |e_1| + |e_2| \quad (84)$$

$$r_{V1} = \begin{cases} 2 & k_3 = 0.1 \\ 1.5 & k_3 = 1 \\ -1 - 0.1 \times (k_1 + k_2 + k_3) & \text{other} \end{cases} \quad e_{sum} \leq 0.01 \quad (85)$$

$$\text{reward} = \begin{cases} r_{V1}, & r_{V1} \geq -500 \\ -1000, & \text{other} \end{cases} \quad (86)$$

$$\text{done} = \begin{cases} 1, & r_{V1} \leq -500 \\ 0, & \text{other} \end{cases} \quad (87)$$

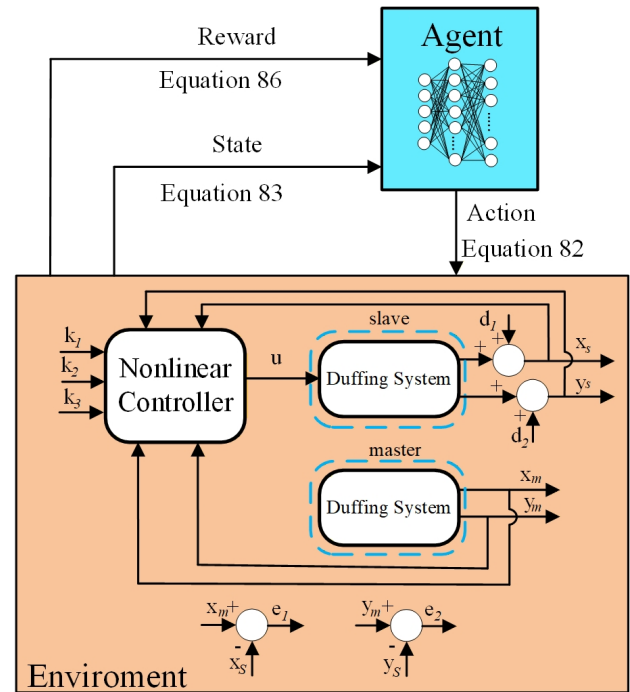


Figure 7 Block diagram of DQN-assisted or DDPG-assisted reinforcement learning agent for synchronization of the Duffing system

■ **Table 8** Action and State Ranges in DQN Framework for Synchronization of the Duffing System

Action	Range	State	Range
k_1	[0.1, 1, 10, 100]	e_1	$(-\infty, \infty)$
k_2	[0.1, 1, 10, 100]	e_2	$(-\infty, \infty)$
k_3	[0.1, 1, 10, 100]		

■ **Table 9** Action and State Ranges in DDPG Framework for Synchronization of the Duffing System

Action	Range	State	Range
k_1	[0.1, 100]	e_1	$(-\infty, \infty)$
k_2	[0.1, 100]	e_2	$(-\infty, \infty)$
k_3	[0.1, 100]		

■ **Table 10** DNN Parameters of DQN for Synchronization of the Duffing System

Layer No	Layer Type	Number of Neurons	Activation Function
1	Feature Input Layer	2 input features	-
2	Fully Connected Layer	500 neurons	-
3	Activation Layer	-	Tanh
4	Fully Connected Layer	64 neurons	-
5	Activation Layer	-	Linear
6	Fully Connected Layer (Output)	64 neurons	-

■ **Table 11** DNN Parameters of DDPG for Synchronization of the Duffing System

Layer Type	Number of Neurons
Input Layer	2 input features
Actor Hidden Layer	500 neurons
Critic Hidden Layer	500 neurons
Hidden Activation Layer	Tanh
Output Activation Layer	Linear
Actor Output Layer (Output)	3 neurons
Critic Output Layer (Output)	1 neuron

■ **Table 12** DQN Training Parameters for Synchronization of the Duffing System

Parameters	Parameter Value	Parameters	Parameter Value
Learning rate	10^{-5}	Epsilon Value	0.05
Gradient Threshold	-	Epsilon Decay	0.99^{iter}
Sample Time	0.02	Minimum Epsilon Value	0.001
MiniBatchSize	32	Max Episode	50
Learning Method	-	Replay Memory	1000

■ **Table 13** DQN Training Parameters for Synchronization of the Duffing System

Parameters	Parameter Value	Parameters	Parameter Value
Actor Learning rate	10^{-5}	Action Filter Coefficient	0.15
Critic Learning rate	10^{-4}	Noise Theta	0.15
Gradient Limit	1.0	Noise Sigma	0.15
Sample Time	0.02	Replay Memory	1000
MiniBatchSize	32	Max Episode	50
Learning Method	-	State Scale	1.0
γ	0.95	τ	0.005

SIMULATION STUDIES

In this study, all simulations and reinforcement learning training processes were performed on a computer equipped with an Intel Core i7-11800H processor operating at 2.3 GHz, 32 GB of RAM, and an NVIDIA GeForce RTX 3070 GPU running Windows 11 Home. MATLAB/Simulink was used as the primary software platform for system modeling, controller implementation, and reinforcement learning integration. Initially, the synchronization models of the Chua and Duffing chaotic systems were developed within the Simulink environment. Subsequently, the nonlinear controller and the reinforcement learning algorithms, namely DQN and DDPG, were integrated into the simulation framework and evaluated under identical operating conditions to ensure a fair performance comparison. Each simulation was conducted over a duration of 50 s, whereas DQN and DDPG agents were trained independently for 50 episodes. The effectiveness of the proposed synchronization strategy was assessed using the obtained system responses, synchronization errors, and quantitative performance indices. The simulation results and comparative analyses are presented in the following subsections through graphical illustrations and tabulated performance metrics.

DQN-Assisted and DDPG-Assisted Synchronization Simulation Studies of the Chua Chaotic System

Synchronization simulations of the Chua chaotic system were performed in the MATLAB/Simulink environment using the system model and the nonlinear controller described in the previous sections. The performance of the proposed DQN- and DDPG-assisted synchronization strategies was comprehensively evaluated through synchronization error signals, the controller parameters generated by the reinforcement learning agents, the control input applied to the slave system, and the corresponding reward values. In addition, the synchronization behavior was assessed by comparing the trajectories of the master and slave systems, while the learning performance of the reinforcement learning algorithms was analyzed using the reward, loss, and cumulative reward variations throughout the training process. The obtained results are presented graphically in Figures 8–16 and quantitatively summarized in Table 14.

In terms of synchronization performance, the error dynamics between the master and slave systems, represented by e_1 , e_2 , and e_3 , are illustrated in the time domain in Figure 8. The results indicate that the slave system gradually converges to the master system, confirming the effectiveness of both synchronization approaches. However, DQN-assisted nonlinear controller exhibits smoother synchronization responses with significantly fewer oscillations, whereas DDPG-assisted nonlinear controller shows noticeable oscillatory behavior, particularly as the simulation time increases. The action values generated by DQN-assisted and DDPG-assisted agents are presented in Figure 9. It can be observed that the action values produced by DQN agent vary approximately between 0.1 and 100, while those generated by DDPG agent remain within the range of approximately 0 to 35. This difference reflects the distinct action generation mechanisms employed by the two reinforcement learning algorithms. The corresponding control signals applied to the slave system are shown in Figure 10. As can be seen, DQN-assisted controller produces control signals with relatively higher amplitudes on average. Although the control signals generated by DDPG-assisted controller also exhibit high amplitudes, they generally remain lower than those produced by DQN-assisted controller.

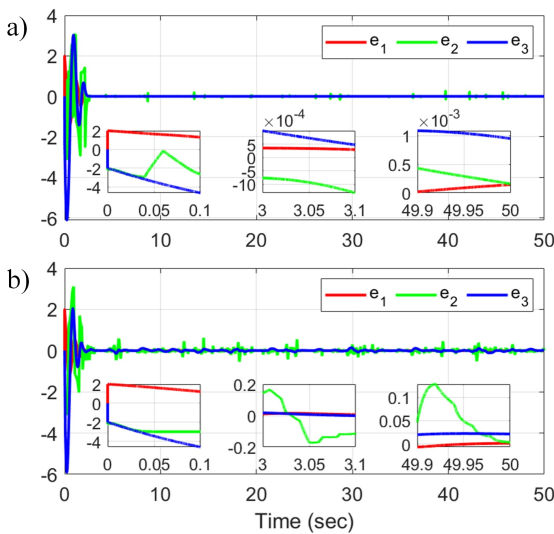


Figure 8 Responses of e_1 , e_2 and e_3 state of the synchronized Chua chaotic system using **a)** DQN-assisted **b)** DDPG-assisted nonlinear controller

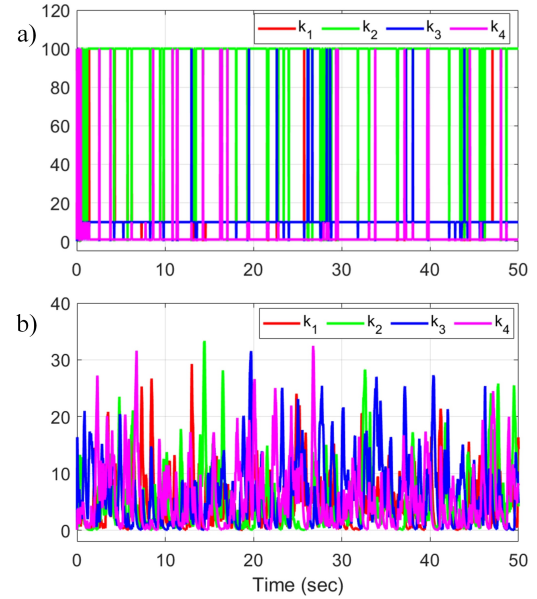


Figure 9 Nonlinear controller parameters by **a)** DQN-assisted **b)** DDPG-assisted for synchronized Chua chaotic system

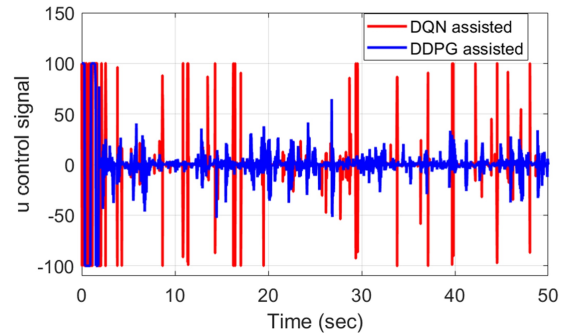


Figure 10 Control signal by nonlinear controller for synchronized Chua chaotic system

The variations of the reward signal and average reward during the synchronization process for DQN-assisted and DDPG-assisted nonlinear controllers are presented in Figure 11. It can be observed that DQN-assisted approach consistently achieves higher reward and average reward values than DDPG-assisted approach throughout the simulation. This indicates that, under identical operating conditions, DQN-assisted method learns a more effective control policy and achieves the desired reward objective more successfully than DDPG-assisted method. In addition, the numerical values of the reward and average reward are reported in Table 15. As shown in the table, DQN-assisted method outperforms DDPG-assisted method with respect to both the reward and average reward metrics. Furthermore, the synchronization performance of the Chua chaotic system is evaluated using the Integral Absolute Error (IAE), Integral Square Error (ISE), Integral Time Absolute Error (ITAE), and Integral Time Square Error (ITSE) performance indices. A graphical comparison of these indices is presented in Figure 12, while the corresponding numerical values are listed in Table 15. As can be observed, DQN-assisted nonlinear controller achieves lower values for all performance indices, indicating superior synchronization accuracy compared with DDPG-assisted approach. In addition, the control effort required by the two synchronization

methods is summarized in Table 15. The DDPG-assisted nonlinear controller yields the lower control effort.

Table 14 Comparison of the reward values obtained by DQN-assisted and DDPG-assisted nonlinear control methods for the synchronization of Chua chaotic system

Method	Reward Value	Method	Reward Value
DQN-assisted reward	1.5000	DDPG-assisted reward	−1.0276
DQN-assisted average reward	1.5000	DDPG-assisted average reward	−1.2414

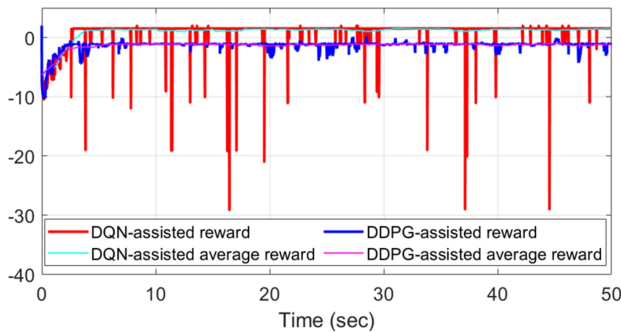


Figure 11 Reward and Average Reward values obtained from the chaotic system synchronized using DQN-assisted and DDPG-assisted nonlinear control

DQN and DDPG agents are continuously trained through interaction with the environment using samples stored in the replay memory. The loss values obtained during the final iteration of training are illustrated in Figure 13. These results indicate that the loss value exhibits an overall decreasing trend over the 50-second simulation period.

Table 15 Performance comparison of DQN-assisted and DDPG-assisted nonlinear controllers for the synchronization of the Chua chaotic system

Performance Metric	Formul	DQN-assisted	DDPG-assisted
IAE	$\int_0^T e(t) dt$	9.655×10^0	1.252×10^1
ISE	$\int_0^T (e(t))^2 dt$	2.484×10^1	2.166×10^1
ITAE	$\int_0^T (e(t))t dt$	4.827×10^2	6.262×10^2
ITSE	$\int_0^T (e(t))^2 t dt$	1.242×10^3	1.083×10^3
Control Effort	$\int_0^T (u(t))^2 dt$	2.3693×10^4	1.9469×10^4

The master and slave system trajectories obtained from the environment designed for the synchronization of the Chua chaotic system are presented in Figure 14. As observed in Figure 14, although the slave system initially exhibits behavior different from the master system, it gradually converges to the master system over time, thereby achieving synchronization. In addition, the three-dimensional phase portrait of the system is also illustrated in Figure 14.

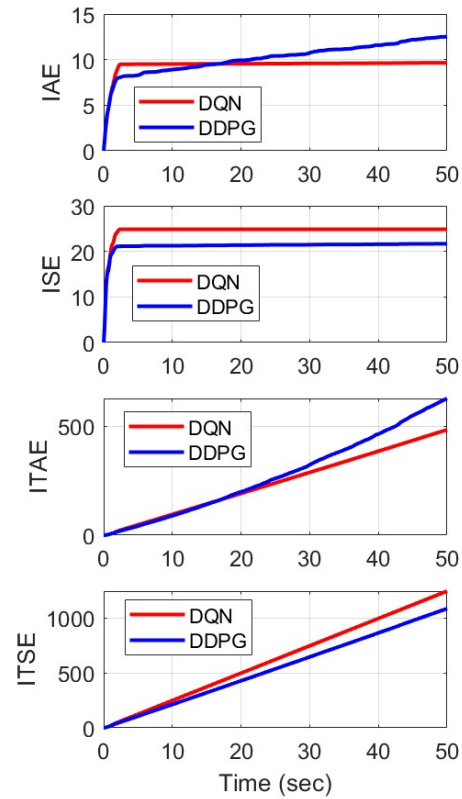


Figure 12 Comparison of IAE, ISE, ITAE, and ITSE performance indices of DQN-assisted and DDPG-assisted nonlinear controllers for the synchronization of the Chua chaotic system

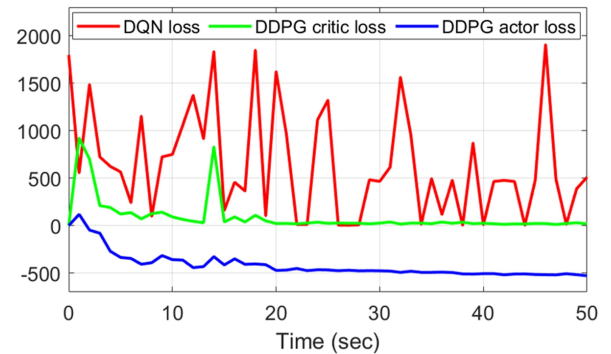


Figure 13 Loss values during synchronization for Chua Chaotic System

During the synchronization of the Chua chaotic system, the reward, loss, and cumulative reward values obtained over 50 training episodes, where each episode consists of a 50-second simulation, are presented for DQN and DDPG agents in Figure 15. The results demonstrate that DQN-assisted approach consistently achieves higher reward values than DDPG-assisted approach throughout the entire training process. Meanwhile, the loss values of both algorithms gradually decrease and converge to stable levels, indicating that the neural networks successfully learn the underlying system dynamics. Note that, for the reward average, the average was calculated using the last 1000 samples of the reward data

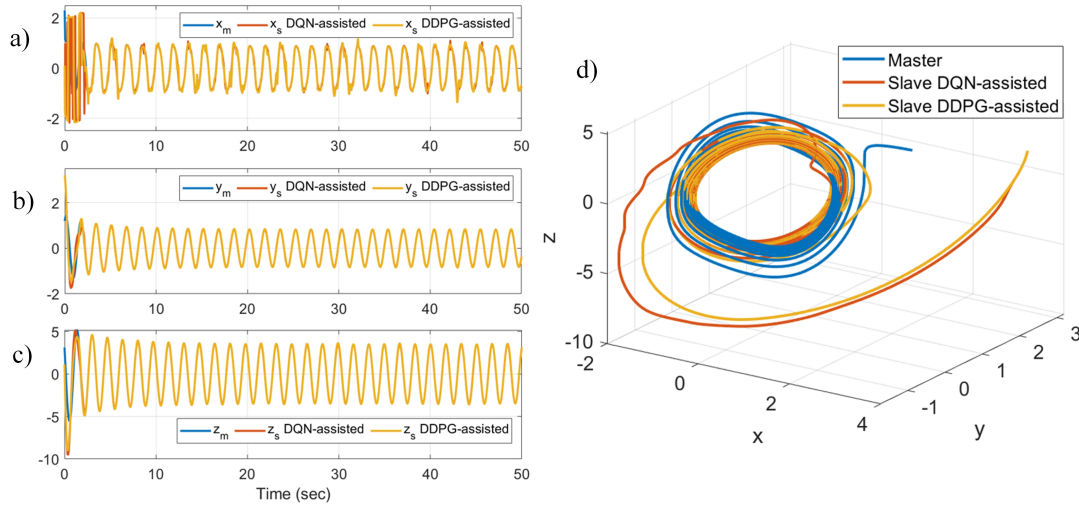


Figure 14 Master and slave states **a)** x state, **b)** y state, **c)** z and **d)** 3D phase portrait during the synchronization of Chua chaotic system using DQN-assisted and DDPG-assisted nonlinear controllers

over time. Furthermore, the cumulative reward obtained by DQN-assisted method is consistently higher than that of DDPG-assisted method. This increasing cumulative reward trend indicates that DQN agent progressively improves its interaction with the environment and learns a more effective control policy. Consequently, the nonlinear controller parameters are determined more accurately, resulting in enhanced synchronization performance. To

proaches successfully maintain synchronization in the presence of external disturbances. However, DQN-assisted approach exhibits smoother synchronization responses with significantly reduced chattering compared with DDPG-assisted approach, demonstrating its superior robustness against disturbances.

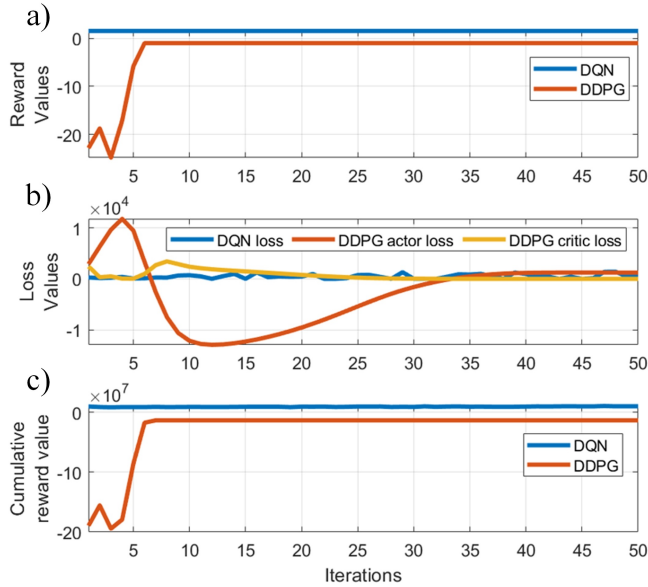


Figure 15 Reward, Loss and cumulative reward values for each iteration during training of DQN-assisted and DDPG-assisted agents for synchronization of Chua Chaotic System

evaluate the robustness of the proposed synchronization strategy, external disturbances d_1 , d_2 , and d_3 were introduced into the general block diagram shown in Figure 6. The disturbance profiles are illustrated in Figure 16c, where step-type disturbances with amplitudes ranging from (-0.25) to (0.25) were applied at different time instants. The synchronization responses obtained using DQN-assisted controller and DDPG-assisted controller are presented in Figures 16a and 16b, respectively. As can be observed, both ap-

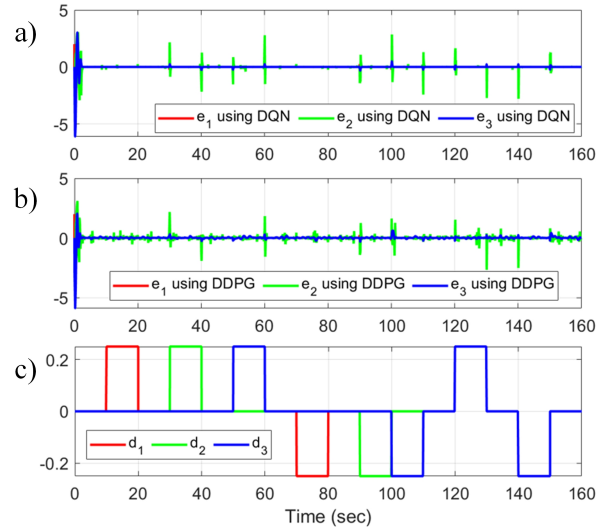


Figure 16 Synchronization performance of the Chua chaotic system under external disturbances: **a)** synchronization errors (e_1 , e_2 , and e_3) obtained using DQN-assisted nonlinear controller, **b)** synchronization errors (e_1 , e_2 , and e_3) obtained using DDPG-assisted nonlinear controller, and **c)** external disturbances (d_1 , d_2 , and d_3) applied to the system states

DQN-Based and DDPG-Assisted Synchronization Simulation Studies of the Duffing System

Synchronization simulation studies of the Duffing system were conducted in MATLAB using the model parameters provided in previous sections. The obtained results are evaluated in terms of the synchronization error signals between the two systems, the nonlinear controller parameters generated by both DQN and

DDPG agents, the control input applied to the slave system, the reward values obtained during synchronization, the trajectories of the master and slave systems, and the loss, and cumulative reward variations observed throughout the training process. These results are presented graphically in Figures 17 to 25.

In terms of synchronization performance, the error trajectories (e_1) and (e_2), representing the differences between the master and slave systems, are shown in the time domain in Figure 17. The results indicate that both DQN-assisted and DDPG-assisted nonlinear controllers successfully synchronize the slave system with the master system, as the synchronization errors gradually converge to zero. However, as illustrated in Figure 17(a), DQN-assisted nonlinear controller drives the synchronization errors to zero more rapidly than DDPG-assisted nonlinear controller shown in Figure 17(b). Although DQN-assisted approach achieves faster convergence, it also exhibits larger transient error amplitudes during the initial stage of the synchronization process. Figure 18 presents the actions generated by DQN-assisted and DDPG-assisted agents based on the observed system states, which are used to determine the parameters of the nonlinear controller. It can be observed that the controller parameters generated by DQN-assisted agent vary approximately between 0.1 and 100, whereas those generated by DDPG-assisted agent remain within the range of approximately 0.1 to 35.

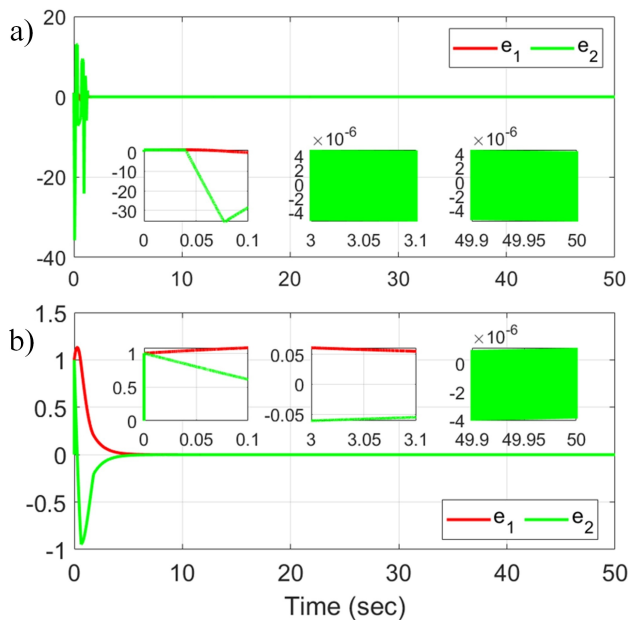


Figure 17 Responses of e_1 and e_2 state of the synchronized Duffing system using a) DQN-assisted b) DDPG-assisted nonlinear controller

The control signal is generated using the parameters of the nonlinear controller determined by the reinforcement learning agents. The control signals produced by DQN-assisted and DDPG-assisted nonlinear controllers are presented in Figures 19(a) and 19(b), respectively. To ensure stable system operation and prevent instability caused by excessively large control inputs, the control signal was constrained by a saturation limit ranging from (-1000) to (1000). As shown in Figure 19(a), the control signal generated by DQN-assisted nonlinear controller occasionally reaches the saturation limits, indicating that the computed control input is clipped when it exceeds the predefined bounds.

The variations of the reward signal and average reward during

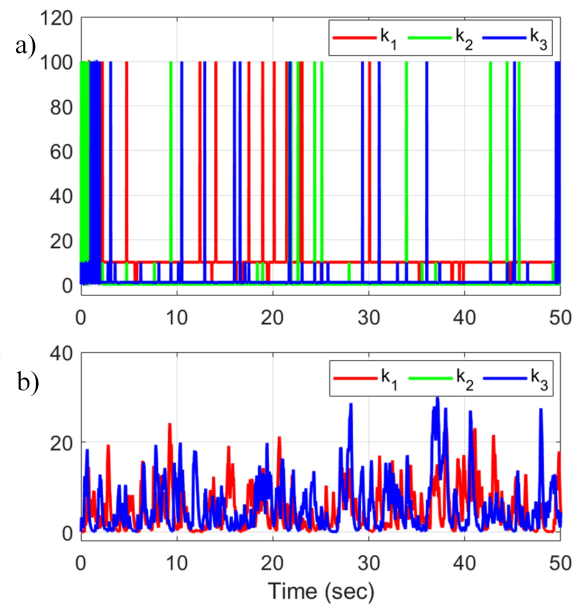


Figure 18 Nonlinear controller parameters by a) DQN-assisted b) DDPG-assisted for synchronized Duffing system

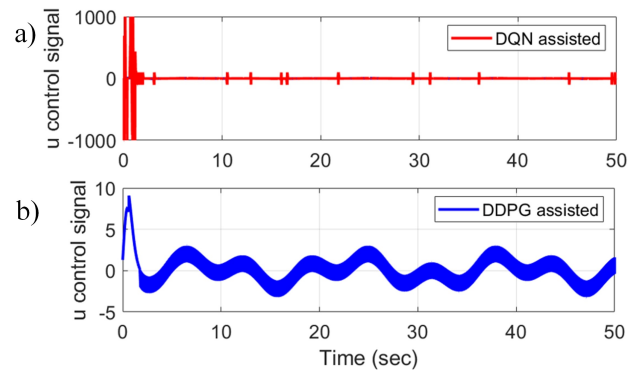


Figure 19 Control signal by nonlinear controller for synchronized Duffing system

the synchronization process for DQN-assisted and DDPG-assisted nonlinear controllers are presented in Figure 17. It can be observed that DQN-assisted approach consistently achieves higher reward and average reward values than DDPG-assisted approach throughout the simulation. This indicates that, under identical operating conditions, DQN-assisted method learns a more effective control policy and achieves the desired reward objective more successfully than DDPG-assisted method. In addition, the numerical values of the reward and average reward are reported in Table 16. As shown in the table, DQN-assisted method outperforms DDPG-assisted method with respect to both the reward and average reward metrics. Note that, for the reward average, the average was calculated using the last 1000 samples of the reward data over time. Furthermore, the synchronization performance of the Duffing chaotic system is evaluated using the IAE, ISE, ITAE, and ITSE performance indices. A graphical comparison of these indices is presented in Figure 25, while the corresponding numerical values are listed in Table 17. As can be observed, DDPG-assisted nonlinear controller achieves lower values for all performance indices, indicating superior synchronization accuracy compared

with DQN-assisted approach. In addition, the control effort required by the two synchronization methods is summarized in Table 17. The DDPG-assisted nonlinear controller yields the lower control effort.



Figure 20 Reward and Average Reward values obtained from the chaotic system synchronized using DQN-assisted and DDPG-assisted nonlinear control

Table 16 Comparison of the reward values obtained by DQN-assisted and DDPG-assisted nonlinear control methods for the synchronization of Duffing chaotic system

Method	Reward Value	Method	Reward Value
DQN-assisted reward	1.5000	DDPG-assisted reward	1.1555
DQN-assisted average reward	-0.1051	DDPG-assisted average reward	-0.5969

DQN and DDPG agents are continuously trained through interaction with the environment using samples stored in the replay memory. The loss values obtained during the final iteration of training are illustrated in Figure 21. These results indicate that the loss value exhibits an overall decreasing trend over the 50-second simulation period.

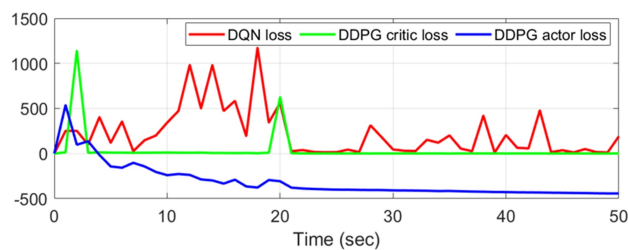


Figure 21 Loss values during synchronization of Duffing System

The master and slave system trajectories obtained from the environment designed for the synchronization of the Duffing oscillator are presented in Figure 22. As observed in Figure 22, although the slave system initially exhibits behavior different from the master system, it gradually converges to the master system over time, thereby achieving synchronization. In addition, the two-dimensional phase portrait of the system is also illustrated in Figure 22.

During the synchronization of the Duffing chaotic system, the reward, loss, and cumulative reward values obtained over 50 training episodes, where each episode consists of a 50-second

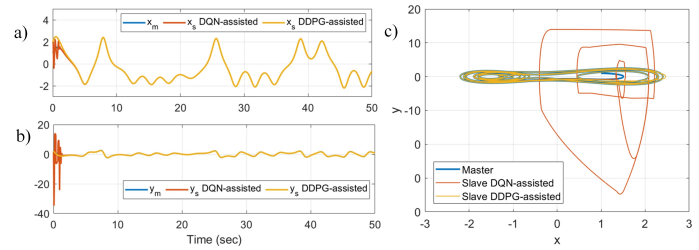


Figure 22 Master and slave states a) x state, b) y state, c) 2D phase portrait during the synchronization of Duffing System using DQN-assisted and DDPG-assisted nonlinear controllers

simulation, are presented for DQN and DDPG agents in Figure 23. The results demonstrate that DQN-assisted approach consistently achieves higher reward values than DDPG-assisted approach throughout the entire training process. Meanwhile, the loss values of both algorithms gradually decrease and converge to stable levels, indicating that the neural networks successfully learn the underlying system dynamics. Furthermore, the cumulative reward obtained by DQN-assisted method is consistently higher than that of DDPG-assisted method. This increasing cumulative reward trend indicates that DQN agent progressively improves its interaction with the environment and learns a more effective control policy. Consequently, the nonlinear controller parameters are determined more accurately, resulting in enhanced synchronization performance.

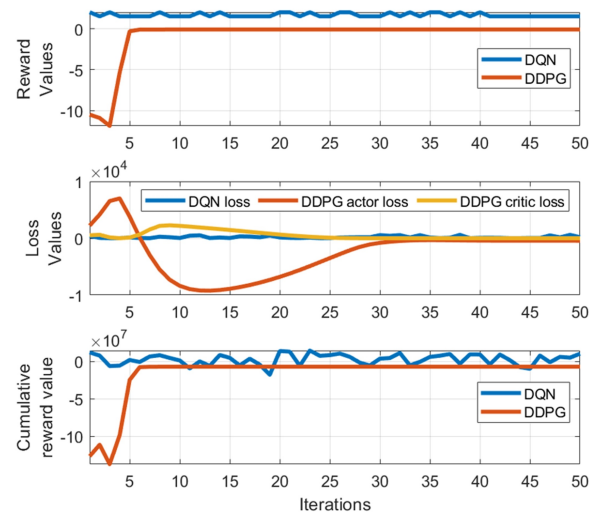


Figure 23 Reward, Loss and cumulative reward values for each iteration during training of DQN-assisted and DDPG-assisted agents for synchronization of Duffing System

To evaluate the robustness of the proposed synchronization strategy, external disturbances (d_1) and (d_2) were introduced into the general block diagram shown in Figure 24. The disturbance profiles are illustrated in Figure 24(c), where step-type disturbances with amplitudes ranging from (-0.25) to (0.25) were applied at different time instants. The synchronization responses obtained using DQN-assisted and DDPG-assisted nonlinear controllers are presented in Figures 24(a) and 24(b), respectively. As can be observed, both controllers successfully maintain synchronization in the presence of external disturbances, demonstrating the robustness of the proposed approaches. However, the transient responses

of the two methods differ noticeably. As shown in Figure 24(a), DQN-assisted nonlinear controller generates control actions with relatively higher amplitudes, resulting in larger synchronization error peaks immediately after the disturbances are applied. In contrast, DDPG-assisted nonlinear controller, shown in Figure 24(b), produces smoother control actions with lower amplitudes, leading to smoother transient responses and reduced error peaks following the disturbance. Nevertheless, the disturbance rejection capability of DDPG-assisted controller is relatively slower, resulting in a longer error settling time compared with DQN-assisted controller. Despite these differences, both methods effectively suppress the external disturbances and ultimately achieve stable synchronization between the master and slave systems.

The comparative results indicate that DQN and DDPG exhibit different performance characteristics depending on the chaotic system and the selected evaluation criterion. Although the DQN-assisted approach achieves higher reward values for both chaotic systems, this does not necessarily lead to lower IAE, ISE, ITAE, and ITSE values. This difference can mainly be attributed to the design of the reward function, which encourages the agents to minimize the instantaneous synchronization error at each sampling instant, whereas the error-based performance indices evaluate the accumulated error over the entire simulation period. In addition, DQN selects controller parameters from a predefined discrete action set, while DDPG generates continuous actions; therefore, their effectiveness may vary depending on the nonlinear dynamics and error evolution of each chaotic system. These findings suggest that system-specific reward functions incorporating accumulated error measures and control effort could further improve the consistency between the reinforcement learning objective and conventional synchronization performance criteria.

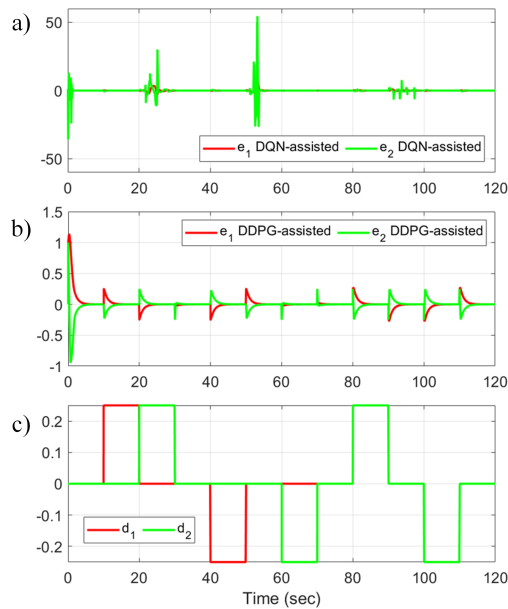


Figure 24 Synchronization performance of the Duffing chaotic system under external disturbances: **a)** synchronization errors (e_1, e_2) obtained using DQN-assisted nonlinear controller, **b)** synchronization errors (e_1, e_2) obtained using DDPG-assisted nonlinear controller, and **c)** external disturbances (d_1, d_2) applied to the system states

Table 17 Performance comparison of DQN-assisted and DDPG-assisted nonlinear controllers for the synchronization of the Duffing chaotic system

Performance Metric	Formul	DQN-assisted	DDPG-assisted
IAE	$\int_0^T e(t) dt$	1.042×10^1	2.727×10^0
ISE	$\int_0^T (e(t))^2 dt$	1.351×10^2	1.871×10^0
ITAE	$\int_0^T (e(t))t dt$	5.212×10^2	1.363×10^2
ITSE	$\int_0^T (e(t))^2 t dt$	6.753×10^3	9.357×10^1
Control Effort	$\int_0^T (u(t))^2 dt$	1.5069×10^5	1.5778×10^2

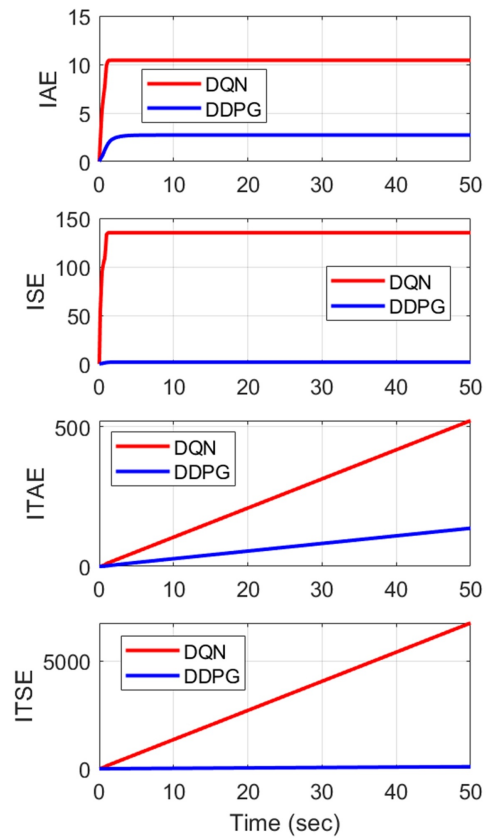


Figure 25 Comparison of IAE, ISE, ITAE, and ITSE performance indices of DQN-assisted and DDPG-assisted nonlinear controllers for the synchronization of Duffing system

CONCLUSION

This study investigated the synchronization of two well-known nonlinear chaotic systems, namely Chua's circuit and the Duffing oscillator, using Lyapunov-based nonlinear controllers enhanced by reinforcement learning. Owing to the inherent characteristics of chaotic systems, including strong nonlinearities and sensitivity to initial conditions, achieving reliable synchronization remains a challenging task. To address this problem, Lyapunov-based nonlinear controllers were designed to stabilize the synchronization error dynamics and ensure convergence between the master and slave systems. Furthermore, the controller parameters were adaptively adjusted online using Deep Q-Learning (DQN) and Deep

Deterministic Policy Gradient (DDPG) frameworks. During the synchronization process, both reinforcement learning agents were trained to maximize the instantaneous reward at each sampling instant, thereby improving the synchronization performance.

The effectiveness of the proposed approaches was evaluated using the reward, average reward, IAE, ISE, ITAE, ITSE, and control effort performance metrics. The results showed that DQN-assisted approach consistently achieved higher reward values and average reward values than DDPG-assisted approach for both the Chua and Duffing chaotic systems, indicating that it learned a more effective reward-maximizing policy under identical operating conditions. However, the remaining performance metrics exhibited different trends depending on the chaotic system. For the synchronization of the Chua chaotic system, DQN-assisted nonlinear controller generally provided superior performance in terms of reward, average reward, IAE, ISE, ITAE, and ITSE. In contrast, for the Duffing chaotic system, DDPG-assisted nonlinear controller achieved better synchronization performance according to IAE, ISE, ITAE, and ITSE and control effort metrics. These findings demonstrate that the relative effectiveness of the reinforcement learning algorithm depends on the characteristics of the chaotic system being synchronized. In addition, the proposed control strategies effectively reduced the high switching amplitudes in the control signals, resulting in smoother control actions and improved practical applicability. To further evaluate the robustness of the proposed methods, external disturbances were introduced during the synchronization of both chaotic systems. The simulation results demonstrated that both DQN-assisted and DDPG-assisted controllers successfully rejected the disturbances and maintained stable synchronization between the master and slave systems.

The findings highlight that combining Lyapunov-based nonlinear control with DQN or DDPG provides an effective and flexible solution for the synchronization of complex chaotic systems. Since the trained reinforcement learning agents require only a forward pass through the neural network during online operation, the computational burden is significantly lower than that of the training stage, making the proposed approach suitable for real-time implementation on modern embedded control platforms. Future studies will focus on extending the proposed approach to fractional-order and time-delay chaotic systems, integrating robust control strategies, and experimentally validating the method on real-time hardware platforms. From a practical perspective, the proposed adaptive control framework has the potential to be applied to nonlinear and chaotic systems requiring real-time synchronization and adaptive parameter adjustment, particularly in areas such as secure communication, power electronics, robotic systems, and industrial control applications.

Availability of data and material

Not applicable.

Conflicts of interest

The author declares that there is no conflict of interest regarding the publication of this paper.

Ethical standard

The author has no financial or non-financial interests to disclose.

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