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A novel unsupervised approach based on the hidden features of Deep Denoising Autoencoders for COVID-19 disease detection

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**A B S T R A C T**

Chest imaging can represent a powerful tool for detecting the Coronavirus disease 2019 (COVID-19). Among the available technologies, the chest Computed Tomography (CT) scan is an effective approach for reliable and early detection of the disease. However, it could be difficult to rapidly identify by human inspection anomalous area in CT images belonging to the COVID-19 disease. Hence, it becomes necessary the exploitation of suitable automatic algorithms able to quick and precisely identify the disease, possibly by using few labeled input data, because large amounts of CT scans are not usually available for the COVID-19 disease. The method proposed in this paper is based on the exploitation of the compact and meaningful hidden representation provided by a Deep Denoising Convolutional Autoencoder (DDCAE). Specifically, the proposed DDCAE, trained on some target CT scans in an unsupervised way, is used to build up a robust statistical representation generating a target histogram. A suitable statistical distance measures how this target histogram is far from a companion histogram evaluated on an unknown test scan: if this distance is greater of a threshold, the test image is labeled as anomaly, i.e. the scan belongs to a patient affected by COVID-19 disease. Some experimental results and comparisons with other state-of-the-art methods show the effectiveness of the proposed approach reaching a top accuracy of 100% and similar high values for other metrics. In conclusion, by using a statistical representation of the hidden features provided by DDCAEs, the developed architecture is able to differentiate COVID-19 from normal and pneumonia scans with high reliability and at low computational cost.

1. Introduction

Since its inception, medical imaging has been a valid tool for making non-invasive medical diagnoses (Suetens, 2009). Among the different techniques, Computed Tomography (CT) has assumed a very important role (Hsieh, 2009). In fact, CT images represent a powerful investigation tool because they contain more detailed information than conventional X-rays. Unlike a conventional X-ray, this computerized version uses a mobile X-ray source that rotates around the patient and generate cross-sectional images of the body, called slices.

Recently, CT scans have been adopted to identify the novel coronavirus pneumonia (NCP) due to SARS-CoV-2 viral infection of the COVID-19 pandemic (Kwee & Kwee, 2020). In this regard, this method has demonstrated a high potentiality, showing a high sensitivity for detection of the disease (Adams et al., 2020; Lerum et al., 2020). Since COVID-19 is spreading rapidly all over the world, a fast and accurate screening is of primary importance for controlling the pandemic.

To this purpose, many researchers have highlighted that the COVID-19 pneumonia is different from other viral (common) pneumonia (CP) (Sharma, 2020). In this regard, some works have shown that cases of NCP tend to affect the entire lungs, unlike common diseases that are limited to small regions (Chen et al., 2020; Sharma, 2020). Pneumonia caused by the COVID-19 shows a typical hazy patch on the outer edges of the lungs. For this reason, CT scans appear to work well, as they are able to bring out three distinctive hallmarks: (i) while normal lung scans appear black, those related to COVID-19 show lighter colored spots or gray; (ii) the lung airspaces are full of fluids due to inflammation (consolidation); and, (iii) pleural effusion is present, i.e. liquid in the spaces around the lungs.

However, CT scans are not always easy to read and interpret by radiologists. In addition, in order to reduce the massive dose of radiation and avoid harmful consequences (such as tumors), it is preferable to perform scans with a low emission of radiation (Chen et al., 2020). In this case, unfortunately, the scanned images often have a degraded quality (such as blur, background noise and low contrast) that can make interpretation ambiguous and difficult to take a certain and precise diagnosis (Al-Ameen & Sulong, 2016).

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In order to solve all the above problems, very recently many studies have been directed towards the use of automatic image classification techniques through Deep Learning (DL) algorithms (Shen, Wu, & Suk, 2017; Zhou et al., 2017), a branch of machine learning that uses architectures that possess many layers of processing (Goodfellow et al., 2016). The author in Sharma (2020) has recently hypothesized that machine learning techniques applied to CT scans can certainly become the first alternative screening test to the real-time reverse transcriptase-polymerase chain reaction (RT-PCR) in the near future.

Although DL techniques have been applied with great success to identify cases of the NCP (Sharma, 2020; Shen, Wu, & Suk, 2017; Zhou et al., 2017), there are nevertheless a number of challenges to be solved (Chen et al., 2020; Hammer et al., 2020). First of all, many solutions have been proposed in the literature, each of which has its own advantages and disadvantages, providing very different results: that is, there is no single solution to the problem (Sarv Ahrahi et al., 2021). Furthermore, the DL architectures have a very large number of free parameters that must be adapted by the optimization algorithm and, in order to achieve the convergence, it is necessary to have a large amount of data, which is not always possible in practice (Goodfellow et al., 2016). Also because it is not certain that having lots of scans available is enough to be of quality (Aiello et al., 2019).

This situation is further worsened by the fact that, since the CPN is a relatively recent disease, the proportion of CT scans related to COVID-19 is very limited with respect to the number of images available in the datasets freely available on the web (Chen et al., 2020). In this regard, the identification of CT scans affected by COVID-19 is a problem more similar to the anomaly detection rather than the traditional classification, since the small number of data present in each dataset (Chandola et al., 2009). It would therefore be advisable to provide an anomaly detection algorithm, light from the computational point of view and capable of identifying CT scans related to COVID-19 with high accuracy.

Motivated by these considerations, in this paper we propose an autoencoder-based approach for the detection of COVID-19 CT scans. Specifically, the denoising version of a deep convolutional autoencoder, here called DDCAE, is proposed to learn a compact and meaningful representation of the normal and common pneumonia CT scans in an unsupervised manner. Autoencoders (AEs), in fact, are unsupervised architectures trained to copy its input to the output; they possess an internal layer (the hidden features or feature vector) that is used to efficiently represent the input (Goodfellow et al., 2016). Generally, an AE is composed of two main sections: an encoder that maps the input into the hidden features, and a decoder that maps the hidden features to a reconstruction of the input. When the encoder and decoder are composed of several layers, the AE is called deep (DAE) (Goodfellow et al., 2016). In image processing, usually convolutional layers have been employed (Masci et al., 2011), particularly appropriate to extract meaningful information from images. This results in a deep convolutional AE (DCAE). In the denoising version, DDCAE, the input is stochastically corrupted, usually using a Gaussian additive noise, while the uncorrupted input is still used as the target for the optimization of the parameters (Alain & Bengio, 2014; Vincent et al., 2008).

After the proposed DDCAE has been trained on a target class (the normal or the common pneumonia), the hidden features are used to construct an average and robust statistical representation of the target class. This is accomplished by averaging all the hidden features obtained by passing the whole training set in the encoder part and then evaluating the histogram of the mean representation. This histogram is used as a reference in the inference phase. For each new test CT scan, the related hidden features are evaluate by using the trained encoder and a test histogram is obtained. At this stage, a suitable measurement of the distance between two distributions is used: if the resulting distance is below a certain threshold, the test image is classified as the same of the target class, otherwise it is considered as an anomaly and labeled as COVID-19.

Specifically, the main contributions of this paper are:

- we propose an ad hoc DDCAE architecture optimized for the detection of anomaly CT scans. The proposed architecture is composed of three convolution layers in order to keep limited the computational complexity while obtaining sufficiently good and robust hidden features to obtain a high discrimination between their statistical representation;
- we propose a statistical distance-based approach to label a test image either as anomaly or not. The employed distance measurements should be suitable for discriminating histograms belonging to different classes. In this paper, we compare between the Kullback–Leibler divergence, the Bhattacharyya distance, and the Euclidean one;
- we perform numerical results on a well-known dataset available in the literature and compare the proposed approach to other state-of-the-art deep architectures. We expect that the proposed approach is able to obtain excellent results by keeping limited the training and inference time.

Let us remark that statistical representations of target classes and autoencoders are well known approaches for the anomaly detection problem. However, in literature these methods are used in a different way (see, for example, Chandola et al., 2009, and references therein). Specifically, the statistical representation is used to characterize the probability density or evaluating some peculiar moments of the instances by directly working on the input space. Autoencoders are typically used in anomaly detection problems by thresholding the reconstruction error (i.e., by comparing the input and the output directly). These state-of-the-art approaches have been demonstrated to be ineffective for the CT scans of COVID19 disease, as pointed out in Section 5.2. On the contrary, the approach proposed in this paper works directly on the latent space generated by the autoencoder. This means that the statistical representation is evaluated on the hidden feature vector, while the final classification is obtained by thresholding suitable-designed inter-histogram distances. To the best of the authors’ knowledge and on the basis of the broad overview of the related literature of Section 2, the proposed approach is novel and not used up to date for the classification of CT scans of infected lungs.

The rest of the paper is organized as follows. Section 2 presents the recent literature on the topic. Section 3 describes the proposed approach in terms of both used architecture and suitable distribution distances. Section 4 introduces the experimental setup, while Section 5 shows the obtained numerical results and their comparison with other state-of-the-art approaches. Finally, Section 6 concludes the paper and outlines some future works.

2. Related work

In recent years, a great attention on automatic classification of medical images has been devoted to the application of Deep Learning approaches. Although many recent works are addressed to traditional x-Ray images (Chandra et al., 2021; Ismael & Şengür, 2020, 2021) and use transfer learning (Vidal et al., 2021), lots of novel methods working on CT scans have been proposed. Two recent and comprehensive reviews embrace several methodologies currently used in medical screening (Ozsahin et al., 2020; Rahman et al., 2021). Obviously, automatic CT scans classification is applied for diverse diseases, as the lung nodule malignancy suspiciousness classification (Shen et al., 2017), but during the last year the main contributions focused on the COVID-19 disease. Among these works, studies are divided into two main families: those based on segmentation and those that perform the classification task directly.

Approaches based on segmentation are usually based on U-Net type architecture to identify relevant part of the CT scans and perform classification focusing the attention only on these sections (Fan et al., 2020; Saood & Hatem, 2021; Vidal et al., 2021; Yao et al., 2021).
Specifically, the work in Vidal et al. (2021) is based on U-Net exploiting a multi-stage transfer learning idea to quickly develop computer-aided diagnosis systems that can be used in real-time on smart-phones. Similarly, Saood and Hatem (2021) performs CT scan segmentation exploiting both the U-Net and the SegNet. The authors of Fan et al. (2020), instead, propose Inf-Net, an “infection segmentation deep Network” introduced to automatically identify infected regions from chest CT slices. Differently form these works, our proposed approach does not resort to image segmentation. Finally, Yao et al. (2021) proposes NormNet, an approach able to recognize normal tissues and separate them from possible COVID-19 lesions. Like our approach, NormNet is trained in an unsupervised manner, however, differently from the proposed work, it uses synthetic lesions constructed by using a set of simple operations and then inserted into normal CT lung scans, while the prediction is performed by a U-Net type architecture. Moreover, the results shown in Yao et al. (2021) do not overcome a precision of 0.905 for the COVID-19 cases and hence it does not outperform our proposed idea.

The main works of the second family are based on the binary classification problem of COVID/NON-COVID images (Elmuogy et al., 2021; Mishra et al., 2020; Shah et al., 2021; Tan et al., 2021). Specifically, the work in Shah et al. (2021) is based on deep Convolutional Neural Networks (CNNs) and proposes a specific configuration called CNet-10 while comparing the results with well-known CNN architectures, such as DenseNet-169, VGG-16, ResNet-50, InceptionV3, and VGG-19. Similarly, in Tan et al. (2021) a “super-resolution” variant of VGG-16 neural network has been introduced. The super-resolution of chest CT images has been obtained by exploiting the SRGAN neural network. The authors in Elmuogy et al. (2021) propose an automatic classification architecture based on a deep neural network called Worried Deep Neural Network (WDNN) that uses transfer learning and provide results by using different pre-trained models. Differently, the paper in Mishra et al. (2020) is based on a fusion approach. The main idea of the fusion approach is that the classification errors made by individual models may be mitigated by combining the individual predictions via a majority voting approach. The baseline models used in Mishra et al. (2020) include VGG16, InceptionV3, ResNet50, DenseNet121, and DenseNet201. Similarly, Silva et al. (2020) proposes a voting-based approach for the screening of COVID-19 by exploiting and extending the EfficientNet neural network along with a data augmentation process and transfer learning. Differently from our approach, works in Elmuogy et al. (2021), Mishra et al. (2020), Shah et al. (2021), Silva et al. (2020) and Tan et al. (2021) are all supervised, hence they have to be trained on both the COVID and NON-COVID images.

Moreover, we point out that there are some few approaches that exploit the deep AEs in medical images (Chen et al., 2017; Li et al., 2020; Xu et al., 2016). Specifically, the work in Xu et al. (2016) proposes a Stacked Sparse Autoencoder (SSAE) plus a softmax classifier for identifying the presence or absence of nuclei in individual image patches related to the breast cancer. Authors in Chen et al. (2017) applied a deep convolutional autoencoder to pulmonary CT scans to detect lung nodules. Once again, the final detection is performed by a softmax classifier. Interestingly enough, the approach in Chen et al. (2017) has been extended for similarity measurement of lung nodules images. Topic of Li et al. (2020) is the COVID-19 diagnosis from chest CT scans exploiting a stacked autoencoder detector model. Authors propose a novel cost function to train the stacked autoencoder, regularized in a different manner for each layer, then the detection is again done by a softmax classifier. Differently from our approach, works in Chen et al. (2017), Li et al. (2020) and Xu et al. (2016) use the autoencoder to automatically construct a set of features and then use a softmax classifier on the top. We instead use the hidden features to construct a statistical representation of the input scans. Moreover, differently from Li et al. (2020) and Xu et al. (2016) that implement stacked autoencoders (trained in a layer-wise fashion), we exploit a deep autoencoder that is computationally more efficient.

In addition, there exist some approaches based on traditional Machine Learning (ML) methods. To this aim, the main goal of the contribution in Gomes et al. (2020) is to check the actual effectiveness of some low-complexity shallow supervised classifiers (namely, Support Vector Machine (SVM), Multi-Layer Perceptron (MLP) and Random Forest (RF)) to detect COVID-19 diseases by texture analysis of chest X-ray images. The goal is to properly classify COVID-19, viral pneumonia, bacterial pneumonia and healthy radiographic images by running the mentioned ML approaches on a set of features composed by the Haralick and Zernike moments. Interestingly enough, the numerical results reported in Gomes et al. (2020) support the conclusion that SVMs equipped with 2–3 degree polynomial kernels are the most performing ones and, in the carried out tests, obtain a good average accuracy, recall, precision and specificity.

Finally, the follow-up paper in Gomes et al. (2021) extends the utilization of shallow ML approaches to the classification of DNA sequences of 25 different virus classes. Specifically, the paper proposes a technique for representing DNA sequences in which each sequence is partitioned into shorter mini-sequences that partially overlap in a pseudo-convolutional fashion, in order to be represented by suitable co-occurrence matrices. These last are the extracted features utilized as input to five types of shallow supervised classifiers, namely, SVM, RF, MLP, Naïve Bayes classifier and Instance-Based-K (IBK) learner (Alpaydin, 2014). Interestingly, the multiclass classification tests carried out in Gomes et al. (2021) support the conclusion that RF classifiers are the most performing ones and they attain average accuracies around 94%.

An overview of the related work is provided in Table 1 that briefly summarizes the main approaches. Overall, on the basis of the carried out overview, we conclude that our approach is unique in: (i) applying a statistical representation of the hidden feature vector, estimated in an unsupervised manner; and, (ii) performing classification by thresholding suitable inter-histogram distances.

### 3. Proposed approach and related deep denoising CAE architectures

The proposed approach is based on a denoising version of a Deep Convolutional Autoencoder (DCAE), here called DDCAE.

Although Autoencoders (AEs) have been introduced at the end of 80s (Bourlard & Kamp, 1988), only recently their deep versions have been exploited in practical applications (Goodfellow et al., 2016). In brief, a Deep AE (DAE) is a feed-forward neural network with 2L + 1 hidden layers trained to (quasi) reproduce its input at the output layer. In this regard, the aim of a DAE is to learn a compact and meaningful representation ℓ̃ (encoding), also called hidden features or feature vector) for a set of (possibly, noisy) input data, using a set of weight parameters. Then, an estimate of the input data is recovered (decoding), usually using tied weights (Goodfellow et al., 2016).

However, when used on image data, it is more convenient to resort to the convolutional version of the DAE. In the Deep Convolutional AE (DCAE) (Masci et al., 2011), each fully connected layer is replaced by a cascade of a suitable number of convolutional, pooling and normalization layers, as described in the following.

Moreover, in literature it is often used a robust variant of the AE, called Denoising AE (Alain & Bengio, 2014; Vincent et al., 2010), in which a stochastically corrupted version of the input is employed to feed the AE (usually, using a Gaussian additive noise with zero mean and variance σ²), while the uncorrupted input is still used as the target for the optimization of the parameters. The general idea of a DDCAE is graphically depicted in Fig. 1.

Fig. 1 shows that the encoder of a DDCAE is composed of the cascade of L Convolutional, Max Pooling, and Batch Normalization (BN) layers, plus and eventual final Dense layer. Not all the depicted layers are used in some specific configurations of the proposed DDCAE.

Although, the role of these layers is well-known in literature, we provide a short description of each of the involved layers to help the non expert reader.
output sample \( Y_l \) are the spatial size of the \( l \) filters, filter size and stride coefficient, respectively, while \( F \) us denote with produce an output map of reduced size with respect to its input. Let \( F \) parallel for all the and another output pixel is produced. This operation is performed in \( s \) output pixel. Then the kernel is moved by a quantity \( \mathcal{W} \) region of the image of the same size of the kernel to produce an \( \mathcal{W} \) maps. Specifically, a kernel function \( \mathcal{W} \) filters (also called kernels) to produce a certain number of feature \( \mathcal{W} \) of local features, implements a set of \( \mathcal{W} \) convolutions by using \( \mathcal{W} \) filters. A stride value greater than the unity will \( \mathcal{W} \) the \( \mathcal{W} \) th convolutional layer, which is responsible for the extraction \( \mathcal{W} \) th layer, and \( \mathcal{W} \) is the set of the scalar samples of the kernel of the \( \mathcal{W} \) th convolutional layer, is provided by the following summation \citep{Goodfellow2016}:

\[
Y_l(i, j, k) = \sum_{h=0}^{k_i-1} \sum_{p=0}^{k_j-1} \sum_{u=0}^{F_l-1} W_l(h, p, u, k) Y_{l-1}(s_i h + i, s_j j + j, u + b_l(k)).
\]  

(1)

for \( 1 \leq i \leq M_i, 1 \leq j \leq N_j, \) and \( 1 \leq c \leq F_l, \) where \( \{W_l(\cdot, \cdot, \cdot, \cdot)\} \) is the set of the scalar samples of the kernel of the \( l \)th 2D filter, \( \{Y_{l-1}(\cdot, \cdot, \cdot)\} \) is the set of scalar features at the input of the \( l \)th channel of \( l \)th layer, and \( b_l(k) \) is the bias term of the \( k \)th filter in the \( l \)th layer. All the convolutional layers, except the last of the decoder, use the ReLU activation function. The ReLU function is defined as \( \text{ReLU}(x) = \max\{0, x\} \). The last layer of the decoder uses instead a sigmoid activation in order to produce a valid pixel values inside the interval \([0, 1]\).

In the pooling layer, used for the down-sampling of the feature maps, each input map is divided into adjacent non-overlapping regions of spatial dimension: \( M \times N \times F \) indicates a convolutional layer (or a filter kernel or an input image) of spatial dimension: \( M \times N \times 3 \), representing the number of rows, columns, and colors.

The \( l \)th convolutional layer, which is responsible for the extraction of local features, implements a set of \( F_l \) convolutions by using \( F_l \) filters (also called kernels) to produce a certain number of feature maps. Specifically, a kernel function \( W_l \) is convolved with a specific region of the image of the same size of the kernel to produce an output pixel. Then the kernel is moved by a quantity \( s \), called stride, and another output pixel is produced. This operation is performed in parallel for all the \( F_l \) filters. A stride value greater than the unity will produce an output map of reduced size with respect to its input. Let us denote with \( F_l, k_i, s_i \) the corresponding number of squared 2D filters, filter size and stride coefficient, respectively, while \( M_i \) and \( N_i \) are the spatial size of the \( l \)th 2D filter output. Mathematically, the output sample \( Y_l(i, j, k) \) generated at the spatial position \((i, j)\) by the \( k \)th spatial filter of the \( l \)th convolutional layer, is provided by the following summation \citep{Goodfellow2016}:

\[
Y_l(i, j, k) = \sum_{h=0}^{k_i-1} \sum_{p=0}^{k_j-1} \sum_{u=0}^{F_l-1} W_l(h, p, u, k) Y_{l-1}(s_i i + h, s_j j + j, u + b_l(k)).
\]  

(1)

for \( 1 \leq i \leq M_i, 1 \leq j \leq N_j, \) and \( 1 \leq c \leq F_l, \) where \( \{W_l(\cdot, \cdot, \cdot, \cdot)\} \) is the set of the scalar samples of the kernel of the \( l \)th 2D filter, \( \{Y_{l-1}(\cdot, \cdot, \cdot)\} \) is the set of scalar features at the input of the \( l \)th channel of \( l \)th layer, and \( b_l(k) \) is the bias term of the \( k \)th filter in the \( l \)th layer. All the convolutional layers, except the last of the decoder, use the ReLU activation function. The ReLU function is defined as \( \text{ReLU}(x) = \max\{0, x\} \). The last layer of the decoder uses instead a sigmoid activation in order to produce a valid pixel values inside the interval \([0, 1]\).

In the pooling layer, used for the down-sampling of the feature maps, each input map is divided into adjacent non-overlapping regions.
according to the size of the pooling region, and the maximum of the region is output. In this way the spatial dimension of the input is reduced after the pooling operation. Instead, the number of input feature maps is equal to the number of output feature maps in the pooling layer. Mathematically, the max pooling operation is performed as:

\[ Z_q(k) = \max\{Y_q(k)\}, \]

where \( Y_q(k) \) is the \( q \)th region of the \( k \)th feature map and \( Z_q(k) \) represents the \( q \)th element of the \( k \)th output feature map.

The batch normalization layer applies a standardization operation on the output of the layer, by forcing a zero mean and a unit variance. This operation works as a regularization, increasing the stability of the neural network and accelerating the training (Ioffe & Szegedy, 2015). This layer normalizes its output using the mean \( \mu_X \) and standard deviation \( \sigma_X \) of the current batch of inputs \( X_i \), by evaluating:

\[ X_{i+1} = \gamma \frac{X_i - \mu_X}{\sqrt{\sigma_X^2 + \epsilon}} + \beta, \]

where \( \epsilon \) is a small constant used to avoid division by zero, while \( \gamma \) and \( \beta \) are a scaling and offset parameters learned during the training phase.

Training of the proposed DDCAE. The training of the proposed DDCAE has been performed by the Adam optimizer, a gradient-based optimization algorithm that exploits the first and second order moments to obtain a smooth and fast convergence (Kingma & Ba, 2015).

Evaluating the target statistical representation. After the training of the DDCAE on a reference class by minimizing the reconstruction error in (5), its encoder has been used to construct a meaningful statistical representation of the image pixels. In order to obtain a robust statistical representation, in this work we evaluate the hidden features for the entire training set \( X \) by using the encoder of the trained DDCAE. Hence, a target hidden feature vector \( \hat{X} \), of length \( N_x \) = \( M \times N \times F \), is obtained as the average of all the \( N_x \) single hidden feature vectors. We expect that, if the number \( N_F \) of images is sufficiently high, this target representation can be a meaningful representative of the target class.

As a statistical representation of the target feature vector \( \hat{X} \), in this paper we choose the (normalized) histogram, principally due to its simplicity and efficiency in computation. A histogram is an estimate of the distribution obtained by dividing the range of values into a sequence of \( N_{bin} \) equally-spaced interval called bins and counting how many values fall into each interval. The histogram is then normalized to sum to unit.

The number \( N_{bin} \) of bins used to construct the histogram should be chosen by a trade-off between numerical stability of the used distance measurement and its discriminating capability. Although this number turned out not to be critical for the final model performance, if it is much less than the length \( N_x \) of the hidden feature vector, we found that an excellent choice to guarantee non-empty bins is by using 50 bins, i.e. \( N_{bin} = 50 \). The only observation is regarding the Euclidean distance that tends to fill the gap between the two classes if \( N_{bin} \) is excessively increased.

In this phase, we also evaluate the distance between the just computed target histogram and all the histograms of the single reference encoded scans, by using suitable probability dissimilarity measurements (introduced in the next subsection). Among these distances, we compute the mean \( d_m \) and standard deviation \( \sigma_d \) values in order to set conveniently a suitable threshold \( TH \) used during the test phase to discriminate between a reference scan from an anomaly one. The idea is that the statistical distance from an anomaly scan should be greater than a reference one, hence the threshold \( TH \) could be set proportionally to the mean distance \( d_m \) plus a term depending on its standard deviation. Mathematically, we set the threshold \( TH \) as follows:

\[ TH = d_m + \eta \sigma_d, \]

where \( \eta \) is a suitable constant. In this case, a \( \eta = 0.3 \) provides good results.

Test of the proposed DDCAE. During the inference phase, each test image passes through the trained encoder and produces its latent feature vector used to evaluate a test histogram. This test histogram will be successively compared to the target one by a suitable distance measurement (the same used during the target computation). In this paper, we focus our attention on two reference classes: the normal one and the common pneumonia (CP) one. If the distance between the test and target histograms is above the set threshold \( TH \), the related image will be marked as COVID (anomaly), otherwise as the reference one. The main idea is sketched in Fig. 2.
Layer type | Kernel size | Stride | Output Shape | Param. #
--- | --- | --- | --- | ---
Conv2D | 3 $\times$ 3 | 1 | (200, 300, 256) | 7168
Batch Normalization | – | – | (200, 300, 256) | 1024
Conv2D | 3 $\times$ 3 | 1 | (200, 300, 128) | 295040
MaxPooling | 2 $\times$ 2 | 2 | (100, 150, 128) | 0
Conv2D | 3 $\times$ 3 | 1 | (100, 150, 64) | 73792
Batch Normalization | – | – | (100, 150, 64) | 256
MaxPooling | 2 $\times$ 2 | 2 | (50, 75, 64) | 0

Total params: 377,280
Trainable params: 376,640
Non-trainable params: 640

Layer type | Kernel size | Stride | Output Shape | Param. #
--- | --- | --- | --- | ---
Conv2D Transpose | 3 $\times$ 3 | 2 | (100, 150, 128) | 73856
Batch Normalization | – | – | (100, 150, 128) | 512
Conv2D Transpose | 3 $\times$ 3 | 2 | (200, 300, 256) | 295168
Batch Normalization | – | – | (200, 300, 256) | 1024
Conv2D Transpose | 3 $\times$ 3 | 1 | (200, 300, 3) | 6915

Total params: 377,475
Trainable params: 376,707
Non-trainable params: 768

3.2. Unsupervised distance-based processing of the latent representation

The main focus of the paper is the evaluation of the dissimilarity between the target histogram and the histogram obtained by the encoder for a test image. If the histogram of the test image is similar to the target one, we can assign it to the corresponding target class, otherwise it is labeled as a COVID-19 image. An example of target, NCP, and CP histograms are shown in Fig. 3.

In literature, the similarity between two histograms can be evaluated by several distance measurements of the underlying distribution (Kullback, 1997). For the aims of this paper, after denoting with $p$ and $q$ the two involved histogram distributions defined over the set of interval bins $I$, we have selected the following three distances.

1. Kullback–Leibler (KL) divergence:

$$d_{KL} = \sum_{i \in I} p_i \log \left( \frac{p_i}{q_i} \right).$$

(8)

where $p_i$ and $q_i$ are the values assumed by the $p$ and $q$ histogram in the $i$th bin, respectively. By definition, the contribution of the $i$th term in the summation in (8) is zero if $p_i = 0$.

2. Bhattacharyya distance:

$$d_B = - \log \left( \sum_{i \in I} \sqrt{p_i q_i} \right).$$

(9)

3. Euclidean distance:

$$d_E = \sqrt{\sum_{i \in I} (p_i - q_i)^2}.$$

(10)

These distances have been normalized by the number $N_{bins}$ of used bins in the histogram in order to render them independent of this choice. The Bhattacharyya distance is widely used in several applications, like image processing, and, differently from the KL one has the advantages of being insensitive to the zeros of distributions. On the other hand, the Euclidean distance is very simple and smooth but it tends to treat excessively equally differences between the distributions.

In the proposed approach, if the distance (chosen between the KL, Bhattacharyya and Euclidean one) between the target and the test histograms is above the set threshold $TH$, the image under test is classified as COVID-19 (CNP), otherwise it is classified as the target class (normal or CP, depending on the used training set).
In this section, we describe the utilized dataset for the reference classes, the employed software environment, the setting of the main parameters, and the metrics used to evaluate the performance of the proposed idea.

4.1. The utilized datasets

In response to the COVID-19 pandemic, the global open source and open access COVID-Net initiative\(^1\) made available some relevant datasets of CT scans in order to accelerate the advancement in machine learning to fight the pandemic (Gunraj et al., 2020). Recently, the COVID-Net team has released a second version of the dataset in two variants (the COVIDx CT-2 A and CT-2B datasets, respectively) (Gunraj et al., 2021). The “A” variant consists of cases with confirmed diagnoses, while the “B” variant contains all of the “A” variant and adds some cases which are assumed to be correctly diagnosed but are weakly verified. In this paper, we address our attention to the “A” variant of the dataset.\(^2\)

The COVIDx CT-2 A dataset has been constructed by collecting many publicly available data sources (Gunraj et al., 2021, 2020) and comprises 194,922 CT slices from 3745 patients. The dataset scans are related to three classes: novel coronavirus pneumonia due to SARS-CoV-2 viral infection (NCP), common pneumonia (CP), and normal controls. For NCP and CP CT volumes, slices marked as containing lung abnormalities were leveraged. Moreover, all the CT volumes contain the background in order to avoid model biases. An example of a representative image for each class is shown in Fig. 4. The issues pertinent to data ethics were ensured during the data collection of the dataset, according to the information reported on the related websites supporting this study.

In this paper, we have randomly selected 3500 and 700 images from the normal and Pneumonia classes for the training and validation of the proposed DDCAE, respectively, and 500 images from each class to test it.

4.2. Utilized simulation environment and setting of the main parameters

All the simulations described in this paper have been implemented in Python environment by using the end-to-end and open-source machine learning platform TensorFlow 2 exploiting the Keras API, with a PC having an Intel Core i7-4500U 2.4 GHz processor, 16 GB RAM, and Windows 10 operating system.

In this section, we describe the utilized dataset for the reference classes, the employed software environment, the setting of the main parameters, and the metrics used to evaluate the performance of the proposed idea.

4.3. The considered performance metrics

In a binary classification problem we are interested in classifying items belonging to a positive class (P) and a negative class (N). With respect to a specific dataset, there are four basic combinations of actual data category and the assigned output category:

- **true positive (TP):** correct positive assignments;
- **true negative (TN):** correct negative assignments;
- **false positive (FP):** incorrect positive assignments;
- **false negative (FN):** incorrect negative assignments.

The set of these four quantities is usually arranged in a matrix layout, called confusion matrix (CM), which allows a simple visualization of the performance of a classification algorithm. Each column of the CM represents the instances in a predicted class while each row represents the instances in an actual class. Moreover, the combination of the previous four numbers in some powerful indicators can be a valid tool to quantitatively measure the performance of a classification algorithm (Alpaydin, 2014). Among all the possible combination, in this paper we focus our attention on the accuracy, precision, recall and F-measure metrics, whose formal definition can be found in Table 5. The accuracy is the ratio between the correct identified instances among their total number. The precision is the ratio of relevant instances among the retrieved instances, while the recall is the ratio of the total amount of relevant instances that were actually retrieved. Finally, precision and recall can be combined in a single measurements called F-measure that is mathematically defined as their harmonic mean.

We also consider the TP rate (formally coincident with the recall metric) and the FP rate. These last measures are, respectively, the ratio between the number of TP and the total positive examples and the ratio between the number of FP and the total negative examples. By plotting the TP rate on the y-axis against the FP rate on the x-axis in a plane, when the discrimination threshold is changed, we obtain the Receiver Operating Characteristic (ROC) curve that is a graphical representation of the performance of a binary classifier. However, the ROC curve is a two-dimensional depiction of classifier performance and often we need of a single scalar value representing the expected performance. A common method is to calculate the area under the ROC

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1. https://alexswong.github.io/COVID-Net/
2. It can be downloaded from: https://www.kaggle.com/hgunraj/covidct.
Table 5
The performance metrics for the evaluation of the proposed model.

| Performance Metrics | Formula |
|---------------------|---------|
| Precision            | $\frac{TP}{TP+FP}$ |
| Recall               | $\frac{TP}{TP+FN}$ |
| F-measure            | $2\frac{TP}{2TP+FP+FN}$ |
| Accuracy             | $\frac{TP+TN}{TP+FN+FP+TN}$ |
| TP rate              | $\frac{TP}{TP+FN}$ |
| FP rate              | $\frac{FP}{FP+TN}$ |

Table 6 demonstrates the effectiveness of the proposed idea. In fact, results in terms of all the considered metrics are generally satisfying and, interestingly enough, they reach the top result of 100% in some of the proposed settings. By a carefully examination of the rows of Table 6, we can draw some general considerations:

- results obtained with reference to the normal class generally outperform those of the CP class. This is justified by the fact that scans of the NCP are more similar to the CP class rather than the normal one, hence discriminating between NCP and CP is a more complicated task with respect to the discrimination between NCP and normal;
  - the clean version of the deep CAE provides worsening results with respect to the denoising versions. This is justified by the fact that the input noise operates as a regularizer providing a more robust classification;
  - the level of the noise should be not too big. In fact, the performance obtained by using the value $\sigma = 0.1$ is lower than the corresponding ones with $\sigma = 0.01$ and $\sigma = 0.05$;
  - the proposed DDCAE with $\sigma = 0.01$ and $\sigma = 0.05$ is able to reach top performance in terms of all the considered metrics;
  - although all the three considered distance measurements (i.e., the KL divergence, the Bhattacharyya distance, and the Euclidean distance) provide similar results, when the performance are not at the top level, Table 6 suggests that the Bhattacharyya distance produces higher scores, while the Euclidean distance the smaller ones. This could be justified by the mathematical expressions of these distances. In fact, the Bhattacharyya distance is quite smooth and automatically takes into account for the possible zero values of a distribution, while in the KL divergence this could be a problem, even if the chosen number $N_{bin}$ of bins assures the absence of zeros in the both distributions. On the other hand, the Euclidean distance, for its nature, produces not so discriminating distance;
  - the DDCAE with $\sigma = 0.01$ provides always the top accuracy of 100%. Just for the normal reference and Euclidean distance, the accuracy is slightly lower, i.e. 99.90%!

Motivated from these considerations, in the following tests and comparisons we use the DDCAE with $\sigma = 0.01$ and the distance are measured by the KL divergence. Moreover, since it is more challenging, we use as reference class the CP one.

In order to give a visual insights of the results in Table 6 and justify the top 100% accuracy, Fig. 6 shows the considered Kullback–Leibler divergence, Bhattacharyya distance, and Euclidean distance in the case of common pneumonia reference dataset and the DDCAE with $\sigma = 0.01$. This figure clearly shows the effectiveness of the proposed idea. In fact, we can see that the NCP scans (the first 500 bars in Fig. 6) are much more distant with respect to the corresponding reference images (the last 500 bars). The differences between the classes is about one order of magnitude for the KL divergence and the Bhattacharyya distance, as we can see in Figs. 6(a) and 6(b), while it is more limited in the case of the Euclidean distance (see Fig. 6(c)). This last case also shows a larger variance of the obtained distances with respect to the first two measures.

In the following set of experiments, we compare the proposed 3-Layer DDCAE by changing the number of hidden layers. Specifically, we test two shallower architectures (with one and two layers, respectively) and a deeper one (with four hidden layers). Since the DDCAE with a single hidden layer performed very poorly, we provide results obtained by an architecture composed of a single dense layer, that is the only yellow layers in Fig. 1. The results obtained by these solutions on the CP reference dataset and employing the KL divergence to measure the histogram distances are shown in Table 7.
Table 6
Results obtained by the proposed DDCAE at different noise level for the two considered scenarios.

| Model               | Accuracy | Precision | Recall | F-measure | AUC    | Accuracy | Precision | Recall | F-measure | AUC    |
|---------------------|----------|-----------|--------|-----------|--------|----------|-----------|--------|-----------|--------|
| Kullback–Leibler divergence |          |           |        |           |        |          |           |        |           |        |
| DCAE 0.00           | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 | 83.40    | 0.8345    | 0.8340 | 0.8342    | 0.8600 |
| DDCAE1 0.01         | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 |
| DDCAE2 0.05         | 99.60    | 0.9960    | 0.9960 | 0.9960    | 0.9990 | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 |
| DDCAE3 0.10         | 92.70    | 0.9272    | 0.9270 | 0.9270    | 0.9790 | 88.33    | 0.8942    | 0.8830 | 0.8868    | 0.9710 |
| Bhattacharyya distance |        |           |        |           |        |          |           |        |           |        |
| DCAE 0.00           | 99.60    | 0.9960    | 0.9960 | 0.9960    | 0.9990 | 98.80    | 0.9881    | 0.9880 | 0.9880    | 0.9930 |
| DDCAE1 0.01         | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 |
| DDCAE2 0.05         | 99.20    | 0.9921    | 0.9920 | 0.9920    | 0.9990 | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 |
| DDCAE3 0.10         | 93.50    | 0.9352    | 0.9350 | 0.9350    | 0.9820 | 87.60    | 0.8810    | 0.8760 | 0.8785    | 0.9510 |
| Euclidean distance  |          |           |        |           |        |          |           |        |           |        |
| DCAE 0.00           | 92.00    | 0.9328    | 0.9200 | 0.9265    | 0.9070 | 91.80    | 0.9314    | 0.9180 | 0.9247    | 0.8930 |
| DDCAE1 0.01         | 99.90    | 0.9990    | 0.9990 | 0.9990    | 0.9990 | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 |
| DDCAE2 0.05         | 92.90    | 0.9391    | 0.9290 | 0.9340    | 0.9560 | 99.80    | 0.9980    | 0.9980 | 0.9980    | 0.9980 |
| DDCAE3 0.10         | 92.90    | 0.9294    | 0.9290 | 0.9292    | 0.9710 | 74.90    | 0.8730    | 0.7490 | 0.8063    | 0.9190 |

Fig. 5. ROC curves of the proposed approach for the considered distance measures in the Pneumonia scenario: (a) DCAE, (b) DDCAE1, (c) DDCAE2, and (d) DDCAE3. The corresponding AUC values are reported in the legend boxes.

Table, the performance tends to decrease for both the increasing and decreasing number of hidden layers. This behavior is uniform for all the considered metrics. Similar results have also been obtained by using the normal class as reference, not shown here for space constraints. The results, shown in Table 7, justify the use of three hidden layers in the proposed DDCAE.

Remark. We point out that we also implement the same methodology by exploiting the idea of Sparse AEs as done in Xu et al. (2016). However, the sparse AE does not yield any good results by nothing of the used metrics. Therefore, we decided to exclude it from the paper. The bad results obtained by sparse AEs are intuitively justified by the fact that our approach is based on the construction of a statistic representation by evaluating the histogram of the hidden feature vector. Since the sparse AE produces a very sparse hidden feature vector, the obtained histogram becomes not so significant.

5.2. Comparisons to state-of-the-art benchmark solutions

In this subsection, we show some comparisons with other state-of-the-art benchmark solutions. These comparisons involve both unsupervised and supervised techniques. Specifically, we employ the DDCAE itself to evaluate the anomalies. In fact, an autoencoder is trained to reconstruct its input: this is meaning that the reconstruction error in (5) should be small for test image belonging to the same class on which the architecture has been trained, otherwise the error should be bigger. Hence, the anomaly scans (i.e., the NCP images) can be obtained by
Table 7  
Results obtained by the proposed DDCAE at different number of layers. The metrics have been evaluated by using the KL divergence on the CP reference dataset. In italic the proposed DDCAE.

| Layers | Accuracy | Precision | Recall | F-measure | AUC  |
|--------|----------|-----------|--------|-----------|------|
| 1      | 63.90    | 0.6594    | 0.6390 | 0.6487    | 0.7250 |
| 2      | 88.20    | 0.7800    | 0.9799 | 0.8686    | 0.9210 |
| 3      | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 |
| 4      | 96.40    | 0.9648    | 0.9640 | 0.9644    | 0.9960 |

Fig. 6. The obtained distances for the case of CP reference using the DDCAE with $\sigma = 0.01$. The considered distances are: (a) Kullback-Leibler divergence, (b) Bhattacharyya distance, and (c) Euclidean distance.

compute the reconstruction error of a test scan and evaluate the statistical representation of such an error by means of the histogram. Then, once again, we perform the distance measurement of this test histogram to the reference one, obtained from the average of all the error images computed from the training scans. The same three distance measurements introduced in Section 3.2 have been employed. We refer to this method as the second benchmark approach or BAP2.

Results for the BAP1 and BAP2 benchmark approaches are shown in the top part of Table 8. For space reasons, only the results related to the CP dataset as reference are shown, but similar results can be obtained by using the normal reference dataset. Regarding the BAP2 approach, the second row of Table 8 is related to the KL divergence, which provide the best results compared to the Bhattacharyya and Euclidean distances.

Results shown in the first two rows of Table 8 clearly show that the benchmark solutions are not suitable to produce high metrics. This is meaning that the hidden features, extracted by the DDCAE, are more informative than those corresponding to the reconstructed images. This, in turn, supports the proposed approach.

Regarding the supervised approaches, in this paper we consider some well-known feed-forward deep networks in the literature, i.e., the AlexNet (Krizhevsky et al., 2012) and the GoogLeNet (Szegedy et al., 2015). Specifically, AlexNet is composed of the cascade of five convolutional layers and three (dense) fully connected ones, while the GoogLeNet is more complicated since it is very deep and constructed by stacking three convolutional layers, nine inception modules, and two dense layers. An inception module is a particular layer obtained by concatenating several convolution operations with different filter sizes and a max pooling operation. Since these architectures are of supervised type, they have been trained by using both the CP and NCP classes in the training set, differently to our approach that has been trained only on the CP class in an unsupervised manner.

The results provided by AlexNet and GoogLeNet are shown in the bottom part of Table 8. As shown in the table, AlexNet performs worse than our approach, since it reaches only 71% accuracy, and similar other metrics. On the contrary, the performance of GoogLeNet are the same as the proposed idea, since it obtains a 100% accuracy. The ROC curves of all the considered approaches in Table 8 are shown in Fig. 7. However, we have to remark that this result is obtained with a deeper approach with a huge number of free parameters compared to the proposed approach, as shown in Table 9 that reports the number of trainable parameters and the training time (in minutes) for all the considered architectures. For the proposed approach, we have also to consider the time needed to compute the target histogram. The complexity of a single histogram computation depends on the length $N_h$ of the hidden feature vector plus the number $N_{bin}$ of bins. Hence, the evaluation of the target histogram has an asymptotic computational complexity of $O(N_h(N_h + N_{bin}))$. This provides an additional time of few seconds, which is negligible with respect to the training of the models. Once again, this consideration, along with the trade-off shown in Table 9, supports the proposed methodology. Moreover, since GoogLeNet is based on a supervised approach, we expect that it may work efficiently only on data belonging to the training classes, differently from our unsupervised approach, as investigated in the following subsection.
5.3. Layer-wise training of DDCAEs

All the numerical results presented up to now refer to an end-to-end training approach in which each noisy input image is utilized to train end-to-end (i.e., one-shot) all the layers composing the underlying DDCAE. In order to evaluate the actual effectiveness of the considered end-to-end training approach, we have also implemented the more sophisticated layer-wise training approach described in Section 3.5 of Vincent et al. (2010). In a nutshell, according to this layer-wise approach (see, in particular, Fig. 3 of Vincent et al., 2010), a shallow denoising AE is considered at first, which is composed by only the first layer of the overall Deep AE. This shallow AE is trained on a set of noisy input training images (see Fig. 1 of Vincent et al., 2010), in order to learn its single-layer encoding function. Afterward, the learnt encoding function of the first-layer is used on a set of clean input training images, in order to train the second-layer of a two-layer denoising AE which is composed by the first two-layer of the underlying DDCAE (see the middle part of Fig. 3 of Vincent et al., 2010). So doing, the second-level encoding function is learnt. The described layer-wise procedure is replicated up to learn the encoding function of the upper-most layer of the underlying DDCAE (see the right part of Fig. 3 of Vincent et al., 2010). Finally, after finishing the layer-wise training procedure, the target histogram is numerically evaluated on a set of clean training images. The numerical results we have obtained by applying the described layer-wise procedure for training the proposed 3-Layer DDCAE of Table 2 are reported in Table 10 under the same experimental setup already considered in Section 5.1 for the (somewhat more challenging) Normal data set (see the columns labeled as “Normal” of Table 6 for the related numerical results).

A comparison of the numerical results reported in Table 10 against the companion ones previously reported in Table 6 point out that the performance improvements arising from the utilization of the implemented layer-wise approach for training the considered DDCAE are, indeed, (very) marginal. Hence, since the implementation complexity of the described layer-wise procedure scales up (at least) linearly with the depth of the considered DDCAE, we conclude that, at least in the here considered application scenarios, the adopted end-to-end one-shot training procedure exhibits a more appealing performance-vs.-implementation complexity tradeoff.

5.4. Robustness of the considered approaches

The aim of this subsection is to evaluate the robustness of the proposed DDCAE, compared to the GoogLeNet architecture, against unexpected image classes, like new variants of coronavirus and/or other classes never used in the training process.

In the following experiment, as in the previous subsection, the GoogLeNet has been trained by using both the CP and NCP classes while our DDCAE has been trained only on the CP class in an unsupervised manner. In order to check the robustness of these two considered approaches, both the architectures will be now tested on a test set composed of 500 normal scans and 500 CP scans. The obtained results are shown in Table 11, which clearly supports the effectiveness of our DDCAE. In fact, since our approach relies on an unsupervised training and a statistical distance measurement, it is able to identify anything that is different from the target class (in our case the CP class). On the other hand, we expect that the GoogLeNet can only assign previously unseen data randomly to the two output classes. This insight is confirmed by looking at the confusion matrices in Fig. 8 that shows how GoogLeNet splits the unseen data with a ratio of 53.8% and 46.2% between the two classes, respectively. The ROC curve of GoogLeNet in this experiment is shown in the blue curve of Fig. 7.
Table 10
Numerical performance of the proposed 3-Layer DDCAE of Table 2 when it is trained according to the layer-wise approach of Vincent et al. (2010) under the Normal dataset. The same simulation setup of Section 5.1 at \( \sigma = 0.05 \) is considered under the Normal datasets.

| Distance          | Accuracy | Precision | Recall | F-measure | AUC  |
|-------------------|----------|-----------|--------|-----------|------|
| Kullback-Leibler   | 99.61    | 0.9961    | 0.9960 | 0.9960    | 0.9992 |
| Bhattacharyya     | 99.22    | 0.9923    | 0.9921 | 0.9922    | 0.9991 |
| Euclidean         | 92.93    | 0.9401    | 0.9292 | 0.9346    | 0.9580 |

Table 11
Robustness of the proposed 3-Layer DDCAE and GoogLeNet to unseen data.

| Architecture      | Accuracy | Precision | Recall | F-measure | AUC  |
|-------------------|----------|-----------|--------|-----------|------|
| 3-Layer DDCAE     | 100.00   | 1.0000    | 1.0000 | 1.0000    | 1.0000 |
| GoogLeNet         | 76.90    | 1.0000    | 0.6996 | 0.6996    | 0.7690 |

Table 12
Main parameters of the implemented supervised shallow classifiers: SVMs with 2-degree (SVM-2D) and 3-degree (SVM-3D) polynomial, and Radial Basis Function (SVM-RBF) kernels; MLPs equipped with single hidden layers composed by 50 (MLP-50), 100 (MLP-100), and 200 (MLP-200) neurons; RFs composed by 100 (RF-100), 500 (RF-500), and 1000 (RF-1000) binary trees.

| Model          | Main parameters                          |
|----------------|------------------------------------------|
| SVM            | 2-degree polynomial kernel (SVM-2D)      |
|                | 3-degree polynomial kernel (SVM-3D)      |
|                | RBF kernel (SVM-RBF)                     |
| MLP            | 50 neurons in the hidden layer (MLP-50)  |
|                | 100 neurons in the hidden layer (MLP-100)|
|                | 200 neurons in the hidden layer (MLP-200)|
| RB             | RF with 100 randomly generated binary trees (RF-100) |
|                | RF with 500 randomly generated binary trees (RF-500) |
|                | RF with 1000 randomly generated binary trees (RF-1000) |

shallow classifiers (Alpaydin, 2014), working on input features that are obtained by extracting suitable Haralick and/or Zernicke moments from X-ray images. Hence, motivated by the interesting results reported in Gomes et al. (2020) on X-ray images, goal of this section is to numerically check the accuracy performance of such of kinds of simple-to-implement ML models for the binary classification of Pneumonia-vs.-COVID CT images extracted by the dataset of Table 3. Being the training of the considered shallow classifiers of supervised-type by design, the dataset of Table 3 has been augmented by including 3500 training plus 700 validation COVID-19 images picked up from the (previously described) CT-2 A dataset. Table 12 describes the main parameters and related taxonomy of the implemented shallow classifiers.

According to Gomes et al. (2020), in the carried out tests, suitable sets of Haralick (Haralick et al., 1973) and Zernicke (Kan & Srinath, 2001) moments extracted by the (previously described) available sets of CP and NCP scans are used as input features to the shallow classifiers of Table 12. Specifically, four (256 × 256) matrices of the co-occurrences of the gray levels of row-wise, column-wise and diagonal-wise adjacent pixels are extracted from each available CT scans and, then, they are employed as Haralick input features to the classifiers of Table 12 (see the seminal paper in Haralick et al., 1973) for an in-depth presentation of the Haralick feature extraction. As detailed in Gomes et al. (2020), the corresponding Zernicke moments are obtained by computing the coefficients of the orthogonal projection of each image onto an orthogonal basis composed by a set polar functions \( V_{n,m}(\rho, \theta) \), with each basis function \( V_{n,m}(\rho, \theta) \) labeled by a pair of non-negative integer indexes \((n, m)\) (see, for example, Eqs. (1) and (2) of Gomes et al. (2020)). In the carried out tests, the same set of \((n, m)\) index pairs reported in Table 3 of Gomes et al. (2020) is considered, so to associate 64 Zernicke moments to each processed image.

The top (resp., bottom) part of Table 13 shows the numerically evaluated results that have been obtained by running the shallow supervised binary classifiers of Table 12 when the described Haralick (resp., Haralick-plus-Zernicke) moments of the CP and NCP images of the dataset are used as input features. A comparative examination of the numerical results of Table 13 leads to two main conclusions. First, under both the tested Haralick and Haralick-plus-Zernicke input feature sets, the SVM classifier with degree-2 polynomial kernel attains the best performance metrics. In contrast, at least in the carried out tests, the implemented RF-based classifiers exhibit the worst performance. Second, a comparison of the top and bottom parts of Table 13 points out that, in all carried out tests, performance improvements are experienced by concatenating the Haralick input features to the corresponding Zernicke ones. Specifically, the experienced accuracy improvement is noticeable and around 14.5% for the (less-performing) MLP-50 classifier, while it reduces to 0.4% for the (most performing) SVM-2D model.

Finally, some insights may be acquired by comparing the performance metrics of the proposed DDCAE models of Table 6 against the
corresponding ones of the shallow models of Table 13. Specifically, the comparison points out that the average accuracies of the most performing DDCAE models (namely, the proposed DDCAE1 and DDCAE2 models equipped with the KL and/or the Bhattacharyya distance of Table 6) reach 100%, while the average accuracy of the most performing tested shallow classifier (namely, the SVM-2D classifier of Table 13) remains limited up to 93%. Furthermore, since the considered shallow classifiers are supervised models, in principle, they are prone to the same robustness issues already pointed out in Section 5.4. Obviously, these pros of the proposed DDCAE models are counterbalanced by some cons arising from considerations on the corresponding implementation complexity. The training times of the shallow models provided in the last column of Table 13 show that all the compared models are faster than the corresponding ones of the proposed DDCAE models (see Table 9). This is due to the facts that these models are shallow and operate on input feature vectors of limited length, as detailed in Gomes et al. (2020). However, although these shallow models can be quickly trained, we remark that the obtained accuracies of Table 13 are not suitable for a reliable system of automatic diagnosis. Hence, all in all, we conclude that the proposed DDCAE models may represent an appealing solution in application scenarios in which very high accuracy (we say, accuracy over than 95%) and robustness against unseen input features are the main quality-of-service requirements. In fact, although the training time of the proposed DDCAE is higher than the corresponding ones of the tested shallow methods, the resulting test accuracy-vs.-training time tradeoffs compare favorably with respect to competing deep methods with similar test accuracies.

### 6. Conclusion

In this paper, we propose an unsupervised approach to detect the new coronavirus pneumonia from CT scans. Since the number of these images is usually limited, we train a deep denoising convolutional autoencoder (DDCAE) on some target classes (normal and common pneumonia) and construct a robust statistical representation by evaluating the histogram of the hidden features averaged over all the training scans. A suitable distribution distance is then used to compute how far this target histogram is from the corresponding histogram evaluated on an open-source dataset, known in literature, for an unknown test scan: if this distance is above a threshold the test image is classified as anomaly, i.e. affected by the COVID-19 disease, otherwise it is classified the same as the target class. Some numerical results evaluated on an open-source dataset, known in literature, demonstrate the effectiveness of the proposed idea, since it is able to obtain the top 100% of the considered metrics (accuracy, precision, recall, F-measure and AUC) with a limited computational complexity, outperforming the corresponding state-of-the-art approaches.

| Model       | Accuracy | Precision | Recall | F-measure | AUC   | Training time |
|-------------|----------|-----------|--------|-----------|-------|---------------|
| SVM-2D      | 93.00    | 0.9386    | 0.9300 | 0.9343    | 0.9940| 1.6           |
| SVM-3D      | 90.20    | 0.9181    | 0.9200 | 0.9190    | 0.9910| 1.8           |
| SVM-RBF     | 91.20    | 0.9252    | 0.9120 | 0.9186    | 0.9700| 1.5           |
| MLP-50      | 61.60    | 0.6160    | 0.6160 | 0.6159    | 0.6600| 6.4           |
| MLP-100     | 70.10    | 0.8083    | 0.7010 | 0.7508    | 0.8000| 9.3           |
| MLP-200     | 76.10    | 0.7947    | 0.7610 | 0.7775    | 0.7800| 12.2          |
| RF-100      | 68.50    | 0.7652    | 0.6850 | 0.7229    | 0.8500| 6.4           |
| RF-500      | 68.70    | 0.7665    | 0.7210 | 0.7431    | 0.9600| 31.8          |
| RF-1000     | 68.90    | 0.7676    | 0.6890 | 0.7262    | 0.9620| 65.3          |

| Model       | Accuracy | Precision | Recall | F-measure | AUC   | Training time |
|-------------|----------|-----------|--------|-----------|-------|---------------|
| SVM-2D      | 93.40    | 0.9417    | 0.9340 | 0.9378    | 0.9950| 1.7           |
| SVM-3D      | 92.70    | 0.9363    | 0.9270 | 0.9316    | 0.9930| 2.4           |
| SVM-RBF     | 91.70    | 0.9788    | 0.9170 | 0.9469    | 0.9600| 1.6           |
| MLP-50      | 76.00    | 0.8132    | 0.7600 | 0.7857    | 0.7900| 7.5           |
| MLP-100     | 77.40    | 0.7874    | 0.7740 | 0.7806    | 0.7200| 10.8          |
| MLP-200     | 78.30    | 0.8123    | 0.7830 | 0.7974    | 0.7800| 13.2          |
| RF-100      | 71.10    | 0.7852    | 0.7110 | 0.7463    | 0.9600| 7.3           |
| RF-500      | 72.00    | 0.7903    | 0.7200 | 0.7535    | 0.9650| 36.5          |
| RF-1000     | 72.10    | 0.7893    | 0.7210 | 0.7536    | 0.9680| 74.0          |

Accuracy is in percentage while the training time is measured in seconds.
In future works, we aim at extending our methodology towards different types of medical images, other than CT, and/or different diseases. We expect, in fact, that the automatic screening of pathological images can take a great advantage by the simplicity of our methodology, in both of the resulting accuracy and prediction time. A second line of future research can be addressed towards to use of Generative Adversarial Networks (GANs) for generating additional examples in the case of new variants of COVID-19, in order to be fast in the automatic discrimination of these scans without awaiting the construction of sufficiently copious dataset. Finally, a third research hint can be focused on the implementation of the proposed methodology in a distributed Cloud/Fog networked technological platforms (Baccarelli et al., 2021, 2017), in order to produce in fast and reliable clinical responses by exploiting the low-delay and (possibly, adaptive)

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