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Stacked Ensemble Machine Learning based Skin Cancer Detection and Classification Model

K. Uma Maheswari[1,*], C. P. Indumathi[2], S. Usha[2], S. Gayathri Priya[3]

[1]Department of Information Technology, University College of Engineering, BIT Campus, Anna University, Tiruchirappalli, India
[2]Department of Computer Science and Engineering, University College of Engineering, BIT Campus, Anna University, Tiruchirappalli, India
[3]Department of Electronics and Communication Engineering, R.M.D. Engineering College, Chennai, India
Emails: umaravi03@gmail.com; cpindumathi@aubit.edu.in; usha@aubit.edu.in; sgp.ece@rmd.ac.in

Abstract

Skin cancer is most top three critical kinds of cancer due to damaged DNA, which is cause death. This damaged DNA begins cells for growing uncontrollably and currently it can be obtaining improved quickly. It is several researches on the computerized examination of malignancy from the skin cancer image. But, study of these images are very difficult taking several troublesome issues such as light reflections on the skin surface, differences from the color illumination, sizes of lesions, and distinct shapes. Thus, the outcome, evidential automatic detection of skin cancer are appreciated for developing the accuracy and efficiency of pathologists at the beginning phases. This manuscript develops a Stacked Ensemble Machine Learning based Skin Cancer Detection and Classification (SEML-SKCDC) approach. The presented SEML-SKCDC technique majorly aims to offer ensemble of three ML models for skin cancer classification. In the presented SEML-SKCDC technique, median filtering and contrast enhancement is performed at the pre-processing stage. To generate feature vectors, the honey badger algorithm (HBA) with EfficientNet method has been exploited in this work. At last, an ensemble of k-nearest neighbor (KNN), random forest (RF), and feed forward neural network (FFNN) approaches are applied for skin cancer classification. The simulation evaluation of the SEML-SKCDC system on skin cancer database depicts the developments of the SEML-SKCDC algorithm with recent methods.

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1. Introduction

Skin cancer becomes most common cancers that cause death across the world. There exist 2 kinds of skin cancer named non-melanoma and melanoma [1]. Initial identification of such lesions might rise the curing rate to 90%. More resemblance between various kinds of skin lesions will make the visual examination tough and results in incorrect examination. Melanoma will start to develop in a cell termed melanocyte [2]. It initiates when healthier melanocytes start to produce out of control, causing a cancerous tumor. It is generally seen on the body parts which is exposed to rays of sunlight, namely on the lips, hands, face, neck, and so on. Melanoma kind of tumours is just cured when it is identified in the earlier stage, or they start to spread to other body parts and result in the painful death of victim [3]. There exist several kinds of melanoma skin tumors namely lentigo malign, nodular melanoma, acral lentiginous, and superficial spreading melanoma. Such tumor cells contain low tendency of spreading to other body parts. Non-melanoma tumours were made a comparison with melanoma tumours. Thus, the critical aspect of skin cancer treatment is initial prognosis [4]. Clinicians normally utilize the biopsy technique for the identification of skin cancer. This procedure becomes time-consuming, painful, and slow. Computer based technologies offer a speedy diagnosis, are convenient, and are considered less expensive ones for identifying skin cancer indications [5]. To observe the skin cancer indications, whether they indicate non-melanoma or melanoma, non-invasive in nature, many methods were devised.

Thus, an automatic mechanism is mandated for skin lesion classification [6]. This classifying mechanism used the methods of artificial intelligence (AI) and image processing. The prior computer-aided techniques for dermatological image classification encounter 2 main difficulties [7]. Firstly, inadequate data. The imaging process becomes next challenging issue where a special gadget, dermoscopy, achieves skin images whereas other medical images like histology images can be gained by utilizing biopsy and microscopy. The previous techniques needed wide pre-processing, feature extraction, and segmentation process for classifying the skin images [8]. DL has transformed the whole landscape of machine learning (ML) in recent years. It can be assumed the most urbane ML subfield is related to artificial neural network (ANN) techniques. Such techniques were simulated by the structure and function of brain [9]. As compared with other traditional techniques of ML, DL mechanisms have reached remarkable outcomes in such applications [10].

In Khamparia et al. [11], a new DL IoHT driven structure is presented for the classification of skin cancer in skin images with the idea of TL. During this work, automated feature is extracted from an image with distinct pretrained models such as SqueezeNet, VGG19, InceptionV3, and ResNet50 that is provided as FC layer of CNN for skin malignant and benign cells classification with dense and max pooling operations. Furthermore, the suggested method is totally incorporated with IoHT architecture and is remotely employed to assist health-care professionals in the treatment and diagnosis of skin lesions. In [12], the author handles the problems of integrating metadata features and images with DL algorithms employed for the classifier of skin lesions. The author developed the Metadata Processing Blocks (MetaBlock), a new method that makes use of metadata for supporting data classification through improvising the most appropriate features derived from the images all over the classifier pipelines.

Chaturvedi et al. [13] devise an automated CAD mechanism for MCS cancer classification having very higher accuracy. The proposed method outpaced professional skin doctors and modern DL algorithms for MCS cancer classification. The author implemented tuning on 7 classes of HAM10000 dataset and carried out a relative study for examining the act of 5 pre-trained CNNs and 4 ensembling methods. Ameri [14] introduces a DL method for identifying skin cancer through skin lesion images. A deep CNN has been formulated for classifying the images into malignant and benign classes. The AlexNet is used as the pre-trained method in a TL approach. The devised technique considers the raw image as the input and mechanically studies beneficial features in the images for classifying purposes. Hence, it removes complicated process of feature extraction and lesion segmentation.

Rashid et al. [15] present a new deep TL technique for melanoma categorization utilizing MobileNetV2. The MobileNetV2 was a deep CNN, which categorizes the sample skin lesion into benign or malignant. Saba et al. [16] developed an innovative automatic technique for skin lesion recognition and detection employing a deep CNN. The modelled cascaded model includes 3 essential steps one is contrast improvement via fast local Laplacian filtering (FlLpF) having HSV color change; next step is extracting lesion boundary by making use of color CNN method by following XOR function; final step is extracting features deeply by implementing TL leveraging Inception V3 method earlier to feature fusion employing hamming distance (HD) methodology. An entropy controlled selecting feature approach was even presented for selecting the most discriminant structures.

This manuscript develops a SEML-SKCDC approach. The presented SEML-SKCDC technique majorly aims to offer ensemble of three ML models for skin cancer classification. In the presented SEML-SKCDC technique, median filtering and contrast enhancement is performed at the pre-processing stage. To generate feature vectors, the honey badger algorithm (HBA) with EfficientNet method has been exploited in this work. At last, an ensemble of KNN, RF, and FFNN approaches are applied for skin cancer classification. The simulation evaluation of the SEML-SKCDC methodology on skin cancer database depicts the enhancements of the SEML-SKCDC technique over other recent methodologies.

2. The Proposed Skin Cancer Classification Model

In this manuscript, a new SEML-SKCDC method was presented for the recognition and classification of skin cancer. The proposed SEML-SKCDC methodology majorly aims to offer ensemble of three ML approaches for skin cancer classification. In the presented SEML-SKCDC technique, median filtering and contrast enhancement is performed at the pre-processing stage. To make feature vectors, the HBA with EfficientNet method has been exploited in this work. At last, an ensemble of KNN, RF, and FFNN models is applied for skin cancer classification. Figure 1 portrays the block diagram of SEML-SKCDC algorithm.

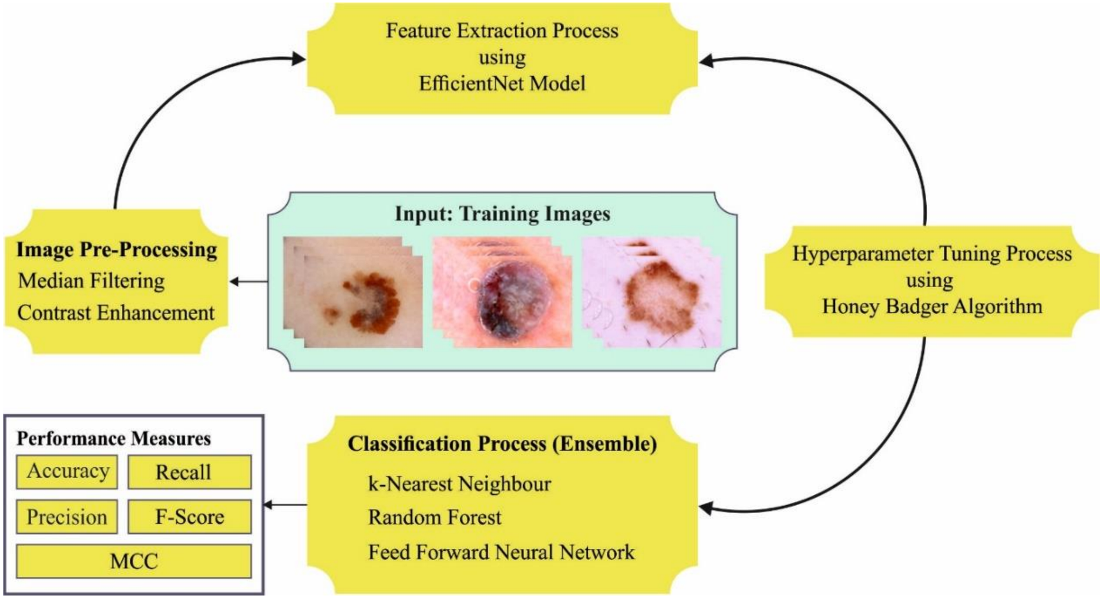

Figure 1. Block diagram of SEML-SKCDC approach

A. Feature Extraction

In the proposed SEML-SKCDC technique, the HBA with EfficientNet model is exploited in this work. According to the observation that better performance and accuracy are achieved through imposing a balance between every network size, EfficientNet was developed through scaling in 3D, viz., resolution, width, and depth, using a subset of fixed scaling coefficient that meets specific limitations [17]. With the compact configuration, there exist overall eighteen convolutional layers, viz., D=18 and every layer is armed using kernel k(5,5) or k(3,3). The input images have RGB color channels of 224 × 224size. The second layer has been scaled up in width to enhance the performance, however, scaled down in resolution to reduce the size of feature maps. Another configuration of the EfficientNet family is produced from EfficientNetB0 through dissimilar scaling values. EfficientNetB7 outperformed a CNN by accomplishing a good performance, but significantly decreasing the parameter count.

To modify the hyper parameter values of the SEML-SKCDC technique, the HBA is used. The HBA was simulated by the smart hunting performance of honey badgers (HB) [18]. HBA accomplishes the balancing amongst exploration as well as exploitation by setting suitable chances. During the HBA technique, the smell intensity of prey I was compared with the focus strength of victim S and the distance amongst the prey as well as HB d_i that allows searching agent for transferring in exploration to exploitation and keep from falling as local optimal. The density factor α implies the randomized control feature, which reduces with time for reducing population diversity throughout iteration. It attains the vital trade-off balancing amongst exploration as well as exploitation. F is offering population diversity from the searching procedure by altering the searching directions. HBA takes 2 modes of finding food sources digging and honey modes:

1. Digging mode: HBs utilize their rat sniffing abilities to gradually method the prey and dig the prey in a cardioid manner. During the digging mode, the HBA place upgrade procedure (x_{new}) is provided as Eq. (1):

$$x_{new} = x_{prey} + F \times \beta \times I \times x_{prey} \quad (1)$$

$$+F \times r_3 \times \alpha \times d_i \times |\cos(2\pi r_4) \times [1 - \cos(2\pi r_5)]|$$

whereas x_{rey} implies the global optimum place of prey still. I refers the smell intensity of prey α signifies the upgrade density factor. β denotes the capability of HB for getting food (default $= 6$). r_3, r_4, and r_5 indicates the 3 distinct arbitrary values amongst $zero$ and one. F implies the flag to alter the searching direction that is provided in Eq. (2):

$$F = \begin{cases} 1\, r_6 \le 0.5 \\ -1 r_6 > 0.5 \end{cases} \quad (2)$$

I refers the prey smell intensities which is compared with the prey concentration strength S and the distance amongst the prey as well as HB d_i. The prey smell intensity I has strong if the prey concentration strength is higher and the distance amongst the prey and HB are closer. HBs are searching quicker if the prey smell intensity is strong. I, S, and d_i are provided correspondingly utilizing in Eqs. (3)-(5):

$$I_i = r_2 \times \frac{S}{4\pi d_i^2} \qquad (3)$$

$$S = (x_i - x_{i+1})^2 \qquad (4)$$

$$d_i = x_{prey} - x_i \qquad (5)$$

whereas r_2 implies the arbitrary number amongst $zero$ and one. The density upgrade factor α is an arbitrary variable, which controls time-varying chance that is utilized for achieving smooth transition in the exploration and development. It can be provided as in Eq. (6):

$$\alpha = C \times \exp\left(\frac{-t}{t_{\max}}\right) \qquad (6)$$

In which C denotes the higher than or corresponding to 1 (default $= 2$). t signifies the present count of iterations and $t_{\max}$ refers the maximal amount of iterations.

2. Honey mode: The HB likes eating bee larvae and pupae, and it is integrated with honey-guide (bird) for defining bee larvae. It can be complex for HB for determining the hive, however, its claws simply break open the hive, but the honey-guide rapidly defines the hive while could not break it. During the honey mode, the HBA place upgrade procedure (x_{new}) is provided as Eq. (7):

$$x_{new} = x_{prey} + F \times r_7 \times \alpha \times d_i \qquad (7)$$

In which r_7 denotes the arbitrary number amongst $zero$ and one.

The HBA system takes a fitness function (FF) for realizing enhanced classifier performances. It describes a positive integer for denoting the better efficiency of candidate outcome. In this case, the minimized classification rate of error was observed that FF as represented in Eq. (8).

$$fitness(x_i) = ClassifierErrorRate(x_i)$$

$$= \frac{No.\ of\ misclassified\ instances}{Total\ no.\ of\ instances} * 100 \qquad (8)$$

B. Stacked Ensemble Learning based Classification

In this work, an ensemble of KNN, RF, and FFNN approaches was applied for skin cancer classification. The driving concept of ensemble method is to integrate the prediction of many base estimators for improving generalizability and robustness through a single predictor. In the study, a stacked ensemble method that assembles FFNN, RF, and KNN methods are developed. Based on the concept, a high level (level_1) meta model is trained on out-of-fold prediction of base model (level_0), which generates a concluding forecast of the total ensemble models. The data training and partitioning method is discussed in the following:

Step1 Divide the overall trained sets into 2 disjointed sets represented by the holdout and learned sets.

Step2 Trained every level_0 base model on the learning set and testing on the holdout set.

Step3 Utilize holdout set prediction as input and target value as output for training the level_1 learner named meta-model.

Step4 Repeating steps 1 to 3 until the whole dataset was utilized for making out-of-fold prediction.

On the one hand, the stacked model is regarded as a means of jointly evaluating the errors of each base generalizer while correcting prediction residual via the level_1 model and working on a specific learning set. At the same time, it is viewed as a tremendous MLP that exploits level_1 model as output layer unit and level_0 model as neural unit of hidden layer to maximize generalizability, robustness, and accuracy of the prediction.

1) RF Model

RF is recognized as a powerful and widespread ML algorithm that might implement classification and regression processes [19]. It is a collective ML methodology using a divide-and-conquer algorithm, which integrates more than one learning mechanism for forming single method to increase the efficiency of the method. Therefore, the method generates different DTs as an improvement of an individual tree in a cut module. The method boosts these different DTs namely the Gini index approach or information gain model. Generally, the higher trees in the forest, the further powerful the classifier, which leads to high performance.

In this study, to categorize a novel object according to features or attributes, every tree offers its calculation, and the model selects the classifier that has the majority voting (the most votes) of the trees in the forest and assists in rectifying the higher difference that implies a model to make a poor prediction while the training data is altered and usually appear in a single DT model. Therefore, RF has a lower bias, since it depends on DTs, and has lower discrepancy. It employs the bagging method (viz., ensemble ML methodology) that integrates several DTs for forming an individual method. The lower variance and bias decrease the problem of overfitting that occurs while a model training implements better with trained dataset however offers imprecise prediction using the test dataset. Consider the case count in a trained subset is N (or the item number in the trained dataset). Next, samples from N cases would be randomly taken however with replacement. Once there exist M input features or variables, a number $m < M$ is quantified so that at every node, m parameters are chosen arbitrarily out of M. The optimal splitting of m is applied to separate the tree node. The value of m remains constant, whereas the forest is grown. Every tree is developed to the biggest range, and there exists no pruning and forecast novel dataset by gathering the prediction of k tree.

Assumed a trained data $D = (X_1, X_2, \cdots, X_n)$, $x_i \varepsilon \mathbb{R}^d$ and quantified class $y_i \in Y$, whereas $Y = \{1,2,\cdots,m\}$, choose k random instances using the replacement from D, and build or fit k DTs in the following:

For $I = 1$ to k.

Choose arbitrary instances, with replacement, from D and Y; as $D_i Y_i$.

Fit h_i on $D_i Y_i$, whereas h_i denotes a DT leaner that is built from the D_i random samples.

Afterward, training, classifying novel X' into the suitable class (attaining the $\hat{y}$ value) is generated by taking the most votes from every DT on X':

$$\hat{y} = \arg \max_{y \in Y} \left(' \textstyle\sum_{i=1}^{k} h_i (X') \right) \qquad (9)$$

In addition, the lower variance and bias benefit of the RF classification denotes that the classification takes lesser time for testing and training when compared to other supervised learning methods. Since RF belong to the lower bias class that decreased the assumption count made through RF for fitting a module, and it requires a maximal of two tuning variables.

2) KNN Model

The presented study is a robust classifier module in the multi-dimension classifier that offers modest performance outcomes. The approximation of classifier considers that neighbours continuously share communal classes and features.

KNN consider that in the d-dimension space, the nearer the two objects, the highly possibly they belong to a similar class [20]. The nearness can be represented as the distance between the points or objects. The distance is evaluated through the Minkowski, Euclidean, Hamming, or Manhattan approaches. In addition, the nearness could be viewed as a comparison between the objects, and it is evaluated by the similarity computational models namely cosine similarity.

KNN is a conventional ML approach that has theoretical assurances: while n or size of dataset D becomes large, there exists some theoretic assurance regarding the efficiency of KNN.

Assume a trained data $D = \{(x_1, y_1), (x_2, y_2), \cdots, (x_n, y_n)\}$, $x_i \varepsilon J \mathbb{R}^d$ and a predetermined subset of class $y_i \in Y$, whereby $Y = \{1,2,\cdots,m\}$, there exists certain distance metric namely the Euclidean distance that measures the distance among two points in the d-dimension problem so that

$$d(X_i, X_j) = x_i - x_{j^2}$$

$$d(X_i, X_j) = \sum_{c=1}^{d} (x_{i_c} - x_{j_c})^2$$

Now, $X_i, X_j \in \mathbb{R}^d$, $X_i = (x_{i_1}, x_{i_2}, \cdots, x_{i_d})$, and $X_j = (x_{j_1}, x_{j_2}, \cdots, x_{j_d})$. In KNN, assume the distance between the new x termed x' and the neighboring point as a similarity measurement as follows

$$\hat{y} = \arg \max_{y \in Y} \sum_{=1}^{k} d\,(x_{i_c}, x_{j_c}) \qquad (10)$$

Assume the similarity between X_i and X_j, whereby X_i denotes a feature vector of, so that $\overline{X_i} = (x_{i_1}, x_{i_2}, \cdots, x_{i_h})$ and $\overline{x_j} = (x_{j_1}, x_{j_2}, \cdots, x_{j_1})$, $x_{i)} x_j \varepsilon \mathbb{R}^d$ is

$$sim\,(x_i, x_j) = \cos\,(\overline{X_{i,}X_j}) = \frac{\overline{X_i}.\overline{X_j}}{|\overline{X_i}||\overline{X_j}|} \qquad (11)$$

Here, simplify the similarity principle and change Eq. (10) as

$$\hat{y} = \arg \max_{y \in Y} \sum_{c=1}^{k} \mathrm{sim}\,(x_{i_c}, x_{j_c}) \qquad (12)$$

Also, KNN has a probabilistic formula. An arbitrary parameter y:

$$y \sim P(y|X, D)$$

In which, $P(y|X, D)$ denotes the fraction of point X_i in $N_k(X)$, and $N_k(X)$ indicate the k-nearest point to X_i as follows

$$\hat{y} = \arg \max_{y \in Y} P(y|x, D) \qquad (13)$$

3) FFNN Model

An artificial neural network (ANN) or connectionist system is ML method stimulated from the biological neural network and could procedure a similar dataset as a human brain [21]. ANN develops linear and non-linear methodologies for time sequence. ANN is extensively applied and accepted as an efficient mechanism for forecasting and optimization. The feed-forward backpropagation neural network (FFNN) structure encompasses input, output, and multiple hidden neurons. FFNN has efficacy in resolving different kinds of challenges. Alternatively, finding an effective FFNN training method is very complex. Resolving FFNN problem by augmenting each network weight. In FFNN, the input dataset (I_n) was multiplied through the weight W_{i_J}. The addition function is the sum of bias (b_i) on layer1 and input with weight (W_{i_J}). $X_2(t)$ indicates activation function.

$$X_1(t) = \sum_{i=1}^{j} W_{i_J}\, l_n(t) + b_1 \qquad (14)$$

$$X_2(t) = f(x_1(t)) = \frac{1}{1+exp^{x_1}} \qquad (15)$$

In layer 2, the resultant in layer1 $(X_2(t))$ was multiplied weight layer2. The addition

function of Layer 2 is a sum of bias with weight $(W_{jk})$and bias (b_2) and output layer 1 with weight $(X_2(t))$.

$$X_a(t) = \sum_{j=1}^{k} W_{jk}\, X_2(t) + b_2 \qquad (16)$$

$$x_4(t) = f(X_3(r)) = \frac{1}{1+exp^{X_3}} \qquad (17)$$

3. Performance Validation

The simulation validation of the SEML-SKCDC approach was tested utilizing the skin cancer dataset, containing 1224 benign samples and 199 malignant samples as depicted in Table 1. A few sample images are showed in Figure 2.

Table 1: Details on dataset

Classes	No. of Instances
Benign	1224
Malignant	199
Total No. of Instances	1423

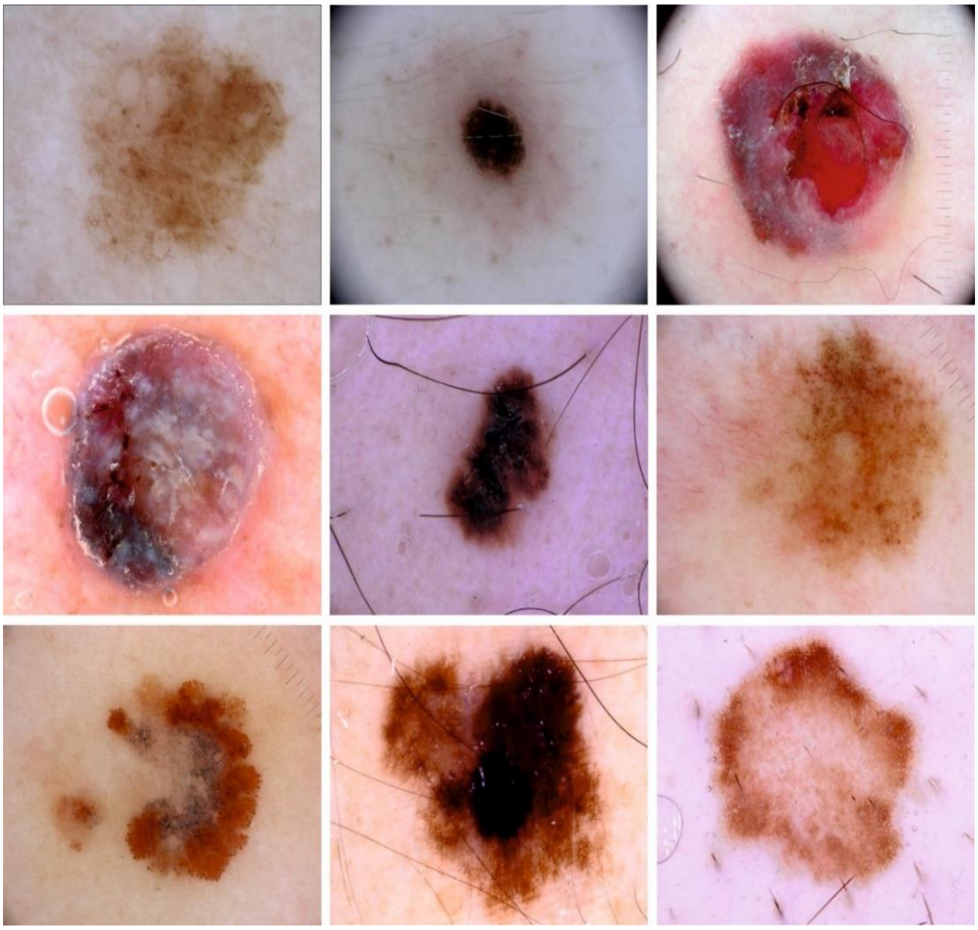

Figure 2. Sample images

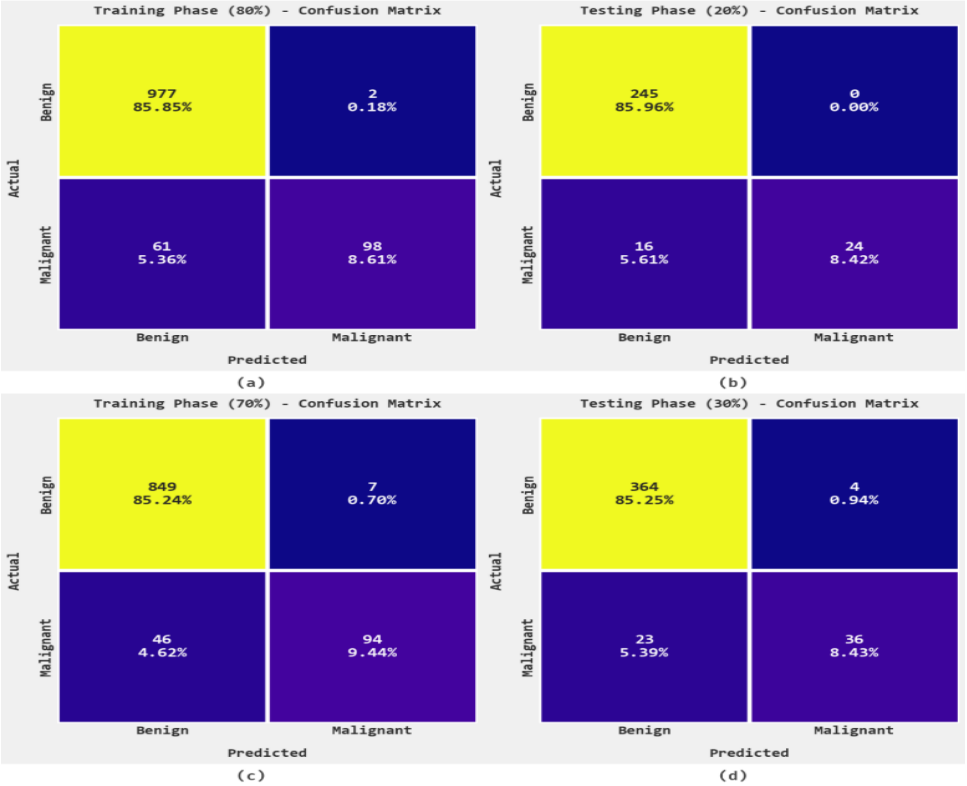

Figure 3. Confusion matrices of SEML-SKCDC approach (a-b) 80:20 of TR data/TS data and (c-d) 70:30 of TR data/TS data

The confusion matrix offered by the SEML-SKCDC model is demonstrated in Figure 3 under diverse training (TR) and testing (TS) data. With 80% of TR data, the SEML-SKCDC approach has identified 977 instances into benign and 98 instances into malignant. In line with, with 20% of TS data, the SEML-SKCDC system has identified 245 instances into benign and 24 instances into malignant. Along with that, with 70% of TR data, the SEML-SKCDC algorithm has identified 849 instances into benign and 94 instances into malignant. Besides, with 30% of TS data, the SEML-SKCDC methodology has recognized 364 instances into benign and 36 instances into malignant.

Table 2 offers the skin cancer classifier result of the SEML-SKCDC technique on 80:20 of TR/TS data. The outcome implied the effectual outcomes of the SEML-SKCDC model.

Table 2: Result analysis of SEML-SKCDC methodology with 80:20 of TR/TS data

Training / Testing (80:20)					
Labels	$Accu_y$	$Prec_n$	$Reca_l$	F_{Score}	MCC
Training Phase					
Benign	94.46	94.12	99.80	96.88	75.23
Malignant	94.46	98.00	61.64	75.68	75.23
Average	94.46	96.06	80.72	86.28	75.23
Testing Phase					
Benign	94.39	93.87	100.00	96.84	75.05
Malignant	94.39	100.00	60.00	75.00	75.05
Average	94.39	96.93	80.00	85.92	75.05

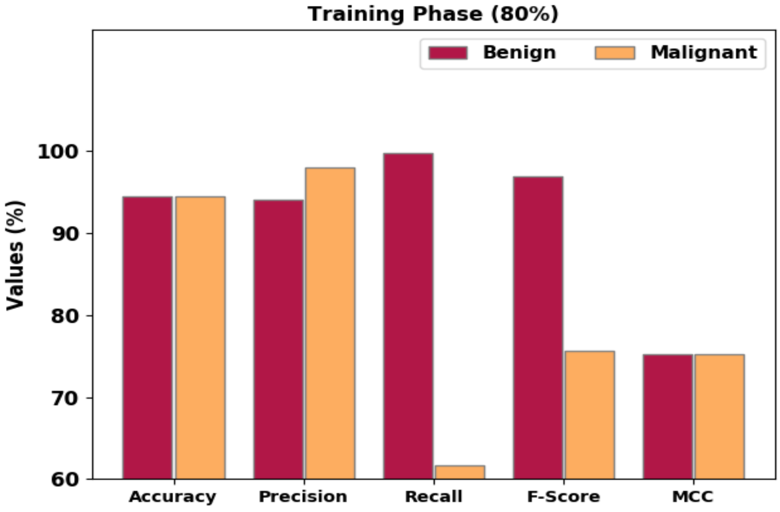

Figure 4. Result analysis of SEML-SKCDC system on 80% of TR data

Figure 4 exhibits the classifier result of the SEML-SKCDC process on 80% of TR data. The SEML-SKCDC model has identified benign class samples with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.46%, 94.12%, 99.80%, 96.88%, and 75.23% respectively. Also, the SEML-SKCDC algorithm has considered malignant class instances with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.46%, 98.00%, 61.64%, 75.68%, and 75.23% respectively. In addition, the SEML-SKCDC model has obtained average $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.46%, 96.06 %, 80.72%, 86.28%, and 75.23% respectively.

Figure 5 depicts the classifier results of the SEML-SKCDC algorithm on 20% of TR data. The SEML-SKCDC model has identified benign class samples with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.39%, 93.87%, 100%, 96.84%, and 75.05% correspondingly. Besides, the SEML-SKCDC system has categorized malignant class instances with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.39%, 100%, 60%, 75%, and 75.05% correspondingly. At last, the SEML-SKCDC technique has obtained average $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.39%, 96.93 %, 80.%, 85.92%, and 75.05% correspondingly.

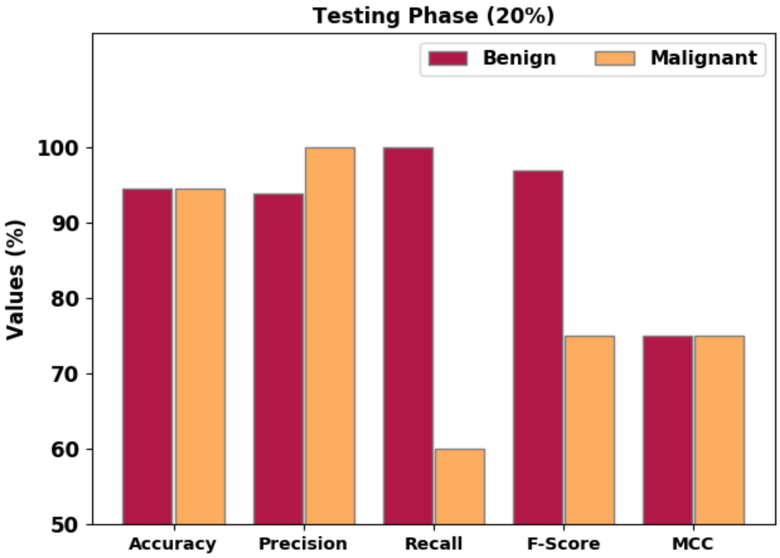

Figure 5. Result analysis of SEML-SKCDC system on 20% of TS data

Table 3 offers the skin cancer classifier result of the SEML-SKCDC method on 70:30 of TR data/TS data. The outcome demonstrated the effectual outcomes of the SEML-SKCDC algorithm.

Table 3: Result analysis of SEML-SKCDC method with 70:30 of TR data/TS data

Training / Testing (70:30)					
Labels	$Accu_y$	$Prec_n$	$Reca_l$	F_{Score}	MCC
Training Phase					
Benign	94.68	94.86	99.18	96.97	76.37
Malignant	94.68	93.07	67.14	78.01	76.37
Average	94.68	93.96	83.16	87.49	76.37
Testing Phase					
Benign	93.68	94.06	98.91	96.42	70.98
Malignant	93.68	90.00	61.02	72.73	70.98
Average	93.68	92.03	79.96	84.58	70.98

Figure 6 illustrates the classifier result of the SEML-SKCDC method on 70% of TR data. The SEML-SKCDC method has identified benign class samples with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.68%, 94.86%, 99.18%, 96.97%, and 76.37% correspondingly. Moreover, the SEML-SKCDC system has categorized malignant class instances with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.68%, 93.07%, 67.14%, 78.01%, and 76.37% respectively. Besides, the SEML-SKCDC algorithm has obtained average $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.68%, 93.96 %, 83.16%, 87.49%, and 76.37% correspondingly.

Fig. 7 shows the classification result of the SEML-SKCDC system on 30% of TS data. The SEML-SKCDC algorithm has identified benign class instances with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 93.68%, 94.06%, 98.91%, 96.42%, and 70.98% correspondingly. Followed by, the SEML-SKCDC system has categorized malignant class samples with $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 93.68%, 90%, 61.02%, 72.73%, and 70.98% correspondingly. Eventually, the SEML-SKCDC method obtained average $accu_y$, $prec_n$, $reca_l$, F_{score}, and MCC of 94.68%, 93.96 %, 83.16%, 87.49%, and 76.37% correspondingly.

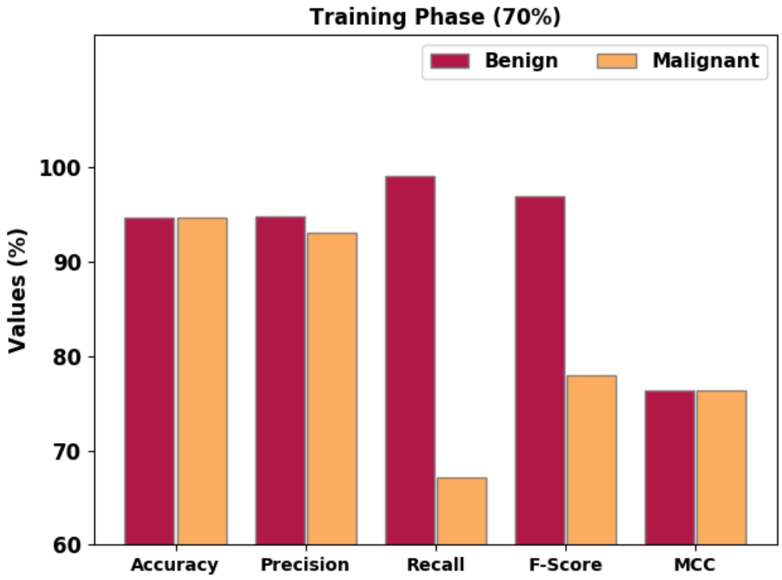

Figure 6. Result analysis of SEML-SKCDC system on 70% of TR data

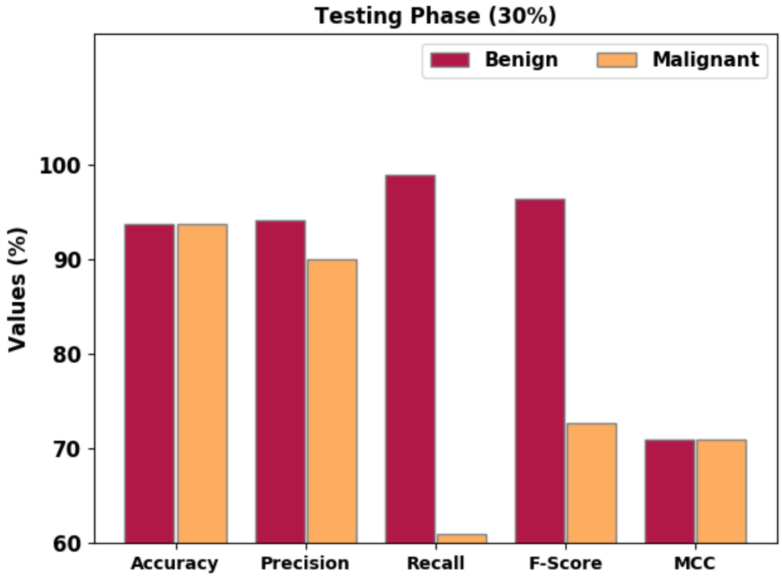

Figure 7. Result analysis of SEML-SKCDC system on 30% of TS data

The training accuracy (TRAC) and validation accuracy (VLAC) acquired by the SEML-SKCDC methodology on test database is depicted in Figure 8. The simulation value exposed that the SEML-SKCDC methodology has reached superior outcomes of TRAC and VLAC. Generally, the VLAC considered that higher than TRAC.

The training loss (TRLO) and validation loss (VLL) obtained by the SEML-SKCDC system on test database are represented in Figure 9. The simulation value revealed that the SEML-SKCDC technique has been able lower outcomes of TRLO and VLLO. In certain, the VLLO is lower than TRLO.

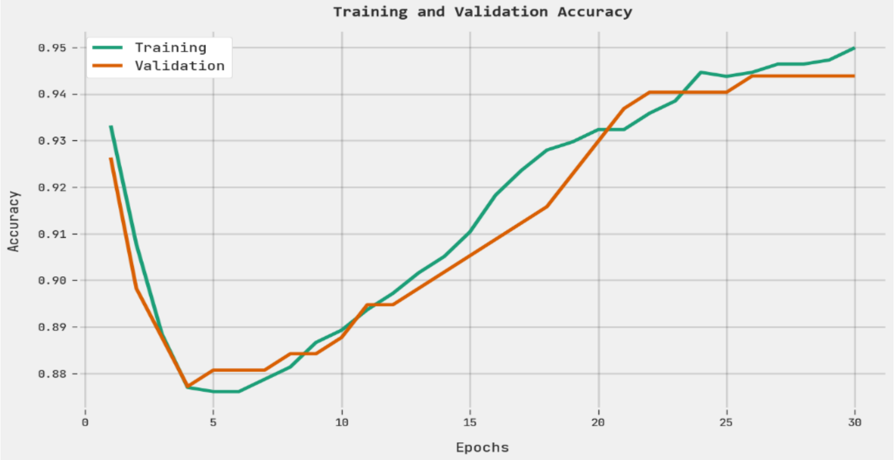

Figure 8. TRAC and VLAC curve of SEML-SKCDC method

Figure 9. TRLO and VLLO curve of SEML-SKCDC method

A PR examination of the SEML-SKCDC approach on test database is represented in Figure 10. The outcome stated that the SEML-SKCDC algorithm has resulted in increased solutions of PR outcomes under various classes.

A widespread ROC examination of the SEML-SKCDC algorithm on test database is displayed in Figure 11. The outcome demonstrated the SEML-SKCDC algorithm has depicted their capability in classifying various classes on test database.

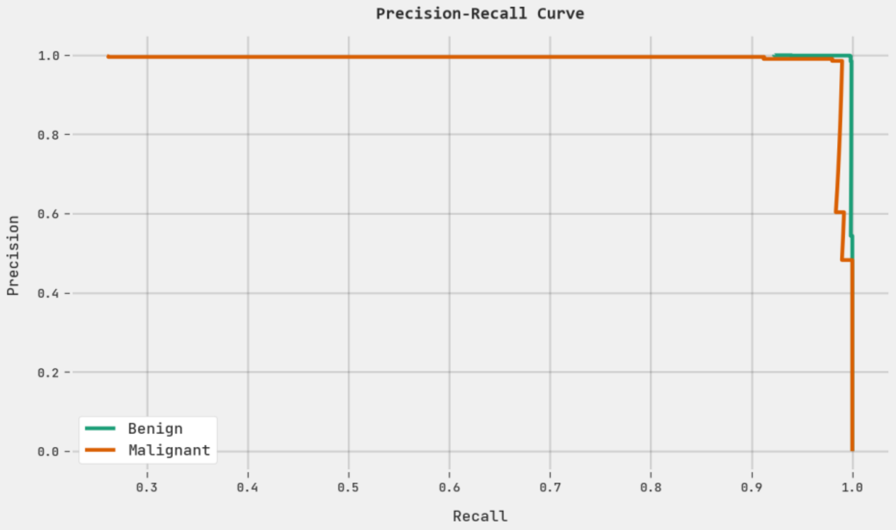

Figure 10. PR curve of SEML-SKCDC algorithm

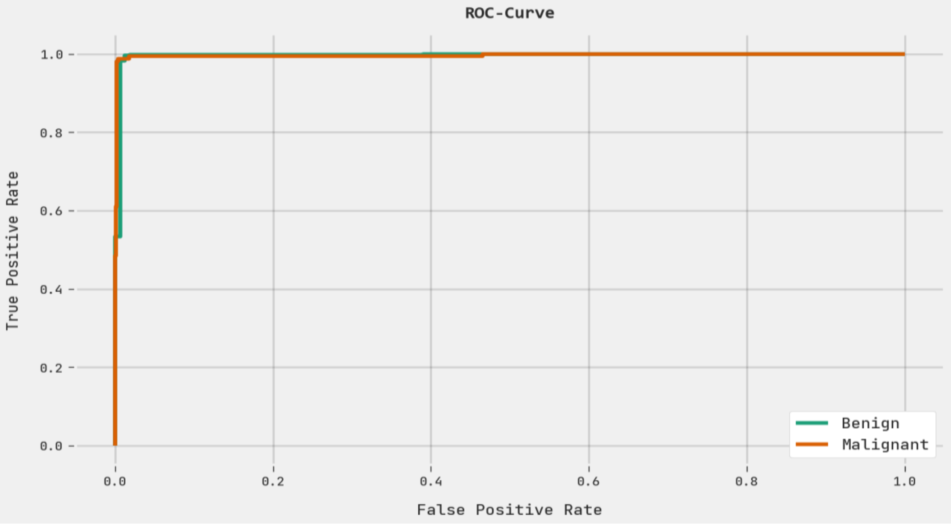

Figure 11. ROC curve of SEML-SKCDC methodology

A wide-ranging simulation analysis of the SEML-SKCDC model with other recent methods is compared in Table 4 and Figure 12 [22-24]. The outcome inferred that the VGG-16 and MobileNet models have accomplished least $accu_y$ values of 86.25% and 88.58% correspondingly. Moreover, the DCNN and ResNet approaches are reported certainly higher $accu_y$ values of 91.79% and 91.10% respectively. However, the SEML-SKCDC system has shown higher solution with other approaches with superior $accu_y$ of 94.39%. These outcomes certain the enhanced outcomes of the SEML-SKCDC approach over other recent approaches.

Table 4: Comparative outcome of SEML-SKCDC system with existing methods

Methods	Accuracy (%)
SEML-SKCDC	94.39
DCNN Model	91.79
ResNet	91.10
VGG-16	86.25
MobileNet	88.58
AlexNet	90.69
DenseNet	88.71

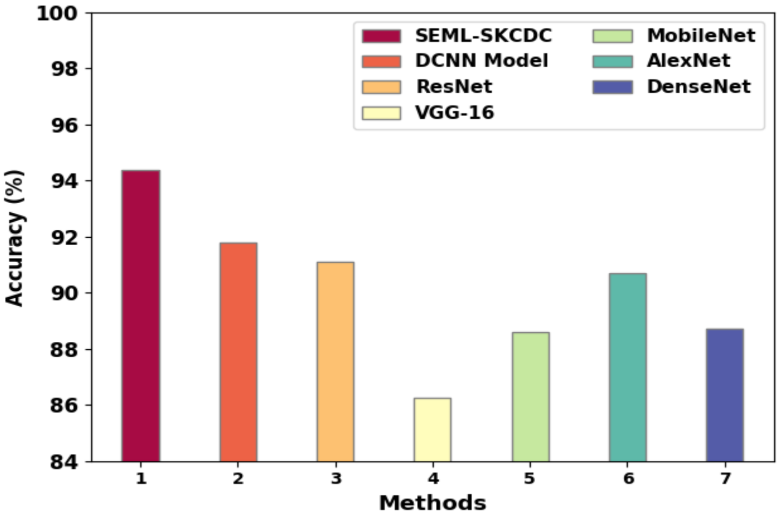

Figure 12. Comparative outcome of SEML-SKCDC approach with recent methods

4. Conclusion

In this manuscript, a new SEML-SKCDC method has been presented for the classification and recognition of skin cancer. The presented SEML-SKCDC approach majorly aims to offer ensemble of three ML techniques for skin cancer classification. In the presented SEML-SKCDC technique, median filtering and contrast enhancement is performed at the pre-processing stage. To generate feature vectors, the HBA with EfficientNet method has been exploited in this work. At last, an ensemble of KNN, RF, and FFNN models was executed for skin cancer classification. The performance evaluation of the SEML-SKCDC algorithm on skin cancer dataset depicts the developments of the SEML-SKCDC algorithm over other recent systems. In future, the presented SEML-SKCDC technique can be extended to real time cloud platform for remote monitoring purposes.

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