

Detection of Covid-19, Skin Cancer and Malaria using AI and Image Processing

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Abstract - Owing to the burgeoning population and with it, the upswing in the number of diseases, the synergy of technology and the healthcare sector has become a pressing need. It's essential to integrate technology like AI to trace, track and detect critical diseases and make frameworks for upcoming ones. There have been several developments in machine learning technology especially, to use it to aid the doctors. It decreases the time taken to diagnose and speeds up the treatment phase.

A large number of data sets consisting of imageries are formed for various ailments and are made open for comprehensive research. These data sets form the basis of AI solutions and deep learning algorithms. The solution we propose uses AI frameworks and data sets available for SARS- CoV 2 also known as Covid19, Malaria and Skin Cancer to classify and label them as healthy or affected.

Key Words: Machine Learning in disease detection, Image Classification, CNN, AI, VGG 19, ResNet 18, Inception V3, DenseNet 201

1. INTRODUCTION

The proposed solution is a streamlined and efficient way of screening three critical diseases using image processing. The solution leverages fine-tuned version of four advanced CNN models namely, ResNet 18, VGG -19, Inception V3 and DenseNet 201 to identify and label the provided chest X-Ray scans/ blood smear/ skin lesions from healthy ones. This opportunity has also been wielded to compare these four models on their accuracy, speed and complexity. [1]

Research has been done on Convolution Neural Networks, Image Processing, ResNet 18, VGG -19, Inception V3 and DenseNet 201 to provide a viable solution that can help in improving the medical technician's ability to detect a particular disease and play a vital role in the reduction of fatalities due to the same. [2] The proposed approach has also taken the intra class resemblances and inter class variations in the color, texture, location, scale and look of the sample image into account for better identification and results. The above has been completed in three phases, the first one used ResNet 18, the second one uses VGG-19 and the final one uses Inception V3 and Densenet 201.

2. CONVOLUTION NEURAL NETWORKS

Convolution neural network is a network of various hidden layers between input and output which help in feature extraction and classification based on probabilistic models.

Any basic CNN model contains the following layers:

- Input layer, its where the input image matrix is given.
- Convolution layer, it basically breaks down the large image matrix into smaller segments and features.
- ReLU or activation Layer, the rectifier linear unit assigns zero to all negative values in the matrix so that the predictions are better.
- Pooling layer, it helps to reduce the dimension of these matrices, there are three types of layers min max and average.
- Then there's the fully connected layer which classifies the objects into the required categories along with their closeness probability.
- SoftMax or logistics layer depending upon the classification type.

And finally, the output layer which shows the most probable match. [3]



Fig 1. Basic CNN Architecture



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3. DETECTION OF DIFFERENT DISEASE USING AI AND IMAGE PROCESSING

3.1 Covid 19 Screening

Covid 19, a highly contagious respiratory disease, caused by a virus named SARS-Cov 2 in its initial phases. World Health Organization traced its origin to Wuhan, China and its first

case to 31st December 2019. Covid-19 was soon declared pandemic and worldwide lockdowns were imposed due to its alarming rate of transmission and severity. More than 523 million people have been infected by it in over 200 countries as of May 2022. Though majority of the infected people only experienced trivial [4] respiratory ailment, people with medical history and other co-morbidities had to endure acute pneumonia like illness pushing the death toll to 6.27 million (as of May 2022). [5][6]

Its symptoms included but were not restricted to loss of taste and smell, shortness of breath, reduction in oxygen levels, fever, nasal congestion, sore throat, dry cough, nausea and chills. [7] [8] The two major detection methods were RTPCR test and HRCT scan. Both of these tests, due to their critical nature and increased workload, took longer time to produce a definite result. Hence, using image classification models on chest X-ray scans is a viable solution. The proposed solution aims to correctly identify Covid-19 infected chest X-ray scans from the viral pneumonia ones using ResNet-18 image classification model. [9]

3.2 ResNet - 18 Model

ResNet18 it's an 8-layer CNN. It has pretrained image classification models with a million images classified into 1000 categories of the size 224x224. [10][11] It works on the residual feedback technique which helps to increase accuracy and diminish the effect of vanishing gradient. [12] It has been tested for various number of layers and it shows a maximum of 3.4% error.

Layer Name	Output Size	ResNet-18	
conv1	$112\times112\times64$	7 × 7, 64, stride 2	
		3×3 max pool, stride 2	
conv2_x	$56 \times 56 \times 64$	$\left[\begin{array}{c} 3\times3,64\\ 3\times3,64\end{array}\right]\times2$	
conv3_x	28 imes 28 imes 128	$\left[\begin{array}{c} 3 \times 3, 128\\ 3 \times 3, 128 \end{array}\right] \times 2$	
conv4_x	$14\times14\times256$	$\left[\begin{array}{c} 3 \times 3,256\\ 3 \times 3,256 \end{array}\right] \times 2$	
conv5_x	$7\times7\times512$	$\left[\begin{array}{c} 3 \times 3,512\\ 3 \times 3,512\end{array}\right] \times 2$	
average pool	$1 \times 1 \times 512$	7×7 average pool	
fully connected	1000	512×1000 fully connections	
softmax	1000		

Fig 2. Full Architecture of ResNet 18 Model

3.3 Malaria Screening

Malaria which is accredited to be a life-threatening disease is caused by the transfer of malarial parasites to an individual's bloodstream due to the bite from female Anopheles mosquito. Though malaria is treatable, it still amounted to about 241 million cases and 627 000 deaths in 2020 as per WHO's Malaria Report. [13]

Early diagnosis of malaria is a vital step towards controlling the disease's severity, a step which is often missed because of two main reasons. One, due to patients' negligence of the symptoms (which often resemble a flu) and two, due to the time-consuming, manual and error-prone testing techniques like Thin and Thick Blood Smear and Polymerase Chain Reaction tests. Hence, using image classification models on blood smears is a robust solution. [14] The proposed solution aims to correctly identify malaria infected blood smears from the normal ones using VGG-19 image classification model.

3.4 VGG - 19 Model

VGG 19 as the names suggests has 19 layers. It has a total of 16 convolution layers using 3x3 convolution filters along with max pooling layers for down sampling and a total of two fully connected hidden layers of 4096 units in each layer followed by a dense layer of 1000 units, where each unit represents one of the image categories in the ImageNet database. The VGG model is typically fine-tuned in the last block (4,5).



Fig. 3 Full Architecture of VGG 19 Model

3.5 Skin Cancer Screening

Generally, cells in the human body follow the property of concat inhibition, that is to grow and spread in a controlled fashion. When cells stop following this, it results in uncontrolled growth of cells. Which is left untreated can be fatal. Such a condition is known as "Cancer".

Skin cancer is a type of cancer where in the cells present in the epidermis (skin) start growing abnormally, forming lesions on it. The exact cause behind it has remained veiled for decades and has been vaguely narrowed down to physical, chemical and biological carcinogens.

It remains a highly mortal disease [15] because of the lack of treatment and awareness in its initial stages on the patients' side and restricted and uncertain tests like biopsy and MRIs on the healthcare infrastructure's side. Hence, using image classification models on skin lesion images is a viable and cheaper solution. The proposed solution aims to correctly identify malignant skin cancer lesion images from the benign ones using ensemble (Inception v3 and DenseNet 201) image classification model. [16][17]

3.6 Inception V3 Model

The Inception V3 model is a 42–48-layers deep model. This model has been trained on ImageNet dataset with an accuracy of 78.1%. Inception V3 takes input in 299 x 299 size. It has various unique and repeated connections. A basic inception V3 model has max and average pool, concatenation, dropout and fully connected layers.

The loss is calculated using SoftMax function. This model reduces the number of parameters used by replacing the single 5×5 convolutions with 3×3 convolutions. It also has good efficiency and less complexity. [18]

Going back to its introduction the Inception models were introduced to overcome overfitting, a. phenomenon that happens because of having too deep layers in a model. Inception V3 uses parallel layers having various sizes and kinds of filters, making it wider rather than deeper hence preventing overfitting. [19]





3.7 DenseNet 201 Model

DenseNet 201 model is a 201 layer pretrained model. It has been trained on ImageNet data. It takes input in 224x224 size images. It has dense and short connections. Its specialty is that each previous layer passes its information to each next layer hence making the connections n(n+1)/2. [20]

Thus, it uses less channels and has more efficiency. It solves the problem of diminishing gradient, increases feature reuse, reduces parameters. Its basic architecture has batch normalization, ReLU and convolution 3x3. Sometimes to reduce complexity 3x3 is replaced by 3x1 and 1x3.

Layers	Output Size	DenseNet-121	DenseNet-169	DenseNet-201	DenseNet-264	
Convolution	112 × 112	7×7 conv, stride 2				
Pooling	56 × 56	3×3 max pool, stride 2				
Dense Block (1)	56 × 56	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	
Transition Layer	56 × 56	1 × 1 conv				
(1)	28×28	2×2 average pool, stride 2				
Dense Block (2)	28×28	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	
Transition Layer 28 × 28		1×1 conv				
(2)	14×14	2×2 average pool, stride 2				
Dense Block (3)	14 × 14	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 24$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 48$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 64$	
Transition Layer 14 × 14		1 × 1 conv				
(3)	7 × 7		2×2 average pool, stride 2			
Dense Block (4)	7×7	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 16$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 48$	
Classification	1×1	7 × 7 global average pool 1000D fully-connected, softmax				
Layer						

Fig 5. Full Architecture of DenseNet 201 Model

In skin cancer screening an ensemble model (Inception V3 and DenseNet 201) has been used for better accuracy and results.



4. METHODOLOGY



5. FINDINGS

The different models proposed above work decently for the available dataset. Different datasets and metrics were used to train, validate and test the performance of these models. To check how accurately it can classify the image (diseases) along with how much time it takes to perform it. The accuracy and time largely depend on the AI model (parameters, no. of layers, etc.) in use, the size of the dataset in use and the computational capacity of the system. For purpose of this paper, we have used an i5-gen CPU at 1.60GHz clocking at 1.80 GHz.

The accuracy for different AI models used for different diseases (showing value of most optimum model we used). Evaluation metrics like test and validation accuracy, confusion matrix and wall time were calculated.

For COVID-19 Screening, the optimum model was ResNet 18, which achieved an accuracy of 97.78%, translating to

accurately labelling and classifying (into COVID-19, pneumonia and normal) 97 images out of 100.

In Malaria Detection, the optimum model was VGG-19, which achieved an accuracy of 96.00% indicating in 96 out of 100 cases it can precisely tell which blood smear is of infected cells.

Skin Lesion, we propose an ensemble model (combination of DenseNet 201 and Inception V3), which achieved an accuracy of 88.52% indicating it accurately classify 88 images out of 100 into seven different types of skin lesions.

The results thus obtained are satisfactory, but there is still scope for achieving better accuracy to make it fit for realworld health cases.

Disease	Dataset	Accuracy
Covid-19 Screening	3000	97.78%
Malaria Screening	26000	96.00%
Skin Cancer Screening	10000	88.52%

Table -1: Findings of the Disease Detection Model

6. LIMITATIONS AND FUTURE SCOPE

Above proposed AI models have shown great accuracy in test/controlled scenarios and have to undergo several iterations with adding more factors determining the presence of infection/disease. Also, the models are not tested in real-life diagnoses and the occurrence of similar symptoms for different diseases can confuse the model. Hence, this can result in a false diagnosis.

The models are tested on a small dataset (approx. 3000 for COVID-19, 10,000 for skin lesions and 26,000 for malaria) which results in faster and more accurate computation. But this posits chances of a dip in efficiency if the large dataset is used.

Techniques like GAN (generative adversarial network) can be used, to create synthetic images using existing datasets. Also, dataset libraries can be expanded by seeking support from healthcare departments of different nations.

The models primarily work on image classification but can be expanded to complete computer aid diagnostic systems by adding patients' history and other demographic factors. For this consultation with medical practitioners, epidemiologists and other experts are required.

An integrated website/application UI can be built, where people can insert their image and can predict from the respective algorithm. Initially starting with researchers and thereby opening for the general public if fit accuracy acquired for former.

Development of a model which can classify images first in different categories (based on input data find whether x-ray or blood smear or skin lesion) and then further in subcategories on its own. Thereby, making the process streamlined for the user on front.

7. CONCLUSION

In this paper, we have proposed the use of AI models to classify the given images and differentiate between healthy and afflicted. We have worked on three different diseases namely, COVID-19, Malaria and Skin lesions. For each disease different dataset is used, chest X-ray for COVID-19, blood smears for malaria and photographs of skin lesions of different types for the skin lesion model. We have used several CNN models on the same datasets to come up with the most optimum model for that particular dataset. In our paper, we evaluated the performance of ResNet-18, VGG-19, DenseNet 201 and Inception V3 Neural networks to learn the pattern of infected and healthy images and toward classifying infected and uninfected images to aid in improved disease screening.

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