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An Efficient Cancer Classification Model using Deep Neural Network with Arithmetic Optimization Algorithm-based Optimal Gene Selection

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***Abstract*— Cancers are the most disastrous and inevitable ailment that occurs in individuals. Due to the hazardous effects of cancer, people get at death in very early age. In today's date, cancer is categorized into many types, which are affected by the external and internal parts of the body. In general, cancers are caused by the growth of abnormal tissues where cancer originates and it is gradually spread to other parts. Therefore, the medical industry struggles to detect the different types of cancer disorders without any loss of people. Hence, the automated detection system is implemented to predict cancer in its early stages to prevent the people gets worsening. Normally, the collection of individual data is another challenging concern. Several methods have been implemented yet they exist with constraints to provide better results. Machine learning models are also used, but it does not tackle the big data collection process and also fail to obtain the relevant features. Henceforth, the deep learning model has emerged for various processes like prediction, classification, and recognition. So, a new and improved classification framework for classifying cancer is executed in this paper. At first, the data is gathered from the benchmark database. From the data, the genes are optimally selected using an Improved Arithmetic Optimization Algorithm (IAOA). Then, the optimally chosen genes are given as input to the "Optimized Deep Neural Network (ODNN)" for classification. The constraints in the DNN framework are optimized by the improved AOA. From the DNN, the classified output is obtained. Various experimentations are carried out by contrasting the developed optimization algorithm enhanced DNN model to verify the efficient working of the suggested cancer classification model. Throughout the result analysis, the accuracy and precision rate of the designed method is 93.42% and 9363% for all datasets.**

Keywords—Cancer Classification; Raw Data; Optimal Gene Selection; Improved Arithmetic Optimization Algorithm; Optimized Deep Neural Network

I. INTRODUCTION

The word "cancer" refers to the most hazardous disease that affects any human part of the body [1]. Cancer is a disease that origins from the submission of abnormal cells or tissues that spread and cause death to individuals. As it is expected as a non-communicable and inevitable disease, cancer increases the death rate and occurs in one-sixth of the infected people [2]. In normal, the cancers have existed in the world with distinct types concerning various human organs. Like, "Breast cancer, skin cancer, lung cancer, brain cancer", etc. are dangerous cancer types that also become non-curable diseases [3]. Therefore, the categorization of cancer disorder is a quite tricky and addressing task for such scholars. Due to the uncontrolled growth of cells, cancer detection is a requisite objective in the medical industry. Conversely, the cancer is categorized into different types as benign (primary stage) and malignant (second stage) [4]. Hence, the cancer classification model is developed to treat the patients on an early time basis.

In recent times, cancer has been the prime reason behind people's deaths all over the world. Thus, the timely cancer detection model saves countless human lives [5]. Normally, the cancer classification model is processed by considering the images, but it fails to attain the desired outcome. Hence, the researchers have taken the gene-related data to find the cancer ailment in humans [6]. In a technical way, the early or rapid identification of cancer types is a crucial part. When it is

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diagnosed with the proper method, thus, it aids in preventing the cancer disease [7]. While handling the data, the system may also face some constraints like more dimensional and smaller size of data samples. In addition to this, the noise present in the data might not get into the deployment of an efficient model [8]. Hence, the rise of intelligent classification models is another challenging job.

Nowadays, machine and deep structured models have been developed for cancer categorization and also pave the way for acquiring more accuracy [8]. Nevertheless, this model also causes the effect of non-trivial tasks and is critical in the statistical analysis of the data. Another downside factor is determining the features from the raw data. Owing to the optimal selection, the system also degrades the performance and reduces the positive measures rate [9]. To avoid such issues, the deep learning model is employed for diagnosing the cancer and its types. Since it has more potential, the deep learning technique emerges with high performance and less error rate [10]. With the intention of carry out this, the novel cancer classification is promoted using an improved heuristic algorithm.

The prime intentions of the new method are discussed as follows:

- ✓ To frame the efficient cancer classification model using an improved heuristic-aided deep learning model for treating the patients significantly.
- ✓ To select the optimal features by using the proposed IAOA approach for maximizing the system efficiency.
- ✓ To design the ODNN model for classifying cancer, where the number of suitable hidden neurons and epoch counts are tuned optimally by IAOA.
- ✓ To validate the efficacy of the recommended model using multiple measures and contrast with traditional techniques.

The introduction division is followed by literature work on the several cancer classification models that are illustrated in Division II. Division III portrays the description of the proposed model and dataset. Then, the feature selection and deep learning model are given in Division IV. Division V discusses the experimental results and the paper is completed in Division VI.

II. DESK STUDY

A. Documentary study

In 2020, Shah *et al.* [11] presented the "Laplacian Score along with Convolutional Neural Network (LS-CNN)" for cancer classification. The raw data was initially fetched from the databases. With the help of collected data, the proposed model performed the classification task. Finally, the effectiveness was examined using different metrics and achieved the desired results. Hence, the suggested system has exploited the higher accuracy values in terms of confusion matrix format.

In 2023, Alrefai *et al.* [12] proposed an integrated model for classifying cancer using three objectives. Further in the second aspect, the "Adaptive Self-Training Method (ASTM)" was utilized for less dimension problems. Lastly, the data was fed into the CNN to identify the cancer disorder. For experimentation, six various microarray dataset has been considered for finding the different cancer types. Rather than the traditional method, CNN has exploited the impressive classification rate. Hence, the simulation results have evinced that it has increased the system's effectiveness.

In 2022, Shen *et al.* [13] explored the hybrid learning of using CNN as well as "Bidirectional Gated Recurrent Unit (BiGRU)" for cancer classification. The proposed work has resolved the dimension reduction problem. In the hybrid model, the CNN was used to fetch the local significant features, which were then subjected to the BiGRU for classification tasks. The enhanced work has captured the pertinent features for evading data sparsity. Thus, the extensive outcome has been revealed to improve the final outcome.

In 2021, Mohammed *et al.* [14] implemented the "One-Dimensional CNN (1D-CNN)" for finding the five types of cancer using RNASeq data. Consequently, the novel method was interlinked with the "Least Absolute Shrinkage and with the integration of Selection Operator (LASSO)" for extracting the features. At last, the system was validated and provided a comparative analysis. Thus, the suggested method has demonstrated that it has acquired higher results in increasing the survival rate of cancer patients.

In 2022, Eissa *et al.* [15] have deployed the intelligent cancer classification model. In the first stage, the original data as DNA methylation loci was getting pre-processed. The implemented method has been performed in two stages. The first stage was used for selecting the essential features, which assisted in decreasing the dimension. Further, the DNN was deployed for classifying cancer diseases and their types. At last, the effectiveness of the framework was evaluated by divergent measures. On the contrary, the simulation outcomes were obtained that revealed an early diagnosis of cancer disorder in terms of high positive rates of recall, precision, and accuracy.

B. Problem Specification

Numerous studies regarding existing classification models are given in Table I. LS-CNN [11] achieves the desired accuracy value while using the multi and binary class datasets. It is further suggested for multi-class or labeled images to classify the cancer types. CNN [12] reduces the dimension issue of handling the data and it also offers superior results for identifying the cancer types. But, it does not support the microarray gene data of RNA-sequence data sources. CNN and BiGRU [13] provide impressive results, which help to increase the performance. However, it becomes less effective by using the multiomics data for classifying the cancer disorder. 1DCNN [14] acquires the more positive measure that proves the system's robustness. Due to the use of the ensemble model, it causes computation burden or complexity. GA and DNN [15] enhance the classification rate and decrease the data redundancy and it also attains the significant features

of input data. On the other hand, it is not used for real-time applications as well as real-time datasets. These challenging drawbacks motivate to design of an intelligent cancer classification model by microarray gene data.

TABLE I. SUPERIORITIES AND CRITICAL ISSUES OF EXISTING CANCER CLASSIFICATION MODEL USING MICROARRAY GENE DATA

Author [citation]	Framework	Superiorities	Critical issues
Shah *et al.* [11]	LS-CNN	• It achieves the desired accuracy value while using the binary class and multi-class datasets.	• It is further suggested for multi-class or labeled images to classify the cancer types.
Alrefai *et al.*[12]	CNN	• It reduces the dimension issue of handling the data. • It also offers superior results for identifying cancer types	• It does not support the microarray gene data of RNA-sequence data sources.
Shen *et al.* [13]	CNN and BiGRU	• It provides impressive results, which helps to increase the performance.	• It becomes less effective by using the multiomics data for classifying the cancer disorder.
Mohammed *et al.* [14]	1DCNN	• It acquires the more positive measure that proves the system's robustness.	• Due to the use of an ensemble model, it causes computation burden or complexity.
Eissa *et al.* [15]	GA and DNN	• It enhances the classification rate and decreases the data redundancy. • It also attains the significant features of input data.	• It is not used for real-time applications as well as real-time datasets.

III. DEVELOPMENT OF IMPROVED HEURISTIC ALGORITHM AND DEEP LEARNING MODEL FOR CANCER CLASSIFICATION

A. Description of Proposed Model

Cancer is a dangerous disease that has recent innovations in the medical domain. Since this disease causes a huge impact, it requires effective detection or classification via different learning methods. The cancer causes more disastrous effects; it needs an early diagnosis model to decrease the death rate. In recent years, expert systems have been developed and employed for detecting various cancer types. Classifiers like “, Naive Bayes (NB), Support Vector Machine (SVM), Artificial Neural Network (ANN)”, etc. are considered. Yet, these models face shortcomings like high computation complexity, feature indetermination, and more false rate, which results to incur the misclassification issue. To surmount the problems, classifiers have been utilized in during the past years for cancer classification. Hence, this paper explores an optimal classifier technique along with an improved heuristic algorithm for cancer classification. Firstly, the input data is garnered from the benchmark datasets. Further, a novel IAOA is introduced for choosing the accurate features for increasing efficiency. A few of the importance of gene selection are discussed as follows. The cancer gene selection is important because it is utilized to reduce the computation complexity and enhance the classification accuracy in the bioinformatics field. The gene selection is an aid to the recommended model for effective diagnosis and prognosis of cancer subtypes. Finally, the resultant genes are fed into the ODNN model for forecasting the cancer disorder. To attain the optimum results, the constraints are accurately optimized by using the IAOA which helps to elevate the classification accuracy. Thus, the efficacy of the model is evaluated with the help of distinct metrics. On the contrary, the recommended system outperforms the classification process and it proves the early diagnosis of cancer ailments. Fig. 1 displays the architectural presentation of the offered model.

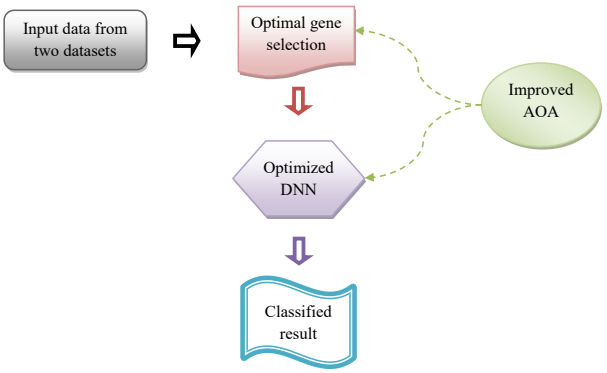


Fig. 1. Architecture view of the proposed cancer classification model using a heuristic-aided deep learning model

B. Dataset Details

This paper utilizes two different datasets for fetching the required input data for processing. Those are described as below.

Dataset 1: It represents the link as "https://data.mendeley.com/datasets/ynp2tst2hh/4": "Access Date: 2023-06-05". It is also named as "Microarray Gene Expression Cancer Data". It encompasses different cancer types as prostate cancer, endometrial cancer, brain cancer, lung cancer, etc.

Dataset 2: The input gene data is extracted from the link given as "https://archive.ics.uci.edu/ml/datasets/gene+expression+cancer+RNA-Seq": Access Date: 2023-06-05". It contains 801 data instances for representing the cancer disorder.

Therefore, the collected data from two datasets is denoted by D_n, where $n = 1,2,\ldots,N$. Here, the term N provides the total gene data.

C. Improved Arithmetic Optimization Algorithm

The novel IAOA is developed for obtaining the optimal solutions, which is inherited from traditional AOA. The IAOA is employed for "optimizing the constraints like features and the suitable number of hidden neurons and epochs" present in DNN. AOA [16] is inspired by the fundamental theory concept of different arithmetic operations. Though the AOA possesses with certain key points, still it lacks points that affect the optimum performance. It does not support the binary and discrete types of population over the iteration. Also, it produces fewer fitness measures for such candidate solutions. It fails to implement some opposition-based aspects for finding the best result. To overcome such issues, an IAOA is proposed here. Hence, the mathematical model of IAOA is discussed below.

Initialization: Considers the population as candidate solutions that are arbitrarily placed and used for both exploration and exploitation stages. After this process, "math optimizer accelerated (moa)" is computed using the below equation as Eq. (1).

$$moa(x) = \min + x \times \left(\frac{\max - \min}{X} \right) \tag{1}$$

Here, the present and average iteration are defined by x and X, respectively. Further, the maximum accelerated value is indicated by $\max$, whereas $\min$ refers the minimum value.

Exploration: This phase is focussed on the two operators as multiplication and division as it offers high decisive or distributed values. The search strategy is done over the space and also formulated by considering the random parameter as $n2$. Thus, the position is upgraded using Eq. (2).

$$a_{u,v}(x+1) = \begin{cases} bt(a_v) \div (mop + \eta) \times ((up_v - lw_v) \times \lambda + lw_v), & n2 < 0.5 \\ bt(a_v) \times mop \times ((up_v - lw_v) \times \lambda + lw_v), & else \end{cases} \tag{2}$$

Term, up and lw represents the upper and lower boundary level and λ is the control parameter. Also, the small integer value is marked by η and then the random value is mentioned as $n2$. The "math optimizer probability (mop)" is denoted by mop. In the conventional approach, the variable mop is calculated by iteration. Owing to the disadvantage, the proposed IAOA is developed for deriving the new formulation mop with the help of fitness. It is given in Eq. (3).

$$\begin{aligned} mop &= mop_{\min} + (mop_{\max} - mop_{\min}) * rn \\ mop_{\max} &= (bstft / wstft) * 0.75 \\ mop_{\min} &= (bstft / wstft) * 0.25 \end{aligned} \tag{3}$$

Here, the best and worst fitness value is measured by $bstft$ and $wstft$, accordingly.

Exploitation: The exploitation process is accomplished by considering the operators as subtraction and addition. This operator can be used to reach the target when the solution lies in a low dispersed area. Henceforth, the best position is revised using Eq. (4).

$$a_{u,v}(x+1) = \begin{cases} bt(a_v) - mop \times ((up_v - lw_v) \times \lambda + lw_v), & n3 < 0.5 \\ bt(a_v) + mop \times ((up_v - lw_v) \times \lambda + lw_v), & else \end{cases} \tag{4}$$

Finally, using four math operators, the best solution is acquired that helps to estimate the optimized value.

IV. Classification of Cancer using Optimal Gene Selection and Optimized Deep Neural Network

A. Optimal Gene Selection using IAOA

This section elucidates the selection process of optimal genes from the input data as D_n. As the data is in raw form, it might constitute noisy data, artifacts, and data redundancy. These issues lead to a decrease the efficiency and affect the classification process. Also, as the normal data contains more redundancies, the model is yet to face the computation burden that degrades the performance as well. To overcome such constraints, optimal genes are requisite to select by using the proposed IAOA approach. The raw data is given into the proposed algorithm, where the data acts as the input population. Thus, the algorithm estimates the optimal genes or features for subsequent processes. Hence, the acquired optimal genes are obtained via IAOA and it is denoted as D_m^{op}.

B. ODNN-based Classification

Once the optimal features are selected, it is subjected to the novel ODNN for classifying the cancer types. The DNN [17] is the most commonly used model in deep learning techniques. Rather than, the hidden layer contains more number of hidden neurons that are processed with weights and bias terms. Here, the resultant feature D_m^{op} is subjected to the input layer of DNN, which passes the features to the next subsequent layer as a hidden layer. In the mid-layer, the activation function is used to do the classification job. Through the training process, the weight is randomly updated to provide the outcome. The formulation of the activation function that considers "Rectified Linear Unit (ReLU)" is shown in Eq. (5).

$$\mathrm{Re}LU : af(D_m^{op}) = \max(0, D_m^{op}) \tag{5}$$

Once the network is trained, the test data is passed to the network to get the classified outcome.

Proposed ODNN: The classical DNN faces some computation burden since it uses multiple hidden layers and neurons. Hence, this model also requires more training samples and more time for processing. These issues lead to performance degradation. In order to overcome this problem, the ODNN model is deployed, where the parameters are tuned by using IAOA. Therefore, the objective function is estimated using Eq. (6).

$$Obj = \underset{\{D_m^{op}, Hn, Ep\}}{\arg\min}\left[\frac{1}{pr} + \frac{1}{mcc} + fpr\right] \tag{6}$$

Here, the hidden neuron contains the limit as 5 to 255 as mentioned in Hn and the "epoch is denoted by Ep that has the limit of [5, 50]". Correspondingly, the precision, "False Positive Rate (FPR) and Mathew Correlation Coefficient (MCC) and" is annotated by pr, mcc and fpr. This fitness function determines the better positive value and the lowest negative value. The schematic diagram of the ODNN model is depicted in Fig. 2.

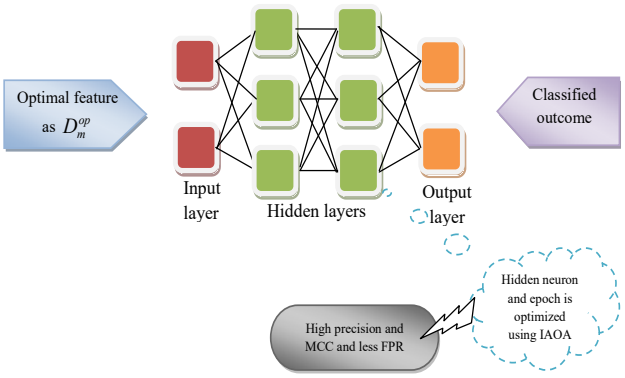


Fig. 2. Schematic diagram of ODNN for cancer classification with optimized parameters

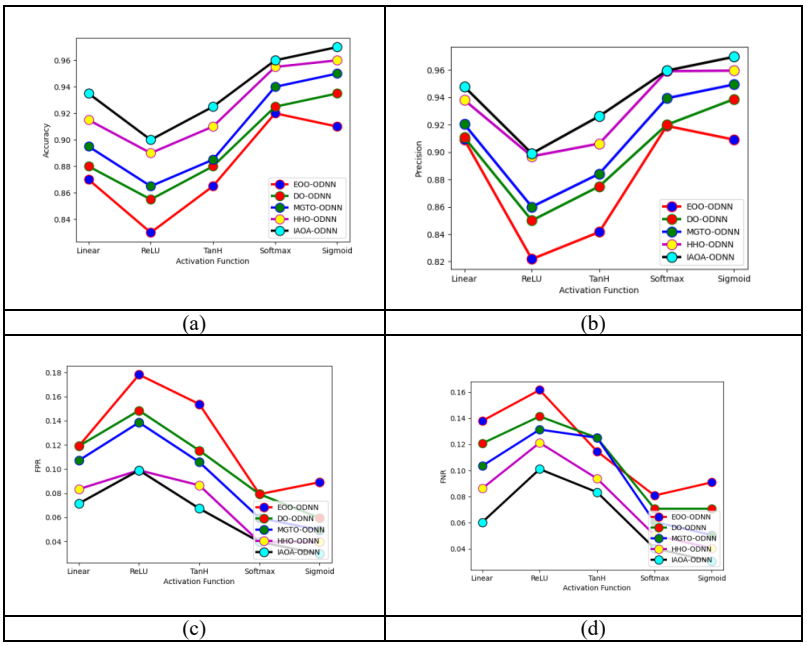
V. Experimental Results Analysis

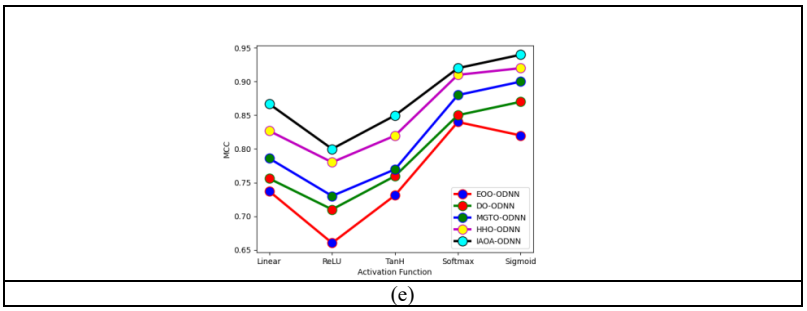
A. Simulation Setup

The given recommended classification method was evaluated over the platform as Python. The extensive results were carried out by using `different measurements. The traditional optimizations like "Eurasian Oystercatcher Optimizer (EOO)" [18], "Dingo Optimizer (DO)" [19], "Modified Gorilla Troop Optimization" (MGTO) [20], and "Harris Hawks Optimization (HHO)" [21] were taken. Similarly, conventional deep learning classifiers were considered as DBN [22], DTCN [23], LSTM [24], and DNN [17]. The metrics used for evaluating the designed model are listed here. (https://en.wikipedia.org/wiki/Sensitivity_and_specificity)

B. Performance evaluation for the suggested cancer classification model for both datasets

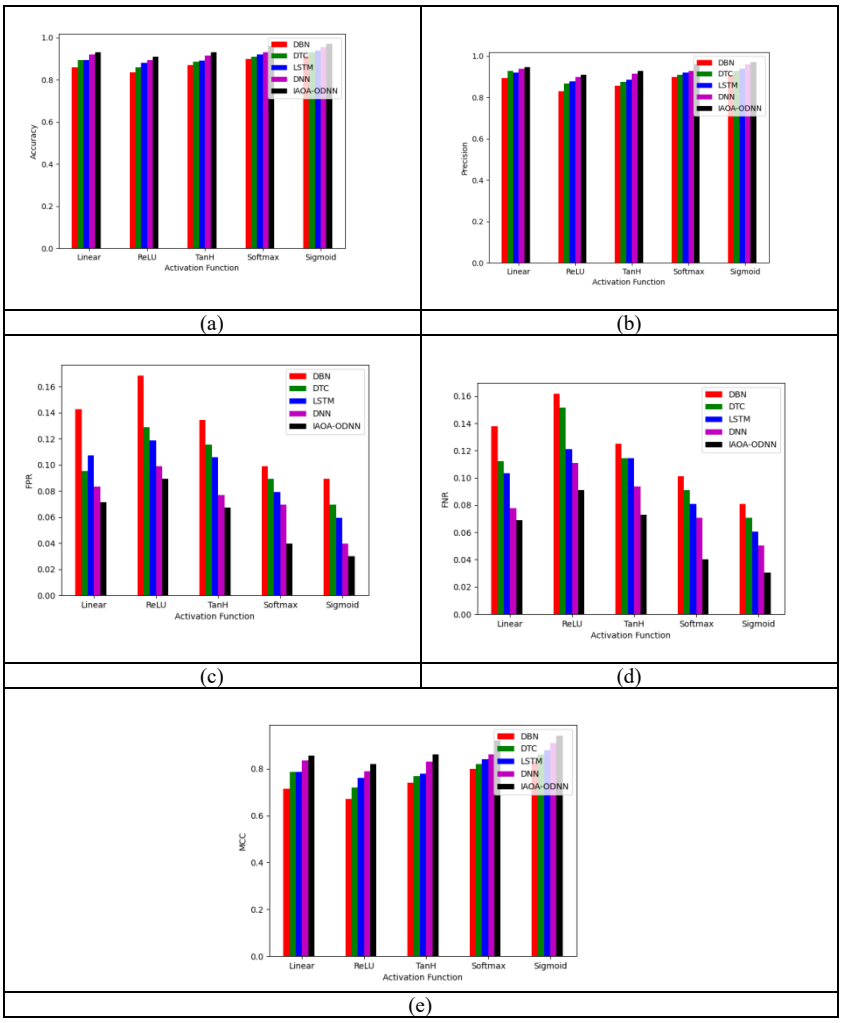
Fig. 3 and Fig. 4 elucidate the efficacy analysis of the enhanced model for dataset 1 compared to existing optimization and classifier models. The efficacy of the model is done by utilizing the different activation functions. The FNR results of the model using dataset 1 compared with algorithms are given in Fig. 3 (b). When the activation function as tanh, the FNR achieves as 28.3% of EOO-ODNN, 23.3% of DO-ODNN, 20.8% of MGTO-ODNN, and 16.6% of HHO-ODNN, which is higher than the proposed IAOA-ODNN, respectively. Similarly, the algorithm and classifier comparison takes place for dataset 2 to evaluate the effectiveness of the cancer classification system which is elucidated in Fig. 5 and Fig. 6. Here, the DBN attains lower; performance at the same time the DNN model attains second better performance. Owing to these, the DBN model does not have the ability to resolve class imbalance issues. It is not applicable to real-time datasets and also for this model, it increases the computation time.





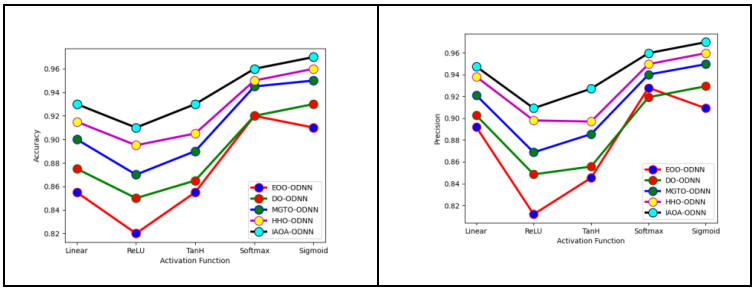
(e)

Fig. 3. Experimental evaluation of the offered cancer classification method by different activation functions in contrast with existing optimization for dataset 1 with regards to "(a) Accuracy, (b) Precision, (c) FPR (d) FNR, and (e) MCC"



(a) (b) (c) (d) (e)

Fig. 4. Experimental validation of the offered cancer classification model by different activation functions in contrast with existing classifiers for dataset 1 with regards to "(a) Accuracy, (b) Precision, (c) FPR (d) FNR, and (e) MCC"



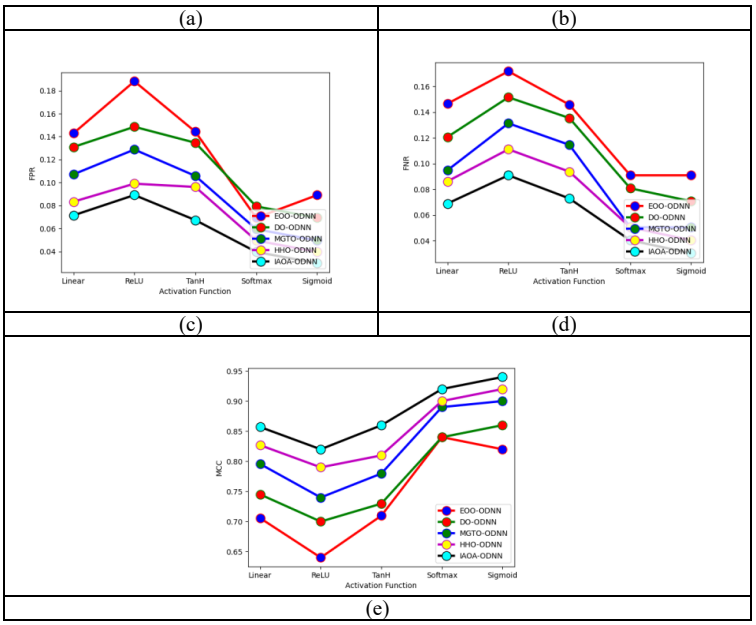


Fig. 5. Experimental validation of the offered cancer classification model by different activation functions in contrast with existing optimization for dataset 2 with regards to "(a) Accuracy, (b) Precision, (c) FPR (d) FNR, and (e) MCC"

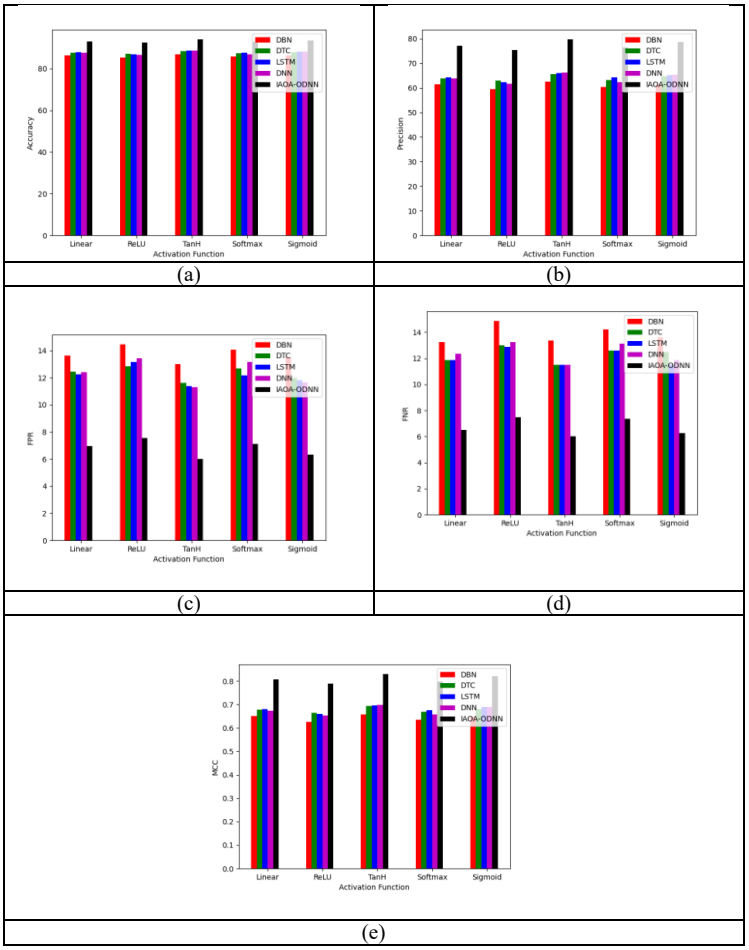


Fig. 6. Experimental validation of the offered cancer classification model by different activation functions in contrast with existing classifiers for dataset 2 with regards to "(a) Accuracy, (b) Precision, (c) FPR (d) FNR, and (e) MCC"

VI. Conclusion

This work has presented the novel cancer classification model using an improved heuristic and deep learning model. Firstly, the gene data was downloaded from the two various datasets. It was then followed by the selection of optimal genes that could be achieved with the help of novel IAOA. Lastly, the optimal genes were given as input to the ODNN for classifying the cancer disorder, where the tuned parameters were acquired using IAOA. The validation was done and measured across diverse measures. For dataset 2, when the network used the activation function as ReLU, the accuracy value for the enhanced model attained higher results rather than 4.34%, 2.17%, 1.08%, and 1.63% of DBN, DTCN, LSTM, and DNN, respectively. Thus, extensive results were acquired that have assisted in easily diagnosing the cancer disease and treating the patients effectively. However, the given recommended approach required more concentration on the target of cancer diagnosis. The enhancement of the classifier using ensemble methods helps to combine multiple genome-wide platforms. In the future, advanced ensemble approaches will be included to combine multiple genome-wide platforms. It is utilized to enhance the efficacy of the designed approach. The hybridization of diverse approaches will help to reduce the complexity of the classification approaches and also it will help to attain a better accuracy rate.

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