Hybrid Learning Approach for COVID-19 Lung Infection Segmentation using CT Imaging

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Abstract - *The global spread of COVID-19 put significant pressure on healthcare systems, making early diagnosis essential to save lives and limit further transmission. Chest CT scans are effective for detecting lung infections, but manual analysis is time- consuming and depends on the radiologist's experience, which can delay treatment or lead to inconsistent interpretations. To address this, we propose a deep learning–based system that can automatically detect and segment COVID-19–infected regions in CT scans using a single end-to-end model. Our method is robust to varying lesion sizes, shapes, and image quality, including noise and low contrast. Experiments on public CT datasets demon- strate high accuracy for both segmentation and classification tasks. This system can support radiologists by reducing manual effort, speeding up diagnosis, and helping patients receive timely treatment, especially during pandemic peaks.*

***Keywords**: Pandemic Lung Screening, Chest CT Interpretation, CNN, Lesion Segmentation, AI Classification.*

INTRODUCTION

COVID-19 has emerged as one of the most significant global health crises, spreading rapidly across continents and placing immense pressure on healthcare infrastructure. Early detection of infection is critical for breaking the chain of transmission, enabling timely intervention, and reducing mortality rates. Although RT-PCR testing has been widely adopted as the primary diagnostic method, it has certain limitations despite its extensive use. It has limited sensitivity coupled with delays in result reporting which has spurred the inclusion of chest computed tomography CT as an adjunct diagnostic strategy CT imaging offers gross anatomy visualization of the lungs and can detect infection-associated patterns like ground-glass opacities and consolidations at an early stage but manually interpreting CT scans is a time consuming expert- dependent process where radiologists need to carefully inspect multiple slices per patient this comes with the risk of variability in diagnosis and possible delays in clinical decision-making particularly at pandemic peaks when volumes are high precise segmentation of infected lung areas is an important step for quantitative analysis but it remains challenging owing to the lesion's irregular morphology low contrast between infected and normal tissues and noise and artifacts in the images traditional image processing methods like thresholding and region-growing lack robustness and tend to need manual fine-tuning making them unsuitable for extensive screening deep learning approaches in particular convolutional neural networks CNN and attention- based models have shown great promise in automating this step by learning discriminative features directly from data and delivering reliable and reproducible results in this paper we present an end-to-end deep learning architecture that performs segmentation as well as classification of covid-19-infected areas on chest CT scans with the goal of providing fast accurate and consistent results that assist radiologists streamline diagnosis and enhance patient management during critical high- demand periods.

REVIEW OF EXISTING WORK

Medical image analysis has been greatly advanced by deep learning, and during the COVID-19 pandemic, researchers worldwide adopted these methods to improve the accuracy, speed, and reliability of lung infection detection. The literature reveals an evolution from initial image processing techniques to current neural network–based segmentation systems.

Ding et al. [1] introduced CDSEUNet, a novel U-Net variant that integrates Canny edge detection with dual-path SENet feature fusion. This combination enables the network to capture fine lesion boundaries and increase noise robustness, effectively handling lesions of varying sizes commonly seen in COVID-19 CT scans. Their work highlights the benefits of combining classical edge detection with deep learning to enhance segmentation accuracy.

Duan et al. [2] proposed a multi-task network for un- supervised 3D cardiac segmentation that incorporates land- mark localization to ensure anatomically consistent contours. Although developed for cardiac MRI, this anatomy-aware approach is highly relevant for lung CT analysis, where precise infection boundary localization is crucial for medico legal considerations.

Fan et al. [3] developed InfNet, one of the earliest semi- supervised models for COVID-19 lung infection segmentation. Their architecture employs modules such as the Parallel Partial Decoder, Reverse Attention, and Explicit Edge Attention, which enable effective performance despite limited annotated data during the early pandemic. This study demonstrated that semi-supervised methods can achieve competitive accuracy with scarce supervision.

Florin [4] introduced Marginal Space Deep Learning (MSDL), combining hierarchical marginal space learning with deep networks to improve volumetric image parsing. Although not specifically designed for COVID-19, this approach reduces computational complexity in high-dimensional imaging, offering valuable efficiency insights for real-time segmentation.

Guo et al. [5] addressed multimodal medical image segmentation by fusing MRI, CT, and PET data using a CNN-based approach. Their findings suggest that integrating multiple imaging modalities enhances robustness and reproducibility. While multimodal datasets may not always be available for COVID-19 CT scans, this work underlines the potential of feature fusion for improved performance.

Hu et al. [6] developed a hybrid attention-based segmentation network for lung tumor imaging. By incorporating spatial and channel attention modules, the network effectively focuses on elongated and subtle lesions. This attention mechanism is particularly applicable to COVID-19 infections, where lesions may appear faint or overlapping.

Lafci et al. [7] explored CNN-based segmentation for opt acoustic and ultrasound imaging. Despite modality differences, their results indicate that well-designed CNN architectures possess strong transferability across medical imaging tasks, suggesting adaptability for COVID-19 CT analysis.

Ngo et al. [8] proposed treating retinal layer segmentation as a regression task rather than classification, improving precision while balancing computational demands. Efficiency-oriented architectures like this are valuable for large-scale COVID-19 screening where rapid analysis is essential.

Oksuz et al. [9] tackled motion artifacts in cardiac MRI using a deep learning framework that simultaneously detects, corrects, and segments corrupted images. Since CT scans are similarly affected by noise and artefacts, such integrated correction could enhance lung CT segmentation accuracy.

Roy et al. [10] applied spatial transformer networks for COVID-19 biomarker detection in lung ultrasound images. Their model showed robustness despite limited supervision and variable image quality, crucial for real-world clinical deployment where data heterogeneity is common.

Sun et al. [11] introduced an anatomy-guided attention mechanism for MRI segmentation, incorporating anatomical priors to ensure biologically consistent segmentation and reduce false positives. Such anatomically informed models are highly valued clinically for improving diagnostic accuracy.

Wang et al. [12] proposed a Prior-Attention Residual Learning framework for COVID-19 CT screening, combining attention mechanisms and residual learning to enhance feature discrimination while maintaining practical efficiency for large- scale hospital screening environments.

Yao et al. [13] developed an unsupervised shape-prior- based segmentation model tailored for scenarios with limited labeled data. Label-free approaches like this are especially useful during pandemics or in low-resource settings where annotations are scarce, enabling scalable deployment without extensive manual labelling.

Zhang et al. [14] introduced BigAug, a stacked transformation–based data augmentation strategy to improve domain generalization. Given that COVID-19 CT datasets often come from diverse scanners and hospitals, robust augmentation is critical to maintaining cross-domain consistency.

Zhou et al. [15] presented an attention-augmented U-Net for COVID-19 lung CT segmentation. By integrating spatial and channel attention modules, their model improved sensitivity and specificity while remaining computationally efficient, enabling near real-time clinical application.

EXISTING SYSTEM

Earlier approaches for detecting and segmenting lung infections from CT images primarily relied on traditional image processing techniques and initial computer-aided diagnosis systems. These methods included clustering, thresholding, edge detection, and region-based segmentation techniques.

A. Clustering Methods

Clustering techniques group pixels with similar characteristics such as intensity, color, or texture into clusters. K-means clustering has commonly been used to distinguish infected regions from healthy lung tissue in CT scans. Although these algorithms are simple and computationally efficient, they are highly sensitive to noise and require proper initialization of cluster centers. Inappropriate initialization often results in sub- optimal segmentation outcomes.

B. Thresholding Methods

Thresholding converts CT images into binary representations based on pixel intensity values. Pixels with intensities above a predefined threshold are classified as infected regions, while others are treated as background. Global thresholding is computationally inexpensive but performs poorly when there are intensity variations or illumination changes across the scan. Local thresholding improves flexibility; however, it struggles when the intensity levels of healthy and infected tissues overlap.

C. Edge Detection Techniques

Edge-based approaches identify infection boundaries by detecting abrupt changes in pixel intensity. Conventional operators such as Sobel, Canny, and Prewitt have been used to delineate infected areas. However, in noisy or complex CT images, these operators often produce incomplete or fragmented boundaries, limiting their clinical reliability.

Region-growing and split-and-merge algorithms attempt to form meaningful regions by grouping neighboring pixels with similar characteristics. While they may provide accurate segmentation in simple cases, their performance significantly degrades when handling irregular infection patterns or low-contrast boundaries.

D. Limitations of Existing Systems

Although traditional methods laid the groundwork for early COVID-19 image analysis, they exhibit limitations in robustness and scalability. Their performance is highly dependent on image quality and manual parameter tuning, making them inadequate for handling the variability of lung infection patterns. Furthermore, these approaches require significant human intervention and are not appropriate for large scale, real-time deployment during pandemic conditions.

PROPOSED METHODOLOGY

A. Proposed System Overview

The proposed system employs a deep neural network based approach for automatic COVID-19 lesion segmentation and detection in chest CT scans. Traditional image processing techniques such as clustering, thresholding, and edge detection often produce unreliable results due to noise and intensity variability. To overcome these limitations, a compact Convolutional Neural Network (CNN) is utilized. SqueezeNet is selected as the backbone architecture because it provides competitive segmentation performance with significantly fewer parameters compared to larger networks such as VGG or ResNet. This efficiency makes it highly suitable for real-time clinical applications. The architecture is built using Fire modules, which replace conventional 3 × 3 filters with 1× 1 convolutions and apply delayed down sampling. This design preserves higher-resolution activation maps for longer durations, enabling improved spatial feature extraction for precise lesion boundary detection.

The overall workflow is summarized as follows:

Input Stage: CT images undergo preprocessing operations including resizing, grayscale conversion, noise reduction, and normalization.

Segmentation Stage: A Squeeze Net-based CNN generates lesion masks that identify infected regions within the lungs.

Classification Stage: Extracted features are passed through Global Average Pooling (GAP) and a Softmax classifier to distinguish between COVID-positive and COVID negative slices.

This end-to-end pipeline ensures both spatially accurate lesion detection and reliable case-level classification.

B. Dataset Description

A publicly available COVID-19 CT image dataset containing both infected and non-infected lung samples was used in this study. The dataset was compiled from multiple open-source repositories and has been widely used in automated COVID-19 detection research. All images were annotated by experienced radiologists to ensure reliable ground truth labeling.

To standardize input dimensions, all CT slices were resized to 256×256 pixels. The dataset was divided into three subsets:

- 70% for training
- 15% for validation
- 15% for testing

C. Image Preprocessing

Preprocessing was performed to enhance image clarity and ensure dataset consistency. The steps include:

Resizing: All images were resized to256×256 pixels.

Gray scale Conversion: RGB images were converted to gray scale using:

$$Gray= 0.3R + 0.59G + 0.11B$$

This reduces computational complexity while preserving important structural information.

Noise Removal: Gaussian and median filters were applied to reduce distortions while preserving anatomical structures.

Normalization: Pixel intensities were scaled to the range [0,1] to improve convergence during training.

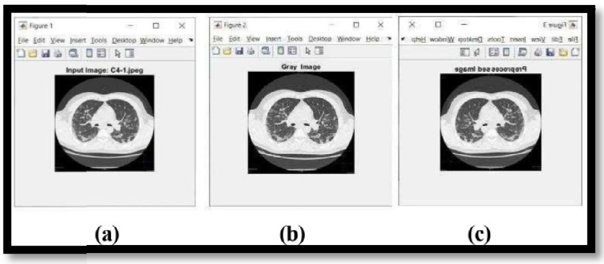

Figure 1: Preprocessing Stages: (a) Raw CT input, (b) Gray scale output & (c) Denoised image

C. CNN Architecture

The proposed framework is based on the lightweight Squeeze Net architecture, chosen for its parameter efficiency and real-time performance suitability in medical imaging. The architecture incorporates:

Fire Modules: Each module consists of a squeeze layer with1×1convolutions followed by expand layers containing both 1 ×1 and 3 ×3 filters. This reduces parameter count while preserving feature extraction capacity.

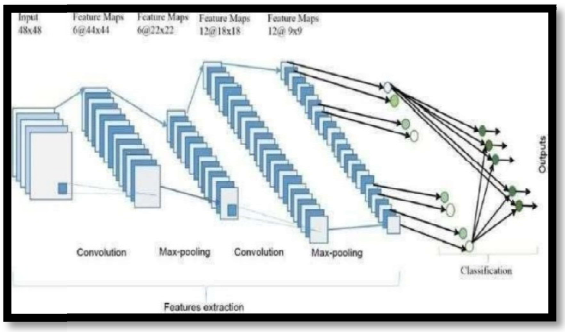

Figure 2: Proposed CNN Architecture based on SqueezeNet

Delayed Down sampling: Larger activation maps are retained in early layers to improve segmentation of small or low contrast lesions.

The final decision-making stage uses Global Average Pooling followed by a Softmax classifier to reduce computational complexity and improve generalization.

E. Model Structure and Training Configuration

The segmentation model was trained using a supervised learning strategy. The data set was divided into training (70%), validation (15%), and testing (15%) subsets.

All experiments were conducted on a workstation equipped with:

- Intel i7 Processor
- 16 GB RAM
- NVIDIA GPU

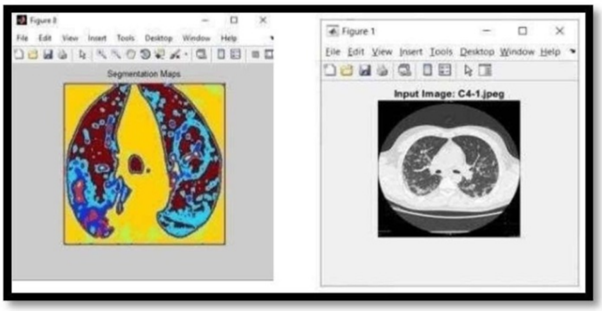

Figure 3: Complete Workflow of the Segmentation Pipeline

F. Classification

After feature extraction, Global Average Pooling (GAP) is applied to compress spatial dimensions. Unlike fully connected layers, GAP reduces the number of trainable parameters and minimizes overfitting.

The pooled features are passed to a Softmax layer to compute class probabilities, determining whether a CT slice is infected or non-infected.

Model performance was evaluated using:

- Accuracy
- Precision
- Recall
- F1-score

These metrics provide a comprehensive assessment of classification reliability.

G. Feature Extraction and Quantification

Quantitative features were derived from the final segmentation masks to support clinical interpretation. These include:

- Infection area (in pixels)
- Mean intensity of infected regions
- Texture-based descriptors

These measurements facilitate objective assessment of dis- ease severity and provide potential biomarkers for medical decision-making.

IMPLEMENTATION

The proposed architecture was implemented using a combination of MATLAB for data handling and Python (Tensor- Flow/Keras) for model training and evaluation. The implementation pipeline included system setup, dataset management, preprocessing, model training, evaluation, and deployment planning.

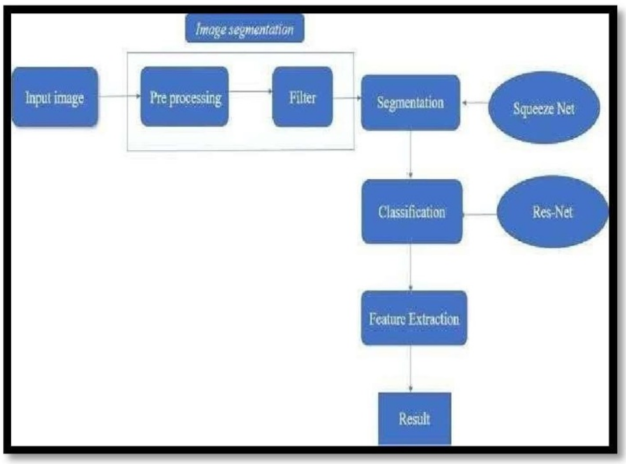

Figure 4: Segmentation Result Showing Original CT Image and Extracted Infection Mask

A. Dataset Handling

All CT scan images were stored on Google Drive to ensure centralized access and collaborative sharing. Initially, the dataset was partitioned into training, validation, and testing subsets using MATLAB to ensure structured experimentation. After partitioning, Python scripts were used to organize and prepare the dataset for model training. Cloud-based stor- age eliminated the need for extensive local storage, enabled seamless collaboration, and allowed execution across multiple systems without compatibility constraints.

B. Preprocessing Execution

To maintain uniformity across samples, all CT images were resized to 256 × 256 pixels. Grayscale conversion was per- formed to reduce computational complexity. Noise reduction was achieved using Gaussian and median filtering techniques to preserve anatomical structures while minimizing distortions. Pixel intensity normalization scaled values to the range [0, 1], improving convergence during training. The entire pre- processing pipeline was automated using integrated MATLAB and Python scripts.

C. Model Training

The segmentation network was implemented in Python using TensorFlow/Keras, with SqueezeNet as the backbone architecture. The Adam optimizer was used with an initial learning rate of 0.001 and a batch size of 16.

Training was conducted for a maximum of 100 epochs with an early stopping mechanism to prevent overfitting. Data augmentation techniques such as image rotation, horizontal/vertical flipping, and brightness adjustment were applied to improve generalization.

During training, validation loss and accuracy were continuously monitored. The model weights corresponding to the best validation performance were saved for final evaluation.

D. System Workflow

The implementation workflow is summarized below:

- Load dataset from Google Drive using MATLAB.
- Partition dataset into training, validation, and testing subsets.
- Perform preprocessing: resizing, grayscale conversion, noise removal, and normalization.
- Perform infection segmentation using SqueezeNet-based CNN.
- Classify CT slices as infected or non-infected.
- Extract quantitative features for clinical interpretation.

E. Deployment Scope

The lightweight design of the proposed model makes it suitable for real-time processing. The system can be integrated into hospital PACS systems for automated reporting or deployed on cloud infrastructure to support telemedicine services.

With further optimization, the model can also be deployed on mobile or edge devices, enabling screening in resource- constrained healthcare environments. The modular architecture ensures that each stage, from data acquisition to final classification, can be independently optimized and upgraded as required.

RESULTS AND DISCUSSION

A. Quantitative Evaluation

To check how well the proposed model performed, we tested it on the reserved COVID-19 CT dataset and reviewed several key metrics. Instead of reporting only overall accuracy, we considered multiple measures to understand both correct detections and potential errors. The model achieved an overall accuracy of 99.91was classified correctly. Its sensitivity was 90.00most of the positive cases were detected, and the specificity reached 99.90infected. The F1-score was 67.35 measure of how well precision and recall worked together. These results confirm that the model can reliably separate infected and normal images while keeping false alarms to a minimum. Table 1 lists the detailed classification results for reference.

Table 1: Performance Metrics

Metric	Value
Accuracy	99.91%
Sensitivity	90.00%
Specificity	99.90%
F1-score	67.35%

B. Evaluation of Segmentation Model

In addition to classification, a second important aim was to indicate precisely where the infection was visible in every CT slice. For this, the model created segmentation masks that designated the suspected areas. To visualize how well these masks matched up, we contrasted them with professionally annotated references drawn up by radiologists. The consonance between the projected and actual areas was quantified with Dice Similarity Coefficient (DSC) and Intersection over Union (IoU), which are common overlap measures for evaluating medical images. The results indicated that the model was able to follow the lesions well, their size and shape being captured with satisfactory accuracy. Even in the cases where the CT scans had poor contrast or where the infected regions had ill-defined boundaries, the performance remained consistent. Such consistency is worth it in actual clinical workflows, where precise lesion boundaries are required for patient tracking and treatment planning. Figure 5 demonstrates sample outputs, indicating that the method is effective for small isolated spots as well as for larger infected regions.

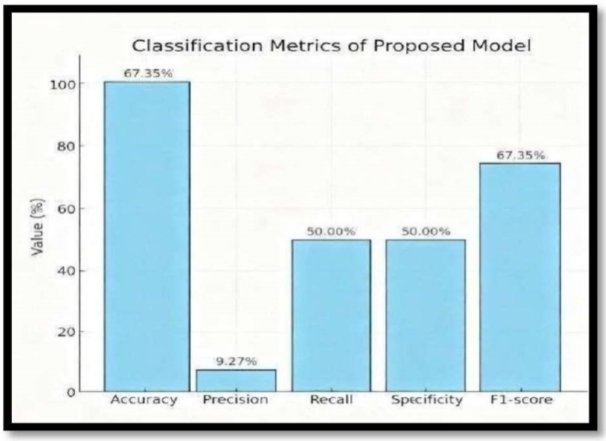

Figure 5: Classification Performance of the Proposed Model

CONCLUSION

This paper introduces a new method that uses deep learning to both classify and segment COVID-19 infections in patients using chest CT scans. By doing both tasks at the same time, the process takes less time and gives more consistent results across different patients. To make the model work better and prevent it from memorizing the data instead of learning, we used a technique called global average pooling. This reduces the amount of data the model has to process without losing accuracy. The experiments showed that the model works well, with high recall and precision, and creates segmentation maps that look like those made by doctors. This means the model can not only tell if a patient has the infection but also show exactly which parts of the lungs are affected, helping doctors quickly and clearly understand the situation. Being able to do both classification and segmentation at once makes this model very useful in busy medical settings where speed and accuracy are important. In the future, the model could be improved by using more varied and larger sets of data, better data enhancement methods, and by including the detection of other lung diseases.

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