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Research Article

A Novel Deep Learning model for detection of Pneumonia and Covid-19 variants from Chest X-ray images

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Abstract:

Pneumonia is an example of a past pandemic and continues to be a serious health concern. In the USA, more than one million people are admitted in hospital with pneumonia every year, leading to about 500,000 deaths. Chest X-ray imaging is an effective and widely utilised method for diagnosing pneumonia and is essential in both healthcare and epidemiological studies. COVID-19, a viral infection initiated in Wuhan, China towards the end of 2019, quickly spread across the globe. It is caused by the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) and has influenced millions globally. Analyzing X-ray images is regarded as the fastest and simplest methods for discovery, available at a minimal cost in many places. CT scans, on the other way, are a mere advanced imaging technique that can identify small changes in the composition of internal organs. This method uses 3-D computer technology along with X-rays for a more detailed examination. While both CT scans and X-rays provide images of internal body compositions, traditional X-ray images can sometimes occlude, making it difficult to see fine details. The proposed model outlines a framework for classifying COVID-19 variants and predicting new ones. As per the results, the proposed ResNet_Seg achieved an F1 score of 99.96%, which is higher than the CNN and other models tested. The performance of these models is assessed using datasets from SARS and MERS, resulting in accurate predictions. Future work will focus on validating these models using statistical methods. A relative analysis of deep learning models, including CNN, ResNet, and Darknet, is conducted, with performance enhancements achieved through the novel segmentation algorithm and hyperparameter fine-tuning. The results offer insights into developing more effective and reliable diagnostic methodologies for pneumonia and COVID-19 using deep learning and machine learning techniques.

1. Introduction

Pandemics and outbreaks are two distinct ways to describe the spread of infectious diseases in communities over time. A pandemic occurs when there is a higher-than-expected rise in cases of illness, injury, or health problems in a particular area or among specific groups over a certain period, with most cases being interconnected. An example of a past pandemic is pneumonia, a serious illness that has led to numerous health complications [1].

In USA, over a million of people are admitted in health centres with pneumonia every year, and the mortality rate is about 50% of the admitted [2]. The World Health Organization (WHO) also reported in 2019 that pneumonia accounted for 14% of mortality among the global children under 5 years. This highlights the need for early-stage identification of pneumonia. By employing deep learning (DL)-based models for pneumonia detection could possibly save lives by helping the patients to get treated before it is too serious and thereby bring down the high mortality rate associated with it [3,4].

Pnuemonia affects the lungs through the inhilation of bacteria, fungi or infections which leads to breating abnormalities and to death in children under 5 years. The most prominently employed technique to detect pneumonia is Chest X-ray (CXR) imaging. Though the CXR imaging is quite efficient and is able to produce path breaking medical research results it requires a lot of experience for the radiologists to identify pneumonia from CXR images.

Although the prominently used method for the detection of pneumonia is CXR imaging, there are certain cons with this model such as time consumption and in some cases difference of opinion among the radiologists [5]. Keeping aside these factors, CXR imaging for pneumonia detection is still the cheaper way compared to other detection methods available. These challenges demand the development of a clinical method to detect pneumonia in the healthcare field without human intervention and errors in an automated manner.

The research using Computer-Aided Design (CAD) is becoming popular now a days for Machine Learning (ML) and its observed that the results produced by existing CAD systems are efficient in terms of breast cancer detection or lung cancer identification etc.,. The most vital task in ML is the process of feature identification which was done manually in the olden days [6-8]. The shortcomings of these manual models are listed below:

- The results arrived were not that significant
- The feature extraction done manually has its own limitations

Recently the feature extraction is automated after the development of DL models such as Convolutional Neural Networks (CNNs) [9]. This automated feature extraction depends on the process of transfer learning, which involves the models that are already equipped with the large data sets namely ImageNet, which are modified for a lesser precise task. The researchers are also imparting the pre-trained models namely Xception, DenseNet, ResNet, VGGNet and AlexNet for the feature extraction process [10-14].

As of this writing, over 702 million cases have been reported, with an estimated 6.9 million resulting in death [15]. In many instances, SARS-CoV-2 can lead to pneumonia, necessitating hospitalization for affected patients. With an R0 value of approximately 2.5 for the original strain, the virus spreads quickly, often straining healthcare systems, including those in developed countries [16]. An accurate method to diagnose pneumonia is required to effectively treat the patients and minimze the related complications are the need of the hour.

CXR and CT scans are wiely used to diagnose medical diseases in an accurate manner [17]. Though the analysis results using CXRs are little slower than other modes, still they are widely used as the primary method across the globe in identifying pneumonia. The properties such as affordability, accessibility and minimized exposure (7 millisievert (mSv) for CT scan vs 0.1 mSv for CXR) to radiation make CXRs the preferred method for diagnosis [18]. The cost of other models like Magnetic Resonated Imaging or CT is bit higher compared to the CXRs, which makes it the most sought method for medical diagnosis [19].

Though there are researches being done in identifying a faster method to diagnose Covid-19 from CXR or CT scans in an automated manner as the manual method requires a lot of processing time and expertise from the radiologists [20]. The expertise in analyzing this is mandate since the Covid-19 resembles various conditions like SARS or Viral Pneumonia (VP) which may lead to wrong diagnosis there by endangering the patient’s life.

2. Literature Review

This part of the paper provides a summary of various ML works in medical image recognition, highlighting both the advantages and drawbacks of them. Various datasets have been employed in the process of training the ML model to accurately identify the disease from the image [21]. One reliable approach in medical image analysis is DL, which can be employed to train models on medical image datasets. In this study, DL models like ResNet-101 and ResNet-50 were applied to detect pneumonia [22] the provided different outcomes based on their individual features.

To handle the variations, an integrated DL strategy was developed by fusing the models with dataset of 14,863 CXRs, achieving a precision of 96%. However, despite this high level of precision, the model faces challenges arising due to the complexity of merging ResNet models. Additionally, artificial neural networks (ANNs) have proven effective in identifying and diagnosing various diseases.

The Pre-processing is done to neglect the irrelevant data, remove the noise and improvise the image quality for better disease detection. Segementation is an important phase in diagnosing pneumonia from Lung images. The dataset collected from 80 patients [23], was fed to a feed-forward network and provided a result with 96% accuracy. The model suffered with lack of accuracy if the input images are distorted or reduced in size.

In recent years, the world has been profoundly influenced by the widespread COVID-19 pandemic with multiple variants and different severity levels ranging from mild to severe [24,25]. The effectiveness of vaccines depends on viral variants, demography of population, and other related aspects. Immunity against SARS-CoV-2 following vaccination is primarily mediated by humoral immunity, with IgG levels generally surpassing IgA levels in response to vaccine antigens. Spike protein-specific IgG has been detected in the airway mucosa, and its presence is further strengthened when combined with mucosal IgA in infected individuals [26].

Delta variant, a more complex disorder was first identified as B.1.617.2 in India in December 2020, quickly became the largely transmissible strain, showing a 66% higher occurrence compared to the Alpha variant in England and exceeding 79% in certain parts of France [27]. The study [28] included 1,542,510 adults with a total of 17,448 Covid-19 positive individuals by swab test. This comprised 2,971 for the wild type, 2,275 for the Alpha variant, 1,493 for the Delta variant, and 10,709 for the Omicron variant.

The CNN model for analyzing vairous lung related diseases [29] consisted of 14,296 images accumulated from 120 CT scans for pneumonia, cancer and tuberculosis patients. The model that was distinctive from other models like VGGNet or LeNet was termed as AlexNet and consisted of 5 layers. It was providing as acccuracy of 0.855 but had limitations that involved the requirement of larger features for training. These higher features might lead the model to suffer from over fitting problem during the training phase 2 individual deep CNNs namely AlexNet and GoogleNet [30] were used to analyze the CXRs to identify tuberculosis. The initial and the finally trained network used ImageNet to categrozie the input images based on the affected regions. The problem with this model was that, it was able to recognize only the tuberculosis and not it’s related or sub diseases. In an attempt to differentiate among the bacterial and viral pneumonia based on CXR images, a CNN model named VGG-16 was utilized [31]. The visualization of the model revealed that the proposed method had an accuracy value of 0.962 and was able to efficiently distinguish among the viral and pneumonial disease.

The authors [32] focussed on ML models for diagnosing pneumonia and reviewed different studies and methodologies used for automated pneumonia detection from CXRs and CT scans. The recent developments, limitations and solutions in ML with an insight over their pros and cons were discussed. The manual detection has several limitations [33]:

- Limited availability of test kits.
- It can be costly, making it inaccessible for some individuals.
- Most tests take five to six hours to produce results, and faster tests, while available, can be unreliable due to their lack of sensitivity and the potential for false negatives.
- COVID-19 is highly contagious, posing a risk to healthcare professionals involved in manual diagnoses. This puts the lives of healthcare workers at risk, and the healthcare system is under significant strain.

Extensive research has been conducted to develop methods for early detection of various lung diseases based on symptoms. Since CXR and CT scans are affordable and accessible for patients in most countries, they have been widely used to identify COVID-19. CXRs were used to detect COVID-19 pneumonia in patients through three CNN models: ResNet-50, InceptionV3, and Inception-ResNetV2. These models bypassed the feature extraction and selection stages, achieving 97% classification accuracy with InceptionV3, 87% with Inception-ResNetV2, and 98% accuracy with ResNet50 [34].

Thorax X-ray based diagnosis using CNN was employed in improvising the image alignment and reduction of noise by Huang Guan Q et al., [35]. Thorax normally attacks smaller areas and the proposed framework helps to reduce the local disrminations in the image. The ChestXRay-14 dataset was used in the proposed model and the results provided an Area under Curve value of 87%. The problem with the model was it lost the performance as the features were modified. Miao Effah et al., [36] investigated the ML applications on forecasting the pneumonia occurence based on non-persistent methods. The review aimed at proposing a tool for the process of earlier identification and treatment of pneumonia without the need of persistent methodologies.

Fusing multiple ML methods improve the accuracy and other related performance metrics in the process of pneumonia detection. Gong Peng et al., [37] explored the relation between the immunity level in patients pre and posr kidney transplant surgery. These ML based methodologies identify the predictive markers that help in diagnosing pneumonia in those patients. Based on the continous monitoring of the immunity data in patients, the diagnosis of pneumonia can be done in an early stage there by helping the patient to get treatment on time.

The COVID-19 pandemic has highlighted the need for accurate predictive models to manage the virus's spread, especially with new variants emerging. This study [38] introduces an AI-driven method to analyze and predict COVID-19 variant dynamics using advanced machine learning algorithms like neural networks and ensemble learning. The model integrates diverse datasets, including genomic sequences, epidemiological data, and environmental factors, to identify and forecast variant spread and impact with high precision. Extensive validation with real-world data shows the model's superior performance over traditional epidemiological models.

This study applies ensemble machine learning models, combining algorithms like random forests, gradient boosting, and neural networks, to predict COVID-19 variant dynamics. Trained on comprehensive datasets including genomic, epidemiological, and sociodemographic information, these ensemble models outperform individual models in prediction accuracy and robustness. The enhanced predictive capabilities offer valuable insights for health authorities to develop effective intervention strategies and resource allocation. This research highlights the potential of ensemble learning in tackling complex public health challenges posed by evolving viral variants [39]. Using advanced neural network architectures, the model [40] processes extensive genomic data to detect patterns and mutations that indicate new variants. Trained on a large dataset of SARS-CoV-2 sequences, it demonstrates high accuracy and sensitivity in forecasting variant emergence. Compared to traditional models, the deep learning approach offers superior prediction accuracy and computational efficiency, providing valuable insights for genomic surveillance and public health strategies.

The COVID-19 pandemic has underscored the importance of accurate predictive models for managing the virus's spread, particularly with the emergence of new variants. The study by R.K. Singh et al., (2024) presents an AI-driven approach to analyze and forecast COVID-19 variant dynamics using advanced machine learning techniques like neural networks and ensemble learning. The model incorporates diverse datasets, such as genomic sequences, epidemiological data, and environmental factors, to accurately predict the spread and impact of variants. Extensive validation with real-world data reveals that this model outperforms traditional epidemiological models. These insights can assist policymakers and healthcare providers in taking proactive measures to control outbreaks and efficiently allocate resources, highlighting the transformative potential of AI in pandemic management.

The study by S.Metha et al., (2024) explores ensemble machine learning models, integrating algorithms such as random forests, gradient boosting, and neural networks, to predict the dynamics of COVID-19 variants. Trained on extensive datasets that include genomic, epidemiological, and sociodemographic information, these ensemble models surpass individual models in both prediction accuracy and robustness. The improved predictive capabilities provide valuable insights for health authorities to devise effective intervention strategies and allocate resources efficiently. This research underscores the potential of ensemble learning in addressing complex public health challenges presented by evolving viral variants.

A deep learning model designed by Y. Feng et al., (2024) to predict COVID-19 variants through the analysis of genomic sequences. By leveraging advanced neural network architectures, the model processes extensive genomic data to identify patterns and mutations indicative of new variants. Trained on a large dataset of SARS-CoV-2 sequences, the model shows high accuracy and sensitivity in forecasting the emergence of variants. Compared to traditional models, this deep learning approach delivers superior prediction accuracy and computational efficiency, offering valuable insights for genomic surveillance and public health strategies.

3. Proposed Methodology

This section provides a detailed description of the workflow and methods used for analyzing medical images related to COVID-19. The discussion covers techniques for both image-level and region-level diagnoses.

3.1 Image Level Diagnosis

This method involves making predictions about the complete radiological image of a patient with COVID-19. Image-level diagnosis can be useful for initially screening COVID-19 suspects, making accurate diagnoses, and isolating infected individuals from healthy ones to help manage the virus spread. DL categorization models have employed image-based analysis techniques for diagnosing and predicting the disease. In image-level diagnosis, labels are assigned in two ways: binary labels that distinguish COVID-19 infected images from normal ones, or multi-class labels that differentiate between COVID-19, normal images, viral pneumonia, bacterial pneumonia, and others.

3.2 Region Level Diagnosis (RLD)

In contrast, RLD focuses on making predictions by assigning labels to smaller sections or specific areas of the CXR image. Each pixel in the figure is categorized as either “COVID-19” or not helping to outline the area of interest. This approach offers more detailed insights into the spread of COVID-19 infection and the unique patterns that emerge. RLD includes DL-based techniques for instance and semantic segmentation, as well as a multi-stage DL approach that combines both classification and segmentation.

Categorization methods have been adapted to screen for COVID-19 in CXR images. They label these images into various categories. Categorization can help with the efficient identification and timely management of COVID-19. Analyzing CXR and CT images carefully requires the expertise of radiologists and can take a lot of time. DL methods can automate the discovery of COVID-19 in radiological images, providing a faster solution. This automation allows medical professionals to spend more time on critical COVID-19 patients, ultimately saving more people.

The proposed study consists of several parts, including image pre-processing, a new algorithm for segmenting images, feature extraction, and categorization using DL models. It utilizes CXR and CT scan images from patients with COVID-19 pneumonia. In the pre-processing stage, color images are converted to grayscale, resized, and filtered. Twenty-four Gabor filters are used to group similar image pixels, resulting in smoother pixels being clustered together. During the segmentation phase, the desired cluster count is created using the k-means clustering technique. Next, attributes are extracted from the segmented images, followed by image enhancement. Finally, different pre-trained models are utilised to accurately categorize images as COVID, pneumonia, or normal. Additionally, the study analyzes a list of symptoms with their severity levels and a list of medications, each linked to treatable symptoms, using a pseudo-selector algorithm. The proposed study includes all of these modules.

The datasets used for disease classification come from various sources. The CXR image dataset includes cases of COVID-19, pneumonia, and normal conditions, and can be found at this Kaggle Dataset [37]. Another dataset, the COVID Radiography Database, has about 3,000 images and can be accessed from COVID-19 Radiography Database [38]. An augmented dataset for COVID-19 and non-COVID-19 cases was collected from GitHub to create a balanced training dataset. Lastly, there is a dataset with 4,173 CT scan images from patients available in COVID Multiclass CT Dataset [39]. The distribution of each dataset is summarized in Table 1.

Additionally, the images in the datasets may be in different formats, so all input figures were resized to 224 × 224 pixels to standardize the data. This preprocessing step ensures that the intensity histograms are uniform across the entire dataset, which is important for the segmentation methods to effectively detect features. By standardizing the images this way, the categorization accuracy of DL models is improved.

The effectiveness of CNNs increases with more data, as it provides better coverage of the feature space. To enhance the training dataset, data manipulation techniques namely vertical flipping, horizontal flipping, and rotation (up to 30 degrees) were used. These techniques ensure that the generated images closely resemble the original dataset and avoid introducing noise that could confuse the model. Additionally, these images maintained the key characteristics needed for diagnosing the disease. The augmented X-ray and CT images were used in both phases of model training.

To ensure balanced exposure during training, the dataset images were shuffled before being input into the network. This prevents the model from developing a bias towards a particular class in each iteration, ensuring that images from different categories, including both Covid-19 positve and negative cases (as well as various types of pneumonia), are mixed throughout the training process.

To address the limitations of current segmentation algorithms, this study proposes using an improved K-Means clustering technique combined with Gabor filters. The input image undergoes preprocessing to make it suitable for further analysis, often involving converting it to grayscale to simplify later operations. Gabor filters are then designed and applied to the pre-processed grayscale image. These filters are effective because they can capture spatial frequency information at various orientations and scales, making them useful for extracting features from texture-rich images, such as medical scans. Relevant features are extracted from each filtered image at the pixel level, which include:

- **Intensity information**: Capturing the brightness values of pixels after filtering.
- **Spatial location**: Identifying the coordinates of each pixel in the image.
- **Texture descriptors**: Extracting local texture information to reveal finer details.

3.3 Classification using DL models

After segmentation, convolutional layers are utilized to extract features from the segmented images. These features are subsequently employed in a CNN-based classifier for classification tasks. The CNN architecture includes convolutional layers, pooling layers for subsampling, and fully connected layers.

Pooling layers then minimize the size of the feature maps while preserving essential information. These features propagate through the network until they reach the final fully connected layer. The last fully connected layer employs a sigmoid activation function to make predictions, generating binary outputs of 0 or 1.The classification phase results in outputs categorized into three classes: images indicating COVID-19 detection, images depicting pneumonia, and images of normal patients.A pseudo selector algorithm calculates scores for medications based on a user's symptoms and their severity levels. For each symptom in the user's list, if a medication can treat that symptom, the algorithm adds the product of the medication's effectiveness for that symptom and the symptom's severity to the medication's score. After computing the scores for all medications, it assigns the calculated scores accordingly. The medications are then sorted in descending order. The medication with the highest score (the most effective one) is returned. Finally, the top suggested medications are displayed to the user.

Proposed CNN Model

The proposed CNN has three convolutional layers that use 3x3 filters and three max pooling layers with 2x2 filters. ReLU activation is used in the convolutional layers to speed up the training process. The CNN is trained on a preprocessed image dataset, allowing it to learn important features and make predictions. The proposed architecture diagram of our model is depicted in Figure 1.

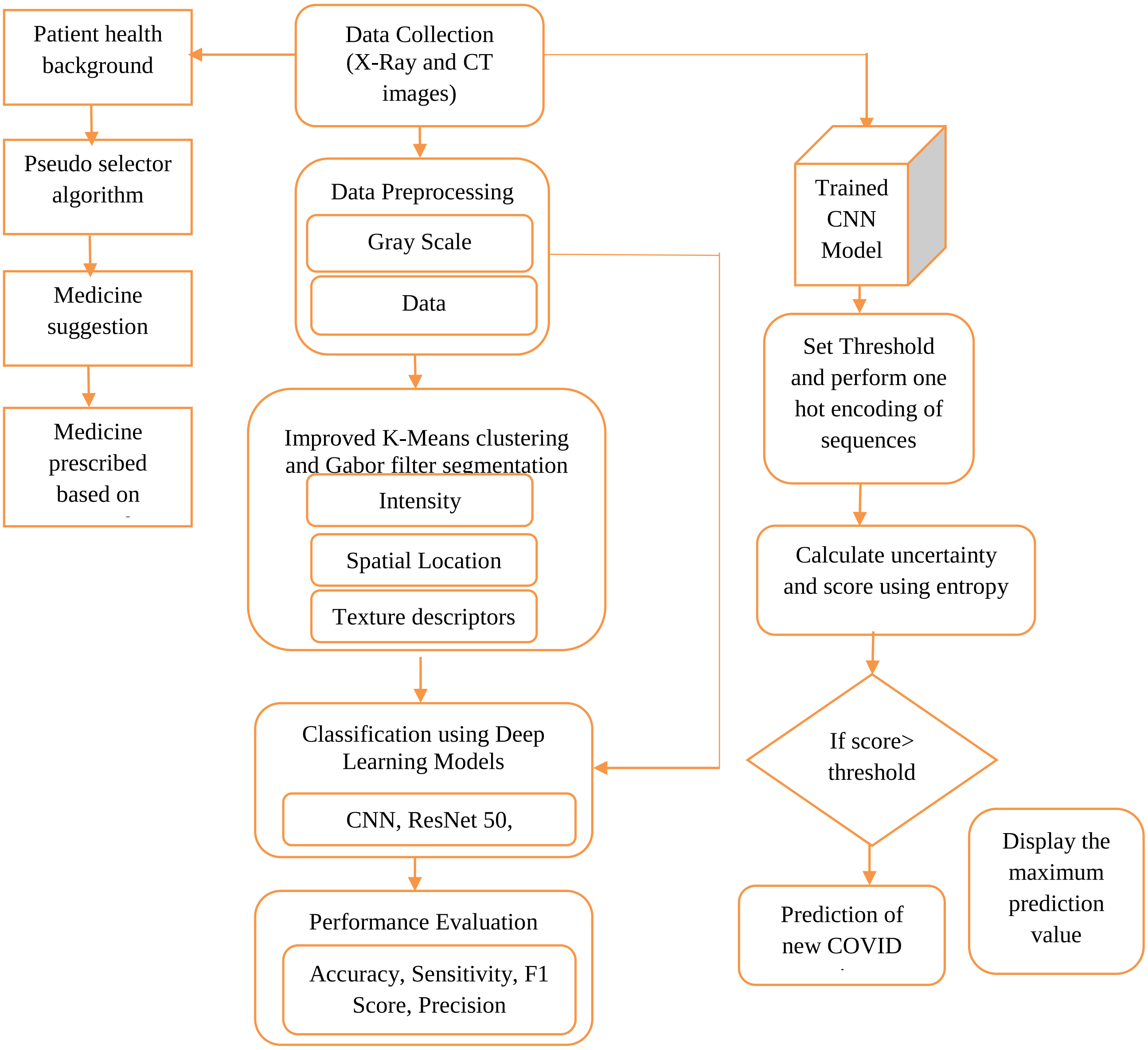

Figure 1. *Architecture diagram of proposed study.*

After training, the CNN's performance is tested on a separate validation or test set to evaluate its effectiveness. Metrics such as accuracy, precision, recall, and F1 score are calculated to assess the network's performance. Additionally, visualizing predictions and analyzing confusion matrices help identify the network's strengths and weaknesses.

After evaluation, the CNN can be further fine-tuned or optimized to advance its performance. This may include adjusting hyperparameters (like learning rate and batch size) or trying out different network architectures. Techniques such as transfer learning, where a pre-trained CNN is adapted for a new task, can also be used to take advantage of existing knowledge and speed up training.

ResNet-50

The main advancement in the ResNet architecture is the use of residual blocks, which tackle the problem of vanishing gradients in deep neural networks. These blocks include shortcut connections, also known as bypass connections or identity mappings, that allow gradients to pass directly through the network without going through many layers. This design greatly improves the ability to train very deep networks.

Dark Net 50

Darknet-50 has 49 convolutional layers that learn hierarchical features from input images. These layers are organized into blocks, with each block containing several convolutional layers, followed by batch normalization and ReLU activation functions. Furthermore, Darknet-50 includes residual connections, inspired by the ResNet architecture. These connections help gradients flow more easily during training, addressing the vanishing gradient problem and making the network easier to train.

The loss function in Darknet-50 ensures that the network learns to predict accurate bounding boxes and effectively classify objects. Darknet is well-known for its speed and efficiency, making it ideal for real-time applications. Its output includes bounding boxes defined by coordinates (x, y, width, height), confidence scores for detected objects, and class probabilities. The architecture frequently uses Rectified Linear Unit (ReLU) activation functions throughout.

4. Results and Discussion

For our model implementation, open source datasets of CXR images and CT scan images are used to classify COVID, pneumonia and normal patients. The dataset is divided into 80% of training and 20% of test datasets. Experimental evaluation of metrics is done to compare the results evaluation results of various models.

The metrics commonly employed to diagnose pneumonia include accuracy, recall, precision, and specificity. These metrics rely on terms such as True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). TP represents cases where pneumonia is correctly identified. TN indicates instances where normal samples are accurately classified. FN refers to cases where pneumonia patients are overlooked by the model, despite having the condition. FP denotes the samples incorrectly flagged as having pneumonia. The formulae for accuracy, recall and precision are given below:

Accuracy measures the amount of accurately predicted data compared on the whole dataset. It is a key metric for assessing the model's performance across different classes present in the dataset. Evaluating accuracy in the proposed model is represented as:

$$Accuracy = \frac{Total\ Correct\ Predictions}{Total\ Predictions}$$

Recall focuses on the comparison between the accurate identification of the positive sample against the all positive samples available in the given data set. The main focus is only on predicting the positive class other than the negative samples that are spread in the dataset.

$$Recall = \frac{TP}{TP + FN}$$

Precision concerns with the count of positive predictions of the model. It is implicitly observed that if the count of positive predcitions is more, the precision value is enhanced significantly and vice versa.

$$Precision = \frac{TP}{TP + FP}$$

Specificity concerns with the count of negative predictions of the model. It is implicitly observed that if the count of negative predcitions is more, the specificity value is enhanced significantly and vice versa.

$$Specificity = \frac{TN}{TN + FP}$$

Similarly, the F1 score serves as an evaluation metric to compare the effectiveness of two classifiers. For example, if one classifier achieves higher precision and the other excels in recall, the F1 score helps gauge the balance between these metrics. In the proposed approach, the F1 score will be used to analyze the trade-off between precision and recall, and the results will be compared to those from prior studies.

$$F1 - Score = \frac{2 * Precision * Recall}{Precision + Recall}$$

The comparative analysis of CNN, ResNet and DarkNet models are compared with the segmented versus and non-segmented images are depicted in this section.

4.1 Framework for COVID 19 variants Prediction

This section presents the proposed framework for classifying COVID-19 variants and predicting new variants. The framework operates in three phases, as illustrated in Figure 2. The segmented images are trained by the ResNet model to classify among 6 types of COVID 19 variants as mentioned in Figure 2.

Classification Network: Classification involves determining which COVID-19 variant corresponds to a given input image. The outcome of this process is a specific class label (e.g., "Variant 1," "Variant 2," etc.), along with the associated probabilities for each class. For instance, if an image is classified as "Variant 1," it signifies that the model has identified this as the most suitable label based on the features it has learned. Essentially, classification focuses on categorizing the input data into predefined classes, specifically identifying which known COVID-19 variant is represented in the image.

Unpredictability Check: Entropy quantifies the uncertainty of predictions. When the probabilities are similar, the entropy is high, indicating uncertainty; conversely, if one probability is significantly higher than the others, the entropy is low, reflecting confidence in the prediction. If the entropy exceeds a specified threshold, the model flags the case as a "New variant" due to the uncertainty. If the entropy is below the threshold, the model selects the variant with the highest probability as the prediction.

Prediction of New Variants: Prediction is a broader concept that refers to estimating an outcome based on input data, which may involve forecasting values, class labels, or behaviors. In this context, prediction includes classification but also extends to other aspects, such as estimating uncertainties or identifying new variants. The outcomes of prediction can consist not only of the predicted class label but also additional information, such as confidence scores and uncertainty metrics. For example, the network might indicate that an image is linked to a specific variant while providing an uncertainty score that reflects its confidence in that prediction. Overall, prediction encompasses the entire inference process based on input data, which can include classification, regression (estimating numerical values), uncertainty estimation, and other forms of inference.

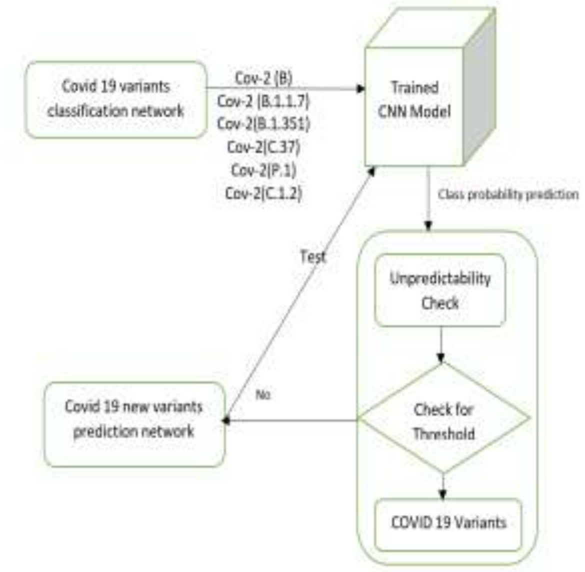

***Figure 2**. Covid Variants Prediction Framework*

The proposed classification network consists of the following steps for effective learning and prediction. The architecture includes:

- Input Layer: Image (224x224x3)
- Convolutional Layer: 64 filters, 7x7 kernel
- Max Pooling: Reduces spatial dimensions
- Residual Blocks: Comprising multiple convolutional layers, introducing skip connections
- Average Pooling: Global pooling to reduce dimensionality
- Fully Connected Layer: Outputs probabilities for each class.

The model is started by loading pre-trained ResNet weights (e.g., from ImageNet) to utilize transfer learning, allowing the model to benefit from existing knowledge. For each new input image, preprocess it consistently (resizing and normalization) before using the trained ResNet model to predict class probabilities. Use the threshold (th = 0.15) for entropy, which helps detect when the model is uncertain about its predictions.Calculate the entropy of these probabilities to evaluate uncertainty: high entropy suggests uncertainty, flagging the case as a "New variant," while low entropy enables the selection of the variant with the highest probability as the prediction. Finally, we can deploy the trained model for real-time predictions, ensuring a user-friendly interface for clinicians or researchers.This structured approach ensures the network effectively learns and generalizes patterns in the nucleotide sequences, facilitating accurate classification and prediction of COVID-19 variants.

Algorithm 1: COVID-19 Variant Prediction

```
X – Load trained CNN model (ResNet)
S – Load image data
T- 0.15 #set threshold value for uncertainty
Preprocessed_img = Resize and normalize the images
Prediction= X(Preprocessed_img)
Score= entropy(prediction)
If score value is > T
New variant predicted
else
Print max(predictions)
```

COVID-19 Variant Prediction

In the proposed method, the entropy metric is used to predict the uncertainty for the COVID 19 variants classification. The uncertainty check is calculated using the following equation.

$$U(C) = -\sum_{j=1}^{n} p(c^j) log\, P(c^j)$$

The COVID 19 variant is predicted using the predefined threshold value and if the uncertainty is greater than the threshold value, then the new variant is predicted. Algorithm 1 depicts the steps involved in the prediction of COVID 19 variants.

The threshold value of 1.5 is selected as a suitable point for distinguishing between confident and uncertain predictions. This empirically tuned value strikes a balance between identifying new variants (associated with high uncertainty) and allowing confident predictions for known variants. While the exact threshold may vary based on the model, dataset, and number of classes, 1.5 serves as an effective midpoint for problems involving six classes (variants).

5. Performance Evaluation

The comparative analysis of various models with the accuracy obtained is represented in table 1.

The graphical results of all the models implemented in the proposed study are depicted in Figures 3 and 4. Figure 3 shows the accuracy graph of all the models and Figure 4 denotes the loss graph values.

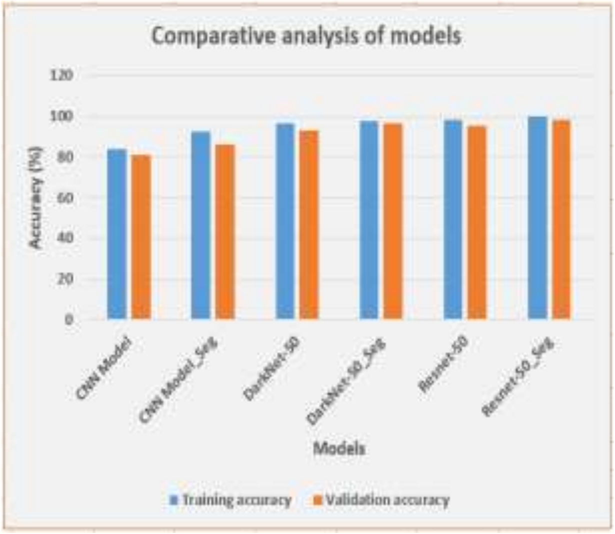

Figure 3. *Comparative analysis for Accuracy Graph*

The loss values of models with and without segmentation is shown below. The proposed models are trained once on unsegmented images and once on segmented images. Model accuracyisimproved by segmented images, e.g. CNN_Seg. The performance of the proposed model is compared with pre-trained networks are shown in the table. Out of all the models, ResNet 50 with segmentation achieved highest accuracy of 99.95%which is higher than the proposed CNN and other models. The proposed ResNet_Seg achieved an F1 score of 99.96%, which is higher than the proposed CNN and other models. The proposed study is evaluated using various metrics like precision, recall and F1 score. The results obtained for the models is shown in table 2. The graphical results of classification with respect to above metrics is depicted in Figure 5.

5.1 Accuracy Graph For Prediction of COVID 19 New Variants

One of the significant contributions of the work is the discovery of new COVID-19 variants.

Table 1. *Comparative analysis of models*

Model	Best Epoch	Training loss	Training accuracy	Validation loss	Validation accuracy	Iteration Count
CNN Model	3	0.48	83.68	0.640	81.24	50
Resnet-50	4	0.131	98.48	0.1580	95.2433	500
DarkNet-50	5	0.194	96.54	0.1279	93.21	500
CNN Model_Seg	4	0.390	92.31	0.615	86.47	150
Resnet-50_Seg	5	0.0052	99.95	0.0087	98.33	200
DarkNet-50_Seg	6	0.078	97.68	0.1059	96.42	200

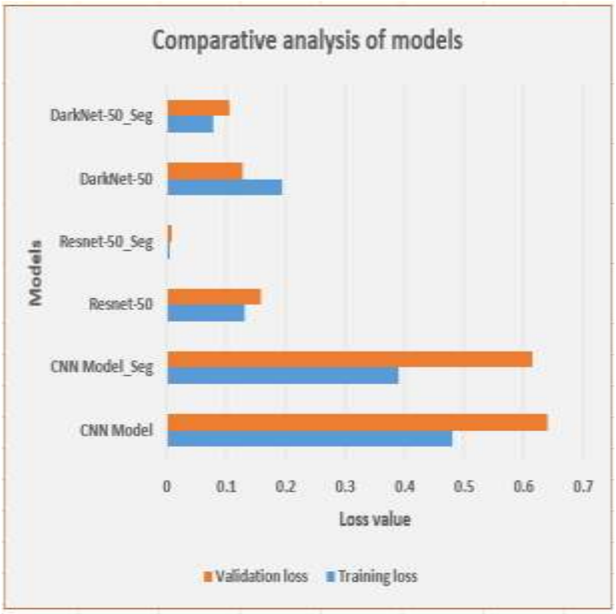

Figure 4. *Comparative Analysis of Loss Graphs*

Table 2. *Performance analysis of models*

Model/Metrics	Accuracy	Specificity	Precision	Recall	F1 score
CNN Model	83.68	87.21	83.91	83.68	83.73
Resnet-50	98.48	99.56	98.72	98.48	98.57
DarkNet-50	96.54	97.89	96.73	96.54	96.61
CNN Model_Seg	92.31	94.45	92.59	92.31	92.47
Resnet-50_Seg	99.95	99.99	99.97	99.95	99.96
DarkNet-50_Seg	97.68	98.25	97.86	97.68	97.79

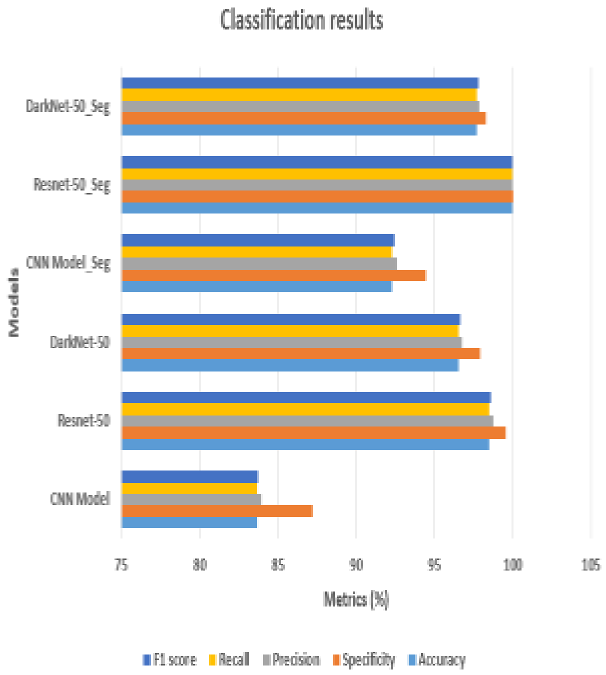

Figure 5. *Comparative analysis of Performance Metrics*

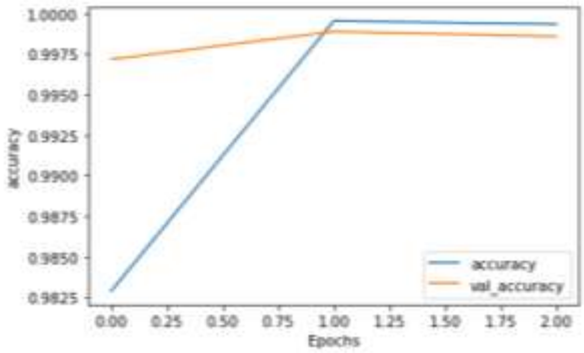

Figure 6. *Covid-19 variant prediction Accuracy*

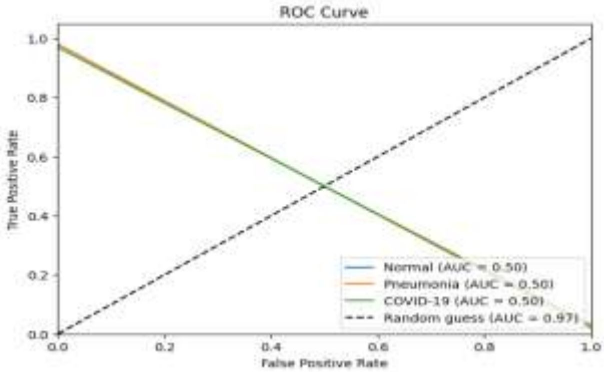

Figure 7. *Covid-19 Variant Prediction ROC Curve*

To evaluate our new variant prediction mechanism, we trained the classification network using six variants and evaluated it with two variants, P.2 and C.1.2. We used the ROC (Receiver Operating Characteristic) curve and AUC (Area Under the Curve) values to assess the effectiveness of the new variant prediction technique. The ROC curve illustrates the trade-off between the TP rate (TPR) and the FP rate (FPR) at various threshold settings. In our context, the TPR represents the proportion of new variant samples correctly identified as new variants, while the FPR represents the proportion of old variant samples incorrectly identified as new variants. Accuracy plots and ROC curves for the prediction of new variants are provided in the Figures 6 and 7.

6. Conclusion

The primary aim of this study is to determine if a user may be infected with COVID-19 and to increase awareness about individual COVID-19 situations. This could help in reducing the spread of the virus in the future. Given the fast transmissibility of this virus, it is crucial to manage its spread through rapid detection and limited contact with infected individuals. DL offers a promising approach for managing this illness and other infectious diseases. Comparisons between different DL models suggest that earlier models, like VGGNet and ResNet, can reach the accuracy of newer models with certain modifications. However, a key advantage of newer models is their ability to minimize model parameters, providing a more lightweight network. Among all the models tested, ResNet 50 with segmentation recorded the highest accuracy at 99.95%, surpassing both the proposed CNN and other models. According to the results presented in the table, the proposed ResNet_Seg attained an F1 score of 99.96%, which is also higher than other models. We tested the performance of these models using datasets from SARS and MERS, yielding accurate prediction results. Future work will focus on validating the models with statistical techniques.

Author Statements:

- **Ethical approval:** The conducted research is not related to either human or animal use.
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