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Classification of COVID-19 in X-ray Images with Genetic Fine-tuning

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Abstract

New and more transmissible SARS-COV-2 variants aggravated the SARS-COV-2 emergence. Lung X-ray images stand out as an alternative to support case screening. The latest computer-aided diagnosis systems have been using Deep Learning (DL) to detect pulmonary diseases. In this context, our work investigates different types of pneumonia detection, including COVID-19, based on X-ray image processing and DL techniques. Our methodology comprehends a pre-processing step including data-augmentation, contrast enhancement, and resizing method to overcome the challenge of heterogeneous and few samples of public datasets. Additionally, we propose a new Genetic Fine-Tuning method to automatically define an optimal set of hyper-parameters of ResNet50 and VGG16 architectures. Our results are encouraging; we achieve an accuracy of 97% considering three classes: COVID-19, other pneumonia, and healthy. Thus, our methodology could assist in classifying COVID-19 pneumonia, which could reduce costs by making the process faster and more efficient.

Keywords: SARS-COV-2, X-ray, convolutional neural networks, fine-tuning, evolutionary genetic systems, Pneumonia.
1. Introduction

Pneumonia affects millions of people each year, which represents significant risks for children, adults aged 65 and over, and individuals with comorbidities. This scenario was aggravated in 2019 by the emergence of the virus SARS-COV-2, which is responsible for the COVID-19 pandemic. In most cases, SARS-COV-2 causes mild and moderate symptoms. However, it can also cause severe pneumonia and lead to death [1].

The transmission of SARS-COV-2 is accelerated. Meanwhile, the pandemic risk depends on several factors, including the availability of testing facilities and socioeconomic factors. In June 2021, the World Health Organization (WHO) reported 181,007,816 confirmed cases of COVID-19 and 3,927,222 deaths globally [2]. In the same year, new and more transmissible SARS-COV-2 variants were discovered in several places around the globe. Among them, we highlight the P.1 variant, which has a 25% to 65% chance of reinfecting people and eight times more chance to lead to death [3]. Early diagnosis is crucial to prevent both the proliferation of SARS-COV-2 and the death of patients.

The standard test to detect COVID-19 is the Reverse-Transcriptase Polymerase Chain Reaction (RT-PCR), which can cost between US$ 120 and US$ 130, and requires a specialized biosafety laboratory to host the Polymerase Chain Reaction (PCR) machine. Thus, the RT-PCR is an expensive and time-consuming test.

Given this, lung X-ray images stand out as an alternative to support case screening. Thereby, it is possible to refer a patient with lung injuries caused by COVID-19 pneumonia to undergo RT-PCR. The COVID-19 pneumonia is characterized in images by peripheral distribution, ground-glass opacity, fine reticular opacity, and vascular thickening. These images have already been used to detect both SARS-COV-1 and Middle East Respiratory Syndrome (MERS) [4].

Generally, the evaluation of these images is done manually by specialists. This can further increase the possibility of inaccurate analyses in the context of the pandemic. The latest Computer-Aided Diagnosis (CAD) systems use
techniques that are based on Deep Learning (DL) to detect pulmonary diseases, among them SARS-COV-2 [5]. The use of CAD systems aims to relieve repetitive work, prevent observational oversights and the number of false negatives, and thus increase work efficiency.

Our work investigates several types of pneumonia detection, including COVID-19, based on X-ray image processing and DL techniques. To address this objective, we present three contributions: 1) An end-to-end methodology to automatically detect pneumonia caused by SARS-COV-2, which could directly assist screening cases of COVID-19, and make the process faster and more efficient. 2) A new genetic fine-tuning method that is based on genetic algorithms to automatically define an optimal set of hyperparameters in the fine-tuning of different CNN architectures when applied to pneumonia classification. 3) A pre-processing step, including data-augmentation, contrast enhancement, and resizing methods to overcome the challenge of the heterogeneous and few samples that can be found in public pneumonia datasets.

The rest of this article is structured as follows: Section 2 reviews the related works; Section 3 describes the proposed method; Section 4 gives the results and discussion; and finally, we draw the conclusion and make several suggestions for future work in Section 5.

2. Related Works

Sivaramakrishnan et al. [6], classified X-ray images of COVID-19 using lung segmentation from the U-Net CNN. They classified the images with five distinct CNNs, as follows: VGG-16, Inception-V3, Xception, DenseNet-121, and NasNet-Mobile. In the experiments, the authors used 12,899 images that were divided into three classes: 314 had COVID-19, 1,583 were healthy, and 11,002 had types of pneumonia. They reported an accuracy of 0.910, an AUC of 0.960, a sensitivity of 0.950, a specificity of 0.850, a precision of 0.910, and an F1-Score of 0.930. Although the result of segmentation with U-Net could be considered acceptable, it involves substantial computational power. We believe that trans-
fer learning and fine-tuning could avoid lesion segmentation and improve the classification rates.

In Brunese et al.’s [7] research, the authors classified X-ray images using a method that highlights chest radiography areas with CNN VGG16. Their study classified 250 COVID-19 images, 3,520 healthy images, and 2,753 images of pneumonia. The results obtained had a sensitivity of 0.960, a specificity of 0.980, an F1-Score of 0.940, and an accuracy of 0.960. However, the authors did not use pre-processing methods that could improve the results.

In Rahimzadeh et al.’s [8] work, the authors used 180 images of SARS-COV-2, 6,054 images of pneumonia, and 8,851 images of healthy people. They applied data augmentation to reduce the differences in the images by classes. They also used resizing (300×300) in the images and the transfer learning of Xception and Resnet50. Although the authors achieved an accuracy of 0.914, they used a small number of COVID-19 images and evaluated using only one validation metric.

Ozturk et al. [9] applied data augmentation to improve the ratio of the number of images by classes and used CNN DarkCovidNet inspired by DarkNet. The images used were 127 images of COVID-19, 500 images of pneumonia, and 500 images of the no-finding type. The results achieved had a sensitivity of 0.853, a specificity of 0.921, a precision of 0.899, an F1-Score of 0.873, and an accuracy of 0.870. In this work, it was not possible to identify whether the images were public.

We used three public image datasets divided into three different classes (i.e., COVID-19, pneumonia, and normal). This context is closer to the possibilities of the real world than the previously mentioned works. We employ two pre-trained CNN architectures and we apply specific data augmentation operations to the type of image. In addition, we employ an Evolutionary Genetic Algorithm in the selection of the hyperparameters when fine-tuning the CNNs. We use the Kappa, Accuracy, F1-Score, AUC, and Precision validation metrics to validate our results.
3. Proposed Methodology

The method adopted in this investigation consists of: 1) acquisition of X-ray images; 2) image pre-processing; 3) data augmentation, focused on the problem, to reduce the existing imbalance among the classes; 4) apply the evolutionary genetic algorithm for the selection of hyperparameters in the fine adjustment of CNNs; and 5) validate the results.

3.1. Image Acquisition

We used three distinct classes (i.e., COVID-19, pneumonia, and healthy). First, we collected images of COVID-19 from two different datasets—the COVID-DB Dataset [10], and the Covid-19 Dataset [11]—which were unified as one. For the pneumonia and healthy classes, we use the NIH Chest X-ray [12] image dataset. All of these image datasets are public. Table 1 summarizes the dataset information and Figure 1 show examples of each class.

| Classes           | COVID-DB [10, 11] | NIH Chest X-ray [12] |
|-------------------|-------------------|----------------------|
| Healthy/No Finding| -                 | 60,412               |
| Pneumonia         | -                 | 307                  |
| COVID-19          | 292               | -                    |

3.2. Image pre-processing

We employ some pre-processing techniques to improve classification, which will be outlined in this section.

The acquired images have different sources, and therefore they vary in their type between 8, 16, and 32 bits. We convert all images to 8 bits because this is the variation with the largest amount of images.

X-rays can have a contrast that makes it difficult to detect diseases because it may not separate the borders of high and low-density tissues well. We use
Figure 1: Examples of the dataset classes: (a) healthy/no finding; (b) pneumonia; and (c) COVID-19.

the Limited Contrast Adaptive Histogram Equalization (CLAHE) technique to improve the contrast, which divides the image by regions to be equalized by their histograms. To avoid the propagation of noise in the region, we use contrast limitation [13].

The images vary in size, from a height of 237 to 4,095 and from a width of between 255 to 4,280. This made it necessary to resize the images to 224 × 224 because this is the standard CNN entry adopted here. To avoid distortions, we applied zero paddings.

When resizing, images can lose important information for learning algorithms. We use the resize based on the max Pool to reduce this loss, which can lead to a faster convergence rate because it selects superior invariant resources that can improve the generalization [14]. Consequently, characteristics that denounce COVID-19 and pneumonia, such as inflammation in the pulmonary alveoli, are more likely to be preserved [15]. Figure 2 shows an image without our pre-processing and the result after pre-processing.

3.3. Data Augmentation

Although the COVID-19 and pneumonia classes have a similar number of samples (292, 307). We use data augmentation to overcome the imbalance, where we employ a set of techniques that improve the training sets’ size and
Figure 2: Pre-processing result: (a) original image; (b) resulting image after pre-processing that applied the CLAHE (zero padding and resizing with the max pool).

quality. Consequently, DL models can improve their learning and generalization [16]. The techniques employed were: rotation varying up to 6º; blur with kernels $3 \times 3$, $5 \times 5$; zoom ranging from 0% to 30%; change in height and width of interval 0.1; brightness range from 10% to 20%; and Gaussian noise between 0% and 8%.

These intervals were selected to simulate different positions, qualities, and exams but preserve the characteristics that could expose the classes.

3.4. Convolutional Neural Network

In this work, we adopted CNNs in the feature extraction and classification of images. CNNs are a specific type of multilayer neural networks, differing from other networks only in their architecture by adding convolutions that enhance characteristics in the image, facilitating their classification [17]. Figure 3 illustrates a generic CNN architecture.

In this work, we adopted two CNN architectures: ResNet50 [18] and VGG16 [19]. We made this choice because it can achieve the best results in the classification of several problems in X-ray images, as well as COVID-19.
Figure 3: Example of a generic CNN architecture based on [17]. In this image, it is possible to visualize the most important processes that CNN employs in the classification of images: from the convolution layer that improves or removes some characteristics of the images; the pooling layer that reduces sample activation map input; and then the characteristics are extracted and sent to the Multilayer Perceptron, which predicts which class the image belongs.

3.5. Transfer Learning and Fine-Tuning

Training a CNN from scratch is complex and requires an enormous amount of data for the model to converge. An alternative is to fine-tune on a pre-trained CNN. Transfer learning with the ImageNet [20] suite helps CNNs improve their performance, even in chest X-ray medical images [21]. A pre-trained CNN with the proper fine-tuning is able to outperform trained CNNs from scratch and is more effective with smaller datasets [22]. Therefore, in this work we employ ResNet50 and VGG16 CNNs pre-trained with ImageNet.

3.6. Hyperparameters

No DL architecture fits all problems. Therefore, it is necessary to select an appropriate set of hyperparameters. The sets of hyperparameters of CNNs applied to fine-tuning include the number of layers, number of neurons per layer, activation function in hidden layers, optimizer, dropout, among others [23].

3.7. Evolutionary Genetic Systems

Evolutionary genetic systems are a branch of artificial intelligence. These algorithms solve problems based on trial and error, using populations based on stochastic and metaheuristic optimization.

Generally, evolutionary computing generates an initial, random population set, with each individual being a possible solution to the problem in question.
New individuals are generated by reproduction between previous individuals selected for their characteristics and ability to solve the problem with each new generation. Some mutations (i.e., small changes in characteristics) can be inserted at random when new individuals are generated, which increases the abundance of phenotypes in individuals [24].

Evolutionary systems produce optimized solutions for a wide range of problems because they are easily adaptable. Consequently, we chose to use them in our methodology to classify COVID-19 because it is a new problem, which makes it difficult to deduce solutions from previous experiences.

3.8. Genetic Fine-tuning

An essential part of fine-tuning is the choice of hyperparameters for the fully connected layers. However, finding a set that guarantees a reasonable convergence rate is complex because the search space is ample. As Neural Networks (RNs) and CNNs developed, they became more complex. This makes them difficult to configure. Although experienced users can optimize some parameters, RNs and CNNs have a complex topology with several hyperparameters [18, 19].

The choice of design is essential because success depends on finding the correct architecture for the problem in question. Much DL research has focused on proposing new architectures and not on new problems [25].

To make the process of choosing hyperparameters more efficient, we developed an evolutionary genetic system, as illustrated in Figure 4. In this system we can make the search more efficient through reproduction, selection of individuals, and mutation. For this work, we selected the CNNs and the following hyperparameters for what we call genetic fine-tuning, see Table 2.

In Table 2, the selection of parameters was based on previous experiences with X-ray and also considering the computational cost in our algorithm. Looking at the options listed in Table 2, our search space has 5,760 possibilities but genetic fine-tuning has optimized it.

- Individual: This consists of a CNN pre-trained with ImageNet; its hyperparameters are contained in an attribute vector that informs how many
Table 2: Hyperparameter search space: types of hyperparameter, and their possibilities and quantities.

| Type               | Hyper-Parameters                        |
|--------------------|-----------------------------------------|
| CNN                | [ResNet50, VGG16]                      |
| Number of layers   | [1, 2]                                  |
| Neurons/layer one  | [512, 768, 1024]                       |
| Neurons/layer two  | [64, 128, 256, 512, 768, 1024]          |
| Activation         | [tanh, relu, selu, elu, exponential]    |
| Optimization       | [adam, sgd, rmsprop, adadelta]          |
| Dropout            | [0.3, 0.4, 0.5, 0.6]                    |

layers, how many neurons per layer, which activation function, and which optimizer and dropout should be used.

- Initial Population: We generated a population of 60 individuals, which are all generated at random and without replicates.

- Reproduction: This occurs by selecting two individuals by a Roulette known as stochastic replacement sampling. Each individual is selected based on their kappa. This step is essential because this is the filtering stage for new individuals who can generate better or worse results.

- New Individual: In each reproduction, a new individual is generated who inherits characteristics from both "father" and "mother" in a process called Crossover.

- Mutation: Whenever a new individual is generated, the mutation can alter a phenotype in its attribute vector. The probability of a mutation occurring is 5%. This percentage was selected because it is not high enough to prevent the transmission of parental characteristics, nor is it low enough to preclude the emergence of new characteristics.

- Selection of Individuals for New Generation: At the end of each generation, 60% of individuals with the best accuracy are selected, and the rest were
discarded. These selected individuals will have a new chance to reproduce
and pass on their characteristics.

- Stop condition: To avoid infinite looping, we determined three stop condi-
tions: first, if any individual reaches 100% \( \kappa \), then the algorithm must
stop; second from the 10th generation on, the average \( \kappa \) of the current
generation should be compared with the previous 5, if the result is lower,
then the algorithm must stop; and finally, if the hundredth generation
arrives, then the algorithm must stop.

![Figure 4: Illustration of the hyperparameter selection steps by our methodology (which is
named genetic fine-tuning).](image)

3.9. Validation Metrics

We adopted the following metrics to evaluate and analyze the performance
of our method, and in particular of the CNNs: Kappa (\( \kappa \)); Accuracy (Acc);
F-Score; Area Under Receiver Operating Characteristic Curve (AUC) and Pre-
cision (Prec).

The \( \kappa \) index is used as a measure to represent the confusion matrix full.
This index is an agreement coefficient for nominal scales that measures the
relationship between agreements.
Acc is a fraction of detection that can be achieved with the selected model.
The F-Score is the average damage of sensitivity and precision.

The Receiver Operating Characteristic Curve (ROC) is a metric that shows the performance of a classification model at all classification thresholds, and the Area under the ROC Curve (AUC) measures the entire two-dimensional area below the entire ROC curve.

Precision measures how many times the model was correct when inferring positive class.

4. Results and Discussion

4.1. Experiments

Using the datasets detailed in Section 3.1, we performed the classification of COVID-19 against the pneumonia and healthy classes. Our goal was to find a set of hyperparameters, in fine-tuning, from CNNs Resnet50 and VGG16, by employing the technique that we call genetic fine-tuning in Section 3.8, which obtained a good rating.

For each individual generated by genetic fine-tuning, the possibility of training for 60 epochs was given with 80% of images in training, 10% in testing, and 10% in the validation. We set it as patience (number of epochs without improvement after which the training will be interrupted) as 22 epochs, which kills individuals without progression.

4.2. Results

In this section, we report and analyse the results obtained with our methodology.

After genetic fine-tuning generated 38 generations, the second stop function, as mentioned in 3.8, was activated because the method was unable to continue improving the $\kappa$ results. Table 3 presents the genetic fine tuning results for the 10 best individuals selected by the algorithm and the two CNNs with their original settings.
Table 3 illustrates that the proposed genetic fine-tuning managed to find better results than the original configurations for the two CNNs. This perception is even greater when comparing the original ResNet50 with the one selected by the algorithm, and the original uses the Global Average Pooling (GAP) layer. GAPs reduce the special dimensions of the three-dimensional tensor by performing an extreme type of dimensional reduction, where they reduce each \( h \times w \) feature map using the mean of these values. The original ResNet50, after the GAP layer, does not use any fully connected layer, except the outgoing one [18]. This fact may have impaired its generalization and restricted learning.

Table 3: Experiment results: the 10 best individuals, their characteristics, and the results obtained.

| CNN   | Layers | Neurons | Neurons | Activation | Optimizer | Dropout | Acc | F-Score | AUC | P  |
|-------|--------|---------|---------|------------|-----------|---------|-----|---------|-----|----|
| ResNet50 | 2  | 1024   | 128   | relu  | adam  | 0.4 | 0.836 | 0.970 | 0.949 | 0.884 | 0.841 |
| ResNet50 | 2  | 1024   | 128   | relu  | sgd   | 0.4 | 0.836 | 0.970 | 0.949 | 0.886 | 0.840 |
| ResNet50 | 2  | 1024   | 256   | relu  | sgd   | 0.3 | 0.816 | 0.965 | 0.947 | 0.872 | 0.828 |
| ResNet50 | 1  | 768    | 0     | selu  | sgd   | 0.3 | 0.658 | 0.955 | 0.931 | 0.756 | 0.741 |
| ResNet50 | 1  | 512    | 0     | elu   | rmsprop | 0.6 | 0.643 | 0.953 | 0.658 | 0.749 | 0.670 |
| ResNet50 | 1  | 512    | 0     | elu   | sgd   | 0.3 | 0.653 | 0.952 | 0.653 | 0.743 | 0.650 |
| ResNet50* | 0  | 0      | 0     | relu  | adam  | 0.0 | 0.650 | 0.962 | 0.825 | 0.834 | 0.786 |
| VGG16  | 2  | 1024   | 128   | relu  | adam  | 0.4 | 0.845 | 0.970 | 0.893 | 0.898 | 0.836 |
| VGG16  | 2  | 1024   | 256   | relu  | adam  | 0.4 | 0.820 | 0.965 | 0.869 | 0.859 | 0.818 |
| VGG16* | 2  | 4.096  | 4.096 | relu  | adam  | 0.0 | 0.751 | 0.962 | 0.825 | 0.834 | 0.786 |
| VGG16  | 2  | 512    | 1024  | tanh  | rmsprop | 0.6 | 0.643 | 0.953 | 0.673 | 0.749 | 0.670 |
| VGG16  | 1  | 512    | 0     | relu  | rmsprop | 0.4 | 0.643 | 0.953 | 0.673 | 0.749 | 0.670 |

**Bold** is the best result for each CNN and the * indicates CNNs in their original settings.

Table 3 shows that ResNet50 and VGG16 obtained similar results, which are in agreement with the state-of-the-art studies. The use of two fully connected layers with 1,024 in the first layer and 128 in the second in the first five individuals showed that two layers combined with this set of neurons bring greater generalization power. The ReLU activation function was very successful, due to its non-linearity. The stochastic gradient descent optimizers, ADAM and SGD, were selected as the best for the algorithm’s problem. The 0.4 dropout showed the best result.
Figure 5 shows the confusion matrix of the two best models, where we can see the successes and errors in each class. ResNet50 in Figure 5 (a) hit all of the images of COVID-19, and missed six images of pneumonia and 14 healthy images. VGG16 in Figure 5 (b) hit all the images of COVID-19, missing two of pneumonia and 18 healthy images.

![Confusion Matrix](image)

Figure 5: The confusion matrices of the two best models (a) ResNet50 and (b) VGG16. The first class is COVID-19, the second class is pneumonia, and the third class is healthy.

The two matrices reveal that the models achieved a good generalization and mainly managed to correct the images of COVID-19, which would be essential in a real pandemic environment. We also found that our methodology managed to separate the classes, even with the unbalanced image datasets.

4.3. Comparison with the state-of-the-art

In this section, we compare the results of our methodology with those found in our state-of-the-art, as shown in Table 4.

Our best result surpassed the others found in our research, as shown in Table 4. The work that had the closest result to ours was that of Luca Brunese et al. [7], which obtained 0.960 accuracy, compared to our 0.970. However, this work presented two validation metrics, which could be unviable for a fair comparison.
5. Conclusion and Future Works

Genetic fine-tuning proved to be a very promising choice for COVID-19 pneumonia classification because we find a set of CNN parameters that outperformed their original setups. The classification of the other classes was also favorable, and is very close to what is desired in a real pandemic environment. Thus, our methodology could assist in classifying COVID-19 pneumonia, which could reduce costs by making the process faster and more efficient.

In our future work, we intend to use genetic fine-tuning in the classification of COVID-19 against other classes and to test it in other contexts related to the classification of medical images.

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Short-Bio

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Highlights

A methodology to automatically detect pneumonia caused by SARS-COV-2.

A Genetic Fine-Tuning applied to CNNs architectures for pneumonia classification.

Pre-processing step to overcome the scarcity and heterogeneity of pneumonia datasets.