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An optimized KELM approach for the diagnosis of COVID-19 from 2D-SSA reconstructed CXR Images

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Abstract

The COVID-19 is proved to be the most infectious disease of the current century with a high mortality rate world-wide. The current RT-PCR test standard for the diagnosis of COVID-19 is an invasive and time-consuming procedure, whereas the chest X-ray (CXR) images provide a non-invasive and time/cost-effective method for COVID-19 diagnosis. The current existing deep learning methods for the detection and diagnosis of CXR images provide biased results for the small size dataset available. Hence, in the present work, a conventional yet efficient method is proposed classifying the CXR images into COVID-19, Pneumonia, and Normal. The proposed approach pre-processes the CXR images using 2D singular spectrum analysis (SSA) for image reconstruction which enhances the feature inputs to the classifier. The features are extracted from the reconstructed images using a block-based GLCM approach. Then, a grasshopper-based Kernel extreme learning machine (KELM) is proposed which finds the optimal features and kernel parameters of KELM at the same instance. From the experimental analysis, it is seen that the present work outperforms that of other competent schemes in terms of classification accuracy with a minimal set of features extracted from the first 2 eigen components of the 2D-SSA reconstructed image with 5 × 5 decomposition.

1. Introduction

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) or now commonly known as COVID-19 is first identified in Wuhan City (Hubei Province, China) and is reported to the world health organization (WHO) in December 2019. Later, in January 2020, it was a global health emergency and by March 2020, it became a global pandemic declared by WHO. To date, it is having a major impact on global health by infecting a large number of people, severe long-term health sequela, and a large figure of mortality rate [1,2]. As per the current statistics, there are around 170 million active cases of COVID-19 with deaths of over 3.5 million around the world. With the changing mutation of the virus, the count is still rising [3].

The current gold standard for the identification of the disease COVID-19 is the reverse transcription polymerase chain reaction (RT-PCR) test which is having low accuracy with a time constraint on it. Also, it is worth mentioning that the procedure associated with the test has to be meticulous about the sample site and most of the users report it to be very uncomfortable [4]. The alternative to this test is using radiography images of the chest using computed tomography (CT) or X-ray techniques. CT scan is comparatively costly and more harmful to the subject than Chest X-ray (CXR). Since the disease is very new to the world, the human expertise for identifying the radiology image for COVID19 is only about 65% [5]. Hence, a computer-aided diagnosis system is an utmost necessity for assisting the doctors as well as the radiologists in the identification of the disease.

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https://doi.org/10.1016/j.ijleo.2021.167572
Received 4 June 2021; Accepted 30 June 2021
Available online 7 July 2021
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The study done by authors of [6,7] has shown that the automatic classification using CXR images gives better results than that of the CT images. Hence, most of the literature adapted CXR-based COVID-19 identification as the standard. To aid the detection of the COVID-19 automatically from CXR images, Apostolopoulos et al. [8] first proposed transfer learning based convolutional neural network (CNN) in March 2020. Following the lead, several deep learning-based architectures are proposed during that year [9–18] using the Cohen JP COVID-19 image data collection [19]. This database is a constantly updating database and till the end of June 2020, accumulated a total of 123 COVID-19 positive images. However, such small number of COVID-19 positive images for the training of deep neural networks (DNN) introduces a high possibility of bias [20]. To expand the size of the small set of COVID-19 images, one of the promising methods is data augmentation [11,13]. Continuous efforts are made employing various machine learning (ML) algorithms where the database of increased number of images are used [21–29]. Chandra et al. [23] proposed a hierarchical classifier using conventional ML algorithms. A cluster-based approach is proposed in [22] using generalized gross neural network (GGNN) and probabilistic neural network (PNN) for multi-class classification of Pneumonia bacterial Normal, viral Pneumonia, and COVID-19 CXRs to make the learning possible from few samples. Hussain et al. [21] proposed a 22 layer CNN model for binary and multi-class classification of COVID-19, Normal, viral Pneumonia, and bacterial Pneumonia CXRs. To train the CNN model, the authors combined all the 8 publicly available CXR datasets. But the number of images in all the classes was less than 1000. For the requirement of large data, Karakanis et al. [24] used deep learning conditional generative adversarial networks (CGAN) to generate the synthetic data followed by CNN models for classification of two and three class CXR images. Two more CNN models are conceived by Gilanie et al. [25] and Das et al. [26] for automated detection of COVID-19 CXR images. Tabik et al. [27] proposed a COVID-SDNet model for predicting COVID-19 using CXR images. The variation they used from the prior mentioned method is using a U-Net approach for the segmentation of lung region from the image and the segmented images as the input to the CNN for more focused features around the lung area only. The same concept is carried out by Rahman et al. [28] while using a 22 layer CNN with a modified version of U-Net segmentation for lung area segmentation from CXR images. Although, most of the aforementioned methods report an accuracy of more than 95%, however, due to the lower number of samples for training the DNNs, the evaluation of the robustness of the proposed models or obtaining a generalized power for clinical setting is dubious [30].

In the proposed article, a conventional algorithm is proposed which reports an improved accuracy even with a small sized dataset. Moreover the proposed work has a significant advantage over DNN networks in terms of computational complexity. The proposed algorithm uses 2 dimensional singular spectrum analysis (2-D SSA) technique to obtain quality noise-free images for better feature extraction in the subsequent stage. Next, a block-wise gray-level co-occurrence matrix (Block-GLCM) is used for extracting the second-order statistical features from the reconstructed images. Further, a bio-inspired evolutionary algorithm, namely, grasshopper optimization algorithm hybridized with kernel extreme learning machine (KELM) is employed for feature selection and also for binary and multi-class classification of COVID-19, Normal, and Pneumonia CXR images.

This paper is organized as follows: Section 2 gives background information about the techniques used in the proposed algorithm. The next section details the stages of the proposed algorithm. Section 4 describes the dataset used for algorithm implementation, experimental setup, and discusses the results obtained. Finally, the conclusion is reported in Section 5.

2. Preliminary background

2.1. 2-D singular spectrum analysis (2-D SSA)

In this paper, to enhance the feature profile of the CXR images, a 2-dimensional singular spectrum analysis (2-D SSA) approach is adopted. 2-D SSA algorithm is based on singular value decomposition (SVD) of a Hankel-block-Hankel (HbH) matrix constructed from the input image of size $N_x \times N_y$ matrix. The structure of the 2-D SSA algorithm consists of four steps, namely, embedding, decomposition, grouping, and reconstruction.

$\bullet$ **Embedding:** This step comprises of HbH matrix construction from the image matrix $(I_{N_x\times N_y})$, i.e.

$$ I_{N_x \times N_y} = \begin{pmatrix} I_{0,0} & I_{0,1} & \cdots & I_{0,N_y-1} \\ I_{1,0} & I_{1,1} & \cdots & I_{1,N_y-1} \\ \vdots & \vdots & \ddots & \vdots \\ I_{N_x-1,0} & I_{N_x-1,1} & \cdots & I_{N_x-1,N_y-1} \end{pmatrix} \tag{1} $$

For the window size of $\ell_x, \ell_y$ whose dimension restricted by $1 \leq \ell_x \leq N_x, 1 \leq \ell_y \leq N_y$ and $1 < \ell_x \ell_y < N_x N_y$, HbH matrix of $\ell_x \ell_y \times k_x k_y$ is created, where $k_x = N_x - \ell_x + 1$ and $k_y = N_y - \ell_y + 1$. The constructed HbH matrix or the trajectory matrix $(T(I))$ could be represented as below,

$$ T(I) = \mathcal{W} = \begin{pmatrix} H_0 & H_1 & H_2 & \cdots & H_{k_y-1} \\ H_1 & H_2 & H_3 & \cdots & \vdots \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ H_{\ell_x-1} & H_{\ell_x} & \cdots & H_{N_y-1} \end{pmatrix} \tag{2} $$

2
where,

\[
H_j = \begin{pmatrix}
I_{0,j} & I_{0,j} & \cdots & I_{k_z-1,j} \\
I_{1,j} & I_{2,j} & \cdots & I_{k_z,j} \\
\vdots & \vdots & \ddots & \vdots \\
I_{k_z-1,j} & I_{k_z,j} & \cdots & I_{N_z-1,j}
\end{pmatrix}
\]  

(3)

- **Decomposition:** The SVD is applied on the trajectory matrix (Eq. (2)) to obtain the nonzero eigenvectors. Mathematically, it can be represented as follows.

\[
\mathcal{W} = \sum_{i=1}^{d} \sqrt{\lambda_i} U_i V_i^T
\]

(4)

Or,

\[
\mathcal{W} = \mathcal{W}_1 + \mathcal{W}_2 + \cdots + \mathcal{W}_d
\]

(5)

Where, \(\lambda_i (1 \leq i \leq d)\) is the nonzero eigen value and \((\lambda_i, U_i, V_i)\) forms the eigentriples of the matrix \(\mathcal{W}\mathcal{W}^T\) with the left and right singular vectors \((U, V)\). By transforming the eigenvectors to window form, eigenimages could be obtained.

- **Grouping:** Grouping could be performed on the basis of analysis of eigen vector to enhance the properties of original image. When the expression of Eq. (5) is obtained, the grouping procedure partitions the set of indices \(1, \ldots, d\) into \(m\) disjoint subsets \(J_1, J_2, \ldots, J_m\). For a subset \(J = i_1, \ldots, i_p\), the matrix \(\mathcal{W}_J\) corresponding to the group \(J\) is defined as \(\mathcal{W}_J = \mathcal{W}_{i_1} + \cdots + \mathcal{W}_{i_p}\). Thus, the grouped matrix decomposition is expressed as

\[
\mathcal{W} = \mathcal{W}_{J_1} + \cdots + \mathcal{W}_{J_m}
\]

(6)

The grouping with \(I_J = \{J\}\) is called elementary.

- **Reconstruction:** The matrices \(I_J\) obtained by grouping may not be Hankelized necessarily, so they need to be Hankelized. This is done in two step Hankelization process. The first hankelization is done within each block (Eq. (2)) and then applied between the blocks (Eq. (7)). The reconstructed \(Z_m \in \mathbb{R}^{N_x \times N_y}\) gives the 2-D image projected from the group \(I_J\), could be expressed as:

\[
Z_J = \begin{pmatrix}
z_{m_{1,1}} & z_{m_{1,2}} & \cdots & z_{m_{1,N_y}} \\
z_{m_{2,1}} & z_{m_{2,2}} & \cdots & z_{m_{2,N_y}} \\
\vdots & \vdots & \ddots & \vdots \\
z_{m_{N_x-1,1}} & z_{m_{N_x-1,2}} & \cdots & z_{m_{N_x-1,N_y}}
\end{pmatrix}
\]

(7)

The projected original image could be expressed using the following expression,

\[
P = Z_1 + Z_2 + \cdots + Z_M
\]

(8)

This helps in the decomposition of an image into several components extracted \(Z_m\) based on the SVD. Each component corresponds to each eigenvalue obtained in the SVD. 2D SSA application in the CXR images for reconstructing the image by taking the most significant eigenvectors gives a better input for feature extraction. Also, it helps in noise suppression from the image which resides in the low eigenvalued pixel vectors.

2.2. **Gray-level co-occurrence matrix (GLCM)**

The GLCM [31] is considered as an efficient approach to represent the second-order statistical feature descriptors of an image. This feature extraction technique helps to study the textural features of an image by exhibiting the spatial relationship between two pixel elements. This relational occurrence of pixel pairs is determined by varying the distance and orientation between the pixels. Each pixel element \(p(x, y)\) in GLCM indicates the sum of the incidence of occurrence of \(x\) in a specific association with the pixel \(y\). It can be implied as \(g(x, y|d, \theta)\). Here, \(d\) and \(\theta\) are the distance and orientation between the pixel pairs, respectively where \(\theta\) can be 0°, 45°, 90°, and 135°. For more details, readers can refer to [32].

3. **Proposed methodology**

The proposed method aims at classifying the CXR images in two ways such as binary (Normal–Abnormal) and multi-class classification (Normal, Pneumonia, and COVID-19). The block diagram of the proposed approach is shown in Fig. 1. In the first stage, 2-D SSA is applied to the images to reconstruct the images to enhance the features of the image and suppress any noise present. In the next stage, feature extraction is done using Block-GLCM followed by feature selection and classification using grasshopper-based KELM. The following subsections describe the working of each block in more detail.
3.1. Application of 2D-SSA on CXR images

The X-ray images generally contain noises like Poisson noise, salt and pepper noise, and speckle noise [33]. These degrade the quality of the noise as well as hinders the feature extraction from the image for classification purposes. Here, the 2-D SSA is applied to the images before feature extraction. SSA application on the CXR images is based on selecting significant components and discarding the less significant components. These less significant and noisy components usually in the low-value eigenvectors. Hence, the reconstructed image with a high value of eigenvector leads to an enhanced image profile for better feature extraction. These feature obtained from the reconstructed images gives better input for the classification. There are two determining parameters of the 2-D SSA application. First, the window size \( \ell \), which provides the total numbers of components extracted in the decomposition stage. The second is in the eigenvalue grouping stage, which selects the extracted components for the desired image reconstruction for feature extraction. Fig. 2 shows examples of reconstructed images with the first and second eigen-components using \( \ell = 5 \) and \( \ell = 10 \).

3.2. Feature extraction using block-GLCM

In the present work, the images are resized to 256 \( \times \) 256, which are further divided into non-overlapping blocks of size 64 \( \times \) 64 to extract the local information in detail. Hence, a total of 16 non-overlapping blocks are generated. Next, a set of 5 statistical descriptors, namely, energy, entropy, correlation, the sum of variance, the sum of average are obtained for all the blocks in 4 different directions using GLCM. Hence, a total of 320 (16 \( \times \) 4 \( \times \) 5) features are obtained from each image.

3.3. Feature selection and classification using grasshopper-based KELM

In the present work, a bio-inspired evolutionary algorithm, namely, grasshopper optimization algorithm is hybridized with kernel extreme learning machine (KELM) classifier to get the optimal features and values of two important parameters of KELM, namely, penalty (\( \lambda \)) and kernel (\( \gamma \)) parameters, simultaneously. The grasshopper optimization algorithm (GOA) follows the behavior of grasshopper swarms to get a globally optimal solution [34]. It may be noted that this optimization algorithm is exploited to obtain the optimal features and kernel parameters of KELM at the same time. KELM is a variant of ELM which is utilized to get improved performance than that of the conventional ELM [35]. In KELM, different kernel functions are implemented for different application purposes. Here, one of the most widely used kernel functions, namely, radial basis function (RBF) kernel is applied. A detailed flow diagram of the present grasshopper-optimized KELM is represented in Fig. 3. The size of the candidate vector is taken as \( s \), where the first two positions indicate \( \lambda \) and kernel (\( \gamma \)) parameters. The next \( s - 2 \) positions indicate the size of the features.

The mechanism of encoding for the candidate vector is done as follows. Each feature is normalized where the value ranges between [0,1]. If the value of the function (see Eq. (9)) of a feature is \( \leq 0.5 \), then that feature is rejected and converted to 0. Else, the corresponding feature is taken into consideration and converted to 1.

\[
\text{Logsig}(s_{ih}) = 1/(1 + \exp(-s_{ih}))
\]  

(9)
Fig. 2. (a)–(c) for Normal, (d)–(f) for Pneumonia, (g)–(i) for COVID-19, Images: Original, Reconstructed image with $\ell = 5$ (eigen components [1-2]), Reconstructed image with $\ell = 10$ (eigen components [1-2]).

Additionally, in the present work, the fitness value of every candidate is the respective classification accuracy and it is represented as follows:

$$fitness_{val} = avgAcc = \frac{\sum_{t=1}^{T} TestAcc_t}{T}$$

where $T$ symbolizes total iterations performed, $avgAcc$ indicates the average of the test accuracy determined by KELM through 5-fold cross-validation.

4. Experimental results and discussions

4.1. Dataset

To start with the implementation of the proposed approach, the CXR images are collected from COVIDx 1.0 [36]. The dataset is a publicly available research dataset which is created by merging three different datasets, namely, COVID-19 Image Data Collection [19], Figure-1-COVID-19 Chest X-ray Dataset Initiative [37] and RSNA Pneumonia Detection Challenge dataset [38]. In the current scenario, the COVID-19 class is primarily sourced from COVID-19 Image Data Collection [19]. The dataset contains a total of 5144 CXR samples out of which 460 are COVID-19, 1266 are Normal, and 3418 are Pneumonia samples. For binary classification, the samples of COVID-19 and Pneumonia are merged to form the samples of abnormal set.

4.2. Experimental setup

The present block-GLCM + PCA + grasshopper-optimized model is implemented using MATLAB 2019a. The dataset is divided into train, validation, and test sets using the k-folded stratified cross-validation (SCV) method to prevent over-fitting. In this work, a 5 independent runs 5-fold cross-validation approach is implemented to get ensure the results are robust and consistent. The results listed below Tables are obtained by taking the mean of the 5 independent runs. To assess the classification performance of the proposed model, different measuring parameters, namely, classification accuracy, sensitivity, specificity, Mathew’s Correlation
Coefficient (MCC), AUC, and F-score are considered via confusion matrix [39]. In the experiment, the value of $\lambda$ and $\gamma$ are set in the range of $[2^{-8}, 2^{-6}, ... , 2^8]$. 

### 4.3. Results obtained prior to 2D-SSA, PCA, and optimization

In the experimental analysis, initially, the results are obtained before 2D-SSA, PCA, and optimization. At the initial stage, a total of 320 number of GLCM features are extracted from the original CXR images without applying 2D-SSA which are then fed to the KELM classifier. The KELM classifies the CXR images into COVID-19, Normal, and Pneumonia. Table 1 shows the results of classification before 2D-SSA, PCA, and optimization. From the table, it is seen that the highest accuracy for the 2-class and 3-class classifications are 85.86% and 83.2%, respectively. However, this performance improved when the original images get pre-processed with 2D-SSA followed by feature reduction and optimization.
4.4. Results after applying 2D-SSA, PCA and optimization

This section discusses the results generated from the CXR images after employing 2D-SSA before the feature extraction stage. Next, the length of the feature vector is reduced using PCA, and then, grasshopper-optimized KELM is applied for feature optimization and classification. The initial length of the obtained feature vector is 320 which is then reduced to 80 using PCA. However, the reduced feature vector may still contain some irrelevant features which degrade the performance of the classifier. Hence, in the present work, grasshopper-optimized KELM is implemented to get the optimized features along with optimal values of $\lambda$ and $\gamma$ at one instance.

To demonstrate the impact of 2-D SSA reconstructed image on the results, Table 2 presents the results obtained for 2-class and 3-class classification by applying PCA and grasshopper-optimized KELM on the original CXR image features obtained by Block GLCM. Then, the results are also obtained using different values of $\ell$ for applying 2D-SSA on CXR images in Tables 3–5. These show the results obtained from the pre-processed images using 2D-SSA for $\ell = 5$, 10, and 20, respectively. C_val and G_val in the table indicate the optimal values of KELM parameters i.e. $\lambda$ and $\gamma$, respectively. Additionally, the values shown in the tables are the average of 5 independent runs. From the tables, it could be concluded that the maximum classification accuracy obtained is 100% for the reconstructed image having $\ell = 5$. Further, it could be observed that the MCC value is lower for 3-class classification when only 1 component is considered while without a significant change in the number of features. Also, when $\ell$ is increasing, the algorithm has additional computation complexity with accuracy declining. Hence, to achieve the highest accuracy for classification, the reconstructed images with $\ell = 5$ and components $[1-2]$ are found to be most appropriate.

Additionally, to show the efficiency of the proposed work, two fundamental evolutionary algorithms, namely, genetic algorithm (GA) and particle swarm optimization algorithm (PSO) are also combined with KELM. The algorithmic parameters of GA, namely, crossover and mutation rate are fixed as 0.4 and 0.01, respectively. Similarly, the parameters of PSO, namely, the acceleration coefficient and the inertia weight are settled to 2.05 and 1, respectively. The comparison among the three approaches, genetic-based KELM, particle swarm-based KELM, and grasshopper-based KELM is made for classification accuracy and illustrated in Fig. 4.
Fig. 4. Line chart illustration of the comparison of three methods in terms of classification accuracy (a) for 2 class (b) for 3 class.

Table 6
Comparative results with proposed algorithm for 2-Class and 3-Class Accuracy obtained in %ge for different existing techniques and respective size of dataset used.

| Literature       | Technique                  | Number of images (COVID19+Pneumonia + Normal) | 2-Class Accuracy (%) | 3-Class Accuracy (%) |
|------------------|----------------------------|-----------------------------------------------|----------------------|----------------------|
| Ioannis et al. [8] | VGG19, MobileNet v2       | 224+714+504                                  | 98.75                | 93.48                |
| Ozturk et al. [9]  | DarkNet                    | 127+500+500                                  | 98                   | 87.02                |
| Togacar et al. [10] | MobileNetV2, SqueezeNet   | 295+98+65                                    | X                    | 99.27                |
| Khan et al. [12]   | CoroNet                    | 285+657+310                                  | 99                   | 95                   |
| Toraman et al. [14] | Convolutional capsnet      | 231+1050 (Normal)                             | 97.24                | X                    |
| Abbas et al. [15]  | DeTrac capsnet             | 196+X                                        | X                    | 95.12                |
| Jain et al. [16]   | Xception Net               | 576+4273+1583                                | 98                   | 98                   |
| Elkorany et al. [17]| COVIDetection-Net         | 300+300+300                                  | 100                  | 99.4                 |
| Ismael et al. [18] | ResNet50 Features + SVM    | 180+X                                        | 94.7                 | X                    |
| Hussain et al. [21]| CoroDet                    | 500+800+800                                  | 99.1                 | 94.2                 |
| Aradhye et al. [22]| GRNN + PNN                 | 69+158+79                                    | 100                  | 92.49                |
| Chandra et al. [23]| Majority vote based classifier ensemble | 434+434+434                      | 98.06                | 93.41                |
| Karakanis et al. [24]| Light weight DNN          | 145+145+145                                  | 98.7                 | 98.3                 |
| Das et al. [26]    | Ensemble learning + CNN    | 438+,+333                                    | 91.62                | X                    |
| Rahman et al. [28] | U-Net+CNN                  | 3616+6012+8851                               | X                    | 96.29                |
| Shakarami et al. [29] | CBIR + AlexNet CNN      | 400+,+400                                    | 99.38                | X                    |
| Proposed Model     | 2D-SSA + Block GLCM + Grasshopper based KELM | 460+3418+1266 | 100                  | 100                  |

From the figure, it is observed that the performance of the proposed grasshopper-KELM exceeds that of the other two evolutionary approaches.

Again, Table 6 provides the accuracy (in %) for 2-class (Abnormal and Normal) and 3-class (COVID19, Pneumonia and Normal) obtained for the existing algorithms and proposed algorithm along with the number of sample images used for implementation. From the table, it is evident that the hand-picked features used for the implementation of the proposed algorithm with the conventional techniques are the best performing.

5. Conclusion

As the current pandemic situation is progressing, it is expected to deal with the diagnosis of COVID-19 as a priority. The existing CNN algorithm results are implausible for the low number of COVID-19 training samples and high computational complexity involved. Hence, in this paper, an efficient approach based on conventional techniques is proposed for the CXR image classification of COVID-19, Pneumonia and Normal. Here, the 2-D SSA technique is used as a pre-processing technique for the CXR image reconstruction to provide noise-free enhanced features to the classifier. The features of the image are extracted using Block-GLCM, which is a proven adequate method for feature extraction. The features obtained are again optimized and classified using grasshopper-based optimized KELM. A maximum accuracy of 100% is obtained for 2D-SSA with $\ell$ value 5 and the first 2 eigen pixel vectors considered. From the analysis of the obtained results, it could be concluded that the proposed model outperforms the existing DNN models.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.
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