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Human Metapneumovirus (HMPV) Classification Using Deep Learning Algorithms

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Abstract: Recently, following the spread of the coronavirus and the emergence of cases hmpv virus, determining the type of pneumonia is essential for taking precautionary measures. Accurate and timely diagnosis is a major challenge X-rays are used for diagnosis, and examining X-ray images and extracting results is a burden on doctors. Therefore, the use of artificial intelligence techniques is crucial to reducing effort and time. In this study, deep learning techniques were used to build a model capable of accurately diagnosing the type of infection. The model was trained on COVID-19 data and then tested on COVID-19 and hmpv data. This study designed a model for the diagnosis of pneumonia. The deep learning techniques using based on the spareable convolution with slandered convolution, two types of data were used: covid data and hmpv data. The model aims to extract patterns from COVID-19 data and generalize them for broader applications. This model was modified and tested on COVID data and then used to diagnose hmpv. The proposed achieved an accuracy of 99.8% and 99.9%.

Keywords: Human Metapneumovirus, Separable CNN, Deep Learning, Viral Classification, Machine Learning, Classification

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1. Introduction

Recently, the use of deep learning techniques has increased due to its ability to use data even if it is unstructured and does not require feature engineering techniques because it extracts features automatically, providing excellent results[1,2].

After a suspected case in the Netherlands, a country in the temperate areas[3] first reported the first cases of hmpv. A instance in Pune, India, was reported by [4] a few years later. It shows the possibility for long-distance viral transmission. Since then, cases of hmpv have been documented in a number of places worldwide, including Canada, the UK, and Australia. This scenario demonstrates the virus's capacity to proliferate and be influenced by environmental factors, such as climate. Given the virus's capacity for adaptation, a method for estimating its possible dissemination is necessary Human Metapneumovirus (HMPV)[5,6,7].

Since there is now no approved vaccine or antiviral medication to cure or prevent HBV infection, the human hepatitis C virus (HBV) has spread extensively around the world and continues to place a heavy medical burden on the local population [8,9]. For instance, over 86% of children under the age of five worldwide are at serious risk of contracting an HBV infection, and the virus is linked to almost 1 million outpatient visits with clinical signs of acute respiratory infections [10,11].

The term artificial intelligence (AI) refers to a wide range of technological advancements that attempt to mimic human cognitive processes and intelligent behavior [12,13,14]. A branch of artificial intelligence called machine learning (ML) is concerned with algorithms that let computers create models for intricate correlations or patterns from empirical data without explicit programming [15]. By using biological neural networks as inspiration, deep learning (DL), a subset of machine learning (ML), outperforms traditional ML models in terms of power and flexibility. DL can address a wide range of challenging [16,17].

Medical imaging has made substantial use of deep learning techniques. Convolutional neural networks (CNNs) in particular have been applied to segmentation and classification challenges [19,20]. In artificial neural networks (ANNs), convolution is a crucial mathematical procedure. Using picture frames, convolutional neural networks (CNNs) can be used to classify data and learn features. There are numerous varieties of CNNs. Depth-wise separable convolutional neural networks are one type of CNN.[21,22,23].

Artificial intelligence was used in the current study.-based potential distribution modelling approach to classify the human seasonal influenza virus and climate sensitivity that influences the occurrence of human seasonal influenza virus based on existing reports and data. Therefore, machine learning is the only effective approach to control the spread of influenza virus.

Related Work

Abdullahi Umar Ibrahim et al (2021) they adopted a transfer learning strategy by employing a Convolutional Neural Network (CNN) to identify viral pneumonia in x-ray images using a pertained AlexNet model. The dataset was divided into 50:50, 60:40, 70:30, 80:20, and 90:10 segments for training and testing, respectively, in order to assess the model's average efficiency. Ten K cross-validation was used to assess the model's performance. The model's performance with the entire dataset was contrasted with the state-of-the-art and cross-validation means. The classification model in terms of sensitivity, specificity, and accuracy has demonstrated high performance. The 70:30 split outperformed the others, with 98.73% accuracy, 98.59% sensitivity, and 99.84% specificity.

.Mohamed Loey et al (2020) they presented classical data augmentation techniques along with conditional generative adversarial networks (CGANs) based on deep learning model for data transfer to detect COVID-19 in chest CT images. . Where, five different models based on deep convolutional neural networks (AlexNet, VGGNet16, VGGNet19, GoogleNet, and ResNet50) were selected. The results show that ResNet50 is the most suitable deep learning model for detecting COVID-19 from a limited chest CT dataset using classical data augmentation with a test accuracy of 82.91%, sensitivity of 77.66%, and specificity of 87.62%.

Shereen Fouad et al (2021) they proposed an intelligent image analysis framework for HPV status determination. The proposed research combines hand-crafted feature extraction and deep learning for epithelial region segmentation. The performance of the proposed method was evaluated on nasal images captured using a 20× objective lens. The experimental results show a classification accuracy of about 91% in detecting HPV status. They also tested the performance of end-to-end deep learning Instead of using manually created features taken from segmented images, classification techniques for HPV status assessment learn directly from the original ISH-processed images. Three well-known image recognition networks (VGG-16, ResNet, and Inception V3) were among the convolutional neural network (CNN) architectures whose performance we evaluated in both pre-trained and scratch-trained versions; nonetheless, their best classification accuracy was 78%. Lang, Daniel M. et al. (2021)They looked into whether deep learning models could use

imaging to determine an individual's HPV status. A transfer learning strategy was employed. Sports videos were used to pre-train a 3D convolutional network.

With an area under the receiver operating curve (AUC) of 0.81 for an external test set, the pre-trained video model demonstrated the ability to differentiate between HPV-positive and HPV-negative instances. The pre-trained video model outperformed a 2D pre-trained architecture on ImageNet and a 3D convolutional neural network (CNN) created from scratch. Apu et al., Md. Shahriar Hossain (2025) In order to comprehend how the public responded to the HMPV outbreak in 2024, they employed sentiment analysis. They achieved 93.50% accuracy in sentiment categorization tasks by using sophisticated transformer models, particularly XLNet. Furthermore, they used SHAP to incorporate explainable artificial intelligence (XAI) to make it transparent how the model determines the main determinants of public opinion. Kiran Purohit et al (2020) They discussed a multi-image augmentation technique based on convolutional neural network (CNN) for the detection of COVID-19 in chest X-ray and chest CT images of suspected COVID-19 patients.

The proposed model shows higher classification accuracy of about 95.38% and 98.97% for CT and X-ray images, respectively. CT images with multi-image augmentation achieve 94.78% sensitivity and 95.98% specificity, while X-ray images with multi-image augmentation achieve 99.07% sensitivity and 98.88% specificity. Li L et al(2020). developed a deep learning model called COVNet to extract visual features from chest CT scans for COVID-19 detection. They used visual features to differentiate community-acquired pneumonia from lung diseases other than pneumonia. However, COVNet is unable to classify the severity of this disease. Fujima et al. (2020) Using a transfer learning technique based on natural images from the ImageNet collection, a 2D convolutional neural network (CNN) was trained on glycogen fluoride PET images to predict HPV status in melanoma patients, achieving an area under the curve of 83%. They did not, however, evaluate their data on an outside cohort, and they did not include tumors with diameters less than 1.5 cm or photos with significant motion abnormalities.

2. Materials and Methods

Dataset

Two X-ray datasets were used in this model: one for COVID-19, which was used for training and testing from Kaggle (<https://www.kaggle.com/datasets/manishkc06/covid19-detection>), as this dataset is imbalance, and the second for testing purposes only (https://www.ncbi.nlm.nih.gov/medgen/?linkname=pmc_medgen&from_uid=5901753)(<https://pubmed.ncbi.nlm.nih.gov/3457928/>). Recent results obtained using radiographic imaging techniques indicate that these images contain important information about the COVID-19 virus.

Dataset Collection

Covid dataset (x-ray) and Hmpv dataset:

This step involves collecting datasets of X-ray images. The two datasets mentioned are:

- a. **Covid dataset:** Contains X-ray images of patients with or without covid-19.
- b. **Hmpv dataset:** Contains X-ray images related to Human metapneumovirus (HMPV), another respiratory illness.

The proposed model

The Covid-19 spreads as easily like any other flu and the number of positive cases grows at an incredibly high exponential rate. If we do not take every necessary measure and utilize all possible diagnostic tools, it would take us a significantly longer amount of time to combat this pandemic X-ray dataset used. deep learning model build for detect if the patient is infecting or not.

According to recent research, radiological imaging techniques may provide important information regarding the COVID-19 virus. The use of cutting-edge artificial intelligence (AI) methods in conjunction with radiological imaging can help detect this illness accurately and help solve the issue of a shortage of skilled medical professionals in isolated communities. A deep learning-based approach for COVID-19 and hmpv classification is depicted in the proposed design in Figure 1.

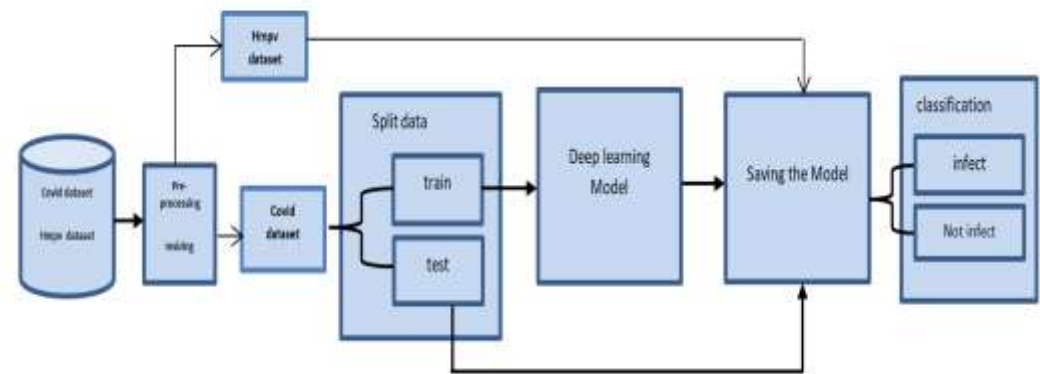


Figure 1. A proposed diagram

The proposed system is composed of three stages. The first phase is the pre-processing the second phase, the CNN (**Convolutional Neural Network (CNN) with residual connections and separable convolutions**) technique, was applied as a deep feature extraction technique. The third phase classifies input data into two categories infect or non-infect. Below is a step-by-step explanation of the process depicted in the proposed model:

Preprocessing phase

Images from both datasets undergo preprocessing and resizing it to a standard input shape suitable for deep learning models. Ensures consistency in the data for better performance and training stability.

Feature extraction phase

This phase consist of the flowing steps

Data Splitting

The dataset is split into two subsets to helps in validating the generalization ability of the model:

1. Train (70%): Majority of the data used to train the deep learning model.
2. Test (30%): Held out to evaluate the model's performance on unseen data

Deep Learning Model

A deep learning model (**Convolutional Neural Network (CNN) with residual connections and separable convolutions**) was trained using the training dataset to learn patterns and features that distinguish between infected and non-infected cases. Training includes adjusting the model's weights using optimization techniques like backpropagation and gradient descent. Figure 2 shows A healthy X-ray and B an infected X-ray.

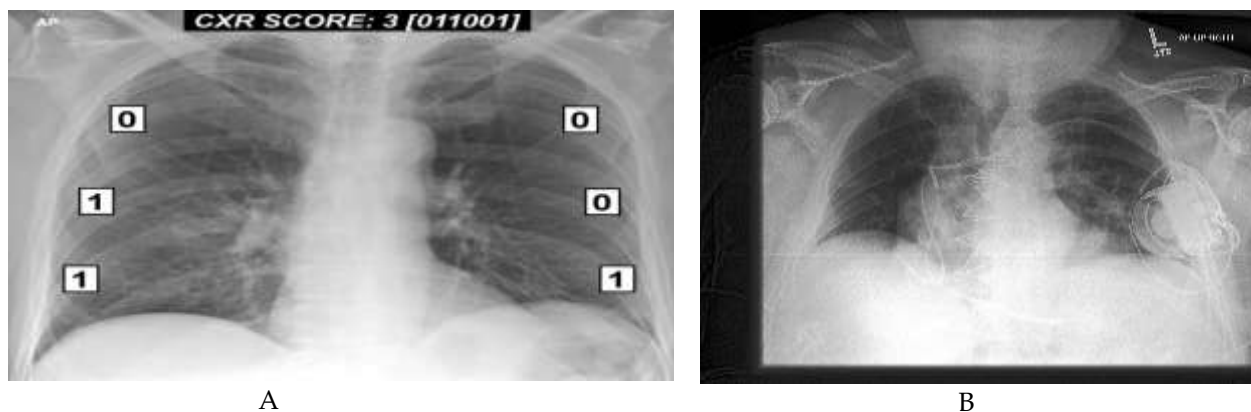


Figure 2. A. Healthy, B. Infect

Model Saving

Once trained, the model is saved for future use, ensuring it does not need to be retrained from scratch every time it is used for classification.

Classification:

The trained model classifies input data into two categories:

1. **Infect:** Indicating a positive case.
2. **Not infect:** Indicating a negative case.

The diagram also includes a feedback loop where the saved model can be retrained with new data, allowing for continuous improvement. This process is crucial in medical diagnostics to enhance the accuracy and reliability of predictions.

3. Results and Discussion

The system's performance outcomes are discussed in this section. Figure 3 show the model architecture overview and detailed of its components a deep learning model architecture based on a Convolutional Neural Network (CNN) with residual connections and separable convolutions.



Figure 3. Model Architecture

1. **Initial Convolution Layer:**
 - a. **Conv2D(32):** A standard convolutional layer with 32 filters.
 - b. **Batch Normalization:** Helps normalize activations to stabilize training.
 - c. **ReLU Activation:** Introduces non-linearity.
2. **Residual Block & Separable Convolutions:**
 - a. The model incorporates **residual connections** using **Conv2D(1x1)** layers.
 - b. Each major block consists of a **SeparableConv2D** layer followed by:
 - c. **batch normalization**
 - d. **relu activation**
 - e. **maxpooling for down-sampling**
3. **Progressive Depth Expansion:**
 - a. The number of filters in the separable convolution layers increases progressively:
 - 1) 64 filters
 - 2) 128 filters
 - 3) 256 filters
 - 4) 512 filters
 - 5) 1024 filters
 - b. This hierarchical feature extraction allows the network to learn complex patterns.
4. **Final Layers:**
 - a. The last **SeparableConv2D(35)** layer suggests that the model outputs **35 feature maps**, likely related to classification categories or feature embeddings.
 - b. **flatten:** Converts the 2D feature maps into a 1D vector.
 - c. **dense layer:** Fully connected layer, likely used for classification.

Key Features of the Model

- a. **Residual Connections:** Helps with gradient flow and prevents vanishing gradients.
- b. **Separable Convolutions:** Reduces computational complexity while preserving performance.
- c. **Batch Normalization:** Ensures stable training by normalizing activations.
- d. **Hierarchical Feature Learning:** Filters increase in depth, capturing low- to high-level features.

The classification of COVID-19 and hmpv textures for two distinct data sets of varying sizes is shown in this paper. The features derived from CNN structures have first been categorized after undergoing fusion and ranking procedures. The accuracy measures were employed to assess the suggested approach. Figure 4 shows the total number of errors the model predicted, illustrating how the CNN performance was evaluated in terms of accuracy scores [24]. The satisfactory fit condition for training the model on the enhanced data is depicted by the learning curves (loss of training and validation) plots in Figure 5. Training and validation losses diminish until they reach equilibrium, and the difference between the two-loss values is negligible. Perhaps it is the consistent training of a good fit that would produce a problem of overfitting, so an early stopping was used when training the model.

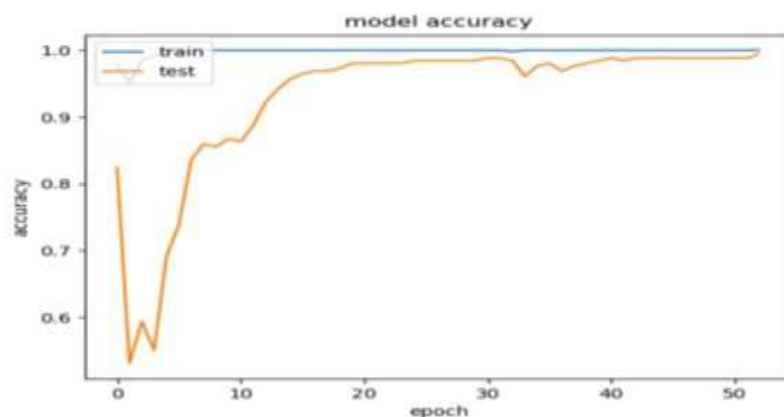


Figure 4. Accuracy learning curves of train and test

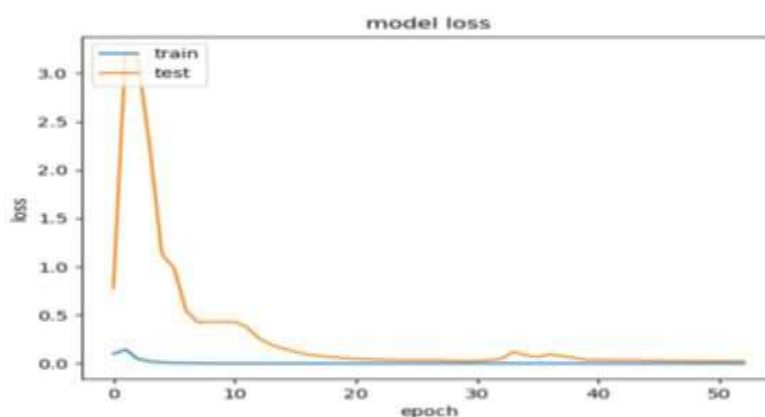


Figure 5. Loss of training and test.

All test samples that make up 30% of the database will be sent to the system during the testing phase without having their labels examined. Two classification techniques used to the test sample will be used to show the findings of the proposed system output during the classification stage: SoftMax utility for identifying HMPV-infected cases. Datasets from the suggested approach employing the SoftMax function yield confusion matrices. This confusion matrix is displayed in Figure 6.

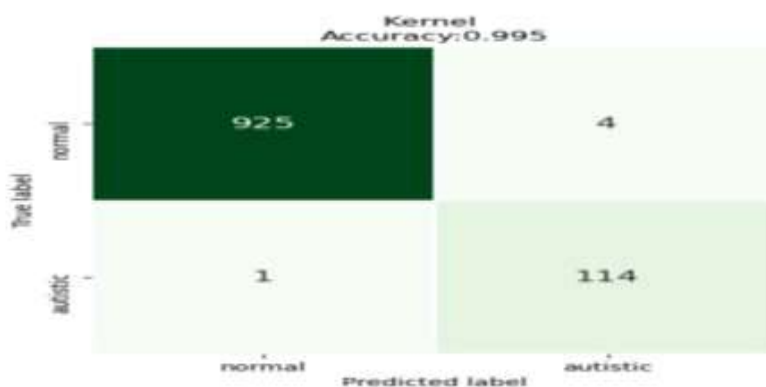


Figure 6. Confusion Matrix of Proposed Method

4. Conclusion

The planned deep learning model effectively leverages chest X-ray for classify and detect infections such as COVID-19 and HMPV. By incorporating essential steps like preprocessing, dataset merging, and data splitting, the model ensures robustness and accuracy in training. The use of a deep learning architecture enables the system to automatically extract and learn complex features from the X-ray images, improving its ability to distinguish between "infected" and "not infected" cases.

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