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CANCER CLASSIFICATION UTILIZING MEDICAL IMAGES

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ABSTRACT
Medical imaging plays a vital role in the early detection and treatment monitoring of lung cancer. Common imaging techniques such as chest X-rays, computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET), and other molecular imaging methods have long been used to diagnose lung cancer. Despite their widespread use, these modalities face certain limitations particularly their lack of automated capabilities for accurately classifying cancerous tissues. This challenge becomes even more critical in patients with overlapping or co-existing conditions, where misdiagnosis can delay treatment. To address this gap, there is a growing demand for diagnostic tools that are not only highly sensitive but also precise in identifying early-stage lung cancer. In recent years, deep learning has emerged as a transformative technology in medical imaging, offering robust capabilities for analyzing both visual and textural data. Leveraging this potential, the present study introduces an enhanced convolutional neural network (CNN) model specifically designed for detecting and classifying lung cancer from chest CT scans. The proposed CNN architecture is capable of categorizing images into four distinct classes: adenocarcinoma, large cell carcinoma, squamous cell carcinoma, and normal tissue. When benchmarked against traditional machine learning approaches specifically the Naïve Bayes Classifier (NBC) the deep CNN model demonstrated superior performance and higher classification accuracy. Evaluation metrics further underscore the model's effectiveness, suggesting that it can significantly aid clinicians in making more accurate and timely diagnoses, ultimately improving patient outcomes.

Keywords: Lung Cancer Detection, Early Diagnosis, Deep Learning in Medical Imaging, Convolutional Neural Network (CNN).

1. INTRODUCTION

Lung cancer remains one of the most lethal forms of cancer globally, accounting for an estimated 1.8 million deaths annually, according to the World Health Organization (WHO). It constitutes nearly 18% of all cancer-related deaths, making early detection and classification vital for patient survival. Among its types, non-small cell lung cancer (NSCLC) represents nearly 85% of cases, while small cell lung cancer (SCLC) accounts for the rest. The five-year survival rate remains below 20%, mainly

due to the lack of early diagnosis. With the advent of medical imaging technologies like CT scans and PET scans, the potential for automated classification using artificial intelligence has gained significant traction, especially to assist radiologists in handling large volumes of patient data efficiently. In recent years, hybrid models combining deep learning for image-based feature extraction with powerful machine learning classifiers like XGBoost for decision-making have demonstrated remarkable improvements in diagnostic accuracy. These models allow for better generalization and interpretation by learning features from image data while leveraging the robustness of gradient boosting frameworks. As healthcare systems worldwide strive for early detection tools that are not only accurate but also explainable, the integration of these technologies becomes indispensable in enhancing clinical decision-making processes for lung cancer diagnosis and treatment planning.

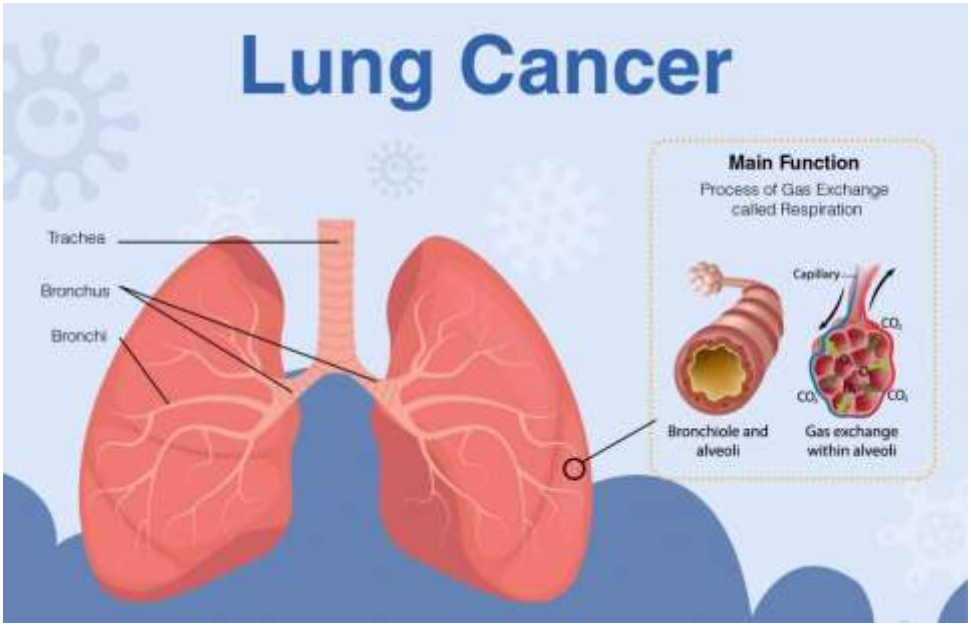

Fig. 1: Lung Cancer Prediction.

2. LITERATURE SURVEY

ALC is a malignancy originating from the lung cells, especially within the epithelial lining of the bronchi, bronchioles, or alveoli [1,2]. It is prevalent and associated with high mortality rates on a global scale. In its earliest stages, LC exhibits no symptoms or presents with moderate manifestations [2]. As a result, it is typically diagnosed in an advanced stage. The delayed identification of a medical condition affects the efficacy of treatment and diminishes the likelihood of achieving long-term survival [3]. The two common types of LC are non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC) [4]. NSCLC is commonly classified into two subtypes: lung squamous cell carcinoma (LUSC) and lung adenocarcinoma (LUAD) [4]. The fine-grained categorization of LC, including LUSC, LUAD, and SCLC, has a significant role in determining the prognosis of LC compared to benign and malignant classifications. The precise classification of LC at the primary diagnostic stage significantly improves therapy efficacy and subsequently increases patients' survival rate [5]. PET and CT are extensively employed as non-invasive diagnostic imaging modalities in clinical practice, serving as valuable tools for assessing the specific diagnosis of LC [6].

The early detection and treatment of LC through effective screening methods are vital in enhancing patient outcomes. Based on the National Lung Screening Trial findings, low-dose helical CT screening is more effective in reducing mortality among high-risk populations [7]. Nevertheless, the screening process for LC is susceptible to yielding false positive (FP) results, leading to increased costs due to unwarranted medical interventions and may induce psychological distress in individuals [8]. Computer-aided diagnosis has notable advantages in LC detection, including enhanced scope in

early cancer screening and a diminished occurrence of FP results throughout the diagnostic process [9].

In the realm of LC detection, there have been notable developments in the form of novel approaches and technologies for enhancing early diagnosis and treatment efficacy [10]. Liquid biopsies are used to examine blood samples for detecting cancers [11]. These diagnostic tests can identify genetic abnormalities and modifications associated with LC. Consequently, these tests offer a non-invasive approach to diagnosing the disease and monitoring the effectiveness of treatment. Low-dose computed tomography (LDCT) screening has emerged as a widely applied method for the timely identification of LC [12]. LDCT scans employ reduced radiation levels compared to conventional CT scans while delivering high-resolution images of the pulmonary region. Novel bronchoscopic methodologies, including electromagnetic navigation bronchoscopy and robotic-assisted bronchoscopy, facilitate the performance of minimally invasive lung lesion biopsies. These tools promote the prompt and precise identification of medical conditions. Integrating genomes, proteomics, and metabolomics has enabled the development of diverse strategies for identifying LC [13]. These methodologies employ several molecular markers to enhance diagnostic precision and discover possible targets for therapeutic intervention.

DL-based LC screening techniques can reduce mortality by detecting the disease in the primary stage [14]. It can aid in lowering false negatives (FN) by detecting subtle or early indicators of LC that humans may leave unnoticed [15]. Imaging modalities including CT, magnetic resonance imaging (MRI), and PET can be integrated using DL algorithms to understand the disease and assist in diagnosis and therapy planning. Cancer staging is directly related to the extent of disease metastasis [15]. A combination of imaging modalities and biopsies of suspicious tissue identifies cancer types. Cancer staging assists caregivers in selecting chemotherapy, immunotherapy, radiation, and surgical strategies [16]. In particular, the higher cancer stage increases the mortality rate. The effectiveness of medical therapies is based on the cancer stages. Providing more accurate and trustworthy diagnoses can help reduce misdiagnosis and unwarranted care. The process of LC screening produces substantial quantities of medical imaging data. DL models effectively analyze CT scans, chest radiography, and other imaging modalities due to their ability to analyze massive data [16,17,18]. Using DL models, physicians may gain insights into a patient's state by combining data from several imaging modalities and other clinical data sources.

Due to privacy concerns and the cost of data acquisition, medical image datasets are typically small. Pre-trained models can apply broader image dataset expertise to medical images, enabling model training with minimal medical data [19]. These models can extract hierarchical information from images, including fine-grained details and crucial patterns. Feature extraction supports the medical image classification models to detect significant patterns, abnormalities, and disease indicators [20]. The process of training CNN models from scratch can pose significant computing costs and require a substantial amount of time. The deep transfer learning technique reduces training time and time spent fine-tuning the model for medical image classification [21].

LC diagnosis and classification rely heavily on PET/CT imaging. PET and CT images are combined in PET/CT-based LC detection models to understand lung lesions' location, size, and metabolic activity. PET/CT scans are employed to monitor the efficacy of cancer treatment. The assessment of therapy success can be facilitated by tracking changes in metabolic activity and tumor growth over a period of time. Differentiating LC types and features with PET/CT imaging allows customized treatment. Bhandary et al. [20] developed a DL framework to detect LC using the CT images. Kanavati et al. [21] proposed a weekly-supervised learning-based model to identify lung carcinoma. Hallitschke et al. [22] built a multimodal LC lesion segmentation technique for annotating the images. They utilized the geodesic distance transformation technique and implemented an ellipsoid-based user simulation scheme. Ardila et al. [23] introduced an end-to-end LC screening model using LDCT

images. Marentakis et al. [24] proposed an LC histology classification technique. Similarly, the studies employed DL models for classifying the medical images to detect LC. Barbouchi et al. [25] introduced a deep neural network for LC classification. They obtained an accuracy of 97% in classifying the PET/CT images.

3. PROPOSED METHODOLOGY

The lung cancer detection framework leverages a combination of traditional machine learning, deep neural networks, and a hybrid model to provide a robust, accurate, and versatile diagnostic tool. By integrating multiple approaches, it balances simplicity and computational efficiency with the ability to capture complex patterns in CT images. The use of the hybrid CNN and XGBoost model enhances feature extraction and classification power, leading to improved prediction accuracy compared to standalone methods. The modular design allows the system to be adaptable for different datasets or related medical image classification tasks, making it highly applicable to varied clinical scenarios. Furthermore, the pipeline's inclusion of comprehensive metric calculations ensures thorough evaluation, enabling clinicians or researchers to assess model reliability effectively.

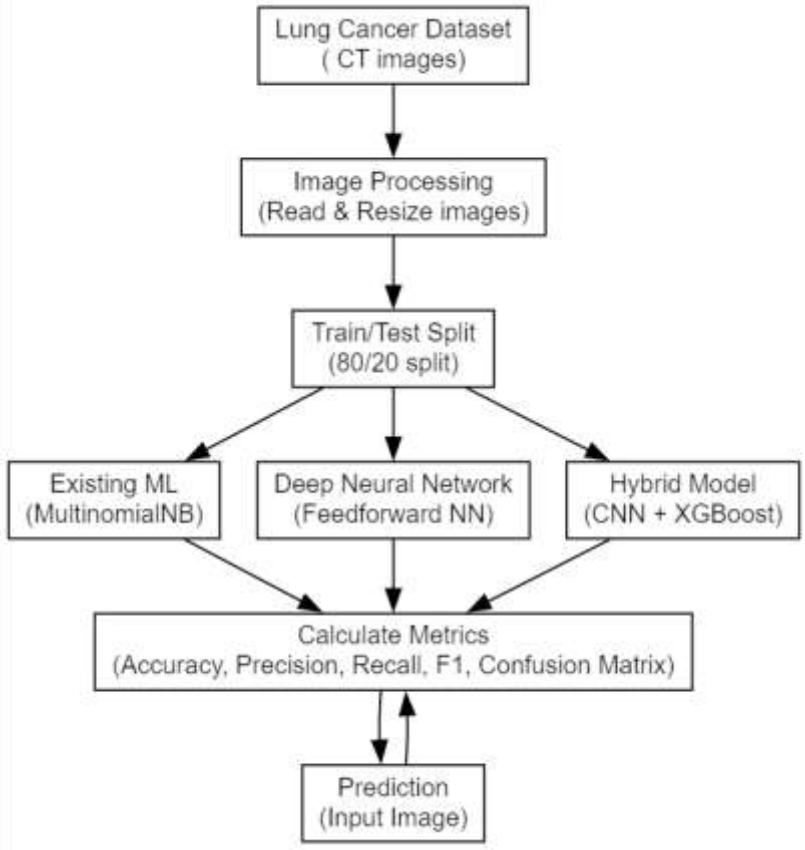

Fig. 2: Proposed System Architecture.

Image preprocessing

Image preprocessing is a critical step in computer vision and image analysis tasks. It involves a series of operations to prepare raw images for further processing by algorithms or neural networks. Here's an explanation of each step in image preprocessing:

Image Read: The first step in image preprocessing is reading the raw image from a source, typically a file on disk. Images can be in various formats, such as JPEG, PNG, BMP, or others. Image reading is performed using libraries or functions specific to the chosen programming environment or framework. The result of this step is a digital representation of the image that can be manipulated programmatically.

Image Resize: Image resize is a common preprocessing step, especially when working with machine learning models or deep neural networks. It involves changing the dimensions (width and height) of the image. Resizing can be necessary for several reasons:

Ensuring uniform input size: Many machine learning models, especially convolutional neural networks (CNNs), require input images to have the same dimensions. Resizing allows you to standardize input sizes. Reducing computational complexity: Smaller images require fewer computations, which can be beneficial for faster training and inference. Managing memory constraints: In some cases, images need to be resized to fit within available memory constraints. When resizing, it's essential to maintain the aspect ratio to prevent image distortion. Typically, libraries like OpenCV or Pillow provide convenient functions for resizing images.

Image to Array: In this step, the image is converted into a numerical representation in the form of a multidimensional array or tensor. Each pixel in the image corresponds to a value in the array. The array is usually structured with dimensions representing height, width, and color channels (if applicable).

For grayscale images, the array is 2D, with each element representing the intensity of a pixel. For color images, it's a 3D or 4D array, with dimensions for height, width, color channels (e.g., Red, Green, Blue), and potentially batch size (if processing multiple images simultaneously).

The conversion from an image to an array allows for numerical manipulation and analysis, making it compatible with various data processing libraries and deep learning frameworks like NumPy or TensorFlow.

Image to Float32: Most machine learning and computer vision algorithms expect input data to be in a specific data type, often 32-bit floating-point numbers (float32). Converting the image array to float32 ensures that the pixel values can represent a wide range of intensities between 0.0 (black) and 1.0 (white) or sometimes between -1.0 and 1.0, depending on the specific normalization used.

This step is essential for maintaining consistency in data types and enabling compatibility with various machine learning frameworks and libraries. It's typically performed by dividing the pixel values by the maximum intensity value (e.g., 255 for an 8-bit image) to scale them to the [0.0, 1.0] range.

Image to Binary: Image binarization is a process of converting a grayscale image into a binary image, where each pixel is represented by either 0 (black) or 1 (white) based on a specified threshold. Binarization is commonly used for tasks like image segmentation, where you want to separate objects from the background.

The process involves setting a threshold value, and then for each pixel in the grayscale image, if the pixel value is greater than or equal to the threshold, it is set to 1; otherwise, it is set to 0.

Binarization simplifies the image and reduces it to essential information, which can be particularly useful in applications like character recognition or object tracking, where you need to isolate regions of interest.

Proposed CNN Feature Extraction

This convolutional neural network (CNN) architecture with transfer learning leverages the power of pretrained models (such as ResNet) combined with additional convolutional layers to efficiently extract hierarchical features from images. It benefits from pretrained weights, which accelerates training and improves performance even with limited data by using learned representations from large datasets. The stepwise pooling reduces spatial dimensions, preserving essential features while lowering computational load. The final dense layers enable flexible classification according to the number of output classes. This approach is well-suited for application-specific image classification tasks, such as medical imaging, where both accuracy and computational efficiency are critical. Moreover, saving the model structure and training history supports reproducibility and future fine-tuning.

Model Initialization and Transfer Learning Setup The model starts by incorporating a pretrained network (e.g., ResNet) to benefit from its learned feature representations. This transfer learning step provides a robust feature extraction base, which can generalize well to the new dataset with fewer training epochs.

Adding Convolutional and Pooling Layers Additional convolutional layers with ReLU activation are added on top of the pretrained base to fine-tune the network for the specific classification task. Each convolutional layer is followed by max-pooling, which progressively reduces the spatial dimensions of the feature maps while retaining important information. This process helps the model focus on the most relevant features and reduces overfitting.

Flattening the Feature Maps After several convolution and pooling layers, the multidimensional feature maps are flattened into a one-dimensional vector. This step prepares the data for the fully connected layers by converting the spatial features into a format suitable for classification.

Dense Layers for Classification The flattened vector is fed into a dense (fully connected) layer with ReLU activation to learn non-linear combinations of the extracted features. Finally, the output dense layer with softmax activation produces probabilities corresponding to each target class, enabling multiclass classification.

Compilation and Training The model is compiled with an optimizer (Adam) and a loss function suitable for multiclass classification (categorical cross-entropy). It is then trained over multiple epochs on the training data, with validation data used to monitor performance and prevent overfitting. During training, the model adjusts its weights to minimize the loss and improve accuracy.

Saving Model and Training History After training completes, the model's weights and architecture are saved separately, enabling future loading and deployment without retraining. Additionally, the training history containing metrics like accuracy and loss over epochs is saved for analysis, helping in performance evaluation and tuning.

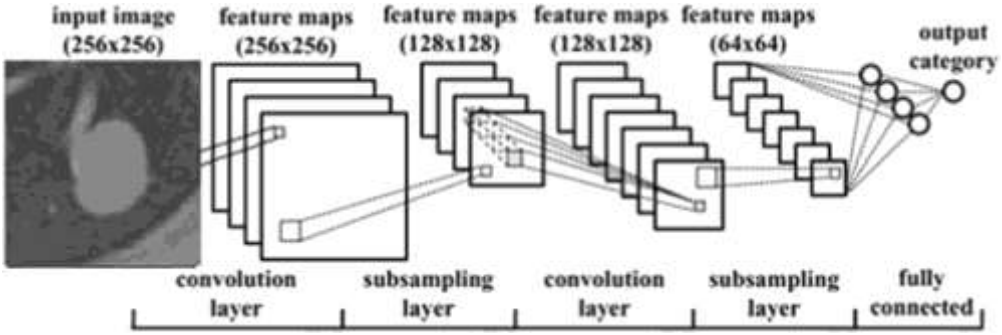

Fig. 3: CNN for Lung Cancer.

4. RESULTS AND DISCUSSION

Figure 4 presents the performance of the CNN with XGBoost model, achieving an accuracy of 91.11%, precision of 93.52%, recall of 90.42%, F1-score of 91.75%, sensitivity of 98.70%, and specificity of 88.46%. The classification report shows excellent class-specific results: adenocarcinoma (0.87, 0.96, 0.92), large cell carcinoma (0.96, 0.82, 0.88), normal (1.00, 1.00, 1.00), and squamous cell carcinoma (0.91, 0.83, 0.87). This model slightly outperforms the DNN, particularly in specificity and normal class detection.

CNN with Xgboost Accuracy : 91.11111111111111
CNN with Xgboost Precision : 93.52468652037615
CNN with Xgboost Recall : 90.41968053044003
CNN with Xgboost FScore : 91.74608131522747
CNN with Xgboost Sensitivity : 98.7012987012987
CNN with Xgboost Specificity : 88.46153846153845

CNN with Xgboost Classification Report

CNN with Xgboost	precision	recall	f1-score	support
adenocarcinoma	0.87	0.96	0.92	79
large cell carcinoma	0.96	0.82	0.88	28
normal	1.00	1.00	1.00	25
squamous cell carcinoma	0.91	0.83	0.87	48
accuracy			0.91	180
macro avg	0.94	0.90	0.92	180
weighted avg	0.91	0.91	0.91	180

Fig. 4: Performance evaluation of CNN with XGboost Classifier

This figure 5 shows the confusion matrix for the CNN with XGBoost model, illustrating its classification performance across the 180 test samples. The matrix likely shows fewer misclassifications compared to NBC, with strong performance for the normal class (perfect precision and recall) and improved predictions for adenocarcinoma and squamous cell carcinoma, aligning with the high accuracy of 91.11%.

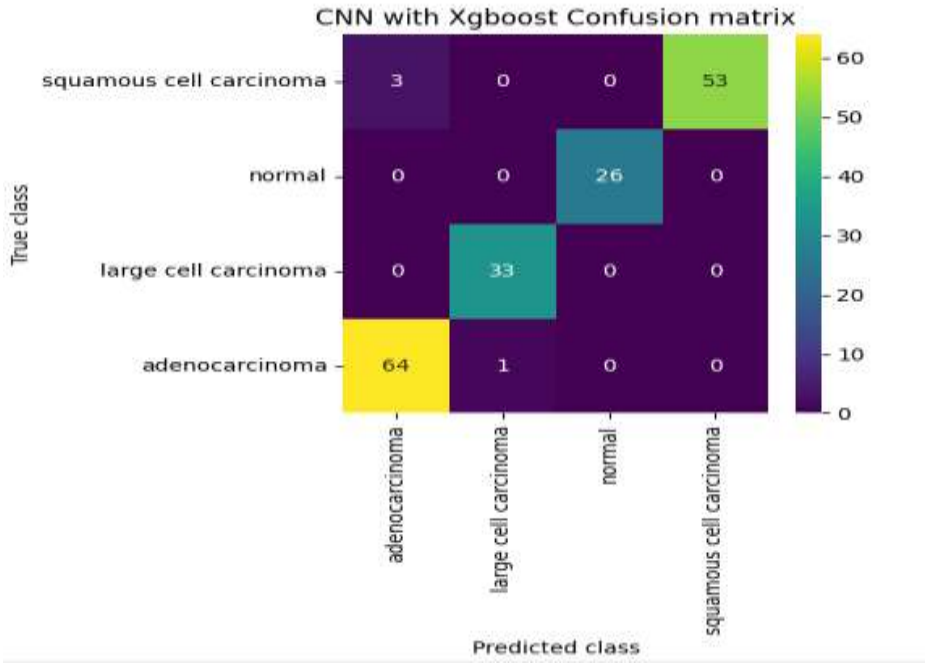

Fig. 5: Confusion matrix of Proposed CNN Model

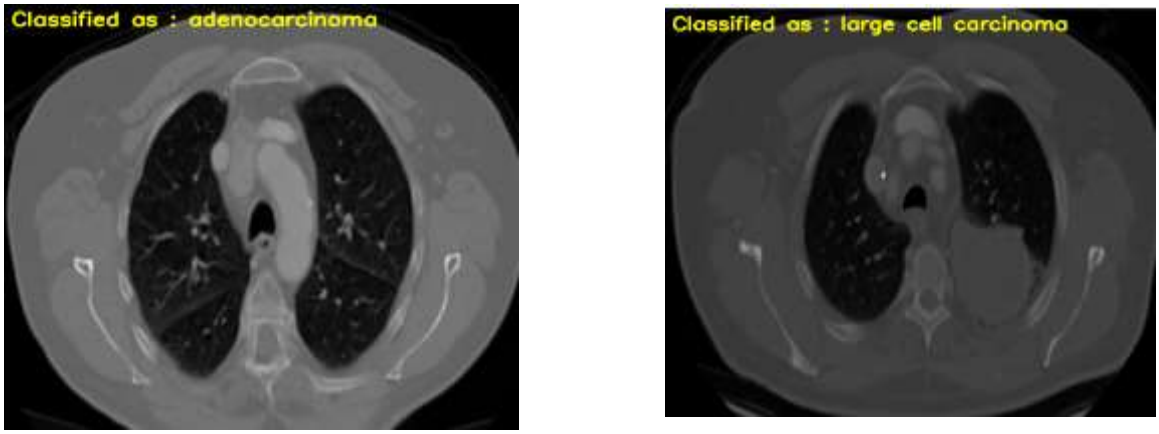

Fig. 6: Predicted output using CNN with XGBoost model

Figure 6 displays sample predictions from the CNN with XGBoost model, likely showing input images alongside their predicted class labels (e.g., adenocarcinoma, normal) and confidence scores. This figure demonstrates the model's practical application, highlighting its ability to accurately classify lung cancer types based on preprocessed images.

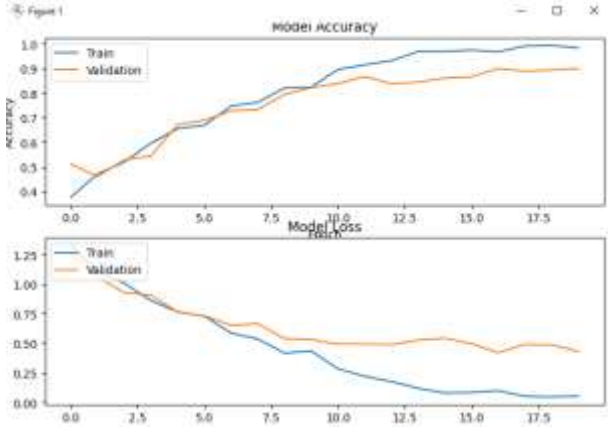

Fig. 7: Training and Validation Accuracy-Loss graph of CNN Model.

This figure 7 plots the training and validation accuracy and loss curves for the CNN model over epochs. It likely shows increasing accuracy and decreasing loss for both training and validation sets, indicating effective learning with minimal overfitting. The high validation accuracy aligns with the reported 91.11% test accuracy for the CNN with XGBoost model.

Table 1 Overall Performance Comparison.

Model	**Accuracy (%)**	**Precision (%)**	**Recall (%)**	**F1-Score (%)**	**Sensitivity (%)**	**Specificity (%)**
NBC	47.22	51.09	51.23	47.78	47.06	82.61
DNN	90.56	92.26	90.47	91.07	100.00	80.00
CNN with XGBoost	91.11	93.52	90.42	91.75	98.70	88.46

The Overall Performance Comparison Table 1 summarizes the performance of three models: NBC, DNN, and CNN with XGBoost. The NBC model performs poorly, with an accuracy of 47.22% and low sensitivity (47.06%), indicating it struggles to correctly identify positive cases. The DNN model significantly improves performance, achieving 90.56% accuracy, 100% sensitivity, and strong precision, recall, and F1-scores, making it effective for lung cancer detection. The CNN with

XGBoost model slightly outperforms the DNN, with a 91.11% accuracy, higher specificity (88.46%), and balanced precision and recall, indicating robust generalization across classes.

5. CONCLUSIONS

An in-depth analysis of the lung cancer detection dataset comprising 900 chest CT images across four classes (adenocarcinoma, large cell carcinoma, squamous cell carcinoma, and normal) highlights clear performance differences among the three evaluated models: Naive Bayes Classifier (NBC), Deep Neural Network (DNN), and a hybrid Convolutional Neural Network (CNN) integrated with XGBoost. The NBC model performed poorly, with an overall accuracy of just 47.22%. It struggled notably with adenocarcinoma (recall: 0.24) and large cell carcinoma (precision: 0.36), indicating its limitations in handling the complexity of medical image classification. In comparison, the DNN model delivered a substantial improvement, achieving 90.56% accuracy, 100% sensitivity, and excellent class-specific results especially for normal tissues, where it recorded an F1-score of 0.98. Slightly outperforming the DNN, the CNN with XGBoost model demonstrated the highest overall performance, reaching 91.11% accuracy, 93.52% precision, and an F1-score of 91.75%. It achieved perfect classification for the normal class (F1-score: 1.00) and showed strong performance in detecting adenocarcinoma (F1-score: 0.92). This superior result is credited to CNN's powerful feature extraction capabilities combined with XGBoost's robust ensemble learning, enabling more accurate and nuanced classification.

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