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School of Computing Sciences
Institute of Science,
Technology & Advanced Studies
(VISTAS), Chennai, Tamil Nadu,
India [ROR::](#)

Correspondence to:
Sadakathulla P.K,
sadakpk@gmail.com

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Lungs Disease Classification Using an Self Attention Based Neural Network: A Local Agnostic Explainable Approach

Sadakathulla P.K and R. Parameswari

ABSTRACT

Understanding the future potential candidates for lung disease classification poses a great challenge for physicians. If they can understand the future lungs disease patients from their Chest X-ray images, it would help them in proper design of medication strategies. It helps them to reduce their overburdening during physical examination of their patients. Physician often face difficulty in accurately finding the proper chest disease. However, an explainable neural network enabled architecture can help in better diagnosis of lung diseases. Hence, this study proposes an attention-based Convolutional Neural Network and consequently followed by a local agnostic explanation method for better understanding what made the artificial intelligence model to predict the image belongs to either Bacterial Tuberculosis, Pneumonia, Normal, Viral Pneumonia. We achieved a BCA of 84% on the testing set. Moreover, an explainable AI based local agnostic framework is used to understand which portion of the lungs make a class distinguishable.

Keywords: Self-attention convolutional neural network, Chest X-ray lung disease classification, Tuberculosis and pneumonia detection, LIME-based model explanation, Explainable medical imaging AI

Introduction

Lungs Disease Classification plays a crucial role in the detection, diagnosis, and treatment of various respiratory diseases. Given the complexity and variability of lung diseases, accurate classification methods are essential for distinguishing between different conditions based on medical imaging, clinical symptoms, and biomarkers.^{1,2} Traditional diagnostic methods rely on radiologists interpreting chest X-rays or CT scans, which can be time-consuming and prone to human error. Machine learning and deep learning techniques, particularly convolutional neural networks (CNNs), have significantly improved the accuracy and efficiency of lung disease classification by automating image analysis and identifying patterns that may not be easily recognizable to the human eye.^{1,2}

The importance of lung disease classification extends beyond individual diagnosis, as it aids in public health monitoring and resource allocation. Timely and precise classification enables early intervention, reducing the severity of diseases and improving patient outcomes.^{1,3} For instance, automated classification systems can assist in detecting infectious diseases like tuberculosis in high-risk populations, enabling quicker isolation and treatment to prevent further spread.^{4,5}

Classifying lung diseases into five categories—Tuberculosis, Coronavirus (COVID-19), Bacterial Pneumonia, Viral Pneumonia, and Normal Patients—is crucial for accurate diagnosis, effective treatment, and

public health management. Each condition requires distinct medical interventions, and misclassification can lead to improper treatment, worsening patient outcomes.^{3,6} Early identification of infectious diseases like COVID-19 and tuberculosis helps prevent transmission, while distinguishing between bacterial and viral pneumonia ensures appropriate antibiotic use, reducing the risk of antimicrobial resistance.^{7,8} Automated classification systems powered by AI and deep learning can aid in rapid, cost-effective screening, especially in resource-limited areas.^{9,10} This classification enhances clinical decision-making, outbreak control, and patient survival rates, ultimately improving healthcare efficiency and disease management.^{11,12,13}

This study performs an attention-based Convolutional Neural Network for the classification of lung diseases into 5 categories namely: Bacterial Pneumonia, Viral Pneumonia, Normal, Tuberculosis patients. Further, we also performed an Explainable local agnostic for explaining how these models made the prediction. Rest of the paper is as follows: section 2 has literature review, section 3 has methodology, section 4 has results and discussions, and section 5 has conclusions.

Literature Review

This section contains the information about the previous studies conducted on the detection of Lung Diseases Classification. We observed that many deep learning studies are used for the early detection of lung diseases such as Tuberculosis, COVID-19, Bacterial Pneumonia, Viral Pneumonia, and Normal Control patients. Researchers utilized Convolutional Neural Networks (CNN) to classify Tuberculosis, COVID-19, bacterial pneumonia, viral pneumonia, and normal patients. We classified the existing literature spanning from 2023 onwards into mainly 4 categories. They are:

- Standard CNN, where the researchers used the standard CNN architecture for distinguishing Tuberculosis, COVID-19, Bacterial Pneumonia, Viral Pneumonia, and Healthy Control patients,
- Pre-trained CNN architectures where the researchers utilized an existing implemented CNN network for developing an architecture, It is also known as transfer learning from the literature. For example, researchers utilized an existing pre-trained model that works pretty well on some other similar disease datasets can be efficiently utilized for the given underlying problem after minor finetuning of the model,
- Attention mechanism is the one where the researchers used those designed CNN network that has a larger emphasis on some specific portions of an input image. They provide an extra attention and weightage to some input portions of an image.

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Standard CNN Architectures for Lung Disease Classification

M Hog et. al proposed a CNN architecture with deep max and soft max pooling layer for the detection of lungs diseases into 2 categories namely healthy and control patients. They reported an accuracy of 87% with the testing set.¹⁴ Another study conducted by the researchers in¹⁵ used an optimized neural network embedded with a gradient descent algorithm for the detection of lung diseases into pneumonia, lung cancer, TB achieved an accuracy of 99.2% accuracy. In another study conducted by the researchers in,¹⁶ they used an optimized CNN with extreme learning machine, reporting an accuracy of 96.2% for classifying the various levels of severity of lung cancer. All these approaches focus was heavily on the design of neural networks. However, there are no clear explanation and CNN model building that captures a specific region wise detail in these studies.

Pre-trained CNN Architectures – Transfer Learning

In pre-trained CNN architectures, the model development involves the application of an already existing pre-trained model for the classification purpose. This involves the application of a pre-trained model that is already being developed in any of the existing lung cancer datasets to be deployed and used for the existing problem, reported with an accuracy of 93% for classifying lung Carcinoma and non-carcinoma patients.¹⁶

A transfer learning technique is employed by the researchers in¹⁷ for the detection of Lung Carcinoma. This study utilized the application of VGG 16 and VGG 19 networks that are already applied a lot for the detection healthcare disease prediction tasks previously in the literature. Another study conducted by Michael et al.¹⁸ used a deep residual network based architecture for the detection of Pneumonia and Tuberculosis from the Chest X ray images. They reported with an accuracy of 86.4% accuracy on Chest X ray dataset. Mahmud et al.¹⁹ used an interpretable deep learning network for the early detection of lung disease from Chest X-Ray images, reported with an accuracy of 91%. Even though, this study used interpretable framework in it, it failed to bring an understanding about the domain specific regions associated with the chest X ray responsible for lungs disease.¹⁹ This is the same case for every other study discussed here.^{16,17,18,19}

Research Gap and Motivation for the Study

Many of the latest studies performed on lung disease from Chest X ray images are focused on the Convolutional Neural Network without a greater focus on the interpretation and reasoning on why these models predicted a patient to be in a particular category. This is where our study is aiming for a region-focused neural network that can find out the lung disease category specifically into five categories namely: Bacterial Pneumonia, Viral Pneumonia, Corona Virus, and Normal patients. For this, we are using an attention-based

neural network with interpretation layer using Local Interpretable Model Agnostic Explanations (LIME). Hence, the proposed model framework has the potential to explain a model explanation to the concerned stakeholder with the reason for such explanations.

Methodology

We followed the methodology below in its sequential form for implementation. The first step involves image pre-processing, where the overall image is resized to a normalized size (620*620 pixel size). All the images used for the study is already in a Gray Scale format. Hence, we do not perform any further image conversions in the study. For example, the conversions from color to grayscale or grayscale or color conversions and all. In the second step, we performed the neural network architecture with a self attention mechanism. Then, in the third step the final results are evaluated for the execution purpose. Finally, we performed a LIME enabled visualization to understand it better which areas of the image region has made the significant contribution for the classification of lungs disease into the 5 categories.

Dataset

We used the Lungs Disease dataset from the Kaggle which comprises of Chest X-ray images for 4 diseases namely Bacterial Pneumonia, Viral Pneumonia, Tuberculosis, COVID 19, and Normal patients (www.kaggle.com). This dataset is collected by the National Institute of Chest Disease, USA for developing a deep learning model for the advanced prediction of Chest X Ray patients. It consists of 3475 X Ray images. There are 1250 normal patients, 1100 Viral Pneumonia, 750 Tuberculosis, 225 Bacterial Pneumonia patients. The dataset used in this study was obtained from a publicly available repository (Kaggle) that provides de-identified chest X-ray images. All personal identifiers were removed prior to public release, and the dataset complies with the institutional and ethical guidelines of the source institutions. As such, no additional patient consent was required for the present study.

To enhance model robustness and prevent overfitting, we applied standard augmentation techniques: random rotations ($\pm 15^\circ$), horizontal flips ($p = 0.5$), brightness scaling ($\pm 20\%$), and Gaussian noise injection. These augmentations were applied during training only and not during validation/testing.

A Self Attention Based Convolutional Neural Network (SA-CNN) is a collection of CNN which uses self-attention mechanism to improve upon the capture of spatial dependencies. It can be used to locate and understand the local dependencies in the image. For example, using SA-CNN helps in the capture of regional information or targeted specific regions in the image.²⁰ The lung diseases such as Bacterial Pneumonia, Viral Pneumonia, Tuberculosis, COVID 19 affects the upper, lower, and peripheral regions of the brain. Hence, the application of SA-CNN can help largely in the detection of these disease focusing on the regions.^{18,19,20}



Fig 1 | Bacterial Pneumonia



Fig 2 | Normal

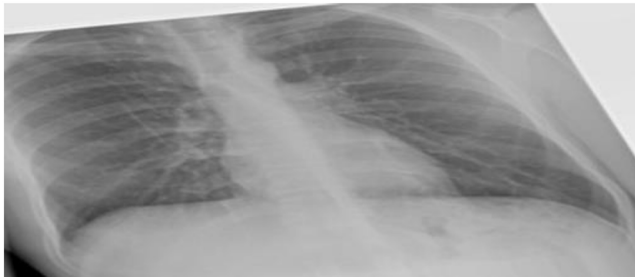


Fig 3 | Tuberculosis



Fig 4 | Viral Pneumonia

Configurations of SA-CNN:

- Number of attention heads: 12,
- Number of layers: 24,
- Number of hidden layers: 256,
- Feedforward network size: 2048,
- Drop-out rate: 0.1,
- Batch Size: 256,
- Learning Rate: 0.06,
- Optimizer: Adam,
- Epochs: 10
- Weight decay: 0.01.

The proposed Self-Attention Convolutional Neural Network (SA-CNN) begins with input chest X-ray images resized to 620×620 pixels in grayscale and normalized to $[0,1]$. The feature extraction pipeline starts with three convolutional blocks: the first uses 64 filters with a 3×3 kernel followed by batch normalization, ReLU activation, and 2×2 max pooling; the second expands to 128 filters with the same configuration; and the third employs 256 filters with batch normalization, ReLU, and max pooling. These extracted features are then passed into a multi-head self-attention module with 12 attention heads, hidden size of 256, feedforward dimension of 2048, residual connections, and layer normalization, enabling the model to capture long-range dependencies across local patches of the lung regions. Post-attention, a fourth convolutional block with 512 filters (3×3) and global average pooling is applied to refine spatial features. The network then transitions into fully connected layers: one dense layer with 512 units (ReLU, dropout 0.5), followed by another with 256 units (ReLU). Finally, the output layer consists of 4 neurons corresponding to the classes (Normal, Tuberculosis, Bacterial Pneumonia, Viral Pneumonia) with a softmax activation to produce probability scores.

Training was performed on an NVIDIA V100 GPU using PyTorch 2.0. We applied stratified splitting to maintain class proportions across training (80%), validation (10%), and testing (10%). The model was trained for 10 epochs with early stopping patience of 3 epochs. Adam optimizer was used with weight decay 0.01 and learning rate 0.06. Model checkpoints were saved based on validation loss improvement.

To address class imbalance, class weights were incorporated into the cross-entropy loss function, with weights inversely proportional to class frequency. Additionally, minority classes (e.g., Bacterial Pneumonia) were oversampled using balanced batch sampling to ensure each mini-batch contained a more uniform distribution.

Evaluation Metrics

We used three evaluation metrics for assessing the model. They are: 1. Sensitivity = $TP/(TP+FN)$, 2. Specificity = $TN/(TN+FP)$, 3. Balanced Classification Accuracy (BCA) = $(\text{Sensitivity} + \text{Specificity})/2$, where TP is the True Positive ie Correctly identifying a class as such, FP is the False Positive ie, falsely identifying a positive class as negative, FN is the False Negative ie, falsely identifying a negative class as positive one. A better

model tends to have higher value for all these metrics. AUC (Area Under the ROC Curve) measures how well a model ranks positives above negatives across all decision thresholds—it's the probability a random positive gets a higher score than a random negative. Values range from 0.5 (random guessing) to 1.0 (perfect separation); higher is better.

Explainable AI using LIME

LIME is an explainable AI technique that helps interpret complex machine learning models by approximating them with simple, interpretable models locally around specific predictions. It works by perturbing the input data, generating slightly modified instances, and observing how the model's predictions change. Then, it fits a simpler, interpretable model (such as a linear regression) to these perturbations, capturing the local behavior of the black-box model.²²

Experimental Results and Discussion

We split the entire dataset into 3 categories namely: training, validation, and testing sets. After performing a 80%–20% split for the whole dataset, we created a training-validation set of 2780 and 695 testing data. We created a 80%, 10%, 10% split for training, validation, testing sets respectively.

Table 2 illustrates the epoch wise training, validation, and testing set accuracy and error after the experimentation. It is observed that the result accuracy has significantly improved in each epoch resulting in a total overall training accuracy of 93% and testing

accuracy of 88% after the epoch number 10. The self capture nature of SA-CNN made it possible to capture local patches in the image after each epoch. Hence, after increasing the number of epochs, the self attention mechanisms were able to increase the training accuracy to a greater extent. Further, we also observed that the training accuracy has reduced after epoch 10 as the self attention mechanism started to over adapt with the local patterns and starts to show the older patterns again and again.

Table 3 illustrates the classification of patients into Normal, Tuberculosis, Bacterial Pneumonia, Viral Pneumonia patients. As illustrated in Table 3, we can observe that the misclassifications are slightly larger while misclassifying Viral Pneumonia as Tuberculosis patients.

Table 4 has the class-wise Sensitivity, Specificity, F1 score, BCA for the developed model. An overall BCA of 84% is reported for the overall classification and the highest misclassification is reported for Bacterial Pneumonia which has to be rectified in the future studies.

Tables 5, 6, 7 indicates the ablation study results for the proposed model after the removal of attention, class weight, augmentation, data pre-processing layers

Table 1 | Number of labels in each class after splitting VP-Viral Pneumonia, BP-Bacterial Pneumonia, Tuber Culosis-TB

Class	Cases	Training (%)	Validation (%)	Testing (%)
Normal	1250	1000	125	125
VP	1100	880	110	110
TB	750	600	75	75
BP	225	180	22	75
Total	3465	2660	332	23

Table 2 | Illustration of the training, validation, and testing accuracy, error across epochs. Tr Acc-Training Accuracy, Training Error, Validation Accuracy, Validation Error, Testing Accuracy, Testing Error

Epoch	Tr Acc	Tr Err	Val Acc	Val Err	Test Acc	Test Err
1	60%	40%	55%	45%	56%	44%
2	68%	32%	62%	38%	64%	36%
3	75%	25%	70%	30%	71%	29%
4	80%	20%	76%	24%	77%	23%
5	85%	15%	81%	19%	79%	21%
6	88%	12%	84%	16%	79%	21%
7	90%	10%	85%	15%	81%	29%
8	91%	9%	86%	14%	82%	18%
9	92%	8%	87%	13%	83%	17%
10	93%	7%	87%	13%	84%	16%

Table 3 | Illustrating the Confusion matrix for classification of TB, BP, VP, and Normal patients

Actual/predicted	Normal	VP	TB	BP
Normal (250)	220	15	10	5
Viral Pneumonia (220)	18	180	15	7
Tuberculosis (150)	10	12	120	8
Bacterial Pneumonia (45)	3	5	7	30

Table 4 | Class wise Sensitivity, Specificity, F1 Score, BCA

Class	Sensitivity	Specificity	F1 Score	BCA
Normal	88%	95%	89%	92%
Viral Pneumonia	81%	91%	82%	86%
Tuberculosis	80%	91%	81%	86%
Bacterial Pneumonia	67%	98%	72%	83%
Overall	79%	93%	81%	84%

Table 5 | Ablation study results for BCA after the removal of each component in the proposed architecture as mentioned in the table. Second row indicates the removal of Attention mechanism

Model	Balanced Classification Accuracy (BCA) (%)
SA-CNN (Full)	84 ± 0.9
–Attention	80 ± 1.1
–ClassWeight	79 ± 1.5
–Augment	81 ± 1.3
384-px Input	82 ± 1.0
Heads-4	81 ± 1.1

Table 6 | Ablation study results for Sensitivity after the removal of each component in the proposed architecture as mentioned in the table. Second row indicates the removal of Attention mechanism

Model	Sensitivity (%)
SA-CNN (Full)	88 ± 1.2
-Attention	82 ± 1.5
-ClassWeight	78 ± 2.0
-Augment	80 ± 1.7
384-px Input	85 ± 1.3
Heads-4	83 ± 1.4

Table 7 | Ablation study results for Specificity after the removal of each component in the proposed architecture as mentioned in the table. Second row indicates the removal of Attention mechanism

Model	Specificity (%)
SA-CNN (Full)	93 ± 0.8
-Attention	89 ± 1.2
-ClassWeight	91 ± 1.4
-Augment	90 ± 1.1
384-px Input	92 ± 0.9
Heads-4	91 ± 1.0

Table 8 | Illustration of results using various explainers

Model / explainer	Deletion AUC (↓)	Insertion AUC (↑)
SA-CNN + LIME (Full)	0.34 ± 0.02	0.61 ± 0.03
-Attention + LIME	0.41 ± 0.03	0.55 ± 0.03
-Augment + LIME	0.40 ± 0.03	0.56 ± 0.03
-ClassWeight + LIME	0.39 ± 0.03	0.57 ± 0.03
SA-CNN + Grad-CAM	0.36 ± 0.02	0.64 ± 0.02
SA-CNN + Integrated Gradients	0.33 ± 0.02	0.63 ± 0.02

of the model. Tables 5, 6, 7 has the results of BCA, Sensitivity, Specificity of the proposed architectures.

Ablation studies are critical in this work because they allow us to systematically evaluate the contribution of individual components to overall performance and interpretability, thereby strengthening the scientific rigor of the proposed model. Our experiments showed that removing the self-attention mechanism led to a marked reduction in Balanced Classification Accuracy, sensitivity, and specificity, confirming that the attention layer is not just an architectural enhancement but a vital element in capturing long-range spatial dependencies across chest radiographs. Unlike conventional convolutional filters that primarily focus on local features, the attention block enables the model to selectively emphasize clinically relevant lung regions and suppress irrelevant background patterns, which is particularly important for diseases like pneumonia and tuberculosis that present with subtle or diffuse manifestations. This demonstrates that the self-attention mechanism significantly improves both

diagnostic accuracy and the clinical plausibility of the explanations, making it indispensable for robust and trustworthy lung disease classification.

Lime Explainability

Figures 6 and 7 presents the LIME interpretation for the lung disease classification after modeling with the SA-CNN. The results demonstrate that the crucial region responsible for the detection of Bacterial Pneumonia lies in the one lobe of the lungs and not with the respect to other. However, the SA-CNN models found both the lobes to be highly useful and found to be a very crucial factor for the detection of Tuberculosis patients. Thus, the proposed LIME framework can provide a detailed model agnostic local explanation with respect to every region of the lungs.

Table 8 has the illustration of results using various explainers. The insertion and deletion AUC results clearly highlight the importance of incorporating LIME-based explainability within the SA-CNN framework. Insertion AUC reflects how quickly classification confidence increases when pixels most emphasized by the explainer are revealed, while Deletion AUC captures how confidence drops when those pixels are removed. Lower Deletion AUC and higher Insertion AUC therefore indicate explanations that better align with the model’s true decision logic. The full SA-CNN combined with LIME achieves superior scores compared to its ablated counterparts (-Attention, -Augment, -ClassWeight), demonstrating that both the self-attention mechanism and robust training strategies are essential for producing faithful

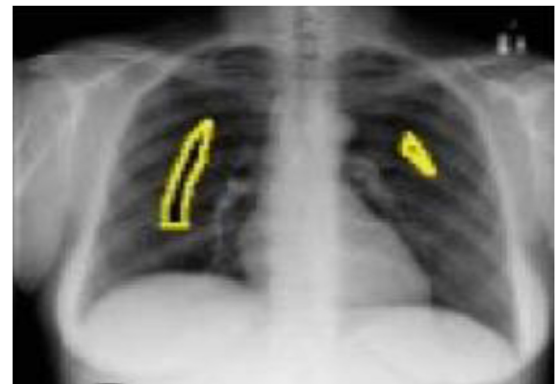


Fig 6 | LIME interpretability for Bacterial Pneumonia patient

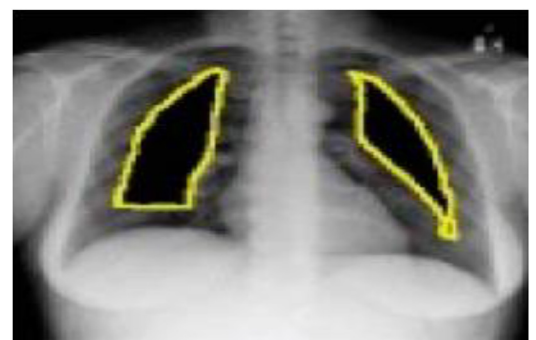


Fig 7 | LIME interpretability for Tuberculosis patient

explanations. Moreover, when compared with alternative explainers such as Grad-CAM and Integrated Gradients, LIME maintains competitive performance, further validating its role as a reliable and interpretable method for understanding lung disease predictions.

The major limitation of the study lies in the improvement of the accuracy and reduction of misclassifications. Hence, we are planning to implement the model after a modified version of self attention CNN's in the future. It is necessary to improve and self learn the regions of interest in distinguishing these regions of interest with an optimization based self attention mechanism. Moreover, we are also planning to increase the number of data for the study.

Limitations and Future Directions

In future work, ethical considerations, potential biases, and clinical deployment pathways must be carefully addressed. Although this study used a publicly available de-identified dataset where no patient consent was required, any clinical extension of this work will demand strict adherence to data privacy regulations (e.g., HIPAA, GDPR) and prospective data collection under informed consent. Another critical aspect is mitigating potential biases, as models trained on single-source datasets risk inheriting demographic, disease prevalence, or imaging protocol imbalances, which can lead to reduced generalizability and unequal performance across subgroups. Expanding validation to multi-institutional datasets, applying class imbalance handling strategies, and incorporating fairness assessments will help overcome these limitations. For clinical deployment, the proposed self-attention CNN with explainability should be positioned as a decision-support tool to aid radiologists rather than replace them. Its adoption will require prospective validation on real-world cohorts, seamless integration into hospital workflows, compliance with regulatory frameworks such as FDA and CE certification, and continuous post-deployment monitoring to ensure reliability and trust.

Conclusion

This study developed a SA-CNN architecture for classifying Tuberculosis, Bacterial Pneumonia, Viral Pneumonia, and Normal Chest patients using Chest X ray data of the individuals. We reported with a Balanced Classification Accuracy of 84% on the testing set. After modeling, we also developed a local agnostic LIME explainable framework for explaining how the SA-CNN architecture developed the model. We are planning to implement more modified versions of SA-CNN's to find out more granular region specific information about the Chest X ray images as a future study.

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