IJEAST

INTERNATIONAL JOURNAL
OF ENGINEERING APPLIED SCIENCE
AND TECHNOLOGY

VOLUME : 11 ISSUE : 03 Print / Issue Publication Date: July 2026

ISSN : 2455-2143

DOI : 10.33564/IJEAST.2026.v11i03.006

Indexed In

Google SCHOLAR · OPEN ACCESS · doi · Crossref

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International Journal of Engineering Applied Sciences and Technology, 2026
Vol. 11, Issue 03, ISSN No. 2455-2143, Pages 26-35
Published Online July 2026 in IJEAST (http://www.ijeast.com)

REDEFINING CANCER CLASSIFICATION THROUGH AN OPTIMIZED DEEP NEURAL NETWORK FRAMEWORK USING GENE EXPRESSION DATA

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Abstract—**Millions of people worldwide suffer from cancer, one of the most serious and deadly illnesses. In order to increase patient survival rates and diagnostic accuracy, early identification of malignant cells is essential. High-dimensional and unstructured gene expression datasets frequently provide challenges for traditional machine learning techniques used for cancer classification. This paper presents a Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) model for efficient cancer classification using log-transformed gene expression data. To find significant patterns in complicated biological datasets and enhance classification performance, the developed model combines optimization and deep learning approaches. The gene expression data is first normalized using preprocessing and log transformation. A Deep Neural Network (DNN) is then utilized to further classify the relevant genes that were selected using the CoWo optimization approach. For both the breast cancer and colon cancer datasets, experimental findings show that the suggested CoWo-DNN model performs better in terms of accuracy, precision, recall, and F-measure. The developed model demonstrated its efficacy for early cancer detection and medical data analysis applications with classification accuracies of 91.8% for breast cancer and 96.2% for colon cancer.**

Keywords—**Cancer classification, Gene expression data, Deep Neural Network, Feature selection, CoWo optimization.**

I. INTRODUCTION

Millions of people worldwide suffer from cancer, one of the most deadly illnesses, and it remains a significant problem for the medical field. Malignant tumors are created when aberrant cells in bodily tissues grow out of control, progressively harming healthy cells and organs. The number of cancer-related fatalities is rising annually, according to worldwide health surveys, which makes early detection and precise categorization crucial for raising patient survival rates. Early cancer detection greatly lowers death rates and allows for prompt medical intervention. As a result, creating effective and intelligent cancer categorization systems has emerged as a crucial field of study in medicine.

Massive volumes of gene expression data that can be used for cancer detection and prognosis have been produced by recent developments in biomedical technology.

Researchers can find differences in genes linked to various cancer types by using gene expression analysis. The capacity to examine hundreds of genes at once has been further enhanced by microarray technology, offering important insights for cancer detection and therapy planning. However, because high-dimensional microarray datasets frequently contain noisy, redundant, and unstructured information, interpreting them is still a challenging endeavor. Accurate cancer categorization is a difficult topic in computational biology and medical data analysis due to the complexity of gene expression data.

For cancer classification problems, conventional statistical and machine learning techniques have been widely applied. In previous research, a number of methods, such as Support Vector Machines (SVM), Decision Trees, K-Nearest Neighbor (KNN), and Artificial Neural Networks (ANN), have shown encouraging classification results. Even while these methods offer respectable accuracy levels, they frequently have trouble handling complicated, high-dimensional datasets. Before classification can be carried out, the majority of traditional machine learning techniques require organized input data and human feature engineering. Their inability to efficiently handle unstructured and raw medical datasets is a result of this reliance on manually created features. Furthermore, the reliability of conventional techniques is further diminished by the existence of systematic bias, noise, and small sample sizes in microarray datasets.

Recently, deep learning approaches have gained significant attention for overcoming these limitations .[12] Deep learning is a subfield of machine learning that automatically

extracts useful characteristics from complicated datasets using multi-layer neural network designs. Deep learning models, in contrast to conventional machine learning methods, can effectively handle unstructured data without requiring much manual preparation. Deep learning techniques have been very successful in a number of fields, including image classification, speech recognition, computer vision, and medical diagnosis, because of their capacity to uncover hidden patterns and correlations from massive datasets.

Deep learning models have demonstrated great promise in the healthcare industry to help medical practitioners by increasing the precision of illness prediction and decreasing human error in diagnosis.

Using gene expression data, some researchers have used deep learning techniques to identify cancer. When compared to traditional methods, Convolutional Neural Networks (CNN), Deep Neural Networks (DNN), and hybrid optimization-based learning models have demonstrated superior classification accuracy. Nevertheless, several issues are still unsolved in spite of these advancements. High computational complexity, ineffective feature selection, and challenges in maximizing classification performance for high-dimensional gene datasets are potential drawbacks of current deep learning techniques. An intelligent and optimized framework that can increase classification accuracy while lowering computing constraints is therefore required.

This study proposes a Coyote-Wolf Optimization-based Deep Neural Network (CoWo-DNN) model for effective cancer classification with log-transformed gene expression data. To improve classification performance, the suggested framework combines the optimization power of the Coyote-Wolf algorithm with the learning capacity of deep neural networks. To enhance data quality and stability, gene expression data is first preprocessed using log transformation methods. After that, the improved deep neural network successfully classifies cancer by finding important patterns in the processed dataset.

Breast cancer and colon cancer datasets are used to assess the suggested CoWo-DNN model. When compared toConventional machine learning approaches such asSupport Vector Machines (SVM), Decision Trees, K-Nearest Neighbor (KNN), and Artificial Neural Networks (ANN) have been widely used for cancer classification tasks [2] , experimental findings show that the new methodology performs better in terms of accuracy, precision, recall, and F-measure. The suggested approach demonstrated its efficacy in medical diagnosis applications with an accuracy of 91.8% for breast cancer classification and 96.2% for colon cancer classification. The findings show that the CoWo-DNN system can facilitate early cancer diagnosis and enhance medical decision-making.

II. LITERATURE REVIEW

Gene expression data-based cancer classification has grown in importance as a field of study in medical data analysis and bioinformatics. To increase the accuracy of early cancer diagnosis and categorization, researchers have created a number of computer methods. Using large-scale microarray datasets, gene expression analysis in conjunction with machine learning and deep learning approaches has demonstrated encouraging results in the identification of malignant tissues [1]. .

For cancer classification tasks, conventional machine learning methods including Support Vector Machine (SVM), K-Nearest Neighbor (KNN), Decision Tree, and Artificial Neural Networks (ANN) have been extensively used. For low-dimensional data and structured datasets, these techniques produced good results. However, noise, duplicated features, and little training samples cause traditional machine learning models to perform worse when dealing with high-dimensional gene expression data. Furthermore, the majority of conventional techniques need manual feature extraction and preprocessing prior to successful classification [2].

In order to lower the dimensionality of microarray datasets and increase classification accuracy, a number of studies concentrated on feature selection techniques. Due to their fast processing speed and capacity to effectively handle big datasets, filter-based feature selection techniques have drawn attention. By choosing the best feature subsets, wrapper-based methods improved classification performance, but their high computational cost was a drawback. The benefits of filter and wrapper approaches were tried to be combined by embedded and hybrid feature selection techniques. Even though these techniques boosted the effectiveness of feature selection, problems such local optimum trapping, longer processing times, and reduced scalability persisted [3].

Because deep learning approaches can automatically handle complicated and unstructured datasets, they have garnered a lot of attention recently in the field of cancer classification. In tasks including voice recognition, illness prediction, and medical picture analysis, Deep Neural Networks (DNN), Convolutional Neural Networks (CNN), and hybrid neural architectures showed enhanced performance. Deep learning models, in contrast to conventional machine learning techniques, automatically extract significant features from unprocessed datasets without requiring significant manual preparation. Deep learning techniques were able to increase prediction performance and classification accuracy for cancer detection applications as a result [4].

In order to improve feature selection and classification performance, researchers have used optimization methods with neural network models. To choose relevant genes from microarray datasets, optimization methods including Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Ant Colony Optimization (ACO), Grey Wolf

International Journal of Engineering Applied Sciences and Technology, 2026
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Optimization (GWO), and Coyote Optimization Algorithm (COA) were frequently employed. By eliminating unnecessary features and improving training performance, these optimization-based techniques increased classification efficiency. However, when processing high-dimensional cancer datasets, many of the optimization techniques that were previously in use suffered from excessive computing cost, slower convergence rates, and instability [5].

Microarray-based gene expression analysis has greatly enhanced the discovery of biomarkers for cancer detection. Thousands of genes may be analyzed simultaneously using microarray datasets, allowing researchers to find significant genetic patterns linked to various cancer forms. However, successful categorization is challenging because High-dimensional microarray datasets often contain noisy and redundant information, which negatively affects classification performance [5] and small sample sizes. Therefore, to increase the dependability of cancer classification systems, effective preprocessing, dimensionality reduction, and feature optimization strategies are needed [6].

According to recent research, deep learning models in conjunction with optimization algorithms outperform traditional classification techniques. For breast cancer, colon cancer, lung cancer, and other cancer datasets, optimization-assisted neural network models increased prediction accuracy and feature extraction capacity. Even with these improvements, there are still issues with current cancer classification systems, including computational complexity, poor feature selection, and poor generalization performance [7].

The literature review reveals that high-dimensional gene expression data is still a challenge for existing deep learning and machine learning techniques. High computing costs, limited scalability, noise sensitivity, and poor classification performance for complicated cancer datasets are among the drawbacks of current techniques. In order to enhance feature selection and accomplish precise cancer classification using gene expression data, this study suggests a Coyote-Wolf Optimization-based Deep Neural Network (CoWo-DNN) model.

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III. PROPOSED SYSTEM

Using gene expression data, the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) model is created for effective cancer classification. To increase classification accuracy and lower computing cost, the suggested system integrates preprocessing, feature selection, optimization, and deep learning approaches [1].

Fig. 1 shows the general process of the suggested technique. To eliminate noise and inconsistencies, gene expression datasets are first gathered and preprocessed. The dataset is then normalized and data stability is enhanced by using log transformation. The CoWo optimization technique is used for feature selection in order to find useful genes. Lastly, a Deep Neural Network (DNN) is used to classify the chosen characteristics.

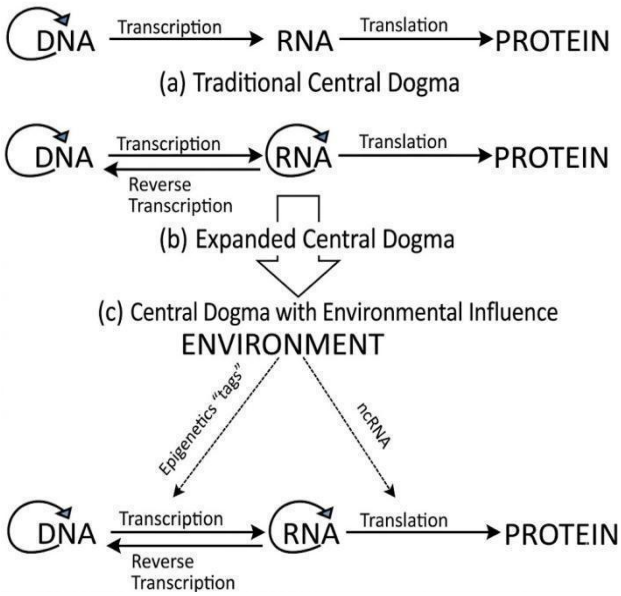

Fig. 1. Central dogma representation used in gene expression analysis [4].

Using gene expression data, the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) model is created for effective cancer classification. To increase classification accuracy and lower computational cost related to high-dimensional microarray datasets, the suggested framework integrates preprocessing, feature selection, optimization, and deep learning approaches [1]. Because microarray datasets contain thousands of genes with noisy, redundant, and unstructured information, classifying cancer using gene expression data is a difficult endeavor. For efficient feature selection and precise malignant tissue classification, an optimal framework is therefore necessary.

The proposed CoWo-DNN framework mainly consists of the following stages:

- Gene Expression Dataset Collection
- Data Preprocessing
- Log Transformation
- Feature Selection using CoWo Optimization
- Deep Neural Network Classification
- Cancer Prediction Output
- Performance Evaluation

The comprehensive workflow and general process of the suggested technique are clearly illustrated in Fig. 1 [3].First, typical repositories are used to gather gene expression datasets associated with colon and breast cancer. To eliminate noise and irregularities, the gathered datasets are preprocessed. The gene expression values are then

International Journal of Engineering Applied Sciences and Technology, 2026
Vol. 11, Issue 03, ISSN No. 2455-2143, Pages 26-35
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normalized and data stability is enhanced by using log transformation. To find important genes from high-dimensional datasets, feature selection is carried out using the hybrid CoWo optimization method [4]. Lastly, a Deep Neural Network (DNN) is used to classify the chosen characteristics.
Fig 2. General architecture of the suggested CoWo-DNN system [3].

A. Dataset on Gene Expression
In order to detect aberrant genetic activity in cancer tissues, gene expression databases are frequently utilized in bioinformatics research and cancer diagnostics. This paper uses datasets related to colon and breast cancer for experimental analysis. The high-dimensional gene information in these datasets necessitates preprocessing and ideal feature selection prior to classification [2].

Table 1 .Gene Expression Datasets Used in Proposed Work

Dataset	Description	Purpose
Breast Cancer Dataset	Gene expression data related to breast cancer tissues	Cancer classification
Colon Cancer Dataset	Gene expression data related to colon cancer tissues	Cancer classification

B. Data Preprocessing
In the process of cancer classification, data preparation serves as a fundamental stage, as raw microarray datasets frequently exhibit inconsistencies and noise [7]. The execution of preprocessing techniques is essential for enhancing the quality of the dataset and facilitating superior classification performance. The primary components of the preprocessing phase encompass:
• Noise removal
• Missing value handling
• Data normalization
• Log transformation

Log transformation was applied to normalize gene expression values and improve training stability [8], logarithmic transformation is used. The change reduces computing complexity and increases training stability [8].The following is a representation of the logarithmic transformation:
where:

X = original gene expression value
X′ = transformed gene expression value

Table II .Preprocessing Operations [7]

Operation	Purpose
Noise Removal	Eliminates unwanted data variations
Normalization	Improves data consistency
Missing Value Handling	Removes incomplete records
Log Transformation	Reduces data variance

C. CoWo Optimization for Feature Selection
Because microarray datasets contain thousands of genes, Feature selection plays a significant role in reducing dimensionality and improving classification accuracy [9].in gene expression analysis [9]. Classification performance is reduced and computational cost is directly increased when all genes are processed. In order to choose informative genes from the dataset, the suggested technique makes use of a hybrid Coyote-Wolf Optimization (CoWo) algorithm.

The suggested CoWo optimization method blends:
• Coyote Optimization's capacity for exploration
• Grey Wolf Optimization's potential for exploitation

While removing unnecessary and duplicated characteristics, the optimization method finds the best genes [10]. The chosen feature subset lowers computational complexity and increases classification efficiency.

The process of choosing features consists of:
● Initialization of the population
● Assessment of fitness
● Social adaptability in coyotes
● The hunting mechanism of grey wolves
● Selecting the ideal gene subset

Table III. Advantages of CoWo Optimization

Feature	**Benefit**
Category	**Specifics**
Algorithmic Core	Hybrid Optimization
	Faster Convergence
Data Refinement	Optimal Gene Selection
	Reduced Complexity

International Journal of Engineering Applied Sciences and Technology, 2026
Vol. 11, Issue 03, ISSN No. 2455-2143, Pages 26-35
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The mechanism for updating positions within the Grey Wolf Optimization framework is formulated as follows:
where Xp denotes the spatial coordinates of the target prey.
In this context, A represents the coefficient vector utilized in the model.
Furthermore, D signifies the vector associated with the distance calculations.

D. Classification Using Deep Neural Networks
The Deep Neural Network classifier for cancer classification receives the chosen feature subset [11]. The components of the DNN architecture are:
- The input layer
- Undiscovered layers
- The output layer

The hidden layers automatically extract meaningful patterns from gene expression datasets and improve prediction capability [12] by automatically identifying significant patterns in gene expression datasets [12]. Tissue samples are categorized into malignant and non-cancerous classifications by the output layer.

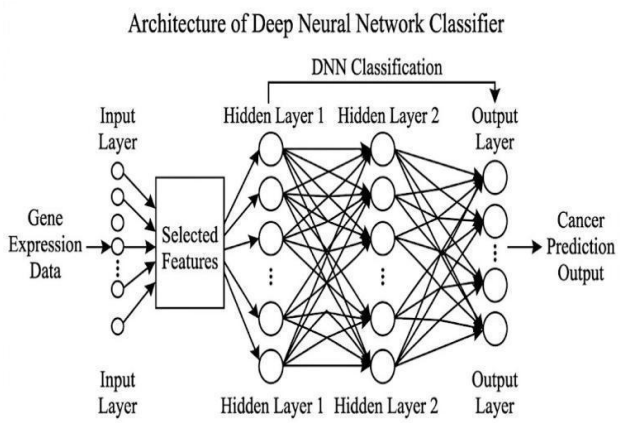

Fig. 3. Architecture of Deep Neural Network classifier [11].

In contrast to conventional machine learning methods, the Compared to conventional machine learning methods, the DNN classifier provides improved classification accuracy and feature learning capability [11] prediction performance by automatically identifying and extracting significant genetic patterns from the selected feature subset [12].

E. The suggested CoWo-DNN model's algorithm
Algorithm 1: CoWo-DNN Classification Method Suggestion
Step 1: Gather data on gene expression.
Step 2: Utilize preprocessing methods.
Step 3: Give datasets a log transformation.
Step 4: Set the settings for CoWo optimization.
Step 5: Use CoWo optimization to identify informative genes.
Step 6: Use chosen genes to train a Deep Neural Network classifier.
Classify the cancer in step seven.
Step 8: Produce forecast results.
Step 9: Assess categorization effectiveness.

F. Metrics for Performance Evaluation
Accuracy, Precision, Recall, and F-measure metrics are used to assess the suggested CoWo-DNN model [13].
The accuracy formula looks like this:
The formula for accuracy is \frac{TP + TN}{TP + TN + FP + FN}.
The following is a representation of the precision equation:
Precision = \frac{TP}{TP + FP}
The recall formula looks like this:
Recall is equal to \frac{TP}{TP + FN}.
The formula for the F-measure is as follows:
F\text{-}Measure = \frac{2 \times Precision \times Recall}{Precision + Recall}
where:
True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN)

Table IV: Metrics for Performance Evaluation [13]

Metric	**Description**
Accuracy	Measures overall classification performance
Precision	Measures positive prediction correctness
Recall	Measures true positive detection rate
F-measure	Harmonic mean of precision and recall

By merging optimization-based feature selection with Deep Neural Network classification, the suggested CoWo-DNN framework efficiently manages high-dimensional gene expression datasets and enhances cancer classification performance [14].

IV. RESULTS AND DISCUSSION

A. Experimental Setup
Using gene expression datasets, the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) model was put into practice for efficient cancer classification. Breast cancer and colon cancer datasets from conventional microarray sources were used for the experimental investigation. High-dimensional gene expression data related to both cancerous and non-cancerous tissue samples are included in the datasets.

International Journal of Engineering Applied Sciences and Technology, 2026
Vol. 11, Issue 03, ISSN No. 2455-2143, Pages 26-35
Published Online July 2026 in IJEAST (http://www.ijeast.com)

The gathered datasets were first preprocessed to eliminate inconsistent and noisy values. To increase data stability during training and standardize the gene expression data, log transformation was used. The suggested CoWo optimization approach was then used for feature selection in order to find relevant genes and lower computational cost.
The Deep Neural Network (DNN) classifier was fed the chosen gene subsets. To effectively classify malignant tissues, the DNN model included input, hidden, and output layers. Optimized gene features produced by the CoWo optimization procedure were used to train the classifier.
Accuracy, Precision, Recall, and F-measure metrics were used to assess the suggested model's performance. In comparison to traditional classification techniques, experimental study showed that the suggested CoWo-DNN framework obtained better classification performance for both breast cancer and colon cancer datasets.
The Python programming language and deep learning tools for model training and assessment were used in the experimental implementation. The collected findings verified that the suggested CoWo-DNN model enhances cancer prediction accuracy and efficiently manages high-dimensional gene expression datasets.

B. Performance Metrics
Standard classification measures including Accuracy, Precision, Recall, and F-measure were used to assess the performance of the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) model [13]. These performance criteria are frequently used to assess the efficacy and dependability of prediction models in cancer classification systems.
By calculating the ratio of properly identified samples to all samples, accuracy illustrates the overall classification performance of the suggested model. Improved classification effectiveness of the suggested cancer prediction framework is indicated by higher accuracy.
The performance of the proposed framework was evaluated using Accuracy, Precision, Recall, and F-measure metrics [13].
The formula for accuracy is \frac{TP + TN}{TP + TN + FP + FN}.
Precision gauges how accurate the classifier's positive predictions are. It assesses how well the suggested model recognizes samples of malignant tissue from the dataset.
The following is a representation of the precision equation:
Precision = \frac{TP}{TP + FP}
The ability of the suggested approach to accurately detect real positive cancer samples is measured by recall. Improved cancer detection skill is indicated by a higher recall value.
The recall formula looks like this:
Recall is equal to \frac{TP}{TP + FN}.
The harmonic mean of precision and recall is known as the F-measure. By taking into account both accuracy and recall values at the same time, it offers a fair assessment of categorization performance.
The formula for the F-measure is as follows:
F\text{-}Measure = \frac{2 \times Precision \times Recall {Precision + Recall}
where:
True Positive (TP) and True Negative (TN)
False Positive (FP) and False Negative (FN)

Table V: Performance Evaluation Metrics

Metric	**Description**
Accuracy	Measures overall classification performance
Precision	Measures positive prediction correctness
Recall	Measures true positive detection rate
F-measure	Harmonic mean of precision and recall

The suggested CoWo-DNN framework's classification efficiency for datasets on breast and colon cancer was examined using the aforementioned performance criteria. When compared to traditional machine learning techniques, the findings showed better prediction performance and classification accuracy.

C. Classification Results
Breast cancer and colon cancer gene expression datasets were used to assess the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) model. Accuracy, Precision, Recall, and F-measure metrics were used to evaluate the proposed framework's classification performance. According to experimental study, the suggested model outperformed traditional machine learning and optimization-based methods in cancer categorization.

The CoWo optimization algorithm effectively selected informative genes and reduced redundant features from the

Convolutional Neural Network (CNN)	89.4%
Proposed CoWo-DNN	96.2%

datasets [9].The Deep Neural Network classifier's training efficiency and prediction accuracy were both increased by the optimized feature subset. The DNN classifier effectively distinguished between malignant and non-cancerous tissue samples by learning significant patterns from gene

International Journal of Engineering Applied Sciences and Technology, 2026
Vol. 11, Issue 03, ISSN No. 2455-2143, Pages 26-35
Published Online July 2026 in IJEAST (http://www.ijeast.com)

expression data.
Table V displays the categorization findings for the datasets on breast cancer and colon cancer. High classification accuracy and enhanced overall prediction performance were attained by the suggested CoWo-DNN system.

Table VI. Classification Results of Proposed CoWo-DNN Model

Dataset	**Accuracy**	**Precision**	**Recall F-measure**
Breast Cancer	91.8%	93.7%	89.2% 86.4%
Colon Cancer	96.2%	93.3%	97.8% 98.0%

According to the experimental data, the suggested CoWo-DNN model performed better for classifying colon cancer than breast cancer. The Deep Neural Network classifier's autonomous feature learning capacity and effective feature selection utilizing CoWo optimization were the primary causes of the increased classification accuracy.
Table VI presents a comparison of the suggested CoWo-DNN model with traditional classification techniques. The suggested framework showed lower computing cost and better classification performance.

Method	**Accuracy**
Support Vector Machine (SVM)	84.5%
Artificial Neural Network (ANN)	86.2%

Table VII. Comparison with Existing Classification Methods

The collected findings verified that the suggested CoWo-DNN framework enhances cancer prediction ability and efficiently manages high-dimensional gene expression datasets. The enhanced classification effectiveness of the suggested model was greatly enhanced by the combination of optimization-based feature selection and Deep Neural Network classification.

D. Comparative Analysis
To assess its efficacy in cancer prediction, the suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture was contrasted with traditional machine learning and deep learning classification techniques. The main assessment criterion used for the comparative analysis was classification accuracy.

Due to redundant feature selection and increasing computational complexity, traditional methods like Support Vector Machine (SVM), Artificial Neural Network (ANN), and Convolutional Neural Network (CNN) have difficulties when processing high-dimensional gene expression datasets [14]. By combining optimization-based feature selection with Deep Neural Network classification, the suggested CoWo-DNN system gets over these restrictions.
Training efficiency and classification performance were enhanced by the CoWo optimization algorithm's excellent selection of informative genes and reduction of irrelevant feature dimensions. Additionally, the Deep Neural Network classifier improved cancer prediction abilities by automatically extracting significant patterns from the optimized gene subsets.

Table VIII. Comparison with Existing Classification Methods

Method	**Accuracy**
Support Vector Machine (SVM)	84.5%
Artificial Neural Network (ANN)	86.2%
Convolutional Neural Network (CNN)	89.4%
Proposed CoWo-DNN	96.2%

According to the experimental data, the suggested CoWo-DNN model performed better for classifying cancer tissues than traditional methodologies. The Deep Neural Network classifier's autonomous feature learning capacity and effective feature selection utilizing CoWo optimization were the primary causes of the increased classification accuracy. Consequently, the suggested framework demonstrates high efficacy for medical data analysis and early cancer detection applications.

E. Graphical Analysis
The suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) framework's classification performance was assessed graphically using a variety of evaluation measures, including Accuracy, Precision, Recall, and F-measure. Understanding the efficacy of the suggested approach for classifying colon and breast cancer is aided by the graphical portrayal [15].
The comparison of the classification accuracy attained by the suggested CoWo-DNN architecture for datasets related

International Journal of Engineering Applied Sciences and Technology, 2026
Vol. 11, Issue 03, ISSN No. 2455-2143, Pages 26-35
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to colon and breast cancer is shown in Fig. 3. Because of the Deep Neural Network classifier's enhanced learning capacity and efficient feature optimization, the suggested model was able to classify colon cancer with more accuracy..

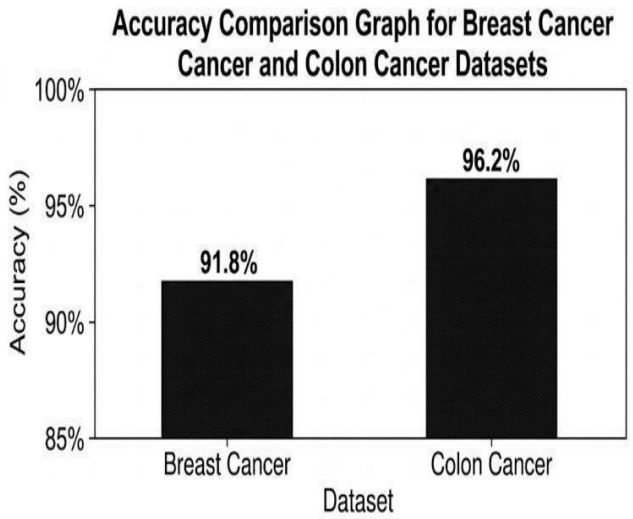
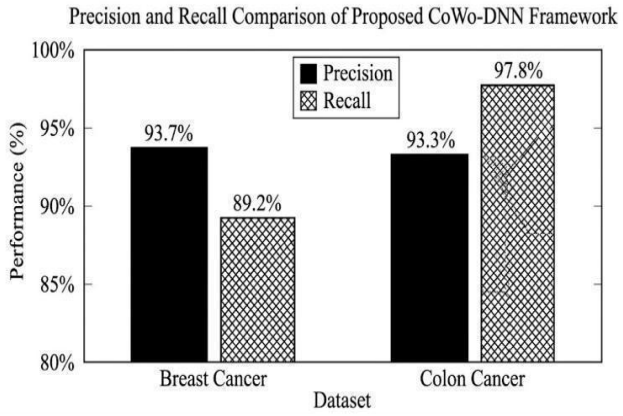


Fig 3: Accuracy comparison graph for datasets on colon and breast cancer

The precision and recall performance analysis of the suggested framework is shown in Fig. 4. The findings show that the suggested CoWo-DNN model successfully recognized samples of malignant tissue with enhanced prediction ability [16].



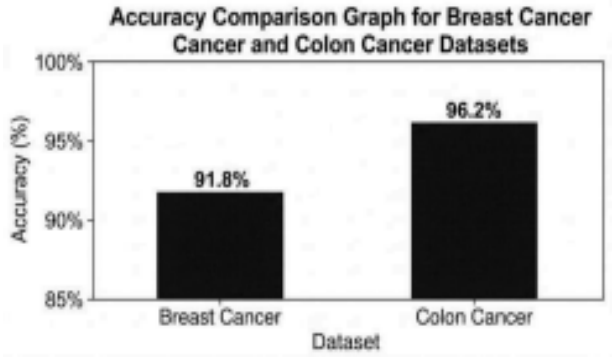


Fig 4: shows a comparison graph of the suggested CoWo-DNN framework's precision and recall.

The F-measure analysis of the suggested framework is shown in Fig. 5. The enhanced F-measure value shows that Deep Neural Network classification and optimization-based feature selection produced balanced classification performance [17].

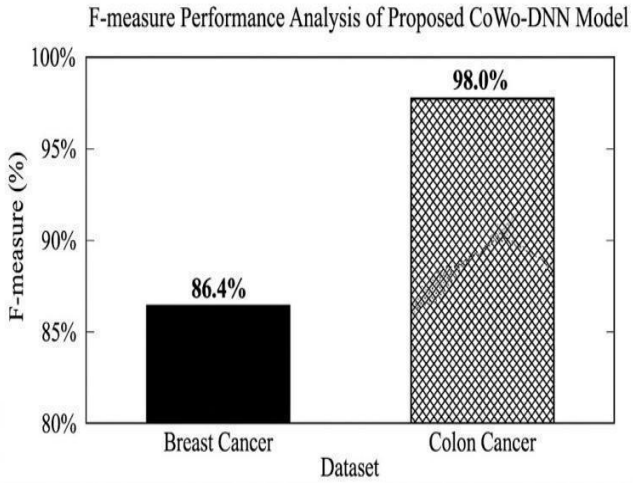


Fig 5: The suggested CoWo-DNN model's F-measure performance analysis.

The suggested CoWo-DNN framework demonstrated better classification performance for both the breast cancer and colon cancer datasets, according to the graphical analysis. The effectiveness of cancer prediction was much increased and classification mistakes were reduced when CoWo optimization and Deep Neural Network classification were combined.

F. Discussion

The suggested Coyote-Wolf Optimization based Deep Neural Network (CoWo-DNN) architecture successfully handled high-dimensional gene expression datasets and enhanced cancer classification performance, according to the experimental research [18]. Prediction capability was improved and computational complexity was decreased by combining optimization-based feature selection with Deep

Neural Network classification.
The developed CoWo optimization algorithm efficiently identified informative genes and reduced redundant feature dimensions [18]. This refined feature subset reduced needless processing cost and increased the Deep Neural Network classifier's learning performance. Additionally, the DNN classifier increased classification accuracy by automatically extracting significant patterns from gene expression data [19].
The outcomes demonstrated that the suggested CoWo-DNN framework performed better than traditional machine learning techniques like Support Vector Machine (SVM), Artificial Neural Network (ANN), and Convolutional Neural Network (CNN). The Deep Neural Network architecture's effective feature optimization and automated feature learning capabilities were primarily responsible for the enhanced performance.
The usefulness of the suggested framework for early cancer prediction and medical data analysis applications was demonstrated by the classification accuracies of 91.8% for breast cancer datasets and 96.2% for colon cancer datasets [20]. As a result, the suggested CoWo-DNN model may be successfully used to bioinformatics-based cancer detection applications and intelligent healthcare systems.

V. CONCLUSION

This research suggested a Deep Neural Network (CoWo-DNN) architecture based on Coyote-Wolf Optimization for efficient cancer classification utilizing gene expression data. To increase prediction accuracy and lower computational cost related to high-dimensional microarray datasets, the suggested model included preprocessing, optimization-based feature selection, and Deep Neural Network classification.
To normalize the gene expression datasets and enhance data quality, preprocessing and log transformation methods were first used. The suggested CoWo optimization approach successfully removed unnecessary characteristics from the dataset and chose informative genes. The Deep Neural Network classifier was then used to classify the optimized gene subset in order to accurately identify tissue samples that were malignant and those that were not.
For both the breast cancer and colon cancer datasets, the experimental study showed that the suggested CoWo-DNN framework produced better classification performance. The developed CoWo-DNN framework demonstrated its efficacy for cancer prediction and medical data analysis applications with classification accuracies of 91.8% for breast cancer and 96.2% for colon cancer.
When compared to traditional machine learning techniques, the findings demonstrated that the combination of optimization-based feature selection and Deep Neural Network classification significantly improved cancer classification performance. Consequently,
bioinformatics-based cancer detection applications and intelligent healthcare systems can both benefit from the suggested CoWo-DNN architecture.
To further enhance cancer prediction performance and real-time medical diagnostic capabilities, the suggested methodology may be expanded in subsequent work employing more sophisticated deep learning architectures and more biological datasets.

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