INDIAN JOURNAL OF SCIENCE AND TECHNOLOGY



RESEARCH ARTICLE



GOPEN ACCESS

Received: 18-08-2024 **Accepted:** 04-09-2024 **Published:** 27-09-2024

Citation: Kalaivani D, Dheepa G (2024) Deep Learning Enhanced CNN with Bio-Inspired Techniques and BCE For Effective Lung Nodules Detection & Classification For Accurate Diagnosis . Indian Journal of Science and Technology 17(37): 3851-3864. https://doi.org/10.17485/IJST/v17i37.2649

Corresponding author.

kalairathin@gmail.com

Funding: None

Competing Interests: None

Copyright: © 2024 Kalaivani & Dheepa. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Published By Indian Society for Education and Environment (iSee)

ISSN

Print: 0974-6846 Electronic: 0974-5645

Deep Learning Enhanced CNN with Bio-Inspired Techniques and BCE For Effective Lung Nodules Detection & Classification For Accurate Diagnosis

D Kalaivani^{1,2*}, G Dheepa³

- **1** Research Scholar, Department of Computer Science, PKR Arts College for Women, Gobichettipalayam, Tamil Nadu, India
- **2** Assistant Professor, Department of Computer Science, PPG College of Arts and Science, Coimbatore, Tamil Nadu, India
- **3** Associate Professor, Department of Computer Science, PKR Arts College for Women, Gobichettipalayam, Tamil Nadu, India

Abstract

Objectives: To propose a new hybrid deep learning model to boost lung nodule detection and classification in combination with a bioinspired method for efficient hyper-parameter optimization to maximize true positive and nodule discrimination rates. Methods: In order to extract the intrinsic and complex features from different lung nodules, deep learning-based enhanced CNN (ECNN) is used. Segmentation masks are generated using Mask-RCNN to isolate and capture the ROIs, which serve as input to CNN. Prior to segmentation and extraction, data cleaning, transformation, and augmentation is done. Hyperparameter optimization is done using a bio-inspired differential evolution method, which helps to identify the learning rate and number of layers to achieve optimal performance. We utilize BCE to quantify the performance of classification tasks. A large-scale CT-DICOM image dataset with 25,1135 images is used for this research work, collected from the cancer imaging archive, which has a clinically proven record of 355 instances with detailed image analysis, tumor location, and bounding boxes with a resolution of 512x512 pixels. 175794 images are used for training, and 75341 images are used for testing and validation. The performance of the new system is assessed using MATLAB, where results are compared with existing models such as SVM-WSS, GCPSO-PNN, and 3D-DLCNN models. Findings: The newly suggested ECNN with DE Bio-inspired model boosts the performance of lung nodule detection and classification with 94.7% accuracy, 93.8% sensitivity, 94.5% specificity, 93.4% F1 score, 92.4% dice coefficient, 0.1 Log Loss and AUC-ROC with 0.93 TPR and 0.07 FPR. **Novelty:** The novel method presents an advanced computational model using deep learning and bio-inspired algorithms for robust classification of lung nodules, which significantly improves the early diagnosis. This CAD model overcomes the limitations of the existing approaches SVM-WSS, GCPSO-PNN, and 3D-DLCNN in terms of segmentation, classification, error detection, and

hyper-parameter tuning.

Keywords: Lung Nodules; Deep Learning; Disease Classification; Image

Processing; ECNN- DE Classifier; CT-DICOM Dataset

1 Introduction

Lung cancer remains one of the leading causes of cancer-related mortality in the world, as per the World Health Organization. Recent advances in imaging techniques combined with artificial intelligence and deep learning models have revolutionized respiratory disease prediction. It is primarily caused by combinations of genetic and environmental factors. Various techniques have been introduced to detect lung nodules and their severity analysis using traditional methods like machine learning, automata processes, mathematical regression, etc., which have limitations like high false positive rates and log loss, which leads to an increase in follow-up procedures and anxiety in patients. The significant gaps found in the prevailing methods are such as inadequate optimization of hyperparameters, robustness and scalability limitations, and lack of integration and nodule discrimination which is the key problem statement of this study. To address the drawbacks of the prevailing approach, a holistic deep learning-based bio-inspired approach is proposed in this research work to integrate deep learning convolutional neural networks with a bio-inspired differential evolution method, Mask-RCNN for deep segmentation and BCE for binary classification, in order to boost the accuracy and true positive rates. The proposed system ECNN with DE & BCE works on the white box method by handling large-scale medical imaging datasets where the process and results are quick and transparent with high patient outcomes. The comprehensive hyper-parameter optimization is done in the real-time scenario before model evaluation, validation, and deployment, which helps the clinicians to test and extract the real-time results after patient screening.

Multi-gene genetic programming (1) methods are employed by selecting automatic features with machine learning applications to detect lung cancer nodules by discriminating 23 crucial features out of 1500 biotic and abiotic features. The model works well on discriminating from protein amino acids with minimal drawbacks of computational complexity and abnormal mutations, which leads to time consumption and an increase in false rates. The complete review of machine learning models (2) for medical image analysis is portrayed by the authors in five different medical applications such as wearable sensors, cancer prediction, medical chemistry, deep imaging, epilepsy detection, etc. SVM, LR, RM, FCN, and GBN are the models used for comparative analysis to project the learning rates and scores. Investigation of state-cell dynamics (3) is carried out to spot the global features in the medical image to identify the cancer at an early stage, which helps the clinicians to diagnose in a better way. This SCD model employs a random screen technique to predict and optimize the learning rates and filters up to 90 Hz folds to progress into the neural networks. A few limitations of the model are that handling large-scale datasets leads to imbalanced data, which affects predicting nodules with high level accuracy. Small data samples from the MASTRO NSCLC (4) collection have been utilized to predict lung cancer using radiotherapy with machine learning models. Histology classification with 3 classes is done using random forest and support vector machine along with inter- and intra-sample cross-validation to minimize data loss and errors. AI-based 3D-DLCNN⁽⁵⁾ is deployed to analyze LC and severity score in response to error points with the KDE and ER-NCN methods. Three class target variables are set to achieve robustness, and statistical outlier detection is employed to calculate the z-score to come out of deviation. Prediction of survivability and risk of mortality is done by using machine learning algorithms with a multilayer approach (6) to classify the lung nodules in a dynamic manner. The method enhances the status of pulmonary disease and analyzes its severity using M-Fold measure with wheel

selection method. Lung nodal status and bio-inspired ML radiomics (7,8) for patient survival prediction were proposed with an encoding and decoding feature extraction model that includes 43 radiomics features with an n value of 78 to evaluate the robustness using AUC-ROC. Few drawbacks are noted in this model in terms of LSDS handling. The QOS-IWDARP optimization model (9,10) helps to reduce the dimensionality and detect dynamic link failure in neural networks where the system automatically responds to the error to set back in an initial stage. It is one of the effective optimization techniques to deal with imbalanced large-scale datasets. The Naive Bays method is employed as an exploitable tool to screen the data for early lung tumor prediction. The method achieves 87% detection and classification accuracy, which is highly adapted by clinicians in terms of screening the initial stage predictions. Casual ML analysis and radiologist-level cancer risk assessment (11,12) were carried out to calculate the heterogeneous treatment effects in lung cancer. Personalized screening strategies are adapted for improved treatment efficacy and to reduce unnecessary interventions. The improvised bio-inspired firefly(13) method was adapted to boost the network optimization to avoid sensor node failure in the LORA network engine, which helps CNN to run fast and provide promising results. Extraction of 3D radiomics (14) features to identify tumors in CT digital images to improve the diagnostic accuracy with short limitations in tumor discrimination rate due to small datasets. The CAD-based brain metastases development for prediction of LC in small cells with machine learning (15,16) method is developed for a personalized patient management system to predict multi-category diseases using an object detection mechanism with deep analysis of images to extract intrinsic patterns to match in the test phase for effective detection and classification of diseases at an early stage. A novel machine learning method SVM-WSS (17) was introduced to integrate multiple methods for dynamic prediction and classification where 89% accuracy is attained with few limitations such as dataset diversity, generalizability to other populations, etc. The GCPSO-PNN model (18) was developed for an effective segmentation and isolation process for medical images to enhance feature selection and extraction mechanisms in order to optimize the genetic population-based method to improve accuracy and efficiency in prediction rate. The scalability is very limited due to computational complexity. QoS is enhanced in networks in order to optimize the routing path to increase the robustness by employing three different population based algorithms (19) for effective data capturing and forwarding from source to destination. Multi-dimensional algorithms, the DL-HPLCP model, and the M-Omic ML (20-22) model were suggested to learn the multi-layer features from all levels for an effective discrimination level between tumor and non-tumor with high accuracy. Extensive training is the only limitation, which consumes a lot of time and leads to late results. Neural network failures are dynamically detected and optimized by RABC⁽²³⁾ with high sensitivity, global DNA methylation fingerprints (24) to difference between various stages in lung cancer using automatic machine learning model which highlights the segmentation and masking approach when implemented in CNN. A cross-cohort analysis (25) machine learning approach is employed to predict lung cancer post-surgery, which helps effective classification with real-time limitation of patient variability. To overcome the limitations of many prevailing approaches, there is a need for a holistic deep learning model with integration of bioinspired techniques for effective lung cancer prediction and classification. The ECNN with DE and BCE model is proposed in this research work with the objective of i) lung nodule prediction with a high depth ratio. ii) hyper-parameter tuning using a bio-inspired approach; iii) complex feature detection using convolutional layers to improve accuracy; iv) binary classification; and v) effective utilization of large-scale CT-DICOM datasets.

2 Methodology

The suggested ECNN with DE bioinspired deep learning model aims to improve the prediction and classification of lung nodules using advanced techniques like as CNN, differential evolution, BCE, cross validation, and Mask R-CNN. This model ensures a robust nodule detection method. A CT-DICOM CIA medical imaging large-scale dataset is utilized for this research work. The new model works with a CT image and extracts the relevant features like nodule size, depth ratio, texture, tumor location, density, edge and boundaries, growth rate, vascular involvement, color, vessel tortuosity, subtle intensity variations, morphological changes, tissue enlargements and fibrosis size, etc. to predict the malignant nodules with a high accuracy rate at an early occurrence for an accurate diagnosis. The major steps involved in nodule detection and classification tasks are pre-processing, segmentation & masking using Mask-RCNN, feature extraction analysis using ECNN, hyper-parameter optimization using bioinspired population-based differential evolution method, and BCE integration for binary classification tasks. The affected regions are isolated in 2 levels, and optimal solutions are demonstrated. We compared the novel results against prevailing machine learning approaches such as SVM-WSS⁽¹⁷⁾, GCPSO-PNN⁽¹⁸⁾, and 3D-DLCNN⁽⁵⁾ models.

Proposed Deep Learning Based ECNN with DE Approach

The 5-layer nodule detection approach takes the merits of CNN, bio-inspired differential evolution, and BCE deep learning architectures to enhance true positive rates with dynamic results. The five layers, which include,

Layer 1: Data Preprocessing Stage (Cleaning, Filtering, Denoising, Resizing, etc.)

Layer 2: Image Segmentation & Masking (Isolation & ROI extraction)

Layer 3: Complex feature extraction using enhanced CNN architecture

Layer 4: Hyper-parameter tuning & optimization using bio-inspired differential evolution

Layer 5: Binary Cross Entropy for Classification Tasks with Cross-Fold Validation

In order to address the complexity and limitations of medical image analysis in lung nodule detection, the adaptive deep learning model is utilized to optimize the features. Let's assume that the images are classified into two Nodule (1), $Severe\ Nodule$ (2) and $Non\ Nodule$ (0). The following are the implementation steps for FS & FE,

Step 1: Input as CT-DICOM digital image

Step 2: Feature extraction

Step 3: Reducing dimensionality using pooling layers with ECNN

Step 4: Optimal Solution / Output probabilities for each class (0, 1, and 2)

Assume that, P(Nodule) = 0.85 and P(Non-Nodule) = 0.15. Now optimize using differential equations by initialization, mutation & crossover, and selection of the best value. Example: The best learning rate α (alpha) is optimized to 0.001 after several iterations. Once the fitness value is calculated apply loss function BCE using the below equation.

$$BCE = -[y.log(p) + (y-y).log(1-p)]$$
 (1)

where, y & p is the actual label and predicted probability for class healthy, lung cancer and severity. Now applying the values,

$$BCE = -[y.log(0.85) + (1-1).log(1-0.85)] = log(0.85) = 0.162]$$
 (2)

Once the BCE is calculated, it helps to update ECNN weights using the optimized learning rate of differential evolution candidate solutions. Here is the mathematical approach to combine ECNN with DE in ten steps.

- Initialize ECNN architecture with convolutional layers, pooling layers, fully connected layers, and activation functions
- Define the hyper parameters like (learning rate, kernel size and filters)
- Formulate objective functions (BCE)
- Initialize differential evolution X_i for bio-inspired population
- Evaluate fitness value (Calculate accuracy) followed by Mutation Operation (F is the factor)
- Crossover operation (Creating a trial vector)
- Selection of fitness value Compare fitness of rates $(U_i and X_i)$ and keep the better one.
- Update final population (Replace X_i with selected vector)
- Train the ECNN network model

2.1. Data Attainment and Pre-processing

The proposed study utilizes the lung CT-DICOM large-scale dataset ⁽²⁶⁾ obtained from the CIA (Cancer Imaging Archive) for training and testing of the ECNN with the DE and BCE models. The DICOM dataset contains both the raw images and the images with annotations; therefore, it is useful in order to test the algorithms based on deep learning and artificial intelligence. It helps the research study to work on the early-stage lung cancer through the CT images of the dataset. The dataset includes 355 instances with sub-features such as tumor location and bounding boxes of 512 x 512 pixels. In total, 251135 images are presented in CT-DICOM, where 175794 are used for training and 75341 are used for testing and validation purposes. The clinical information of the dataset has patient records such as gender, age, weight, category (male & female), tumor size, metastasis, histopathological grading, smoking history, etc. These attributes are very important for analyzing the patient data in medical imaging studies, especially for lung cancer diagnosis and treatment planning.

Figure 1 points the CT-DICOM lung image, which is annotated and taken as a sample. Various stages of lung cancer are predicted and showcased in the bound square box with slice intervals of marking the edges. The images are masked by experts, which help to predict the lung cancer patients out of 355 instances. A, B, E, and G cells are spotted & grouped according to histopathological records.

2.2. ECNN Implementation for nodules detection

Measuring In order to extract the complex features from the image resulted by the segmentation process, again the CNN is applied by feeding the segmented image to neural networks. As CNN is designed with multiple convolutional layers, it performs FS, FE, and FC. Here the kernels (filters) detect the local features such as edges, textures, patterns, and depth ratio of the lung

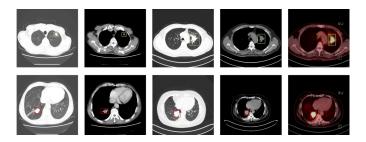


Fig 1. CT-DICOM image dataset with slice intervals

nodules, which perform dot products, and highlight the specific patterns that have rich nodules. As the network layers go deeper, the multiple layers are set to capture intrinsic features and patterns such as sharp boundaries, speculations, etc., which are very crucial for malignant nodules. Spatial dimensions are reduced by pooling layers, which enhances computational efficiency, making the model more robust in nodule detection in terms of position and size inside the DICOM image. The features are flattened and sent to fully connected layers to make the final predictions, where clinicians can check and record the classes L1, L2, and L3 for diagnosis. Let's assume 3x3 filters are applied to 5x5 DICOM image patch, the output will be recorded as,

$$Output = 3x3 \ (i-1, j=1) \ Filter \ (i,j) \ x \ Image \ (i,j) + Bias$$
 (3)

where, i, j are the kernel positions corresponds to the filter matrix. If the filter values are [1,0,-1;1,0,-1;1,0,-1], [1,0,-1;1,0,-1;1,0,-1], [1,0,-1;1,0,-1], the image patch values are [4,5,6;3,7,1;2,8,9], [4,5,6;3,7,1;2,8,9] and [4,5,6;3,7,1;2,8,9], and the bias is 0: The output will be 1×4)+ (0×5) + (-1×6) + (1×3) + (0×7) + (-1×1) + (1×2) + (0×8) + (-1×9) =-7. The filter positions i and j loop through all the elements of the 3xx3 kernel and their equivalent positions in 5x5 image patch. The CNN computes each element of the filter and multiplies it by the corresponding element in the image patch, sums these products and adds the bias to get the output value.

2.3. Mask-RCNN for Image Segmentation

After preprocessing, deep segmentation of the CT DICOM image is done in 2 levels using Mask R-CNN, which uses the metrics of CNN to extract the feature maps from the given CT lung image input. For an accurate & deep segmentation process, isolation of ROIs is very important where the clinicians can check the nodules depth ratio that is likely to be found. The feature maps are sent through different layers of neural networks to spot the potential regions to mask where the rich nodules are present. The model generates bounding boxes to highlight the isolated areas. On the other hand, all the misalignments are minimized effectively to boost the precision. Two levels are created: one is classification and bounding box refinement and the other level is masking predicted nodules. The bounding box has region coordinates, the classification branch has nodules ROIs, and the masked image has a tissue-segmented mask in the image. The deep pixel-level segmentation allows the neural network to identify rich nodules with a high degree of accuracy, even if they are small or have an irregular shape. The segmented nodules are then taken to the feature extraction and classification stage, in which more characteristics of the nodules are determined and target levels are recorded. By giving accurate and detailed segmentation, Mask R-CNN ensures that the enhanced CNN with differential evolution can target the right features to boost the nodule detection and classification.

2.4. Integration of Bio-Inspired DE for hyper parameter optimization

The In order to boost the lung nodule detection using the convolutional neural network model, the bioinspired differential evolution method has a crucial role in hyper optimization of the data captured by CNN layers. DE is a population-based optimization model that optimizes the complex features by enhancing the candidate solutions based on fitness scores. The learning rate, number of layers, batch size (epochs), filter sizes, etc. are fine-tuned with the help of the differential evolution method. One of the major advantages of using the population-based method is that it handles complex, high-dimensional, and nonlinear CNN hyperparameters with the help of mutating the candidate solutions (hyper parameter sets). Once the hyperparameters are optimized, the CNN is boosted with its ability to extract the complex affected regions and features from the input DICOM image, which helps to discriminate between lung cancer, healthy, and severity scores. The network parameters are fine-tuned, allowing CNN to learn entire patterns in the given input for early and accurate nodule detection. The objective

function of bio inspired is represented as,

$$Minimize \ F\left(\emptyset\right) \ = \ -\frac{1}{N} \ \underset{i=1}{\overset{N}{N}} L\left(\ y_{i}, f\left(x_{i} \ ; \emptyset\right)\right) \tag{4}$$

where, $F(\emptyset)$ is loss function, \emptyset represented hyper parameters, L is the loss between the true label y_i and the predicted output $f(x_i;\emptyset)$ for each input x_i in the proposed model. The candidate solutions are generated with the following steps,

- Initialization: Each candidate represented as a vector contains hyperparameters of CNN.
- **Mutation:** For each candidate (target vector), select candidates randomly and generate a new vector by adding the weighted difference between 2 of these candidates to the 3rd candidate.
- Crossover: Perform a crossover between the target vector and the mutant vector to generate a trial vector.
- **Selection:** Evaluate the fitness value and compare the target vector.
- Iteration: Repeat the steps until the optimization generates the best set of hyperparameters to enhance CNN.

2.5. BCE for Binary Classification Tasks

The model uses the BCE approach to optimize the binary classification tasks in a multi-class framework. Here the classification tasks are carried out in each step between healthy vs. lung cancer and lung cancer vs. severity analysis by computing the probability ratio by using the sigmoid function. This hierarchical process ensures that the model handles multi-class predictions between total sample DICOM images, true label, and predicted probability. This effectively balances the classification ratio across different lung nodules isolated by CNN layers. BCE allows the neural network layers to focus on nodule discrimination to predict the presence and absence of disease, which is very important to boost the TPR. Clinical decisions can be taken easily when the results are proven with more accuracy. The imbalanced datasets are handled effectively to avoid false positive rates. By using BCE, CNN learns to predict even the exceptional but in critical cases.

2.6. ECNN with DE and BCE Architecture Diagram

The deep learning-based enhanced CNN with DE integrated with Mask R-CNN a BCE for efficient nodule detection and classification with three target classes L1, L2, and L3, which represent healthy, lung cancer, and severity score analysis. The new model begins with a CT-DICOM raw image as input, followed by the initiation of preprocessing as stage 1. During data preprocessing, normalization, noise reduction, image resizing, and data augmentation (flips and rotation) are carried out for effectiveness. The preprocessed data is passed to Mask R-CNN for image isolation and localization to extract ROI in terms of masking the affected region in two levels. Level 1 includes outline masking, and level 2 shows the inline masking of ROIs. The segmented ROIs serve as an input to convolutional neural networks to detect the complex features for lung nodules with multilayer functionality. The networks are fully connected, and CNN is trained in such a way that differential evolution is applied to search hyper-parameter space. Determine which parameters are hyper so that they can be adjusted in terms of learning rate, number of layers, number of filters, etc. The bio-inspired DE approach considers a collection of solutions and combines them over time to improve the performance level of CNN. BCE is employed for binary classification tasks in three classes.

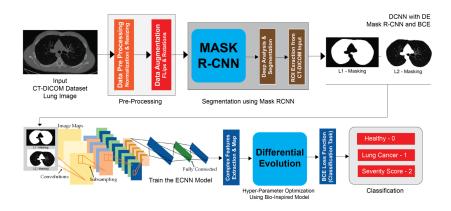


Fig 2. ECNN with DE & Mask R-CNN Architecture Diagram

2.7. Validation of ECNN with DE & BCE Model

After the class predictions by the proposed ECNN with DE bio-inspired model, the cross-validation technique is performed for validation to enhance the robustness and generalization towards unseen data. The model is fine-tuned to boost the level of accuracy in lung nodule prediction and severity analysis with elevated AUC-ROC in terms of TPR and FNR. 10 fold cross validation is used, where K-1 fold is training and remaining as validation to train the model.

$$Cross\ Validation\ results = cross_val_score\ (model,\ X,\ Y,\ cv = k\ fold)$$
 (5)

where, X is the data and Y is the target data with an ECNN-DE classifier model to implement random state functions with k-fold data points. To reduce the variability, the cross-validation is repeated multiple times to generate results. Each set is used once here as a validation set, and the model is trained on all other samples.

2.8. Confusion Matrix - True Label Predictions

As the classes are L1, L2, and L3, which state healthy (0), lung cancer (1), and severity score (2) analysis of the suggested model, the 3x3 confusion matrix is performed for training and testing phases shown in Figure 3 & Figure 4. Heatmap values are generated to project the predicted true values for each class. The complete analysis is done to predict TPR & FPR, which are the main metrics in the model.



Fig 3. Confusion Matrixes for Training Datas



Fig 4. Confusion Matrixes for Testing Datas

ECNN with Mask R-CNN, DE and BCE Step by Step Process

- 1. Input: CT-DICOM CIA Lung Image Large Scale dataset
- 2. **Begin:** Load the Image Dataset $dataset = load(lung_data.mat)$

3. Initial Processing - Normalize & Resize

```
images = imresize(dataset.images,[inputHeight,inputWidth])
images = images / 255.0;
```

 $\textbf{Data Augmentation } A_{Images} = img Data Augmenter (\textit{RandRotation}, [-40, 10], \textit{RandXReflection}, true) \\$

4. Segmentation using Mask-RCNN

```
[bboxes, masks, labels] = detect(maskRCNN, images);\\ segmentedROIs = applyMasks(images, masks);\\ ROIs = cropROI(segmentedROIs, bboxes);
```

5. Complex Feature Extraction using ECNN

```
layers = [imageInputLayer([inputHeight,inputWidth,numChannels])
  convolution2dLayer(3,32,'Padding','same')
  batchNormalizationLayer
  reluLayer
  maxPooling2dLayer(2,'Stride',2)
  fullyConnectedLayer(128)
  reluLayer
  fullyConnectedLayer(numClasses)
  softmaxLayer
  classificationLayer];
```

6. Training the Proposed Model ECNN with DICOM Dataset

```
Options = trainingOptions ('adam', 'MaxEpochs', 50, 'InitialLearnRate', 1e-4, 'ValidationData', valData); \\ net = trainNetwork (ROIs, labels, layers, options);
```

7. Hyperparameter Optimization using Bio Inspired Model

```
hyperparameters = [learningRate,numFilters,numLayers];\\ bounds = [lowerBounds; upperBounds];\\ [optimalParams,fval] = differentialEvolution;\\ optimalNet = trainNetwork(ROIs,labels,optimalLayers,options);\\
```

8. Classification using BCE (Binary Task) & Training Classifier

```
layers(end) = classification Layer('Loss', 'binary Cross Entropy'); \\ final Net = train Network(ROIs, labels, optimal Layers, options); \\ [preds, scores] = classify(final Net, test Data); \\ metrics = evaluate Model(preds, test Labels); \\
```

9. Cross Validation & Deployment (K-Fold)

```
CrossValMetrics = crossval(@(Xrain,Ytrain,Xest) trainAndTest(Xrain,Ytrain,Xest),k);
save('lungNoduleModel.mat','finalNet');
app = lungNoduleDetectionApp(finalNet);
```

- 10. Output: Lung Cancer detection, classification & severity score
- 11. Comparative Analysis using MATLAB & Graphs using PYTHON
- 12. Creation of User Interface For Deployment
- 13. End

Performance Evaluation Metrics of ECNN-DE

The newly proposed ECNN with DE bio-inspired nodule detection model is mainly focused on deep image segmentation & masking with local and global feature extraction in terms of extracting multifaceted patterns to enhance the ratio of nodule discrimination. Mask-RCNN segments & masks isolated region in the DICOM image, which helps ECNN model boost the detection rate using CNN multi layers and the differential evolution method. MATLAB is used to evaluate the performance of DL model with the evaluation metrics such as accuracy, sensitivity, specificity, AUC-ROC, dice coefficient, F1-score, log loss,

and AUC-ROC. The results are compared against SVM-WSS⁽¹⁷⁾, GCPSO-PNN⁽¹⁸⁾, and 3D-DLCNN⁽⁵⁾ models. The following is the formula to calculate the values of PEM using ECNN with the DE model.

 Accuracy: Calculates the proportion of accurate lung nodule discriminations out of the total samples tested by the new ECNN with DE bio-inspired model. It is the balanced ratio of classified and predicted from the total samples.

$$Accuracy = \frac{(TPR + TNR)}{(TPR + TNR + FPR + FNR)} \times 100$$
 (6)

 Sensitivity & Specificity: The complete TPR and TNR values are measured out of actual positive and actual negative samples in the given dataset.

$$Sensitivity = \frac{TPR}{(TPR + FNR)} \times 100 \tag{7}$$

$$Specificity = \frac{TNR}{(TNR + FPR)} \times 100$$
 (8)

• **Dice Coefficient:** During the segmentation & masking tasks, the dice coefficient values are measured between predicted and actual data. It is the measure of overlap by the new ECNN model.

$$Dice\ Coefficient\ \frac{2_*TP}{(2_*TP+FPR+FNR)} \times 100 \tag{9}$$

AUC-ROC: The imbalanced datasets are computed and measure the complete trade-off between P&R and assess the TPR
and FPR with multiple iterations and batch sizes.

$$AUC \mid ROC \ (TP \& FP) \quad TP = \frac{TPR}{(TPR + FNR)}, FP = \frac{FPR}{(FPR + TNR)}$$
(10)

Logarithmic Loss: LLV penalizes the false classification rates that show the performance of the ECNN with the DE model

$$F\mathbf{1} - Score = \frac{2_*(Precision_*Recall)}{(Precision + Recall)}$$

where the probability score range is between 0 and 1.

$$Log \ Loss = -\frac{1}{N} \underset{i=1}{N} \left(y_i \ \log \left(p_i \right) + (1 - y_i) \ \log \ (1 - p_i) \right) \tag{11}$$

• **F1** -**Score:** To measure and uphold an ideal weighing scale between precision and recall, the F1 metric is calculated to provide a harmonic mean.

$$F1 - Score = \frac{2_*(Precision_* Recall)}{(Precision + Recall)}$$
 (12)

$$MCC = \frac{T_1}{\sqrt{T_2 \times T_3 \times T_{4 \times} T_5}} \times 100$$
 (13)

where, LNP represents Lung Cancer Nodules Prediction and the distinct MCC (Matthews Correlation Coefficient) provides a balanced measure even the classes are imbalanced which is derived using the below equation, $T_1 = (TPR \times TNR - FPR \times FNR)$, $T_2 = (TPR + FPR)$, $T_3 = (TPR + FNR)$, $T_4 = (TNR + FPR)$, and $T_5 = (TNR + FNR)$.

3 Results and Findings

This section showcased the promising results of the proposed deep learning-based bio-inspired ECNN with DE method integrated with Mask-RCNN and BCE loss function. The performance metrics portrayed how the new method overcomes the limitations and shortcomings of the existing lung nodules classification models. The model vigorously works on feature extraction and efficient segmentation in order to boost the nodule discrimination in three classes L0, L1 & L2 (healthy, cancer and severity). The results are compared with three prevailing approaches such as SVM-WSS⁽¹⁷⁾, GCPSO-PNN⁽¹⁸⁾, and 3D-DLCNN⁽⁵⁾. This iterative nodule detection and classification model helps clinicians diagnose the disease in a robust manner. The CT-DICOM CIA dataset is used for this study. Out of 251135 images, 175794 are used for training, and 75341 are used for testing and validation purposes. Figures 5, 6, 7, 8, 9 and 10 shows the graphical representation of comparative analysis with the X axis as models and the Y axis as percentage.

3.1. Accuracy

Figure 5 clearly shows the accuracy rate of the new deep learning-based ECNN with DE bio-inspired model. As the binary classification tasks are done using the BCE loss function, it helps to quantify the data during the training and testing phases to boost the nodule detection performance. The pre-trained weights are updated to minimize the loss and maximize the accuracy rate. Fine tuning and cross-validation are performed to generalize the unseen data and improve the robustness of the model ECNN with DE. The complex patterns are captured to isolate ROIs by CNN and Mask-RCNN, which helps to overcome the limitations of the existing approaches. 94.7% accuracy is achieved during the testing phase, which is comparatively higher than SVM-WSS⁽¹⁷⁾, GCPSO-PNN⁽¹⁸⁾, and 3D-DLCNN⁽⁵⁾.

Table 1. Comparative Analysis of LC Accuracy

Metrics / Models	SVM-WSS (17)	GCPSO-PNN (18)	3D-DLCNN ⁽⁵⁾	ECNN with DE & BCE (Proposed)
Accuracy (It-1)	71.26	78.48	84.52	92.45
Accuracy (It-N)	73.18	80.08	87.68	94.73

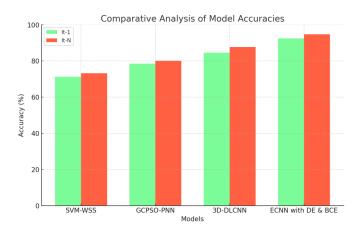


Fig 5. Accuracy

3.2. Sensitivity & Specificity

Figure 6 depicts the comparative analysis of sensitivity and specificity. The ECNN with DE model uses Mask-RCNN for deep segmentation and masking; the complex patterns are captured and isolated for efficient performance. The image intensities are standardized for a consistent range for multiple epochs. The target classes are exactly identified and recorded and passed through the convolutional layers to detect the features in a dynamic manner. The ECNN generates feature maps that represent the characteristics of the lung nodules to classify and learn their severity analysis. In order to avoid overfitting and increase the training diversity, data augmentation is performed. 93.81% sensitivity and 94.62% specificity are achieved, which shows the outstanding performance of the proposed model.

Table 2. Comparative Analysis of LC Sensitivity & Specificity

Metrics / Models	SVM-WSS (17)	GCPSO-PNN (18)	3D-DLCNN ⁽⁵⁾	ECNN with DE & BCE (Proposed)
Sensitivity	76.52	81.78	86.35	93.81
Specificity	78.65	83.40	88.48	94.52

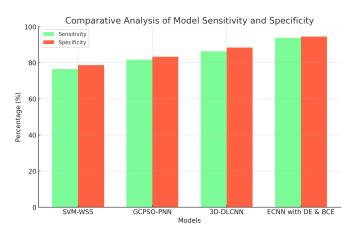


Fig 6. Sensitivity & Specificity

3.3. F1 Score

The F1-Score comparative analysis of the proposed bio-inspired ECNN with DE classifier model is showcased in Figure 7. The false positive and false negative instances are recorded in all iterations in order to provide a harmonic mean and balance the datasets. As the BCE loss function is applied, the classification tasks of the model are enhanced optimally to discriminate the nodules in an effective manner. The precision and recall are optimized with the help of pre-trained CNN networks and hypertuning such as learning rate, batch size, and layer bifurcations. 93.4% F1-Score is achieved by the model, which is remarkably high compared to the prevailing approaches to ensure quality of feature and nodule retrieval and discrimination processes.

Table 3. Comparative Analysis of LC F1 Score

Metrics / Models	SVM-WSS (17)	GCPSO-PNN (18)	3D-DLCNN ⁽⁵⁾	ECNN with DE & BCE (Proposed)
F1 Score (It-1)	75.35	80.68	86.55	91.30
F1 Score (It-N)	78.18	82.74	88.76	93.42

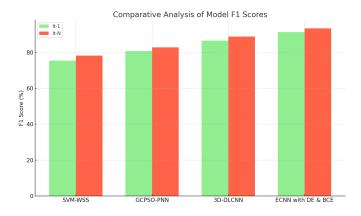


Fig 7. F1 Score

3.4 AUC-ROC Analysis

The AUC-ROC analysis ranging from 0 to 1 is presented in Figure 8. The true positive and true negative rates are measured and computed as AUC, which helps to assess the performance of the proposed ECNN with DE model against existing approaches such as SVM-WSS ⁽¹⁷⁾, GCPSO-PNN ⁽¹⁸⁾, and 3D-DLCNN ⁽⁵⁾. With efficient training of large-scale CT-DICOM images, the iterations are set for threshold values to capture and record each and every result for detailed analysis. During the testing phase, the discrimination features are isolated and recorded in all iterations with different classification thresholds. The new system yields the remarkable results of AUC-ROC with 0.93 TPR and 0.16 FPR, which is higher than the other computational methods that help clinicians use this model in a better way.

Table 4. Comparative Analysis of LC AUC-ROC

Metrics / Models	SVM-WSS (17)	GCPSO-PNN (18)	3D-DLCNN ⁽⁵⁾	ECNN with DE & BCE (Proposed)
TPR	0.62	0.70	0.79	0.89 - 0.93 (N)
FPR	0.39	0.31	0.23	0.11 - 0.07 (N)

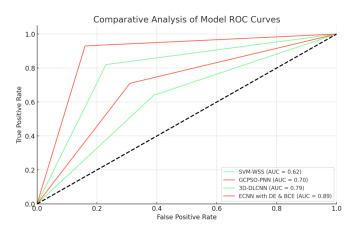


Fig 8. AUC-ROC

3.5. Dice Coefficient

The dice coefficient comparative analysis is highlighted in Figure 9. The deep segmentation task is carried out to mask the ROIs using the Mask-RCNN method to isolate the affected region. The complete overlap is measured between the predicted and actual data during segmentation to compare the levels of iteration. The decision threshold has been adjusted to optimize the trade-off to capture the values from each iteration for better analysis. The loss function is carried out for effective binary classification, which helps the system to perform better. The dice score is achieved with 92.44%, which is relatively high as the other models have shown less performance. This helps the clinical experts to make better decisions in using this CAD system for effective nodule detection and classification.

Table 5. Comparative Analysis of LC Dice Coefficient

Metrics / Models	SVM-WSS (17)	GCPSO-PNN (18)	3D-DLCNN ⁽⁵⁾	ECNN with DE & BCE (Proposed)
Dice Score (It-1)	77.19	83.17	85.45	90.78
Dice Score (It-N)	79.80	85.16	87.76	92.44

3.6. Logarithmic Loss Analysis

Loss-loss is calculated, and results are compared and portrayed in Figure 10. It is well calibrated the predicted probabilities, which are not directly impacted by class imbalance. The low confidence scores are thoroughly evaluated and validated to correct the errors. To prevent the model, introducing the label smoothing helps reduce the log loss. 0.04 log loss is recorded when using

ECNN with a DE bioinspired model, which is remarkable in producing actual results with minimal false rates. The risk is completely reduced in this new model as the input image crosses multiple convolutional layers to generate an optimal solution. Hyper-parameter tuning also plays a major role in reducing the log loss to the core.

Table 6. Comparative Analysis of LC Logarithmic Loss

Metrics / Models	SVM-WSS (17)	GCPSO-PNN (18)	3D-DLCNN (5)	ECNN with DE & BCE (Proposed)
LLV (It-1)	0.47	0.35	0.26	0.10
LLV (It-N)	0.37	0.28	0.19	0.04

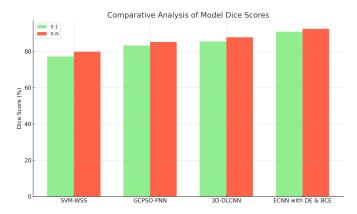


Fig 9. Dice Coefficient

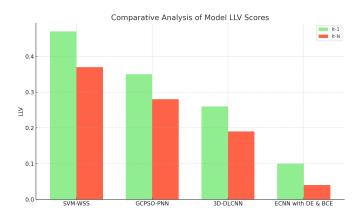


Fig 10. Logarithmic Loss

4 Conclusion

In this suggested deep learning model, hyper-parameter tuning and effective nodule discrimination of lung nodules is the main focus to support the clinical experts to detect and classify for accurate diagnosis with the help of deep learning with bioinspired methods. The proposed work used ECNN to learn the complex features from lung nodules after initial pre-processing and deep segmentation. Hyper-parameter tuning is done by employing a bio-inspired differential evolution population-based method to optimize the performance of the proposed model. Classification tasks are performed using binary cross entropy to measure the performance of predicted and actual nodule classification. Mask-RCNN is used for segmentation in order to isolate the region of interest, which serves as input to CNN layers. The CT-DICOM CIA dataset is used for this research work, which has 355 subjects with clinically proven records, which helps to train and test the model in a robust manner. After 20 epochs with 15 batch sizes, the proposed ECNN with DE model attains 94.7% accuracy, which is relatively high compared

to the existing approaches such as SVM-WSS, GCPSO-PNN, and 3D-DLCNN models. In addition to that, 93.8% sensitivity, 94.5% specificity, 93.4% F1 score, 92.4% dice coefficient, 0.1 log loss, and AUC-ROC with 0.93 TPR and 0.07 FPR are achieved by the model. The model is fine-tuned later by doing multiple iterations to enhance the accuracy and true positive rates. The classification tasks are performed in 2x2 matrixes, where the results are recorded at every stage to compare them in different iterations.

Though the model yields promising results, some of the notable limitations are there to be enhanced in the future, such as computational complexity, time consumption of handling large scale data, 3D image transformations, micro annotations, early automatic classifications, etc., which will help clinicians to diagnose in a better way.

References

- 1) Sattar M, Majid A, Kausar N, Bilal M, Kashif M. Lung cancer prediction using multi-gene genetic programming by selecting automatic features from amino acid sequences. *Computational Biology and Chemistry*, 2022;98. Available from: https://doi.org/10.1016/j.compbiolchem.2022.107638.
- Shehab M, Abualigah L, Shambour Q, Abu-Hashem MA, Shambour MKY, Alsalibi AI, et al. Machine learning in medical applications: A review of state-of-the-art methods. Computers in Biology and Medicine. 2022;145. Available from: https://doi.org/10.1016/j.compbiomed.2022.105458.
- 3) Hughes NW, Qu Y, Zhang J, Tang W, Pierce J, Wang C, et al. Machine-learning-optimized Cas12a barcoding enables the recovery of single-cell lineages and transcriptional profiles. *Molecular Cell*;82(16):3103–3118. Available from: https://doi.org/10.1016/j.molcel.2022.06.001.
- 4) Ubaldi L, Valenti V, Borgese RF, Collura G, Fantacci ME, Ferrera G, et al. Strategies to develop radiomics and machine learning models for lung cancer stage and histology prediction using small data samples. *Physica Medica*. 2021;90:13–22. Available from: https://doi.org/10.1016/j.ejmp.2021.08.015.
- 5) Eldho KJ, Nithyanandh S. Lung Cancer Detection and Severity Analysis with a 3D Deep Learning CNN Model Using CT-DICOM Clinical Dataset. *Indian Journal of Science and Technology*;2024(10):899–910. Available from: https://doi.org/10.17485/IJST/v17i10.3085.
- 6) Faccioli R, Heise L, Fonseca C, Liaw W, Lauricella L, Pêgo-Fernandes P, et al. 01 Machine Learning for Prediction of Survival and Risk of Mortality in Patients with Lung Cancer Undergoing Resection. *Journal of Thoracic Oncology*;16(10). Available from: https://doi.org/10.1016/j.jtho.2021.08.188.
- 7) Presti GL, Corso F, Tini G, Garau N, De Angelis S, Bellerba F, et al. OD168 Radiomic analysis for prediction of nodal status in lung cancer simulated data: comparison of machine learning methods. *Physica Medica*. 2021;92. Available from: https://doi.org/10.1016/S1120-1797(22)00285-X.
- 8) Devi PA, Megala D, Paviyasre N, Nithyanandh S. Robust AI Based Bio Inspired Protocol using GANs for Secure and Efficient Data Transmission in IoT to Minimize Data Loss. *Indian Journal of Science and Technology*;2024(35):3609–3622. Available from: https://doi.org/10.17485/IJST/v17i35.2342.
- 9) Nithyanandh S, Jaiganesh V. Quality of service enabled intelligent water drop algorithm based routing protocol for dynamic link failure detection in wireless sensor network. *Indian Journal of Science and Technology*;2020(16):1641–1647. Available from: https://doi.org/10.17485/IJST/v13i16.19.
- 10) Xie Y, Meng WY, Li RZ, Wang YW, Qian X, Chan C, et al. Early lung cancer diagnostic biomarker discovery by machine learning methods. *Translational Oncology*. 2021;14(1):100907–100907. Available from: https://doi.org/10.1016/j.tranon.2020.100907.
- 11) Hu L, Lin JY, Sigel K, Kale M. Estimating heterogeneous survival treatment effects of lung cancer screening approaches: A causal machine learning analysis. Annals of Epidemiology. 2021;62:36–42. Available from: https://doi.org/10.1016/j.annepidem.2021.06.008.
- 12) Trajanovski S, Mavroeidis D, Swisher CL, Gebre BSBG, Veeling R, Wiemker T, et al. Towards radiologist-level cancer risk assessment in CT lung screening using deep learning. *Computerized Medical Imaging and Graphics*. 2021;90. Available from: https://doi.org/10.1016/j.compmedimag.2021.101883.
- 13) Nithyanandh S, Omprakash S, Megala D, Karthikeyan MP. Energy Aware Adaptive Sleep Scheduling and Secured Data Transmission Protocol to enhance QoS in IoT Networks using Improvised Firefly Bio-Inspired Algorithm (EAP-IFBA). Indian Journal of Science and Technology;2023(34):2753–2766. Available from: https://doi.org/10.17485/IJST/v16i34.1706.
- 14) Lin X, Jiao H, Pang Z, Chen H, Wu W, Wang X, et al. Lung Cancer and Granuloma Identification Using a Deep Learning Model to Extract 3-Dimensional Radiomics Features in CT Imaging. Clinical Lung Cancer;22(5):756–766. Available from: https://doi.org/10.1016/j.cllc.2021.02.004.
- 15) Deng F, Zhou H, Lin Y, Heim JA, Shen L, Li Y, et al. Predict multicategory causes of death in lung cancer patients using clinicopathologic factors. *Computers in Biology and Medicine*. 2021;129. Available from: https://doi.org/10.1016/j.compbiomed.2020.104161.
- 16) Visonà G, Spiller LM, Hahn S, Hattingen E, Vogl TJ, Schweikert G, et al. Machine-Learning-Aided Prediction of Brain Metastases Development in Non-Small-Cell Lung Cancers. Clinical Lung Cancer;24(8):311–322. Available from: https://doi.org/10.1016/j.cllc.2023.08.002.
- 17) Chaturvedi P, Jhamb A, Vanani M, Nemade V. Prediction and classification of lung cancer using machine learning techniques. *IOP Conference Series: Materials Science and Engineering*. 2021;1099:12059–12059. Available from: https://doi.org/10.1088/1757-899X/1099/1/012059.
- 18) Jagadeesh K, Rajendran A. Improved model for genetic algorithm-based accurate lung cancer segmentation and classification. *Computer Systems Science and Engineering*;2023(2):2017–2032. Available from: https://doi.org/10.32604/csse.2023.029169.
- 19) Nithyanandh S, Jaiganesh V. Interrogation of Dynamic Node Link Failure by Utilizing Bio Inspired Techniques to Enhance Quality of Service in Wireless Sensor Networks. 2020. Available from: http://hdl.handle.net/10603/400513.
- 20) Chen N, Zhou R, Luo Q, Liu Y, Li C, Zhang J, et al. Combining Dosimetric and Radiomics Features for the Prediction of Radiation Pneumonitis in Locally Advanced Non-Small Cell Lung Cancer by Machine Learning. *International Journal of Radiation Oncology*. 2023;117(2). Available from: https://doi.org/10.1016/j.ijrobp.2023.06.732.
- 21) Vani Rajasekar MP, Vaishnnave S, Premkumar, Sarveshwaran VV, Rangaraaj. Lung cancer disease prediction with CT scan and histopathological images feature analysis using deep learning techniques. *Results in Engineering*. 2023;18. Available from: https://doi.org/10.1016/j.rineng.2023.101111.
- 22) Chen Z, Chen Z, Kang J, LI Y, Xiao W, CHEN J, et al. P1.01-05 A Predictive Model for Postoperative Recurrence of Lung Cancer Based on Multi-omic Machine Learning. *Journal of Thoracic Oncology*. 2023;18(11):S183–S184. Available from: https://dx.doi.org/10.1016/j.jtho.2023.09.283.
- 23) Nithyanandh S, Jaiganesh V. Reconnaissance Artificial Bee Colony Routing Protocol to Detect Dynamic Link Failure in Wireless Sensor Network. International Journal of Scientific & Technology Research. 2019;10(10):3244–3251. Available from: https://doi.org/10.35940/ijstr.b2271.0986231.
- 24) Katase S, Ichinose A, Hayashi M, Watanabe M, Chin K, Takeshita Y, et al. Development and performance evaluation of a deep learning lung nodule detection system. *BMC Medical Imaging*. 2022;22(1). Available from: https://dx.doi.org/10.1186/s12880-022-00938-8.
- 25) Rehman Z, Qiang Y, Wang L, Shi Y, Yang Q, Khattak SU, et al. Effective lung nodule detection using deep CNN with dual attention mechanisms. *Scientific Reports*. 2024;14(1). Available from: https://dx.doi.org/10.1038/s41598-024-51833-x.
- 26) Li P, Wang S, Li T, Lu J, Huangfu Y, Wang D. A Large-Scale CT and PET/CT Dataset for Lung Cancer Diagnosis (Lung-PET-CT-Dx). 2020. Available from: https://doi.org/10.7937/TCIA.2020.NNC2-0461.