An Investigation on Inception V3 Network Models for Disease Severity Identification

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KEYWORDS

Health, Covid-19, Disease, public health

ABSTRACT

Due to the high incubation period of COVID-19 and the use of restricted data, it is difficult to anticipate the number of casualties and the rate at which the virus would spread in the COVID-19 scenario. Monitoring those who are impacted and those who have interacted with them is perhaps the most difficult procedure. Since COVID-19 does require 14 days to incubate, it is doubtful that patients have been detected earlier. Patients have the ability to influence everyone they interact with while they are in the designated incubation period. Typically, the various machine learning algorithms are given the COVID-19 deep properties in order to classify the illness severity levels. Consequently, this may help in the early diagnosis of COVID-19. The created a deep feature extraction and classification model that successfully classified the COVID-19 severity levels using a variety of deep and machine learning algorithms. It has the ability to classify COVID-19 severity levels for early, accurate diagnosis. Ultimately, the results showed that the Inception V3 classifier outperformed all other models in both feature extraction and classificational, successfully extracting deep features from CT images and classifying the severity levels of COVID-19 infection. The testing results also showed that the classification of deep characteristics achieves promising use in COVID-19 severity prediction and diagnosis.

1. Introduction

The relationship between a person's ability to defend themselves against diseases without a diagnostic might be emphasised in this developing field of medical diagnosis [1]. Various biological technologies assess the impact of human sickness rather than focussing on a reduction process based on one or two primary organs, which is typical of any illness. The field of biomedical research has progressed to the point where large databases containing comprehensive and systematic information on the chromosome, transcriptome, epigenome, microbiome, and exposome can be used to study and understand individual disease-causing events from an integrated standpoint. Particular elements that influence an individual's resistance to diseases include nutritional status, anatomical abnormalities, cognitive impairment, diabetes, protein calorie deprivation, physical stamina, one-nucleotide polymorphisms, and toxic agents like smoking and polluted air [2]. The assessment of an individual's risk of contracting COVID-19 or the care of a patient who has already contracted the virus can be aided by the application of machine learning and deep learning techniques for analysing the many threats and their interactions. While determining the severity of a patient's illness has been the subject of numerous study, this acknowledgement is a necessary analytical prerequisite for developing an appropriate COVID-19 diagnosing system [3]. Therefore, it is essential to develop a quick, accurate, and automated approach for COVID-19 seriousness assessment in order to help physicians anticipate when an ICU authorisation would be required [11]. Features taken from the pre-learned deep learner structures have been used as

a result. To determine the severity levels based on the Inception V3 model, deep features related to the illness severity per CT image are retrieved in this model.

The work is described as follows: Introduction part is portraying in section 1 as well as the studies of several research papers portrayed, part 2 highlights the suggested method and defines the performance metrics in part 3. Part 4 describes the results of the research and the work is completed in part 5 [6].

2. Literature Review

A fully automated method [4] has been proposed to use U-Net-based deep convolutional networks for brain tumour segmentation. To optimise the effectiveness, a thorough picture enrichment process was used in this procedure. In order to segment the brain tumour, a soft dice-based loss factor that was adaptive to unlabelled samples was also used. However, the cross-validation approach was used to examine this strategy, which might provide an unbiased predictor. However, using this technique on independent testing data could result in a highly objective analysis. There were several parameters that required effective fine-tuning as well. Additionally, it performed less well when segmenting the Low-Grade Glioma (LGG) cohort's tumour locations. Image processing and DL have proposed automated tissue image segmentation [5]. Initially, a few preprocessing techniques, such as wavelet denoising, were used to extract the precise outlines of distinct tissues from diverse MRI brain imaging datasets. After that, CNN was used with DL to achieve automated picture segmentation. Parallel computing was also shown. These methods increased the number of training samples while drastically reducing processing time. However, the dataset under consideration only includes adult data, but samples of all ages should be collected. Additionally, the 3D contour of the margins of various tissues could not be seen. Based on the CNN structure, a segmentation and categorisation of lung parenchyma [14] has been created. Initially, a dataset for CNN training was automatically created using a clustering algorithm. It was then decided to split the CT slices into picture patches using a k-means clustering approach. Additionally, a size-junction, a cross-shaped verification, a simultaneous analysis, and a patch development were used to create the final dataset. Finally, CNN received this dataset in order to classify Chronic Obstructive Pulmonary Disease (COPD) [9]. However, the patches' dimensions remained unchanged, and its impact on CNN's efficiency was not examined.

3. Methodology

Figure 1 shows the graphical representation of the "Naive Version" conception module. Convolution is applied to the input using three distinct filter sizes (1x1, 3x3, 5x5). The max-pooling process is also carried out. The next inception module receives the concatenated outputs. A major issue with this module is that, when applied on top of a convolutional layer with a lot of filters, even a small number of 5 x 5 convolutions may be very costly. When pooling units are included, the issue is exacerbated because there are exactly as many output filters as there were in the stage before. The number of results would inevitably rise from stage to stage as the pooling layer's output and the convolutional layers' output were combined. As a result, dimension reductions are introduced into the architecture [7].

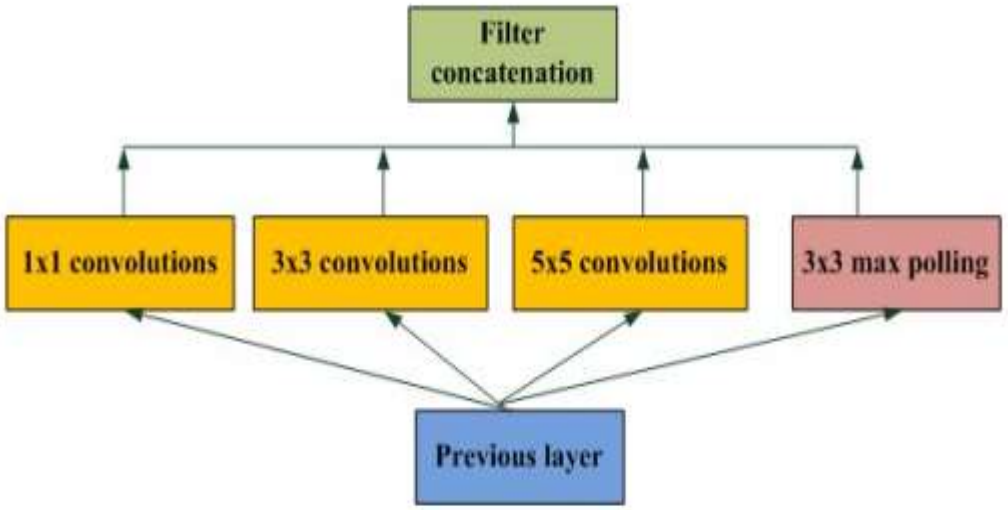

Figure 1: Inception module, Naive Version

Figure 2 shows a graphical representation of the Inception Module with reduced dimensions. Convolutional and pooling layers operate in parallel with one another rather than each one alone. The feature maps' dimensions are decreased by inserting 1 x 1 convolutional layers before the 3 x 3 and 5 x 5 layers because doing otherwise would result in an excessive number of outputs. [8].

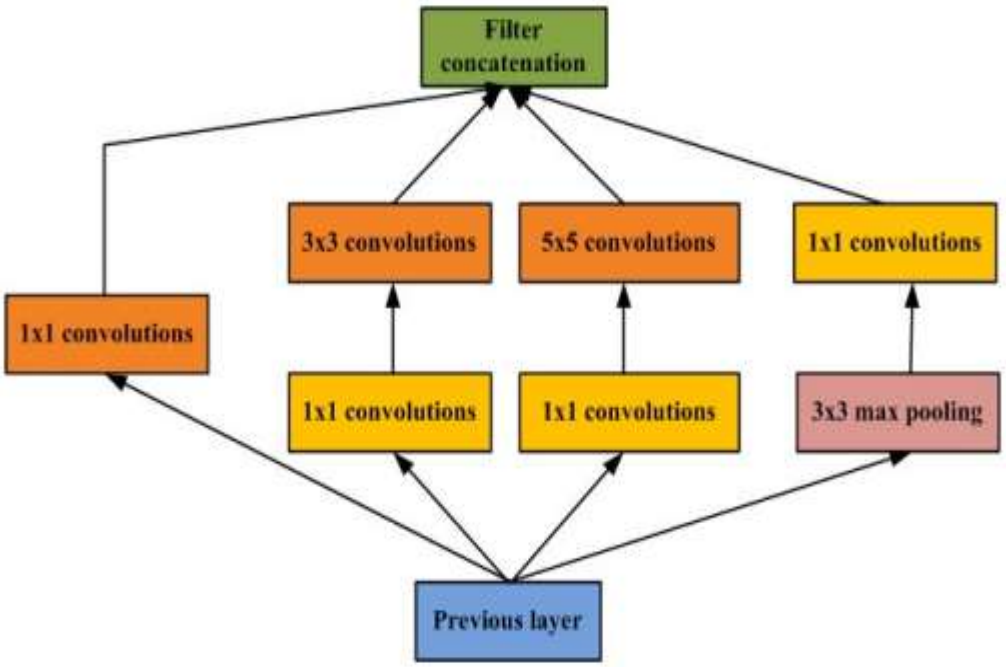

Figure 2 Inception Module

One well-known model that can be applied to transfer learning is the Inception V3 model. As was covered earlier in the section, the model was initially trained on more than a million photos from 1,000 classes. Retraining the last layer involves using the knowledge that was acquired by the model during its initial training on a smaller dataset, which produces highly accurate classifications without requiring a lot of computer resources or training. By cutting the current dropout, fully-connected layer, and softmax layers and introducing a new fully-connected, softmax layer, the Inception V3 is fine-tuned [13]. Training with the CT dataset updates the weight of the recently added layers during the fine-tuning phase. Prior to the images being classified, their features are extracted. With the exception of

the freshly inserted, perfectly connected layers, the weight of the older layers is frozen. The number of classes in the tomato dataset is matched by the new softmax layer on the top layer of the model [12]. The target class is the one with the highest probability, and the softmax function returns the probabilities values for the ten classes. The model is adjusted using the Adam optimiser and a learning rate of 0.001 [10].

4. Results and discussion

First, images of tCovid -19 were used to train the Inception V3 model for 14 epochs. Figure 3 shows the variation in training and validation accuracy calculated by the Inception V3 model. In the earlier epochs, from 1 to 8, the accuracy increases more quickly. From epoch 9 to 11, it increases gradually. From epoch 12 to 14, the accuracy stays constant.

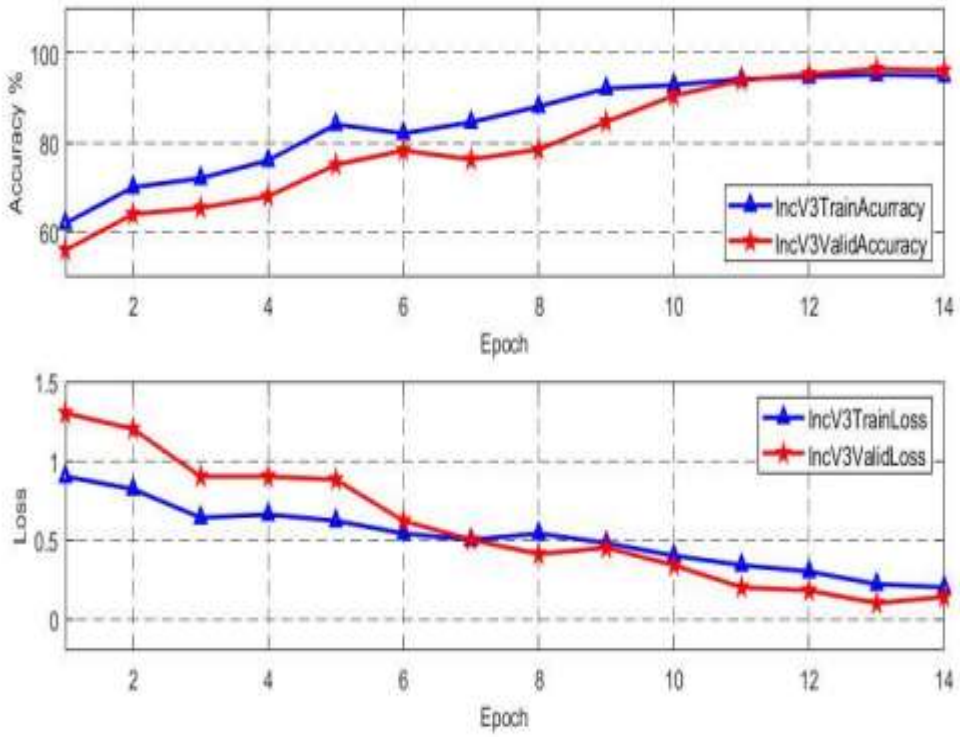

Figure 3: Experimental setup

Similarly, Figure 3 shows the training and validation loss values of the model for each epoch. As seen in Figure 3, the loss value decreases with later epochs after being large in the early ones. It is found that the model performs better for Inception V3 when the number of epochs is increased.

The Inception V3 model is evaluated using performance measures like recall, accuracy, precision, and F1 score. Section 3.7 discusses how the accuracy, precision, recall, and F1 score are calculated. The models' efficacy is evaluated using the Top 1 and Top 5 accuracies. Of the classes that are probably predicted, the class with the highest possibility of being accurately predicted is matched by the top accuracy. Similarly, Top 5 accuracy matches correctly predicted class with any one of the top 5 predicted classes.

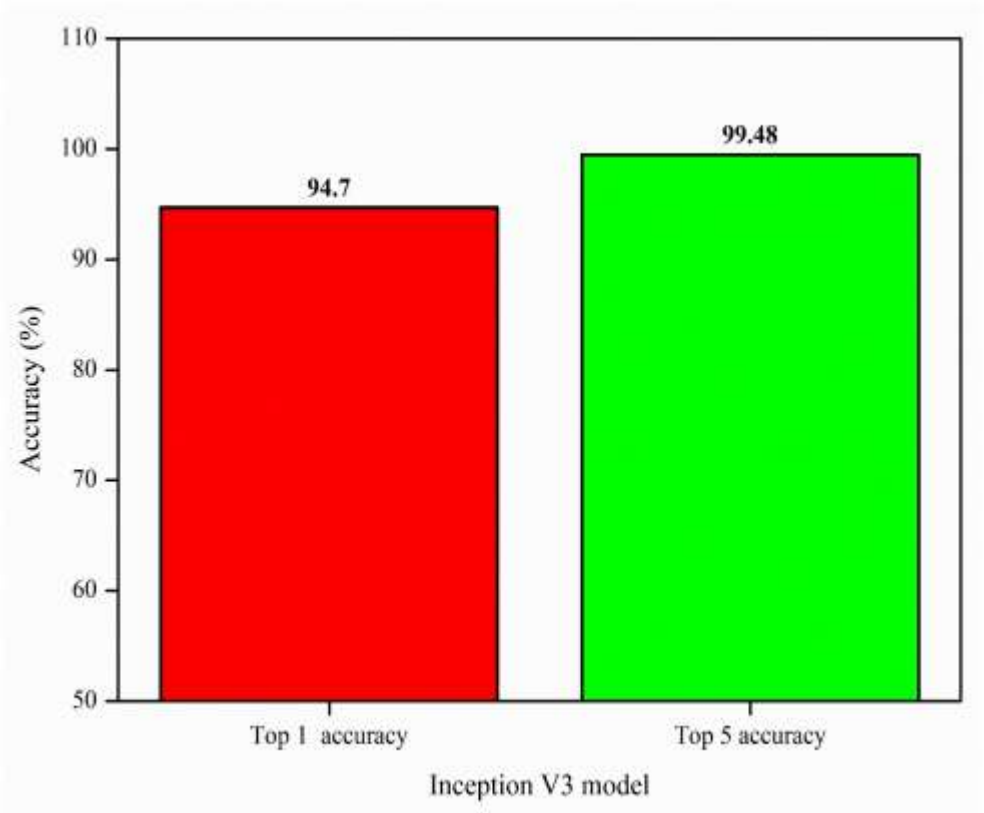

Figure 4: Comparison of Top 1 and Top 5 accuracy obtained by Inception V3 m**odel**

On the CT test dataset, Figure 4 presents a comparison of the accuracy of the Inception V3 models in the Top 1 and Top 5 categories. The size of the model, batch size, number of parameters, training and testing times for each image, and model size are used to quantify the Inception V3 model's complexity. The Inception V3 model requires 132 hours of training, has a 92 MB model size, 32 batch sizes, and 23.9 million parameters

5. Conclusion and future scope

The chapter summarizes the proposed Inception V3 model with a transfer learning approach to create a classifier to categorise illnesses. Furthermore, in order to achieve a higher recognition accuracy, choosing an appropriate classifier for disease diagnosis is necessary. Using image recognition, the suggested Inception v3 model can successfully categorise ten tomato classes. The accuracy of disease categorisation utilising dataset photos can be effectively increased through the fine-tuning of the Inception V3 model. Based on transfer learning, the Inception V3 model achieves Top 1 accuracy of 94.70% and Top 5 accuracy of 99.48%, as demonstrated by the experimental results. The suggested model obtains 0.9360, 0.9363, and 0.9354 for precision, recall, and F1 score, respectivel.

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