

Mixup Data Augmentation for COVID-19 Infection Percentage Estimation

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Abstract. The outbreak of the COVID-19 pandemic considerably increased the workload in hospitals. In this context, the availability of proper diagnostic tools is very important in the fight against this virus. Scientific research is constantly making its contribution in this direction. Actually, there are many scientific initiatives including challenges that require to develop deep algorithms that analyse X-ray or Computer Tomography (CT) images of lungs. One of these concerns a challenge whose topic is the prediction of the percentage of COVID-19 infection in chest CT images. In this paper, we present our contribution to the COVID-19 Infection Percentage Estimation Competition organised in conjunction with the ICIAP 2021 Conference. The proposed method employs algorithms for classification problems such as Inception-v3 and the technique of data augmentation *mixup* on COVID-19 images. Moreover, the *mixup* methodology is applied for the first time in radiological images of lungs affected by COVID-19 infection, with the aim to infer the infection degree with slice-level precision. Our approach achieved promising results despite the specific constraints defined by the rules of the challenge, in which our solution entered in the final ranking.

Keywords: Computer Vision · Inception-v3 · Computer Tomography

1 Introduction

In December 2019 a significant increase of pneumonia cases was reported in Wuhan, Hubei Province, China [9]. These cases are due to an infection with a novel coronavirus. In the following weeks, infections spread across China and other countries around the world [5]. On January 30, 2020, the World Health Organization (WHO) declared the outbreak a Public Health Emergency of International Concern [25]. On February 12, 2020, the WHO baptized the disease caused by the novel coronavirus “coronavirus disease 2019” (COVID-19) [26]. Numerous epidemiological studies have been conducted to model the outbreak and the trend of the pandemic [15, 16]. At the same time, a group of international experts, with a range of specialisations, are working to try to contain and defeat the pandemic. During these months, the radiological imaging techniques,

e.g. X-rays and Computed Tomography (CT), are demonstrating to be the most effective diagnostic tests of this disease including the follow-up assessment and evaluation of disease evolution [21, 3] as well as the quick detection of proper interventions especially for asymptomatic cases. Actually, a clinical study with 1014 patients in Wuhan China, has shown that chest CT analysis can achieve 0.97 of sensitivity, 0.25 of specificity, and 0.68 of accuracy for the detection of COVID-19 [1]. Similar observations were also reported in other studies [4, 19] suggesting that radiological imaging may help support early screening of COVID-19. Nevertheless, this practice requires a complex effort by radiologists. For this reason, many Computer Vision systems [6–8, 24, 2] have been developed and proposed to offer a diagnostic tool that can help the decision-makers in the medical and health centers. The goal is a rapid and accurate identification of COVID-19 infection in radiography images (i.e. x-ray or CT imaging) of lungs. Given the significant scientific and social impact of COVID-19 infection, multiple research initiatives have been proposed worldwide. One of these is the First International Workshop on Medical Imaging Analysis for COVID-19 (MIA COVID) that is associated with 21st International Conference on Image Analysis and Processing (ICIAP 2021). The workshop proposes an associated challenge about the estimation of the percentage of COVID-19 Infection from thoracic CT scans. We as IPLab team¹ of the Department of Mathematics and Computer Science of the University of Catania participated in the challenge. In this paper, we present our results in the MIA COVID challenge, in which we entered in the final top-score ranking (seventh ranked out of 50 participants). The paper illustrates the methodology employed to predict the percentage of COVID-19 infection in CT slices of lungs achieving the best results by the application of the *mixup* data augmentation technique during the training of the neural network. We believe that our method would help radiologists in diagnosing infection related to COVID-19. To encourage research on this topic, we publicly release our codes and models at the following url: <https://github.com/ausilianapoli/Percentage-Covid-Estimator>.

The paper is structured as follows: Section 2 describes related work in relation to our work, Section 3 describes all the details of the MIA challenge concerning COVID-19, the methodology and approach used to solve the challenge problem are described in Section 4, whereas the experiments are detailed in Section 5. Finally, the manuscript concludes with some considerations regarding the results obtained and possible future works in Section 6.

2 Related Works

In recent years, there has been an increasing number of algorithmic solutions based on computer vision methods to several tasks and practical applications, among others, significant examples are the applications of computer vision in the field of medical imaging [12, 18]. Nowadays, computer vision is used in solving problems involving COVID-19. Research in this area is very fervent, given the

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pandemic state of the world today. Indeed, the combination of Computer Vision techniques with various imaging modalities can assist to increase the efficiency of COVID-19 detection worldwide [3]. Gudigar et al. [6] have published a survey in which they collected and filtered 184 papers that are the most influential in the field of Computer Vision applied to COVID-19, which deals with classification issues. Generally, in these problems the input data are CT images or X-ray images of patients. For instance, Heidari et al. [7] use chest X-ray images to detect COVID-19 induced pneumonia. They fine-tune a VGG16 [14] based on Convolutional Neural Network (CNN) model pre-trained on ImageNet [20] challenge database yielding 94.5% classification accuracy in three-classes scenario (i.e., pneumonia induced by COVID-19, other pneumonia and normal cases). Moreover, Hellwan et al. [8] finetuned an Imagenet pre-trained DenseNet-201 [31] on a dataset of chest CT images, achieving an accuracy of 97.8% in a two-classes scenario (i.e. COVID-19 vs no COVID-19). Vantaggiato et al. [24] propose an Ensemble-CNNs approach to distinguish chest X-ray images between healthy, COVID-19 and pneumonia resulting in an accuracy of 100%. The CNNs employed are ResNext-50 [28], Inception-v3 [23] and DenseNet-161. Bougourzi et al. [2] introduce a new problem in this research field. It is the estimation of the percentage of COVID-19 infection from CT scans. For this purpose, the authors collected a dataset of 183 CT scans and 3986 slices and the dataset was named Per-COVID-19. The authors employed the Inception-v3 neural network pre-trained on ImageNet to perform transfer learning. However, this work is different from the previous ones because it deals with a problem of regression instead of classification. For this reason, the loss function employed is Huber Loss and performance is measured with Mean Absolute Error (MAE), Pearson Correlation (PC) and Root Mean Square Error (RMSE), obtaining 5.34 MAE, 0.9330 PC and 9.44 RMSE.

We decided to work on the latter problem with a strong emphasis on data augmentation that deals with a suite of techniques that enhance the size and quality of training datasets such that better deep learning models can be developed using them. Traditional methods of data augmentation are proven to be a good practice in many fields [22]. One of these is the color space augmentation which, among other things, leaves plenty of room for creativity as shown in [17, 27]. A not conventional type of transformation, e.g. *mixup* [29], regards the combination of two or more original images to generate the new one. The *mixup* authors tested it with state-of-the-art models on some datasets such as ImageNet and CIFAR. These experiments have shown that this data augmentation technique improves the generalisation error. Moreover, the *mixup* technique is employed in chest CT imaging with success. The authors in [30] apply this method on chest CT images to do predictions about pulmonary adenocarcinoma with much improved performance compared to experiments without *mixup*. For these reasons, we choose to employ *mixup* in COVID-19 chest CT images. To the best of our knowledge, this is the first study introducing *mixup* into COVID-19 image computing.

3 Challenge

The MIA COVID 2022 has launched a scientific challenge which task is the estimation of the percentage of COVID-19 infection from thoracic CT scans. The presence of COVID-19 is diagnosed through the reverse transcription polymerase chain reaction. Nowadays, this test is considered as the global standard method for COVID-19 diagnosis [13]. Furthermore, the presence of COVID-19 is confirmed by the CT scan manifestations identified by two experienced thoracic radiologists. In this way, the authors of [2] have built a dataset for the competition’s participants (i.e., Per-COVID-19).

The challenge has three sets: Train, Validation, and Test. The Train set contains 132 CT scans, from which 128 CT scans have COVID-19, and the rest 4 CT scans have not any infection type (i.e., healthy). Instead, the Validation set includes 57 CT scans, from which 55 CT scans are affected by COVID-19, and the rest 2 CT scans are healthy. Moreover, no information was provided for the Test set that consists of 4449 CT scans. Finally, the infection labels are available only for the Train set. The Figure 1 shows some CT scans from the three sets of data.

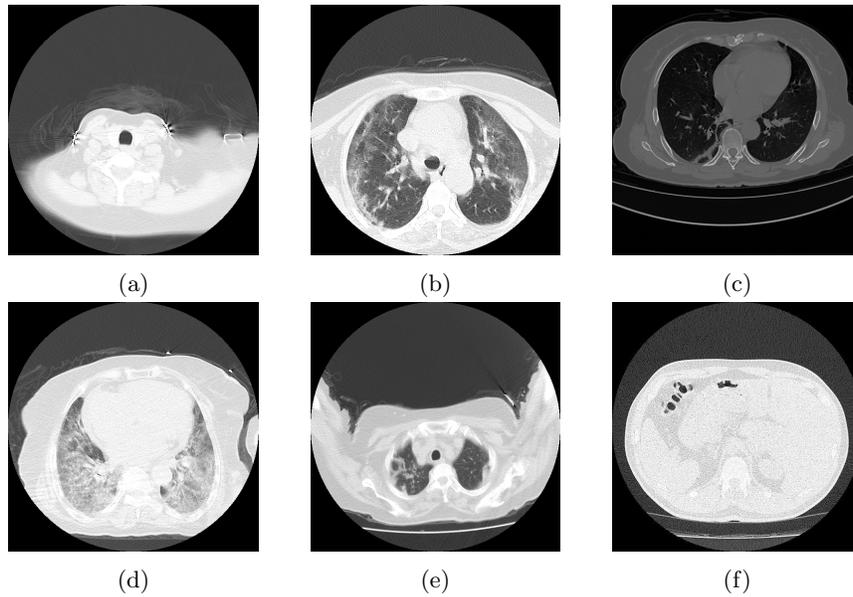


Fig. 1: Sample CT scans included in the three sets of data: **(a)** and **(d)** are train images with respectively 0% and 100% infection percentage; **(b)** and **(e)** are validation images; **(c)** and **(f)** are test images.

The challenge requires that proposed approaches estimate the percentage of COVID-19 infection from each slice using deep learning techniques. Moreover,

there are some limitations for the participants and the proposed approaches. Only ImageNet’s pre-trained models and lung nodule segmentation models are allowed. Thus, the use of other pre-trained models is not allowed. In addition, it is forbidden to use data other than that provided by the challenge with respect to Train, Validation and Test sets. Finally, the challenge’s organisers have established also the evaluation metrics - that are MAE, PC and RMSE - for all approaches. The most important evaluation criterion is the MAE. In the event of two or more competitors achieving the same MAE, the PC and the RMSE are considered as the tie-breaker.

4 Methodology

The COVID-19 pandemic increased considerably the workload in hospitals. This has led to the development of various techniques to make diagnosis faster and more accurate. In this context, computer vision is contributing by developing deep learning algorithms that can predict the rate of infection in chest CT of the patients.

For these reasons, there are an increasing number of research works in this field. Thus, we decided to propose a novel methodology based on a data augmentation technique that firstly is applied on COVID-19 lung images. The technique is *mixup* that creates convex combinations of pairs of samples and their corresponding labels [29]. This means that a *mixup* process is simply averaging out two images and their labels correspondingly as new data. Specifically, *mixup* augmentation is explained with the following equations

$$\begin{aligned}\hat{x} &= \lambda \cdot x_i + (1 - \lambda) \cdot x_j \\ \hat{y} &= \lambda \cdot y_i + (1 - \lambda) \cdot y_j\end{aligned}\tag{1}$$

where \hat{x} is a blend of two images that are x_i and x_j , while \hat{y} is the mixed label of labels y_i and y_j . Instead, λ is a beta distribution generated with a number between 0 and 1 that specifies the weight of the two samples in contributing to the new data. The definition of *mixup* implies that the two samples belong to different classes. Otherwise, this technique would not be applied properly. This is valid for classification problems which are the general and most frequent use case of *mixup*. However, we deal with a regression task and therefore the choice of the two samples is random. Examples of new images generated with *mixup* are shown in Fig. 2.

The *mixup* augmentation creates virtual examples that significantly increase the diversity of data available regardless of the neural architecture employed. Thus, the technique improves the generalisation error of the neural network making it more robust. These are the benefits introduced by the use of this technique that does not compromise the training time of a neural network. Actually, *mixup* inside the training pipeline does not bring computational overhead since it is fast and needs only a few lines of code.

In our approach, we employ the neural network Inception-v3 pre-trained on ImageNet. Inception-v3 is a widely-used neural network for image recognition. Thus, this network is employed in classification problems. Since we deal with a regression task, we replace the last layer of the original Inception-v3 with a fully connected layer with a single output that is the probability of COVID-19 infection. We choose the Huber loss function [10] as criterion. The loss function is defined for N batch size, and $Y = (y_1, y_2, \dots, y_N)$ are the ground-truth and $\bar{Y} = (\bar{y}_1, \bar{y}_2, \dots, \bar{y}_N)$ are their corresponding estimated percentages. The Huber loss function is defined by

$$L_{Huber} = \frac{1}{N} \sum_{i=1}^N l_i \quad (2)$$

where N is the batch size and l_i is defined by

$$l_i = \begin{cases} 0.5(x_i - \bar{y}_i)^2, & \text{if } |x_i - \bar{y}_i| \leq \delta \\ \delta |x_i - \bar{y}_i| - 0.5\delta^2, & \text{otherwise} \end{cases} \quad (3)$$

where δ is a hyperparameter.

5 Experimental Results

The approach described in the previous Section has been trained and validated by means of the dataset released by the challenge described in Section (§3). All experiments and setups are reported in detail in the following subsections.

5.1 Neural Network Model Setup

We use the three sets of data provided by the challenge with their respective purposes namely Train set for training our approach, Validation set for validating it and Test set for the final rank. Images have been normalised to the range $[0, 1]$ using the mean and standard deviation of ImageNet challenge database. We employ the *mixup* augmentation as described previously and we generate the beta distribution λ with its parameter = 0.2 in Eq. (1). The Fig. 2a is generated from image x_i with 0% infection and image x_j 98% resulting with 38% COVID-19 infection; the Fig. 2b derives from image x_i with 13% infection and image x_j 5% resulting with 10% COVID-19 infection; the last Fig. 2c is mixed from image x_i with 33% infection and image x_j 44% resulting with 37% COVID-19 infection. Moreover, we have used other traditional data augmentation techniques that are:

- gaussian blur with kernel 5×5 ;
- color jitter;
- random horizontal flipping;
- random vertical flipping;
- random cropping 492×492 followed by a resizing to 512×512 ;
- rotation with a random degree of $\pm 10^\circ$.

We train our network for 50 epochs with an initial learning rate of 0.0001 with decays by a factor 10 every 10 epochs and batch size equals 20. The weight decay hyperparameter is set to 0.5 to regularize the network. Another hyperparameter varies during the training i.e. δ in the Huber loss function. It decreases from 15 to 1 by 0.5 step every epoch. Finally, we use Stochastic Gradient Descend (SGD) as optimizer.

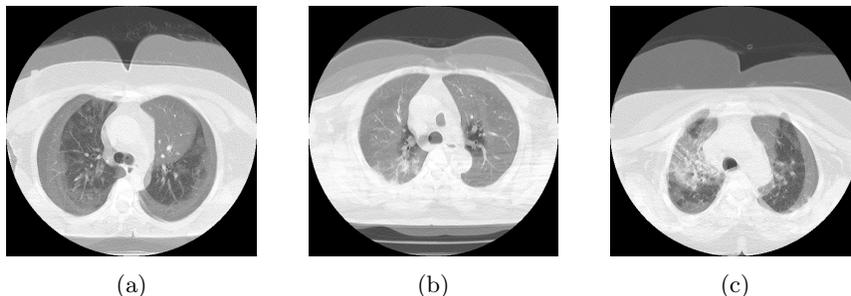


Fig. 2: Examples of new data generated with mixup augmentation technique from training images

5.2 Results and Discussion

We employ the evaluation metrics suggested by the challenge’s organisers i.e. MAE, PC and RMSE. The Table 1 shows the results of our best model for each phase of the challenge. In the final rank our approach is placed seventh. To interpret the network predictions, we also produce saliency maps to visualise the areas of the image most indicative of the infection using CAMERAs [11]. To generate the saliency maps, we feed an image into the fully trained network and choose the final convolutional block of the Inception-v3 network to obtain these maps. The Figures 3 and 4 show some prediction and their saliency maps respectively for Validation set and Test set. Analysis of the saliency maps shows that the algorithm focuses on the highest density areas, i.e., those with a grey level close to white. This is meaningful because the COVID-19 infection involves an increase in density within the lungs resulting in whitish areas. It is important to note that the lungs are surrounded by other tissue that shows up as a thick whitish area that confuses the algorithm. Actually, it happens that the focus is on these regions where there is no COVID-19 infection.

The experiments show that the proposed method is valid for processing COVID-19 chest CT images. The validation MAE is better than the threshold for admission to the final phase of the challenge (i.e. 5.294). Moreover, in this phase we improved the results achieved by Bougourzi et al. [2] that deal with our same problem but on the entire labeled Per-COVID-19 dataset. Actually, the Train set of the challenge is a subset of the Per-COVID-19 database and

Table 1: Results achieved by IPLab team during all challenge’s phases.

Phase	MAE	PC	RMSE
Validation results	4.953	0.944	8.604
Testing results	6.536	0.709	9.976
Final ranking ($0.3 * Validation + 0.7 * Testing$)	6.061	0.779	9.016

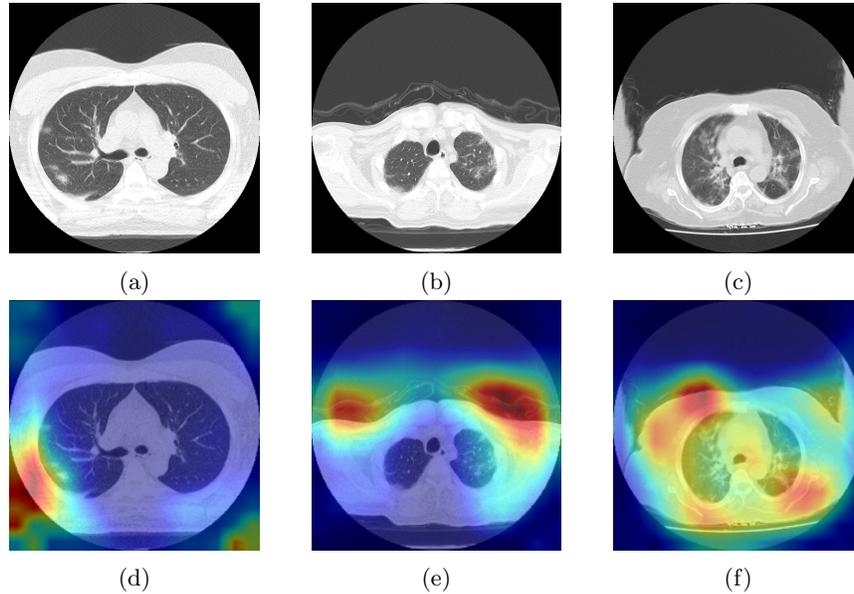


Fig. 3: Some predictions on images from Validation set and their saliency maps: **(a)** has 3% COVID-19 infection estimated by the model while **(d)** is its saliency map; **(b)** has 18% COVID-19 infection estimated by the model while **(e)** is its saliency map; **(c)** has 41% COVID-19 infection estimated by the model while **(f)** is its saliency map.

labels are provided for only this subset. This limitation together with the impossibility of using external data sources promotes the occurrence of overfitting. Actually, there are signs of overfitting in the performance on the Test set since these are worse than the ones in the Validation set. This is due to the limited amount of data available for the above-mentioned reasons and the diversity of testing images whose details are illustrated in the following. In addition, it was not possible to fine-tune the network after the results about the Test set due to the challenge rules². Despite the limitations imposed and the difficulties ex-

² <https://github.com/faresbougourzi/Covid-19-Infection-Percentage-Estimation-Challenge>

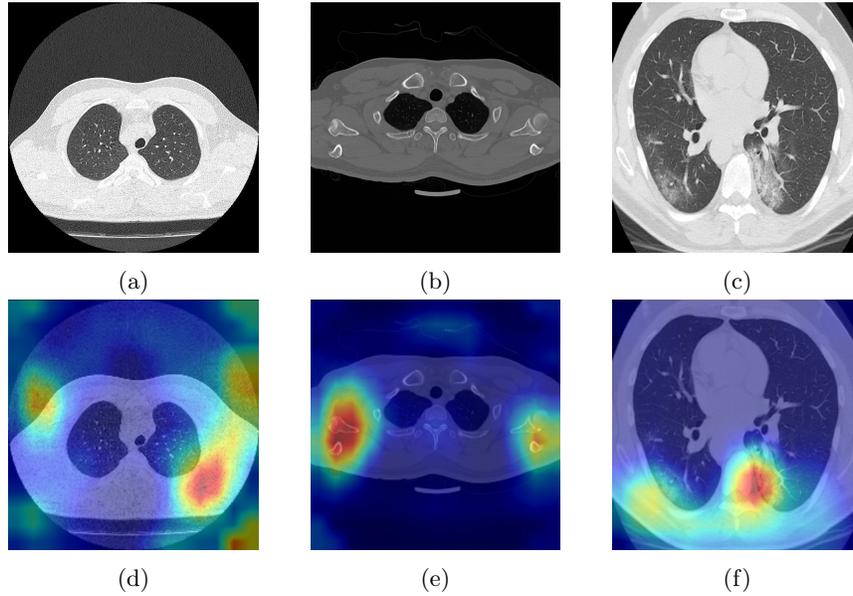


Fig. 4: Some predictions on images from Test set and their saliency maps: **(a)** has 2% COVID-19 infection estimated by the model while **(d)** is its saliency map; **(b)** has 14% COVID-19 infection estimated by the model while **(e)** is its saliency map; **(c)** has 16% COVID-19 infection estimated by the model while **(f)** is its saliency map.

hibited, the proposed method is promising and valid given that the estimated predictions can be plausible as shown in the images reported in this manuscript.

Considerations about Test set. As previously mentioned, the Test set is different from other datasets. Actually, the Fig. 5 shows that the source of the Testing set is not the same as the other two data sets for the following reasons:

- the size of the images is not always the same (i.e. 512×512) unlike Train set and Validation set as shown in Fig. 5a for which our model predicts 18% COVID-19 infection;
- the colour gamut in Train set and Validation set is the same but not in the Test set for some images as displayed in Fig. 5b for which our approach estimates 7% COVID-19 infection;
- the presence of text in the images (e.g. Fig. 5c for which the model predicts 64% COVID-19 infection), while Train and Validation images have no text.

This negatively affects the performance on the testing set.

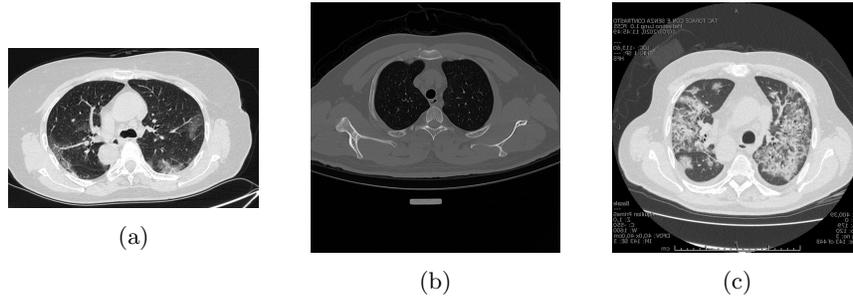


Fig. 5: Some images of Test set that reveal the different source of the data.

6 Conclusions

The COVID-19 pandemic significantly affected everyone’s life, as well as any type of organisation and public service. Hospitals are the most affected target due to the large number of cases of patients admitted for this infection, and indirect consequences to patients affected by other diseases, overload of the healthcare personnel, and the subsequent crisis of any care service. The diagnostic techniques available are good for diagnosing this disease. However, science and research are making a considerable contribution to the development of new diagnostic methods that are faster and more accurate. In this context, computer vision offers tools that could support medical decisions in the presence of radiological images of the lungs. Actually, many research works deal with the COVID-19 detection in chest X-ray or CT resolving a classification task. Moreover, the MIA COVID 2022 workshop has organised a challenge that requires deep learning algorithms for predicting the percentage of COVID-19 infection in chest CT images of patients. This is a regression task to which we have chosen to participate by adopting state-of-the-art classification algorithms. Specifically, we employ the Inception-v3 neural network together with the data augmentation *mixup* technique. The proposed method reaches the final classification by passing the Validation and Testing phases. Our results show that the approach is promising despite the limitations given by the constraints defined by the challenge rules. For these reasons, we plan to overcome the limitations imposed by the challenge such as the prohibition to use external data to those provided by the challenge. As future work, we thought to give as input to our approach the output of a lung segmentation network. Other improvements may be carried out by the exploitation of pre-trained models designed for lungs’ micro nodules segmentation, in order to make transfer learning on the available Per-COVID-19 dataset. In addition, we plan further experiments on the *mixup* method to evaluate its advantages and disadvantages in an uncontrolled domain such as misalignment of the chest in the CT images. We would also like to compare *mixup* technique with random noise as the adding noise to the training data could improve generalisation and prevent overfitting.

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