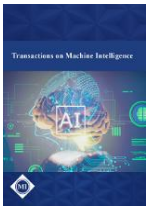
Transactions on Machine Intelligence 2(3) (2019) 128-140

ISSN Online: 2821-1693

Transactions on Machine Intelligence

Journal Homepage: https://tmachineintelligence.ir/index.php/TMI



Predicting the Severity of Non-Alcoholic Fatty Liver Disease Using ANFIS Optimized by Particle Swarm Optimization and Genetic Algorithm

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ARTICLE INFO

Article History:
Received 2 June 2019
Received in revised form 11 July 2019
Accepted 4 September 2019
Available online 5 September 2019

Keywords:
Liver Disease, ANFIS Algorithm, Particle Swarm Optimization Algorithm, Genetic Algorithm, Classification

ABSTRACT

The liver is a vital organ and the largest gland in the human body, responsible for numerous essential functions such as metabolism, digestion, protein synthesis, and the removal of harmful toxins. It plays a central role in maintaining overall health and ensuring the body's proper functioning. Malfunction or damage to the liver can lead to a variety of serious health issues, including liver failure, cirrhosis, and fatty liver disease, all of which can significantly impact a person's quality of life and life expectancy. Early detection and accurate diagnosis of liver diseases are crucial for timely treatment, prevention, and minimizing the risk of further complications. Traditional diagnostic methods for liver diseases often involve invasive procedures, which can be expensive, time-consuming, and uncomfortable for patients. This research explores an innovative, non-invasive approach to diagnose and assess the severity of fatty liver disease by analyzing blood test results. The study applies various advanced techniques, including the Adaptive Neuro-Fuzzy Inference System (ANFIS), ANFIS combined with Particle Swarm Optimization (PSO), and ANFIS with Genetic Algorithms (GA), to a dataset collected from the Tabriz University research center. These methods are compared in terms of their accuracy and efficiency in predicting the severity of fatty liver disease, providing valuable insights into the potential of machine learning algorithms for medical diagnostics. The findings aim to contribute to the development of more accessible, cost-effective, and non-invasive diagnostic tools for liver diseases.

1. INTRODUCTION

In recent decades, scientific advancements have increasingly focused on utilizing artificial intelligence and various machine learning algorithms to predict and prevent diseases at early stages, thereby reducing potential treatment costs and mortality rates [1-10]. Liver diseases, among these, affect diverse segments of the population. Because symptoms of liver disease often remain hidden for years, progressively impairing bodily functions, early

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http://dx.doi.org/10.47176/TMI.2019.128

diagnosis is particularly crucial in today's society. Physicians continuously seek various methods to predict this disease statistically and probabilistically in different patients to enable timely prevention and treatment.

For the first time in this paper, the severity of liver disease is determined using blood test results without the need for ultrasound or liver biopsy examinations. Blood test results from 400 different patients at the Tabriz University Medical Research Center were collected. This data includes blood test results of healthy individuals and those with grade 1, 2, and 3 fatty liver disease. Fourteen different factors, whose influence on liver disease has been confirmed by specialists, were examined. The Adaptive Neuro-Fuzzy Inference System (ANFIS), ANFIS-Particle Swarm Optimization, and ANFIS-Genetic algorithms were applied to the new data, and the resulting severity of liver disease is analyzed and discussed.

The second chapter of this paper reviews liver data and various machine learning algorithms, examining the characteristics of these data and the algorithms used for their classification, and providing a historical overview of previous work using different classification algorithms in various sciences. Chapter three examines the methods used and how they were applied. Chapter four includes simulations and the results of applying the discussed methods to the data, comparing the algorithms. Finally, chapter five summarizes the results and provides recommendations for future research.

2. LITERATURE REVIEW

Human ability to find relationships and model various functions among data with different features and dimensions has always been error-prone. However, machine learning algorithms offer a suitable solution for extracting the best model among these data and solving classification problems [11]. These algorithms have proven highly effective by providing appropriate models for solving classification problems, enabling a better understanding of future system behavior and solving complex issues [12, 13]. The purpose of reviewing the articles presented in this section is to evaluate the performance of the ANFIS algorithm in various scientific fields to understand its performance and use it in this paper for modeling and evaluating results.

In article [14], prostate disease is introduced as a widespread disease similar to liver disease, highlighting the importance of early diagnosis. By collecting data with features affecting the diagnosis of this disease, relationships and disease identification are pursued. The complexity of finding precise relationships among many features justified the use of machine learning algorithms, advancing information analysis through artificial intelligence. The primary method used is ANFIS, a combination of neural networks and fuzzy systems. Various parameters of the ANFIS algorithm needing determination and optimization are handled through three different methods: error backpropagation, least squares, and a proposed method based on genetic algorithms. The evaluation criteria for the results include accuracy, precision, and mean squared error, all functions of error. In this study, the genetic algorithm performed better and was more practical.

Article [15] also selected ANFIS for model building and prediction. This algorithm was applied to the BUPA liver dataset, using error backpropagation and least squares algorithms for parameter optimization. The article describes the algorithm as multilayered, using five different ANFIS layers for prediction. The research concluded that the multilayer algorithm was faster and more accurate, noting the limitation of numerous layers when the data had many features.

The complexity of dynamic systems, including chaotic systems, necessitates the use of artificial intelligence, with fuzzy algorithms proving highly effective as estimators and predictors [16, 17]. Combining these fuzzy systems with neural networks creates the ANFIS algorithm, where error backpropagation significantly enhances result accuracy [18].

This paper presents a new method for optimizing ANFIS algorithm parameters. Particle Swarm Optimization (PSO) is used for parameter updates, with simulation results indicating superior performance and reduced complexity and calculations compared to error backpropagation and least squares [19]. Given the body's functioning and disease detection complexities, predictive results have consistently contained errors, prompting the creation of a framework and model based on neuro-fuzzy algorithms. This model, operating on liver features obtained from blood tests, detects samples with abnormal values and is applicable to other diseases, including hepatitis [20].

Article [21] introduces the ANFIS algorithm for constructing a model to predict iron rust rates. Existing data were classified using PSO for parameter determination, modeling after the natural and social behaviors of bird flocks [22, 23]. Simulation results compared with genetic algorithms confirmed the efficacy of PSO in error reduction and optimal parameter identification.

In article [24], ANFIS is shown as a robust method for modeling various data, such as air pollution levels from fossil fuels, with optimal performance indicated by error reduction.

This paper introduces a hybrid method for diagnosing hepatitis, combining ANFIS and genetic algorithms with a set of experimental data. Comparing previous articles' results based on accuracy and sensitivity, the hybrid method demonstrated superior performance, achieving a 97% accuracy rate in classification [25].

3. MODEL STRUCTURE

The structure of an ANFIS system [26], shown in Figure 1, consists of five layers that represent the Takagi-Sugeno inference system. If an ANFIS system has n inputs and p rules, then the first layer will have n×p neurons, and the other four layers will have p neurons each. For simplicity, we consider a system with two inputs and two rules, as shown in Figure 1. Our fuzzy system has two inputs, x and y , and the rules are defined as in Equations (1) and (2). We will now examine the outputs of each layer in Figure 1.

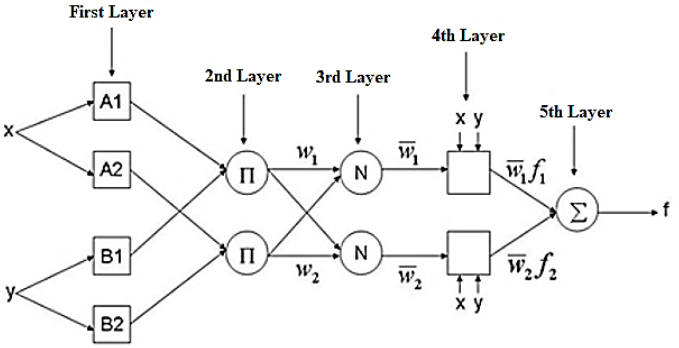

Fig. 1. Structure of the Adaptive Neuro-Fuzzy Inference System (ANFIS)

$$Rule1: \text{if } x \text{ is } A1 \text{ and } y \text{ is } B1 \text{ then } f1 = p1x + q1y + r1 \quad (1)$$

$$Rule2: \text{if } x \text{ is } A2 \text{ and } y \text{ is } B2 \text{ then } f2 = p2x + q2y + r2 \quad (2)$$

Layer 1: In this layer, the inputs pass through the membership functions, and O represents the output as defined by Equations (3) and (4).

$$O_{1,i} = \mu Ai\ (x) \quad for \quad i = 1,2 \quad (3)$$

$$O_{1,i} = \mu Bi\ (x) \quad for \quad i = 3,4 \quad (4)$$

The membership functions can be any suitable parametric functions, but Gaussian functions as in Equation (5) are commonly used.

$$\mu\ (x) = \frac{1}{1+\left|\frac{x-c_i}{a_i}\right|^{2\,b_i}} \quad (5)$$

Here, {ai , bi , ci} is the set of parameters, known as the premise parameters. The number of these parameters is equal to n × p × 3.

Layer 2: The output of this layer, as defined by Equation (6), is the product of the input signals, corresponding to the "if" part of the rules.

$$O_{2,i} = wi = \mu Ai(x)\mu Bi(y) \quad for \quad i = 1,2 \tag{6}$$

Layer 3: The output of this layer, as shown in Equation (7), is the normalized version of the previous layer's output.

$$O_{3,i} = \overline{w}i = \frac{w_i}{w_1 + w_2} \quad for \quad i = 1,2 \tag{7}$$

Layer 4: The output of this layer, as described in Equation (8), involves the set of parameters {pi , qi , ri}known as the consequent parameters. The total number of consequent parameters is n × (p + 1).

$$O_{4,i} = \overline{w}i\, f_i = \overline{w}i\,(pi\, x + qi\, y + ri) \quad for \quad i = 1,2 \tag{8}$$

Layer 5:The final layer, as shown in Equation (9), sums up the results to produce the overall output.

$$O_{5,i} = \sum_i \overline{w}_i f_i = \frac{\sum_i w_i f_i}{\sum_i w_i} \tag{9}$$

4. PARTICLE SWARM OPTIMIZATION (PSO) ALGORITHM

The PSO algorithm is a nature-inspired optimization method first introduced by Kennedy and Eberhart in 1995. This method is derived from the collective behavior of animal groups such as birds and fish. In this method, a number of entities, referred to as particles, are dispersed in the search space. Each particle evaluates the objective function at its current position. It then updates its position based on a combination of its own best-known position and the best-known positions of neighboring particles. The direction and speed of movement are influenced by these factors. After all particles move, one iteration of the algorithm is completed. The best solution found by each particle from the start of the program to the current iteration is stored. This process is repeated several times until the desired solution is obtained. The position and velocity of a particle at a new time step are determined by Equations (10) and (11):

$$v_{k+1} = v_k + c_1 rand(0,1) \times [\, pbest_k - present_k] + c_2 rand(0,1) \times [\, gbest_k - present_k] \tag{10}$$

$$present_{k+1} = present_k + v_{k+1} \tag{11}$$

In these equations, present indicates the position, v represents the velocity, and c_1 and c_2 are learning constants.

5. GENETIC ALGORITHM

Genetic algorithms are a subset of evolutionary algorithms and a group of optimization methods inspired by the natural evolution process. Evolutionary algorithms use variations and replacement operations to improve or replace populations to enhance the best solution. The number of solutions generated by the genetic algorithm equals the number of chromosomes or population size. A chromosome consists of genes, which are the parameters of the problem. The initial chromosomes generate the initial solutions for the genes. After creating the initial chromosomes, the evolutionary cycle begins. In each generation, a set of new chromosomes is selected from the previous set, forming the basis for all subsequent optimizations. To achieve this, an objective function must be defined, which is a function of the differences between the predicted values based on certain features. The fitness function, as shown in Equation (12), is derived from the objective function, where i denotes the chromosome or population number.

$$Fitness\ Function\ [i] = \frac{1}{1 + Objective\ Function[i]} \tag{12}$$

Chromosomes with higher fitness values have a greater probability of forming the new population. The roulette wheel mechanism calculates the probability of fitness values and cumulative probabilities. Random numbers between 0 and 1 are generated equal to the number of chromosomes. If any of these random numbers fall between the cumulative probability of populations i and i+1, the i+1-th population replaces the previous population associated with that random number. Some chromosomes in the population pair through a process called crossover, producing new chromosomes called offspring, which combine the genes of their parents. In one generation, some chromosomes undergo mutation, meaning the gene value is randomly replaced with a new value. The number of chromosomes undergoing crossover and mutation is controlled by the crossover and mutation rates. The final step of the generation is replacement, where the entire previous generation is replaced by the newly produced generation. A genetic algorithm typically terminates after a specified number of generations or based on predefined stopping criteria, returning the fittest solution in the population as the best overall solution.

6. MODEL EVALUATION CRITERIA

One of the most critical issues after designing and building a model is its evaluation to verify its performance accuracy. Therefore, it is necessary to review evaluation criteria. The Root Mean Square Error (RMSE) measures the differences between predicted values by the model and actual values. This criterion is a useful tool for comparing prediction errors across datasets. RMSE is the square root of the mean squared error (MSE), and its value is always non-negative. The closer this value is to zero, the lower the error. If the predicted value is $\hat{\mathbf{X}}$ and the actual value is x, and n is the number of data points, these criteria are defined by Equations (13) and (14):

$$RMSE\,(\hat{X}) = \sqrt{MSE\,(\hat{X})} \tag{13}$$

$$MSE\,\left(\hat{X}\right) = \frac{1}{n}\sum_{i=1}^{n}(x_i - \hat{x}_i)^2 \tag{14}$$

7. SIMULATION AND RESULTS

The primary data include results from 400 different patients, among which 100 are healthy and 300 have liver disease. Out of these 300 patients, 100 have grade 1 fatty liver, 100 have grade 2, and 100 have grade 3 fatty liver. The data were randomly shuffled before applying the algorithm, and the system was trained based on 13 features using 80% of the data. The remaining 20% of the data were used to test and validate the results.

The results of applying the ANFIS algorithm to the training, test, and entire datasets are shown in Figures 2, 4, and 6, respectively. Figures 3, 5, and 7 indicate the errors obtained and the differences between actual and predicted values, with the results presented in Table 1. The closer these fluctuations are to zero, the better the results obtained.

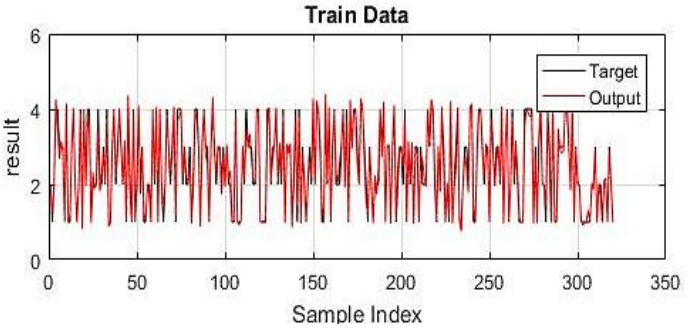

Fig. 2. ANFIS on Training Data

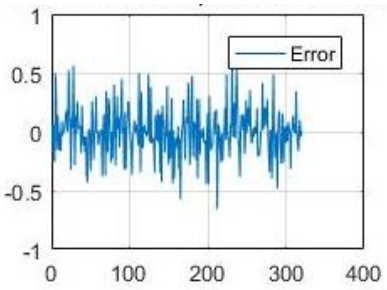

Fig. 3. ANFIS Error on Training Data

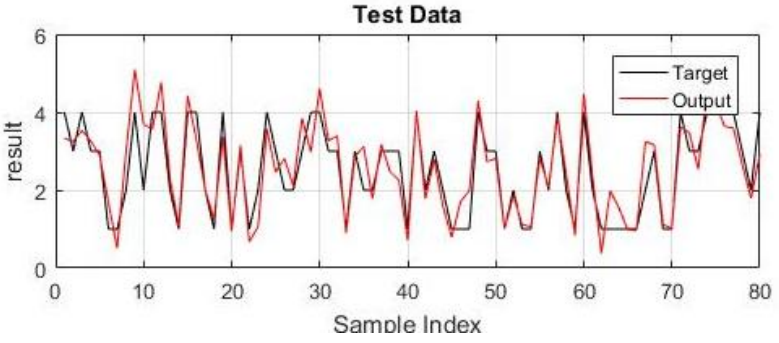

Fig. 4. ANFIS on Test Data

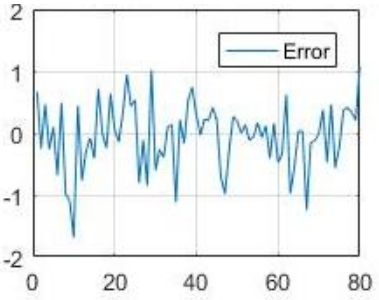

Fig. 5. ANFIS Error on Test Data

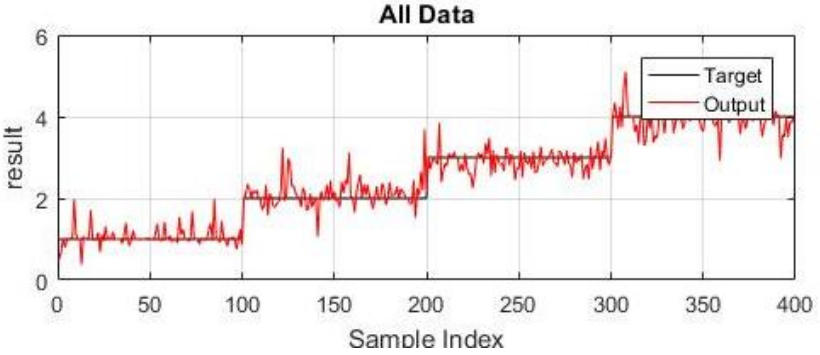

Fig. 6. ANFIS on All Data

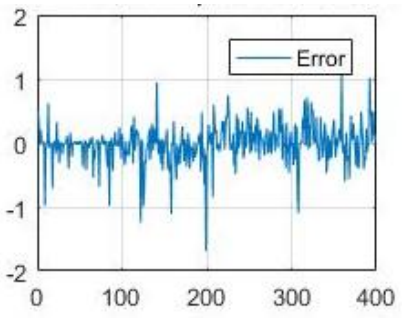

Fig. 7. ANFIS Error on All Data

Table 1. ANFIS Error for Disease Severity

Data	MSE	RMSE
Train Data	0.0883	0.2973
Test Data	0.1874	0.4329
All Data	0.1332	0.3651

The simulation results for the ANFIS-Genetic Algorithm on training, test, and all data are shown in Figures 8, 10, and 12, respectively. Figures 9, 11, and 13 depict the errors and the differences between the actual and predicted values. The results are summarized in Table 2.

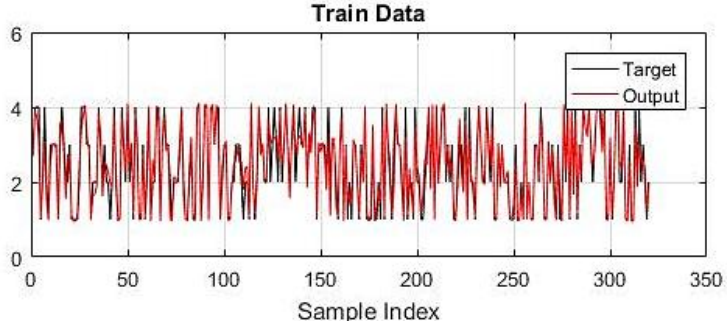

Fig. 8. ANFIS-Genetic Algorithm on Training Data

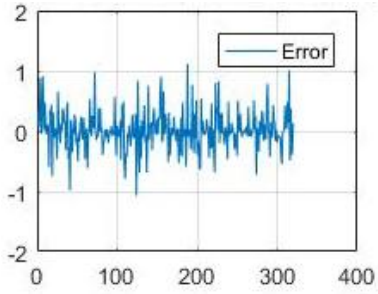

Fig. 9. ANFIS-Genetic Algorithm Error on Training Data

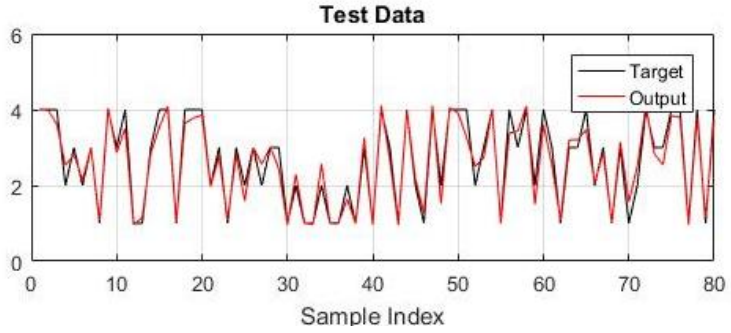

Fig. 10. ANFIS-Genetic Algorithm on Test Data

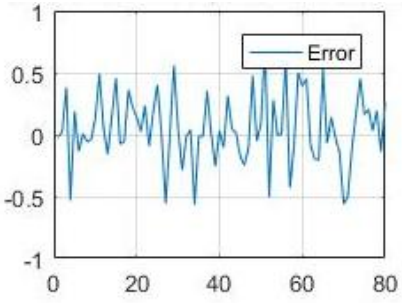

Fig. 11. ANFIS-Genetic Algorithm Error on Test Data

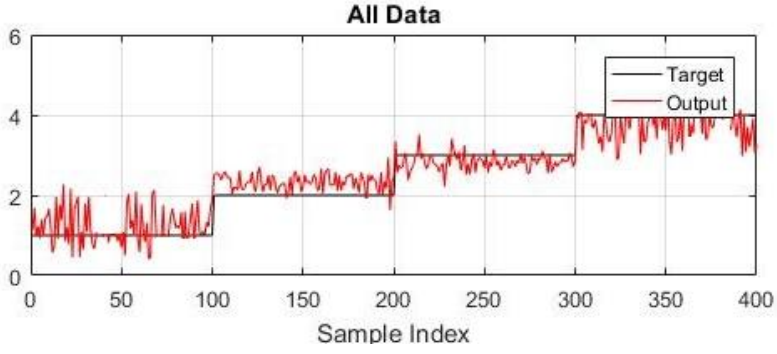

Fig. 12. ANFIS-Genetic Algorithm on All Data

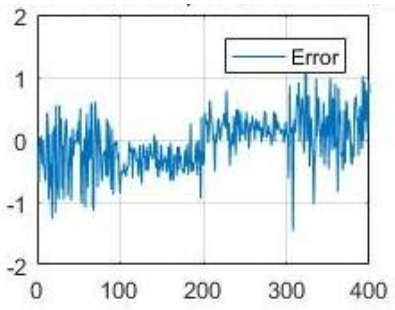

Fig. 13. ANFIS-Genetic Algorithm Error on All Data

Table 2. ANFIS-Genetic Algorithm Error for Disease Severity

Data	MSE	RMSE
Train Data	0.1271	0.3566
Test Data	0.0829	0.2880
All Data	0.1074	0.3278

The Particle Swarm Optimization (PSO) algorithm has also been applied to the data. The simulation results for the ANFIS-PSO Algorithm on training, test, and all data are shown in Figures 14, 16, and 18, respectively. Figures 15, 17, and 19 depict the errors and the differences between the actual and predicted values. The results are summarized in Table 3.

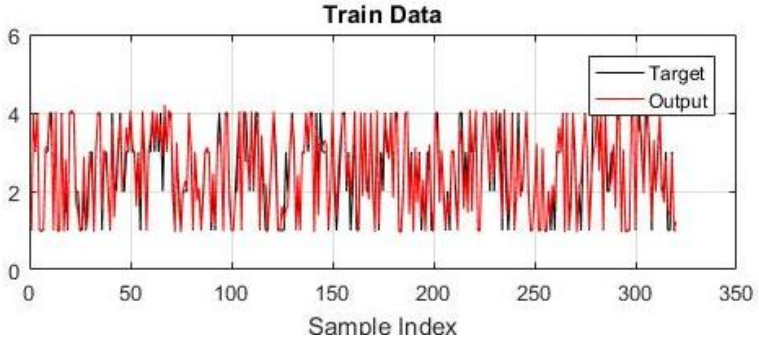

Fig. 14. ANFIS-PSO Algorithm on Training Data

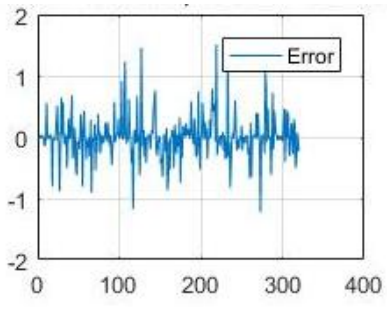

Fig. 15. ANFIS-PSO Algorithm Error on Training Data

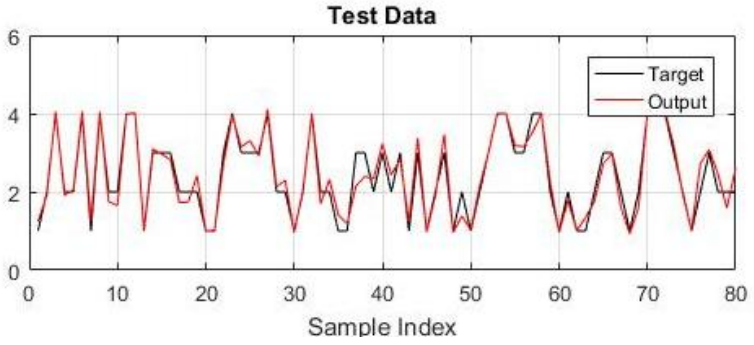

Fig. 16. ANFIS-PSO Algorithm on Test Data

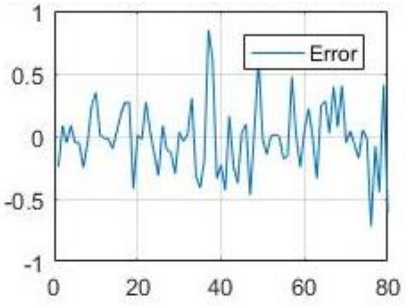

Fig. 17. ANFIS-PSO Algorithm Error on Test Data

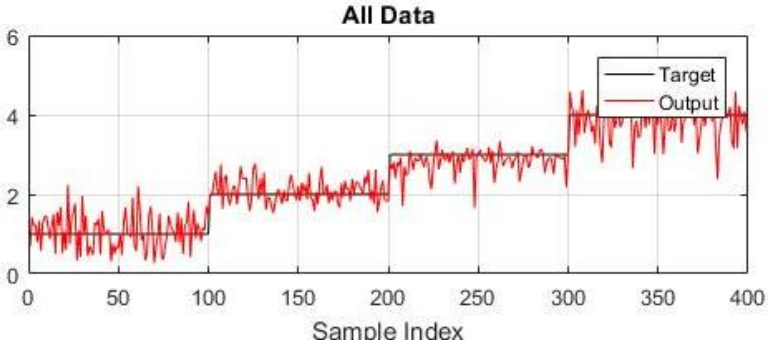

Fig. 18. ANFIS-PSO Algorithm on All Data

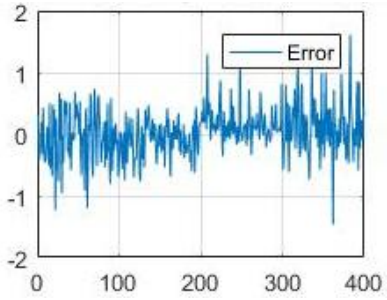

Fig. 19. ANFIS-PSO Algorithm Error on All Data

Table 3. ANFIS-PSO Algorithm Error for Disease Severity

Data	MSE	RMSE
Train Data	0.0956	0.3094
Test Data	0.0748	0.2736
All Data	0.0849	0.2915

8. CONCLUSION

By comparing the results obtained in Tables 1-3, the Particle Swarm Optimization (PSO) algorithm has the lowest error and provides values closer to the actual objective function. The Genetic Algorithm (GA) also provided accurate predictions but was slightly less precise than PSO. Both optimization algorithms have improved the performance of the ANFIS model. Given the obtained results and the error values, the ANFIS model with optimization algorithms has demonstrated accurate performance.

Transparency Statement

The data supporting this study are available upon reasonable request to the corresponding author, subject to ethical and confidentiality considerations.

Acknowledgments

We would like to express our gratitude to all individuals who contributed to this project.

Declaration of Interest

The authors declare that they have no competing interests.

Funding

This research received no specific grant from any funding agency, commercial, or not-for-profit sectors.

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