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FULL-LENGTH ARTICLE

A Global-best Harmony Search based Gradient Descent Learning FLANN (GbHS-GDL-FLANN) for data classification

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Abstract While dealing with real world data for classification using ANNs, it is often difficult to determine the optimal ANN classification model with fast convergence. Also, it is laborious to adjust the set of weights of ANNs by using appropriate learning algorithm to obtain better classification accuracy. In this paper, a variant of Harmony Search (HS), called Global-best Harmony Search along with Gradient Descent Learning is used with Functional Link Artificial Neural Network (FLANN) for classification task in data mining. The Global-best Harmony Search (GbHS) uses the concepts of Particle Swarm Optimization from Swarm Intelligence to improve the qualities of harmonies. The problem solving strategies of Global-best Harmony Search along with searching capabilities of Gradient Descent Search are used to obtain optimal set of weight for FLANN. The proposed method (GbHS-GDL-FLANN) is implemented in MATLAB and compared with other alternatives (FLANN, GA based FLANN, PSO based FLANN, HS based FLANN, Improved HS based FLANN, Self Adaptive HS based FLANN, MLP, SVM and FSN). The GbHS-GDL-FLANN is tested on benchmark datasets from UCI Machine Learning repository by using 5-fold cross validation technique. The proposed method is analyzed under null-hypothesis by using Friedman Test, Holm and Hochberg Procedure and Post-Hoc ANOVA Statistical Analysis (Tukey Test & Dunnett Test) for statistical analysis and validity of results. Simulation results reveal that the performance of the proposed GbHS-GDL-FLANN is better and statistically significant from other alternatives.

1. Introduction

Data Analysis is an analytical process of examining data to discover useful information and draw conclusions which help in decision making. It integrates diversified techniques under Statistic, Engineering and Science. Since 1990, data are being collected in numerous speed and in large volume in the area

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of web, business management, e-commerce, remote sensors, microarrays gene expression, scientific simulations, production control and engineering design, transactions, stocks and bioinformatics, etc. These explosive growths of data collection and the need of automated extraction of novel, valid, unknown and potentially useful information from the data in large databases gave birth to many data analysis methodology, which includes Data Mining and Business Intelligence.

Data mining is the process of identifying novel, understandable and previously unknown patterns in data which helps in decision making. Most tricky and challenging decision making processes in day to day human life is classification, which helps to make decision from past experience. In data mining, the Classification is defined as a variety of data analysis process that can be used to assign important classes to unknown patterns. Classification task predicts definite class labels and constructs a model based on the training dataset which is used to classify anonymous patterns.

In the recent years, many classification tasks have been proposed in emerging areas of science and engineering which includes document classification [1–3], Sentiment classification [4–7], Fault classification [8–11], Text classification [12–14], Image classification [15–18] and Gene Expression classification and Bio Medical Data classification [19–23] and others [24–30], which have given new shape, motivation and direction to application of the classification task in data mining.

Although a number of traditional classification methods are proposed by many researchers [31–35], first time, Zhang et al. [34] realized that artificial neural network models are alternative to various conventional classification methods which are based on statistics. The artificial neural networks (ANNs) are capable of generating complex mapping between input and the output space; thus, they can form arbitrarily complex nonlinear decision boundaries. Along the way, there are already several artificial neural networks, each utilizing a different form of learning or hybridization. As compared to higher order neural network, the classical neural networks (Example: MLP) are suffering from slow convergence and unable to automatically decide the optimal model for classification. In the last few years, to overcome the limitations of conventional ANNs, some researchers have focused on higher order neural network (HONN) models [36,37] for better performance.

2. Literature survey

In this paper, it is an attempt to design higher order neural network model with competitive learning based on new meta-heuristic optimization algorithm for classification of benchmark datasets from the well known machine learning data repository.

Prior to this, a Chebyshev Functional Link Artificial Neural Network model (Chebyshev-FLANN) with Chebyshev polynomial functional expansion for prediction of financial indices is proposed by Patra et al. [38]. The performance of FLANN and chFLANN is found nearly equivalent and training time for FLANN and chFLANN is noticed as almost half of the MLP. Among MLP, FLANN and Chebyshev-FLANN, the chFLANN is found best among these three. Also it is observed that FLANN and chFLANN are efficient and have less complex architecture as compared to MLP.

Misra and Dehuri [39] have proposed a classification method by using FLANN and simulation results show that proposed FLANN model is capable to handle linearly non-separable classes by increasing the dimension of input space through functional expansion. The execution time and accuracy of this model is found to be better than the other alternatives.

A hybrid functional link artificial neural network (HFLANN) based on genetic algorithm (GA) for optimal input feature selection by using functionally expanded selected features is proposed by Dehuri et al. [40] which address nonlinear nature of classification problems. Through experimental results, the HFLANN is proven to be better in optimal set feature selection as compared to RBFN and FLANN with back propagation learning.

A comprehensive survey on FLANN is made and an efficient PSO based back propagation learning is proposed by Dehuri and Cho [41]. In this paper, the basic concept of FLANN, associated basis functions, learning schemes and development of FLANNs over time are discussed. Also the authors have used PSO based back propagation learning scheme on Chebyshev-FLANN for classification and the proposed method is proved to be better as compared to FLANN by testing with benchmark datasets.

An efficient FLANN for stock price prediction of the closing price of US stocks is suggested by Patra et al. [42] and found to be better in performance in terms of more accurate predictions of stock. In this paper, a FLANN with trigonometric functional expansion (Trigonometric-FLANN) is used and shown to be better result as compared to MLP-based prediction model.

A FLANN based prediction model for prediction of causing genes in gene diseases is proposed by Sun et al. [43]. In this study, three classifiers (i.e. MLP, SVM, FLANN) have been implemented and compared. The performance of the FLANN classifier is found to be better over MLP and SVM.

For better prediction of the stock market indices, Chakravarty and Das [44] have proposed a Functional Link Neural Fuzzy (FLNF) Model and compared with FLANN based prediction model in terms of root mean square error. The simulation results show that the FLNF performs better over FLANN. Also the authors have addressed the issue of falling in local minima in case of back propagation learning by employing Particle Swarm Optimization.

A classification method based on FLANN is achieved by Majhi et al. [45] for classification of online Indian customer behavior and the proposed FLANN model found to be superior in classification accuracy than other statistical approach (discriminant analysis). Also authors have suggested to use psychographic and cultural information for further improvement of the proposed method.

An accurate hybrid FLANN classifier (HFLNN) is proposed by Dehuri and Cho [46] by selecting an optimal subset of favorable input features. This is achieved by eliminating features with fewer or no predictive information. The proposed method is found to be better as compared to FLANN and RBFN.

Forecasting of stock exchange rates is achieved with Genetic algorithm (GA) based FLANN model by Nayak et al. [47] and proposed method is compared with MLP, GA based MLP and GA based FLANN models. The authors have claimed that the FLANN-GA is found better in almost all cases.

Bebarta et al. [48] have implemented few variants of FLANN model (Power FLANN, Legendre FLANN, Chebyshev FLANN and Laguerre FLANN) for forecasting stock price index and performances are measured in terms of standard deviation error, squared error, etc. All the four proposed methods are implemented and found to be simple and efficient to predict the various Indian stock data.

A Bat inspired optimization based FLANN classification method is proposed by Mishra et al. [49]. The method is compared with FLANN and hybrid PSO based FLANN classification method. In this paper, bat algorithm is used to adjust the weights of the FLANN efficiently which results in high accuracy for classification. The simulation results show that the proposed method outperforms FLANN and hybrid PSO based FLANN classifiers.

Various dimension reduction strategies are projected by Mahapatra et al. [50] for the Chebyshev FLANN classifier and have been used for cancer classification. The basic idea used in this paper is to perform PCA, FA, DFT and DCT techniques to reduce dimension of the data and then Chebyshev FLANN classifier is applied for better classification. It is observed that the combination of DCT feature reduction technique along with Chebyshev FLANN classifiers outperforms other possible alternatives.

Mishra et al. [51] have developed MLP, FLANN and PSO-FLANN classification models for classification of biomedical data. In this paper, to extract important input features, an efficient dynamic classifier fusion (DCF) is proposed along with principal component analysis (PCA) scheme. After extraction of optimal input features, LMS classifier is performed along with PSO based Back propagation learning algorithm. Although MLP is a traditional ANN, surprisingly, in this study, PSO based Back propagation learning-MLP is found to be better as compared to FLANN and PSO-FLANN.

An Improved PSO (IPSO) based FLANN classifier (IPSO-FLANN) is proposed by Dehuri et al. [52] and

Table 1 FLANN models and learning methods used for various applications in recent years.

Author(s)	Model used	Learning method employed	Application
Park and Pao [244]	FLANN	Back Propagation	Pattern Recognition
Patra and Kot [242]	Chebyshev FLANN	Back Propagation	System Identification
Abu-Mahfouz [247]	FLANN	Back Propagation	Detection of Gear Faults
Patra et al. [38]	FLANN	Back Propagation	Prediction
Patra et al. [38]	Chebyshev FLANN	Back Propagation	Prediction
Mishra and Dehuri [39]	FLANN	Back Propagation	Classification
Dehuri et al. [40]	FLANN	GA + Back Propagation	Classification
Patra et al. [42]	FLANN	Back Propagation	Stock Price Prediction
Dehuri and Cho [41]	FLANN	PSO + Back Propagation	Classification
Abbas [250]	FLANN	Back Propagation	System Identification
Sun et al. [43]	FLANN	Back Propagation	Disease Gene Prediction
Nanda et al. [251]	FLANN	Back Propagation	Identification of MIMO Plants
Chakravarty and Das [44]	FLNF	Back Propagation	Prediction of Stock Indices
Majhi et al. [77]	FLANN	Gradient Descent	Forecasting of Stock
Majhi et al. [77]	FLANN	Recursive Least Square	Forecasting of stock
Emrani et al. [253]	FLANN	PSO + Back Propagation	System Identification
Majhi et al. [45]	FLANN	Back Propagation	Classification of Consumer Behaviour
Dehuri and Cho [46]	FLANN	GA + Back Propagation	Classification
Sicuranza and Carini [56]	FLANN	Back Propagation	Noise Control
Nayak et al. [47]	FLANN	GA + Back Propagation	Forecasting
Bebarta et al. [48]	FLANN	Back Propagation	Forecasting and Classification
Bebarta et al. [48]	Power FLANN	Back Propagation	Forecasting and Classification
Bebarta et al. [48]	Laguerre FLANN	Back Propagation	Forecasting and Classification
Bebarta et al. [48]	Legendre FLANN	Back Propagation	Forecasting and Classification
Bebarta et al. [48]	Chebyshev FL ANN	Back Propagation	Forecasting and Classification
Mishra et al. [49]	FLANN	BO + Back Propagation	Classification of Microarray Data
Mahapatra et al. [50]	Chebyshev FL ANN	Back Propagation	Classification of Cancer Data
Mishra et al. [51]	FL ANN	Back Propagation	Classification of Bio-Medical Data
Dehuri et al. [52]	FL ANN	IPSO + Gradient Descent	Classification
Sicuranza. and Carini [59]	Recursive FLANN	Back Propagation	Noise Control
George and Panda [57]	FLANN	Back Propagation	Noise Control
Mili and Hamdi [53]	FLANN	PSO + Back Propagation	Classification
Mili and Hamdi [53]	FLANN	DE + Back Propagation	Classification
Parija et al. [58]	FLANN	Back Propagation	Location management
Ali and Haweel [60]	Legendr-FLANN	Back Propagation	Channel Equalization
Durga and Tarun [61]	FLANN	Back Propagation	Wind Power Forecasting
Durga and Tarun [61]	Legendre-FLANN	Back Propagation	Wind Power Forecasting
Durga and Tarun [61]	Chebyshev-FLANN	Back Propagation	Wind Power Forecasting
Cui et al. [62]	FLANN	Back Propagation	Identification of Model
Naik et al. [54]	FLANN	PSO + GA + Gradient Descent	Non-linear Data Classification
Naik et al. [55]	FLANN	HMBO + Gradient Descent	Non-linear Data Classification
Naik et al. [63]	FLANN	HS + Gradient Descent	Non-linear Data Classification

compared with MLP, support vector machine (SVM), RBFN, FLANN with gradient descent learning and Fuzzy Swarm Net (FSN) model. Initially, IPSO is used to optimize the weight value of Functional link ANN and finally, functionally expanded (using trigonometric basis functions) input patterns are supplied to FLANN for classification. The proposed method is found to be simple and better as compared to MLP, SVM, FLANN with gradient decent learning and FSN.

Mili and Hamdi [53] have developed a good number of FLANN based classifier such as PSO based FLANN, GA based FLANN and Differential Evolution (DE) based FLANN for classification task. These classifiers are compared and tested with various expansion functions. In their study, the authors have concluded that the proposed methods are performing better in terms of accuracy and convergence as compared to traditional FLANN.

An efficient classification method based on FLANN and a hybrid learning scheme based on PSO and GA have been proposed by Naik et al. [54] and it is found to be relatively better in performance as compared to other alternatives. The PSO, GA and the gradient descent search are used iteratively to adjust the parameters of FLANN until the error is less than the required value, which helps the FLANN model to get better classification accuracy.

Naik et al. [55] have designed a Honey Bee Mating Optimization (HBMO) based learning scheme for FLANN classifier and compared with FLANN, GA based FLANN and PSO based FLANN classifiers. The proposed method mimics the iterative mating process of honey bees and strategies to select eligible drones for mating process, for selection of best weights for FLANN classifiers.

Along with these applications, many recent applications of FLANN model with various hybrid learning schemes from the period 2000–2015 are listed in Table 1.

Table 1 represents various recent applications of FLANN models with varieties of hybrid learning methods to solve real life applications.

3. Background study of the proposed work

From all the FLANN models discussed in literature survey (Table 1), few of them (Table 2) implement some form of learning methods which learns from past data in Classification tasks in Data mining. Almost all the higher order ANNs (HONNs) including functional link higher order ANN (FLANN) are sensitive to random initialization of weight and rely on the learning algorithm adopted. Although a selection of efficient learning algorithm for HONNs helps to improve the performance, initialization of weights with optimized weights rather than random weights also plays important roles in efficiency of HONNs.

In related works (Table 2), it is noticed that, all most all the previously published works have addressed the issue of random initialization of weight in FLANN by using various optimization algorithms such as Genetic Algorithm (GA) [64,65], Particle Swarm Optimization (PSO) [66], and Honey-Bee Mating Optimization (HBMO) [67,68]. In these papers, various optimization algorithms (GA, PSO, Improved PSO, HMBO, etc.) are used to select the best set of weight for FLANN models for various nonlinear data classification. Although it is reported that these optimization techniques are successfully used in FLANN models for improved models such as GA based FLANN (GA-FLANN) [40], PSO based FLANN (PSO-FLANN) [41], IPSO based FLANN (IPSO-FLANN) [52], HS based FLANN (HS-FLANN) [63] and HBMO based FLANN [55] (HBMO-FLANN), the major negative aspects of these implementations are the requirement of various complicated mathematical operators such as (i) Mutation and Crossover operator in GA in GA-FLANN, (ii) Position and Velocity calculation in PSO in PSO-FLANN and IPSO-FLANN and (iii) Crossover and Mutation in HBMO in HBMO-FLANN. The performance of these models depends upon the way of implementation of these mathematical operations (such as selection of crossover operation, mutation operation and mutation rate) and any changes in these factors may lead to increase in time and space complexity of the algorithm.

Considering these, some new variants of Harmony Search [69] are used in FLANN learning model with Gradient Descent learning scheme for classification. Many researchers are attracted toward the study of harmony search and its applications due to the fact that, HS algorithms have few mathematical requirements as compared to earlier meta-heuristic optimization algorithms and can be easily used for optimization problems. We have surveyed about 170 published papers

Table 2 Various FLANN models and learning methods used for data classification in recent years.

Author(s)	Model used	Learning method employed	Application
Mishra and Dehuri [39]	FLANN	Back Propagation	Classification
Dehuri et al. [40]	FLANN	GA + Back Propagation	Classification
Dehuri and Cho [41]	FLANN	PSO + Back Propagation	Classification
Majhi et al. [45]	FLANN	Back Propagation	Classification of Consumer Behaviour
Dehuri and Cho [46]	FLANN	GA + Back Propagation	Classification
Bebarta et al. [48]	FLANN	Back Propagation	Forecasting and Classification
Nayak et al. [47]	FLANN	Back Propagation	Forecasting of Stocks
Mishra et al. [49]	FLANN	BO + Back Propagation	Classification of Microarray Data
Mahapatra et al. [50]	Chebyshev FL ANN	Back Propagation	Classification of Cancer Data
Mishra et al. [51]	FL ANN	Back Propagation	Classification of Bio-Medical Data
Dehuri et al. [52]	FL ANN	IPSO + Gradient Descent	Classification
Dehuri et al. [52]	MLP	Back Propagation	Classification
Dehuri et al. [52]	SVM	Back Propagation	Classification
Dehuri et al. [52]	FSN	Back Propagation	Classification
Naik et al. [55]	FLANN	HMBO + Gradient Descent	Non-linear Data Classification
Naik et al. [63]	FLANN	HS + Gradient Descent	Non-linear Data Classification

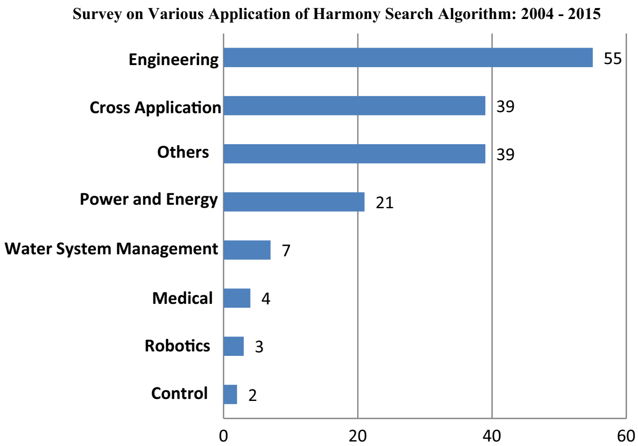

Figure 1 Various contributions on applications of harmony search algorithms.

on application of harmony Search algorithms till the year 2015 in the scientific databases of Elsevier, IEEE and Springer.

It is found that, various papers have been published in the area of different application of HS (Fig. 1) which includes engineering (32.353%), water system management (4.118%), medical (2.353%), robotics (1.765%), control (1.176%), power and energy (12.353%), cross application (22.941%) and others (22.941%). Starting from the development of HS, it has been a keen interest among the diversified researchers and has been used in various real life applications [70–239] (Table 3).

Inspired from successful applications of harmony Search algorithms, in this paper, an attempt has been made to address the intricacy in adjusting the set of weights of the FLANN model by using appropriate learning algorithm. Here the problem solving approach of the Global-best Harmony Search along with learning ability of the Gradient Descent Learning (GDL) is used to obtain the optimal set of weight of FLANN model. The objective is to design an Ease-of-use FLANN model with Global-best Harmony Search technique which requires very few mathematical operation as compared to other meta-heuristics.

In this paper, an attempted has been made to design a FLANN model with hybrid Global-best Harmony Search (GbHS) and Gradient descent search based learning method for classification. The performance in terms of classification accuracy of the proposed method is compared with some of the existing popular methods such as MLP, SVM, and FSN and found that the results are exceeding over others.

Table 3 Various applications of harmony search algorithms.

References	Application area
Lee and Geem [70], Lee et al. [71], Saka [72,73], Zarei et al. [74], Kaveh and Talatahari [75], Fesanghary et al. [76], Fesanghary [77], Kaveh and Shakouri [78], Khazali et al. [79], Parizad et al. [80], Wei et al. [81], Verma et al. [82], Barzegari et al. [83], Nezhad et al. [84], Zhang and Hanzo [85], Gao et al. [86], Jafarpour and Khayyambashi [87], Sarvari and Zamanifar [88], Yadav et al. [89], Erdal et al. [90], Srinivasa et al. [91], Kudikala et al. [92], Mehdizadeh et al. [93], Kermani et al. [94], Gao et al. [95], Bekda and Nigdeli [96], Harrou and Zeblah [97], Del Ser et al. [98], Fesanghary et al. [99], Kaveh and Ahangaran [100], Shariatkhah et al. [101], Degertekin [102], Askarzadeh and Rezazadeh [103], Landa-Torres et al. [104–107], Manjarres et al. [108,109], Gil-Lopez et al. [110], Del Ser et al. [111], Manjarres et al. [112], Yoo et al. [113], Huang et al. [114], Niu et al. [115], Askarzadeh and Masoud [116], Li et al. [117], Akin and Saka [118], Wang et al. [119], Zhai et al. [120], George et al. [121], Ouyang et al. [122], Wang et al. [123], Tarkeshwar et al. [124]	Engineering
Geem [125], Ayvaz [126,127], Geem [128], Geem et al. [129], Ayvaz [130], Cisty [131]	Water/Ground Water System Management
Panchal [132,133], Gandhi et al. [134], Landa-Torres et al. [135]	Medical
Tangpattanakul et al. [136], Yazdi et al. [137], Xu et al. [138]	Robotics
Coelho et al. [139], Das Sharma et al. [140]	Control
Vasebi et al. [141], Coelho and Mariani [142], Ceylan and Ceylan [143], Geem [144], Sinsupan et al. [145], Gao et al. [146], Ceylan et al. [147], Coelho et al. [148], Sui et al. [149], Sivasubramani and Swarup [150], Geem [151], Khorram and Jaberipour [152], Pandi and Panigrahi [153], Sivasubramani and Swarup [154], Chatterjee et al. [155], Afshari et al. [156], Sirjani et al. [157], Sirjani and Mohamed [158], Sirjani et al. [159], Javaheri and Goldoost-Soloot [160], Mukherjee [161]	Power and Energy
Geem [162], Alexandre et al. [163], Geem [164], Wang et al. [165], Diao [166], Cobos et al. [167], Sarvari et al. [168], Hoang et al. [169], Alia et al. [170], Mandava et al. [171], Forsati and Mahdavi [172], Kaizhou et al. [173], Gao et al. [174], Han et al. [175], Yadav et al. [176], Wang et al. [177], Ayachi et al. [178], Ramos et al. [179], Navi et al. [180], Chandran and Nazeer [181], Ahmed et al. [182], Yusof et al. [183], Ko and Sim [184], Li et al. [185], Pan et al. [186,187], Ren et al. [188], Fu and Zhang [189], Jing et al. [190], Peiying et al. [191], Diao and Shen [192], Krishnaveni and Arumugam [193], Ezhilarasi and Swarup [194], Li et al. [195], Hua et al. [196], Ahmad et al. [197], Habib et al. [198], Salcedo-Sanz et al. [199], Gao et al. [200]	Cross-Application
Geem [201], Geem and Choi [202], Geem and Williams [203], Fourie et al. [204], Mun and Geem [205,206], Coelho and Bernert [207], Ma et al. [208], Zou et al. [209,210], Fourie et al. [211], Mohsen et al. [212], Cheng and Yong [213], Bo et al. [214], Kattan et al. [215], Wong and Guo [216], Jaberipour and Khorram [217], Wang et al. [218], Huang et al. [219], Zou et al. [220], Kayhan et al. [221], Wang et al. [222], Kulluk et al. [223], Kattan and Abdullah [224], Alsewari and Zamli [225], Taleizadeh et al. [226], Landa-Torres et al. [227], Kulluk et al. [228], Salcedo-Sanz et al. [229], García-Torres et al. [230], Plasencia et al. [231], Turky et al. [232], Valian et al. [233], Yuan et al. [234], Kong et al. [235,236], Gökçe and Ayvaz [237], Gupta and Jain [238], Salman et al. [239]	Others

The remaining part of this paper is organized as follows: Preliminaries in Section 4, proposed method in Section 5, experimental setup in Section 6, simulation results and performance comparisons in Section 7, proof of statistical significance in Section 8, conclusion in Section 9 and references.

4. Preliminaries

4.1. Functional link artificial neural network architecture

The Functional Link Artificial Neural Network (FLANN) [240] is a class of Higher Order Neural Networks that make use of higher combination of its inputs [241,242] and has been successfully used in many applications such as pattern recognition [243,244], classification [245–247], channel equalization [248], system identification [249–253] and prediction [254]. Even if it has a single-layer network, still it is capable to handle nonlinear separable classification task as compared to MLP.

In FLANN, the dimension of input pattern increases artificially through the functional expansion and then the extended and transformed input data are used to train the feed forward network. During functional expansion, various mathematical functions, such as sine, cosine, and log, are used to transform an original input pattern to its extended version. The number of input terms during functional expansion depends upon the number of attribute of an input pattern. The basic structure of FLANN is depicted in Fig. 2.

The functionally expanded values for dataset x can be generated by using Eq. (1), where $x_i(j)$ stands for jth attribute value of ith pattern and 'x' is a dataset in a form of matrix of order $m \times n$.

$$\varphi(x_i(j)) = \{x_i(j), \cos \Pi x_i(j), \sin \Pi x_i(j), \cos 2\Pi x_i(j), \sin 2\Pi x_i(j) \ldots \cos n\Pi x_i(j), \sin n\Pi x_i(j)\} \quad (1)$$

Total $2n + 1$ number of functionally expanded values are generated for an input attribute value $x_i(j)$ of a pattern x_i, intern,

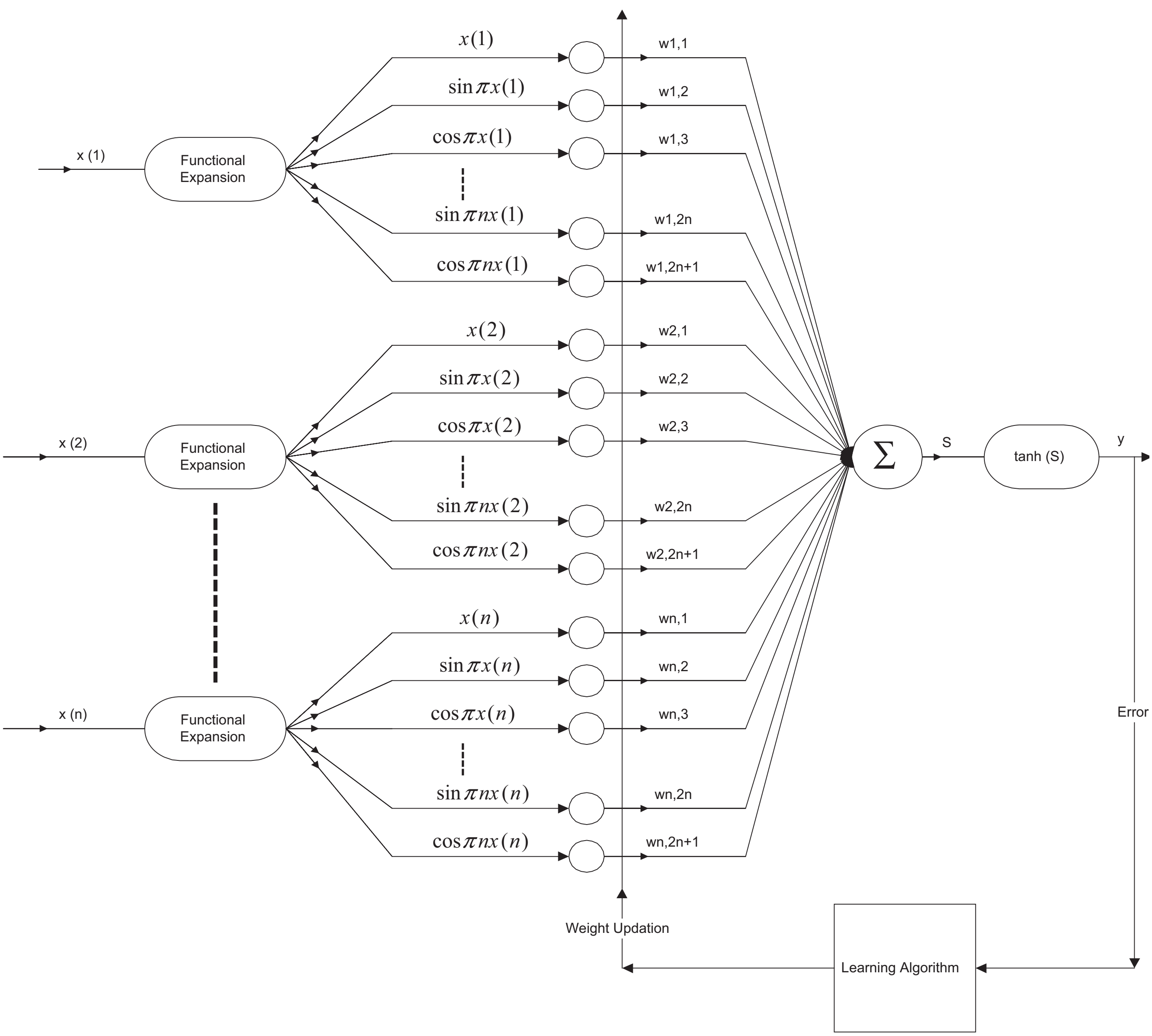

Figure 2 Functional link artificial neural network architecture.

$(n * (2n + 1))$ number of expanded values are generated for a single input pattern x_i. In Eq. (1), value for i and j can be ranged from $i = 1,2\ldots m$ and $j = 1,2\ldots n$, where m and n are number of input pattern and number of attribute values of each input pattern respectively except class level (probably last column of dataset x). Hence, the complete functionally expanded values for dataset x is represented using Eq. (2).

$$\varphi = \{\{\varphi(x_1(1)), \varphi(x_1(2)) \ldots \varphi(x_1(n))\}^T, \{\varphi(x_2(1)), \varphi(x_2(2)) \ldots \varphi(x_2(n))\}^T \ldots \{\varphi(x_m(1)), \varphi(x_m(2)) \ldots \varphi(x_m(n))\}^T\} \quad (2)$$

The weights of FLANN are set randomly prior to the above functionally expanded values 'ϕ' are the input to FLANN classifier. Total $n * (2n + 1)$ number of weights are set for each individual pattern, as each input pattern is transformed to $n * (2n + 1)$ number of functionally expanded values. Random initialization of weight-set for each individual pattern can be visualized as Eq. (3).

$$W_i = \{w_{i,1}, w_{i,2}, \ldots w_{i,2n+1}\}, \quad \text{for } i = 1,2\ldots n \quad (3)$$

where W_i is the weight vector initialized randomly for a single input pattern. Hence, initialization of set of weight for input patterns of dataset 'x' can be viewed as a weight vector $W = \{W_1, W_2 \ldots W_m\}^T$, where W_i is the set of weight for ith pattern in the dataset x. The dataset 'x' is supplied to FLANN in terms of functionally expanded values 'ϕ' and the net output is obtained as follows.

- First, values of S is calculated as $S = \varphi X W = \{s_1, s_2 \ldots s_m\}$.
- Then, the net output Y is computed as $Y = f(S) = \{f(s_1), f(s_2) \ldots f(s_m)\} = \{y_1, y_2 \ldots y_m\} = \{\tanh(s_1), \tanh(s_2) \ldots \tanh(s_m)\}$. Here tanh is used as activation function and net output y_i is for input pattern x_i.

Based on net output y_i and given target value t_i, error of FLANN is calculated and a suitable learning method is adopted to adjust weight values of FLANN.

4.2. Gradient descent learning scheme

Gradient descent learning is the most commonly used training methods in which weights are changed in such a way that network error is declined as rapidly as possible. The learning of FLANN model using Gradient descent method with error of the network is described below.

- Error of kth input pattern is generated as $e(k) = Y(k) - t(k)$ which is used to compute error term $\delta(k) = \left(\frac{1-y_k^2}{2}\right) \times e(k)$, for $k = 1,2\ldots m$, where m is the number of input pattern in a dataset.
- Then, weight factor of 'ΔW' can be computed as $\Delta W_q = \left(\frac{\sum_{i=1}^{L} 2 \times \mu \times \varphi_i \times \delta_i}{L}\right)$, for $q = 1,2\ldots L \times (2n + 1)$. Where $\varphi = (\varphi_1, \varphi_2 \ldots \varphi_L)$, $e = (e_1, e_2 \ldots e_L)$ and $\delta = (\delta_1, \delta_2 \ldots \delta_L)$ are the vector which represent sets of functional expansion, set of error and set of error term respectively where L is the number of input patterns.
- Finally, weight updation is done as $w_{new} = w + \Delta W$ where $w = (w_1, w_2 \ldots w_{L\times(2n+1)})$ and $\Delta W = (\Delta W_1, \Delta W_2 \ldots \Delta W_{L\times(2n+1)})$.

Basically, a better learning algorithm helps the ANN model for fast convergence. Further, a use of competitive optimization technique can, not only improve the convergence of a learning algorithm, but also enhance accuracy of an ANN based classifier. In the next subsection, a new meta-heuristic optimization technique, known as Harmony Search technique and its variants have been described.

4.3. Variants of harmony search

The Harmony Search (HS) [69] is a meta-heuristic algorithm inspired by musical process of searching for a perfect shape of harmony. The algorithm is based on natural musical processes in which a musician searches for a better state of harmony by tuning pitch of each musical instrument, such as jazz improvisation. The music improvisation by pitch adjustment in the Harmony Search is analogous to local and global search process to find better solution in any optimization techniques.

4.3.1. Harmony search

This section contains brief review on working procedure of the harmony search algorithm. In general, basic steps of harmony search can be expressed as follows:

Step 1 Initialize a harmony memory (HM) with randomly generated solution vectors (Harmonies)
Step 2 Repeat Steps 3 and 4 until no further significant growth in fitness of solution vector is noticed or the maximum number of iterations is reached
Step 3 Improvise HM to get New Harmony Memory (NHM)
Step 4 Update the HM based on comparison between solution vectors of HM and NHM in terms of fitness. If any harmony in HM is less fit than harmony in NHM, then harmony in HM is excluded by adding harmony from NHM
Step 5 Exit

Basically, the harmony memory (HM) is a group of predefined number of solution vectors similar to a population of particle in PSO or chromosome in GA. Initially HM is initialized with random solution vectors and gradually, solution vectors in HM are improved by using Step-3 of harmony search procedure known as HM improvisation step. This step is entirely controlled by the parameters: Harmony Memory Consideration Rate (HMCR), Pitch Adjustment Rate (PAR) and Bandwidth (bw).

In HS, the HMCR controls the balance between exploration and exploitation and it is set between 0 and 1. The searching procedure behaves as purely random search, if the HMCR is set to 0 and a value 1 for HMCR specifies 100% of previous solution vectors from HM are taken into consideration for next generation, which means, there is no chance to improve the harmony from outside the HM. In this way, HMCR keeps the balance between exploration and exploitation. Another parameter PAR determines the rate of adjustment of solution vectors based on the bandwidth (bw) which is usually a variable, and behaves as step size.

The HMCR and PAR determine Memory Consideration Probability (MCP), Pitch Adjustment Probability (PAP) and Random Probability (RP) as follows:

$$\mathrm{MCP} = \mathrm{HMCR} * (1 - \mathrm{PAR}) * 100$$
$$\mathrm{PAP} = \mathrm{HMCR} * \mathrm{PAR} * 100$$
$$\mathrm{RP} = 100 - \mathrm{MCP} - \mathrm{PAP}$$

Basically, Improvisation of HM is governed by these parameters (MCP, PAP, and RP).

Example: If HMCR = 0.99 and PAR = 0.45 then MCP = 0.9 * (1 – 0.45) * 100 = 49.5 and PAP = 0.9 * 0.45 * 100 = 40.5 and RP = 100 – 49.5 – 40.5 = 10. Which means, during harmony improvisation phase (Step-3), 49.5% of solution vectors are migrated (without any changes) from previous harmony memory (HM) to New Harmony Memory (NHM), 40.5% of solution vectors are gone through pitch adjustment and then included into NHM and 10% of solution vectors are gone through modification by adding randomly generated values with existing solution vector in HM.

In HS, the bw and PAR are fixed and pitch adjustment is done according to Eq. (4).

$$\mathrm{HM}_i(t+1) = \begin{cases} \mathrm{HM}_i(t+1) = \mathrm{HM}_j(t) - \mathrm{rand}(1) * \mathrm{bw} \text{ if } \mathrm{rand}(1) < 0.5 \\ \mathrm{HM}_i(t+1) = \mathrm{HM}_j(t) + \mathrm{rand}(1) * \mathrm{bw} \text{ if } \mathrm{rand}(1) > 0.5 \end{cases} \quad (4)$$

In Eq. (4), $\mathrm{HM}_i(t+1)$ is the next ith harmony at time $t + 1$ and $\mathrm{HM}_j(t)$ is the jth randomly selected harmony for pitch adjustment at time t.

In recent years, many Harmony Search variants (Fig. 3) have been proposed by the researchers by incorporating some modifications to the original HS algorithm [69]. Further, these variants are some modifications of three major variations of HS and those are Improved HS, Global-best HS and Self Adaptive HS. These variants have some common steps and are different in strategies of solving optimization problem. Overall strategies and steps involved with these variants of Harmony Search have been demonstrated in Fig. 3.

4.3.2. Improved harmony search

The Improved Harmony Search (IHS) [255] is an initial variant of HS, which employs a novel strategy for generation of new solution vectors that not only enhances accuracy but also improves the convergence rate of basic HS algorithm. The authors have claimed the better performance of IHS over HS by eliminating constant parameters (bw, PAR) in HS algorithm and incorporating dynamically changes in PAR and bw with iteration number.

The IHS is free from the fixed values of PAR and bw in the HS algorithm by decreasing bw and increasing PAR with an iteration number and found considerable influence on the quality of solutions. The mechanism of dynamically decreasing of bw with iteration is inspired from the strategy of decreasing the learning rate of neural networks dynamically [256].

Unlike HS, the bw and PAR are not fixed and this value changes according to HS iterations which is achieved by using Eqs. (5) and (6).

$$\mathrm{bw(iter)} = \mathrm{bw}_{\max} \times exp\left(\frac{ln\frac{\mathrm{bw}_{\min}}{\mathrm{bw}_{\max}}}{N} \times \mathrm{iter}\right) \quad (5)$$

In Eq. (5), bw(iter) is the bandwidth in particular iteration ‘iter’, $\mathrm{bw}_{\min}$ and $\mathrm{bw}_{\max}$ are the minimum and maximum bandwidth respectively and N is the number of solution vector in the population.

$$\mathrm{PAR(iter)} = \mathrm{PAR}_{\min} + \frac{\mathrm{PAR}_{\max} - \mathrm{PAR}_{\min}}{N} \times \mathrm{iter} \quad (6)$$

In Eq. (6), PAR(iter) is the pitch adjustment rate in particular iteration ‘iter’, $\mathrm{PAR}_{\min}$ and $\mathrm{PAR}_{\max}$ are the minimum and maximum pitch adjustment rate and N is the number of solution vector in the population.

4.3.3. Global-best Harmony Search

Inspired from successful use of PSO in numerous applications, Omran and Mahdavi [257] have developed Global best Harmony Search (GbHS), which borrowed the concepts from PSO to enhance its performance of HS optimization. Instead of dynamically increasing PAR, authors have suggested to employ the small constant PAR which may prevent overshooting and oscillation that normally occurs in IHS.

In GbHS, it eliminates the difficulties of selecting appropriate bandwidth (bw) by directly adopting the current best pitch (Global best) from the harmony memory and adjusting other solution vectors to improve their qualities in the HM without pitch adjustment step. This process of HM improvisation is analogous to selection of local best (LBest) and global best (GBest) particle (In PSO) from population based on which, changing of position of particles is obtained. The performance of GbHS is found to be significantly better than HS and IHS in terms of quality of solution and convergence rate.

4.3.4. Self adaptive harmony search

In, SAHS [258], the pitch adjustment step in IHS has been modified to incorporate better utilization of its own experiences, by updating the new harmony according to the maximum and minimum values in the HM. Here, the objective is to simplify pitch adjustment step by introducing a new strategy of adjusting new harmony by using maximum and minimum values in HM encountered so far, thereby eliminating bw altogether from HS procedure.

Like IHS, in SAHS, the bw and PAR change with HS iterations. The SAHS is different from IHS in pitch adjustment mechanism as illustrated in Eq. (7).

Let minHM and maxHM denote the lowest and the highest values of the ith variable in the HM respectively and then harmony in HM is further adjusted by the following Equations:

$$\mathrm{HM}_i(t+1) = \begin{cases} \mathrm{HM}_i(t+1) = \mathrm{HM}_j(t) + [\max(\mathrm{HM}) - \mathrm{HM}_j(t)] \times \mathrm{rand}(1) & \text{if } \mathrm{rand}(1) < 0.5 \\ \mathrm{HM}_i(t+1) = \mathrm{HM}_j(t) - [\mathrm{HM}_j(t) - \min(\mathrm{HM})] \times \mathrm{rand}(1) & \text{if } \mathrm{rand}(1) > 0.5 \end{cases} \quad (7)$$

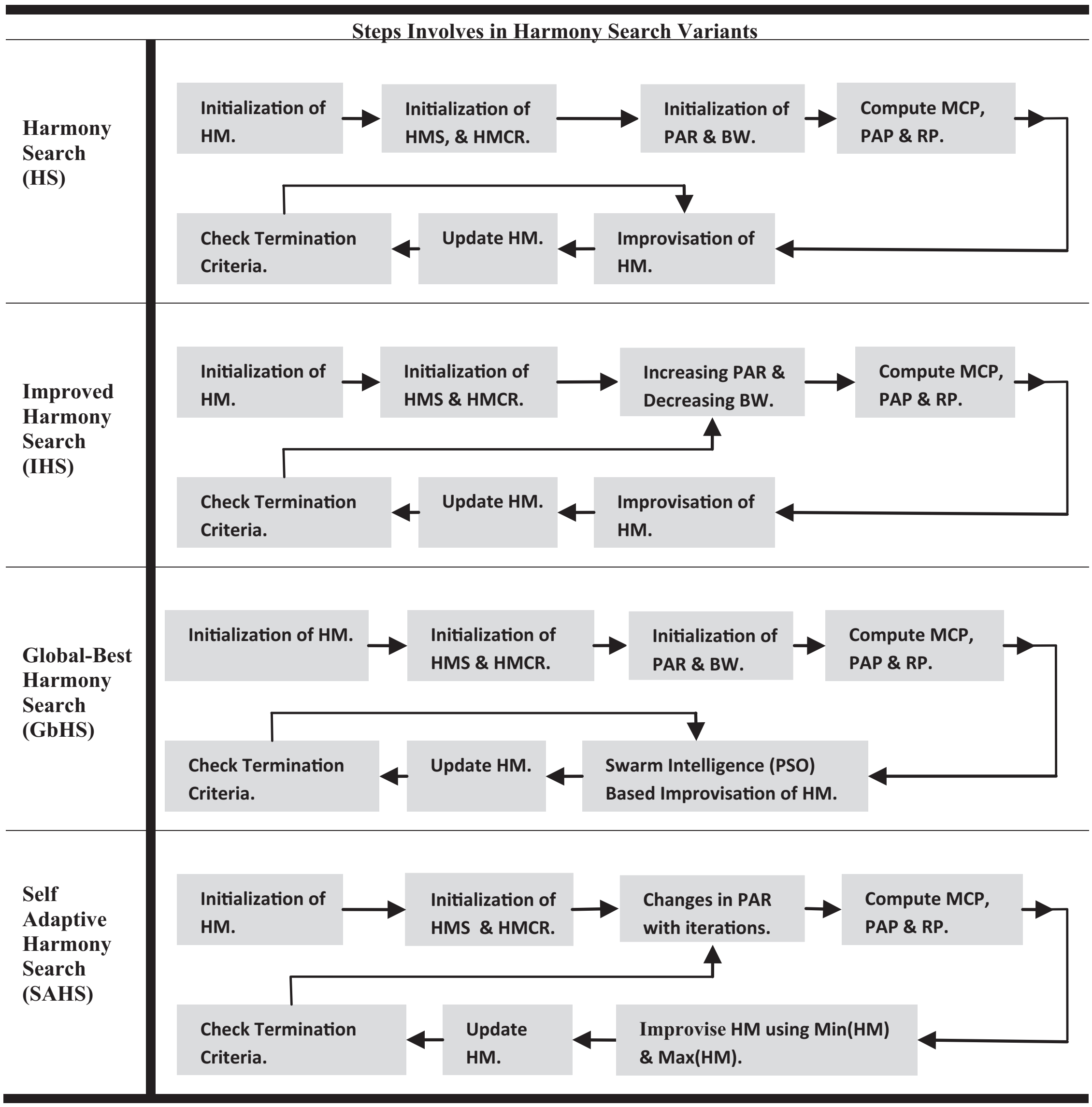

Figure 3 Harmony search variants.

where $\mathrm{HM}_i(t+1)$ is the next ith harmony at time $t + 1$, $\mathrm{HM}_j(t)$ is the jth randomly selected harmony for pitch adjustment at time t, min(HM) and max(HM) are the minimum and maximum values of entire harmony memory (HM) and rand (1) is a uniform number in the $[0, 1]$ range without 1.

5. Proposed method

In this section, we have considered four FLANN classifiers with Gradient descent learning based on four variants of Harmony Search algorithm. In this paper, a deep experimental analysis on Harmony Search algorithm and its different variants (i.e. Improved HS, Global-best HS and Self Adaptive HS) has been done and an attempt has been made to use the problem solving strategies of these variants to improve performance of FLANN classifiers. Here the objective is to select the best set of weight (Weight-set) from a set of randomly selected weight-sets (Population) for FLANN model for classification task. This paper mainly focused on Global-best HS based Gradient Descent Learning-FLANN model (GbHS-GDL-FLANN) for classification and the objective is to investigate the performances of Global-best HS (GbHS) to enhance classification accuracy of FLANN classifier as compared to basic HS (HS), Improved HS (IHS) and Self Adaptive HS (SAHS). Also, the performance of GbHS-GDL-FLANN is compared with other meta-heuristic algorithm (GA based FLANN and PSO based FLANN) to get generalized performance. The pseudo codes developed during implementation of proposed GbHS based Gradient descent learning FLANN (GbHS-GDL-FLANN) are presented in Section 5.1. The simulation results and the comparisons of performance of these hybrid FLANN classifiers (FLANN, GA-GDL-FLANN, PSO-GDL-FLANN, HS-GDL-FLANN, IHS-GDL-FLANN, GbHS-GDL-FLANN and SAHS-GDL-FLANN), MLP, SVM and FSN are discussed in Section 7.

5.1. Global-best Harmony Search based Gradient Descent Learning-FLANN (GbHS-GDL-FLANN)

Initially (Fig. 4), the population of weight-sets (HM) is randomly initialized. Each weight-set is a possible candidate set of weight of FLANN for classification of the dataset. Each individual weight-set in HM can be defined as follows:

$$W_i = \left(w_{i,1}, w_{i,2} \ldots w_{m\times n\times(2\times k+1)}\right) \tag{8}$$

In Eq. (8), the $(2 \times k + 1)$ is the number of functionally expanded values for a single value in input pattern (for a chosen value of k), n is the number of values (features) in a single input pattern and m is the number of patterns in the dataset. The set of weight-sets in the HM (population) is represented as Eq. (9).

$$\text{HM} = (W_1, W_2 \ldots W_m) \tag{9}$$

The objective of this study is to improve the quality of weight-sets by using Global-best HS and to find the best weight-set from the population (HM). The problem solving strategies of Global-best HS are used here to improve the qualities of harmonies in harmony memory (HM) and the complete flow of execution can be realized by using Fig. 4 and pseudo codes (Algorithms 1–4). Initially, the harmony memory (HM) is initialized with 'n' numbers of weight-sets for FLANN. Each weight-set W_i is set to FLANN and the FLANN model is trained with a particular dataset. Based on output of the

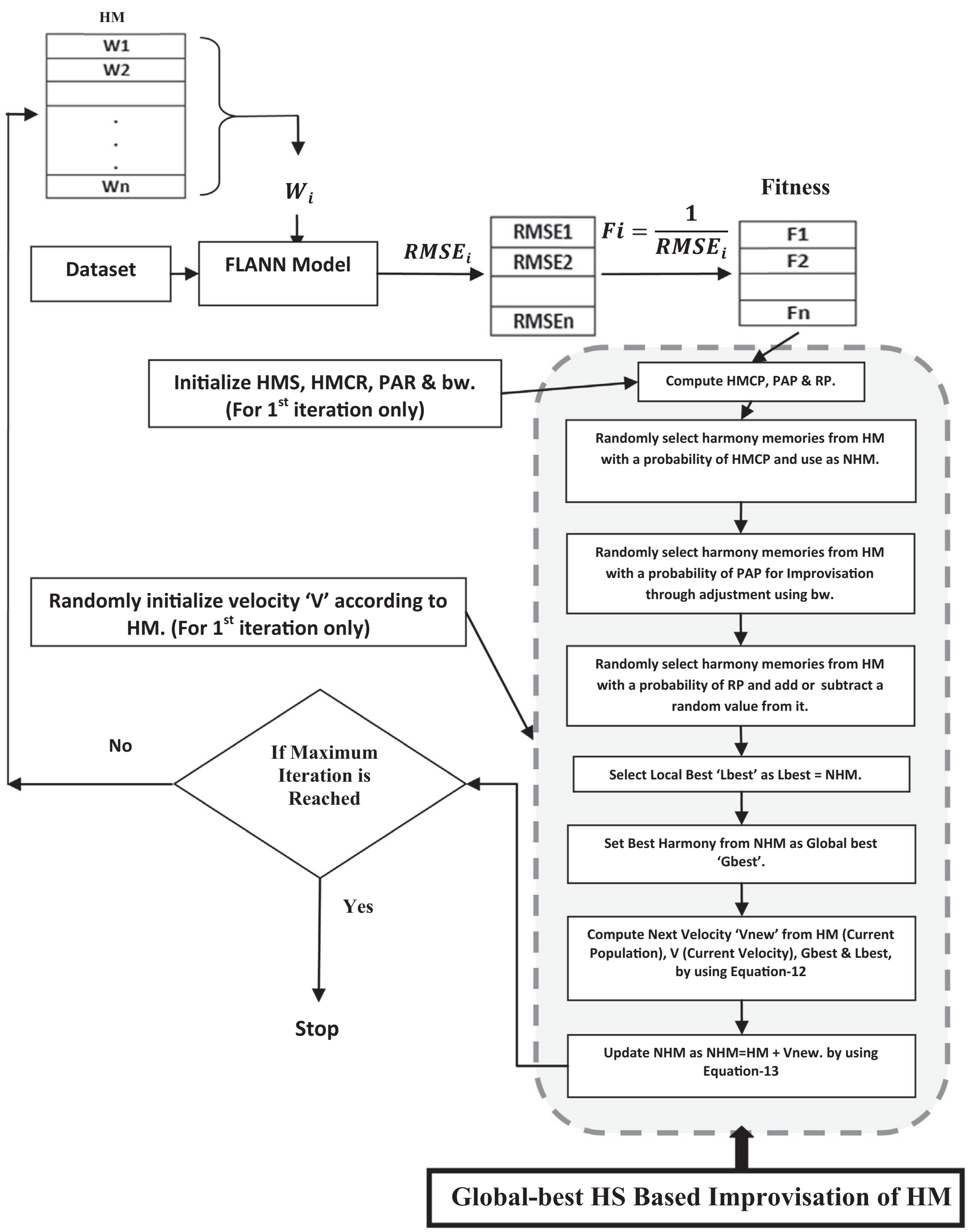

Figure 4 Overview of proposed scheme.

FLANN and given target value, error of the network is obtained. For a specific dataset, the root mean square error (RMSE) (Eq. (10)) for each Weight-set W_i is computed by using output of the FLANN (Algorithm 4) and given target value. Based on RMSEs, fitness of the weight-sets is computed by using Eq. (11).

The Root Mean Square Error (RMSE) of predicted output values $\hat{y}_i$ of a target variable y_i is computed for n different predictions as follows:

$$\mathrm{RMSE} = \sqrt{\frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{n}} \tag{10}$$

$$F_{W_i} = 1/\mathrm{RMSE}_i \tag{11}$$

In Eq. (11), W_i is the ith weight-sets in the population, $RMSE_i$ is the root mean square error of ith weight-set and F_{W_i} is the fitness of ith weight-set W_i.

After evaluation of fitness values for each weight-set in HM, the HM goes through HM improvisation process based on Global-best Harmony Search (GbHS). During this, the parameters: HMS (Harmony Memory Size), HMCR (Harmony Memory Consideration Rate), PAR (Pitch Adjustment Rate) and bw (Bandwidth) are set and based on which MCP (Memory Consideration Probability), PAP (Pitch Adjustment Probability) & RP (Random Probability) are computed (Algorithm 1). Basically, the Harmony Search procedure is governed by these parameters.

Algorithm 2 represents pseudo-codes for Harmony Memory improvisation in which, initially, among all weight-sets (harmonies) in HM, some are randomly selected with a probability of MCP (Memory Consideration Probability) and included into New Harmony Memory (NHM). Here the objective is to migrate some weight-sets (harmonies) from HM into NHM without any changes on them, which serve as new harmonies. For the improvement of weight-sets through pitch adjustment, some weight-sets are selected randomly from HM with a probability of PAP and then they are adjusted based on the variable distance bandwidth (bw) which is similar to the local search method with a step size bw. Similarly, with a probability of Random Probability (RP), some weight-sets are selected randomly and added to NHM by suitably adding or subtracting a random value on it. Although Global-best Harmony Search is suggested to bypass the pitch adjustment step, better result also can be obtained through pitch adjustment of harmonies.

After the generation of harmonies NHM from HM through Harmonic Memory Consideration, Pitch Adjustment and Random Selection phases with probabilities of MCP, PAP and RP respectively, all the harmonies in NHM are treated as local best particles (LBest) from which the harmony with best fitness is chosen as global best particle (GBest). Here, the population of harmonies in HM is analogous to population of particles in PSO. The next velocities (Vnew) of harmonies (particles) is computed by using V (Initial Velocity), LBest and Gbest from Eq. (12). After obtaining next velocity Vnew, the next position of harmonies in NHM is computed from Eq. (13) (Algorithm 2).

$$V_i(t+1) = V_i(t) + c_1 * \mathrm{rand}(1) * (\mathrm{lbest}_i - X_i(t)) + c_2 * \mathrm{rand}(1) * (\mathrm{gbest}_i - X_i(t)) \tag{12}$$

$$X_i(t+1) = X_i(t) + V_i(t+1) \tag{13}$$

After improvisation of HM by using Glabal-best Harmony Search optimization, the HM is updated by based on comparison of fitness of weight-sets in HM and NHM. If the fitness of ith weight-set in HM is less than fitness of ith weight-set in NHM, then HM(i,:) will be replaced by NHM (i,:) else HM(i,:) serves as new harmony for next iteration. The pseudo codes for HM updation procedure are represented in Algorithm 3. These processes are continued iteratively until maximum iteration is reached or increase in fitness of weight-sets in HM in subsequent iteration is not significant. The complete schemes of the proposed method can be realized in Fig. 4.

Algorithm 1. Global-best-Harmony-Search-GDL-FLANN (GbHS-GDL-FLANN) Procedure

% HMS: Harmony Memory Size, HMCR: Harmony Memory Consideration Rate, PAR: Pitch Adjustment Rate.
% Randomly initialize a harmony memory (HM) with size HMS.
HM = −1 + (1 − −1).*(rand (m, l));
% *Where* m is the number of weight-set in population and l is the length of each weight-set.

% Initialization of HMS, HMCR and PAR.
HMS = 40;
HMCR = 0.9;
PAR = 0.3;
bw = zeros(1,l) + 0.0001;

% Compute MCP(memory consideration probability), PAP(pitch adjustment probability) and RP(randomization probability).
MCP = HMCR*(1-PAR)*100;
PAP = HMCR*PAR*100;
RP = 100-MCP-PAP;

Iter = 0;
While (1)
% Improvisation of Harmony Based on Global-best HS Optimization
Function NHM = ImprovizationOfHarmonyMemory (HM, HMS, MCP, PAP, RP, bw);

% Updation of HM
Function HM = UpdateHarmonyMemory(HM, NHM);
% Check for Termination Criteria.
if **(iter > = MAX_ITERATION)**
break;
end if
iter = iter + 1;
End While

Algorithm 2. ImprovizationOfHarmonyMemory Procedure

Function NHM = **ImprovizationOfHarmonyMemory**(HM, HMS, MCP, PAP, RP, bw)
for **i = 1:1:HMS**
r = rand(1)*100;
% Select jth weight-set randomly from harmony memory with memory consideration probability (MCP) which serve as New Harmony Memory (NHM).

(*continued on next page*)

```
If (1 < = r && r < = MCP)
        j = floor (mod((rand(1)*1000),
        HMS)) + 1;
        NHM(i,:) = HM(j,:);
Endif
% Select jth weight-set randomly from
harmony memory with a probability of
PAR for pitch adjustment to improve
quality of weight-set in HM which serves
as new harmony memory (NHM). The
PAR and appropriate bandwidth (bw)
serve the purpose. It is similar to the local
search method with step size of variable
distance bandwidth.
If (MCP + 1 < = r && r < = MCP + PAP)
    j = floor(mod((rand(1)*1000), HMS))
    + 1;
    r1 = rand(1);
    If (r1 < = 0.5)
        for k = 1:1:lbw, where lbw is the
        length of bw
            NHM(i,k) = HM(j,k) −
            rand(1)*bw(1,k);
        End
    Else
        for k = 1:1:lbw, where lbw is the
        length of bw
            NHM(i,k) = HM(j,k)
            + rand(1)*bw(1,k);
        End
    End
endif
% Select jth weight-set randomly from
harmony memory with a probability of RP
which serve as new harmony memory
(NHM). In this phase, a jthweight-set is
selected randomly from HM and added to
NHM by suitably adding or subtracting a
random value from it.
If (MCP + PAP + 1 < = r && r < = MCP
+ PAP + RP)
        j = floor(mod((rand(1)*1000),
        HMS)) + 1;
        NHM(i,:) = HM(j,:) + (−0.1
        + (0.1 − −0.1).*rand(1));
Endif

% Global best Harmony 'gbest' Selection:
Select best harmony (weight-sets) from
population having highest fitness among all
weight-sets in the population (HM).
  lbest = NHM; for i = 1:1:HMS
        w = lbest(i,:);
        Flbest(i,1) = fitfromtrain
        (φ, w, t, μ);
  end
  [mx,mxi] = max(Flbest);
  gbest = lbest(mxi,:);
% Compute next velocity 'Vnew':
Compute next velocity Vnew from lbest,
gbest, NHM and current velocity V.
  c1 = 2; c2 = 2;
  For i = 1:1:rlbest, where rlbest is the
  number of row in lbest
            For j = 1:1:clbest, where clbest is
            the number of column in lbest
                Vnew(i,j) = V(i,j) +
                rand(1)*c1*(lbest(i,j)
                − HM(i,j)) + rand
                (1)*c2*(gbest(1,j) −
                HM(i,j));
            End
        End
        % Generate next position of harmony
        NHM from old NHM and new velocity
        'Vnew'.
        NHM = HM + Vnew;
    endfor
end
```

Algorithm 3. UpdateHarmonyMemory Procedure

```
Function HM = UpdateHarmonyMemory (HM, NHM)
        % Update the HM: If the new harmony
        (weight-sets) in NHM is better than the
        harmony in the HM, then add the new
        harmony into the HM by excluding the worst
        harmony from the HM.
        for i = 1:1:HMS
            w = HM(i,:);
            F1(i,1) = fitfromtrain (φ, w, t, μ);
        endfor
        for i = 1:1:HMS
            w = NHM(i,:);
            F2(i,1) = fitfromtrain (φ, w, t, μ);
        endfor
        lf = length(F1);
        for i = 1:1:lf
            if (F1(i,1) < F2(i,1))
                HM(i,:) = NHM(i,1);
            end if
        endfor
end
```

Algorithm 4. fitfromtrain Procedure

function F = **fitfromtrain** ($\boldsymbol{\varphi}, w, t, \mu$)

$S = \varphi \cdot w$

$Y = \tanh(S)$;

If $\varphi = (\varphi_1, \varphi_2 \ldots \varphi_L)$, $e = (e_1, e_2 \ldots e_L)$ and $\delta = (\delta_1, \delta_2 \ldots \delta_L)$ are vector which represent set of functional expansion, set of error and set of error tern respectively, then the weight factor of w 'ΔW' is Computed as follows: $\Delta W_q = \left(\frac{\sum_{i=1}^{L} 2 \times \mu \times \varphi_i \times \delta_i}{L}\right)$.

Compute error term $\delta(k) = \left(\frac{1 - y_k^2}{2}\right) \times e(k)$, for $k = 1, 2 \ldots L$ where L is the number of pattern.

$e = t - y$;

Compute root mean square error (RMSE) by using Eq. (10) from target value and output.

$F = 1/\text{RMSE}$, where F is fitness of the of FLANN model.

end

6. Experimental setup

In this section, the environment for simulation, the dataset used for training & testing phase and the parameter setting for proposed methods during simulation are presented.

All the classification methods (FLANN, GA-FLANN, PSO-FLANN, HS-FLANN, IHS-FLANN, SAHS-FLANN and GbHS-FLANN) are implemented in Matlab (Version 9.0) in a system with Window XP operating system. After obtaining the results of simulation, statistical analysis has been carried out using SPSS statistical tool (Version 16.0).

The benchmark datasets (Table 4) used for classification are originated from UCI machine learning repository [259] and processed by KEEL software [260].

Table 4 represents the list of benchmark datasets which is used to evaluate the models. All the datasets are presented along with their number of patterns, number of attributes (without class attribute) and number of classes.

The detail descriptions about all these dataset can be obtained at 'http://archive.ics.uci.edu/ml/' and 'http://keel.es/'.

6.1. Parameters setting used for simulation

6.1.1. FLANN parameter

During the learning of the FLANN model, the gradient descent learning method is used by setting 'μ' to 0.13. The value of 'μ' is obtained by testing the models in the range 0–3. Each value in the input pattern is expanded to 11 number of functionally expanded input values by setting $n = 5$. (As FLANN model suggests to generate $2n + 1$ number of functionally expanded input values for a single value in the input pattern.)

6.1.2. Harmony search parameter

Harmony Memory Size (HMS): 40
Harmony Memory Consideration Rate (HMCR): 0.9
Pitch Adjustment Rate (PAR): 0.3
Bandwidth (bw): 0.0001

6.1.3. Improved harmony search parameter

Harmony Memory Size (HMS): 40
Harmony Memory Consideration Rate (HMCR): 0.9
Pitch Adjustment Rate (PAR): $\text{PAR}_{\min} = 0.01$, $\text{PAR}_{\max} = 0.9$
Bandwidth (bw): $\text{bw}_{\min} = 0.0001$, $\text{bw}_{\max} = \frac{1}{20\times(UB-LB)}$

Table 4 Dataset information.

Dataset	Number of pattern	Number of features (excluding class label)	Number of classes
Monk 2	256	06	02
Iris	150	04	03
Heart	256	13	02
Hayesroth	160	04	03
Wine	178	13	03
Ionosphere	351	33	02
Hepatitis	80	19	02
Pima	768	08	02
New Thyroid	215	05	03
Bupa	345	06	02
Dermatology	256	34	06

6.1.4. Global-best Harmony Search parameter

Harmony Memory Size (HMS): 40
Harmony Memory Consideration Rate (HMCR): 0.9
Pitch Adjustment Rate (PAR): 0.3
Bandwidth (bw): 0.0001

6.1.5. Self adaptive harmony search parameter

Harmony Memory Size (HMS): 40
Harmony Memory Consideration Rate (HMCR): 0.9
Pitch Adjustment Rate (PAR): $\text{PAR}_{\min} = 0.01$, $\text{PAR}_{\max} = 0.9$

7. Results and comparisons

In this section, the classification accuracies (Eq. (14)) obtained from various methods for all benchmark datasets with their comparison results are represented. These classification accuracies (Tables 6–8) are observed individually for training and testing phase.

$$\text{Classification accuracy} = \frac{\sum_{i=1}^{n}\sum_{\substack{j=1,\\ i=j}}^{m}\text{CM}_{i,j}}{\sum_{i=1}^{n}\sum_{j=1}^{m}\text{CM}_{i,j}} \times 100 \tag{14}$$

In Eq. (14), the CM is the confusion matrix which represents number of well classified and miss classified pattern after classification operation.

Here n and m are no. of row and no. of column of CM respectively and they are supposed to be equal (i.e. $n = m$).

7.1. Cross validation

The Cross-Validation [261] is a statistical method to estimate generalized performance of the learned model from data which compare learning algorithms by dividing data into two segments: training set & testing set, which are used to train and evaluate the model respectively. In k-fold cross-validation [262], the data are partitioned into k equally or nearly equally sized fragments on which training and validation are performed such that, in each test different fold of the data is used for training and validation.

In this paper, all the datasets used for classification are prepared for cross validation by using 5-folds cross validation technique. During the preparation of datasets for 5-fold cross validation, 5 pairs of dataset sample are created and each pair contains datasets for training and testing phase.

Table 5 represents 5-fold cross validated Newthyroid dataset in which dataset is divided into 5 pair datasets. Each pair contains dataset for training and testing which are used to train and test the models respectively.

For example (Table 5), the 'newthyroid-5-1tra.dat' and 'n ewthyroid-5-1tst.dat' data are a pair of datasets sample of New Thyroid dataset which is used for training and testing phase for a single run respectively. As 5-fold cross validation is employed, the New Thyroid datasets contains 5 such pair of dataset sample for training and testing the algorithms.

The 5-fold cross validated dataset for NEW THYROID dataset is presented in Table 5. All other datasets are prepared for 5-fold cross validation in the same fashion and collected from KEEL Dataset Repository [260]. The average classification accuracies on 5-fold cross validation dataset during training and testing phase are listed in Tables 6–8. In Tables 6–8, the average of classification accuracies of algorithms on 'new thyroid-5-1tra.dat', 'newthyroid-5-2tra.dat', 'newthyroid-5-3tr a.dat', 'newthyroid-5-4tra.dat' and 'newthyroid-5-5tra.dat' is posted as the classification accuracy in training phase for New Thyroid dataset. Similarly, the average of classification accuracies of algorithms on 'newthyroid-5-1tst.dat', 'newthyr oid-5-2tst.dat', 'newthyroid-5-3tst.dat', 'newthyroid-5-4tst.da t' and 'newthyroid-5-5tst.dat' is posted as the classification accuracy in testing phase.

Table 6 describes the comparison of classification accuracies of FLANN, GA based FLANN (GA-FLANN), PSO based FLANN (PSO-FLANN) and HS based FLANN (HS-FLANN) classifiers and Table 7 represents comparison of other 4 classifiers: HS based FLANN (HS-FLANN), Improved HS based FLANN (IHS-FLANN), Self-Adaptive HS based FLANN (SAHS-FLANN) and Global-best HS based FLANN (GbHS-FLANN), which are based of variants of Harmony Search technique.

After comparison of proposed method with hybrid models (Tables 6 and 7), we have made some comparison with other similar approaches in the same area. The projected method (GbHS-FLANN) is compared with Multi-Layer Perceptron [52], Support Vector Machine [52] and Fuzzy System Nets [52]. Table 8 represents the average classification accuracies of the GbHS-FLANN, MLP, SVM and FSN for both training and testing phase. The average of training and testing accuracies on the datasets are listed in Table 9. The overall statistic on performance of all the methods in this study is shown in Fig. 5. From the simulation results (Table 9), it clearly indicates that the proposed GbHS-FLANN outperforms over the other results in all the tested datasets.

In this study, the performance of GA, PSO, HS, IHS, SAHS and GbHS is analyzed in order to know the improvement of harmonies (weight-sets) in the population by these algorithms in different generation. The changes in fitness of weight-sets in different generations are observed in all the 11 number of datasets and Figs. 6–16 demonstrate the improvements of fitness of weight-sets in the population.

8. Proof of statistical significance

In this section, the statistical comparison of classifiers over multiple datasets [263] is presented to argue the projected method is statistically better and significantly different from

Table 5 Datasets in 5-fold for cross validation.

Dataset	Data files	Number of pattern	Task	Number of pattern in class-1	Number of pattern in class-2	Number of pattern in class-3
New Thyroid	newthyroid-5-1tra.dat	172	Training	120	28	24
	newthyroid-5-1tst.dat	43	Testing	30	07	06
	newthyroid-5-2tra.dat	172	Training	120	28	24
	newthyroid-5-2tst.dat	43	Testing	30	07	06
	newthyroid-5-3tra.dat	172	Training	120	28	24
	newthyroid-5-3tst.dat	43	Testing	30	07	06
	newthyroid-5-4tra.dat	172	Training	120	28	24
	newthyroid-5-4tst.dat	43	Testing	30	07	06
	newthyroid-5-5tra.dat	172	Training	120	28	24
	newthyroid-5-5tst.dat	43	Testing	30	07	06

Table 6 Comparison of results among FLANN, GA-FLANN, PSO-FLANN and HS-FLANN.

Datasets	Classification accuracies of classifiers in %							
	FLANN		GA-FLANN		PSO-FLANN		HS-FLANN	
	Training	Testing	Training	Testing	Training	Testing	Training	Testing
Monk 2	93.828	92.043	96.545	93.199	97.453	95.466	97.914	96.537
Iris	96.847	97.368	97.13	98.166	97.352	98.65	97.857	99.472
Heart	88.963	78.481	89.407	79.074	89.778	79.852	89.917	80.222
Hayesroth	90.359	82.313	91.063	83.562	91.266	83.937	91.547	85.063
Wine	92.76	93.186	94.368	95.536	97.762	95.627	97.597	95.570
Ionosphere	79.482	80.927	87.336	89.152	92.372	90.18	91.552	90.069
Hepatitis	73.519	70.593	80.275	75.826	80.028	75.42	82.481	76.273
Pima	78.416	78.76	78.64	78.80	80.126	79.47	80.683	80.581
Thyroid	93.918	76.558	94.198	77.535	94.302	78.791	94.407	79.256
Bupa	72.16	72.76	74.321	75.5	76.384	76.75	76.318	76.358
Dermatology	96.358	92.442	96.946	93.859	97.011	94.08	97	93.872

Table 7 Comparison of results among HS-FLANN, IHS-FLANN, SAHS-FLANN and GbHS-FLANN.

Datasets	Classification accuracies of classifiers in %							
	HS-FLANN		IHS-FLANN		SAHS-FLANN		GbHS-FLANN	
	Training	Testing	Training	Testing	Training	Testing	Training	Testing
Monk 2	97.914	96.537	97.929	96.552	98	96.634	98.019	96.692
Iris	97.857	99.472	97.871	99.695	97.869	99.541	98.164	99.58
Heart	89.917	80.222	89.924	80.275	89.932	80.295	89.95	80.361
Hayesroth	91.547	85.063	91.557	85.193	91.602	85.26	91.582	85.247
Wine	97.597	95.570	97.902	95.63	97.927	95.783	98.152	95.923
Ionosphere	91.552	90.069	91.893	90.173	92.735	90.672	92.95	91.363
Hepatitis	82.481	76.273	82.638	76.334	82.533	76.294	82.586	76.306
Pima	80.683	80.581	80.835	80.593	80.738	80.587	82.733	81.53
Thyroid	94.407	79.256	94.437	79.263	94.426	79.261	94.804	79.335
Bupa	76.318	76.358	76.475	76.925	76.618	77.426	78.236	78.754
Dermatology	97	93.872	97.046	94.382	97.176	94.762	97.369	95.442

Table 8 Comparison of results among MLP, SVM, FSN and GbHS-FLANN.

Datasets	Classification accuracies of classifiers in %							
	MLP		SVM		FSN		GbHS-FLANN	
	Training	Testing	Training	Testing	Training	Testing	Training	Testing
Iris	98.15	94.00	91.69	91.70	97.182	96.00	98.164	99.58
Heart	82.63	80.42	85.20	84.19	85.19	84.86	89.95	80.361
Wine	96.14	92.29	79.06	73.66	97.87	93.69	98.152	95.923
Ionosphere	74.61	73.28	83.74	83.74	90.54	87.5	92.95	91.363
Hepatitis	60.42	60.83	76.27	63.18	76.57	72.52	82.586	76.306
Pima	76.61	77.19	79.68	75.37	75.27	76.39	82.733	81.53
Thyroid	79.78	79.77	90.70	90.76	96.74	94.39	94.804	79.335
Bupa	67.52	67.39	74.57	68.53	65.19	65.00	78.236	78.754
Dermatology	86.78	80.63	95.49	87.65	96.28	90.65	97.369	95.442

Table 9 Comparison of average classification accuracy of MLP, SVM, FSN and GbHS-FLANN.

Datasets	Average classification accuracies of classifiers in %			
	MLP	SVM	FSN	GbHS-FLANN
Iris	96.075	91.695	96.591	98.872
Heart	81.525	84.695	85.025	85.1555
Wine	94.215	76.36	95.78	97.0375
Ionosphere	73.945	83.74	89.02	92.1565
Hepatitis	60.625	69.725	74.545	79.446
Pima	76.9	77.525	75.83	82.1315
Thyroid	79.775	90.73	95.565	87.0695
Bupa	67.455	71.55	65.095	78.495
Dermatology	83.705	91.57	93.465	96.4055

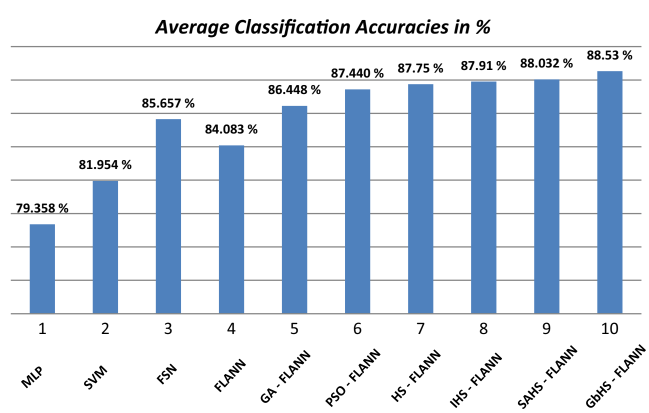

Figure 5 Comparisons of results of proposed method with all related work.

other alternative classifiers by using Friedman test [264,265]. List of datasets on which these tests have been carried out and the assigned ranks to each of the considered methods is presented in Table 10.

8.1. Friedman test

The Friedman test is a nonparametric statistical method which computes average ranks of algorithms (Eq. (15)) and compares them. In Eq. (15), r_i^j is the rank of the jth of k number of classifiers on ith of N number of datasets.

In Table 10, all the classification models are ranked based on their performance on datasets. Each classifier is assigned with a rank which is mentioned with brackets. The models with lowest and highest rank are considered to be models having best and worst performance respectively.

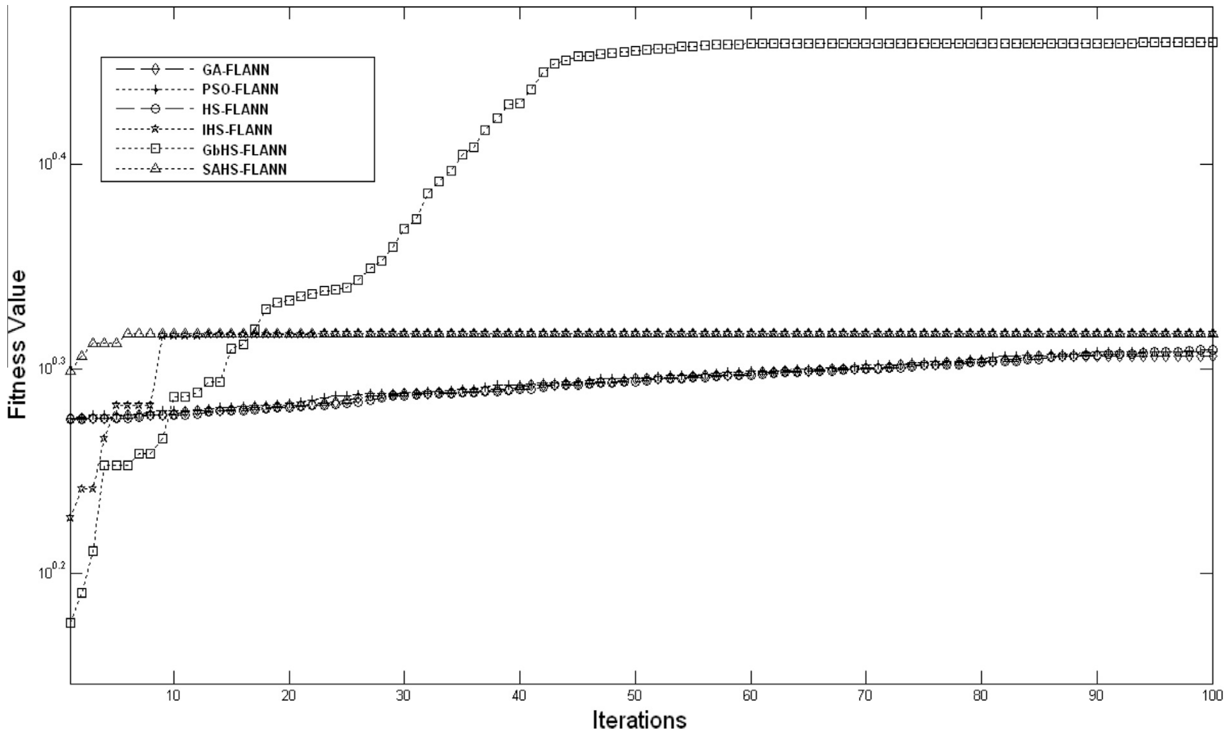

Figure 6 Improvements in fitness of population in different iterations observed in MONK2 dataset.

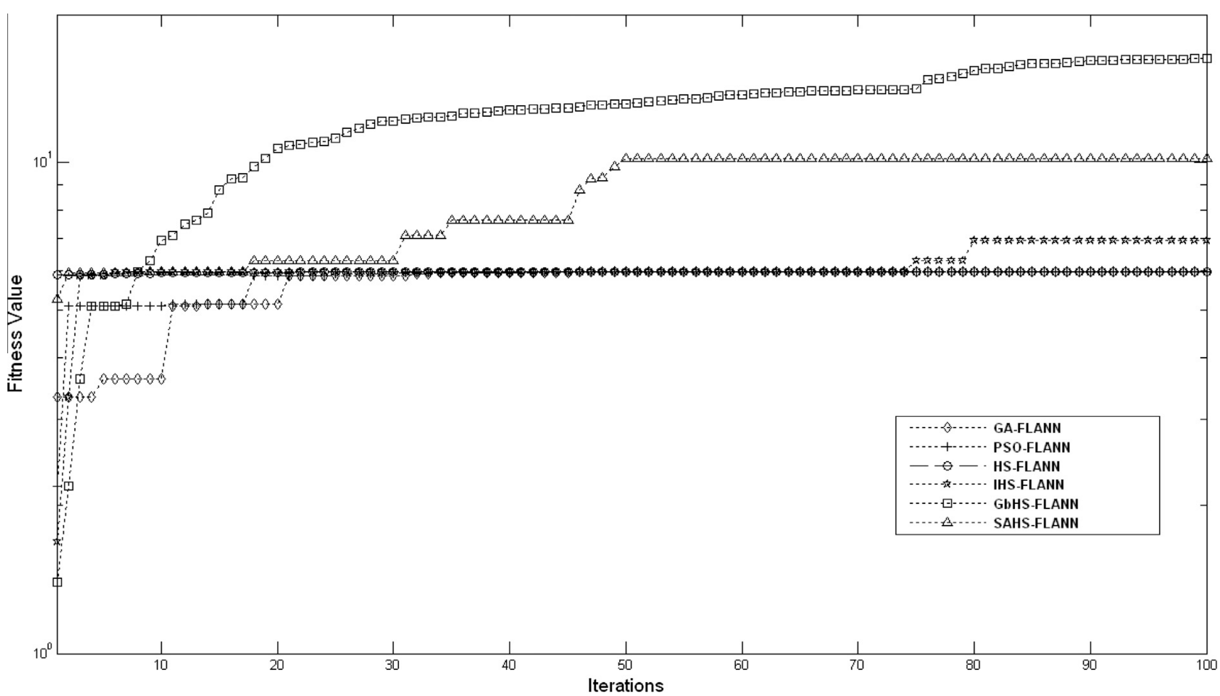

Figure 7 Improvements in fitness of population in different iterations observed in IRIS dataset.

In Table 10, the ranks of each classifier on various datasets are shown in brackets. Based on r_i^j, the average ranks of seven classifier is found from Eq. (15).

$$R_j = \frac{1}{N}\sum_i r_i^j \tag{15}$$

The average ranks for all classifiers are found as follows:

$$\{R_1 = 7, R_2 = 5.91, R_3 = 4.636, R_4 = 4.364, R_5 = 2.636, R_6 = 2.273, R_7 = 1.182\}$$

The X_F^2 value is computed from the average rank R_j of each classifier by using Eq. (16). In this study, we got the value of X_F^2 as 61.232. From the value of X_F^2, the Friedman statistics F_F is computed by Eq. (17) and found as 128.42281.

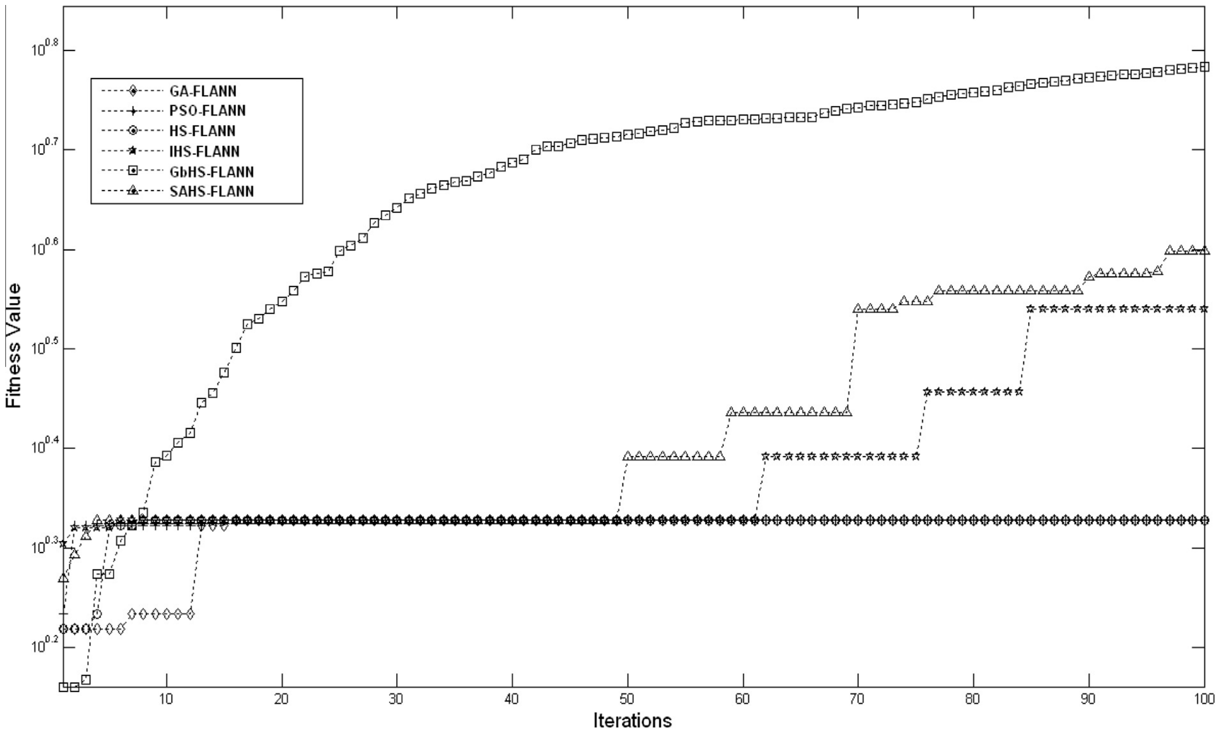

Figure 8 Improvements in fitness of population in different iterations observed in HEART dataset.

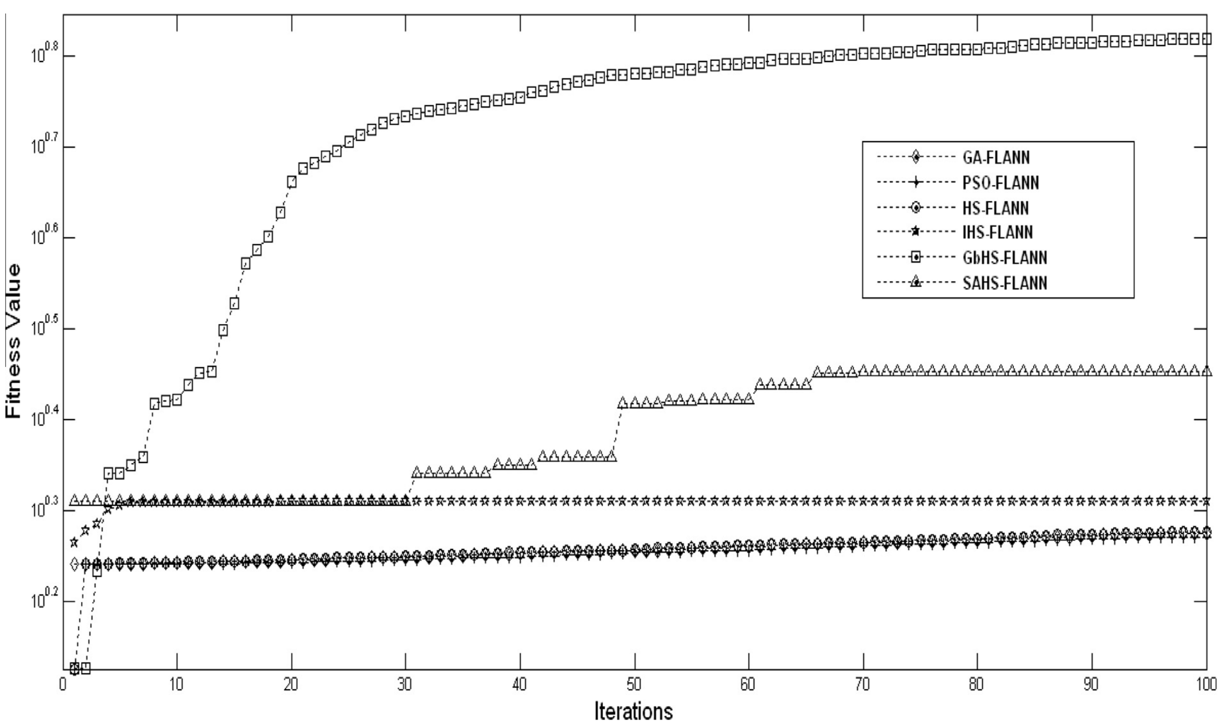

Figure 9 Improvements in fitness of population in different iterations observed in HAYESROTH dataset.

The Friedman statistic is distributed according to X_F^2 with $(k-1)$ degree of freedom under the null-hypothesis (H_0) and the critical value of the F-distribution can be obtained from F_F with $(k-1)$ and $(k-1)*(N-1)$ degree of freedom. In our case, for the 7 number of classifiers and 11 number of datasets, $F_F = 128.42281$ with $7-1=6$ and $(7-1)*(11-1)=60$ degrees of freedom, a crucial value = 3.12 is obtained from suitably selecting $\alpha = 0.01$. Density plot for degree of freedom (6, 60) is obtained and displayed in Fig. 17.

The null-hypothesis is clearly rejected as critical value 3.12 is less than F_F statistic 128.42281.

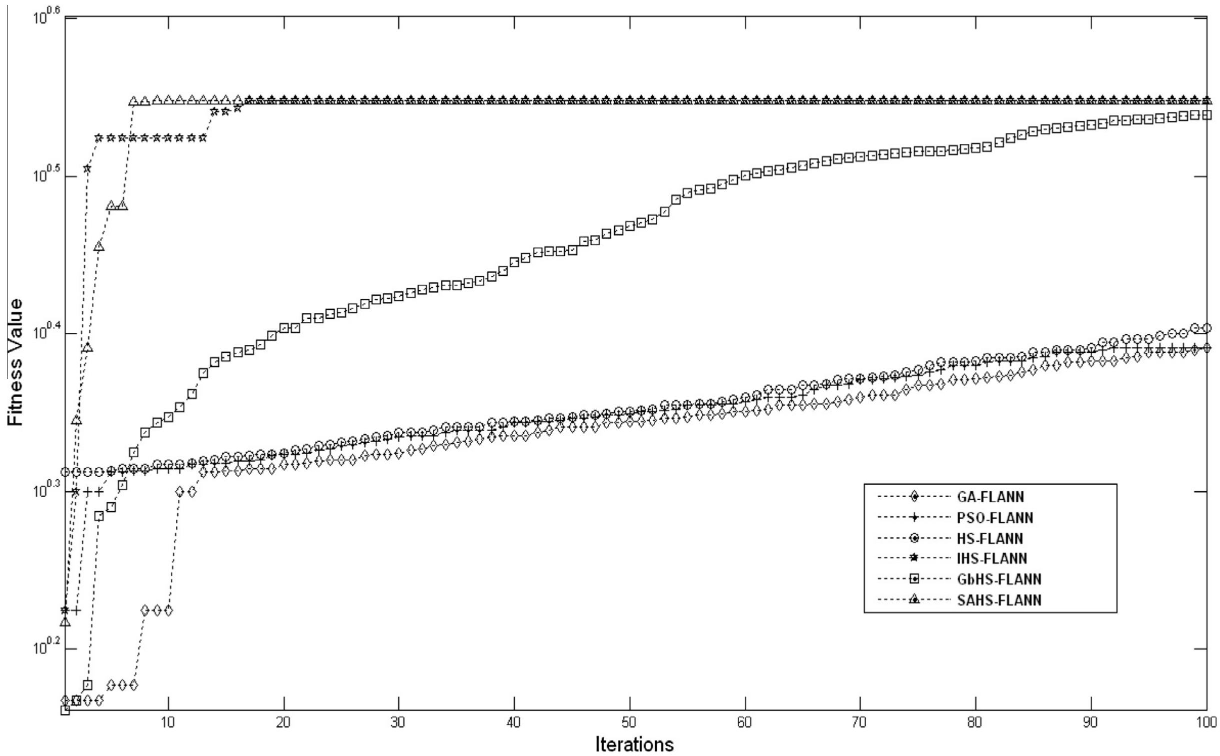

Figure 10 Improvements in fitness of population in different iterations observed in WINE dataset.

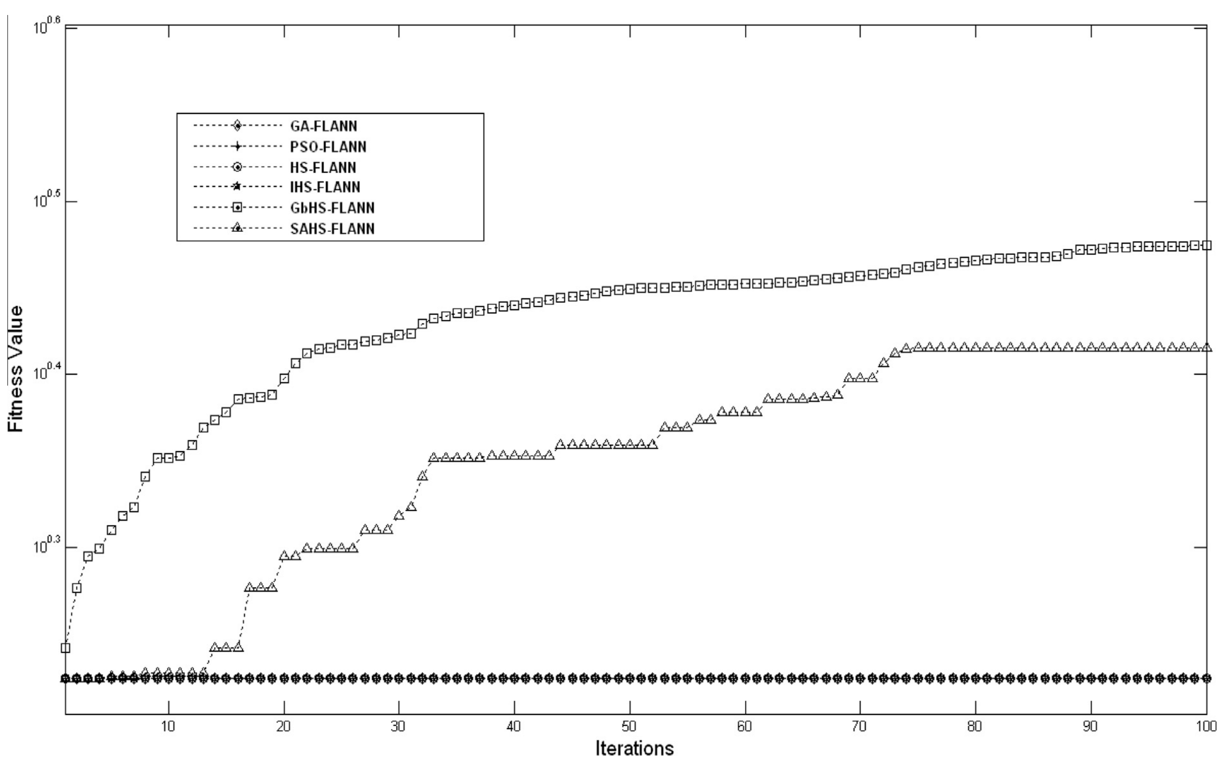

Figure 11 Improvements in fitness of population in different iterations observed in IONOSPHERE dataset.

H_0: All the classifier has same rank, hence they are equivalent.

$$X_F^2 = (12N/k(k+1))\left(\sum_j R_j^2 - \frac{k(k+1)^2}{4}\right) \quad (16)$$

$$F_F = \left((N-1)X_F^2\right)/\left(N(K-1) - X_F^2\right) \quad (17)$$

After the rejection of null-hypothesis from Friedman test, in order to evaluate performance by pairwise comparison of proposed classifier with another classifier based on z-score value

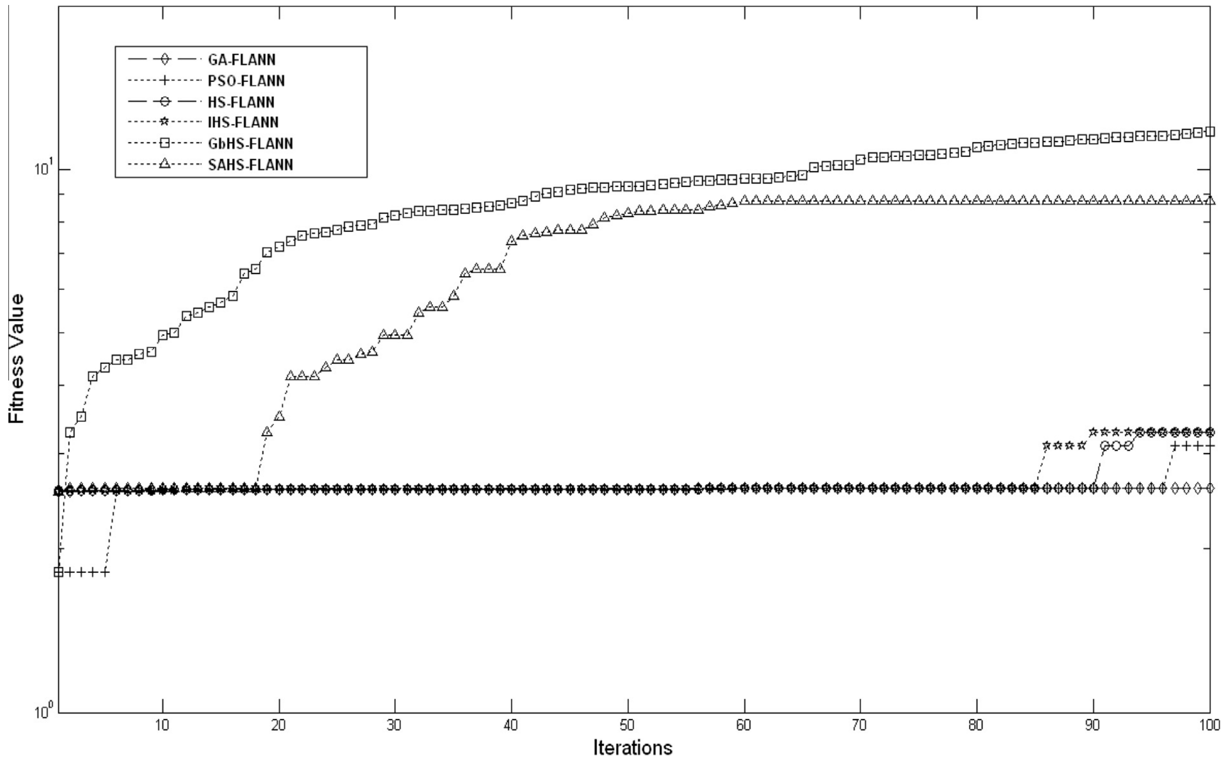

Figure 12 Improvements in fitness of population in different iterations observed in HEPATITIS dataset.

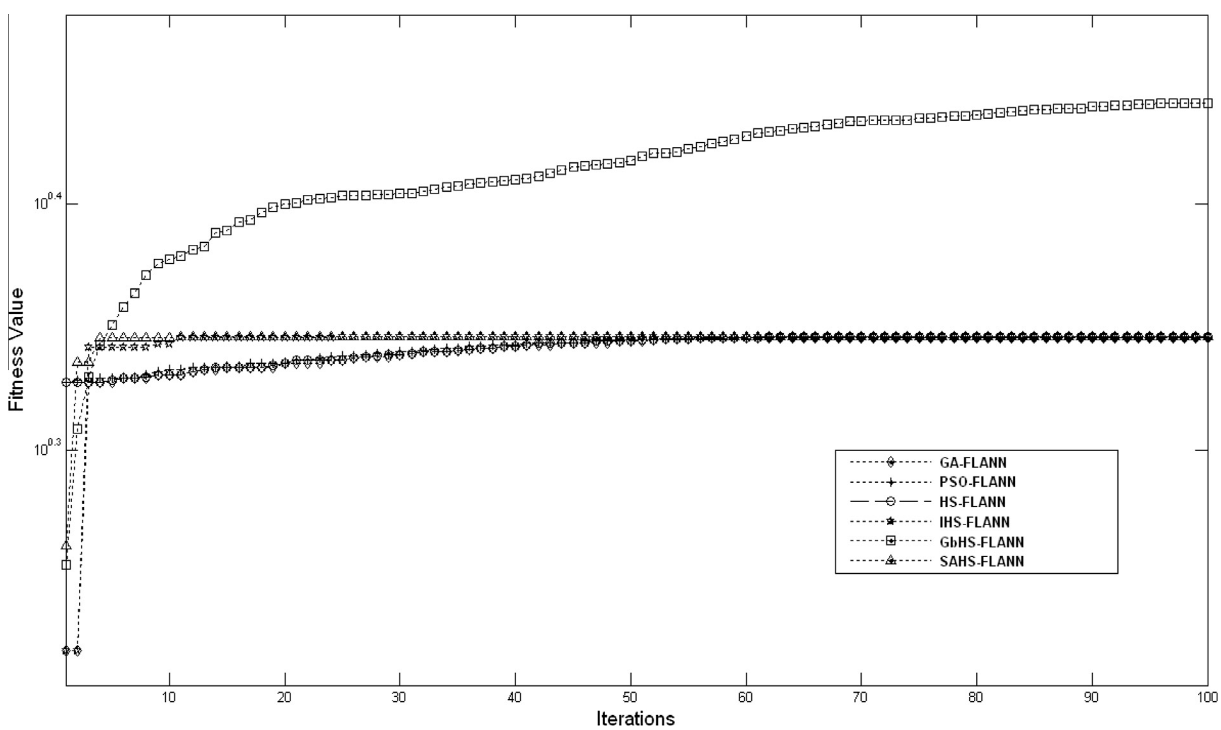

Figure 13 Improvements in fitness of population in different iterations observed in PIMA dataset.

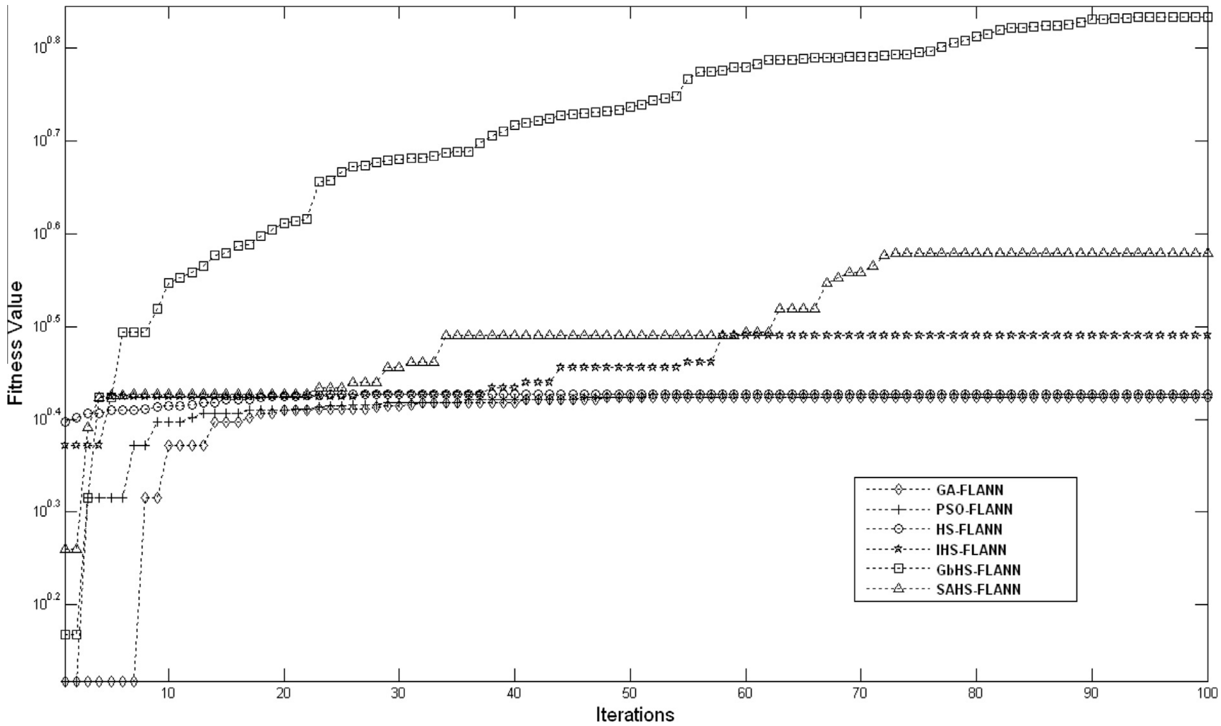

Figure 14 Improvements in fitness of population in different iterations observed in NEW THYROID dataset.

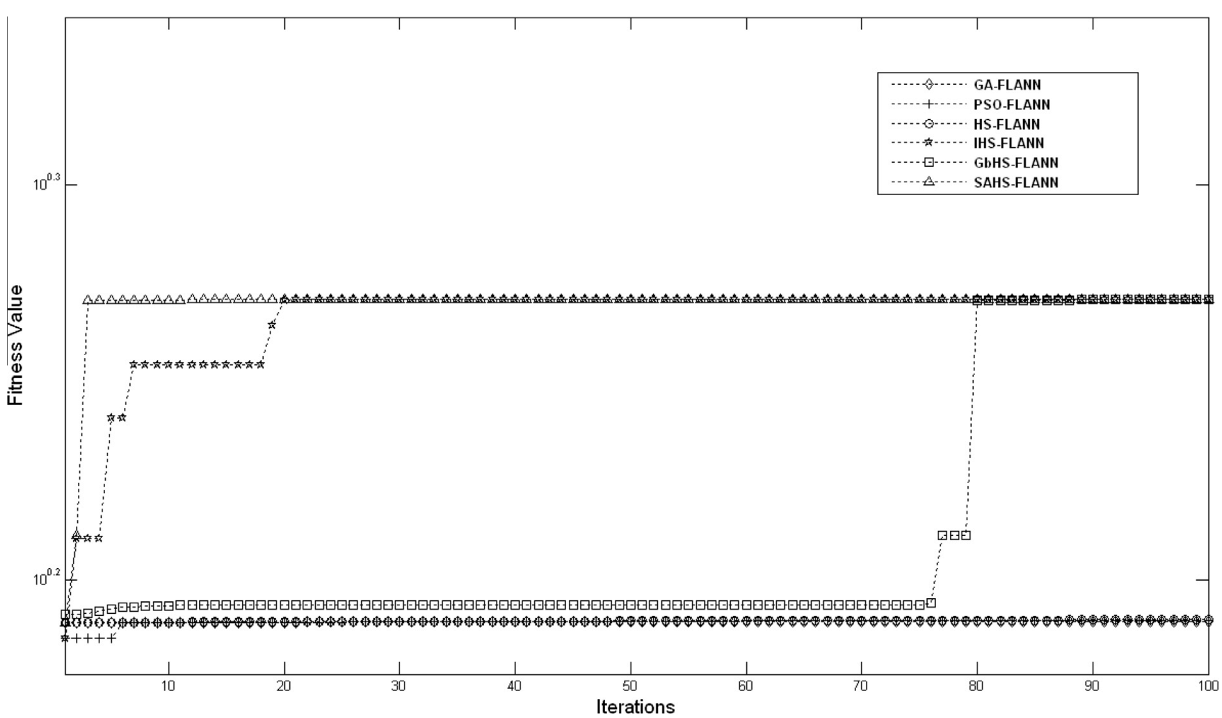

Figure 15 Improvements in fitness of population in different iterations observed in BUPA dataset.

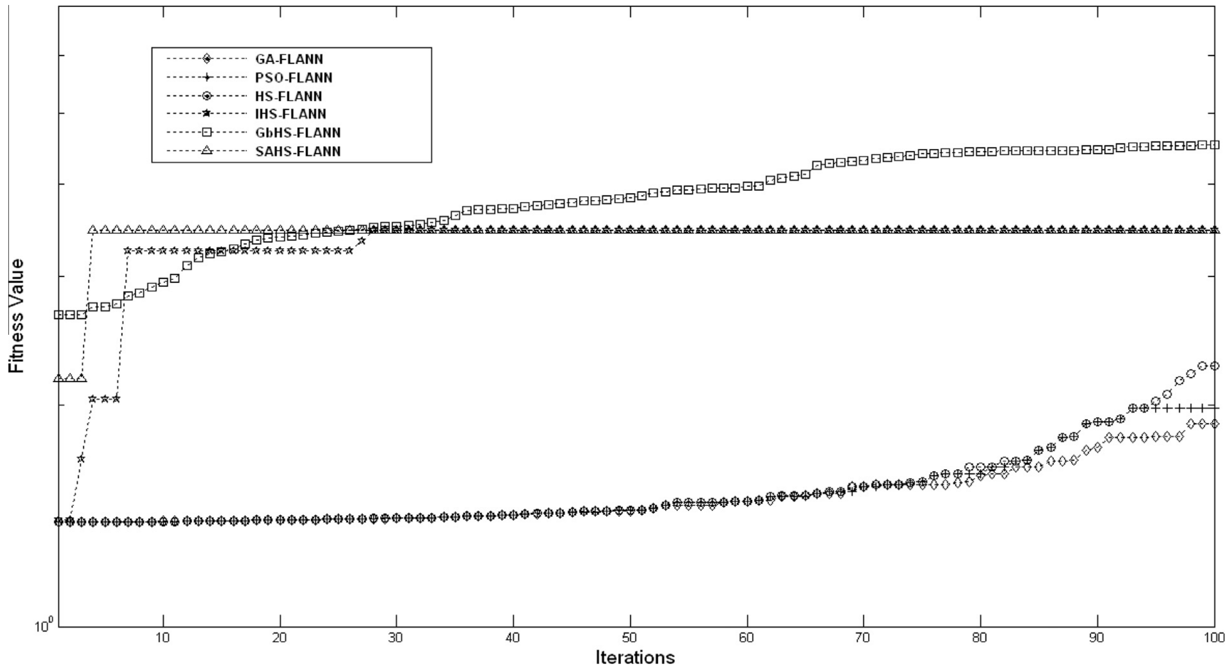

Figure 16 Improvements in fitness of population in different iterations observed in DERMATOLOGY dataset.

Table 10 Ranks of classifiers on various datasets based on the classification accuracy on train and test set.

Datasets	Average classification accuracies of classifiers in %						
	FLANN	GA-FLANN	PSO-FLANN	HS-FLANN	IHS-FLANN	SAHS-FLANN	GbHS-FLANN
Monk 2	92.9355 (7)	94.872 (6)	96.4595 (5)	97.2255 (4)	97.2405 (3)	97.317 (2)	97.3555 (1)
Iris	97.1075 (7)	97.648 (6)	98.001 (5)	98.6645 (4)	98.783 (2)	98.705 (3)	98.872 (1)
Heart	83.722 (7)	84.2405 (6)	84.815 (5)	85.0695 (4)	85.0995 (3)	85.1135 (2)	85.1555 (1)
Hayesroth	86.336 (7)	87.3125 (6)	87.6015 (5)	88.305 (4)	88.375 (3)	88.431 (1)	88.4145 (2)
Wine	92.973 (7)	94.952 (6)	96.6945 (4)	96.5835 (5)	96.766 (3)	96.855 (2)	97.0375 (1)
Ionosphere	80.2045 (7)	88.244 (6)	91.276 (3)	90.8105 (5)	91.033 (4)	91.7035 (2)	92.1565 (1)
Hepatitis	72.056 (7)	78.0505 (5)	77.724 (6)	79.377 (4)	79.486 (1)	79.4135 (3)	79.446 (2)
Pima	78.588 (7)	78.72 (6)	79.798 (5)	80.632 (4)	80.714 (2)	80.6625 (3)	82.1315 (1)
Thyroid	85.238 (7)	85.8665 (6)	86.5465 (5)	86.8315 (4)	86.85 (2)	86.8435 (3)	87.0695 (1)
Bupa	72.46 (7)	74.9105 (6)	76.567 (4)	76.338 (5)	76.7 (3)	77.022 (2)	78.495 (1)
Dermatology	94.4 (7)	95.4025 (6)	95.5455 (4)	95.436 (5)	95.714 (3)	95.969 (2)	96.4055 (1)
Friedman's rank in average	7	5.91	4.636	4.364	2.636	2.273	1.182

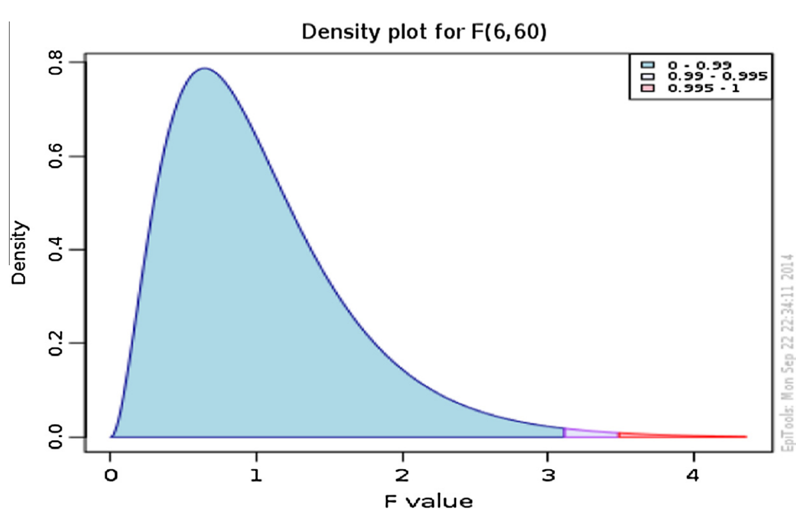

Figure 17 Density plot.

Table 11 Result of Holm and Hochberg procedure.

i	Classifiers	z-values	p-values	$\alpha/(k-i)$
1	GbHS-GDL-FLANN: GDL-FLANN	6.31616	0	0.001667
2	GbHS-GDL-FLANN: GA-GDL-FLANN	5.13283	1.427543e−7	0.002
3	GbHS-GDL-FLANN: PSO-GDL-FLANN	3.74974	0.000089	0.0025
4	GbHS-GDL-FLANN: HS-GDL-FLANN	3.45445	0.000276	0.003333
5	GbHS-GDL-FLANN: IHS-GDL-FLANN	1.5785	0.057225	0.005
6	GbHS-GDL-FLANN: SAHS-GDL-FLANN	1.18441	0.118125	0.01

Table 12 Tukey test results.

Multiple comparisons						
(I) Algorithm	(J) Algorithm	Mean difference (I–J)	Std. error	Sig.	90% confidence interval	
					Lower bound	Upper bound
Sample: Tukey HSD						
FLANN	GA-FLANN	−2.19986	1.02109	.322	−4.9552	.5554
	PSO-FLANN	−3.18255	1.02109	.031	−5.9378	−.4272
	HS-FLANN	−3.56841	1.02109	.009	−6.3237	−.8131
	IHS-FLANN	−3.70368	1.02109	.006	−6.4590	−.9484
	SAHS-FLANN	−3.81955	1.02109	.004	−6.5748	−1.0642
	GbHS-FLANN	−4.22895	1.02109	.001	−6.9843	−1.4737
GA-FLANN	FLANN	2.19986	1.02109	.322	−.5554	4.9552
	PSO-FLANN	−.98268	1.02109	.962	−3.7380	1.7726
	HS-FLANN	−1.36855	1.02109	.833	−4.1238	1.3868
	IHS-FLANN	−1.50382	1.02109	.761	−4.2591	1.2515
	SAHS-FLANN	−1.61968	1.02109	.691	−4.3750	1.1356
	GbHS-FLANN	−2.02909	1.02109	.424	−4.7844	.7262
PSO-FLANN	FLANN	3.18255	1.02109	.031	.4272	5.9378
	GA-FLANN	.98268	1.02109	.962	−1.7726	3.7380
	HS-FLANN	−.38586	1.02109	1.000	−3.1412	2.3694
	IHS-FLANN	−.52114	1.02109	.999	−3.2764	2.2342
	SAHS-FLANN	−.63700	1.02109	.996	−3.3923	2.1183
	GbHS-FLANN	−1.04641	1.02109	.948	−3.8017	1.7089
HS-FLANN	FLANN	3.56841	1.02109	.009	.8131	6.3237
	GA-FLANN	1.36855	1.02109	.833	−1.3868	4.1238
	PSO-FLANN	.38586	1.02109	1.000	−2.3694	3.1412
	IHS-FLANN	−.13527	1.02109	1.000	−2.8906	2.6200
	SAHS-FLANN	−.25114	1.02109	1.000	−3.0064	2.5042
	GbHS-FLANN	−1.0211	1.02109	.995	−3.4158	2.0948
IHS-FLANN	FLANN	3.70368	1.02109	.006	.9484	6.4590
	GA-FLANN	1.50382	1.02109	.761	−1.2515	4.2591
	PSO-FLANN	.52114	1.02109	.999	−2.2342	3.2764
	HS-FLANN	.13527	1.02109	1.000	−2.6200	2.8906
	SAHS-FLANN	−.11586	1.02109	1.000	−2.8712	2.6394
	GbHS-FLANN	−.52527	1.02109	.999	−3.2806	2.2300
SAHS-FLANN	FLANN	3.81955	1.02109	.004	1.0642	6.5748
	GA-FLANN	1.61968	1.02109	.691	−1.1356	4.3750
	PSO-FLANN	.63700	1.02109	.996	−2.1183	3.3923
	HS-FLANN	.25114	1.02109	1.000	−2.5042	3.0064
	IHS-FLANN	.11586	1.02109	1.000	−2.6394	2.8712
	GbHS-FLANN	−.40941	1.02109	1.000	−3.1647	2.3459
GbHS-FLANN	FLANN	4.22895	1.02109	.001	1.4737	6.9843
	GA-FLANN	2.02909	1.02109	.424	−.7262	4.7844
	PSO-FLANN	1.04641	1.02109	.948	−1.7089	3.8017
	HS-FLANN	1.0211	1.02109	.995	−2.0948	3.4158
	IHS-FLANN	.52527	1.02109	.999	−2.2300	3.2806
	SAHS-FLANN	.40941	1.02109	1.000	−2.3459	3.1647

and p-value, the post-hoc test has been carried out by using the Holm procedure [263,266,267].

8.2. Holm and Hochberg procedure

In this section, the Holm [268] and Hochberg [269] procedure is used to compare classifiers with their p-value and $\alpha/(k-i)$. During this test, the z-value is obtained from Eq. (18) and based on z-value, p-value is computed from the table of the normal distribution.

$$z = \left(R_i - R_j\right) \bigg/ \sqrt{\frac{k(k+1)}{6N}} \tag{18}$$

where z is the z-score value, k is the number of classifiers, N is the number of datasets and R_i and R_j are average rank of ith and jth classifier respectively.

Table 11 presents comparison of All 7 classifier based on z-value, p-value and $\alpha/(k-i)$, where 'i' is the classifier's number.

In the Holm [268] and Hochberg [269] procedure, the null-hypothesis (H_0) is rejected if p_i – value is less than the corresponding value of $\alpha/(k-i)$. In Table 11, all classifiers are compared with proposed method with respect to p_i – value and $\alpha/(k-i)$ values. For example, while comparing between GbHS-FLANN and PSO-FLANN, the p_i – value 3.74974 is less than $\alpha/(k-i)$ value 0.000089. Hence the null-hypothesis is rejected in this case.

By using the Holm test, when we compared the p_i – value with $\alpha/(k-i)$, it was observed that, in almost all the cases p_i – values is less than $\alpha/(k-i)$ values. Hence, it is clear that the null-hypothesis is rejected. Thus, the proposed classifier 'GbHS-FLANN' is statistically better and significantly different from other classifiers (except IHS-FLANN and SAHS-FLANN) in performance on cross validated data and outperforms other classifiers. In a more close observation, while comparison with IHS-FLANN and SAHS-FLANN, the GbHS-FLANN is found better than IHS-FLANN and SAHS-FLANN in performance but it is not much significantly different.

8.3. Post-Hoc ANOVA Statistical Analysis (Tukey Test & Dunnett Test)

After the rejection of the null-hypothesis from Friedman test in Section 8.1 and Holm procedure in Section 8.2, in this section, the Post-Hoc ANOVA Statistical Analysis has been carried out by using Tukey Test [270] & Dunnett Test [271] to get generalized statistic on the performance of all classifiers.

The ANOVA [272] is the general statistical technique for testing the differences between more than two related performances of the classifiers measured on the same datasets for training and testing. During ANOVA test, the null-hypothesis is to be considered is that: "all classifiers are same in performances and differences in performances are simply random". In ANOVA test, total variability in classifier's performances is investigated and classified into three categories: between-classifiers variability, between the datasets variability and between-error variability. It divides the total variation into the variability between the classifiers, variability between the datasets and the residual (error) variability. The null-hypothesis can be rejected if and only if, the between-classifiers variability is larger than the between-error variability.

In this paper, the statistics on all classifier's performance is computed under post-hoc-ANOVA test by using SPSS (Version: 16.0) statistical tool. All the methods are executed for 10 numbers of runs on each dataset. The test has been carried out with 90% confidence interval, 0.1 significant level and linear polynomial contrast. To get the differences between the performances of classifiers, we have used post-hoc ANOVA test by using mostly used Tukey test and Dunnett test. The Tukey test is carried out for comparisons of performance of all classifiers with each other and the Dunnett test for comparisons of all classifiers with base classifier (proposed classifier). The results from Tukey test and Dunnett test are presented in Tables 12 and 13 respectively.

In Tukey test (Table 12), all the methods are compared pairwise with respect to mean difference, standard error and level of significance. The null-hypothesis is rejected if the between-classifiers variability is larger than the between-error variability. For example, while comparing the proposed method (GbHS-FLANN) with PSO-FLANN, we noticed that, the between-classifiers variability (1.04641) is larger than the between-error variability (1.02109). Hence, the null-hypothesis is rejected in this case. According to this observation, we found the rejection of null-hypothesis in all most all cases (4 out of 6).

In Dunnett test (Table 13), only the proposed method is compared with other alternative methods with respect to mean difference, standard error and level of significance. The criteria for the rejection of null-hypothesis are same as Tukey test. For example, while comparing the proposed method (GbHS-FLANN) with GA-FLANN, we notice that, between-classifiers variability (2.02909) is larger than the between-error variability (1.02109). Hence, the null-hypothesis is rejected in this case. The rejection of null-hypothesis is noticed in all most all cases.

Table 13 Dunnett test results.

Multiple comparisons

(I) Algorithm	(J) Algorithm	Mean difference (I–J)	Std. error	Sig.	90% confidence interval	
					Lower bound	Upper bound
Sample: Dunnett t (2-sided)						
FLANN	GbHS-FLANN	−4.22895	1.02109	.000	−6.5736	−1.8843
GA-FLANN	GbHS-FLANN	−2.02909	1.02109	.197	−4.3737	.3156
PSO-FLANN	GbHS-FLANN	−1.04641	1.02109	.806	−3.3911	1.2982
HS-FLANN	GbHS-FLANN	−1.0211	1.02109	.971	−3.0052	1.6841
IHS-FLANN	GbHS-FLANN	−.52527	1.02109	.991	−2.8699	1.8194
SAHS-FLANN	GbHS-FLANN	−.40941	1.02109	.998	−2.7541	1.9352

As a conclusion of these tests, we noticed that, the mean differences (between-classifiers variability) among classifiers are larger than the standard errors (between-error variability) (except between GbHS-FLANN & IHS-FLANN and GbHS-FLANN & SAHS-FLANN) (Table 12). Also in Dunnett test (Table 13), while comparing GbHS-FLANN with other classifiers, we observed same as that of Tukey test. In both Tukey test and Dunnett test, the rejection of null-hypothesis holds for all most all classifier (out of 6 classifiers, rejection of null-hypothesis holds for 4 classifiers). Hence, as a whole, the null-hypothesis can be rejected.

9. Conclusion

From multiple comparison of classifiers by using Tukey test and Dunnett test (Tables 12 and 13), and rejection of the null-hypothesis of post-hoc test, clearly the proposed method is found significantly better and different from other methods. This is because, in all most all the cases, we noticed that, the mean differences (between-classifiers variability) among classifiers are larger than the standard errors (between-error variability). In Friedman test, the null-hypothesis is rejected as the critical value of the F-distribution is found less than F_F statistic, which proves the proposed classifier is statistically significant from other classifiers. After the rejection of the null-hypothesis in Friedman test, all classifiers are compared pairwise in terms of the z-values, p-values and $\alpha/(k-i)$ from the ANOVA post-hoc test by using the Holm procedure (Table 11). We observed that, in all most all the cases, p-values are less than $\alpha/(k-i)$ values thereby rejection of null-hypothesis.

From rigorous test under well known statistical methods (Friedman test, Post-hoc test by Holm and Hochberg procedure, Tukey test and Dunnett test), we claim the proposed GbHS-FLANN classifier is better and outperforms other alternatives (FLANN, GA-FLANN, PSO-FLANN, HS-FLANN, IHS-FLANN, SAHS-FLANN). Also it can be computed with a low cost due to less complex architecture of FLANN and Global-best HS requires less mathematical computation and is free from complicated operators (like crossover in GA) and parameters (like c1, c2 in PSO). The future work is comprised of integration of other improved variants of HS with other higher order neural network in diverse applications of data mining.

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