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# Enhanced Lung Disease Classification through Deep Learning Fusion with CLBP, Attention Graphs, and Bee Colony Optimization

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**Abstract:** The identification and classification of lung diseases based on clinical images is critical to ensuring that physicians diagnose and treat the diseases properly. DeepAttentionCLBP-BeeNet is a new model proposed in this study to improve the accuracy of lung disease classification. In this model, both machine and deep learning algorithms are used to extract relevant information from chest radiographs/CT scan images. Contrast Local Binary Patterns (CLBP) are used for data preprocessing, texture detection, and improving the discriminative capacity of retrieved features. Attention Graphs can capture architectural entailments and temporal boundaries of disease symptoms, which enables more precise classification. When it comes to optimizing the number of parameters, the Bee Colony Optimization algorithm is used. The presented methodology is particularly successful, surpassing convention and improving treatments beyond expectations. Overall, it has a good accuracy of 97% as well as a precision of 96.1%; The specificity was at 96.7% while the recall and sensitivity were both at 97.3%, and F1-score value equal to 97.1%.

***Keywords:*** *Artificial Bee Colony optimization, Convolutional Neural Network, Deep Learning, Local Binary Patterns, Lung Diseases*.

## 1. Introduction

Chronic lung diseases are one of the foremost health issues across the globe and remain associated with high illness and mortality rates around the world. The disease diagnosis is crucial in controlling progression and determining an appropriate treatment process. Diagnostic imaging particularly chest radiographs and CT scans are essential diagnostic tools in lung examination, giving detailed information on the structural and functional changes within pulmonary system. However, the semantic analysis of such pictures can sometimes turn into a highly computational and time-consuming pursuit which requires quite some degree of specialization and the outcome varies from one observer to another. The newly developed deep learning, which took place within the last several years, has revolutionized medical image analysis, offering the possibility of automated as well as data-driven approaches for classification and detection of diseases based on images. Hence, there exists a wide range of models in deep learning, specifically Convolutional Neural Networks (CNNs), that perform well in multiple medical imaging scenarios, including lung diseases' classification. As presented, CNNs can effectively learn hierarchical representations from raw image data and, consequently, it can effectively identify the complex patterns and features associated with various diseases. Howevessr, CNNs have limitations such as it often requires large quantities of labeled data for training and can be less interpretable, thus making it challenging to understand why it reached certain conclusions about the data. Lung cancer broadly results from the malignant growth in the lungs of tissues, the affected persons may develop the following signs and symptoms; a cough which may be persistent, chest pain, spitting of blood, change in voice especially hoarseness, difficulty in breathing and wheezing. Some of the major forms of the lung cancer include Squamous Cell Carcinoma, Large Cell Carcinoma and Adenocarcinoma.

### 1.1. Lung Cancer Types

**Adenocarcinoma:** This is the most common type of lung cancer, it accounts for roughly 40% of all lung cancer cases, and is also known as non-small cell lung cancer (NSCLC) in about three-fourths of the patients. It is produced by glandular cells that covers the lining of alveoli and giving mucus. Different types of lung cancer also show variations; adenocarcinoma is seen commonly in patients who never smoked, in females or in the younger population. Almost always, it forms in the peripheral zones of lungs and is generally known to develop slower compared to others. Lung cancer is more likely when a person smokes, but that is not the only cause, as radon, asbestos, and other carcinogens also increase the risks.

**Large Cell Carcinoma (LCC):** A prevalent category of lung cancer, comprising approximately 80% of illness, and the type that occurs in big, abnormal-looking cells this type makes up only 10-15 % of NSCLC. LCC can form anywhere in the lung but is more common on the outer edges. It tends to grow and spread more quickly than other

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forms of NSCLC; therefore, early detection of the illness is a critical factor in determining treatment efficacy.

**Squamous Cell Carcinoma (SCC):** A Cancer that starts in squamous cells in lining of bronchi in the middle of the chest and constitutes approximately 25-30% of all lung cancers. It has the strongest correlation to smoking among the NSCLC's. Squamous cell carcinoma tends to develop in the middle area of the lungs including the bronchi and may be presented with features such as hemoptysis, pleurisy and dyspnoea among others. Similar to other lung cancers, where its aggressiveness and treatment outcomes are established by the tumor stage and the patient's general conditions.

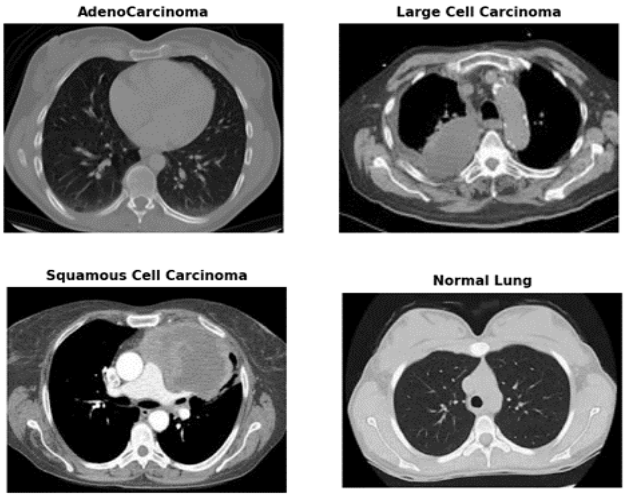


**Fig. 1.** Visualizing different types of Lungs Cancer and Normal Lung

The aforementioned types of lung cancer are closely related and share symptoms such as coughing, chest pains, and shortness of breath coupled with unexplained weight loss. Depending on the type and extent of the disease, surgery, chemotherapy, radiation therapy, and selective therapy may be performed individually or in combination. High levels of awareness are stressed since the chances of the disease being detected early and treated hike survival outcomes. Further, lung diseases are not restricted to depicting a single vague synthesized form, but can exhibit several complex disease forms which should be well captured by our models. To address these challenges, we introduced the incorporation of deep learning techniques, fused with other methods such as texture analysis, attention mechanism, and optimization techniques.

In this context, we propose a novel hybrid model in this study named DeepAttentionCLBP-BeeNet to optimize the classification of lung diseases shown in Figure 9. This model integrates Contrast Local Binary Patterns technique for data preprocessing, attention mechanisms, and Bee Colony Optimization for feature extraction and feature selection, and utilizes the Inception model for classification. By fusing these techniques, our objective is to formulate a comprehensive and efficient framework for the classification of lung diseases that addresses the limitations of individual approaches. This paper will examine the methodology, implementation specifics, experimental outcomes, and implications of the DeepAttentionCLBP-BeeNet model. Additionally, we will evaluate its performance against existing methods, underscore its potential applications in clinical settings, and ultimately contribute to the progression of automated lung disease diagnosis, thereby enhancing patient outcomes and healthcare provision. Moreover Figure 2. represents the workflow of proposed hybrid model

### 1.2. Workflow

The important contributions of this research article are as follows. We utilize Contrast Local Binary Patterns for texture characterization, it captures local texture patterns by computing binary patterns based on the contrast between a central pixel and its neighbors. Attention Graph network mechanisms empower models to concentrate on relevant regions of interest, enhancing both their interpretability and performance. Bee Colony Optimization is an optimization technique inspired by the honey bees foraging behavior. It's used to identify the most informative features from the data.

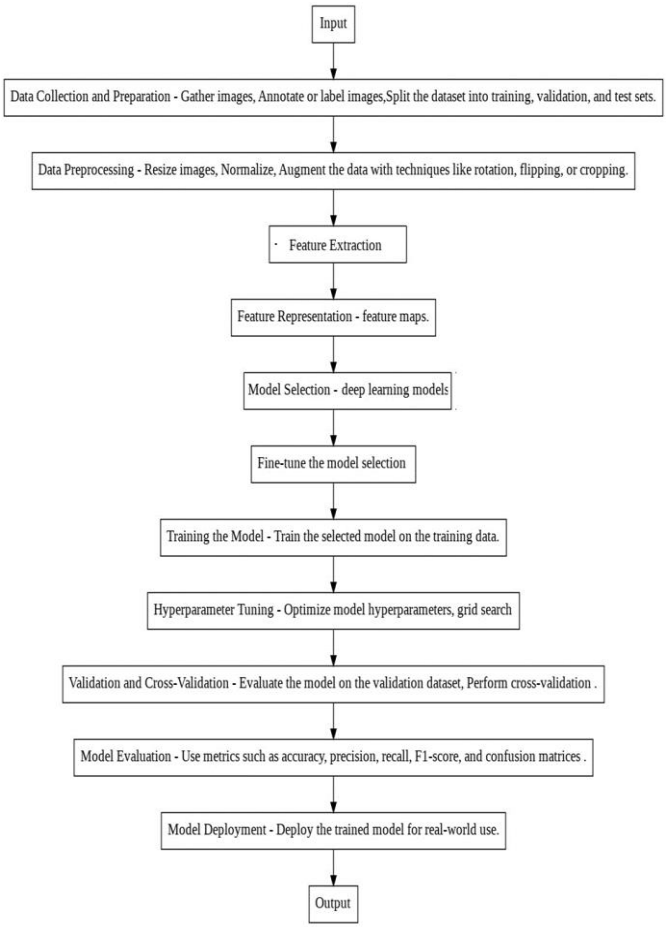


**Fig 2.** Represents workflow of proposed model

The Inception model is used for image classification tasks

It's known for its ability to capture multi-scale features through the use of inception modules. We assess the effectiveness of our proposed framework by evaluating its performance using key metrics such as Accuracy, Precision, Recall, and F-measure. We compare these metrics between our proposed framework and traditional algorithms to gauge the superiority or parity of our approach.

This article follows a structured approach to outline the research process comprehensively. In Section 2, we conduct a literature survey, delving into relevant existing studies concerning Deep Learning and its extensive utilization in medical image processing. Section 3 shifts focus to the dataset, exploring various data pre-processing techniques and introducing proposed methodologies, accompanied by a detailed explanation of the dataset. Section 4 is devoted to presenting the results of the study. Finally, Section 5 serves as the conclusion, where we summarize our findings as well as the implications of the findings are discussed.

## 2. Related Work

For the classification of lung diseases, there have been established developments of certain methodologies in an attempt of reducing the errors and enhancing the speed of the invention. Deep learning, particularly the convolutional neural network (CNN) [12-17], has emerged as a key tool for differentiating thoracic disorders from medical imaging in recent years. Nelson et al. [1], introduce a new valuable contribution to this area in developing CancerDetectNN, which is actually a stoke computer application that is aimed at enhancing the effectiveness in the detection of lung cancer. Introducing the new algorithms, CancerDetectNN also enhances the approach towards detecting malignant areas in lung images and also reduces the required computation for training. This must be very encouraging in enhancing the identifying and diagnosing ability so as to create enhanced patients benefits.

Bhola et al. [2] proposed the technique of lung cancer detection using transfer learning along with EfficientNetB2 model. They have chosen a target application for their work, namely, the use of deep learning methods for automatic tumor detection in the CT images. To apply transfer learning, the structure is trained initially on a vast amount of data to learn and select features helpful for returning scores that differentiate between normal and abnormal CT images. This methodology can play a role in improving the decision of outlining the position of the tumor and improving effectiveness and speed of the lung cancer diagnosis. An Automated Hybrid CNN Hopfield Neural Network (CHNN) model deployed by Vidyasri et al. [3], adds another type of approach on how to solve the classification and detection of lung diseases. Their work employs the transfer learning to improve disease categorization with lesser False Negative and False Positive rates. In deployed CHNN model, the CNN algorithm helps in the automation of lung diseases classification and detection, while the Hopfield neural networks (HNNs) technique provides a complete architecture for such processes. This new structure combined some perspectives of CNNs and HNNs, which can help to enhance the capability of this model in detecting different pathologies of lung applied from medical images.

A deep learning (DL) model based on VGG19 proposed by Goram Mufarah M et al. [4] was used in a study for the diagnosis pulmonary opacity, lung cancer, COVID 19, tuberculosis and pneumonia at stages involving multiclass classification. Architecture includes three CNN layers for feature extraction, a fully connected network for classification phase. Kim, S., et al. [5] used an EfficientNetv2-M DL network to closely examine the raw CXR images from two datasets. Their work provided recognizable accuracies of normal, pneumonia, and pneumonia classes, achieving 82.15% accuracy for the NIH dataset and 82.20% for the SCH dataset, which additionally incorporates tuberculosis classification.

Arora, R. et al. [6], deployed the Multi Lung Disease Classification (MLDC) technique to identify COVID-19, pneumonia, tuberculosis, and healthy lung categories. Their methodology integrates a feature extraction technique alongside two distinctive classifiers: the quantum classifier (QC) and the artificial neural network (ANN). MLDC attains impressive accuracies of 95.6% for MLDC-ANN and 97.5% for MLDC-QC, all while maintaining lower computational costs.

Hong et al. [7], propose a CNN method for categorizing lung diseases from X-ray images. They use two datasets, NIH and Soonchunhyang University Hospital, and preprocess images with Center Crop. Fine-tuning an EfficientNet model with Noisy Student learning and Multi Global Average Pooling, they achieve 85.32% accuracy on the NIH dataset and 96.1% accuracy, with 92.2% sensitivity and 97.4% specificity, on the Soonchunhyang University Hospital dataset, with an average inference time of 0.2 seconds

Sami, Azam [8], developed LungNet22, a CNN model tailored for accurate lung disease classification. It efficiently categorizes 10 disease classes, including Pneumonia, Nodule, Mass, Pulmonary Fibrosis, Tuberculosis, Effusion, Pulmonary Opacity, COVID19, Pneumothorax, and the Normal class. The dataset, containing 80,000 X-ray images, undergoes preprocessing and balancing via eight augmentation techniques. Initially, eight pre-trained CNN models are evaluated, with VGG16 achieving the highest accuracy of 92.95%. Consequently, LungNet22 is built on the VGG16 architecture to further

enhance classification accuracy. Ramya Mohan et al. [9], introduce MIDNet18, a CNN designed for identifying the lung infections from chest CT images. MIDNet18, derived from a tailored Medical Image Analysis and Detection network, attains high accuracy with a simplified framework structure and minimal complexity. Compared to conventional algorithms like LeNet5, VGG19, VGG16, and ResNet50, MIDNet18 demonstrates significantly superior accuracy, particularly surpassing LeNet5, VGG19, and VGG16, and marginally outperforming ResNet50.

Hassaan Malik et al. [10] develop BDCNet, a pioneering model that integrates VGG-19 with CNN. This novel technique is used across multiple publicly available standard datasets to efficiently detect COVID-19 and other chest tract disorders. Pre-trained CNN models like as ResNet-50 model, Inception V3 model, VGG-16 and VGG-19 model exhibit impressive accuracy rates ranging from 95.10% to 97.35%, suggesting that the BDCNet model has the potential to revolutionize early disease identification. Furthermore, San-li Yi et al. [11], present a five-classification pulmonary disease model featuring the RED-CNN network, utilizing state-of-the art feature extraction modules such as Res2Net, ECA, and Double Blaze Block. Through the amalgamation of datasets encompassing COVID-19, tuberculosis, and other pulmonary diseases, a comprehensive dataset is curated. A rigorous series of experiments were conducted with 5-fold cross-validation, RED-CNN model achieves impressive metrics including accuracy (91.796%), precision (92.062%), recall (91.796%), F1 score (91.892%), and Jaccard scores (86.176%). Due to high death rate of lung cancer, early detection is especially essential because lung diseases are difficult to diagnose and treat. Jumin Zhao et al. convolutional neural network (CNN) to identify lung nodes as malignant or benign in CT images. Their multistream multitask network merges multi-scale embeddings, and multi-attribute classification via a new loss function to address attribute correlations. The model performed well, with AUC (0.979), accuracy (93.92%), sensitivity (92.60%), and specificity (96.25%).

Here are some potential gaps:

- One of the most profound challenges that still confronts the field of medical imaging is the limited availability of large, diverse, well-annotated datasets to conduct such experiments. The scarcity of such high-quality lung imaging data can restrain the development and validation of strong classification systems.
- Lung diseases can vary in the size, shape and texture patterns in imaging characteristics. That it will handle such variability with sufficient vigor and so that it will allow for a consistent and accurate classification across different disease presentations.
- Manual CT scan analysis is time-consuming and prone to inaccuracies or errors, highlighting the need for automated, reliable classification systems.
- Using hybrid strategies that incorporate multiple algorithms can complicate result interpretation and increase computational complexity and resource requirements. Ensuring efficient model training and inference on standard computing platforms is crucial for practical deployment.
- Developing an effective feature extraction process is challenging, and poor feature selection can lead to suboptimal classification performance.

Addressing these gaps will improve the robustness, interpretability, and clinical relevancy of lung disease classification models. Here we propose a novel methodology for the categorization of the lung disease which combines deep learning Inception model, CLBP texture feature, attention graphs, and Bee Colony Optimization (BCO). Based on the proposed integrative convolutional network, texture analysis, attention mechanism, and optimization techniques are combined to make the classification model more accurate and stable, which is expected to be utilized in lung disease diagnosis and treatment.

## 3. Methodology

### 3.1. Data set Preparation

The dataset was collected from the public domain on Kaggle, includes approximately 1,000 images categorized into three types of chest cancer: Squamous Cell Carcinoma (260 images), Adeno Carcinoma (338 images), Large Cell Carcinoma (187 images). Additionally, there is a normal lung cell category with 215 images. The sample dataset shown in Figure 1, with the class-wise distribution represented in Figure 3. The dataset is divided into three sets: training (613 images), testing (315 images), and validation (72 images). The class-wise distribution of the dataset after the train, validation and test split shown in the Table 1 and Figure 4.

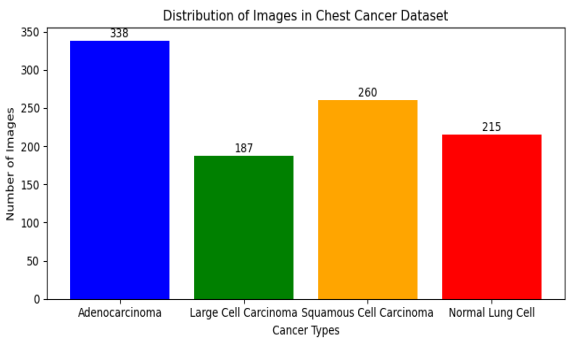


**Fig 3.** Demonstrates the distribution of the dataset, including Adeno Carcinoma, Large Cell Carcinoma, Squamous Cell Carcinoma, and normal lung images**.**

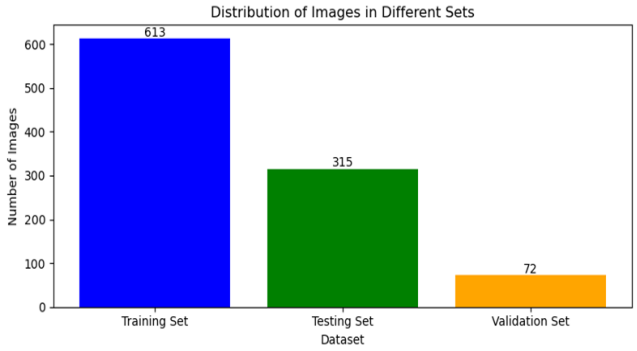


**Fig 4**. Demonstrates the distribution of the dataset into training, testing and validation set

**Table 1.** The class-wise distribution of dataset after the train–test split

| Lung Disease type | Train set | Validation set | Test set | Total |
|---|---|---|---|---|
| Adeno Carcinoma | 195 | 23 | 120 | 338 |
| Large Cell Carcinoma | 115 | 21 | 51 | 187 |
| Squamous Cell Carcinoma | 155 | 15 | 90 | 260 |
| Normal Lung | 148 | 13 | 54 | 215 |
| **Total** | 613 | 72 | 315 | 1000 |

### 3.2. Image preprocessing techniques to CT scan images

Lung disease diagnosis and classification using CT scan images are crucial for effective treatment planning and patient care. In this paper, we enhance lung disease classification by applying various image preprocessing techniques to CT scan images. We explore techniques such as normalization, resizing, histogram equalization, Gaussian blur, thresholding, edge detection, and rotation. These techniques aim to improve image quality, enhance contrast, reduce noise, and highlight relevant features for accurate disease classification.

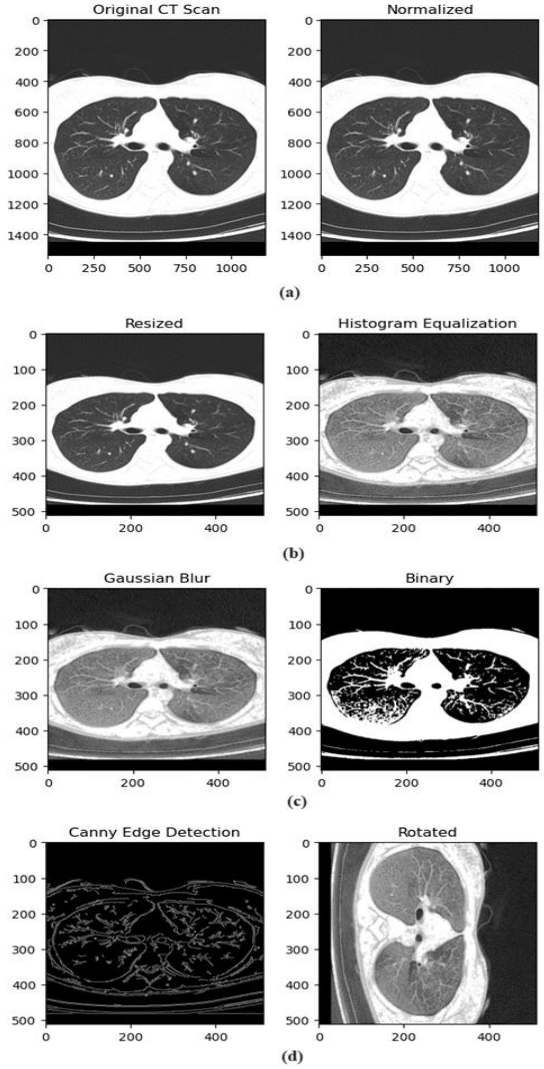


**Fig 5.** Preprocessing techniques applied to CT Scan Image

Normalization, imagine scaling, histogram equalization, Gaussian blurring, data thresholding, edge detection, and rotations are some of the techniques used to enhance and analyze images focused on the current data. Normalization (as seen in Figure 5a) normalized the pixel intensities of the images to more acceptable values. Resizing (Figure 5b) decreases the input image size into the range that various current datasets can tolerate, while histogram equalization (Figure 5b) employ stretching out of frequent intensity values that were concealed to reveal hidden information in pictures. Gaussian blur (Figure 5c) smooths the images such that most of the noise and detailed features are filtered out to prepare the images for subsequent processing. Thresholding (Figure 5c) converts the grayscale images to binary whereby proper features of the images that need to be emphasized are separated from the background. Edge detection which is illustrated in Figure 5(d) is used to detect the existence of gradients on an image and their magnitudes to define the shape and structure of objects. Finally, rotation (Figure 5d) switches image positions up and down, left and right for standard orientation or augmentation to advance the perspective and

make analysis.

The Figure 6 displays some of the more popular thresholding techniques applied to a CT scan image, and demonstrates image and threshold image side by side. Every subplot shows one kind of the thresholding methods considering the image, Otu's thresholding, adaptive thresholding and manual thresholding. This comparison assists in the evaluation of the performance of each technique to segment the important features on CT scan image

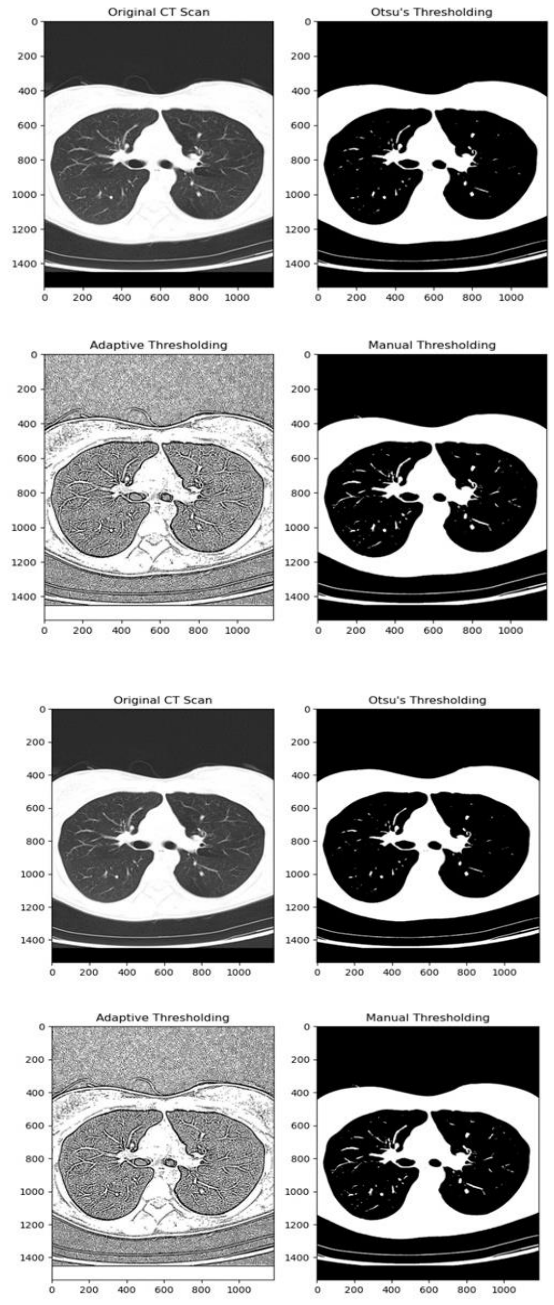


**Fig 6.** Thresholding Techniques Applied to CT Scan Image

Figure 7 shows the lung image obtained by the medical imaging, whose both qualitative and quantitative analyses were recorded with a normal result. The first is a visual inspection based on the structural form of the image and its anatomy traits. Then a histogram analysis to evaluate how intensities of pixels are distributed in the image. This analysis technique does not so much reveal the luminance distribution of the image; but it does tell us something very useful about how light or dark the image is as a whole, and the contrast ratio of the image. If you compare that same histogram to the original image, then it can help you to understand a comprehensive way about the visual characteristics of an image and distribution of its brightness.

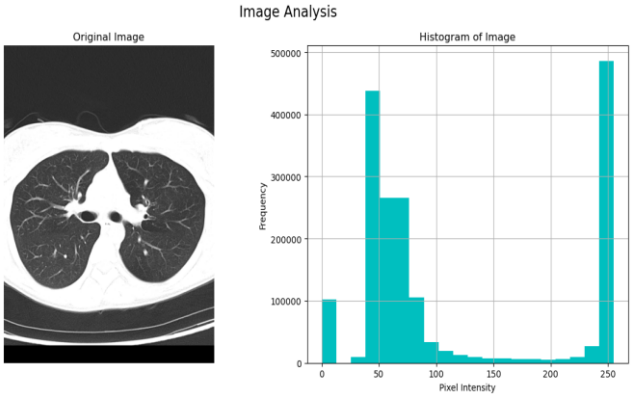


**Fig 7.** Demonstartes the Original Image and Histogram Analysis

### 3.3. Data Preprocessing with CLBP

Before extracting features, the medical images are first preprocessed by using Contrast Local Binary Patterns (CLBP), which is a texture descriptor commonly used in image processing for selecting those patterns of the local texture. The CLBP quantifies the local contrast inside the image patch, thus, strengthening the discriminative capability of features of medical images, which is proving to be invaluable to lung diseases' classification. Local binary pattern basic idea is to threshold a local neighborhood around each pixel and generates a binary number. Here's a step-by-step explanation of how LBP works:

1. **Local Neighborhood:** For each pixel in the image, consider a local neighborhood (usually a 3x3 window).
2. **Thresholding:** Subtract each of its adjacent pixel values with the center pixel value. If the neighbor is greater than or equal to the center value then output 1 otherwise 0. The final output is a binary representation of the pattern.
3. **Binary Pattern:** This produces a binary number (for a 3×3 window, it gives 8 binary digits).
4. **LBP Code:** This binary number represents the LBP code for the center pixel; convert them to a decimal form.
5. **Histogram:** Display a histogram of the LBP

codes for the whole image or a sub-region of interest.

Contrast Local Binary Patterns (CLBP) is an extended version of LBP that incorporates additional information to enhance texture classification. The three components which make up CLBP are: CLBP_S (sign component), CLBP_M (magnitude component) and CLBP_C (center component). These components together provide a more comprehensive description of texture.

Here's the step-by-step algorithm for using CLBP for lung cancer identification from CT images:

**Step 1:** Pre-processing

a. Input Raw CT image

b. Normalize the pixel intensity values to a fixed range (e.g., [0,1])

$$I_{\text{norm}} = \frac{I - I_{\min}}{I_{\max} - I_{\min}} \quad (1)$$

c. Apply noise reduction filter:

$$I_{\text{denoise}} = \text{filter}(I_{\text{norm}}) \quad (2)$$

**Step 2:** Local Binary Patterns (LBP) Calculation

a. Starting from each pixel, compare its value with the neighbors

b. Assign binary values based on the comparison:

$$S(x) = \begin{cases} 1 \ if \ x \geq 0 \\ 0 \ if \ x < 0 \end{cases} \quad (3)$$

Where x is the difference between the pixel value and its neighbor.

**Step 3:** Contrast Local Binary Patterns (CLBP) Calculation

a. Compute the sign component CLBPs

$$\text{CLBP}_S = \sum_{p=0}^{P-1} s(g_p - g_c) \cdot 2^p \quad (4)$$

Where $g_p$ and $g_c$ are the gray levels of the neighbors and center pixel respectively, and P denotes the number of neighbors.

b. Compute the magnitude component $\text{CLBP}_M$

$$\text{CLBP}_M = \sum_{p=0}^{P-1} m(|g_p - g_c| - \tau) \cdot 2^p \quad (5)$$

while τ stands for a threshold and equation for m(x) is provided

$$m(x) = \begin{cases} 1 \ if \ x \geq 0 \\ 0 \ if \ x < 0 \end{cases} \quad (6)$$

c. Compute the center component CLBPc

$$\text{CLBP}_C = s(g_c - \tau) \quad (7)$$

**Step 4:** Generate Feature vector for each Region of Interest and combine feature vectors from all ROIs:

Combined_FeatureVector = concatenate ([Feature Vector1, Feature Vector2……., Feature Vector n])

**Step 5:** Classify the combined feature vector using a pre-trained model

Classification Result = Model.predict(Combined_Feature Vector)

### 3.4. Feature Extraction with Attention Graphs

Attention Graphs are employed to model spatial relationships and contextual information among disease patterns in medical images. By focusing on relevant regions of interest, attention graphs enable the classification model to extract meaningful features, facilitating more accurate disease classification. Here's a step-by-step algorithm to perform feature extraction using attention graphs:

**Step 1:** Input Representation

a. Graph Definition: Firstly, define a graph G = (V, E) in which the set V contains vertices and the set E contains the edges between the vertices.

b. Feature Matrix: Prepare the feature matrix X, where Xi is the feature vector for one particular node i.

c. Adjacency Matrix: Keep track of the connections between the nodes and create the adjacency matrix A.

**Step 2:** Initialize Parameters

a. Initialize Weights: Create the weight matrices W required for the neural network layers in the function.

b. Attention Mechanism Parameters: Initialize the parameters of the attention mechanism such as for instance attention weights α.

**Step 3:** Attention Mechanism

a. Compute Attention Coefficients: For each pair of nodes (i, j) connected by an edge, calculate the attention coefficient $e_{ij}$ as follows:

$$e_{ij} = \text{LeakyReLU}(a^T[WX_i | WX_i]) \quad (8)$$

where a is a learnable weight vector, ‖ denotes concatenation, and LeakyReLU is the activation function.

b. Normalize Attention Coefficients: Normalize the attention coefficients across all node i's neighbors j using a SoftMax function.

$$\alpha_{ij} = \frac{\exp(e_{ij})}{\sum_{k \in \mathcal{N}(i)} \exp(e_{ik})} \quad (9)$$

where N(i) specifies the set of node i's neighbors.

**Step 4:** To compute the aggregated feature representation for each node i, use normalized attention coefficients.

$$h_i' = \sigma\left(\sum_{j\in\mathcal{N}(i)} \alpha_{ij} W \mathrm{X_i}\right) \quad (10)$$

where sigma(σ) is a nonlinear activation function (such as ReLU).

**Step 6:** Update the node features for the next layer or iteration:

$$\mathrm{H'} = \sigma\left(\sum_{\mathrm{i}\in\mathcal{N}(\mathrm{i})} \alpha_{\mathrm{ii}} \mathrm{W\, H_i}\right) \quad (11)$$

where H is the updated feature matrix from the previous layer or the initial feature matrix X.

**Step 7:** Stacking Layers (Optional)

Stack Multiple Layers: Repeat steps 3 to 5 to stack multiple attention layers if a deeper representation is needed.

**Step 8:** Readout and Output

a. Graph-Level Representation (Optional): If a graph-level representation is required (e.g., for graph classification), apply a readout function (e.g., sum, mean, or max) to aggregate node features.

b. Feature Extraction Output: Extract the final node or graph-level features for downstream tasks such as classification, regression, or clustering.

### 3.5. Fine-Tuning with Bee Colony Optimization technique

Bee Colony is a metaheuristic optimization technique stimulated by the honey bees foraging behavior. In the context of lung disease classification, Bee Colony Optimization is utilized to fine-tune the parameters of the classification model, optimizing its performance for accurate disease classification. Bee Colony Optimization algorithm for fine-tuning parameters of a classification model for lung disease classification:

Steps:

1. **Initialization:** Initialize a population of parameter sets for your classification model. These parameter sets represent potential solutions that the algorithm will explore.
2. **Employed Bees Phase:** Each employed bee evaluates the fitness of its assigned parameter set by using it to train the classification model and then testing it on a validation set. The fitness function could be based on metrics like accuracy, sensitivity, specificity, or a combination of these.
3. **Onlooker Bees Phase:** Onlooker bees select parameter sets based on the probability that their corresponding employed bees have high fitness values. This probability could be determined by the fitness of the employed bee relative to the other employed bees.
4. **Scout Bees Phase:** After a specified number of iterations (or generations), parameter sets that have not been improved are replaced with fresh randomly generated sets.
5. **Repetition:** Steps 2-4 are repeated for a predetermined number of iterations or until a termination condition is fulfilled (such as convergence).
6. **Best Solution:** After the algorithm completes, the parameter set with the highest fitness value (or best-performing model) is chosen as the final solution.
7. **Evaluation:** Analyze the final model's performance on a separate test set with the chosen parameter set. Evaluated measures such as sensitivity, accuracy, specificity, and other metrics, to assess the model's ability for generalization.

The step-by-step explanation shows how the parameters of a classification model can be optimized using the Bee Colony Optimization technique to enhance the categorization of lung diseases.

### 3.6. Proposed Architecture

To assist feature extraction, that would allow our classification model to categorize a disease based on chest radiographs or CT scans, we use the Inception model's ability to extract features from hierarchies of varying order. The Inception model is a widely used deep architecture technique that has been constructed using CNN for the purpose of image identification tasks. To enhance the categorization of the various lung diseases the novel approach of DeepAttentionCLBP-BeeNet framework has adopted the following techniques. First, the model applies the CLBP algorithm to the lung images, where it favors the representation of texture information by computing both the local binary patterns and local contrasts of the image patches. Thus, the preprocessing step that follows in this study serves the purpose of enabling the model to analyze texture patterns that are important for disease differentiation. Following that, the model utilizes Attention Graphs to provide key areas of the images from CLBP enhancement to draw salient features. These attention mechanisms help in filtering noise and on incorporating features that are essential for classification.

Furthermore, the model employs Bee Colony Optimization (BCO) to enhance feature selection where honey bees go out in search of food, and those found in the new area are exploit optimal solution in understanding and

implementing the solution space. BCO helps in picking the key discriminative features from the regions learned by the attention guide regions, enhancing feature representation. Lastly the features that have been chosen are passed to the Inception model which is a deep CNN used for image classification. The Inception model is useful in the identification of representations from the enhanced images using CLBP and ensures accurate classification of the lung diseases from the obtained features. In summary DeepAttentionCLBP-BeeNet model provides a three-level implementation framework that includes texture improvement, feature location, feature selection, and classification based on cutting-edge methods; it is a feasible strategy for enhancing the classification of lung diseases.

The Figure 8 shows the deeper network architecture of DeepAttentionCLBP-BeeNet model which begins with the input lung image. The image is first processed with CLBP preprocessing then followed by construction of an attention graph, selection of features based on the Bee Colony Optimization, and finally the Inception model is used for classification. Lastly, based on the information extracted from the image, the model produces the predicted disease classification.

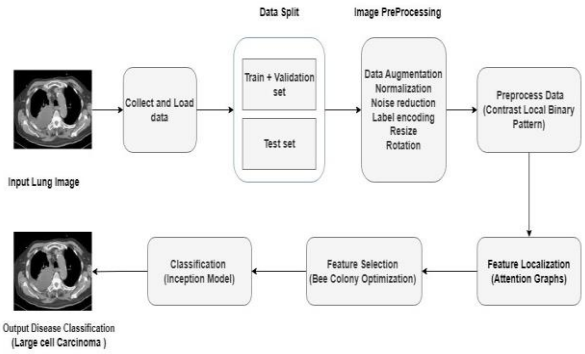


**Fig 8.** show proposed hybrid DeepAttentionCLBP-BeeNet model

## 4. Results

Experimental outcomes determine efficiency of the proposed methodology in accurately classifying lung diseases from medical images. Comparative analysis against conventional methods reveals significant improvements in classification accuracy, highlighting the potential of the DeepAttentionCLBP-BeeNet model for enhancing diagnosis and patient care.

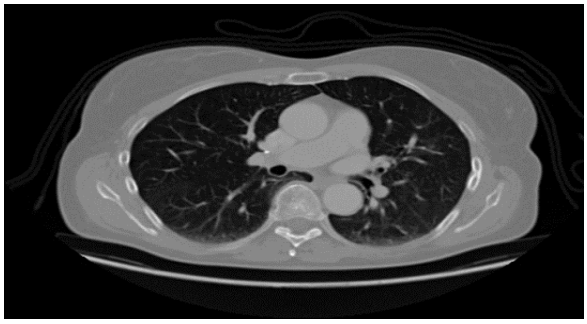

**Fig 9.** shows an axial computer tomography image of the human lung.

The simulation results provide insight into the system's behaviour under varied input and conditions. The findings may include numerical or graphical representations of the simulated system's dynamics, behaviour, and conclusions. Figure 9 shows the simulation findings for axial computer tomography of the human lung. A computed tomography (CT) scan is a medical diagnostic tool that examines the internal structures of the thorax, identifying diseases or anomalies and scheduling treatment appointments. It provides a cross-sectional image of the body, allowing medical workers to evaluate areas such as the heart, lungs, and bones that wouldn't be viewable with traditional X-rays.

The confusion matrix and classification report presented below demonstrate that the proposed model was quite effective, classifying patients with a high degree of efficiency at 97% accuracy. The classification results shown in the confusion matrix in Figure 10 show that the model produces satisfactory classification results with the lowest number of misclassified occurrences across classes. For example, the model is 95.83% accurate in classifying Adeno carcinoma (ACC) instances (115 samples correctly classified as ACC out of 120 ACC samples) and 96.08% accurate in classifying Normal instances (53 samples correctly classified as Normal out of 54 Normal samples). The results of the classification report are provided in Table 2 demonstrates the model's correctness, as precision, recall, and F1-score values are all greater than zero. The mean values obtained for each class were 94, indicating both a high sensitivity and precision. The macro and weighted averages of accuracy, recall, and F1-score are similar to the computed averages, which are approximately 0. 96 and 0.97, emphasizing the model's consistent performance across different classes, ensuring minimal bias towards any specific class.

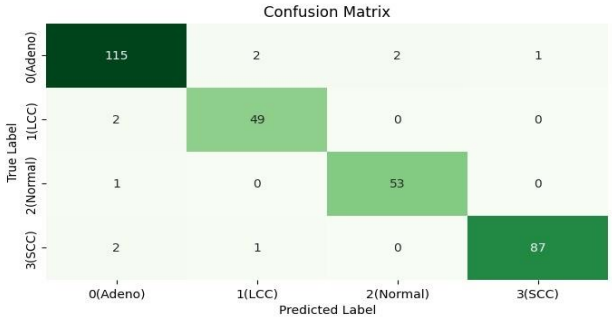


**Fig 10.** Analysis of Lung Disorder Detection.

**Table 2.** depicts classification report

| Labels | Precision | Recall | F1score | support |
|---|---|---|---|---|
| 0 | 0.96 | 0.96 | 0.96 | 120 |
| 1 | 0.94 | 0.96 | 0.95 | 51 |
| 2 | 0.96 | 0.98 | 0.97 | 54 |
| 3 | 0.99 | 0.97 | 0.98 | 90 |
| Accuracy | | | 0.97 | 315 |

### 4.1. Performance Metrics of the proposed model.

The DeepAttentionCLBP-BeeNet Networks leveraging Contrast Local Binary Patterns for data preprocessing, Attention Graphs for feature localization and selection, Bee Colony Optimization for parameter tuning, and the Inception model for detection and classification capabilities. We evaluated the model's performance using key metrics like the precision, accuracy, recall and F1 score. These metrics are computed as follows:

Accuracy calculated as

$$Accuracy = \frac{TP + TN}{TP+FP +TN+FN} \quad (12).$$

Precision (P) is determined as

$$Precision(P) = \frac{TP}{TP + FP} \quad (13).$$

To compute recall (R), use the formula

$$Recall\ (R) = \frac{TP}{TP+FN} \quad (14).$$

The F1 score is computed as the harmonic mean of precision and recall

$$F1_{Score} = \frac{2*P*R}{P+R} \quad (15)$$

True Positive (TP) represents the count of correctly detected positive instances. False positives (FP) are instances that were incorrectly identified as positive, while false negatives (FN) are the number of positive cases that were mistakenly classified as negative. Metrics are crucial for evaluating model accuracy, especially in image recognition applications. Using the proposed framework, we determined the accuracy, recall, sensitivity, specificity, and precision of the current technique. Figure 11 illustrates the changes in each metric across epochs, allowing observation of the model's performance trends. The legend indicates the corresponding line for each metric.

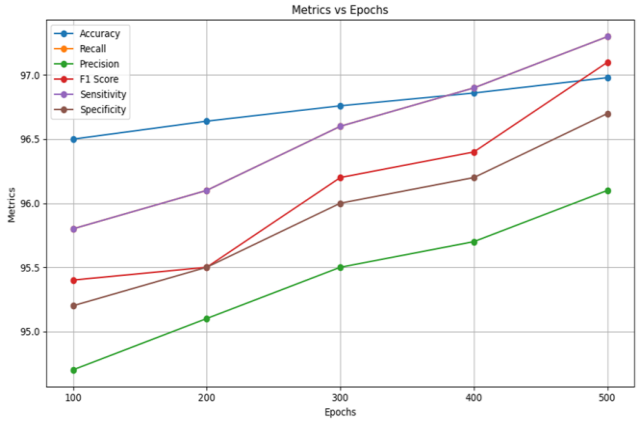


**Fig 11.** demonstrates the progression of each metric throughout epochs.

By identifying spatial links in medical images, the DeepAttentionCLBP-BeeNet strategy improves feature extraction performance. Figure 12 displays the accuracy vs. specificity performance statistic for the suggested method. At 100 epochs, the accuracy is 96.5%, and at 500 epochs, it is 96.7%. A specificity of 95.2% is obtained after 100 epochs, whereas 96.7% is obtained after 500 epochs.

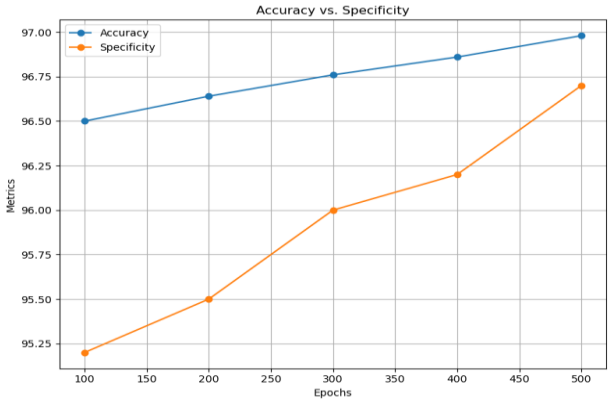


**Fig 12.** illustrates performance comparison between Accuracy and Specificity.

The DeepAttentionCLBP-BeeNet model, by capturing spatial connections in medical images, enhances feature extraction efficiency. This procedure substantially boosts the model's recall at each epoch. Specifically, at 100 epochs, the recall is 95.8%, and at 500 epochs, it is 97.3%. The Precision vs. Recall achieved with the proposed approach is depicted in Figure 13, where a precision of 94.7% is achieved at 100 epochs, and 96.1% is achieved at 500 epochs.

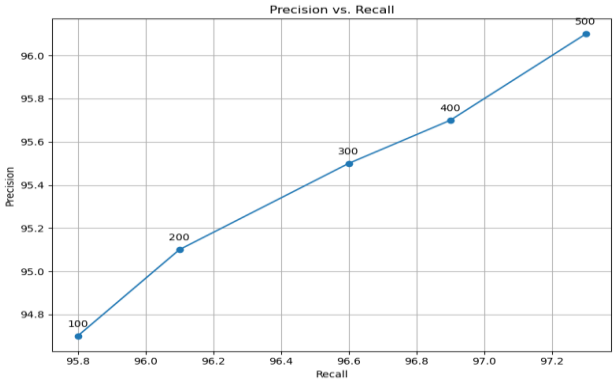


**Fig 13.** showcases the Precision vs. Recall attained at each epoch through the proposed approach

An F1-score of 95.4% is attained at 100 epochs, while at 500 epochs, it rises to 97.1%. The suggested fusion inception model adeptly detects subtle variations amid intricate backgrounds, thereby improving detection and classification efficiency. This method notably enhances the model's F1 score across all epochs as illustrated in Figure 12. At 100 epochs, a sensitivity of 95.8% is observed, which increases to 97.3% at 500 epochs, as depicted in Figure 11. The hybrid model, which combines contrast local binary pattern, attention graph, Bee optimization network, and inception model techniques, improves feature extraction and preprocessing efficiency by mitigating the impact of density alterations. This method notably boosts the performance metrics of the model across all epochs, as illustrated in Table 3

**Table 3.** depicts performance metrics across epochs

| Epochs | Accuracy | Recall | Precision | F1 Score | Sensitivity | Specificity |
|---|---|---|---|---|---|---|
| 100 | 96.5 | 95.8 | 94.7 | 95.4 | 95.8 | 95.2 |
| 200 | 96.64 | 96.1 | 95.1 | 95.5 | 96.1 | 95.5 |
| 300 | 96.76 | 96.6 | 95.5 | 96.2 | 96.6 | 96.0 |
| 400 | 96.86 | 96.9 | 95.7 | 96.4 | 96.9 | 96.2 |
| 500 | 96.7 | 97.3 | 96.1 | 97.1 | 97.3 | 96.7 |

### 4.2. Comparison of the proposed model.

The efficiency of the proposed method in terms of the accuracy, precision and sensitivity, recall, and specificity is compared with those of standard classification algorithms such as RF, SVM, BNN and Adaboost. This comparison will reveal how well the proposed approach copes with the tasks in pre-processing, feature extraction, detection, and classification stages and give a detailed discussion of these measures. While on one hand, we investigate beyond the measures of performance, on the other hand, we verify the angles like accuracy and sensitivity to support the efficacy of the introduced strategy in handling diagnostics in order to enhance the investigation of lung disorders in research domains like pre-processing, feature extraction, detection, and classification.

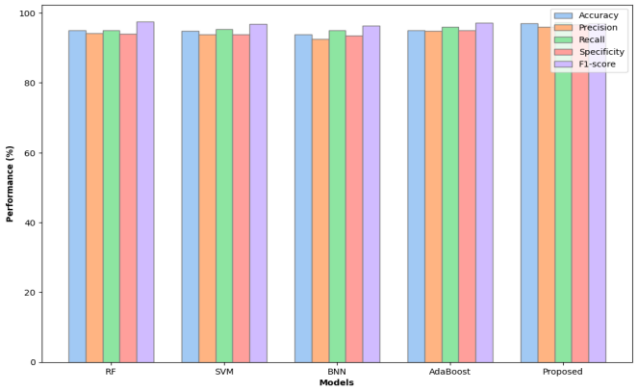


**Fig 14.** Comparison of different models with proposed DeepAttention CLBP Bee Optimization Network

The enhancement of pre-processing and feature extraction is proposed to be achieved by the use of Attention graph, Contrast Local Binary Pattern, and Bee Binary Optimized Network, where the use of the proposed method eases the impacts of density variation and mischaracterization. The comparison of the accuracy of the proposed model with existing methods is shown in Figure 14. With an accuracy of 96.7%, the proposed algorithm outperforms RF, SVM, BNN, and Adaboost, which attain accuracies of 95%, 94.9%, 93.9%, and 95.1% respectively. Similarly, the precision of the proposed model is 96.1%, outperforming RF, SVM, BNN, and Adaboost with precisions of 94.25%, 93.8%, 92.55%, and 94.9% respectively. The proposed approach obtains 97.3% recall, which is better than the recalls of 95.9%, 95.35%, 95%, and 96.1% achieved by RF, SVM, BNN, and Adaboost, respectively.

**Table 4.** Comparison of proposed method with existing techniques

| Parameters | RF | SVM | BNN | AdaBoost | Proposed |
|---|---|---|---|---|---|
| Accuracy | 95% | 94.9% | 93.9% | 95.1% | 96.7% |
| Precision | 94.25% | 93.8% | 92.55% | 94.9% | 96.1% |
| Recall | 95.1% | 95.35% | 95% | 96.1% | 97.3% |
| Specificity | 94.1% | 93.8% | 93.5% | 95.1% | 96.7% |
| F1-score | 97.51% | 96.89% | 96.37% | 97.13% | 97.1% |

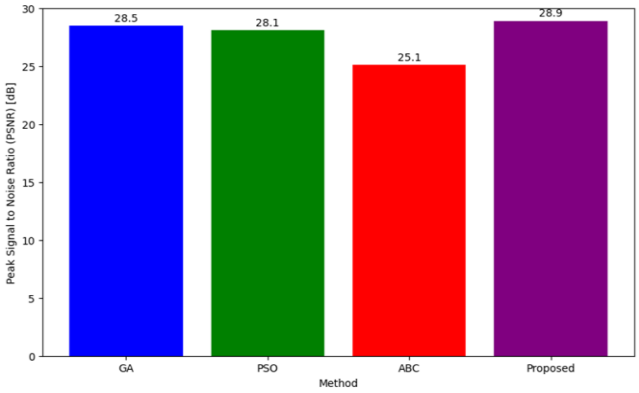


**Fig 15.** Comparison Peak signal-to-noise ratio with existing models.

The proposed method's Peak signal-to-noise ratio is compared with the existing approaches in Figure 15. The suggested strategy's peak signal-to-noise ratio is contrasted with multiple other approaches, such as Particle Swarm Optimization (PSO), Genetic Algorithm (GA), and Artificial Bee Colony (ABC) [16]. Peak signal-to-noise ratio for the suggested approach is 28.9 dB, compared to 28.5 dB, 28.1 dB, and 25.1 dB for GA, PSO, and ABC. The proposed technique enhanced Bee Binary Optimized Network improves pre-processing and feature extraction by mitigating the effects of mischaracterization and density fluctuations. Table 4 illustrates the comparative assessment of five methods: Random Forest, Support Vector Machine, Bayesian Neural Network, AdaBoost, and the proposed model. The proposed model outperforms the others across multiple metrics including Accuracy (97%), Precision (96.1%), Recall (97.3%), Specificity (96.7%), and F1-score (97.1%).

**Table 5**. Comparison of proposed method with existing technique

| Parameter | GA | PSO | ABC | Proposed |
|---|---|---|---|---|
| Peak signal to noise ratio | 28.5 dB | 28.1 dB | 25.1 dB | 28.9 dB |

The comparative evaluation of the proposed technique against le Particle Swarm Optimization (PSO), Genetic Algorithm (GA) and Artificial Bee Colony (ABC), demonstrates its superiority in Peak Signal-to-Noise Ratio (PSNR) as illustrated in the Table 5. The proposed method attains higher scores, achieving a PSNR of 28.9 dB, surpassing GA's 28.5 dB, PSO's 28.1 dB, and ABC's 25.1 dB Furthermore, the proposed approach exhibits superior specificity and sensitivity balance, contributing to its overall accuracy.

## 5. Conclusion

In conclusion, this study introduced the DeepAttentionCLBP-BeeNet, which is a new multi-modal approach to improving the classification of lung diseases. With CLBP feature extraction carried out through the Contrast Local Binary Patterns method for data preprocessing alongside the Attention Graph used for feature extraction, the Bee Colony Optimization for the tuning of parameters and the Inception model used for the classification of the data, the used methodology can be seen to present sufficiently positive results. Still, it is significant noting that, in our model we have achieved a remarkable performance measure whereby accuracy was 97%, and precision was 96.1%, F1 score of 97.1%, recall of 97.3%, specificity of 96.7%, and sensitivity of 97.3%. The results show that proposed multimodal approach better than conventional methods, suggesting that quarry diagnosis and subsequently patient treatment can be made more accurate. In the further development of the research area, future research activities may include the fine-tuning of the classification model and implementation of other deep learning strategies for improving overall performance.

## Author contributions

**Sirikonda Shwetha** has worked on conceptualization, methodology, original draft preparation, visualization, software, and validation tasks. The manuscript was investigated and reviewed by **Dr. Nagavelli Ramana**, who was responsible for investigation.

## Conflicts of interest

The authors declare no conflicts of interest.

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