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Integrating Novel Deep Neural Networks on the Analysis of Fractional Epidemiological Models in both Populations with Disease Infection

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Abstract:

Deep Neural Networks (DNNs) have become one of the most significant tools utilized in analyzing complicated systems, surpassing the ability to comprehend complexities. The study provides the advantage of DNNs' interest to improve the analysis of intricate patterns and produce insightful findings. It is crucial to comprehend the dynamics of infectious disease spread in ecological systems, especially when it comes from predator to prey, because of its significance for a variety of real-world situations. In complicated regulation environments, the size range of prey and predator populations is influenced by the complicated interactions between infections and predator-prey relationships. The analysis of fractional epidemiological models in both populations with disease infection (FEM-BPDI) is performed through the novel application of artificial intelligence, particularly Deep Neural Networks (DNNs). Datasets for Deep Neural Networks are generated using the fde12 solver. Training, testing, and validation phases are applied to the DNNs models to acquire solutions for the FEM-BPDI under different epidemiological scenarios. Several statistical metrics, such as mean-squared error analyses, auto-correlation of error (ACE), correlation input and error (CIE), error histogram visualizations, and expected regression measurements, are used to show the efficiency that DNNs are at solving the FEM-BPDI. The model's stability and resilience in forecasting disease dynamics are highlighted by a low Mean Squared Error (MSE) that is obtained. Also, the small or negligible Absolute error provides more evidence of the suggested technique's efficacy. This study highlights the critical role that AI-powered Deep Neural Networks play in improving the comprehension and forecasting of fractional epidemiological models in the context of dual population dynamics, providing invaluable insight into the dynamics of disease transmission and ecosystem control.

Keywords: Deep Neural Networks (DNNs), Supervised Learning, Fractional Epidemical Model. Intelligent computing, bio informatics. Infectious diseases.

1. Introduction

Artificial intelligence and mathematical computation experienced an enormous transformation in the last few years with the introduction of Deep Neural Networks (DNNs). Deep neural networks (DNNs), which derive inspiration from the architecture and operations of the human brain, have become highly effective computational tools that can extract intricate relationships and patterns from enormous quantities of data. Advances in a variety of fields, including finance [1], healthcare [2], natural language processing [3], and epidemiology [4], have been driven by their capacity to acquire high-level characteristics and perform highly complex computations. DNNs play a critical role in AI-based statistical analysis because of their capacity to automatically analyze and interpret large amounts of data. This allows researchers to predict outcomes, find patterns in the data, and extract useful intelligence. Through the utilization of sophisticated computational techniques, DNNs enable forecasters to address challenging problems. By applying DNNs to fractional models, new avenues for study and accuracy in forecasting are opened, providing a promising path toward the accurate and efficient handling of complex phenomena. Scientists can find important variables, unearth subtle dynamics, and produce trustworthy forecasts with remarkable accuracy by combining DNNs with fractional models.

The analysis of fractional epidemiological models, in especially, benefits greatly from the use of Deep Neural Networks (DNNs) in the numerical solution of disease transmission models. These models are crucial for comprehending disease dynamics in populations where infection crosses species boundaries, including variations such as the susceptible-infective-susceptible (SIS) model. Researchers can more accurately predict the spread of the disease and the efficacy of control measures by using DNNs to analyze and simulate the complex interactions between susceptible individuals and infected individuals. Our understanding of disease transmission dynamics is greatly enhanced by utilizing the power of Deep Neural Networks (DNNs) in numerical solutions and analyses of fractional epidemiological models. This integration makes it possible to make more accurate predictions, to identify the key variables that influence the spread of diseases, and to develop disease control and prevention strategies that are more successful. By using DNNs, we can find complex patterns in epidemiological data and draw conclusions that can guide healthcare practices, interventions, and public health policies all of which can help reduce the burden of disease and enhance population health outcomes. The literature cited in references [5-10] provides evidence of recent research conducted in the field of intelligence computing.

For a comprehensive understanding of many practical environmental problems, dynamical systems that depict the transmission of infection from prey to predator are essential to study. Complex regulatory effects on the numbers of both predators and prey are produced in predator-prey ecosystems by the interaction between infectious diseases and predator-prey dynamics. In a fractional-order predator-prey model, susceptible predators can become infected from other infected predators as well as from their prey, as this research investigates. More complexity to the system is added by the notable non-reproduction of infected prey and predators. Statistical scientists and environmentalists have long been fascinated by the intricacies of the prey-predator relationship. Outstanding studies have been generated as a consequence, showcasing different kinds of relationships via functional responses. Alfred J. Lotka first created [11] and Vito Volterra [12] then examined the fundamental framework for modeling the interactions between predators and their prey. The foundation for comprehending these dynamic relationships was established by their groundbreaking work, which made it possible to create complex models that are still evolving and offer new perspectives on environmental systems. A range of ecological frameworks are used to thoroughly examine the dynamics of relationships among populations of predators and prey. A wide range of elements are included in these models, including cannibalistic connections, feedback control processes, migratory behaviors, refuges for prey, predator harvesting strategies, stage-structured population dynamics, and diseases that affect both prey and predator populations [13–17]. Mathematical biology extensively studies epidemiological models that deal with infectious diseases within a single species. Since its introduction, the susceptible-infective-recovered (SIR) model by Kermack and MacKendrick [18] has generated a great deal of research interest. Scientists have studied the effects of a variety of factors on populations in the presence of disease, such as cannibalism, feedback control mechanisms, stage-structured populations, supplementary feeding for predators, migration, prey refuges, and predator harvesting. These studies have been conducted in along with significant research on the classical SIR model. Authors have provided significant findings on prey-predator models, in which the disease affects only predator species, in Refs. [19–22]. On the other hand, some research focuses exclusively on disease within prey species using epidemiological models

[23–25]. According to certain studies, parasites can also change the behavior or outward features of their host, rendering it more susceptible to predators [26]. Venturino [27] investigated the dynamics between two rival species when one is afflicted with a disease that does not transcend species boundaries. A susceptible–infective–susceptible (SIS) prey–predator model with logistic growth in the prey species was proposed by Hethcote et al. [28], emphasizing the fact that infected prey are more susceptible to predators. Their study revealed a number of fascinating inferences, showing that coexistence can be fostered by disease in prey species. Interestingly, they provided examples of how the disease's heightened susceptibility among infected prey contributes to its eradication from the environment, where it would otherwise persist as an endemic.

Infections that cross species boundaries are also the subject of study [29–33]. In-depth research is done on the diseases that spread from animals to people, like Severe Acute Respiratory Syndrome (SARS) and avian flu (H5N1), which is caused by a microbe that overcomes the species barrier [34, 35]. COVID-19, the coronavirus that is currently circulating, represents a situation in which the virus spreads from animal hosts to humans and then from humans to humans. This two-way border crossing emphasizes the possible danger that flu viruses present and the continued need for research to clarify how some pathogens come to be able to cross species boundaries [36]. A model of parasite contamination in which the disease transcended species boundaries was studied by K. P. Hadeler [37]. They established a critical limit condition because they understood that infections could spread from prey to predators through predation and that parasites carried by predators could infect prey. This requirement defined the point at which an endemic state could change to a situation that allowed healthy prey and predators to coexist. Another fascinating discovery was that predators could persist through parasitization if they could not survive only on healthy prey in circumstances where they could not cross a certain threshold of transmission.

The study of fractional calculus has drawn more attention from applied mathematics researchers in recent years. This trend has gained traction because fractional calculus can provide a more realistic explanation for physical phenomena. Several studies have shown that when modeling complex and nonlinear phenomena, integer-order differential operators may not always be the best choice. This is due to the fact that classical derivatives frequently miss important physical characteristics like heterogeneous behaviors, random walk behavior, anomalous diffusion, and non-Markovian processes. The idea of local differential operators has been put forth to overcome these drawbacks and accurately depict these natural processes in conjunction with power-law formulations and non-local differential operators. The complexity of the natural world has inspired mathematicians and physicists to create complex mathematical operators that accurately represent and capture phenomena witnessed in the real world. Given that fractional derivatives incorporate memory effects through integration and retain information about past states, their inclusion in the context of evolution equations is especially important. Bolton et al. [38] used a verified dataset to show how fractional-order models are superior in practice to integer-order models.

In the present work, we postulate a scenario in which predators come into contact with infected prey while predating, thus becoming infected. Furthermore, since both infected prey and predators are unable to procreate, our model permits the spread of infection from predator to predator. We present a fractional-order Holling type-II eco-epidemiological model to study this theoretical situation. With the addition of recovery terms and disease transmission between predators, our model is more effective at representing the complex dynamics of prey-predator interactions in ecosystems. Interestingly, the addition of infection spanning species boundaries in both populations adds something new to the body of knowledge on ecological models of disease transmission. By using Deep Neural Networks (DNNs) and doing a comparative analysis afterwards, we reveal how well our work clarifies these intricate dynamics. We are able to better understand these phenomena and offer insightful information for ecological research strategies by utilizing the capabilities of DNNs. Our thorough comparative analysis, made feasible by DNNs, demonstrates the strength and efficacy of our research in clarifying the complex dynamics of ecological systems impacted by the spread of disease. Recent work on intelligent computing has been done in the references [39–45].

The article is divided into two sections: Section 2 explores the basics of fractional derivatives and Section 2.1 presents the mathematical model for predator-prey dynamics. For the suggested Deep Neural Networks (DNNs) technique, Section 3 describes the methodology used in detail. In Section 4, there are discussions about DNN simulations and results from FEM-BPDI. In conclusion, Section 5 provides a summary of the findings.

Nomenclature	
FEM-BPDI	The analysis of fractional epidemiological models in both populations with disease infection
DNNs	Deep Neural Networks

Fde12	fractional differential equation
ɤ	Consistent rate of recruiting for the population of susceptible prey
B_2	The rate at which an illness spreads from infected prey to susceptible predator
B_1	The rate at which an illness spreads from infected prey to susceptible prey
B_3	The rate at which an illness spreads from infected predator to susceptible predator
σ_4	The infected predators' natural death rate
σ_2	The infected prey's natural death rate
σ_3	Susceptible predators' natural death rate
σ_1	Rate of natural death for susceptible prey
ϓ_2	Predation rate of infected preys
ϓ_1	Predation rate of susceptible prey
$\mathit{\Lambda}_1$	The recovery rate of infected prey.
$\mathit{\Lambda}_2$	The recovery rate of the infected predator
â	Rate of half-saturation of susceptible prey
ɓ	Rate of half-saturation of infected prey

2. Mathematical Modeling

These symbols, which stand for $\text{Ñ}_s(\text{ʈ})$, $\text{Ƥ}_s(\text{ʈ})$ and $\text{Ñ}_i(\text{ʈ})$, $\text{Ƥ}_i(\text{ʈ})$, respectively, signify the sizes of the populations of susceptible prey population, susceptible predator population, and infected prey population infected predator population. The symbol for a time variable is t. The following assumptions supported the formulation of the model:

i. When a species of prey comes into contact with ill. prey, it becomes infected.
ii. There are two different ways in which the predator population is infected:
    a) by eating infected prey.
    b) by getting into contact with infected predators.
iii. Prey that is infected as well as predators recover.
iv. The Holling type-II functioning response is a characteristic of the predation pattern displayed by predators.
v. There is a direct correlation between the growth rate of predators that prey on susceptible prey and their own growth rate.
vi. Prey that is infected does not reproduce.
vii. Predators that are infected do not reproduce.
viii. The probability of obtaining healthy prey is lower than that of infected ones, suggesting that $'\Upsilon 2 > '\Upsilon 1$.
ix. The death rate of healthy prey and predators is lower than that of infected ones. So, $\sigma_2 > \sigma_1 \, and \, \sigma_4 < \sigma_3$.

The following is the suggested fractional mathematical model [46]

$$\begin{cases} {}_{\mathrm{t_0}}^{C}D_{\mathrm{t}}^{\tilde{\alpha}}\ \tilde{\mathrm{N}}_s = \text{ɤ} - \sigma_1\tilde{\mathrm{N}}_s - B_1\tilde{\mathrm{N}}_s\tilde{\mathrm{N}}_i + \Lambda_1\tilde{\mathrm{N}}_i - \frac{'\Upsilon 1\tilde{\mathrm{N}}_s(\text{Ƥ}_s+\text{Ƥ}_i)}{1+\hat{a}\tilde{\mathrm{N}}_s} \\ {}_{\mathrm{t_0}}^{C}D_{\mathrm{t}}^{\tilde{\alpha}}\ \tilde{\mathrm{N}}_i = B_1\tilde{\mathrm{N}}_s\tilde{\mathrm{N}}_i - \Lambda_1\tilde{\mathrm{N}}_i - \sigma_2\tilde{\mathrm{N}}_s - \frac{'\Upsilon_2\tilde{\mathrm{N}}_i(\text{Ƥ}_s+\text{Ƥ}_i)}{1+\text{б}\tilde{\mathrm{N}}_i} \\ {}_{\mathrm{t_0}}^{C}D_{\mathrm{t}}^{\tilde{\alpha}}\ \text{Ƥ}_s = \Lambda_2\text{Ƥ}_i + \frac{\dot{e}'\Upsilon_1\ \tilde{\mathrm{N}}_s\text{Ƥ}_s}{1+\hat{a}\tilde{\mathrm{N}}_s} - B_3\text{Ƥ}_i\text{Ƥ}_s - \sigma_3\text{Ƥ}_s - \frac{B_2\tilde{\mathrm{N}}_i\text{Ƥ}_s}{1+\text{б}\tilde{\mathrm{N}}_i} \\ {}_{\mathrm{t_0}}^{C}D_{\mathrm{t}}^{\tilde{\alpha}}\ \text{Ƥ}_i = \frac{B_2\tilde{\mathrm{N}}_i\text{Ƥ}_s}{1+\text{б}\tilde{\mathrm{N}}_i} - B_3\text{Ƥ}_i\text{Ƥ}_s - \sigma_4\text{Ƥ}_i - \Lambda_2\text{Ƥ}_i \end{cases} \tag{1}$$

The following initial conditions are included in the proposed fractional mathematical model:

- $\tilde{\mathrm{N}}_s(\mathrm{t_0}) > 0$,
- $\text{Ƥ}_s(\mathrm{t_0}) > 0$,
- $\tilde{\mathrm{N}}_i(\mathrm{t_0}) > 0$,
- and $\text{Ƥ}_i(\mathrm{t_0}) > 0$.

Where $\mathrm{t_0}$ denotes the beginning of time. All the values of the variables ɤ, σ_1, σ_2, σ_3, σ_4 B_1, B_2, ,$'\Upsilon_1$, $'\Upsilon_2$, Λ_1 and Λ_2 are positive. The following biological interpretations are given in the nomenclature.

3. AI Power Insights Intelligent Computing for Deep Neural Networks

Artificial intelligence has undergone a revolution due to deep learning, which has made machines capable of extraordinary performance across a range of domains. Deep learning models can automatically learn complicated traits and descriptions from raw data by utilizing enormous amounts of data and powerful computational resources, doing away with the need for human feature development. Deep learning is an area of machine learning that mimics the intricate decision-making capabilities of the human brain using multi-layered neural networks, or deep neural networks. Deep Neural networks, or DNNs, are fundamentally simple computationally units that process inputs and generate outputs. After receiving one or more inputs, each neuron adds a weight to the inputs, and then runs the resultant information through an activation function. By including loops in their network architecture, deep neural networks (DNNs) improve on the capabilities of conventional neural networks by enabling them to retain a memory of prior inputs. Because of this property, DNNs work especially well with sequential data, like time series or natural language. However, problems like vanishing and exploding gradients can make training DNNs difficult. These issues occur when gradients that are used to update weights during backpropagation become unnecessarily large or small, which impairs learning.

We first use the fde12 solver to solve fractional ordinary differential equations (ODEs) to develop a dataset for training deep neural networks (DNNs). The complex behaviors governed by fractional ODEs are captured in a robust dataset by the fde12 solver, which is especially good at handling their complexities. The dataset is split into three parts after it is generated: testing, validation, and training sets. This section makes sure the DNNs can validate their learning while in training, learn from the training data efficiently, and then be tested on unseen data to see how well they perform. When training a DNN, the training data is fed into the network, which processes the inputs via several layers of neurons. Every neuron receives inputs that have been weighted and summed, and the output is then processed by an activation function. Here, we employ the Rectified Linear Unit (ReLU) activation function, which adds non-linearity and facilitates the network's ability to process intricate patterns in the data. Convergence is a procedure through which the DNN modifies the weights of the connections between neurons during training to reduce the error in its predictions. Figures 4 to 11 show the outcomes of this training process and demonstrate how well the DNNs were able to model and predict the behavior of the fractional ODEs. These figures show how effective DNNs are as a potent tool for identifying and forecasting intricate dynamic systems. Deep neural networks (DNNs) are used in various frameworks to solve fractional ordinary differential equations that are present in epidemic models. The following is a summary of the main steps in this process.

i. Identify the factors and elements that must be determined or handled into consideration during the initial stage.
ii. The next step involves compiling a dataset of input-output pairs, where the inputs are the parameters and variables related to the epidemic model.
iii. With the dataset given, train the deep neural networks (DNNs). Divide the dataset into training validation and, testing sets. Use optimization algorithms such as gradient descent to iteratively train the DNNs and modify their weights and biases. Reducing the difference between expected and actual results is the goal of this procedure.
iv. Metrics such as R-squared value, mean squared error (MSE), and root mean square error can be used to evaluate the DNN model's efficiency. It may be necessary to make changes to the structure of the model or training parameters to improve effectiveness.
v. To make sure the trained DNN model is accurate and reliable, evaluate its generalization ability using untested data. Confirm the model's effectiveness in a variety of novel scenarios by comparing its predictions to experimental data or well-known solutions.
vi. Repeat steps 2 through 5 to improve the model repeatedly if new data becomes available or if it is not precise.

Activation functions play a crucial role in introducing nonlinearity in Deep Neural Networks (DNNs), which enables models to extract complex patterns from data. Sigmoid, Tanh, and Rectified Linear Unit (ReLU) are examples of common activation functions that have unique characteristics. Rectified Linear Unit, or ReLU, is one of the most popular activation functions in deep learning among them all. By producing zero if the input value is negative and the input value if it is positive, it uses a simple nonlinear transformation. The following is the definition of the equation for ReLU:

$$f(\alpha) = \max(0, \alpha), \tag{2}$$

ReLU's ease of deployment and computational effectiveness make it an attractive option for Deep Neural Networks (DNNs), especially when handling large-scale problems. Its capacity to sustain gradients over several layers contributes to more efficient training by reducing problems such as disappearing gradients that arise with other activation functions. Moreover, ReLU is a mainstay of neural network architectures since it speeds up convergence and lessens overfitting. DNNs effectively capture complex patterns with little computational overhead by utilizing ReLU activation. This guarantees that the system can identify complex connections in the data, which makes for strong predictions and better performance when dealing with difficult tasks. The improved performance attained by using ReLU activation in DNNs is shown in Figures 4 to 11.

Figure 1 presents an overview of the construction of AI-based Intelligent Computing for Deep Neural Networks (DNNs). A multiple-layer flow chart illustrating the technique's computational processes is shown in Figure 2. Figure 3 presents comprehensive descriptions outlining the proposed approach. The numerical results obtained by using deep neural networks are displayed in Table 1. This table presents information about the model's effectiveness and ability to forecast. Table I also provides a comprehensive summary of the model's effectiveness across various parameters and situations related to the FEM-BPDI model, according to simulations performed with Deep Neural Networks (DNNs).

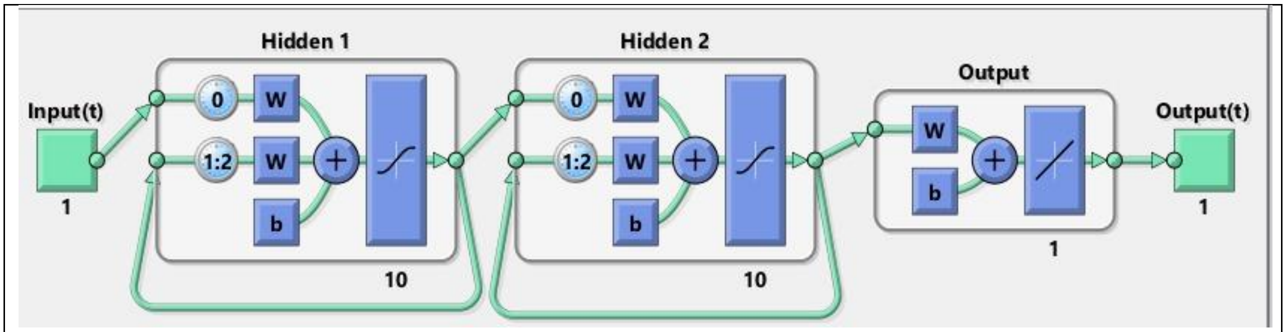


Figure 1: Architecture of AI-based Intelligent Computing for Deep Neural Networks (DNNs).

Table I: Displays the outcomes of Deep Neural Networks (DNNs) simulations for the FEM-BPDI model.

Scenarios	Cases	Performance	Gradient	MU	Time	Epoch
1	1-4	9.36E-12	2.24E-07	1.00E-08	1000	14
2	1-4	2.52E-12	9.87E-08	1.00E-08	445	21
3	1-4	1.85E-11	1.59E-06	1.00E-07	1000	49
4	1-4	9.57E-12	3.15E-04	1.00E-09	1000	47

The results of the Deep Neural Networks (DNNs) simulations for the FEM-BPDI model are shown in Table I. It contains findings for four situations, each of which consists of four different cases and offers in-depth explanations of the outcomes of each case. The results of using Deep Neural Networks $(DNNs)$ to simulate solving the FEM-BPDI model for Scenarios 1 through 4 are shown in Tables 1. These metrics offer a thorough assessment of the predicted accuracy and resilience of the model. Additionally, the metrics expected values for $MSE, MAE, and\ RMSE$ in a perfect or well-fitted model should all be zero, signifying that there is no prediction error. A perfect model fit is highlighted by an R^2value of 1, which denotes perfect correlation between predicted and observed data. Metrics used to evaluate model performance include MSE, MAE, RMSE, NSE, and$R^{2}{}^{2}$. These metrics give a complete picture of the model's predicted accuracy and resilience. In an ideal or completely fitted model, the expected values for MSE, MAE, and RMSE are zero, indicating no prediction error. An R^2 value of 1 indicates a perfect match between expected and observed data. A model is considered accurate and dependable when its MSE, MAE, and RMSE values are near to zero and R^2 is close to one. These statistical findings, which offer a numerical evaluation of model performance, show the data's dependability and credibility. Rough evaluation is made possible by metrics like MSE, $MAE, RMSE, NSE, and\ R^2,$ which guarantee that the model appropriately represents the underlying patterns in the data. The reliability and consistency of the predictions are confirmed by low values of MSE, MAE, and RMSE in conjunction with a highR^2, which strengthens the trust in the data and the predictive power of the model.

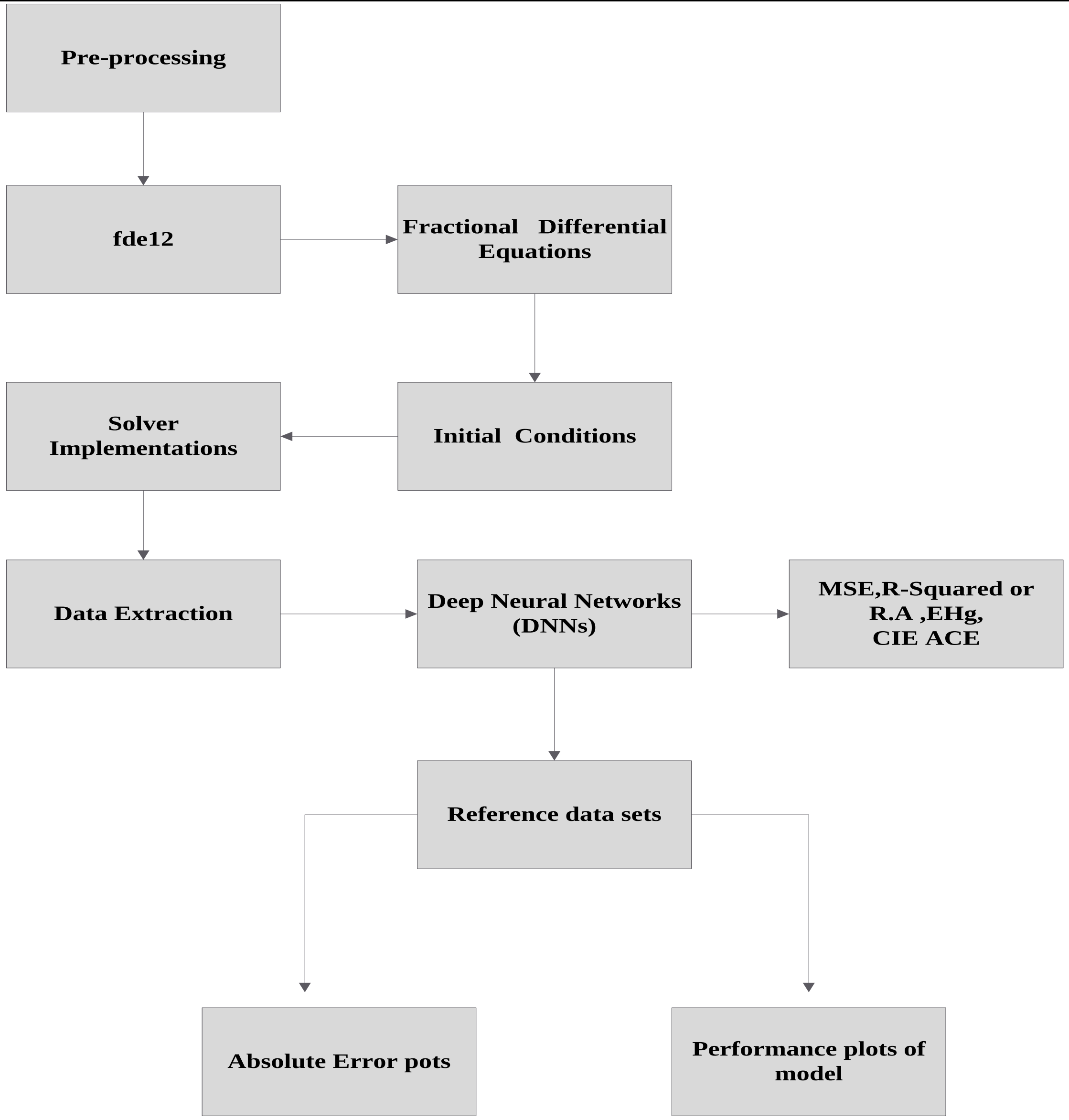
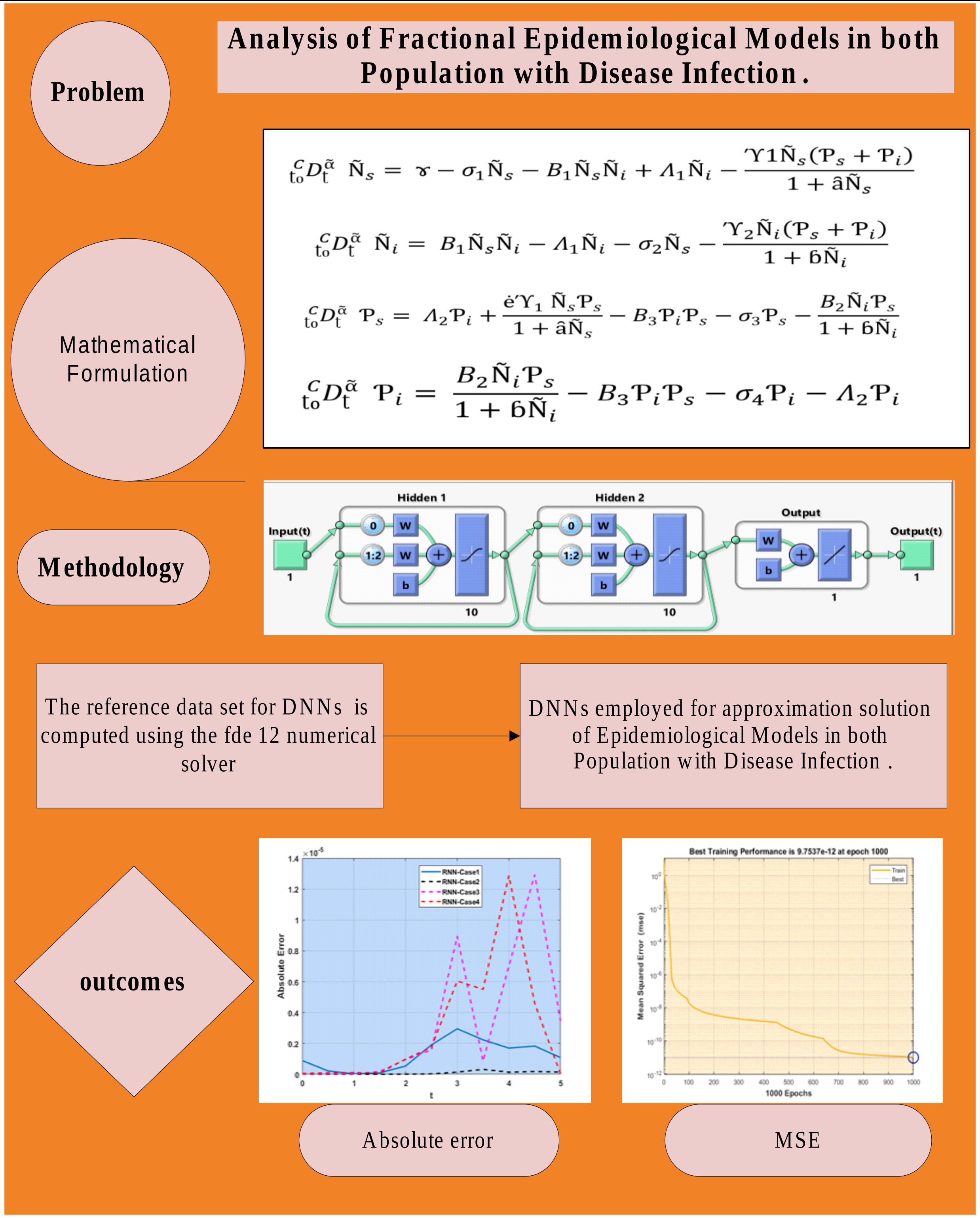


Figure 2: A multiple-layer flow chart illustrating the technique's computational processes



Problem

Analysis of Fractional Epidemiological Models in both Population with Disease Infection.

Mathematical Formulation

$$
\begin{aligned}
{}_{t_0}^{C}D_t^{\tilde{\alpha}}\ \tilde{N}_s &= ɤ - \sigma_1\tilde{N}_s - B_1\tilde{N}_s\tilde{N}_i + \Lambda_1\tilde{N}_i - \frac{\Upsilon 1\tilde{N}_s(Ƥ_s + Ƥ_i)}{1 + \hat{a}\tilde{N}_s}\\
{}_{t_0}^{C}D_t^{\tilde{\alpha}}\ \tilde{N}_i &= B_1\tilde{N}_s\tilde{N}_i - \Lambda_1\tilde{N}_i - \sigma_2\tilde{N}_s - \frac{\Upsilon_2\tilde{N}_i(Ƥ_s + Ƥ_i)}{1 + б\tilde{N}_i}\\
{}_{t_0}^{C}D_t^{\tilde{\alpha}}\ Ƥ_s &= \Lambda_2Ƥ_i + \frac{\dot{e}\Upsilon_1\ \tilde{N}_sƤ_s}{1 + \hat{a}\tilde{N}_s} - B_3Ƥ_iƤ_s - \sigma_3Ƥ_s - \frac{B_2\tilde{N}_iƤ_s}{1 + б\tilde{N}_i}\\
{}_{t_0}^{C}D_t^{\tilde{\alpha}}\ Ƥ_i &= \frac{B_2\tilde{N}_iƤ_s}{1 + б\tilde{N}_i} - B_3Ƥ_iƤ_s - \sigma_4Ƥ_i - \Lambda_2Ƥ_i
\end{aligned}
$$

Methodology

The reference data set for DNNs is computed using the fde 12 numerical solver

DNNs employed for approximation solution of Epidemiological Models in both Population with Disease Infection .

outcomes

Absolute error

MSE

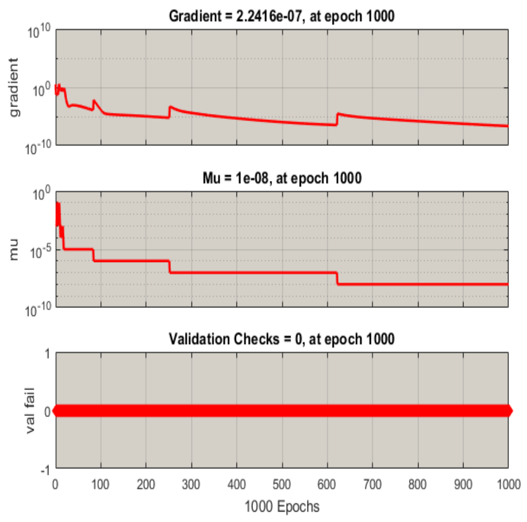
Figure 3: Presents comprehensive descriptions outlining the proposed approach.

4. Results and discussions

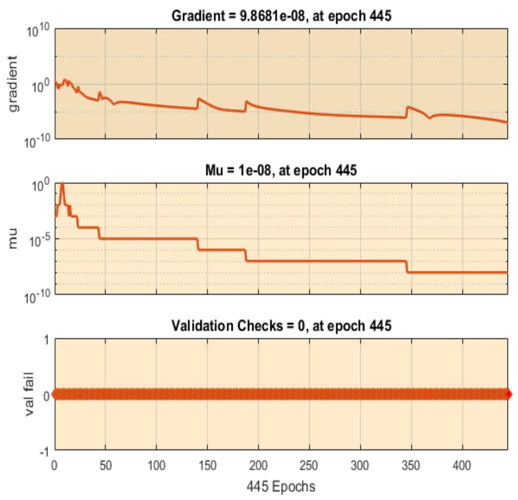
The evaluation and clarification section of our research on Deep Neural Networks (DNNs) is very important since it is essential for efficiently classifying and analyzing data. A brief synopsis of the empirical results obtained from using DNNs is provided in this section. The profound implications and ramifications of these findings are then thoroughly discussed, with an emphasis on neural networks, to clarify their applicability to both the larger field of artificial intelligence and the study's purpose. We support further investigation, optimization, and development of DNN structures and their diverse applications. We highlight the significance of continued research and development efforts aiming at maximizing DNN efficiency, supporting interpretability, and broadening their applicability across various domains by explaining the way our findings act as a catalyst for raising the bar within artificial intelligence. The revolutionary potential of DNNs in driving creative developments in AI deserves special attention. DNNs are a key component in the development of intelligent systems because they enhance the capacity for sequential data analysis and decision-making. The principal aim of this study is to clarify the best approaches for handling the complexities present in epidemiological models by utilizing deep neural network (DNN) techniques. The main goal is to gain a thorough understanding of these models so that disease dynamics may be analyzed and predicted more accurately. The dynamical system's impressive results are shown in Figure 4, which demonstrates the use of transition states (TS). In particular, the dynamical model's observed gradients, which are measured as 2.24E-07, 9.87E-08, 1.59E-06, and 3.15E-04, are strong indicators of the model's dependability and resilience in terms of faithfully capturing the dynamics of the Epidemiological Model. By incorporating transition states, the model demonstrates an improved ability to represent the complex nuances and variations present in the course of the disease. Scientists can feel confident using the dynamic Epidemiological Model in their future research endeavors because of the clear and concise visual representations provided in Figure 4. The minimal Mean Squared Error (MSE) is shown in Figure 5 as a graphic depiction of the way well the model captured the dynamics of the system under investigation. The remarkably low mean square errors (2.24E-07, 9.87E-08, 1.59E-06, and 3.15E-04, respectively) at epochs 14, 21, 49, and 47 verify the model's strong performance in predicting target values during critical training stages. These findings support the model's dependability and practical applicability by highlighting its remarkable flexibility and potential for advancement. An important metric for assessing the reliability and efficacy of deep neural networks (DNNs) is the correlation between the input and error (CIE).

The correlation values between -20 and 20 lag periods are plotted on the graph. The y-axis measures the strength of the correlation, while the x-axis indicates the lag, or offset in the data point sequence. The temporal dynamics within DNNs can be profoundly understood through the CIE analysis, as illustrated in Figure 6. The network may be capturing some periodic or recurrent patterns in the input data, according to the cyclical pattern of correlations. By better understanding these correlations, the architecture and training procedure of the model can be improved, potentially improving its predictive ability and decreasing errors. The baseline for zero correlation is shown by the black dashed line. Deviations from this line show that the input has a quantifiable effect on the error. The majority of correlations fluctuate around this baseline, but at some lags, noticeable deviations become apparent, suggesting a large input influence.

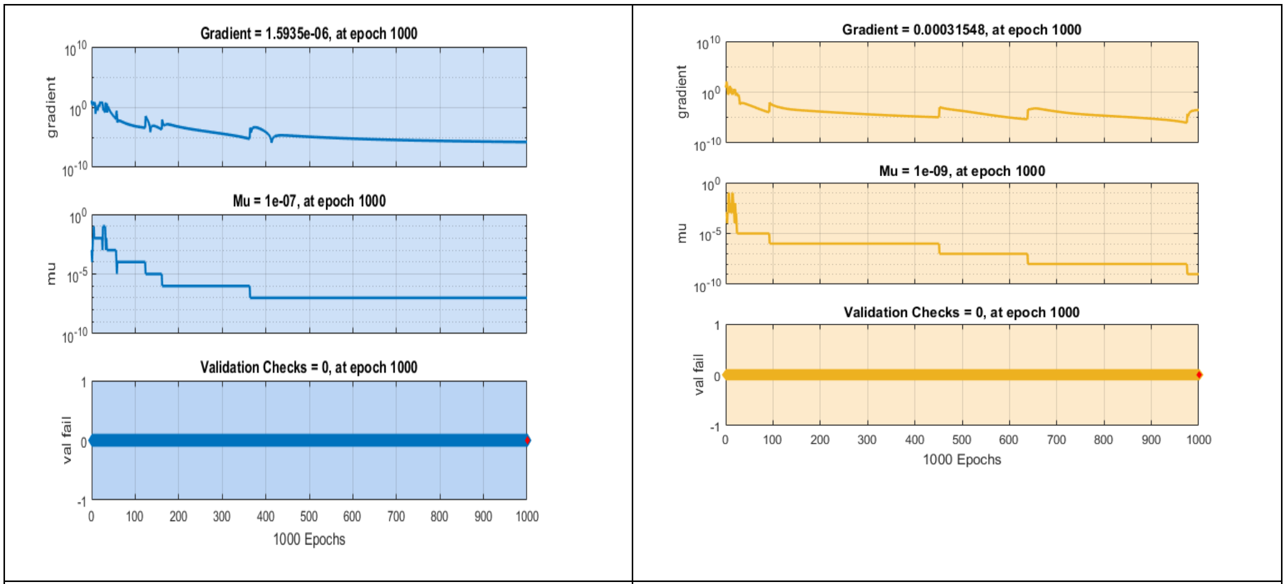
The significance of comprehending temporal dependencies in deep neural networks (DNNs) is highlighted by the graph. We are able to determine which historical inputs have a significant influence on the predictions made today by examining the correlation between input lags and errors. This realization is critical to enhancing the predictive accuracy and optimizing the model construction because it identifies critical time points that affect network performance and provides guidance for better feature engineering and data preprocessing techniques. The correlation analysis plays a crucial role in optimizing the efficiency of deep learning models, managing temporal dependencies, and improving their entire reliability. Figure 7 shows the auto-correlation of error (ACE) for deep neural networks (DNNs) at various lags. The y-axis indicates the auto-correlation values, and the x-axis shows the lag period, which runs from -20 to 20. The temporal dependencies within the errors are displayed on the graph, demonstrating how previous errors affect subsequent ones. Prominent peaks and troughs suggest enduring error patterns by indicating significant auto-correlation at particular lags. The critical lags where error correlation is significant are highlighted by the red dotted lines, which represent the confidence limits. Values outside of these ranges are statistically significant. By addressing error persistence and improving temporal prediction accuracy, this analysis is essential for optimizing DNN performance. The error histogram (Er.H) for a variety of deep neural network (DNN) cases is shown in Figure 8. The range of prediction errors is shown by the x-axis, and their frequency is indicated by the y-axis. The histogram shows the concentration and dispersion of departures from the actual targets, offering insights into the distribution of prediction errors. Whereas a wider distribution denotes notable deviations, a high frequency of errors closes to zero indicates good prediction accuracy. The histogram peaks indicate typical error magnitudes, and the tails indicate instances of extreme errors. For the DNN models to function better overall and be more robust, this analysis is essential for identifying and eliminating biases. The Time Series Response Plots (TSRP) using Deep Neural Networks (DNNs) for all Cases are shown in Figure 9. The graph provides insights into the behavior and performance of the DNN models in a variety of situations by illustrating the dynamic response trends over time. The Regression Analysis (RA) results using Deep Neural Networks (DNNs) for all Cases are shown in Figure 10. The graph, which illustrates the relationship between input variables and predicted outcomes through regression analysis, clarifies the efficacy and predictive power of the DNN models in a variety of scenarios. Regression analysis (RA) in Figure 10 also shows an excellent match of the data points with the regression line, suggesting strong accuracy in forecasting. The data points' closeness to the line indicates that the Deep Neural Networks (DNNs) used in the various Cases have strong capacity for prediction. Additionally, the analysis highlights the way the DNN models capture and explain the variance in the data, supporting their dependability for forecasting tasks, with an R-Square value that approaches 1.



a) Training state of CI



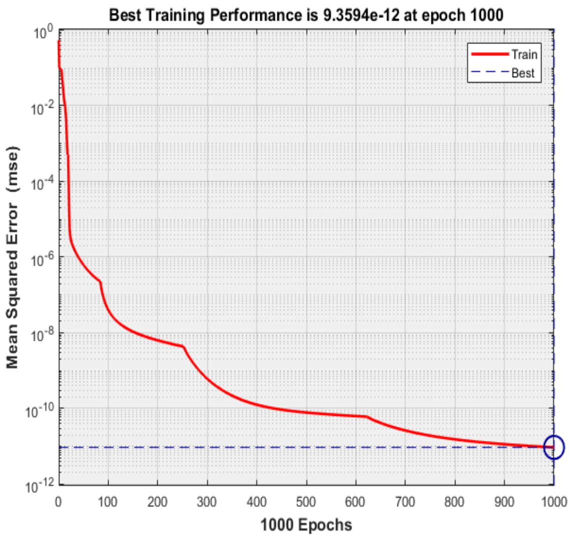
b) Training state of CII



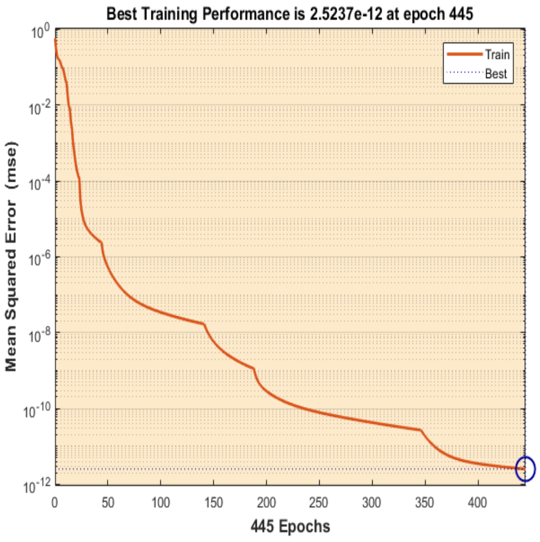
c) Training state of CIII

d) Training state of CIV

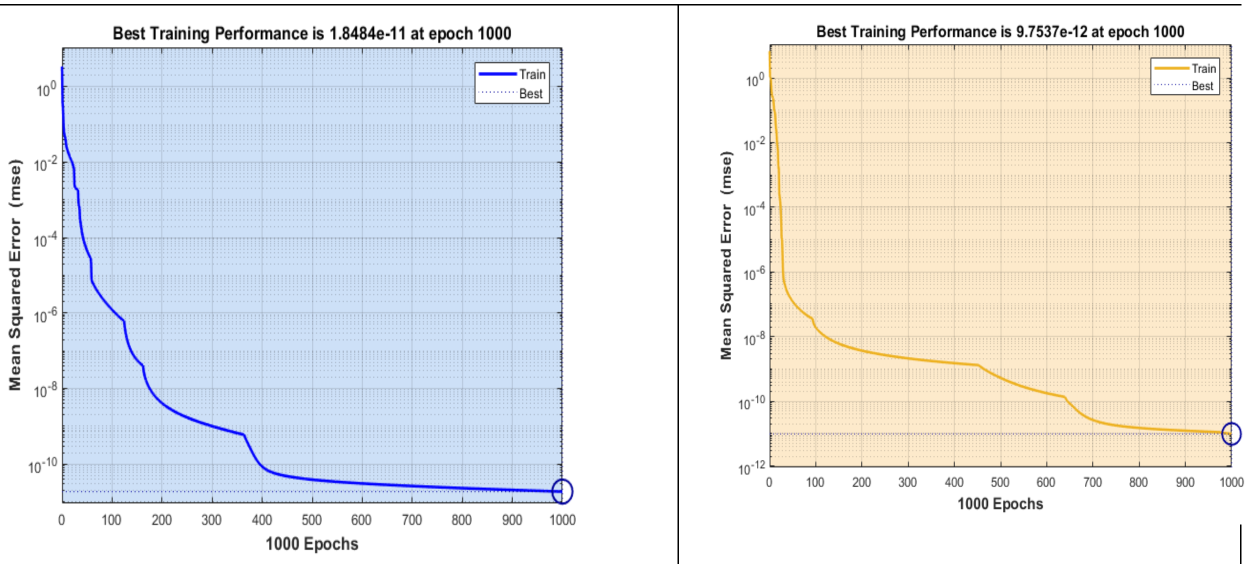
Figure 4: Training state (TS) representations for all Cases adopting DNNs.



a) MSE for CI



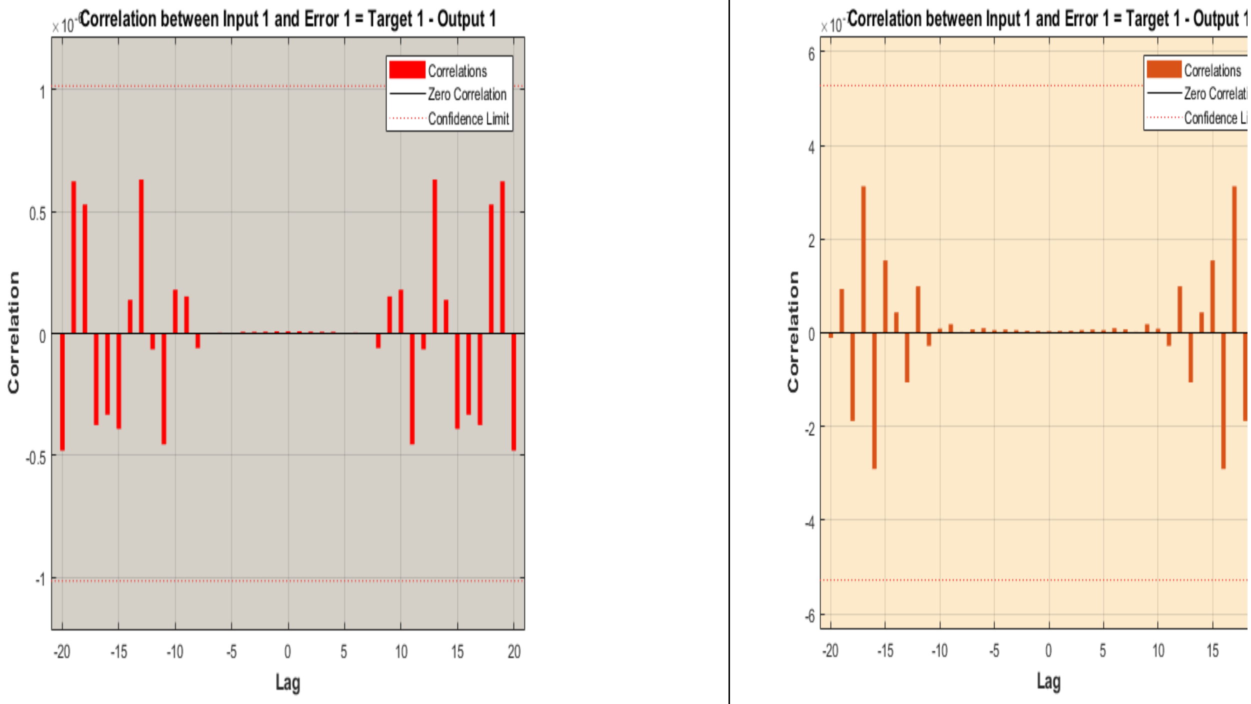
b) MSE for CII



c) MSE for CIII

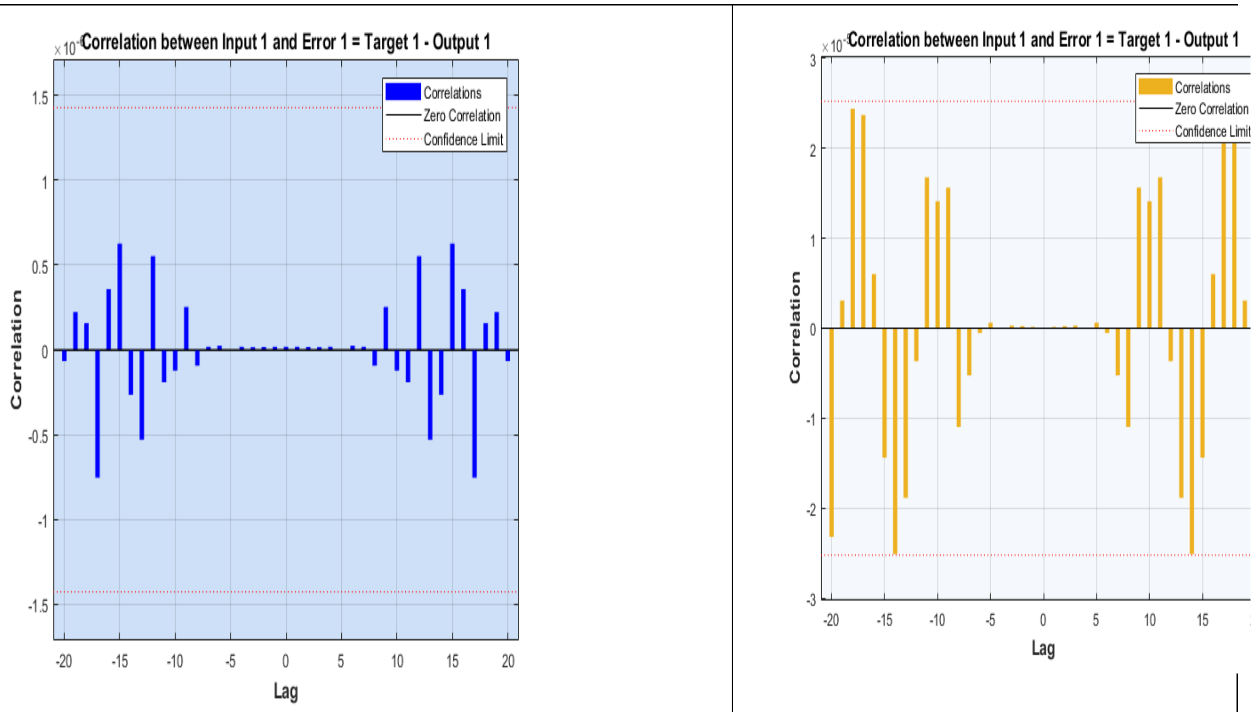
d) MSE for CIV

Figure 5: Mean Square Error (MSE) representations for all Cases adopting DNNs.



a) CIE for CI

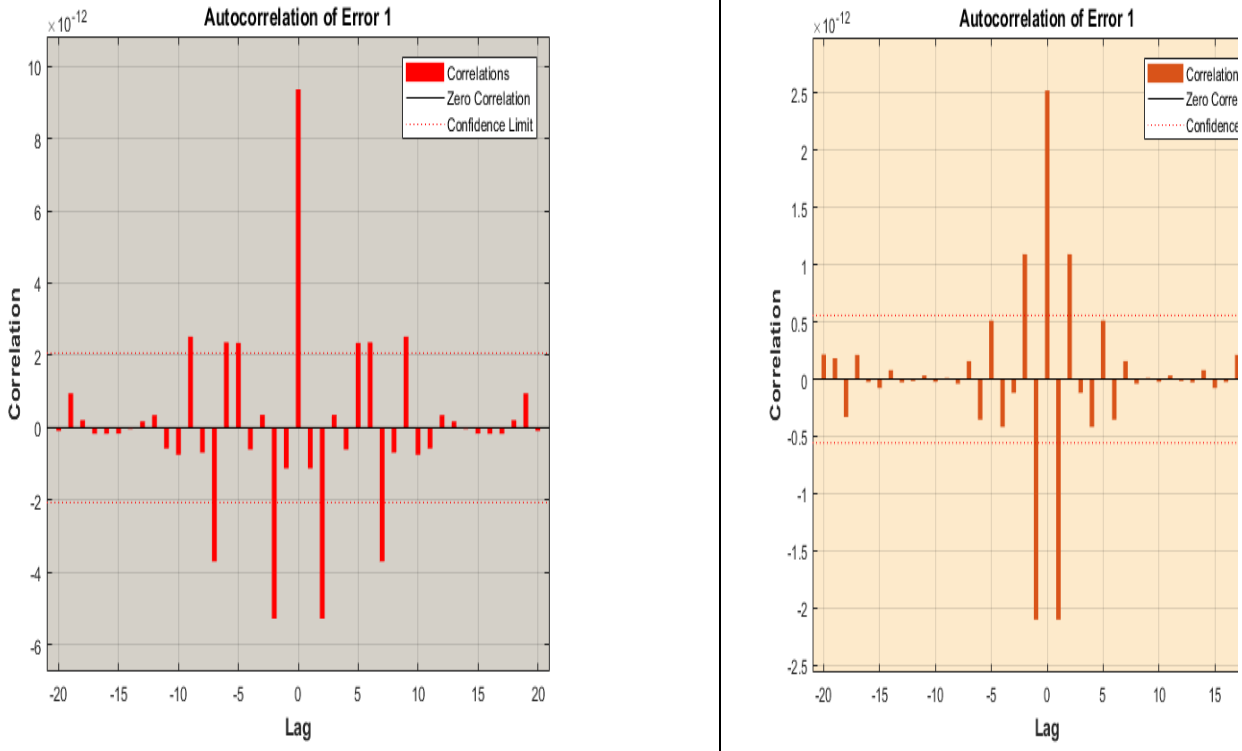
b) CIE for CII



c) CIE for CIII

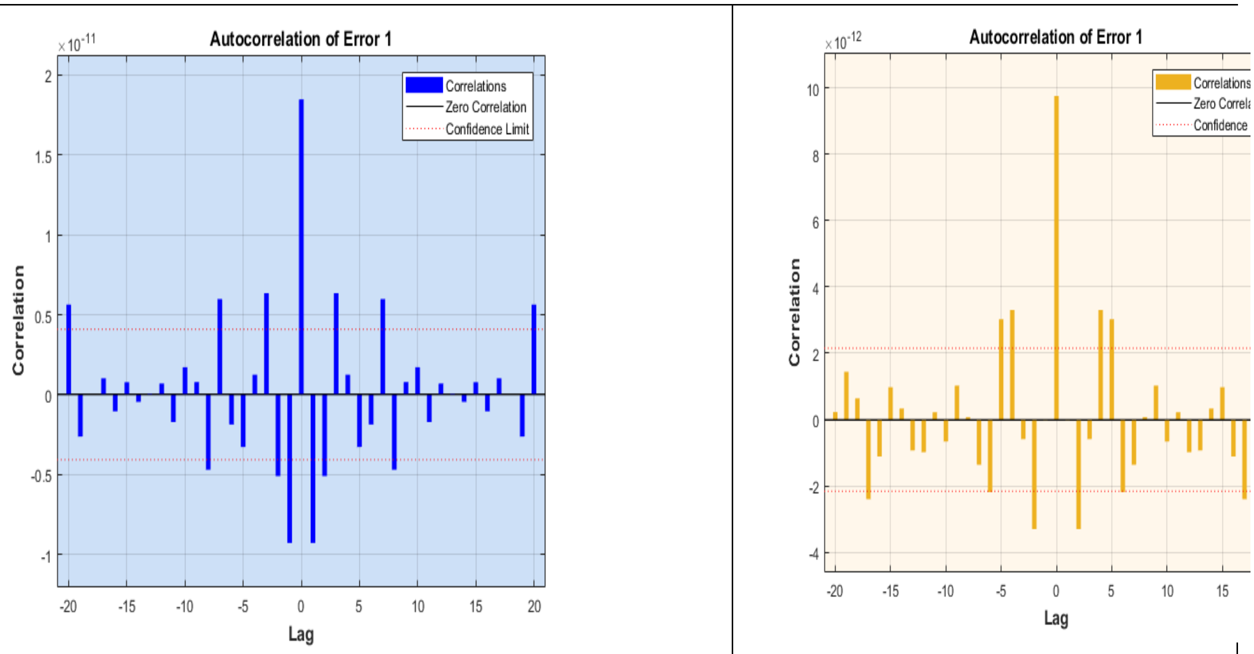
d) IE for CIV

Figure 6: Correlation Input and Error (CIE) for all Cases adopting DNNs.



a) ACE for CI

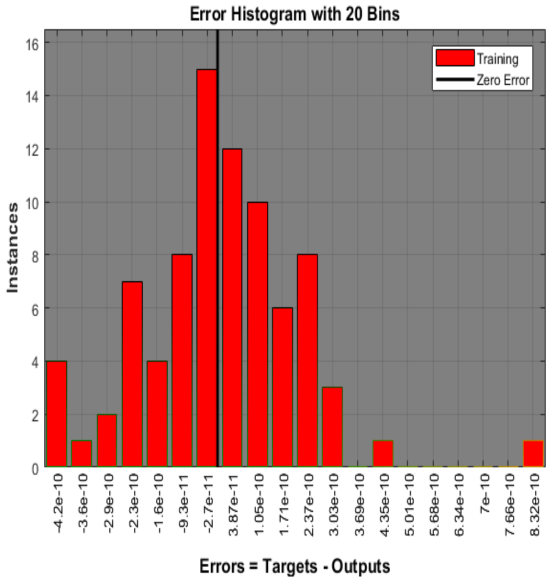
b) ACE for CII



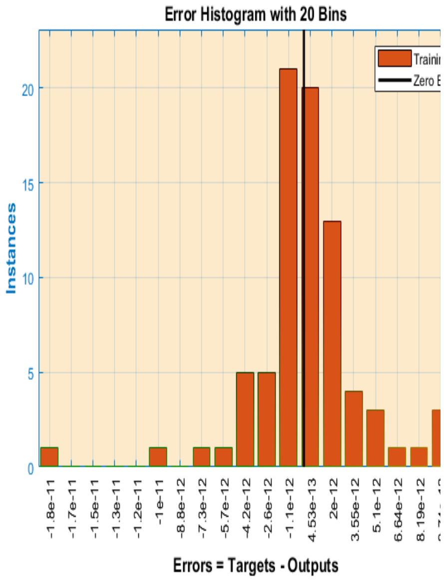
c) ACE for CIII

d) ACE for CIV

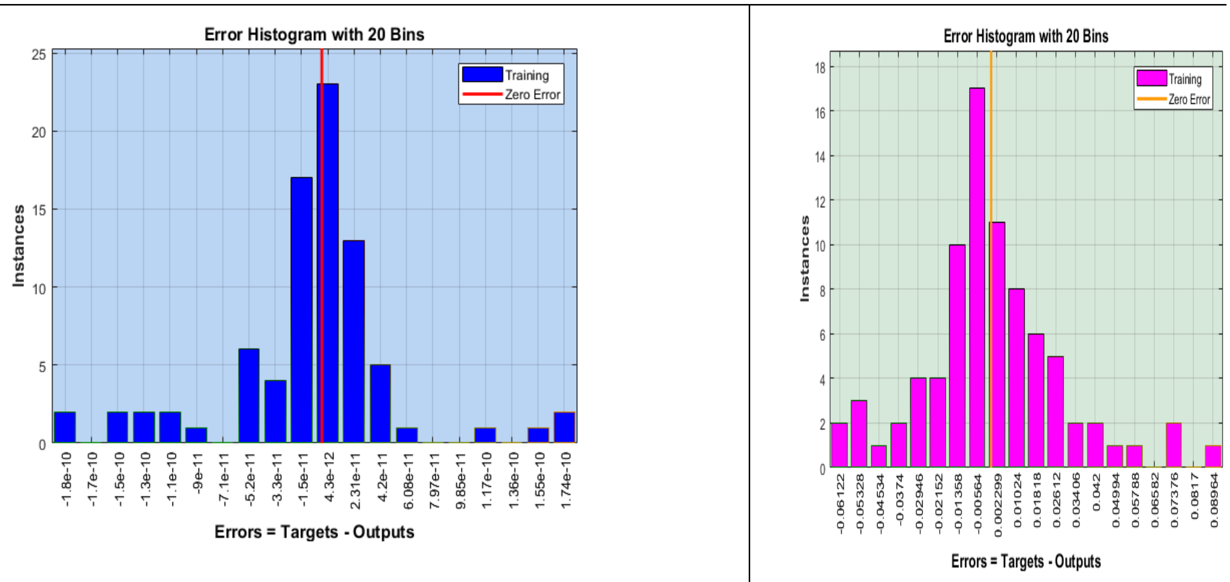
Figure 7: Auto-Correlation of Error (ACE) for all Cases adopting DNNs.



a) (EHg) Analysis for CI



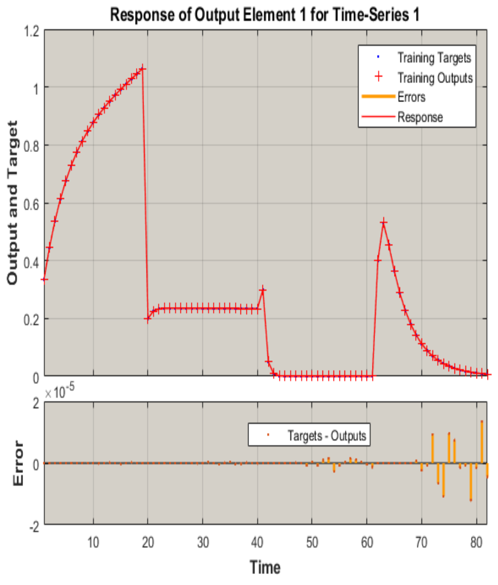
b) (EHg) Analysis for SII/CI



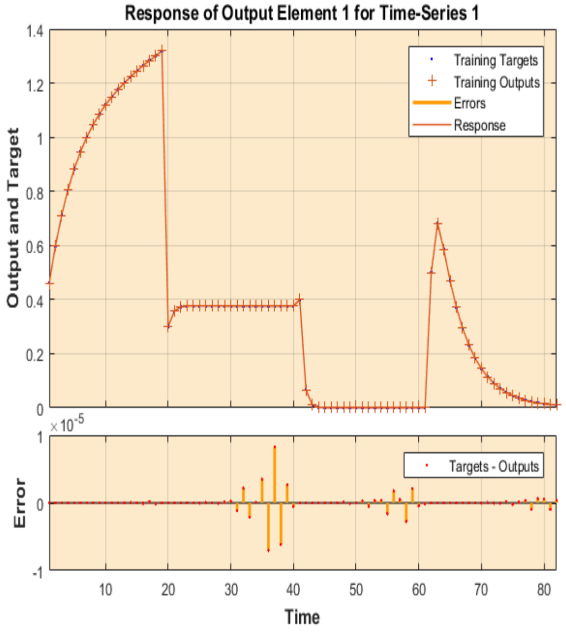
c) (EHg) Analysis for SIII/CI

d) (EHg) Analysis for SIV/CI

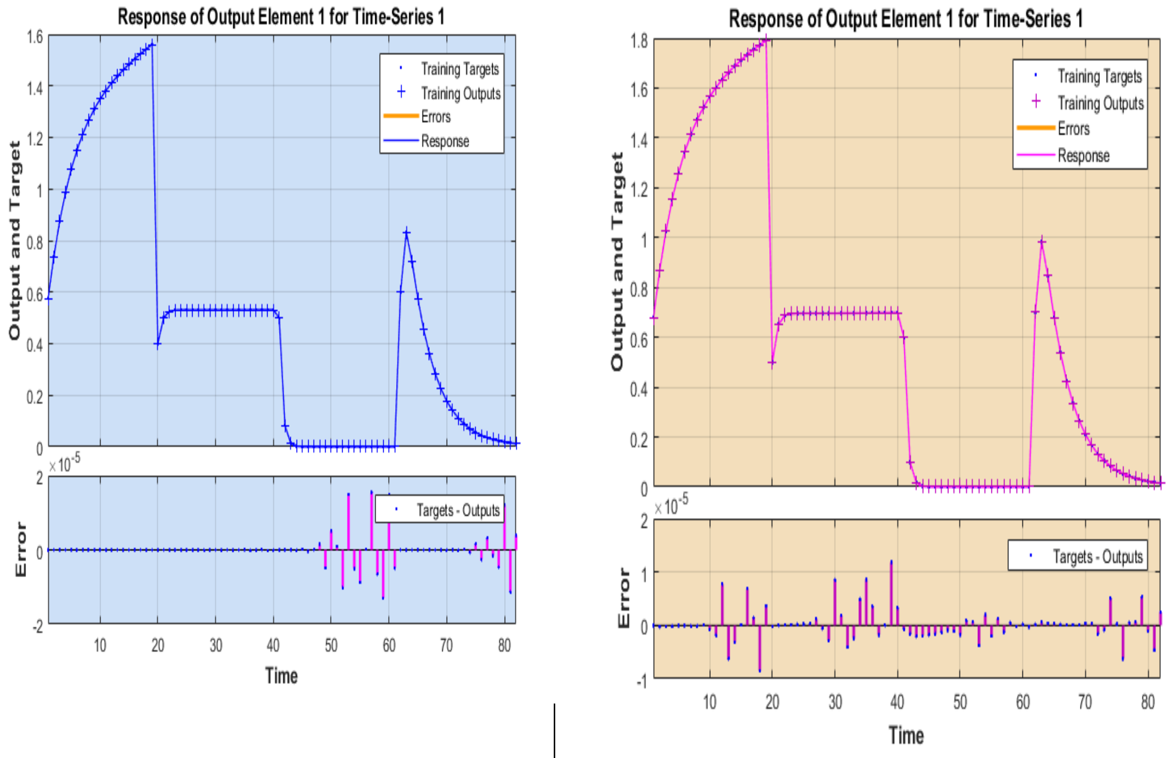
Figure 8: Error Histogram (Er.H) representations for all Cases adopting DNNs..



a) TSRP for CI



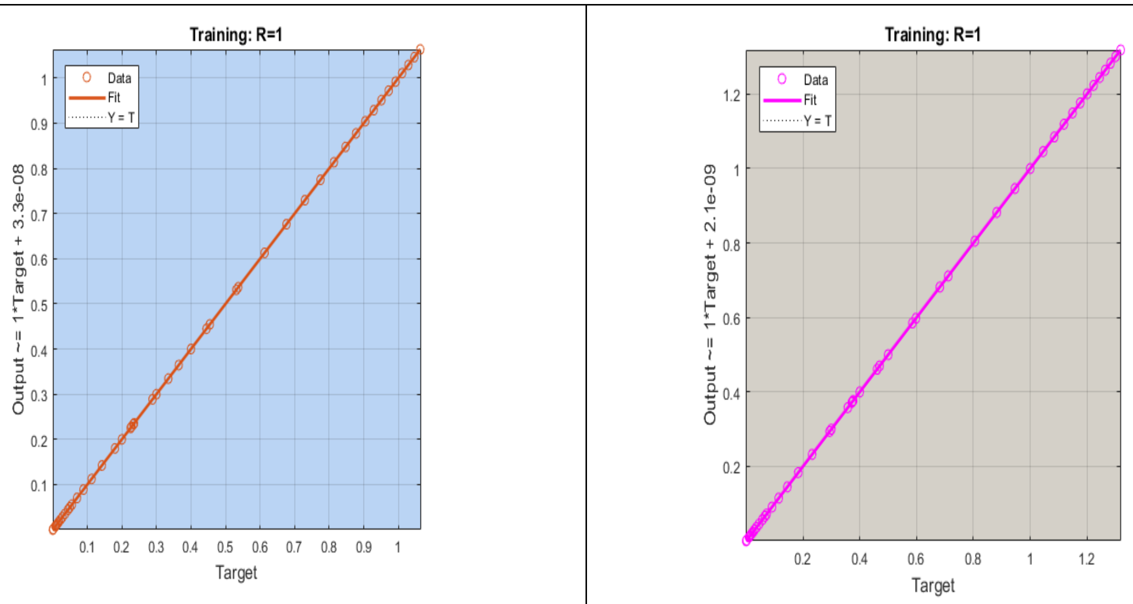
b) TSRP for CII



c) TSRP for CIII

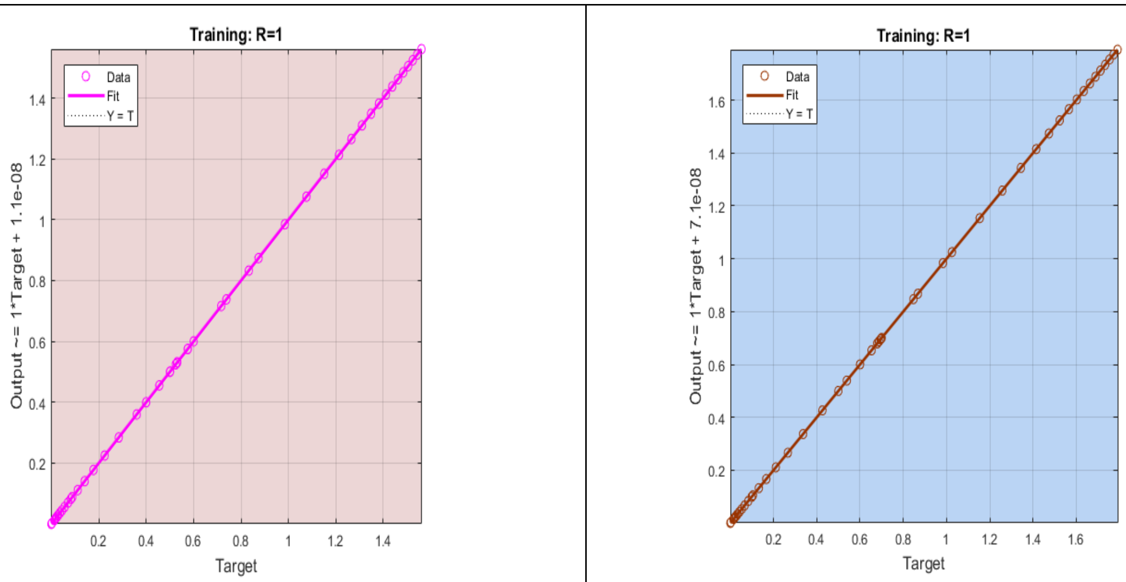
d) TSRP for CIV

Figure 9: Time series response plots (TSRP) for all Cases adopting DNNs.



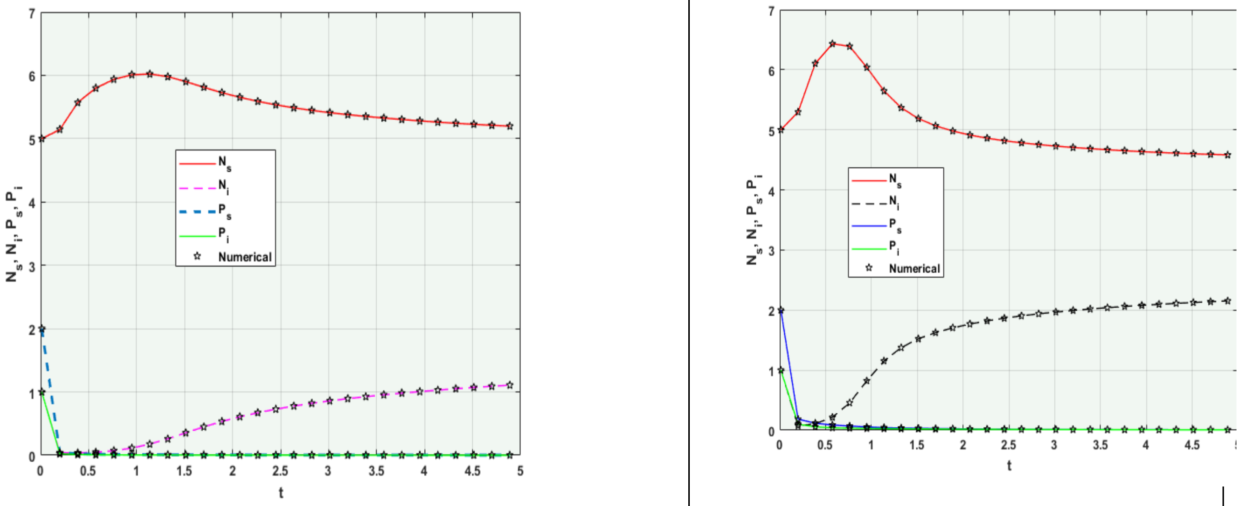
a) RA for SI/CI

b) RA for SII/CI

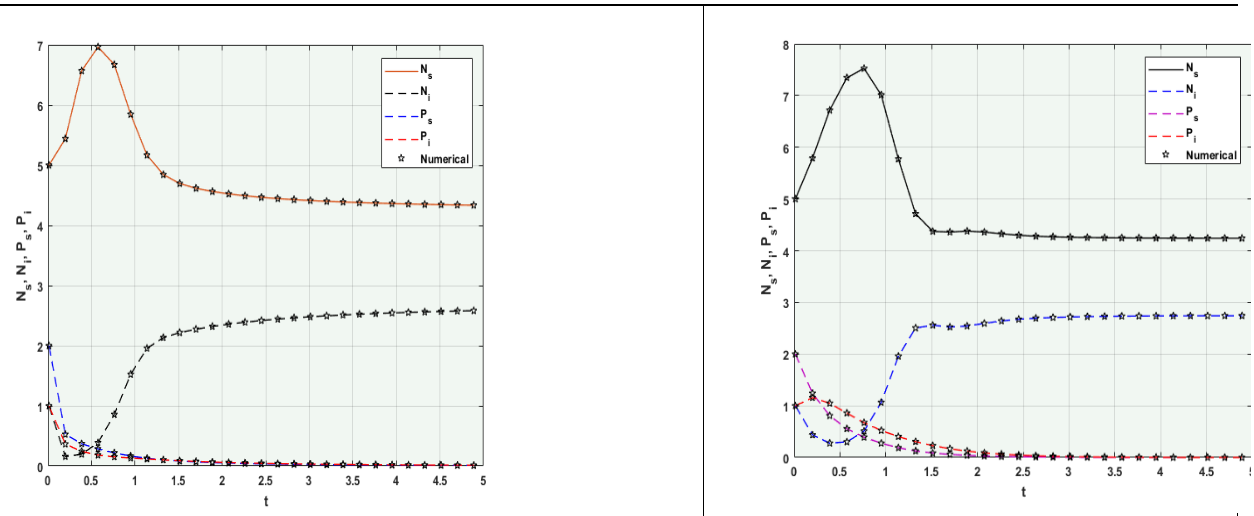


c) RA for SIII/CI **d) RA for SIV/CI**

Figure 10: Regression analysis (RA) for all Cases adopting DNNs.



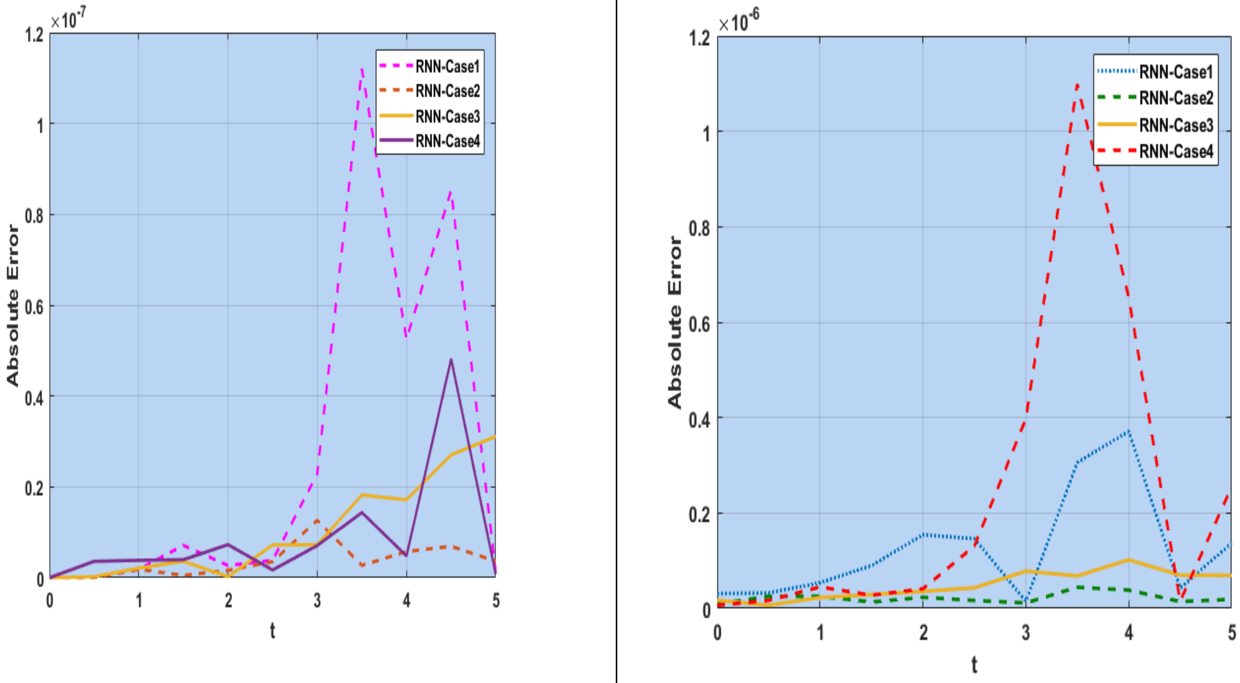
a) Case-I **b) Case-II**



c) Case-IIII

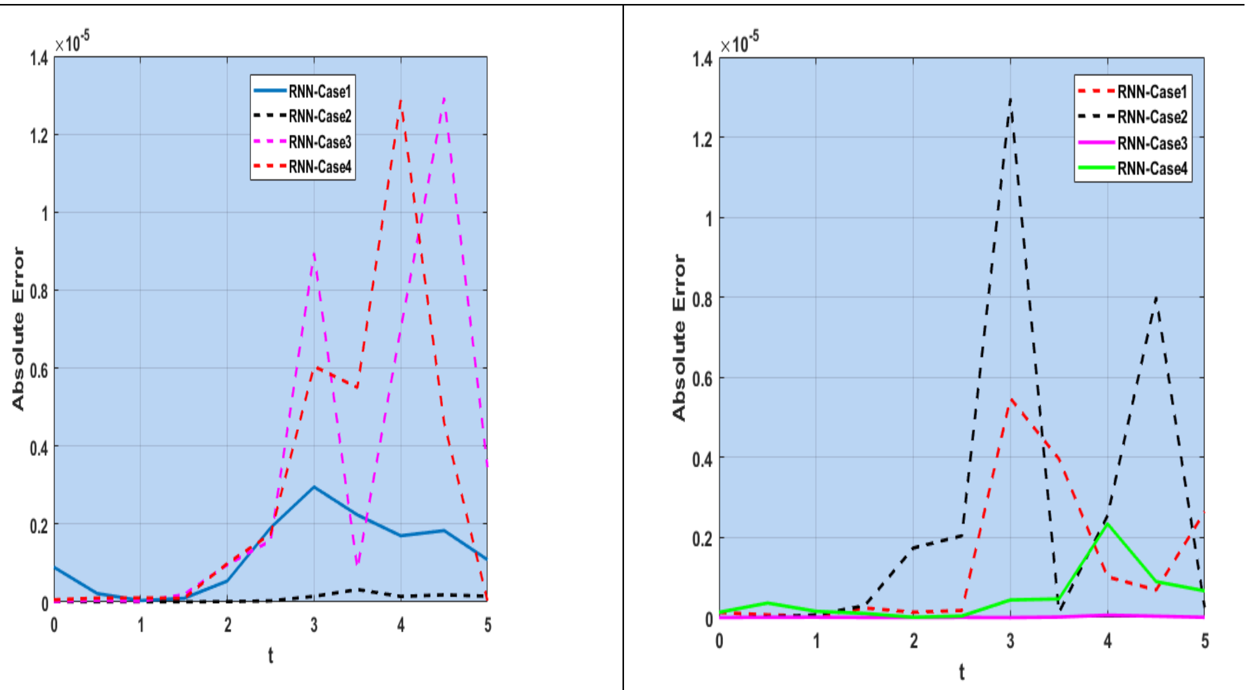
d) Case-IV

Figure 10: Comparisons measures using AI based DNNs procedure to solve FEM-BPDI **model.**



a) Ab. Err: Case-I

b) Ab. Err: Case-II



c) A.Er : Case-III

d) Ab. Err: Case-IV

Figure 11: Ab. Err using the stochastic DNNs procedure to solve the FEM-BPDI model.

The graphical simulations that illustrate the comparison of AI-based Deep Neural Networks (DNNs) used for FEM-BPDI model solving are presented in Figure 10. Four different cases, each with fractional orders of 0.25, 0.50, 0.75, and 1.0, were simulated using the fde12 solver. The objective was to evaluate the way the DNN process performed in generating a target solution that, based on empirical data, not only fit the reference solution but also showed superior predictive ability. An analysis of four different cases is shown in Figure 10, where the FEM-BPDI epidemiological model is solved by AI-based Deep Neural Networks (DNNs). These stars represent solutions that the DNN procedure effectively predicted, demonstrating its exceptional capacity to match reference solutions with strong forecasting abilities. This graphical illustration highlights the way DNNs perform in producing reliable and precise results in the complicated realm of the FEM-BPDI model. A sign of the AI approach's strong reliability is the close match between the numerical solutions and the DNN predictions. This alignment demonstrates the ability of DNNs to precisely represent the complex dynamics of epidemiological models. This represents an important step in the application of AI to epidemiological modeling and forecasting, as the efficacy of the DNN methodology in solving the FEM-BPDI model. Absolute error is the term used to describe the difference between the actual observed values in the dataset and the predicted values produced by the DNN model when using Deep Neural Networks (DNNs) for modeling and prediction. By calculating the amount of the difference between the model's predicted values and the actual values, it can be used to determine the precision of the model. Because the DNN model predicts things accurately and reliably, it is important to achieve the lowest possible absolute error. The model performs better and has higher precision when its absolute error is smaller, indicating that its predictions are closer to the actual observed values. In many applications, especially those involving finance, healthcare, and engineering, where accurate forecasts are critical to the process of making decisions, minimizing absolute error is paramount. As a result, the DNN model's ability to precisely capture the underlying patterns and relationships in the data is indicated by the smallest absolute error, which generates predictions and decisions that are more trustworthy. Figure 11 presents a Absolute Error (Ab. Err) produced during the FEM-BPDI model solving process using stochastic Deep Neural Networks (DNNs). This minimal absolute error performs as a crucial metric that illustrates the effectiveness of the suggested method. The graph illustrates the efficacy and accuracy of the stochastic DNNs approach in obtaining precise solutions in the empirical domain of the FEM-BPDI model, thus emphasizing its potential for both scientific advancement and practical application. The achievement of a minimal absolute error provides strong evidence of the effectiveness of our suggested method, highlighting its dependability and resilience. This result not only validates the correctness of our method but also emphasizes how it can completely change current practices. This kind of success acts as a catalyst for more research and application of this novel method across a range of scientific fields.

5. Conclusion

Mathematical modeling has become a very popular tool for understanding and analyzing the spread and control of infectious diseases as a result of the increase in environmental contamination. As a result, to depict complex scenarios, the literature offers a wide variety of intricate models for epidemics and predator-prey relationships. To the best of our knowledge, no prior research has included the use of a fractional derivative in a predator-prey model that includes disease dynamics in both species. This work offers new insights into the complex relationships between infection and population dynamics by discussing the formulation and implications of such a fractional-order predator-prey model. An important finding is that the disease can be eliminated from the system by increasing the attack rate of infected prey. On the other hand, the vulnerable population of predators can be preserved from disappearance by lowering the order of the fractional derivative. These results unequivocally show that the fractional derivative is an important factor in regulating the dynamics of the system under consideration. In this work, we effectively showcased the use of deep neural networks (DNNs) for fractional epidemiological model analysis and simulation in disease-infected populations. Our method makes use of DNNs' learning and computational power to simulate the complex dynamics present in fractional-order systems, which are becoming more and more known for their capacity to represent memory and genetic characteristics in epidemiological processes. Our models' outcomes show that DNNs can efficiently approximate fractional differential equation solutions, giving researchers and public health officials a useful tool to more precisely forecast the course of infectious diseases. The following are our main findings:

- Beyond the capabilities of traditional integer-order models, the DNNs demonstrated superior accuracy in simulating the complex behaviors of fractional-order systems, which is relevant to disease dynamics in the real world.
- The efficacy of the suggested approach in simulating diverse epidemiological scenarios suggests its adaptability to a range of infectious diseases.
- By employing DNNs, computational complexity was greatly decreased, increasing the viability and efficiency of analyzing large-scale epidemiological data.
- Time series plots show how well the data was handled and how precisely outcomes were obtained.
- The developed DNNs show effectiveness, dependability, and robustness throughout the computation, as shown by getting mean squared error regression matrices, and histogram error representations. The reliability and efficacy of the models are further supported by time series plots, autocorrelation graphs, and correlation input-by-error plots.
- A model's stability is indicated by a low Mean Squared Error (MSE), which reflects the model's accuracy and resilience in making predictions.
- The model's strength is demonstrated by the achievement of minimal or negligible absolute error, which shows how well-predictive and precise it is at gathering data patterns.

An important development in the computational study of infectious diseases is the combination between fractional epidemiological models and deep neural networks. Scientists and public health officials can use this novel approach as a powerful tool to enhance disease prediction, control, and prevention approaches. To further validate the predictive power of the suggested model and evaluate its applicability in various epidemiological contexts, future research could investigate the integration of real-world data. The performance and generalizability of the model for more precise disease forecasting may also be improved by looking into possible improvements to neural network topologies and training approaches.

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