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RESEARCH ARTICLE

Lung Cancer Detection and Severity Analysis with a 3D Deep Learning CNN Model Using CT-DICOM Clinical Dataset

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Abstract

Objectives: To propose a new AI based CAD model for early detection and severity analysis of pulmonary (lung) cancer disease. A deep learning artificial intelligence-based approach is employed to maximize the discrimination power in CT images and minimize the dimensionality in order to boost detection accuracy. **Methods:** The AI-based 3D Convolutional Neural Network (3D-DLCNN) method is employed to learn complex patterns and features in a robust way for efficient detection and classification. The pulmonary nodules are identified by 3D Mask-R-CNN at the initial level, and classification is done by 3D-DLCNN. Kernel Density Estimation (KDE) is used to discover the error data points in the extracted features for early removal before candidate screening. The study uses the CT-DICOM dataset, which includes 355 instances and 251135 CT-DICOM images with target attributes of cancer, healthy, and severity condition (if cancer is positive). Statistical outlier detection is utilized to measure the z-score of each feature to reduce the data point deviation. The intensity and pixel masking of CT-DOCIM is measured by using the ER-NCN method to identify the severity of the disease. The performance of the 3D-DLCNN model is done using the MATLAB R2020a tool and comparative analysis is done with prevailing detection and classification approaches such as GA-PSO, SVM, KNN, and BPNN. **Findings:** The suggested pulmonary detection 3D-DLCNN model outperforms the prevailing models with promising results of 93% accuracy rate, 92.7% sensitivity, 93.4% specificity, 0.8 AUC-ROC, 6.6% FPR, and 0.87 C-Index, which helps the pulmonologists detect the PC and identify the severity for early diagnosis. **Novelty:** The novel hybrid 3D-DLCNN approach has the ability to detect pulmonary disease and analyze the severity score of the patient at an early stage during the screening process of candidates. It overcomes the limitations of the prevailing machine learning models, GA-PSO, SVM, KNN, and BPNN.

Keywords: Artificial Intelligence; Disease Prediction; Lung Cancer; Deep Learning; Cancer Detection; Computational Model; 3D-DLCNN

1 Introduction

Enhancing pulmonary nodule detection and severity analysis are the main focus of this research study, as pulmonary cancer is one of the major global health concerns, which presents a significant challenge to accurate prediction in oncology. Various computational methods were introduced for candidate screening using machine learning as a problem-solving technique to detect the pulmonary nodule at an early stage for effective diagnosis. Some of the research gaps and current challenges identified during the background study are: i) slowdown in managing variation in nodule size; ii) poor severity analysis; iii) less feature extraction (N-Size, N-Shape, Voxel Value, Intensity, etc.) iv) increase in FPR; v) low discrimination power and high dimensionality, etc. are considered the limitations of the prevailing machine learning approaches. Also, recent efforts have mainly focused on the utilization of 2D networks, where nodules and severity analysis at an early stage were found with minimal accuracy.

In order to overcome the shortcomings, there should be an efficient AI-based problem-solving technique to predict pulmonary cancer and its types, NSCLC and SCLC, along with severity score analysis at an early stage. In order to overcome the limitations of prevailing approaches, a new AI-based hybrid approach was developed to predict pulmonary cancer along with severity analysis with the use of 3D-DLCNN from level 0 to level n. 3D-Mask-RCNN and KDE, which are used for nodule detection during initial level screening and error data point discovery and removal for efficient classification. All the morphological changes are recorded in special coordinates and depth inside the lungs to ensure the maximum possibility of nodule discrimination from tissues, which impacts the minimization of false rates. The CT-scanned clinical dataset is used for training and testing purposes.

ANN, KF, RNN ML[(1)] models was proposed to predict lung cancer and CT image processing. 82 CT scans were used with 70 sample patient reports. The K-means technique is employed for image segmentation and masking. The image quality is enhanced using a geometric radiant filter model. The accuracy is boosted to 83%, where the complex dataset cannot be processed in a robust manner, which is one of the drawbacks of ML models. A multiview image restoration and fusion ML model[(2)] was introduced to detect lung cancer, where 4642 tomography images with nodule sizes ranging from 3 to 27 mm are used. Four stages of cancer reports were used as target attributes and implemented using ResNet-18 with two layers. The sensitivity and specificity are boosted and balanced, which results in 87% accuracy. The shortcomings of this MV-IRF model are 41% false rates when using DICOM images. ML, EL, and PSO models[(3)] were employed to assess the performance of LC detection using a simulation tool. Deep image analysis was done before the candidate screening process to detect the pulmonary nodules and their region accurately. Though only 659 images are tested, less time is taken to identify the optimal value. The process begins after the image is restored and enhanced. The limitations are that error points are not calculated during candidate screening, which leads to an increase in false rates. IWD-ARP optimization and DL-based LC detection using chest radiographs[(4,5)] were proposed by the authors, where FPR mean was assessed with the independent clinical reports. The sensitivity and specificity are maximized, and the blind spots in the scanned images were noted, which leads to effective identification of nodule-affected regions in the dataset. A five-fold cross-validation technique is employed. The image is optimized in IWD-ARP to enhance the prediction value and boost accuracy. The major shortcomings of this model are that pixel and root masking are not applied to detect the inner nodule region and voxel value. Lung PET-CT-DX-DICOM[(6)] images are utilized in this study, and the data values of the patients are taken as samples for implementing 3D layers.

Various ML algorithms [7] are used for comparative analysis to detect pulmonary cancer, which has drawn special attention in the healthcare sector, which helps the doctors with prognosis effectively. To enhance medical diagnosis power, these algorithms act as CAD tools for cancer prediction in all scenarios. ANN was employed for accurate detection of LC nodules, where time consumption is the major drawback. QoS was enhanced using EABIFBA [8], where the bioinspired algorithm was proposed for optimization and query mechanism. The system security features are maximized to prevent vulnerabilities. CNN and Google-Net DL [9] models were proposed by the researchers, where ANN is one of the techniques employed to maximize the probability of discrimination power in nodule identification. VGG-18 was used as the base layer in the classifier networks. Some of the limitations of the above models are, lack of nodule discrimination power in root region, finite accuracy etc.

A 2D-CNN [10] approach was proposed to detect lung cancer from CT-scanned images. The LUNA-18 dataset was used with an annotation that understood the data in the specific region of the CT images. The deep ensemble 2D method detects the LC nodules and their severity score, which increases the accuracy level. The drawback of this model is that it reads only a 2x2 pooling filter size where the activation function is mapped in the kernel for a better outcome and optimal value. SVM classifiers [11] are used to detect the symptoms of lung cancer patients at an early stage. Here the limitations are, more pre-processing time due to noisy data, and the SMOTE method was compared against the SVM classifier by using an ensemble classifier. RNSRP-BIP and LC screening and diagnosis methods [12,13] wereproposed by the authors for effective optimization and nodule identification in CT images. A detailed review and comparison were done using classification and segmentation techniques with the help of machine learning models. The advantages and disadvantages were portrayed by the authors, which helps to articulate this article in a unique way. Class imbalance issues are handled by SDP model [14] where the defects are predicted in all ML models and demonstrated. The classification model helps the author to use perfect prediction models for disease detection, classification, simulation, database extraction etc. A PSO genetic algorithm [15] model was proposed for lung cancer prediction in two groups. One is GA, and another is PSO. The data was collected from various sources, and the results are compared against traditional methods. 118 samples were tested, and 214 samples were trained in this model, where accuracy was boosted up to 81%. The researchers proposed the HKASC approach for lung cancer classification with an SVM model [16] with 587 CT images, and FFBPNN was employed for pre-processing. The data is combined with a three-piece mechanism group: i) feature extraction by SURF-A; ii) the GAO process; and iii) FFBPNN and classification using KASC. 98.08% accuracy was achieved with the effect of root depth on classification investigated at limits. The shortcomings are in order to refine the proposed hybrid algorithm to overcome potential complications. An Extended E-KNN algorithm [17] was suggested by the authors where 2D images are utilized. The MGF technique was used to extract features and edge detection. ML combination models were deployed to predict the cancer stage and analyze the input data in various forms. The cropped image was rooted in various pre-processing steps, and it was filtered before candidate screening and feature marking. Global features are marked to train and test the data for nodule identification. BPNN with HWT [18] was proposed to identify lung cancer with the help of a watershed image segmentation model. BOWW, E-SIFT, BPNN, etc. were employed to detect the cancerous nodule at the initial screening stage for easy diagnosis. This system automatically detects the LC and its severity score and provides the optimal results. The only drawback is that the 3D images cannot be processed in this model, which fails to advance medical diagnosis methods. A novel BPNN, link failure detection model, and glow-warm swarm algorithm [19–22] was proposed by the researchers, who stated that classification and prediction using medical datasets should undergo complete pre-processing and annotations to achieve better results. Also, they pointed out that noisy data must be filtered and removed completely with the help of error removal models and check points during the initial stage to boost the accuracy level, and while using CT images, the regions should be marked in a deep manner for better nodule detection to avoid false positive rates and iteration data errors. The complete 2D and 3D process of nodule detection was explained by the researchers, which helped identify a suitable algorithm for nodule detection [23–25]. To overcome all the shortcomings of the existing approaches the new AI and DL based 3D-DLCNN approach was proposed.

The main objectives of 3D-DLCNN are: i) pulmonary nodule detection; ii) classification of target attributes; iii) identifying the changes in CT regions; iv) dynamic usage of the CT-DICOM dataset; v) KDE error removal during candidate screening; vi) enhancing the prediction rate, etc. The following are the important steps to be followed before implementation:

- **Image Pre-Processing:** Complete pre-processing is done using the standard HLM method, where 3D images are easily processed in a short span of time.
- **3D Pixel Masking:** All dimensions are masked using 3D Mask-R-CNN to identify the nodule fractions in the specific regions to measure the optimal value or region.
- **Three Convolutional Layers:** Three level map values are identified in the input cropped CT-DICOM images, where the L1, L2, and L3 values are measured.
- **Outlier Detection:** As the CT images are in slice thickness, the outlier detection is done using SOD to measure the pixel intensity value and recorded in L1. These values are used in order to match the pattern in a dynamic way to identify the

pulmonary nodules at an early stage.

2 Methodology

The newly proposed unique AI-based deep learning pulmonary disease detection model mainly focuses on nodule identification at an early stage by utilizing CT-DICOM clinical datasets with the help of a three-dimensional convolutional neural network approach. This 3D approach boosts the accuracy level and analyzes the c-index to identify the severity. Global features like N-Size, N-Shape, Voxel Value, Intensity, etc. are extracted from the DICOM dataset for implementation to detect nodules at the pre-mature stage. During candidate screening, nodules are identified using 3D Mask-R-CNN, whereas classification is achieved by DL-CNN. The z-score is calculated for each feature extracted to reduce the data point deviation during nodule detection. In addition to this, error points are removed at an early stage to get optimal results. The significant spots are identified by 3D-DLCNN, where the severity score, nodules, and healthy attributes are measured. The method is compared against the prevailing machine learning approaches called GA-PSO [15], SVM [16], KNN [17], and BPNN [18]. The drawbacks of the existing models are addressed by the 3D-DLCNN approach.

2.1 Proposed Methodology

The proposed model initially learns the complex patterns and features in the CT-DICOM dataset, followed by four stages of implementation of the AI-based model.

Stage 1: Initial candidate screening will be done by 3D-Mask-R-CNN.

Stage 2: Identification of true nodules & Classification of types (NSCLC and SCLC).

Stage 3: Error Detection and Removal followed by measurement of Z-score.

Stage 4: Maximizing the discrimination power and minimizing false-positive rates.

The suggested Three dimensional DL-CNN model considers spatial relationships and shape characteristics, enhancing its diagnostic potential. The following are the processing steps: initially, the input CT-DICOM clinical image is passed through a series of down-sampling layers in 3D-Mask-R-CNN. These 3D layers reduce the spatial resolution and encode high-level information about the image. The encoded features are then concatenated with features from earlier stages of processing. This combination of early and later features helps the model maintain fine details while considering high-level information. After feature concatenation, the data goes through several up-sampling transposed convolution layers. These layers decode the high-resolution information, which is essential for identifying or spotting the exact location and size of pulmonary nodules. Given the depth of the network (over 30 convolutional layers), KDE is used to detect the error data points and recover them for efficient processing. Due to huge memory constraints, the larger CT-DICOM images are divided into smaller, overlapping volumes with a pixel value of 128x128x128. Each of these volumes is processed separately to manage memory usage. After processing, the results are combined to form the complete output.

The output of the model is a 16x16x16 matrix of (x, y, z) coordinates, diameter, nodule probability, and severity analysis. (x, y, z) coordinates represent the spatial position of a candidate region within the 3D input volume and also the 3D location of a region within the CT scan. The diameter indicates the size of the candidate region. In the context of lung cancer detection, nodules can vary in size. A larger diameter suggests a larger nodule, and vice versa. Nodule Probability and severity analysis is a measure of how likely it is that the candidate region contains a nodule. It's a probability and severity score, with higher values indicating a higher likelihood of being a nodule. The output of 3D-DLCNN is parameterized by three different anchors, which are essentially templates used to predict the size and location of potential nodules. These anchors are based on certain nodule sizes observed in the CT-DICOM dataset. The anchor sizes are set to 3mm, 7mm, and 20mm. The following is the equation to measure the nodule size in clinical dataset to perform prediction.

$$Nodule_{Diameter} = Maximum\ Feret\ Diameter\ (CT - DICOM) \tag{1}$$

where, *Feret Diameter* size is the straight line distance across the nodule. Based on the prediction tasks the relevant features are extracted from DICOM clinical dataset and optimal value is measured. The model inferences are measured by nodule probabilities and model prediction. The equation is derived as,

$$Nodule_{Probabilities} = 3DDLCNN\_Model_{Predict}\ (Preprocessed\ CT - DICOM) \tag{2}$$

where x, y, and z coordinates the DLCNN nodule detected values. It determines the spatial location of the pulmonary nodule in the CT-DICOM-scanned image dataset. The 3D-Voxel value is measured and classified as a part of the nodule detection optimal value. The process involves 3D CNN layers, pooling and fully connected layers for efficient detection.

2.2 Data Attainment, Acquisition and Pre-Processing of CT-DICOM Clinical Images

This proposed AI-based novel 3D-DLCNN model uses CT-DICOM pulmonary scanned clinical images, which consist of 355 samples of 251135 LC-HD 3D images, fewer than 2 categories male and female. The target attributes with clinically proven results are normal (0), LC nodule identified (2), and severity condition (3) if positive. The CT-DICOM clinical-scanned images have results of fasting and normal. 200x200 pixel images with a 4.70 mm slice thickness are the measurements of the image. Transition scanning was performed from the base of the head to the lung upper layer. All annotations are recorded in PASCAL-VOC format. The reconstructions of CT-DICOM images were made using the CT protocol with the help of the hybrid segmentation method. 75% of DICOM images are used for training, and 25% are used for testing purposes. Table 1 shows the clinical dataset values of the sample patients.

Table 1. CT-DICOM Clinical Dataset (Screened from Scanned Pulmonary Image Values)

P.ID	Age	LC	Gen	Diagnosis	Severity Analysis			Z-Score	Clinical Results
					S1	S2	S3		
#012	51	N2	0	1	0.78	-0.88	1.6	3.1	
#014	54	N1	1	2	-1.72	0.12	2.1	2.3	
#016	56	N3	1	0	-0.72	0.12	1.7	1.4	
#018	67	N2	0	0	0.03	-1.63	0.8	1.8	
#020	48	N1	1	1	-0.97	-0.13	0.5	1.9	
#022	47	N3	0	2	-0.72	0.37	0.8	3.1	
#024	77	N2	0	2	2.03	-1.38	2.1	2.7	**Male: 121**
#026	71	N1	0	2	-0.22	-0.88	1.1	2.8	**Female: 234**
#028	79	N3	0	0	2.78	-1.13	1.5	0.77	**Normal: 156**
#030	55	N2	0	0	2.03	-2.13	2.3	1.88	**LCD: 81**
#032	81	N1	0	0	0.03	-1.63	1.6	1.65	**Severity: 118**
#034	56	N3	0	1	3.03	-0.63	2.4	0.64	**S1 Level: 91**
#036	43	N1	1	2	1.28	-1.38	1.4	0.78	**S2 & S3 : 27**
#038	64	N2	1	0	1.53	-1.13	2.1	0.61	
#040	37	N3	0	1	0.28	0.37	0.4	0.56	
#042	39	N2	1	1	0.03	-1.13	0.8	0.35	
#044	69	N1	1	0	1.53	-1.13	1.1	0.28	
#046	33	N1	0	2	0.28	-0.13	0.9	0.45	

(Out of 20K image screened values, few samples are displayed for reading)

2.3 KDE, SOD and ER-NCN

During the candidate screening, the noise data points may occur in any one of (x,y,z) the coordinated. At that time, KDE calculates the number of errors points and eliminates them in the final optimal calculation. This process is done early before the candidate screening for better identification of nodules with the help of extracted global and local features. The abnormalities and severity score analysis is done by SOD, where the data regions are identified accurately in the form of a z-score and match the patterns in the trained images. The potential nodules are detected with the help of the pixel intensity ratio captured by ER-NCN to reduce false positive and false negative rates. The targeted diagnosis levels are calculated over a specific period of time based on the threshold values. Variations may occur in normal anatomy across individuals. These models are integrated into 3D-DLCNN to perform efficiently and boost the AUC-ROC level and C-Index value to predict pulmonary cancer at an early stage. Data points with feature values are used during vocal identification at the last stage. The following equation is used to calculate the error data points during screening of candidates.

$$Error\ Data\ Points = \{x_i \,|f\,(x_i\,) < THRESHOLD_{Limit}\} \tag{3}$$

where, x_i represents data point and $f\ (x_i)$ represents density data point using KDE. Threshold limit is sent to consider the potential errors. The below equation clearly states the calculation of z-score and pixel intensity SOD value in CT scanned

images.

$$Z_{Score} = x_i - \frac{X_j}{SOD_{Value}} + Predicted_{Value}\,(CTDICOM) \tag{4}$$

where, SOD_{Value} is standard outlier detection values that are calculated to identify the pixel points and the intensity level during implementation.

2.4 3D-DLCNN Candidate Screening Architecture Diagram

The input cropped image (CT-DICOM) is taken for initial screening, and the values are converted into 128 bits, 64 bits, 32 bits, 16 bits, and 8 bits and concatenated with the help of two layers. Masking values are derived after concatenation, where CNN MAP values are identified. The 3x3x3 values are calculated to predict the optimal solutions, where they state the target attributes in the form of x, y, and z coordinates. Pooling and fully connected layers are formulated in the CT-scanned images.

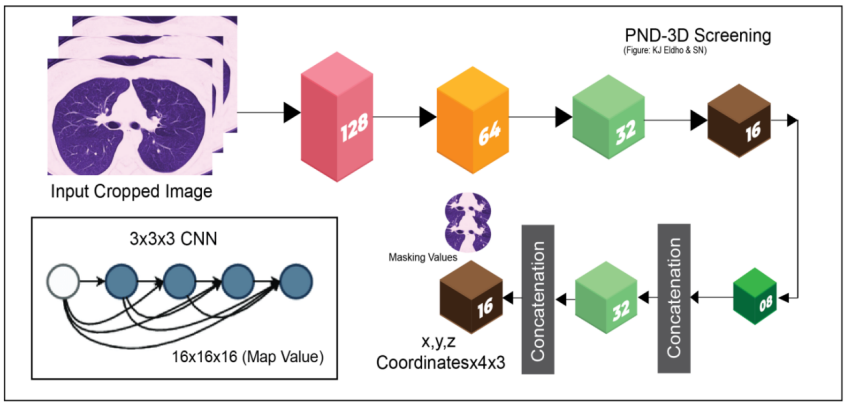

Fig 1. 3D-DLCNN Proposed Architecture Diagram

3D-DLCNN Pulmonary (Lung) Nodule Detection Algorithm

1. **Input:** MATLAB settings with CT-DICOM Dataset
2. **Begin**:
3. Load the CT scan images from DICOM dataset$data.CTDICOM$
4. Perform pre processing $segmented\ images = perform\ (image\ segmentation\ (CTDICOM)$
3D-DLCNN_model = create_3D-DLCNN model()Train 3D-DLCNN model(3D-DLCNN_model, train_data)
evaluation metrics = evaluate 3D-DLCNN model(3D-DLCNN_model, test_data)
return pre-processed images
thresholded_predictions = apply_threshold(3D-DLCNN_model.predict(test_data))
5. **Train Classifier** using $Predicted\ Values\_V$
6. **Apply KDE** for $test_{data}(CTDICOM)$
7. Calculate Z-Score with **Statistical Outlier Detection**
$test_{data}(SOD_{CTDICOM} = S_{Value})$
8. Measure pixel intensity using ER-NCN
$Predicted_{Value} = ERNCN\,(Trained\ Data) + Predicted\ Value$
9. Nodule Identification using $3D_{Featuremeasurement}$
10. Generate **3D-DLCNN output image (0,1,2)**
11. Record the Values $Predicted\ Values\_V$
12. **Output:** Nodule Detection & Severity Analysis
13. **End**

2.5 Output Map Dimensions

Each input region is associated with an output for each of these three anchors, so you have three sets of predictions for each candidate region. Additionally, there are five features (coordinates, diameter, and nodule probability) predicted for each anchor.

Therefore, the output map is of the shape 16x16x16x4x3, where 16x16x16 represents the spatial grid in the 3D volume and 4 corresponds to the features (x, y, and z coordinates, diameter, nodule probability, and severity score). 3 indicate the three anchors, each with its own set of predictions.

2.6 Real - Time Implementation with 3D-DLCNN

Assume that a process of 3D CT scans of a patient's chest. Inside this CT scan, the model is scanning small cubic regions (candidates) of size 16x16x16. For each candidate, the model predicts:

i) (x, y, z) coordinates to locate the candidate within the 3D volume.

ii) Diameter to estimate its size.

iii) Nodule probability and severity analysis to assess the likelihood of containing a nodule.

For each of these predictions, there are three variations (one for each anchor) to account for different nodule sizes. This output provides valuable information about potential nodule locations, sizes, and their likelihood of being cancerous, aiding in the early detection of lung cancer. Ground truth labels are determined based on the intersection of anchors with actual nodules. If the intersection over the union is 0.5 or greater, it's considered positive; if the overlap is less than 0.2, it's negative. Only positive anchors contribute to regression loss. The final loss for each anchor is calculated using the predicted probability (p) and regression values (t) compared to the ground truth (p^* and t^*). The training and testing values might differ depends on iterations.

1. **Performance Evaluation Metrics of 3D-DLCNN**

The new 3D-DLCNN AI-based deep learning model is suggested to identify pulmonary disease and its severity analysis at an early stage. The model is compared against the prevailing models such as GA-PSO[15], SVM[16], KNN[17], and BPNN[18]. The performance is evaluated using the MATLAB simulation tool, which helps process the CT-DICOM dataset from the initial level to the final results. Various iterations have been carried out to get the optimal results, and the results are displayed in graphical format for better understanding. Five PEM metrics are used to analyze the novelty of the proposed AI-based model. After pre-processing is carried out, the simulation starts to evaluate and compare the models to check the accuracy and severity analysis of 3D-DLCNN. The following are the performance metrics used for analyzing the new model by comparing it with the baseline versions. The results are discussed in Section 3.

- **Sensitivity and Specificity:** Sensitivity deals with all the positive instances that are detected by a proposed model (3D-DLCNN) out of actual positive cases. Specificity measures the entire number of negative instances detected by the model out of the actual negative cases in CT-DICOM dataset images.

$$LC_{Sensitivity} = \frac{TPR}{(TPR+FNR)} \times 100 \tag{5}$$

$$LC_{Specificity} = \frac{TNR}{(TNR+FPR)} \times 100 \tag{6}$$

- **Accuracy:** Calculates the ratio of actual predictions against the number of samples by 3D-DLCNN and balances the positive and negative LC predictions. Correctly classified samples will be taken into consideration for comparative analysis.

$$LC_{Accuracy} = \frac{(TPR+TNR)}{(TPR+TNR+FPR+FNR)} \times 100 \tag{7}$$

- **AUC-ROC:** The performance of TPR and FPR is evaluated based on features extracted at various threshold values, which range from 0 to 1. The hyperparameters of the CT-DICOM are adjusted to optimize performance.
- **False Positive & False Negative** - Measures the percentage of negative predicted value by the proposed 3D-DLCNN model. High precision is maintained to minimize FPR in every iteration.

$$LC_{FalsePositiveRate} = \frac{FP}{(FP+TN)} \times 100 \tag{8}$$

$$LC_{FalseNegativeRate} = \frac{FN}{(FN+TP)} \times 100 \tag{9}$$

- **C-Index:** Evaluates the discrimination power and severity score in the binary classification tasks generated by the suggested AI-based deep learning model.

$$LC_{CIndex} = \frac{No.of\ concordant\ pairs}{(No.of\ CP + No.of\ Discordant\ Pairs)} \tag{10}$$

$$Matthews\ \ Corelletion\ Coefficient = \frac{T_1}{\sqrt{T_2 \times T_3 \times T_{4\times} T_5}} \times 100 \tag{11}$$

where, *LC denotes Lung Cancer Prediction* and the evaluation metrics equation is derived using, $T_1 = (TPR \times TNR - FPR \times FNR)$, $T_2 = (TPR + FPR)$, $T_3 = (TPR + FNR)$, $T_4 = (TNR + FPR)$, and $T_5 = (TNR + FNR)$.

3 Results and Discussions

This chapter clearly portrays the performance of the AI-based pulmonary cancer disease prediction by employing the three-dimensional deep learning CNN method to boost feature discrimination power and accuracy and to identify the LC severity score. The 3D-DLCNN-DLCNN is implemented, and comparative analysis is made against the prevailing disease prediction models such as GA-PSO [15], SVM [16], KNN [17], and BPNN [18]. It is observed that the new model outperformed the existing approaches in terms of nodule detection, classification, 3D-screening, and feature extraction. It overcomes the limitations of machine-learning prediction models. The results are compared and discussed, along with its unique features at all performance metric levels. The analysis and findings are shown below in Figures 2, 3, 4, 5 and 6 in the form of a MATLAB graph with X and Y axis coordinates.

3.1 Sensitivity and Specificity Analysis

The analysis of sensitivity and specificity is showcased in Figure 2. The suggested AI-based DL model for pulmonary detection followed a unique learning method for complex patterns in CT-DICOM images, where the filtering, screening, and segmentation methods were done in a robust manner. It is noteworthy that the proposed 3D-DLCNN model effectively discriminates between positive and negative cases among the dataset, which dominates the baseline versions. Initial nodule screening is done by the 3D Mask-R-CNN method. 92.7% sensitivity and 93.4% specificity are marked after 10 epochs and 40 iterations, which is relatively high compared to other models.

Table 2. Sensitivity and Specificity analysis results

Metrics / Schemes	GA-PSO [15]	SVM [16]	KNN [17]	BPNN [18]	3D-DLCNN (Proposed)
Sensitivity	72.33%	75.42%	81.34%	87.63%	92.7%
Specificity	73.16%	76.31%	82.44%	88.09%	93.4%

3 .2 Accuracy Analysis

Figure 3 portrays the accuracy of LC prediction at all levels by the proposed 3D-DLCNN model. The method is compared against the prevailing disease prediction models such as GA-PSO [15], SVM [16], KNN [17], and BPNN [18]. As the error points are removed at an early stage, the feature discrimination power is maximized. Three different anchors are set during implementation with various sizes, where each input is associated with three predictions in a candidate region. Due to the vigorous 3D classification technique, the accuracy is boosted to 93.45%, where it outperforms the existing models. It is proven that the model has high potential for effectively identifying pulmonary disease at an early stage.

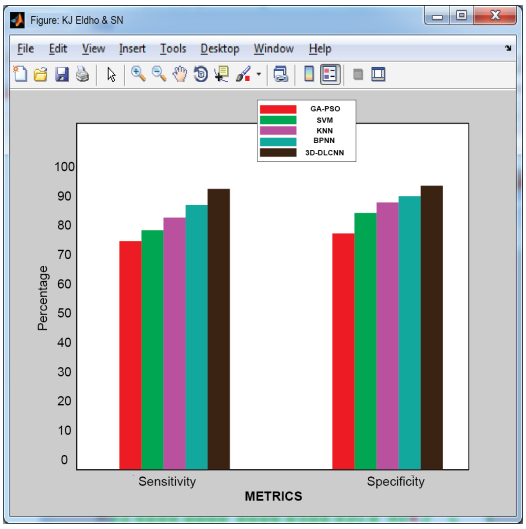

Fig 2. Sensitivity and Specificity

Table 3. Accuracy analysis results

Metrics / Schemes	GA-PSO [15]	SVM [16]	KNN [17]	BPNN [18]	3D-DLCNN (Proposed)
Accuracy (It-1)	71.81%	79.12%	81.67%	84.31%	90.06%
Accuracy (It-N)	75.02%	81.31%	85.16%	88.33%	93.45%

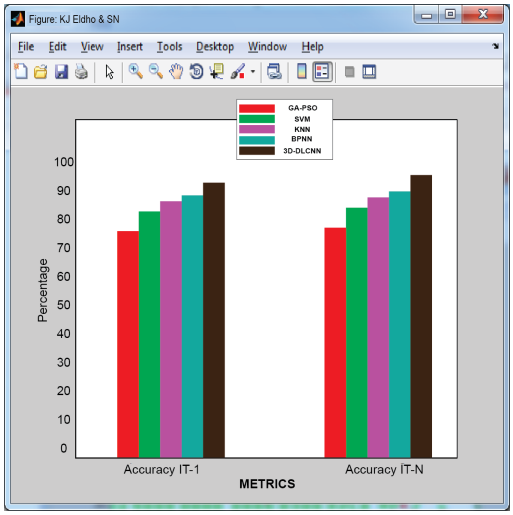

Fig 3. Accuracy

3.3 C-Index Analysis

Figure 4 demonstrates the c-index level of the suggested 3D-DLCNN model, which shows the complete evaluation of the pairs of instances and predicted probabilities. The discrimination power is correctly identified by the c-index. As the model achieved 0.87, perfect discrimination was noted. All possible pairs of instances are considered, and we assess whether the 3D-DLCNN correctly ranks according to predicted probabilities. The severity score is analyzed here, and ER-NCN is employed where the pixel intensity is measured. The D-score is compared against GA-PSO [15], SVM [16], KNN [17], and BPNN [18]. Based on the predicted probability, the last stage is measured after all iterations, and the results are marked.

Table 4. C-Index analysis results

Metrics / Schemes	GA-PSO [15]	SVM [16]	KNN [17]	BPNN [18]	3D-DLCNN (Proposed)
C-Index Level	0.62	0.69	0.72	0.73	0.82
Last Stage	0.65	0.71	0.75	0.78	0.87

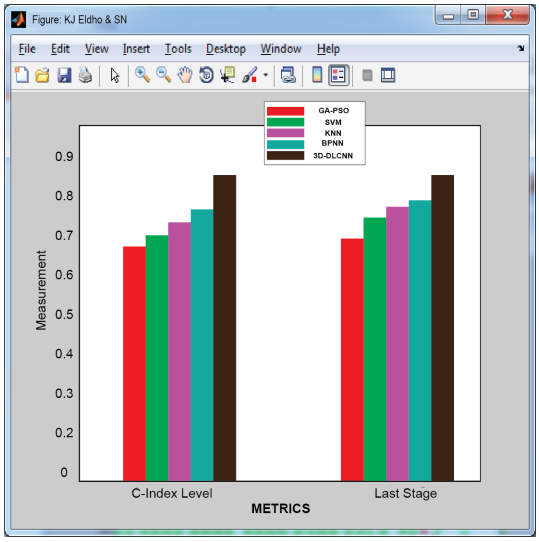

Fig 4. C-Index

3 .4 AUC-ROC Analysis

Figure 5 displays the measured AUC-ROC of 3D-DLCNN LC prediction algorithm. Setting the lowest and maximum threshold values comes before putting them into implementation and beginning the iteration. The threshold value is set in order to achieve a balance between specificity and sensitivity rates. The random classifier levels are assessed in terms of TPR and FPR. To get the maximum TPR and lowest FPR in every iteration, the CT-DICOM images are evaluated and trained using CNN. AUC-ROC provides promising results in disease prediction to prove the potential of the model. 0.8 TPR and 0.5 false curves fall on the graph during implementation, which is relatively best compared to existing machine learning LC prediction models.

Table 5. AUC-ROC analysis results

Metrics / Schemes	GA-PSO [15]	SVM [16]	KNN [17]	BPNN [18]	3D-DLCNN (Proposed)
TPR	0.5	0.57	0.61	0.65	0.8
False Curve	0.2	0.4	0.51	0.34	0.5

3.5 FPR & FNR Analysis

Figure 6 portrays the FPR and FNR rates of the new 3D-DLCNN model. To reduce the data point deviation at different levels, the statistical outlier detection method is employed. 6.6% FPR and 6.4% FNR are achieved, which is outstanding compared with the prevailing models. The deep pixel and segmentation model helps in maximizing feature extraction and severity score analysis. Each image's pixel intensity levels are measured. The model is compared against GA-PSO [15], SVM [16], KNN [17], and BPNN [18]. It is mentioned as a type one error and a type two error. It is highly related to sensitivity, specificity, and AUC-ROC. In all iterations, the levels are measured, and the results are compared. The process of z-score analysis is also one of the unique methods for low FPR and FNR. It is noted that BPNN closely comes in as the best detection, while 3D-DLCNN shows the perfect classification level, which yields low FPR and FNR.

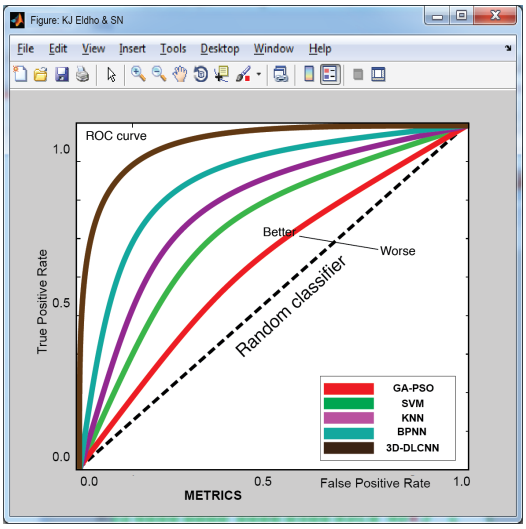

Fig 5. AUC-ROC

Table 6. FPR & FNR analysis results

Metrics / Schemes	GA-PSO [15]	SVM [16]	KNN [17]	BPNN [18]	3D-DLCNN (Proposed)
FPR	32.17%	28.45%	22.51%	20.02%	6.6%
FNR	30.03%	26.7%	20.19%	19.01%	6.4%

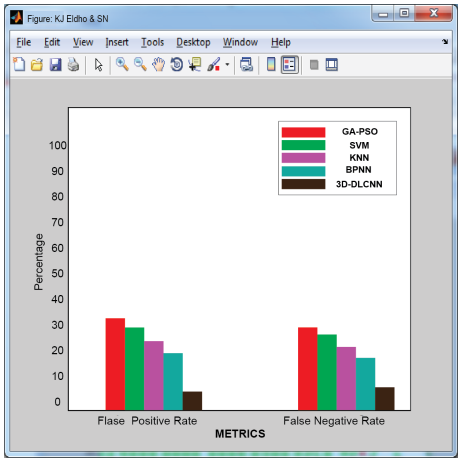

Fig 6. FPR & FNR

4 Conclusion

The novel AI-based 3D deep learning convolutional neural network classifier is employed for pulmonary cancer detection and classification at an early stage by identifying the complex patterns in CT-DICOM images extracted from the dataset. During the initial level, the nodules are spotted in the CT images extracted by utilizing 3D Mask-R-CNN. Feature selection and extraction are done by 3D-DLCNN, which is unique in identifying patterns in extracted images. The DICOM dataset is used with 355 instances and 251135 CT images with target values of 0, 1, and 2, which indicate cancer, normal, and severe. 75% of the dataset is used for training and validation, and 25% is for testing purposes. As a part of error recovery before the candidate screening, KDE is used. The SOD mathematical method is used to calculate the z-score to reduce data point deviation. Intensity and pixel masking are done by using ER-NCN to identify the severity score of the patient if the cancer is positive. After 10 epochs, accuracy is boosted to 93% with 92.7% sensitivity, 93.4% specificity, 0.8 AUC-ROC, 6.6% FPR, and 0.87 C-Index. The proven

implementation results show that the new 3D-DLCNN model outperforms the current approaches, GA-PSO, SVM, KNN, and BPNN.

The noted limitations of this model are: i) a greater requirement for clinical validation; ii) high computational resources; iii) very limited labeled data in terms of obtaining clinically extensive datasets; iv) a lack of interpretability and crucial decision-making processes; v) the performance may be suboptimal when applied to a different or diverse patient population; and vi) high image quality is required for 3D processing to avoid noise and artifacts. This model may be enhanced further to overcome the minor limitations mentioned.

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