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Classifying healthy and infected Covid-19 cases by employing CT scan images

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ABSTRACT

A broad family of viruses called coronaviruses may infect people. The infection's symptoms are often relatively minor and resemble a normal cold. Since the coronavirus disease of 2019 (Covid-19) has never been observed in humans, anyone can contract it, and no one has an innate immunity to it. The detection of Covid-19 is now a critical task for medical practitioners. computed tomography (CT) scans can be considered as the best way to diagnose Covid-19. For patients with severe symptoms, imaging might help to assess the seriousness of the disease. Also, the CT scan can be helpful for determining a plan of care for a patient. This work focuses on classifying Covid-19 cases for healthy and infected by presenting a powerful scheme of recognizing CT scan images. In this study will be provided by proposing a model based on applying deep feature extractions with support vector machine (SVM). Big dataset of CT scan images is employed, it is available in the repository of GitHub and Kaggle. Remarkable result of 100% have been benchmarked as the highest evaluation after investigations. The proposed model can automatically detect between healthy and infected individuals.

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1. INTRODUCTION

Coronavirus disease 2019 (Covid-19) is a type of virus that obtained significant attentions. The first case of Covid-19 was reported on the 1st of December 2019. It named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). It may be originated in an animal, then, changed to cause disease for humans. Since less than 7 months, it has now become a serious global threat. It caused more than 9 million injuries and 525,000 deaths. Currently, there is no preventative treatment for Covid-19. In this epidemic, unprecedented efforts to discover and develop new vaccines and therapeutic strategies against this new Covid-19 are rapidly increased. While hundreds of therapies/vaccines are still investigated and at an early stage of clinical developments. The first cases occurred in Wuhan, China. Then, Covid-19 has rapidly spread around the world [1]. In recent years, Covid-19 has caused a serious threat to the public health [2], [3]. Considering the rapidly increasing cases and severity disease, the World Health Organization (WHO) declared global health emergency on the 30th of January 2020 [4]. Despite of implementing worldwide efforts to prevent the virus spreading such as applying social distances and quarantining infected persons, its infections could not be prevented. Therefore, the WHO declared that Covid-19 is a pandemic on the 11th of March 2020 [5].

The symptoms of Covid-19 and its clinical characteristics for those patients who got infected are common. They have similar characteristics of influenza virus including fever, myalgia, cough, headache, shortness of breath, expectoration, nasal tampon, and fatigue. In severe cases, the infection can result in death [6]. The incubation period is not exactly clear, but depending on the immune system status of patients, it differs from few days to 2 weeks after infection [7]. For the treatment and management of Covid-19, an early diagnosis is essential. Particularly at the epicenter of the epidemic, chest computed tomography (CT) imaging may be a more accurate, feasible, and quick way to detect Covid-19 [8]. The chest CT scan is a routine imaging method for diagnosing lung cancer, pneumonia, asthma, pulmonary thrombosis, and Covid-19 cases [9]-[11]. Also, CT scan is considered a relatively fast and easy-to-perform imaging device [12]-[14]. Recent researchers found that the sensitivity of CT scan for Covid-19 infection can provide higher accuracy compared to X-Ray and it has substantially improved diagnostic facility over X-Ray [15], [16]. The CT scan should be considered in the initial assessment for suspected Covid-19 infections instead of X-Ray in terms of avoiding radiation exposure risk. Furthermore, the reverse-transcription polymerase chain reaction (RT-PCR) testing provides lower sensitivity than the CT scan [17]. This study is aiming to classify a big data of CT scan images into healthy and infected Covid-19 cases by combining between the deep learning (DL) and support vector machine (SVM). Comprehensive work is provided to face challenges, solve problems, and attain a high classification accuracy. The main contributions of this work are as follows:

- a. During data processing, deep features are extracted by passing them through a network with multiple layers to obtain useful features.
- b. Combining between the deep extracted features and SVM in one efficient model.
- c. Classifying between healthy and infected Covid-19 cases by applying a big data of CT images. In this paper, remaining sections after this introduction are distributed as follows: section 2 reviews previous studies, section 3 describes the materials and methods, section 4 provides the results and discussions, and section 5 declares the conclusions.

The traditional machine learning (ML) methods, such as multi-layer perception (MLP), almost employ shallow structures to handle a constrained sample size and computing unit count. The performance and generalization capacity of complicated classification tasks should be adequate when the objective has rich meanings.

The DL network based on the convolutional neural network (CNN) has been developed in recent years. It has been widely used in the field of image processing. It has become powerful and universal. Newman *et al.* [18] offer a new reconstruction approach based on the CNN, and they show its benefits in terms of speed and reliability. Have been presented a classification method that robustly provides correct results while preserving controllable storage costs. It uses the truncation of local tensor singular value decompositions. There was a way for calculating particular pairwise match scores that might be helpful, for instance, with object identification issues where pose and position varied. Three CNN techniques were covered by Wang *et al.* [19].

In general, the feature extraction, trained, and hybrid approaches are these. The network model is more like a biological neural network. In that it preserves the network's deep structure while reducing the necessary parameters. Been demonstrated deep circuits' associated groups of functions are known as deep architectures. The foundation of DL algorithms is the parameterization of such circuits and the adjustment of their parameters to roughly optimize some training objective. Study also concentrated on representation learning at many levels, or DL. The goal was to identify more abstract characteristics at higher levels of representation that would make it simpler to distinguish between the numerous explanatory elements that are present in the data. Have been recommended in order to learn the complex functions that can represent high-level abstractions (for example, in vision, language, and other artificial intelligence (AI)-level tasks). As a result, it is simpler to train and has strong generalization energy [20], [21].

This benefit is especially pronounced when the network input is a multi-dimensional picture since it may use the network input immediately without going through the laborious feature extraction and data reconstruction steps that standard recognition methods need. Consequently, a CNN may be thought of as an MLP. However, a CNN is built to detect two-dimensional structures that are extremely invariant to translation, scaling, tilting, and other types of deformations [22]–[24].

More and more image data is being kept online due to the fast advancement of mobile internet technologies. Particularly in the sphere of medicine, images have replaced words as an essential source of information [25]–[28]. Under this background, it seems that it is very important to suggest an intelligent classification method which can deal with significant images as CT data of Covid-19 and provide accurate healthy/infected decision. The deep features are retrieved by running the CT images through a network with various layers to provide effective features. and getting flawless outcomes by merging the SVM and deep retrieved features into a single effective model.

2. MATERIALS AND METHODS

2.1. Dataset

The dataset that is used in this work basically includes CT scan images. Its data is randomly collected as mentioned in the open sources of GitHub repository and Kaggle [29], [30]. Chest CT scan images in this dataset have been obtained from patients and they have been interpreted and reported by expert radiologists. The CT scan images are of type portable network graphics (PNG) and each image matrix has a size equal to 512×512 pixels. The dataset includes 8,439 items, with 7,495 Covid-19 infected patients and 944 Covid-19 uninfected patients (healthy or negative cases). Multiple examples of the CT scan images for infected and uninfected Covid-19 cases are shown in Figure 1. Where Figure 1(a) shows cases of infected people with Covid-19, while Figure 1(b) shows cases of uninfected Covid-19 people.

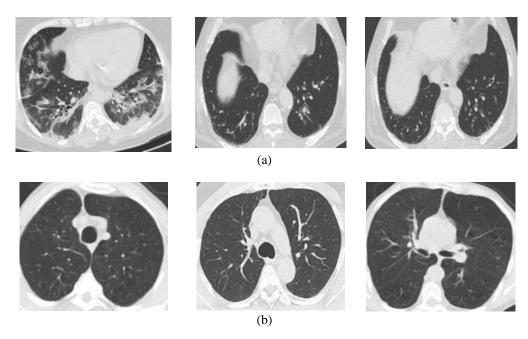


Figure 1. Multiple examples of the CT scan image for (a) infected Covid-19 cases and (b) uninfected Covid-19 cases

2.2. Machine learning

ML is an important area in the AI. It considers an algorithm strategy that has the ability to learn from data, then, predict outputs from other data [31]. In recent years, ML has quickly been expanded in terms of data analysis and consideration, allowing applications to work intelligently [32]. ML is typically considered as the most popular and contemporary technology, since it allows systems to learn and improve their experiences. In addition, it surpasses in classifying objects (and many other related tasks) [33]. The efficacy and efficiency of an ML solution is mostly depends on the type and quality of data, and the performance of an employed learning algorithm. Learning algorithms are selected according to the ML applications of feature extraction, regression, dimensionality reduction, clustering and classification [34], [35]. Furthermore, DL has been evolved as a part of the larger ML family [36] and can be used to intelligently analyses data.

Despite the good performances of deep learning networks, there are still many good reasons encouraging to use classic ML methods. For example, there are researchers who have found using the SVM method can provide a high prediction accuracy compared to other classifiers [37]. Hence, an efficient model to classify chest CT scan images of Covid-19 into healthy and infected cases will be presented. We used in this study a ML approach that utilizes the powers of CNN and SVM, where this can better lead to classify CT scan images into infected and uninfected Covid-19 cases. This work involves multiple important parts: image preprocessing, deep feature extraction and classifier, then, comparisons. The proposed model is shown in Figure 2.

2.3. Deep feature extraction

In this study, deep feature extraction is suggested via a proposed model. It consists of multiple layers as demonstrated in Figure 2 starting from the input layer, which collects original input matrix pixels. In this study, PNG images, each with the dimensions of (width×height) pixels, are used all the data 16-bit gray scale images composed of 512×512 pixels. After that, the data is sent to a batch normalization (BN) layer for standardizing the

input values. This technique operates on the input data over a sequence of steps. Mathematically BN calculates the mean and variance of features for mini-batches, then the mean is subtracted and each value is divided by the standard deviation of a mini-batch. This stabilizes the learning process and enables faster training.

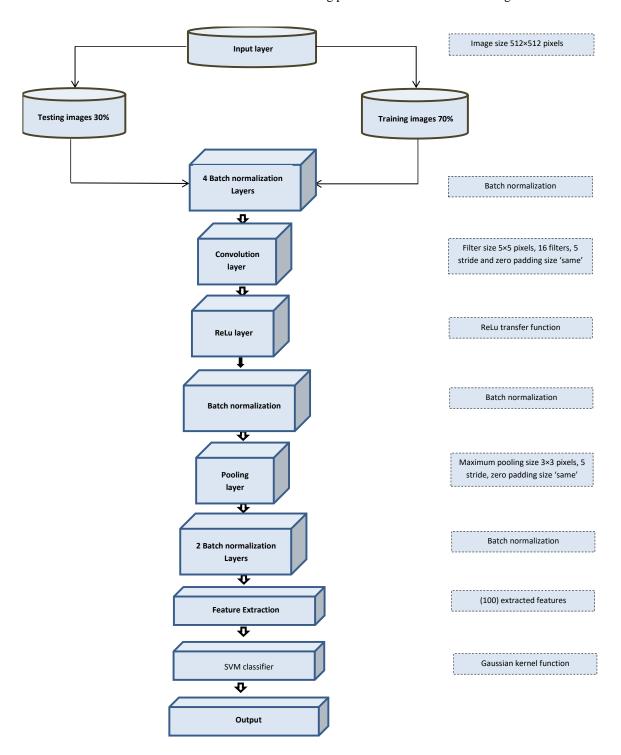


Figure 2. The proposed efficient model to classify chest CT scan images of Covid-19 into healthy and infected cases

Usually, normalization remapping the variances between values which may significantly affect the processes in the next layers. Mathematical expressions for the operations in a BN layer are given as (1) [38]:

$$\mu_{\beta} = \frac{1}{m} \sum_{i=1}^{m} x_i \tag{1}$$

where μ_{β} represents the batch mean, m represents the number of BN batch inputs, β represents the current batch and x_i represents the input values to the BN layer.

$$\sigma_{\beta}^{2} = \frac{1}{m} \sum_{i=1}^{m} (x_{i} - \mu_{\beta})^{2}$$
 (2)

where σ_{β}^2 represents the batch variance and σ represents the standard deviation of BN batch inputs.

$$\widehat{x}_{l} = \frac{x_{l} - \mu_{\beta}}{\sqrt{\sigma_{\beta}^{2} + \varepsilon}} \tag{3}$$

where $\hat{x_i}$ represents the normalized value and ε represents the smoothing it prevents division by zero within the operation, ensuring numerical stability. 0.00005 is the value of the smoothing factor.

$$y_i = \gamma \widehat{x}_i + \beta \equiv BN_{\gamma,\beta}(x_i) \tag{4}$$

where y_i is the value of the final operation, the scaling γ is for the scaling and β is for the shifting. It is possible to learn the scaling and shifting parameter values. BN makes sure that the teachable parameters have the ideal values during neural network training in order to enable precise normalization for each mini batch. Additional BN layer is adopted after the convolution and rectified linear unit (ReLU) layers. Subsequently, the deep features are extracted and applied to the SVM. The operations of convolution and ReLU layers have been highlighted in [39]-[42]. Consequently, the obtained deep features are fed to the SVM in order to classify between the infected Covid-19 cases and healthy cases.

2.4. Support vector machine

SVM is an effective classification technique. It is based on two ideas. The first idea is mapping the values of a feature vector into a high dimensional space with a nonlinear method. The second idea is separating the mapped values by a margin hyper plane. The plane may well classify the mapped values [43]. This method is highly preferred because of its high performance and less computational power. It can usually solve linear and non-linear problems. Initially, the data which is required to be classified are imported. Then, it is represented as unique points in a high dimensional space, where each point is represented in a vector of features.

$$x \in \mathbf{R}^d \tag{5}$$

where \mathbf{R}^d represents the vector space with d dimension. The lengths of vectors are also called norms. The length of vector \mathbf{x} is calculated as:

$$||\mathbf{x}|| = \sqrt{x_1^2 + x_2^2 + x_3^2} \tag{6}$$

where x_1, x_2 and x_3 represent different values in the vector **x**. The direction of vector **x** is calculated as:

$$\left\{ \frac{x_1}{||\mathbf{x}||}, \frac{x_2}{||\mathbf{x}||}, \frac{x_3}{||\mathbf{x}||} \right\} \tag{7}$$

In real world applications, finding the perfect classes for many training datasets takes long time. Usually, some parameters are adopted in order to control the accuracy and SVM classifier. One of the most important parameters is the kernel function. Amazing issue about kernel is that we can utilize it to go to higher dimensions and perform smooth calculations. The kernel plays important role in learning with the hyper plane, it is done by transforming the problem by using a certain algebra. Different SVM algorithms use differing kinds of kernel functions such as linear, radial basis function (RBF) and Gaussian kernel. For linear kernel, the equation of predicting a new input using the dot product between the input x and each support vector x_i is calculated as (8):

$$f_{liner}(x, x_i) = \sum_{i} (x_i x_i)$$
 (8)

RBF is one of the most used and preferred kernel functions in the SVM. Usually, it is chosen for non-linear classification. It is calculated as (9):

$$f_{RBF}(x, x_i) = e^{(-\text{gamma} * ||x - x_i||^2)}$$
 (9)

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where, gamma varies between 0 to 1, the most preferred value is 0.1. Gaussian kernel is used for removing the cross term in mathematical functions. It can be calculated as (10):

$$f_{Gaussian}(x,x_i) = e^{\left(\frac{-||x-x_i||^2}{2\sigma^2}\right)}$$
(10)

where, σ represents the standard deviation [44].

3. RESULTS AND DISCUSSION

A public Covid-19 or severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) lung CT scan dataset is employed. It consists of 8439 CT scan images, 7495 positively Covid-19 infected patients and 944 negatively Covid-19 infected patients. The data was obtained from genuine patients in radiology centers of teaching hospitals in Tehran, Iran. Image are acquired as 512×512 pixels in PNG format.

Training and testing are done by using a computer that has specifications as follows: Dell-brand laptop with 32 GB of RAM, an intel core (TM) i5 8th Gen processor clocked at 3 GHz, and other specifications. The CPU is the basis for all implementations. Used learning parameters in the deep feature extraction are listed in Table 1. Adam optimizer was chosen as the best option because the magnitudes of parameter updates are invariant to gradient rescaling, its step sizes are approximately bounded by the hyper parameter step size, it does not require a stationary objective and it works with sparse gradients. In addition, Adam's implementation is simple, computationally efficient and needs minimal memory [45]. In this study, 0.0001 learning rate is employed, which yielded a significant improved generalization accuracy. Minimum batch size of 128 is utilized for training, it allows computational speedups. Number of epochs is determined equal to 100, which provides sufficient time and performance for updating the weights. Verbose frequency and validation frequency are both equal to 20 as this allows the network to apply its computational power and this might perform better in training.

Table 1. Specifications for the deep feature extraction algorithm

Training parameter	Value	
Optimizer	Adam	
Initial learn rate	0.0001	
Max epochs	100	
Minimum BatchSize	128	
Verbose frequency	20	
Validation frequency	20	

In the exploited SVM, every training option helps in detecting and classifying the healthy and unhealthy persons from Covid-19 by employing CT scan images. It can be observed from Table 2 the SVM options which are considered here. For the first option the constraint box (CB) value is used equal to 1. It allows to set the CB for the soft margin and usually this value can be a scalar or a vector of the same length as the training data. In the options of type 'Kernel function', 'Kernel scale parameter' and 'Kernel offset parameter', the following values are used: Gaussian, 0.3 and 0.1, respectively. Gaussian operations can be utilized for the general supervised learning to solve probabilistic classification and regression problems. The algorithm implements an 'optimization routine' based on an iterative single data algorithm (ISDA). This makes the work fast and solves critical problems, when the learning phase of the SVM is proportional to the number of training data pairs. The classified predictors list's selected option is set to 'vector of positive integers'. Accordingly, each component of the vector is an index value that designates the category of the relevant predictor for that element. The index values range is from 1 to the number of predictors employed in training. 'Categorical array' is utilized in the option 'names of classes to use for two-class learning'. Each element must match a row in the array for this option to be valid. To establish the training's class order and the position of each argument's input or output dimensions in relation to that order. In the 'Observation weights' option, a 'numeric vector' of positive values is combined with weights. The software compares the weights of the observations in each row. In 'number of folds' has been used equal to 10-fold cross validation (CV) to train the classifier. This method divides the initial samples into training and testing sets in order to compare the performance of predictive models.

Table 3 and Figure 3 show the lowest obtained value for the classification is 29.19% with the value of polynomial kernel function equal to 0.3. While the accuracy rate is increased to 95.91% after using the automatic (auto) value of for the same kernel function. Wheres, the SVM classifier gives close accuracies by implementing the linear kernel function for the two options of auto and 0.3 as they respectively obtain 88.42% and 89.63%. Our method reaches its best results after utilizing the Gaussian kernel function, where it

achieves the accuracy of 97.98% for the auto and a remarkable value of 100% for 0.3. Deep feature extractions with the SVM (together as one embedded technique), therefore, can enhance the capability of classifying Covid-19 cases into healthy and infected. It has yielded much more accurate results than applying a single CNN method only, where this gave the accuracy of 72%.

Table 2. Classifier parameters for the SVM

SVM parameters	Value
СВ	1
Kernel function	Gaussian
Kernel scale parameter	0.3
Kernel offset parameter	0.1
Optimization routine	ISDA
Categorical predictors list	Vector of positive integers
Names of classes to use for two-class learning	Categorical array
Observation weights	Numeric vector
Number of folds	10

Table 3. The effects of various SVM kernel functions on testing our proposed algorithm

SVM testing options	Value of function	Accuracy (%)
Polynomial Kernel Function	Auto	95.91
Polynomial Kernel Function	0.3	29.19
Linear Kernel Function	Auto	88.42
Linear Kernel Function	0.3	89.63
Gaussian Kernel Function	Auto	97.98
Gaussian Kernel Function	0.3	100

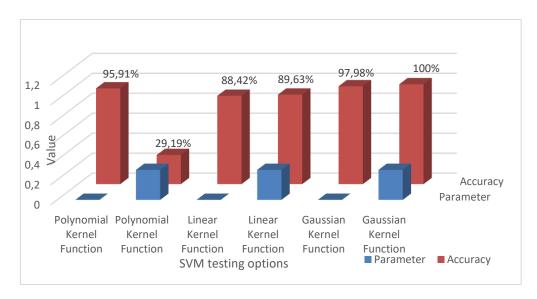


Figure 3. The performances of different SVM kernel functions on testing our suggested algorithm

4. CONCULUSION

In this paper, an effective model for classifying Covid-19 chest CT scan images into healthy and infected cases was presented. We applied a ML strategy in this work which exploited the power of deep feature extractions with the SVM. This included several key components: image pre-processing, deep feature extraction and classification. In evaluating this model, we used a large dataset of CT scan images. The model proved to be effective, where in the evaluation it obtained a very high accuracy of 100%. This was better performance than applying a single CNN alone, which gave a small and unsatisfied accuracy of 72%.

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