



# Neutrosophic Fuzzy Simple Additive Weighting with Artificial Intelligence for Sustainable Heart Disease Recognition and Classification

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## Abstract

Heart disease (HD) is considered the main cause of death rate around the world. Multiple systems and biomedical instruments in hospitals take large amounts of medical data. Thus, understanding the data linked with HD is vital to enhance the prediction performance. The timely intervention of HD is the most important factor in preventing patients from additional damage. In recent times, non-invasive medical procedures, including artificial intelligence-based approaches have been used in the healthcare sector. Particularly machine learning (ML) applies various techniques and algorithms that are extensively applied and are especially effective in accurately detecting HDs within short period. However, HD prediction is a challenging task. The largest size of medicinal database has made it a challenge for clinicians to understand the complicated feature relations and make disease predictions. Therefore, this study presents a Neutrosophic Fuzzy SAW with Artificial Intelligence for Sustainable Heart Disease Recognition and Classification (NFSAW-AISHDC) technique in Healthcare Sector. The NFSAW-AISHDC technique mainly focuses on the adoption of neutrosophic fuzzy simple additive weighting (NFSAW) with feature selection process for HD detection. The NFSAW-AISHDC method exploits min-max scalar to scale the input medical data. For feature selection, the NFSAW-AISHDC method uses beluga whale optimization (BWO) algorithm to choose feature subsets. Moreover, the NFSAW-AISHDC technique applies NFSAW approach to the identification of HDs. The performance values of the NFSAW-AISHDC methodology undergoes using benchmark database. The experimental outcome underlined the promising results of the NFSAW-AISHDC method with other models.

**Keywords:** Heart Disease Recognition; Artificial Intelligence; Beluga Whale Optimization; Neutrosophic; SAW; Feature Selection

## 1. Introduction

With the development of the information era, computer-aided systems are produced a large quantity of raw data, improving the new core of control [1]. Gaining significant knowledge from this type of data will be a complex task for medical specialists. Artificial Intelligence (AI), machine learning (ML), Data mining, and deep learning (DL) are

comparatively advanced and potential technologies for acquiring correlations or recognizing important datasets employing advanced statistical methods [2]. Medical data mining and knowledge consideration are established as a moderately innovative and emerging field, which is interesting to several researchers. With the enhancement of medical information collection, medical specialists can analyze ailments better [3]. Moreover, computational biomedical techniques will increase the decision-making method and accomplish superior prediction outcomes in various diseases like cancers, heart diseases (HDs), skin infections, kidney diseases, and diabetes. Among these diseases, cardiovascular diseases (CVD) are recognized to be the higher mortality rate in major countries all over the world. HD is quickly improving in the worldwide [4]. According to report from the WHO, in 2016 nearly 17.90 million persons died due to HD. Such number accounts for nearly 30% of each death around the world [5]. Approximately 55% of HD patients die in the first three years, and the treatment expenses for HD should be about 4% of the annual medical expenses. Detecting the improving statistics, precise and earlier detection and treatment of such a difficult disease is more crucial for disease avoidance and efficient application of clinical resources [6].

The medical science domains have greatly improved over a period of time because of the new technological developments. Particularly, ML is extensively employed in the domain of CVD medication and can be demonstrated as a possible space [7]. Mainly, medical datasets include relevant and redundant features. Unwarranted features will not provide any important data for the prediction task and then produce the noise in the report of target (output class) that causes prediction errors [8]. Moreover, these features improve the difficulty of ML techniques and develop the system to execute gradually because of raised training time. In order to address the dimensionality process those features connected to the target must be chosen or recognized from databases and offered as inputs to ML methods [9]. Remarkable feature selection (FS) could be supported to increase effectiveness by diminishing the system complexity and improving prediction accuracy which has been extremely significant in medical analysis [10].

This study presents a Neutrosophic Fuzzy SAW with Artificial Intelligence for Sustainable Heart Disease Recognition and Classification (NFSAW-AISHDC) technique in Healthcare Sector. The NFSAW-AISHDC technique mainly focuses on the adoption of neutrosophic fuzzy simple additive weighting (NFSAW) with FS process for HD detection. The NFSAW-AISHDC method exploits min-max scalar to scale the input medicinal data. For feature selection, the NFSAW-AISHDC approach employs beluga whale optimization (BWO) algorithm to choose feature subsets. Moreover, the NFSAW-AISHDC technique applies NFSAW approach to the identification of HDs. The performance assessment of the NFSAW-AISHDC method take place using benchmark dataset.

## **2. Literature Review**

In [11], an innovative Inception v3 with a VGG16 was developed. This method connects progressive image analysis methods including noise reduction and contrast improvement. The blood vessel segmentation and Optic disc identification of the relevant features have been removed in the fundus images. The Inceptionv3 model was first utilized for capturing complex hierarchical designs with the images. Otherwise, analyze the use of the VGG16 model. Papandrianos et al. [12] considered the supervised learning-based ultimate observer image classification employing an RGB-CNN architecture in heart images for diagnosing CAD. This system utilizes DenseNet-121 and VGG-16 pretrained networks. For experimental purposes assessing the technique, it discovers an extensive analysis of DL model setups along with diverse robust analysis and exploitation metrics. Moreover, the technique employs the data augmentation method. Obayya et al. [13] proposed an Automated CVD Analysis employing Honey Badger Optimizer with Modified DL (ACVD-HBOMDL) method. Firstly, the method implements min-max scaler for preprocessing the clinical information. For choosing an optimum subset of features, the HBO method has been employed. For CVD classification, DL modified neural network (DLMNN) method could be employed and the hyperparameters could be optimally selected through Bayesian optimization (BO).

In [14], an effective decision support method, also called an assistive model was developed in this study. It produces the usage of an optimization method and a DL method. The effectiveness of conventional methods to predict CVD by utilizing medical information could be prevented with the integration of the two techniques. For sufficient sample sizes of synthesized instances, the optimization method elects the correct factors for generating the preeminent prediction in an improved method. In [15], a DL-based technique, especially the CNN with bidirectional long and short-term memory (Bi-LSTM) was presented. Major appropriate features have been chosen through FS that were proficient by prioritizing and electing features that were extremely rated in the complete disease database. Later, the CNN + BiLSTM-based hybrid DL method could be utilized for predicting CVD.

In [16], an innovative deep neural network (DNN) called as FibrosisNet method was presented that identified and categorized fibrosis after it existed. The introduced method comprises 17 diverse sequence layers for accomplishing the fibrosis identification targets. Moreover, deep transfer-learning (DTL) methods have been implemented for various

well-known convolution neural networks (CNNs) techniques for determining fibrosis identification systems. Khanna et al. [17] presented an innovative IoT and DL-allowed healthcare disease diagnosis (IoTDL-HDD) system. This method employs a BiLSTM feature extraction algorithm for extracting valuable feature vectors through the ECG signals. Intended to increase the effectiveness of the Bi-LSTM method, the AFO technique was utilized as a hyperparameter optimization. In addition, a fuzzy DNN (FDNN) method was utilized in allocating suitable classes to the ECG signals.

### 3. The Proposed Method

In this study, we have projected a novel NFSAW-AISHDC method in healthcare sector. The NFSAW-AISHDC technique mainly focuses on the adoption of NFSAW with FS process for HD detection. It contains three major processes involved min-max normalization, BWO-based FS, and NFSAW-based disease detection. Fig. 1 represents the entire flow of NFSAW-AISHDC methodology.

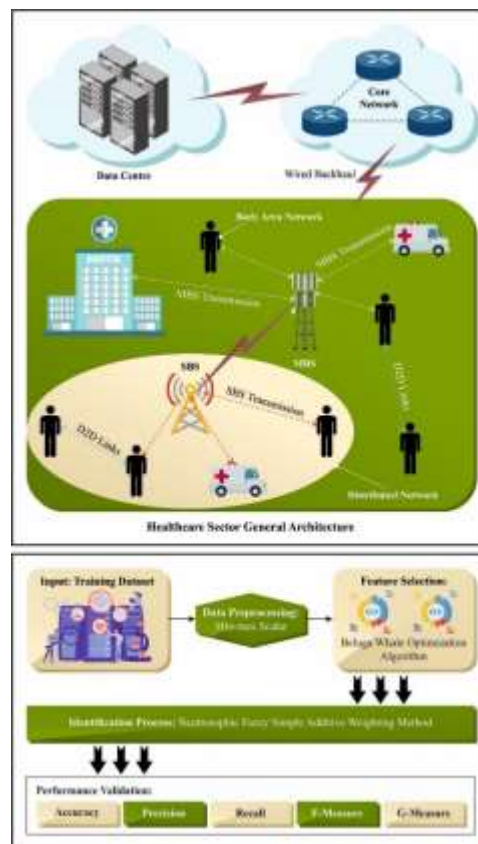


Figure 1: Overall flow of NFSAW-AISHDC technique

#### A. Min-Max Normalization

At primary, the NFSAW-AISHDC method exploits min-max scalar to scale the input data. Min-max scaling, otherwise known as normalization [18], is an approach utilized in data pre-processing to rescale mathematical features to a specific range within  $[0,1]$ . This procedure includes subtracting the smallest values of the feature from each value and later separating by the difference between the minimum and maximum values. Therefore, it ensures that each feature is on a comparable scale, which prevents specific variables from dominating others due to differences in magnitude. Min-max scaling is especially suitable in ML approaches that rely on distance calculation or optimization algorithms, which enables improved performance and more effective model training across different datasets.

## B. BWO based Feature Selection Process

For feature selection, the NFSAW-AISHDC technique uses BWO algorithm to choose feature subsets. BWO algorithm is an innovative heuristic algorithm proposed and made by pretending the beluga whale's behavior [19]. The algorithm gathers many algorithmic benefits. It can be commonly functional to unimodal and multi-modal optimizer issues by adjusting parameters to decrease the parameter control count. The algorithm is separated into 3 core parts as global exploration stage, local development stage, and the fall stage.

### i) Initialization stage

At the establishment of the algorithm implementation, the population of beluga whales is produced by randomization. In the solution space, the global search ability is definite. On the other hand, the development phase manages the local search ability in the solution space. In combination with the whale fall prospect, the existing location of the whale can be altered. The BWO algorithm first produces an initial population of whales  $X$  randomly:

$$X = \begin{bmatrix} x_{1,1} & x_{1,2} & \dots & x_{1,d} \\ x_{2,1} & x_{2,2} & \dots & x_{2,d} \\ \vdots & \vdots & \ddots & \vdots \\ x_{n,1} & x_{n,2} & \dots & x_{n,d} \end{bmatrix}, \quad (1)$$

Here,  $n$  denotes the population size, and  $d$  signifies the variable space dimensionality. For every beluga whale, the corresponding fitness value is revealed in Eq. (2).

$$F_X = \begin{bmatrix} f(x_{1,1}, x_{1,2}, \dots, x_{1,d}) \\ f(x_{2,1}, x_{2,2}, \dots, x_{2,d}) \\ \vdots \\ f(x_{n,1}, x_{n,2}, \dots, x_{n,d}) \end{bmatrix}. \quad (2)$$

Whales arrive at a global exploration stage or a localized exploitation stage based on the factor of equilibrium  $B_f$ . Eq. (3) is the formulation of the equilibrium factor  $B_f$ .

$$B_f = B_0 \left( 1 - \frac{T}{2T_{\max}} \right), \quad (3)$$

Whereas  $T$  represents the amount of existing iterations, and  $T_{\max}$  denotes the highest number of iterations.  $B_0$  is randomly generated number in the range (0 and 1). If  $B_f > 0.5$ , the whale arrives in the global development stage. Or else, it goes into the local development stage.

### Global exploration stage

In this stage, BWO incorporates the swimming behavior of beluga whales in dissimilar poses by synchronization or mirroring. As per its features, the BWO algorithm implements the location upgrade tactic in Eq. (4) during the global search.

$$\begin{cases} x_{i,j}^{T+1} = x_{i,p_j}^T + (x_{r,p_1}^T - x_{i,p_j}^T) (1 + r_1) \sin(2\pi r_2), j = \text{even} \\ x_{i,j}^{T+1} = x_{i,p_j}^T + (x_{r,p_1}^T - x_{i,p_j}^T) (1 + r_1) \cos(2\pi r_2), j = \text{odd}, \end{cases} \quad (4)$$

Here,  $x_{i,j}^{T+1}$  signifies the novel coordinates of the  $i^{\text{th}}$  beluga in the dimension of  $j^{\text{th}}$ , and it is a randomly generated number selected in the  $d^{\text{th}}$  dimension.  $r_1$  and  $r_1$  are random values in the range [0 and 1].

### Partial development stage

The development stage of BWO was stimulated by the feeding behavior of beluga whales. Beluga whales can travel to unite in hunting based on the position of close beluga during foraging. Thus, beluga whales search by dividing every other's position data. In the development stage, the Lévy fight plan is employed to enhance the performance of convergence of the technique (by supposing that belugas can take prey with the Lévy fight plan). The beluga whale development procedure is signified by

$$x_i^{T+1} = r_3 x_{best}^T - r_4 x_i^T + C_1 L_F (x_r^T - x_i^T), \quad (5)$$

Whereas,  $x_i^{T+1}$  represents the following generation of individuals of the  $i^{\text{th}}$  solution,  $x_{best}^T$  indicates the existing optimum solution,  $x_r^T$  is the randomly nominated solution,  $x_i^T$  signifies the  $i^{\text{th}}$  solution,  $r_3$  and  $r_4$  are randomly produced numbers in the range [0 and 1], and  $C_1$  refers to the adaptive equilibrium factor, the BWO set  $C_1 = 2r_4(1 - T/T_{\max})$ .  $L_F$  is the factor of Lévy fight. Fig. 2 represents the steps involved in BWO.

### Whale fall stage

During migration and foraging, other usual hunters disturb them, which can cause their position to alter. This trouble can cause belugas to drop, and these dropped belugas can attract other animals to reproduce here. To pretend this behavior of whale-fall, the BWO algorithm arbitrarily picks few belugas to drop with a definite prospect during the

iterative procedure to pretend small variations in the population. In the algorithm of BWO, it is assumed that if  $B_f$  is lesser than  $W_f$ , the algorithm goes into the whale fall stage. The fall probability of the whale population is  $W_f = 0.1 - 0.05 \frac{T}{T_{max}}$ . The position of the whale fall is revealed in Eq. (6).

$$X_i^{T+1} = r_5 X_i^T - r_6 X_r^T + r_7 X_{step}, \tag{6}$$

Here,  $r_5, r_6$ , and  $r_7$  are randomly produced numbers from the interval of 0 and 1.  $X_{step}$  denotes the step size of the beluga fall, and its value is connected to the iterations count that calculated as

$$X_{step} = (ub - lb) \exp\left(-C_2 \frac{T}{T_{max}}\right), \tag{7}$$

Whereas,  $X_{step}$  denotes the step factor among the falling probability and size of population, the BWO is set as  $C_2 = 2nW_f$ .  $lb$  and  $ub$  are the lower and upper boundaries, correspondingly.



Figure 2: Steps involved in BWO

The fitness function (FF) deployed in the BWO method is aimed to have a balance among the amount of attributes elected and the classifier accuracy, Eq. (8) illustrates the FF to assess the solution.

$$Fitness = \alpha \gamma_R(D) + \beta \frac{|R|}{|C|} \tag{8}$$

In Eq. (8),  $\gamma_R(D)$  infers the classifier error value. The cardinality of elected subset is represented by  $|R|$  and the total feature counts within database is indicated by  $|C|$ , the parameters  $\alpha$  and  $\beta$  indicate the importance of classifier quality and subset length.  $\in [1,0]$  and  $\beta = 1 - \alpha$ .

### C. Heart Disease Detection using NFSAW

At last, the NFSAW-AISHDC technique applies NFSAW approach to the identification of HDs. It is considered a basic model of fuzzy sets and neutrosophic ideas [20].

Definition1. An intuitionistic fuzzy set  $Z$  in  $X$  is a mathematical object [21].

$$Z = \{ \langle x, \mu_Z(x), \nu_Z(x) \rangle \mid x \in X \},$$

Where the membership and nonmembership degrees are represented as  $\mu_Z(x)$  and  $\nu_Z(x)$ , correspondingly

$$\mu, \nu \in [0,1], \quad (9)$$

$$0 \leq \mu + \nu \leq 1. \quad (10)$$

$$\pi = 1 - \mu - \nu \quad (11)$$

If  $\mu(x) = 0$  or  $\nu(x) = 0$  or  $\mu(x) = 1$  or  $\nu(x) = 1$  then we see in  $X$  the area where  $\mu(x) = 1$ , while  $\nu(x) > 0$  and is decreasing or increasing.

If  $\mu(x) = 1$ , then some event is takes place. Thus, there is no place for the hesitation and opposite event, viz.,  $\nu(x) = 0$  and  $\pi(x) = 0$ .

Consider whether Admiral Nelson can be considered a gentleman depends on the personal opinions of an instance of 100 individuals.

Twenty individuals regarded Nelson as a gentleman due to his courageous defense of his country, while thirty others did not perceive him as such because of his association with piracy, and the others found it challenging to judge. The hesitation degree  $\pi = 0.5$ , the degree of membership  $\mu = 0.2$  and the nonmembership  $\nu = 0.3$ .

Consider that every person completely rejected Nelson's belongs to gentlemen. It is clear that in this case we have  $\mu = 0$  then  $\nu = 1$  and  $\pi = 0$ . In fact, every person under the instance refused to identify Admiral Nelson as a gentleman, thus,  $\pi = 0$ . Eventually,  $\mu = 0$  implies the total acceptance of Nelson not being a gentleman, viz.,  $\nu = 1$ . then  $\mu + \nu + \pi = 1$ , and  $\mu = \pi = 0$ , then  $\nu = 1$ .

$$\text{If } \mu = 0, \text{ then } \nu = 1, \pi = 0, \text{ if } \mu = 1, \text{ then } \nu = 0, \pi = 0. \quad (12)$$

There is no special suggestion regarding the dependencies among the  $\mu, \nu$  and  $\pi$  components in the  $A - IPS$ , but they are dependent on each other.

The study discuss the methodological issues of  $A - IFS$  and  $A - IVIFS$ .

When allocating real values to  $\mu$  and  $\nu$ , the expert experiences an difficulty. Sometimes experts claim that the sum  $\mu + \nu$  should be higher than 1. To least alleviate or avoid at these problems, the  $A - IFS$  were introduced.

With regard to  $A - IPS$ , the fundamental of Neutrosophic Set theory ( $NST$ ) is given below:

Definition2. Neutrosophic Set  $Z$  in  $X$  is a mathematical object

$$Z = \{ \langle x, \mu_Z(x), \nu_Z(x), \pi_Z(x) \rangle \mid x \in X \}, \quad \mu, \nu, \pi \in [0,1], \quad (13)$$

$$0 \leq \mu + \nu + \pi \leq 3 \text{ for the completely independent component,} \quad (14)$$

$$0 \leq \mu + \nu + \pi \leq 1 \text{ for the dependent components.} \quad (15)$$

Note that the difference between  $NST$  and  $A - IFS$  is the complete independence of component. The event  $\mu = 1, \nu = 1$  and  $\pi = 1$  is allowable in the  $NST$  based on the independence hypothesis. Assume  $\mu, \nu$  and  $\pi$  as the degrees of truth, false and uncertainty. Therefore, complete truth ( $\mu = 1$ ), with the common sense and formal logic, the degree of false is 0 ( $\nu = 0$ ) without uncertainty ( $\pi = 0$ ). The higher degree of truth is mandatory together with the low degree of false and uncertainty. Note that  $\mu = 1, \nu = 1, \pi = 1$  and  $\mu = 0, \nu = 0, \pi = 0$  are taken as a paradox. the  $A - IFS$  theory is effective to apply theories without paradoxes and undergoes in the opposite asymptotic limit  $\mu = 1, \nu = 1, \pi = 1$  and  $\mu = 0, \nu = 0, \pi = 0$  of the  $NST$ .

The main constraints  $0 \leq \mu + \nu + \pi \leq 1$  in the  $NST$  is better than  $-IFS(\pi + \mu + \nu = 1)$ .

The scale values of linguistic variables are enclosed.

#### i) Fuzzy sets

The fuzzy set is a set of objects with a range of membership grades. This is considered by the membership function (MF) which allots to every object ranging among 0 and 1.

#### ii) Linguistic Variables

A linguistic variable is a duration from a natural language which is resultant utilizing fuzzy logic.

#### iii) Fuzzy Membership

The MF on the universe of discourse  $Z$  is definite as  $\mu_A(z): Z \rightarrow [0,1]$  for the fuzzy subset  $A$ , where every element of  $Z$  is mapped to a value among *zero* and *one*.

Triangular MF (TMF)

The TMF is definite by an upper limit  $c$ , lower limit  $a$ , and a value  $b$ , whereas  $a < b < c$ .

$$\mu_A(z) = \begin{cases} 0, & z \leq a \\ \frac{z-a}{b-a}, & a < z \leq b \\ \frac{c-z}{c-b}, & b < z < c \\ 0, & z \geq c \end{cases} \quad (16)$$

It is definite by  $A = \{z; (a, b, c)\}$ .

Neutrosophic Set

Assume  $U$  as the universe of discourse and  $M$  as a sub-set of  $U$ . The element  $z \in U$  has grade of indeterminacy, true, and false memberships in  $M$ . The representation of neutrosophic number is  $z(T, I, F) \in M$  and  $T, I, F$ , which are neutrosophic modules. Then  $M_{NS} = \{z, T_M(z), I_M(z), F_M(z): z \in Z\}$  is named a neutrosophic set,

Whereas  $0 \leq T_M(z) + I_M(z) + F_M(z) \leq 3$ , and indeterminacy-MF  $I_M: Z \rightarrow [0,1]$ , false MF  $F_M: Z \rightarrow [0,1]$  and truth-MF  $T_M: Z \rightarrow [0,1]$ .

Step1. Define the criteria  $C_j$  in a cluster of experts  $E_k$  for the problem of decision-making.

Step2. Pick the above three membership rate values of every condition by the specialists with respect to linguistic variables.

Step3. Fuzzify the linguistic variables of every condition with regard to fuzzy triangular numbers.

Step4. Discover the average fuzzy scores  $L_j^i$  of triangular fuzzy numbers  $(p_1^1, q_1^2, r_1^3), (p_2^1, q_2^2, r_2^3), \dots, (p_j^1, q_j^2, r_j^3)$ , normalized weight  $w_j$  and defuzzified values for every condition

Average fuzzy scores  $L_j^i = \frac{(p_1^i + p_2^i + \dots + p_j^i)}{j}$ , while  $i = 1, 2, 3$ .

Defuzzified value ( $e$ ) =  $\frac{p+q+r}{3}$ , whereas  $p = L_j^1, q = L_j^2, r = L_j^3$

Normalized values ( $w$ ) = sum of all defuzzified values or Defuzzified values of the conditions/.

Step5. Discover the centroid weight value  $W_j = \frac{\alpha+2\beta+\gamma}{4}$ , whereas  $\alpha, \beta$  and  $\gamma$  are normalized weighted values of three MFs, correspondingly.

Step6. Allocate the related neutrosophic rate values to every alternative  $A_i$  over a condition  $C_j$  as linguistic variables by specialists' view.

Step7. Repeat step4, and discover the scores of average fuzzy and the defuzzified of every substitute on conditions.

Step8. The procedure normalized decision matrix for three MFs equivalent to another condition.

Step9. Estimate  $N_{ij} = \frac{a_{ij} + \lambda b_{ij} + (1-\lambda)c_{ij}}{2}$ , whereas  $a$  denotes the normalized value of truth membership,  $b$  and  $c$  define the value of normalized indeterminacy and false membership.

Step10. Discover the joined normalization neutrosophic decision matrix.

Step11. Compute the overall scores of every alternate utilizing  $TS = N_{ij} * W_j$ . Lastly, the greatest value is selected as the finest alternate.

#### 4. Performance Validation

The performance study of the NFSAW-AISHDC algorithm takes place utilizing the dataset [22], which is combined with instances (Cleveland: 303/Hungarian: 294/Switzerland: 123/Long Beach VA: 200/Stalog (Heart) Data Set: 270). Table 1 defines the details of database.

Table 1: Details on database

Classes	No. of Instances
Normal	561
Disease Affected	629
Total No. of Instances	1190

Fig. 3 establishes the confusion matrices created by the NFSAW-AISHDC algorithm under various epochs. The outcomes inferred that the NFSAW-AISHDC methodology has effectual recognition of the normal and disease samples under all classes.

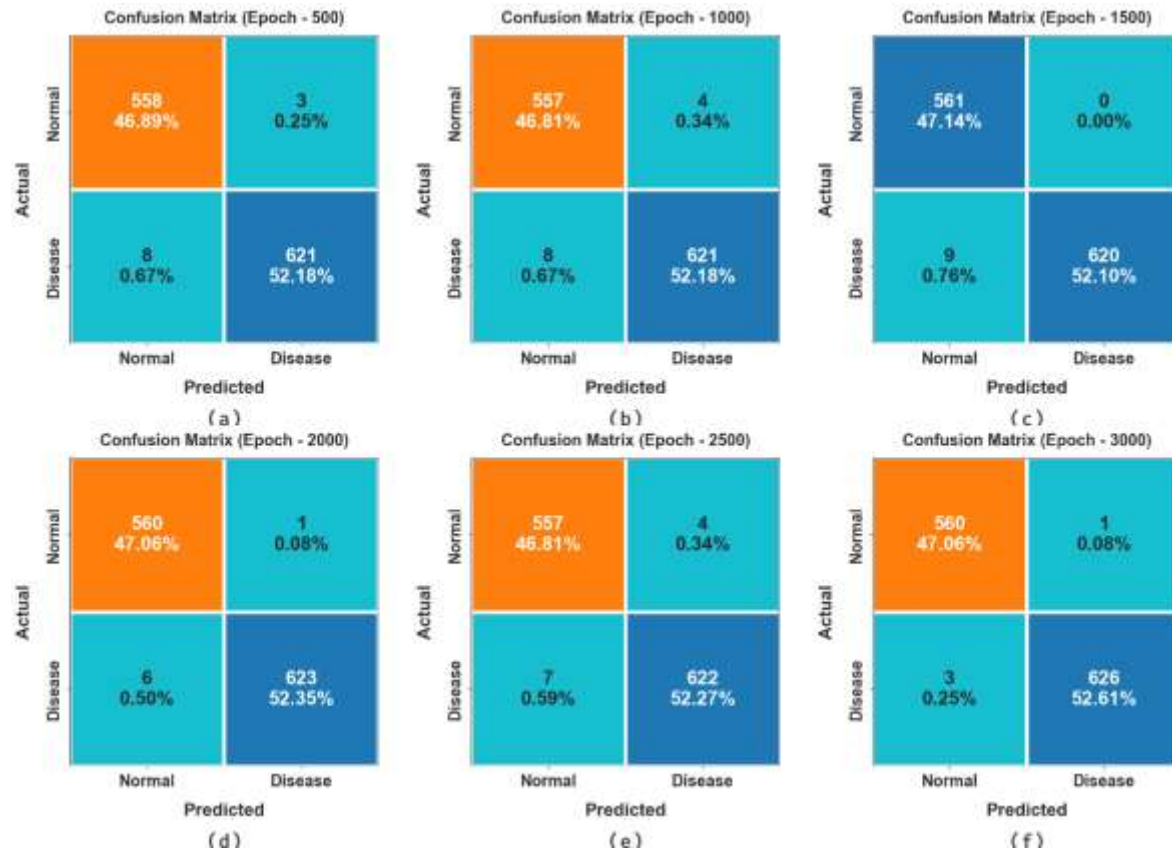


Figure 3: Confusion matrices of NFSAW-AISHDC technique (a-f) Epochs 500-3000

The disease detection outcomes are displayed by the NFSAW-AISHDC approach under distinct epochs in Table 2 and Fig. 4. The table values state that the NFSAW-AISHDC methodology recognized the normal and diseased samples proficiently.

Table 2: Disease detection outcome of NFSAW-AISHDC technique under several epochs

Classes	<i>Accu<sub>y</sub></i>	<i>Prec<sub>n</sub></i>	<i>Reca<sub>l</sub></i>	<i>F<sub>Measure</sub></i>	<i>G<sub>Measure</sub></i>
Epoch - 500					
Normal	99.47	98.59	99.47	99.02	99.02
Disease	98.73	99.52	98.73	99.12	99.12
Average	99.10	99.05	99.10	99.07	99.07
Epoch - 1000					
Normal	99.29	98.58	99.29	98.93	98.93
Disease	98.73	99.36	98.73	99.04	99.04
Average	99.01	98.97	99.01	98.99	98.99
Epoch - 1500					
Normal	100.00	98.42	100.00	99.20	99.21
Disease	98.57	100.00	98.57	99.28	99.28
Average	99.28	99.21	99.28	99.24	99.24
Epoch - 2000					
Normal	99.82	98.94	99.82	99.38	99.38

Disease	99.05	99.84	99.05	99.44	99.44
Average	99.43	99.39	99.43	99.41	99.41
Epoch - 2500					
Normal	99.29	98.76	99.29	99.02	99.02
Disease	98.89	99.36	98.89	99.12	99.12
Average	99.09	99.06	99.09	99.07	99.07
Epoch - 3000					
Normal	99.82	99.47	99.82	99.64	99.64
Disease	99.52	99.84	99.52	99.68	99.68
Average	99.67	99.65	99.67	99.66	99.66

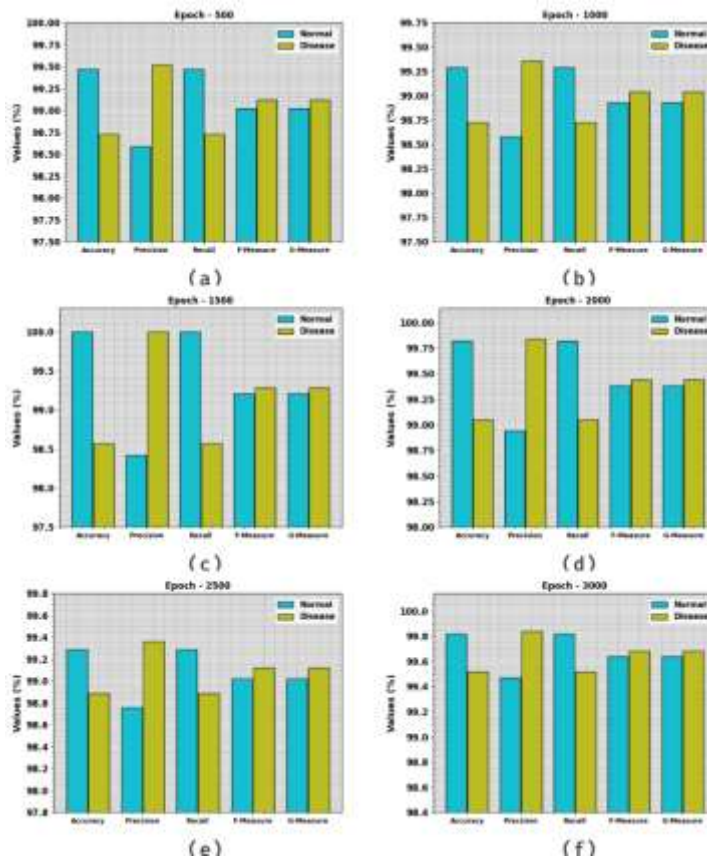


Figure 4: Disease detection outcome of NFSAW-AISHDC technique (a-f) Epochs 500-3000

With 500 epochs, the NFSAW-AISHDC technique gains average  $accu_y$ ,  $prec_n$ ,  $reca_l$ ,  $F_{score}$ , and  $G_{measure}$  of 99.10%, 99.05%, 99.10%, 99.07%, and 99.07%. Additionally, with 1000 epochs, the NFSAW-AISHDC system attains gains average  $accu_y$ ,  $prec_n$ ,  $reca_l$ ,  $F_{score}$ , and  $G_{measure}$  of 99.01%, 98.97%, 99.01%, 98.99%, and 98.99%. Meanwhile, with 1500 epochs, the NFSAW-AISHDC approach obtains average  $accu_y$ ,  $prec_n$ ,  $reca_l$ ,  $F_{score}$ , and  $G_{measure}$  of 99.28%, 99.21%, 99.28%, 99.24%, and 98.99%. Moreover, with 2000 epochs, the NFSAW-AISHDC method reaches average  $accu_y$ ,  $prec_n$ ,  $reca_l$ ,  $F_{score}$ , and  $G_{measure}$  of 99.43%, 99.39%, 99.43%, 99.41%, and 99.41%. Finally, with 3000 epochs, the NFSAW-AISHDC algorithm achieves average  $accu_y$ ,  $prec_n$ ,  $reca_l$ ,  $F_{score}$ , and  $G_{measure}$  of 99.67%, 99.65%, 99.67%, 99.66%, and 99.66%.

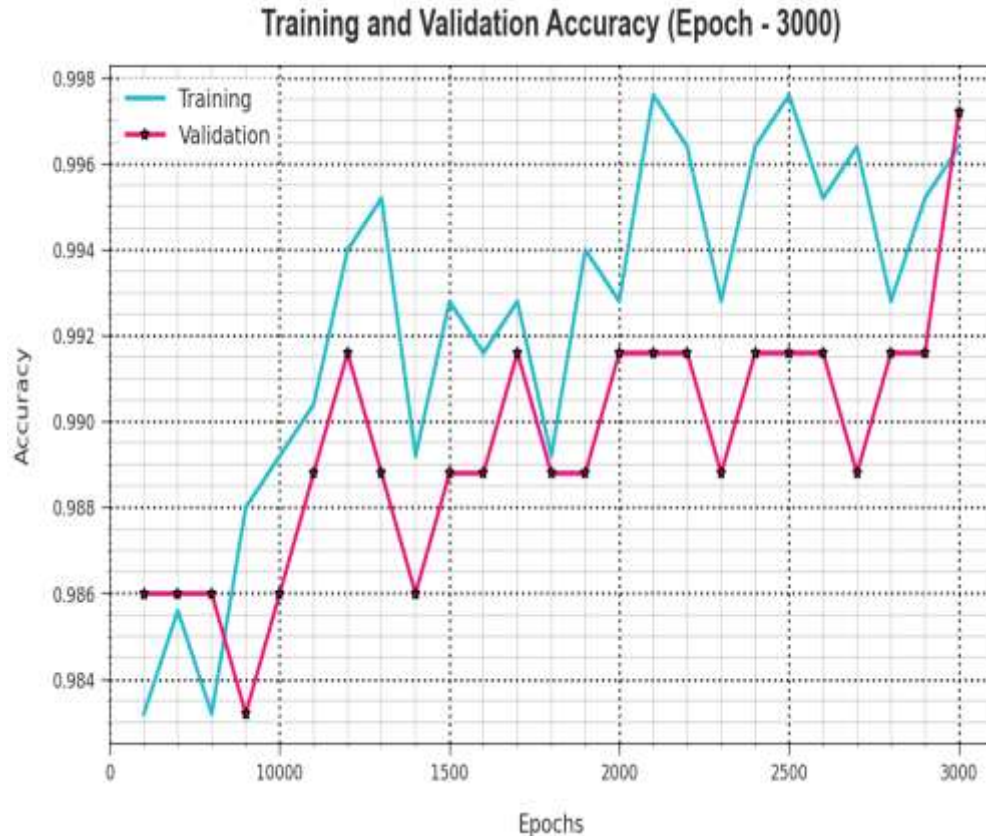


Figure 5:  $Accu_y$  curve of NFSAW-AISHDC technique under 3000 epochs

The evaluation of the NFSAW-AISHDC approach is graphically defined in Fig. 5 in the procedure of TRAA and VALA curves under 3000 epochs. The value exhibition valuable interpretation of the behaviour of the NFSAW-AISHDC algorithm over several epoch counts, signifying its learning procedure and generalization abilities. Remarkably, the figure supposes a steady enhancement in the TRAA and VALA with development in epochs. It ensures the adaptive nature of the NFSAW-AISHDC model in the pattern recognition method on both TR and TS datasets. The uprising direction in VALA outlines the capability of the NFSAW-AISHDC methodology in adapting to the TR data and also excelling in offering correct classifier of unobserved data, pointing out the robust generalization abilities.

Fig. 6 determines a complete representation of the TRLA and VALL results of the NFSAW-AISHDC methodology under 3000 epochs. The progressive reduction in TRLA outperforms the NFSAW-AISHDC algorithm optimizer the weights and lessening the classifier error on TR and TS datasets. The figure indicates a clear understanding of the NFSAW-AISHDC method's link with the TR data, emphasizing its proficiency in capturing patterns from TR and TS data. Remarkably, the NFSAW-AISHDC system continually grows its parameters in reducing the alterations among the predictive and real TR classes.

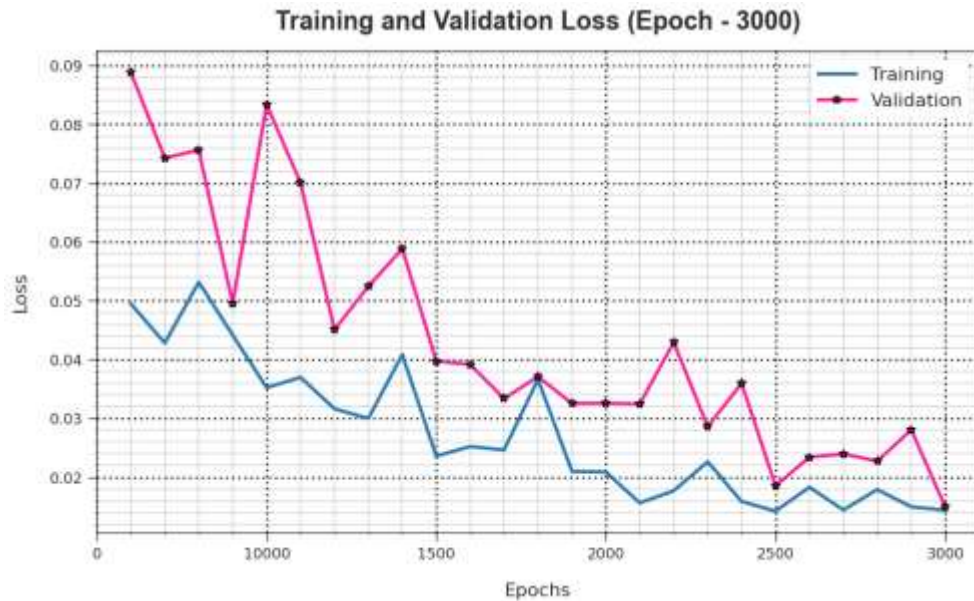


Figure 6: Loss curve of NFSAW-AISHDC technique under 3000 epochs

Examining the precision-recall (PR) curve, as demonstrated in Fig. 7, the outcome ensured that the NFSAW-AISHDC algorithm progressively accomplishes improved PR values over each class under 3000 epochs. It verifies the greater capabilities of the NFSAW-AISHDC algorithm in the identification of various classes, demonstrating the ability the detect classes.

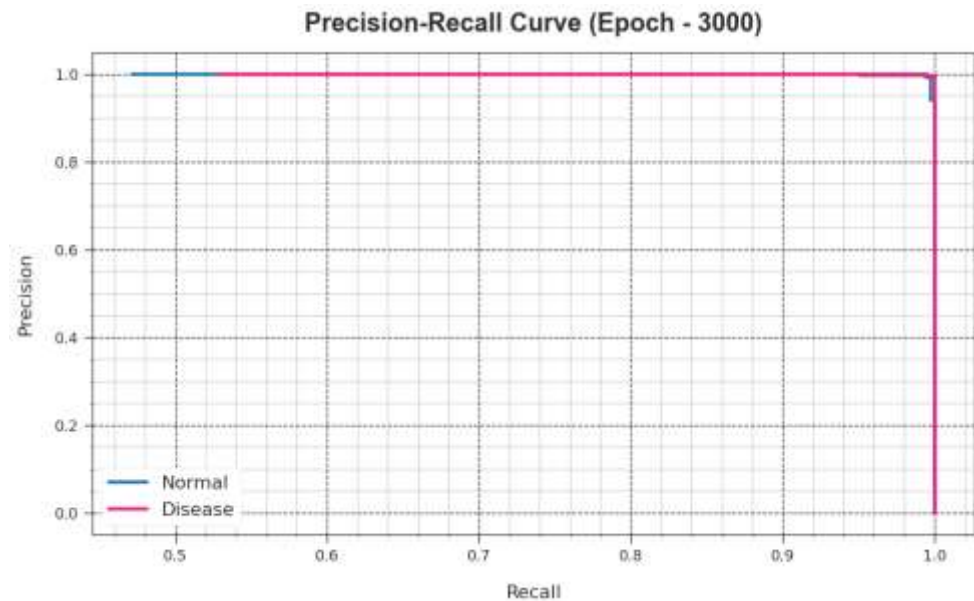


Figure 7: PR curve of NFSAW-AISHDC technique under 3000 epochs

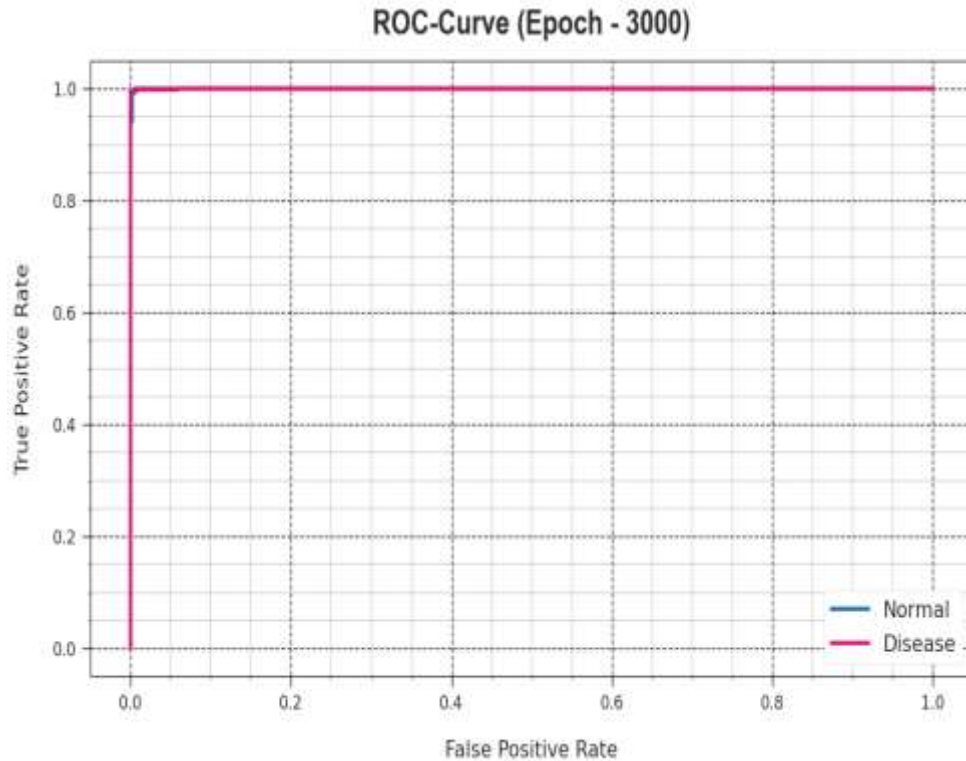


Figure 8: ROC curve of NFSAW-AISHDC algorithm under 3000 epochs

Additionally, in Fig. 8, ROC curves generated by the NFSAW-AISHDC methodology are exhibited in the classification of various classes under 3000 epochs. It offers detailed consideration of the tradeoff among TPR and FRP under various detection threshold values and epoch counts. The figure emphasized the higher classifier solutions of the NFSAW-AISHDC methodology under all classes, outlining the efficiency in addressing several classifier problems. The outcomes of the NFSAW-AISHDC methodology are compared with recent algorithms in Table 3 and Fig. 9 [13].

Table 3. Comparative analysis of NFSAW-AISHDC system with recent models

Methods	$Accu_y$	$Prec_n$	$Reca_l$	$F_{Measure}$
NFSAW-AISHDC	99.67	99.65	99.67	99.66
ACVD-HBOMDL	99.41	99.46	99.40	99.42
SC Model	98.87	98.45	97.62	98.15
J48 Algorithm	97.62	97.55	98.43	98.23
ANN Algorithm	95.57	95.18	94.87	95.29
Bagging Algorithm	95.01	94.41	94.72	94.44
REPTree Algorithm	92.93	92.95	92.48	93.21
SVM Model	84.52	84.98	83.98	84.00

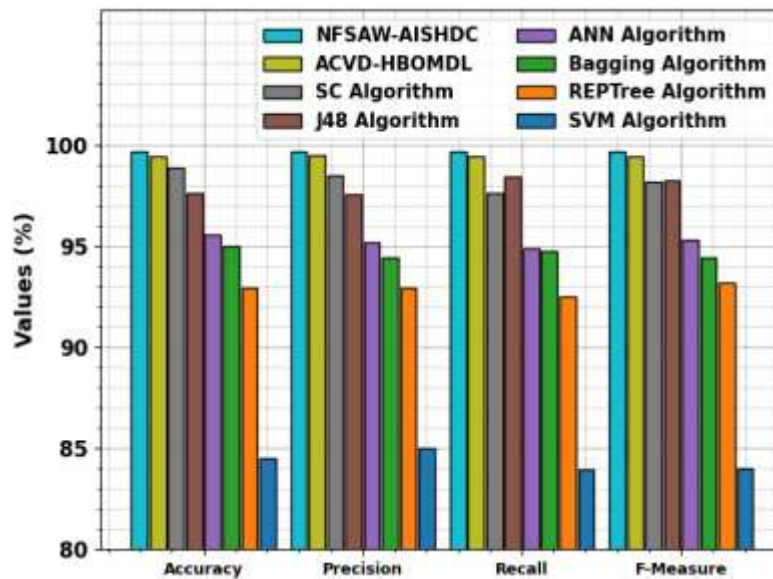


Figure 9: Comparative analysis of NFSAW-AISHDC technique with recent models

The outcomes imply that the SVM system gains worse performance over other models. In line with this, the REPTree, bagging, and ANN models have reported slightly boosted results. Although the ACVD-HBOMDL, SC, and J48 models have resulted in considerable performance, the NFSAW-AISHDC technique demonstrates superior performance with increased  $accu_y$ ,  $prec_n$ ,  $reca_l$ , and  $F_{score}$  of 99.67%, 99.65%, 99.67%, and 99.66%. Hence, the NFSAW-AISHDC technique can be applied for improved detection of HDs.

## 5. Conclusion

In this paper, we have projected a novel NFSAW-AISHDC methodology in healthcare sector. The NFSAW-AISHDC technique mainly focuses on the adoption of NFSAW with FS process for HD detection. It contains three major processes involved min-max normalization, BWO-based FS, and NFSAW-based disease detection. Primarily, the NFSAW-AISHDC method exploits min-max scalar to scale the input data. For feature selection, the NFSAW-AISHDC technique uses BWO algorithm to choose feature subsets. Moreover, the NFSAW-AISHDC technique applies NFSAW approach to the identification of HDs. The performance assessment of the NFSAW-AISHDC method takes place using benchmark dataset. The experimental outcomes underlined the promising results of the NFSAW-AISHDC methodology with other models.

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