Indonesian Journal of Electrical Engineering and Computer Science
Vol. 34, No. 1, April 2024, pp. 134~143
ISSN: 2502-4752, DOI: 10.11591/ijeecs.v34.i1.pp134-143

An optimal model for detection of lung cancer using convolutional neural network

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Article Info

Article history:

Received Jul 10, 2023
Revised Jan 21, 2024
Accepted Jan 23, 2024

Keywords:

Benign
CNN lung cancer
Computed tomography
Malignant
Mean average precision

ABSTRACT

In terms of frequency and mortality, lung cancer ranks second among all cancers worldwide for both men and women. It is suggested that pattern classification and machine learning be applied to the identification and categorization of lung cancer. Convolution neural network (CNN) techniques divide the input data into groups according to the distinctive characteristics of the input. Using a standard approach to analyze a large number of computed tomography images, early detection of lung cancer can save lives. The suggested effort is centered on identifying the precise type of cancer and making predictions about whether it is benign or aggressive. The deployment of proposed model is an attempt to improve the accuracy of the system. The proposed work showed an overall accuracy of 98.4% during the detection of lung cancer and 98.8% accuracy towards the prediction of specific type in the lung cancer. Mean average precision score of 97.17% and 98.75% test and validation respectively. 0.96, 0.93, and 0.95 for malignant test data.

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1. INTRODUCTION

As the second most common disease and the primary cause of cancer-related death for both men and women globally, lung cancer is undoubtedly a serious global health concern [1], [2]. In comparison with other cancer forms, it has a high fatality rate. Globally, there are about 1.8 million new cases (13% of all cancer cases) and 1.6 million fatalities (19.4% of all cancer deaths) from lung cancer annually. Tumors formed by unchecked and aberrant cell proliferation are a hallmark of lung cancer [3], [4]. Cigarette smoking is the primary cause of lung cancer, accounting for about 85% of cases in men and 75% in women [5]. Lung cancer is a major cause of death in developing nations, accounting for 19.4% of cases. Patients with lung cancer have a very high chance of survival if they are diagnosed early. An early diagnosis of the condition greatly increases the likelihood of therapy effectiveness. As a result, efficient techniques and instruments are required for the early detection and diagnosis of lung cancer. Because fuzzy logic enables result-oriented analysis, it has been acknowledged as a useful tool in previous lung cancer forecasts [6], [7]. By leveraging fuzzy logic, it is possible to make more accurate predictions, improving the chances of early detection and potentially better patient outcomes. It is crucial to remember that the word “cancer” refers to a wide range of conditions that affect more than 100 distinct human tissues, including the breast, skin, lung, colon, prostate, blood, and more. Depending on the kind and stage of the disease, cancer symptoms can vary

greatly [8]. A healthcare professional should be consulted for a proper evaluation and diagnosis, even though there are common non-specific symptoms like frequent respiratory infections, shortness of breath, decreased appetite, fatigue, weight loss, pain, skin changes, bowel or bladder function changes, abnormal bleeding, persistent cough, speech changes, fever, and the presence of lumps or masses. To battle lung cancer and lessen its influence on world health, early identification, prompt treatment, and continued research are crucial [9], [10].

Lung cancer constitutes a substantial portion of cancer-related fatalities, contributing to about 20% of all cancer-related deaths. The global prevalence is underscored by the reported figures of 21 million new cases and 1.8 million deaths in 2018 [11]. In the United States, the impact is further emphasized, as the American Cancer Society projected an anticipated 142,670 lung cancer deaths in 2019, with 76,650 in men and 66,020 in women [12]–[14].

Lyu *et al.* [15] proposed using deep learning algorithms to recognize lung nodules in thoracic magnetic resonance (MR) pictures. Unlike many other computed tomography (CT) nodule detection approaches, this suggested method uses the entire image as input and does not require candidate extraction. This solution uses the faster R-convolution neural network (CNN) architecture, which consists of two modules: the region proposal network (RPN) and the fast R-CNN detector [16]. The fast R-CNN detector is used to classify the recommended regions that the RPN generates for each image. The approach was evaluated using the first Affiliated Hospital of Guangzhou Medical University dataset, and the findings indicated that the proposed model had an 85.2% sensitivity for detecting lung cancer. This illustrates the potential application of deep learning approaches to improve the efficacy and precision of thoracic magnetic resonance imaging-based lung cancer detection.

CNN is a type in deep learning algorithm, has drawn a lot of interest in the medical community due to the potential for a wide range of uses. Given the substantial impact early detection and diagnosis of lung cancer can have on patient outcomes and survival rates, it is imperative that cutting edge techniques and technologies be further investigated and developed. An explanation of the paper's structure is provided below. The first section introduces different state-of-the-art CNN architectures and discusses lung cancer. The second section discusses the performance matrices that were used and the architecture of the created model parameters. The experimental findings and debate are covered in more detail in the third section. The conclusion is found in the last portion of the paper.

2. METHOD

AI, or artificial intelligence, refers to a system's ability to extract information from external data and use that information to achieve specific goals through learning. Machine learning is a fundamental concept in AI, where a computer learns from large amounts of training data to create a mathematical model that can make decisions and predictions in real-world scenarios [17]–[19]. Conversely, deep learning is a branch of machine learning that uses artificial neural networks as its base. It utilizes neural networks with multiple layers of algorithms, each providing different interpretations of the data being processed. Deep learning's primary goal is to automatically learn hierarchical data representations, which will enable the system to carry out challenging operations like picture recognition and natural language processing, among others. In the context of lung cancer analysis, Figure 1 shows the general workflow of AI techniques [20]. The process involves using convolution tools for feature extraction. This step involves identifying and labelling various aspects of a lung CT image to enable further analysis. CNNs' crucial convolution layers are utilized to apply filters to lung CT scans and extract characteristics like edges, textures, and forms. The predictions about lung cancer are subsequently generated by running these extracted features through one or more fully connected layers. The combination of convolution layers and fully connected layers in a deep learning model enables the system to automatically learn and extract relevant features from the input data, leading to accurate predictions or classifications in lung cancer analysis [21]–[24]. Overall, AI, machine learning, and deep learning techniques have revolutionized many fields, including medical image analysis, and hold great potential in improving the accuracy and efficiency of lung cancer detection and analysis.

An optimal CNN model for lung cancer detection typically begins with convolution layers that extract intricate patterns and features from medical images like CT scans. These layers are followed by pooling layers to reduce dimensionality and retain essential information. Incorporating multiple convolution blocks, such as residual or inception modules, helps capture hierarchical representations, enhancing the model's ability to discern subtle nuances in the images. Batch normalization and dropout layers mitigate over fitting while aiding in faster convergence during training. Transfer learning, leveraging pre-trained CNN architectures like visual geometry group (VGG), resent, or efficient Net, often proves effective, allowing fine-tuning on specific lung cancer datasets to achieve higher accuracy and efficiency in detecting malignancies within medical imaging data. Regular evaluation and optimization of

hyper parameters, alongside robust validation techniques, contribute significantly to the model's overall performance and reliability.

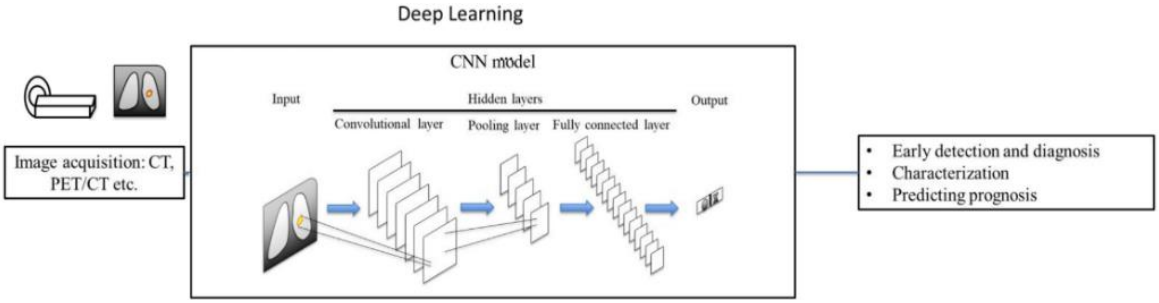

Figure 1. Deep learning model for lung cancer analysis

2.1. Proposed model

It should be noted that a closer inspection of the research paper or other pertinent documentation related to the suggested model would be necessary to fully comprehend the specifics of the architecture, such as the quantity and number of layers, activation functions, regularization strategies, and optimization techniques. The general architecture of the suggested model, as shown in Figure 2, probably shows how the various layers are arranged and connected, including the quantity of convolution layers, the composition of fully connected layers, and any other elements or adjustments particular to the suggested model. Lung CT image convolution layers are necessary in this situation to extract relevant characteristics from the input data. To recognize edges, textures, forms, or other significant characteristics that may be suggestive of lung cancer, these layers apply filters. Using the retrieved features, the fully connected layers oversee classifying or predicting things. These layers combine the information from the convolution layers to discover patterns and relationships within the data.

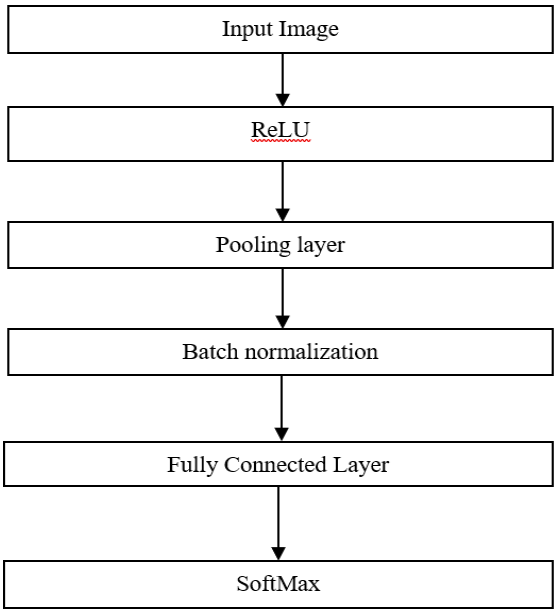

Figure 2. Proposed architecture

Rectified linear activation function (ReLU): the ReLU function is commonly used in neural networks to introduce non-linearity. It's defined as f(x)=max (0, x). This function helps the network learn complex patterns and improves training by preventing vanishing gradients.

Pooling layer: pooling layers diminish the input volume's width and height in space. Max pooling, which divides the input into smaller parts and retains the maximum value from each zone, is a popular pooling procedure. This helps in reducing computational complexity and controlling over fitting.

Batch normalization: in a neural network, batch normalization normalizes the activations of every layer. It uses learnable parameters to scale and shift each feature map after calculating its mean and variance within a mini-batch and normalizing the results. This technique helps in stabilizing and accelerating the training process by reducing internal covariate shift.

Fully connected layer: dense layers, or fully connected layers, link each neuron in one layer to every other layer's neuron. A fully connected layer's output can be expressed mathematically as f(x)=Wx+b, where x is the input, b is the bias vector, and W is the weight matrix. In the later stages of neural networks, these layers are frequently used to aggregate learnt features for tasks involving regression or classification.

SoftMax function: In the output layer of a neural network, the SoftMax function is frequently utilized for classification tasks. It creates probability from the raw scores (logits). The (1) defines the SoftMax function equation for a vector z of length K (where K is the number of classes).

$$\sigma(\overrightarrow{z})_i = \frac{e^{z_i}}{\sum_{j=1}^{k} e^{z_i}} \quad (1)$$

Here, e^z is the exponentiation of the i^{th} element of the input vector z, and the denominator is the sum of the exponentials of all elements in the vector, ensuring that the output probabilities sum up to 1.

Performance metrics: statistical measures such as recall, precision, false measure, sensitivity, specificity, accuracy, and G-measure, as well as false match false acceptance rate (FAR) (accepting a fictitious user) and false mismatch false rejection rate (FRR) (rejecting an actual user), can be used to gauge how well the system is performing. As stated in (2), the recall is the ratio of the number of true-positives (TP) to the total of TP and false-negatives (FN).

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \quad (2)$$

Precision is the ratio between the sum of TP and true-negatives (TN) to the sum of TP, TN, false-positives (FP), and FN as given in (3).

$$\text{Precission} = \frac{\text{TP+TN}}{\text{TP+FN+FP+FN}} \quad (3)$$

The ratio of the harmonic mean of recall and precision to the summation of recall and precision is known as F measure and it can be expressed as in (4).

$$\text{F} - \text{measure} = \frac{2\times \text{Re call}\times \text{Pr ecision}}{\text{Re call} + \text{Pr ecision}} \quad (4)$$

Sensitivity is also named as TP rate and it can be computed using the (5) expression:

$$\text{Sensitivity} \text{S}_\text{e} = \frac{\text{TP}}{\text{TP+TN}} \quad (5)$$

in specificity, TN and TP are used to calculate the negative characteristics and the specificity is also called as TN rate.

$$\text{Specificity S}_\text{p} = \frac{\text{TN}}{\text{TP+TN}} \quad (6)$$

The accuracy can be determined on the basis of sensitivity and specificity, and it can be computed as in (7):

$$\text{Accuracy A} = \frac{\text{TN+TP}}{\text{TP+TN+FP+FN}} \quad (7)$$

3. RESULTS AND DISCUSSION

The following steps provide an organized representation of the many phases of the research process.

– Step 1: relevant data is gathered from appropriate sources, and then preprocessing takes care of any anomalies, missing numbers, or inconsistencies to make sure the data is prepared for more examination.

- Step 2: it is critical in identifying the important variables or characteristics from the pre-processed dataset that are needed for the modelling stage. This step separates the most important features for the next training phase using algorithms and statistical techniques.
- Step 3: in deep learning for lung cancer prediction, ReLU serves as the activation function, introducing non-linearity to model the complex relationships in image data. Pooling layers help capture important features while reducing spatial dimensions, batch normalization stabilizes and accelerates training, fully connected (FC) layers enable the extraction of intricate patterns, and SoftMax is applied in the output layer to transform model predictions into probability distributions, facilitating the identification and classification of lung cancer based on medical imaging features.
- Step 4: here, development of CNN model with support vector machines (SVM) classifier- a deep learning method renowned for its accuracy and robustness is used during the model training phase. This model "learns" from the data after being trained using the chosen features from the previous step, allowing it to generate predictions or classifications.
- Step 5: here, trained model is evaluated where its performance is measured using metrics, such as the Accuracy, area under the ROC curve (AUC)-receiver operating characteristic (ROC) score. This score offers information about how well the model can differentiate between different classes, guaranteeing accurate and trustworthy outcomes.

Dataset: the dataset used in the proposed method includes annotated images such as CT accurately labelled by medical professionals to denote the sub types accurately. An optimal dataset also has been incorporated with metadata, like patient history, treatment outcomes, and clinical details, to enable the development of robust machine learning models. With this it is capable of detecting, classifying, and potentially predicting the progression of lung cancer. Striking a balance between volume and diversity within the dataset ensures the model's generalizability and efficacy in real-world scenarios, fostering advancements in early detection, and personalized treatment strategies.

In the proposed work, the primary job in the suggested work is the detection of a tumor's existence in the CT lung image, which is followed by the classification of a certain class in the same. Finally, findings are contrasted with the suggested model and other state-of-the-art methodologies as well as with pre-defined models like Alex-Net and VGG16. A comprehensive dataset for training and testing in lung cancer detection ideally encompasses diverse patient demographics, various stages of the disease, and a range of imaging modalities. The LIDC-IDRI lung CT scan dataset has been used to train and evaluate the model for the suggested task. The dataset, which consists of 500 records total, is split into two groups: a training set, which makes up 70% of the dataset, and a test set, which makes up 30% of the dataset plus a validation set. A 70%: 20%: 10% split is used to separate the dataset into three sets: one for training, one for validation, and one for testing. Prior to being applied to the suggested model, the photos are pre-processed to a size of 227×227×3.

3.1. Cancer detection

The mean average precision (mAP) curve is the starting point for everyone when examining the properties of any deep learning model. The performance of the proposed approach in detecting cancer in a CT scan is displayed in Figure 3. An example mAP curve generated for training and validation with the proposed model is shown in Figure 3. The maximum validation accuracy occurs at epoch 12, while the least loss occurs at epoch 25. From the mAP curve, it is possible to see that accuracy rises as epoch grows while loss reduces.

Table 1 depict the accuracy, mAP, and loss between training and validation respectively. The procedure of the suggested technique involved 25 epochs and 250 iterations. The results shown the model outperformed with an accuracy of 100% during fold 4. The model has undergone 5-fold cross-validation to evaluate its precise performance. Overall accuracy of the system is found to be with 98.44% for cancer detection. Similarly, training and validation accuracy results in 97.19% and 98.95% respectively. Finally, training and validation loss results in 0.04344 and 0.0352 respectively for the same number of epochs. In addition to accuracy, precision, recall, AUC, and F1-score are other crucial metrics that were looked at in this study to assess overall performance. The same 5-fold cross validation is used to calculate and tabulate these metrics for each class, and the results are shown in Table 2. The value for these metrics is often more than 0.9.

3.2. Identification of lung cancer type

For categorization, CNN is most effective. The model addresses a four-category multiclass classification problem. The characteristics of the tumor cells serve as the basis for this classification.Adenocarcinoma (Calss-1), Large cell carcinoma (Calss-2), Squamous cell carcinoma (Calss-3)

and Normal (Calss-4) are the major 4 types of cancers and these classes are identified using proposed model. The accuracy and loss curve for the detection of lung cancer is shown in Figure 4.

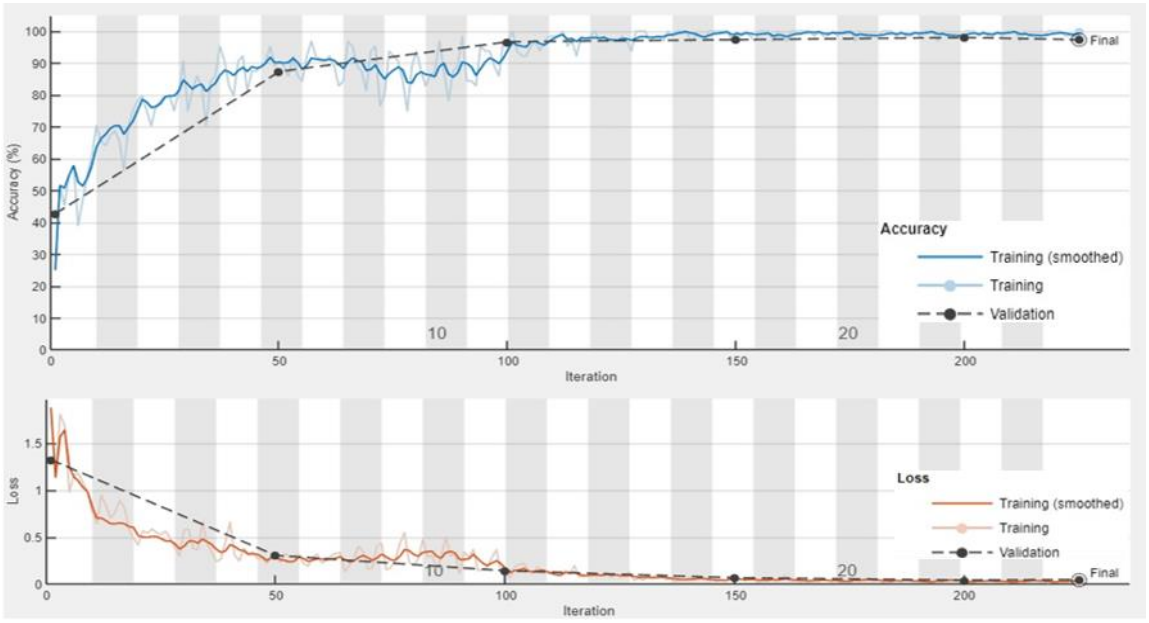

Figure 3. MAP plot for cancer detection

Table 1. Accuracy of proposed model for cancer detection

Fold	Accuracy (%)	mAP		Batch loss	
		Training (%)	Validation (%)	Training (%)	Validation (%)
1	98.70	95.31	98.68	0.0888	0.0468
2	98.70	97.00	100.0	0.0459	0.0181
3	97.40	98.00	97.37	0.0246	0.0572
4	100.0	97.00	100.0	0.0331	0.0166
5	97.40	98.44	98.68	0.0248	0.0373
Average	98.44	97.19	98.95	0.04344	0.0352

Table 2. Critical metrics for each class with 5-fold cross validation

Fold	Class	AUC	Precision	Recall	F1-score	Accuracy
Fold 1	Benign	1	0.96	1	0.98	0.98
	Malignant	1	1	0.96	0.97	0.98
	Normal	1	1	1	1	1
Fold 2	Benign	1	1	0.96	0.98	0.98
	Malignant	1	0.96	1	0.98	0.98
	Normal	1	1	1	1	1
Fold 3	Benign	0.99	1	0.92	0.96	0.97
	Malignant	0.99	0.92	1	0.96	0.97
	Normal	1	1	1	1	1
Fold 4	Benign	1	1	1	1	1
	Malignant	1	1	1	1	1
	Normal	1	1	1	1	1
Fold 5	Benign	0.99	0.96	1	0.98	0.98
	Malignant	0.99	0.96	0.96	0.96	0.97
	Normal	1	1	0.96	0.98	0.98

After completion of cancer detection identification of its types is continued in the work. For this, training and validation accuracy results in 98.75% and 99.50% respectively which is slightly higher than detection as in Table 3. Finally, training and validation loss results in 0.030 and 0.033 respectively for the same number of epochs used earlier. AUC, F1-score, precision, recall, and AUC were among the other crucial measures that were evaluated in addition to accuracy in order to determine performance. An extensive assessment of the model's performance can be obtained by utilizing the 5-fold cross-validation

technique to calculate and tabulate these metrics for every class. The results summarized in Tables 4 and 5 show that in most cases, the values for these metrics are more than 0.9, indicating strong performance of the model.

The ROC-AUC values presented in Figure 5 for the proposed model are consistently above 0.9 across all classes. This implies that the model demonstrates exceptional accuracy in distinguishing between the classes, further highlighting its robustness and effectiveness in the classification task. A comparative analysis of pre-trained models and a proposed model was conducted to assess their performance in the detection of lung cancer. Table 6 presents the performance metrics, including accuracy, precision, recall, and F1-score, for the VGG-16 model alongside the proposed model. Similarly, Table 7 summarizes the results for the Alex-Net model in comparison with the proposed model. These tables collectively provide insights into the effectiveness of the models in the context of lung cancer detection. Percentage of increase has been computed in comparison with pretrained models and proposed model. Pre-trained as well as proposed model outperforms well during the prediction of cancer. Standard evaluation metrics are used to measure the performance of the models. From the results it concludes that proposed model is significantly better than that of the pre-trained models like VGG-16 and Alex-Net. A comparative analysis on our own model with state of art of models has been tabulated as in Table 8. This indicates about the accuracy is moderately better than the existing models.

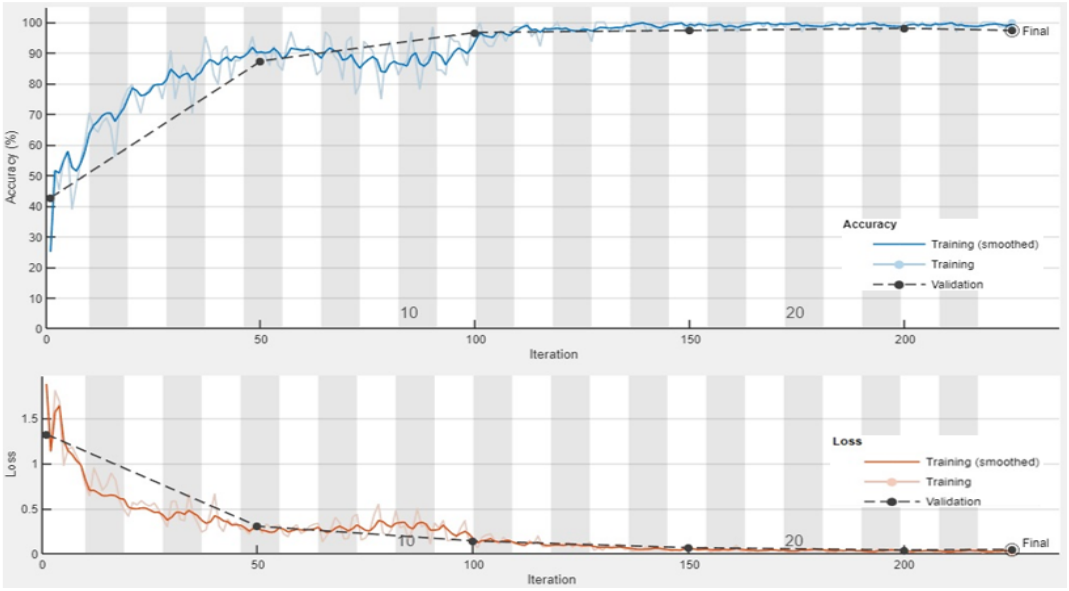

Figure 4. mAP plot to find stages of lung cancer

Table 3. Accuracy of proposed model for cancer detection

Fold	Proposed model				
	Accuracy%	mAP		Batch loss	
		Training (%)	Validation (%)	Training (%)	Validation (%)
1	98.7	100.0	100.0	0.012	0.020
2	98.0	97.0	98.67	0.038	0.037
3	98.7	98.0	100.0	0.051	0.032
4	99.3	100.0	98.33	0.021	0.048
5	99.3	98.44	99.33	0.028	0.028
Average	98.8	98.75	99.50	0.030	0.033

Table 4. AUC for each class with 5-fold cross validation

Fold\Class	Adenocarcinoma	Large cell carcinoma	Squamous cell carcinoma	Normal
1	0.999	1	0.999	1
2	0.999	0.999	0.999	1
3	0.999	1	0.99	1
4	0.998	0.995	0.995	1
5	1	0.999	0.999	1
Average	0.999	0.998	0.998	1

Table 5. Deep learning metrics for each class

Fold	Class	AUC	Precision	Recall	F1-score	Accuracy
Fold1	Class-1	0.999	1	0.98	0.98	0.987
	Class-2	1	1	1	1	1
	Class-3	0.999	0.974	0.975	0.974	0.987
	Class-4	1	1	1	1	1
Fold2	Class-1	0.999	0.962	1	0.980	0.987
	Class-2	0.999	1	0.965	0.982	0.993
	Class-3	0.999	0.974	0.949	0.961	0.98
	Class-4	1	1	1	1	1
Fold3	Class-1	0.999	0.98	0.98	0.98	0.987
	Class-2	1	1	1	1	1
	Class-3	0.999	0.975	0.974	0.974	0.987
	Class-4	1	1		1	1
Fold4	Class-1	0.999	1	0.94	0.969	0.98
	Class-2	0.999	0.966	1	0.982	0.993
	Class-3	0.999	0.927	0.974	0.95	0.973
	Class-4	1	1	1	1	1
Fold5	Class-1	1	1	1	1	1
	Class-2	0.999	0.967	1	0.982	0.993
	Class-3	0.999	1	0.974	0.987	0.993
	Class-4	1	1	1	1	1

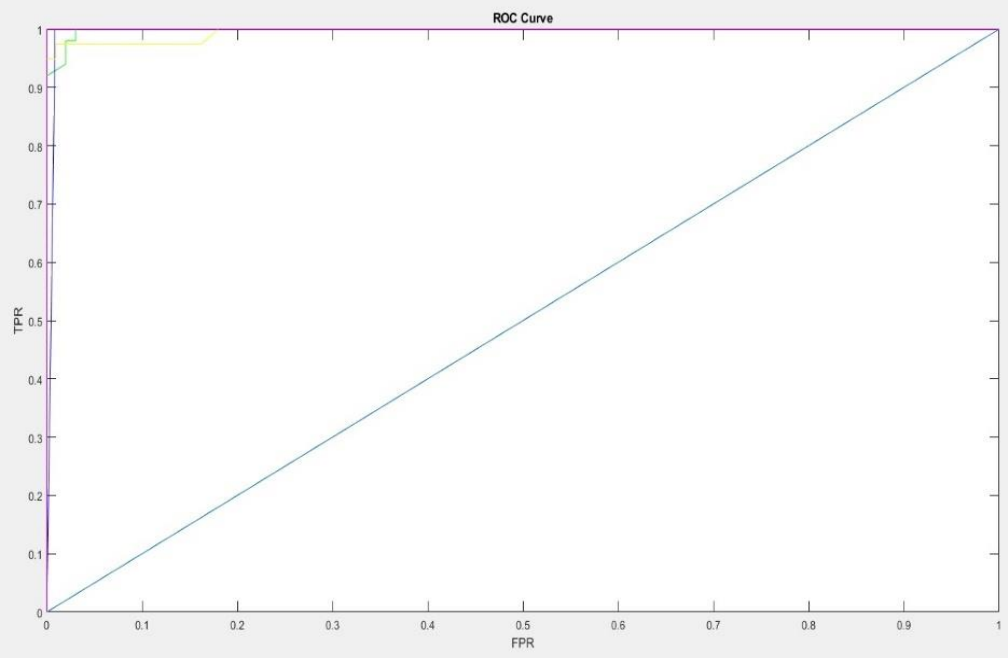

Figure 5. ROC plot for stage detection

Table 6. Comparison of CNN model with VGG-16

Evaluation metrics	VGG-16	Proposed model	(%) of increase
Accuracy	0.9560	0.9844	2.971
AUC	0.9800	0.9970	1.735
Precision	0.9521	0.9840	3.350
Recall	0.9567	0.9840	2.854
F1-score	0.9556	0.9830	2.749

Table 7. Comparison of CNN model with Alex-Net

Evaluation metrics	Alex-Net	Proposed model	(%) of increase
Accuracy	0.9702	0.9844	1.464
AUC	0.9814	0.9970	1.590
Precision	0.9703	0.9840	1.412
Recall	0.9743	0.9840	0.996
F1-score	0.9660	0.9830	1.760

Table 8. Comparison of our model with state of art of models

Sl. No	Authors	Year	Accuracy in (%)
1	Shi *et al*. [25]	2019	87.8
2	Mastouri *et al*. [26]	2020	91.99
3	Mothkur and Nagendrappa [27]	2022	96.56
4	Proposed model	2023	98.44

4. CONCLUSION

This work is being done in order to show that the suggested model, as disparate to a pre-trained model using lung CT image datasets, is more effective and accurate in diagnosing lung cancer. Using the LIDCIDRI dataset, lung cancer detected in CT scan pictures was identified based on the encouraging outcomes of deep learning techniques. This report examined the most recent studies on deep learning methods for CT image-based lung cancer diagnosis and detection. The performance metrics were determined after the following dataset was evaluated and trained using the suggested methodology. The suggested method achieves detection and type identification accuracy of 98.44% and 98.8%, respectively, for lung cancer. A ROC-AUC value of more than 0.99 has been attained in both cases. The suggested model outperforms the pre-trained models by a wide margin, according to the results. The inventors claim that the recommended diagnostic system gives renowned physicians a precise and quick diagnosis.

ACKNOWLEDGMENT

Authors would like to thank Prof. K Byrappa, Provice chancellor of Adichunchanagiri University, Dr. B K Narendra, Dean Engineering and Principal, BGSIT, ACU, Dr. M B Anandaraju, Professor, Department of ECE, BGSIT, ACU, Dr. P S Puttaswamy, Professor and Head, Department of ECE, BGSIT, ACU, and Dr. Nagaraju C, Professor, NIE, Mysore for their support, and valuable suggestions.

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