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Research Article

Designing a SegClassNet Model based on New Loss Function for Skin Disease Classification

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ABSTRACT—

Classification of skin diseases is becoming highly vital in modern healthcare diagnosis systems since humans have been impacted by several types of skin disorders. The identification and classification of different skin disorders have been performed by few transfer learning models. Among those, Segmentation and Classification Network (SegClassNet) model can use dilated convolution and dropout layer in encoder-decoder network to segment the skin lesion images. Also, ResNet18-based Deep Convolutional Neural Network (DCNN) was used to classify the skin disease images. But, this DCNN utilizes the classical loss functions which restrain the network to learn discriminative features from skin lesion images. Hence, this article proposes a novel model called Fine-tuned SegClassNet (F-SegClassNet) by adjusting the ResNet18 layers with a combined triplet and group loss. First, a modified SegNet is employed to segment the augmented skin lesion images. Also, dropout layer is used to avoid the overfitting problem. Then, the embedding from segmented images is learned into the Euclidean space by using DCNN ResNet-18 model. Then, l_2 distance is computed among corresponding segmented images from Euclidean space for learning discriminative features of skin disease images using combined triplet and group loss function. Moreover, the segmented input images are classified by using these l_2 distances. Finally, the experimental results demonstrate that the proposed model attains an average accuracy of 93.37% for HAM dataset than the other existing models.

Keywords—Skin diseases, Transfer learning, SegClassNet, ResNet18, Discriminative features, Triplet loss function, Group loss, Euclidean space

I. INTRODUCTION

Skin or dermatological diseases are the more diverse and complex sub-fields of medicine due to their complexities in handling symptoms and their differences in various conditions. Skin diseases are frequent amongst other diseases, particularly those that are vulnerable to spread, and can prove to be toxic to melanoma if they are not recognized in their earlier stages. In modern years, the occurrence of skin diseases has risen significantly related to the ratio of other types of diseases [1-2]. Many investigations advise that one-fifth of peoples are prone to be impacted by skin disorders and thus its categorization is very complicated.

So, automated categorization of such disorders plays a major function through analyzing various visual signs like skin lesion anatomy, the human structure representation, color, shaping and lesion alignment. Based on the independent analysis of human skin characteristics, the categorization is highly difficult and also the skin features are not automatically extracted. To solve these problems, transfer learning model has been suggested to classify the skin diseases by using the pre-trained deep learning structures [3]. The pre-trained classifiers are mainly used to update the weights of neural networks based on the recurrent backpropagation instead of initializing the random weight values.

In the past centuries, several pre-trained DCNN structures include AlexNet, GoogLeNet, VGGNet, etc., are implemented to classify the skin diseases [4-5]. From this viewpoint, a novel cross-domain skin disease classification model [6] has been developed by the two-stage progressive transfer learning using fully supervised Residual Network (ResNet152) structure pre-trained on ImageNet to modify the network structure on the intermediate set. Also, cycle-GAN learning has been applied as a domain adaptation method for translating the skin features from source to the target domain. Even though it realizes good performance, the visual knowledge of DCNN was not efficient for skin-like images. To tackle this challenge, skin images were segmented by the SegNet i.e., deep encoder-decoder network and the segmented images were classified by the DCNN [7]. On the contrary, the fine-delineating the margins between the ROIs in the lesion images was not achieved.

As a result, a modified SegNet with Classification called SegClassNet has been designed [8] in which the skin lesion images augmented by cycle-GAN were taken as input. Originally, the dilated convolution was executed rather than standard convolution for extracting the multi-scale contextual features with no loss of resolution. Then, those features were concatenated by the encoder and transferred to the decoder followed by the dropout layer. The dropout layer was engaged by the Dynamic Conditional Random Fields (DCRFs) to avoid the overfitting issue and provide the segmented lesion images. Further, the segmented images were instantly fed to the ResNet-18 for classifying the skin disease categories. However, it uses standard loss functions which restrain the network to train discriminative features from skin lesion images.

Therefore in this paper, an F-SegClassNet is proposed by fine-tuning the layers of ResNet-18 with a combined triplet and group loss. First, a modified SegNet is employed to segment the augmented skin lesion images. Also, dropout layer is used to avoid the overfitting problem. Then, the embedding from segmented images is learned into the Euclidean space by using DCNN ResNet-18 model. Then, l_2 distance is computed among corresponding segmented images from Euclidean space for learning discriminative features of skin disease images using combined triplet and group loss function. Moreover, the segmented input images are classified by using these l_2 distances. Thus, the efficiency of end-to-end training is improved.

The remaining sections are prepared as follows: Section II studies the related works for skin diseases classification. Section III describes the methodology of F-SegClassNet model and Section IV presents its effectiveness. Section V summarizes the research and recommends the future improvement.

II. LITERATURE SURVEY

Yang et al. [9] designed a new melanoma classification technique depending on CNN. Initially, a region average pooling was ussed to extract the features. After, an end-to-end classifier fused with segmentation was introduced which uses the segmented lesion area to direct the classification by region average pooling. At last, a linear classifier RankOpt was applied depending on the area under the ROC curve for optimizing the classifier outcome. But, its accuracy was not effective and needs to extract more features to classify the melanoma.

Harangi [10] developed an ensemble deep learning-based method for categorizing the skin lesion through combining multiple CNN structures. In this method, the CNNs were aggregated into one model where the final classification was done depending on the weighted output of the member CNNs. But, its classification accuracy was still not highly efficient.

Seeja & Suresh [11] developed automated skin lesion segmentation using deep learning technique. Initially, CNN-based U-net method was applied to segment the skin lesion images. After, different features were extracted through the Local Binary Pattern (LBP), edge histogram, histogram of oriented gradients and Gabor filter. These features were given to the SVM, random forest, K-nearest neighbor and naive bayes classifiers for classifying the skin lesions into melanoma and benign. But, the accuracy of these classifiers was very less.

Nida et al. [12] developed a deep learning technique depending on RCNN and fuzzy C-means clustering for automatically segmenting the melanoma region in the dermoscopic images. It consists of 3 different tasks: i). refining the skin images, ii) localizing the melanoma area and iii) segmenting the melanoma. But, it needs to classify the types of skin diseases.

Khan et al. [13] designed a technique for localizing and recognizing the skin cancer using a mixture of deep learning algorithm and Iteration-controlled Newton-Raphson (IcNR)-based feature selection scheme. First, a novel contrast stretching method depending on bee colony algorithm to enhance the lesion images. Then, the enhanced images with their ground truths were fed to the faster Region-based

CNN (RCNN) to obtain the segmented images. Moreover, DenseNet201 and IcNR schemes were applied for extracting and choosing the deep features. At last, the selected features were classified by the multilayered feed forward neural networks. But, the border lesions were not effectively classified since the lesion representation of every image was distinct to every other.

Almaraz-Damian et al. [14] developed a novel system for identifying and classifying the melanoma and nevus skin lesions using fused handcrafted and deep features. At first, the lesion image was enhanced, filtered and segmented for obtaining the Region-Of-Interest (ROI). Then, the handcrafted features and deep features were extracted through ABCD rule and CNN, respectively. These features were combined by the mutual information measures. Further, linear regression, SVM and relevant vector machines were applied to classify the skin diseases. But, it was not able to perform multiclass classification.

Banerjee et al. [15] developed a deep learning-based You Only Look Once (YOLO) algorithm for identifying the melanoma from dermoscopic and digital images. First, the skin lesion images were pre-processed and boundary of the affected region was detected based on the graph-based segmentation method. Then, the ABCD rule was applied to extract the features from the segmented images. Moreover, YOLO-v3 was applied to classify the skin lesion features. But, it needs to learn the broader range of datasets having multiple lesions.

Adegun & Viriri [16] designed a pixel-wise classification of skin lesion images was executed for recognizing the melanoma pixels. Also, an end-to-end and pixel-by-pixel learning using deep encoder-decoder convolutional networks with softmax classifier were applied to learn the complex features of skin lesions. But, this method only under-performs in less than 10% of the image samples which may obtain by missing labels.

III. PROPOSED METHODOLOGY

In this section, F-SegClassNet model is described in brief. First, the skin image dataset is acquired and then multi-domain adaptation is performed by using cycle-GAN to map the features of the skin images from the source domain to the target domain. After that, a modified SegNet is used to segment the skin lesion images with high-resolution features. Moreover, the segmented images are classified by the ResNet18 with a new loss function i.e., combined triplet and group loss functions. The determination of both loss functions for training ResNet18 is described in below. The block and architecture diagrams of F-SegClassNet model for skin diseases classification is depicted in Figure 1 & 2.

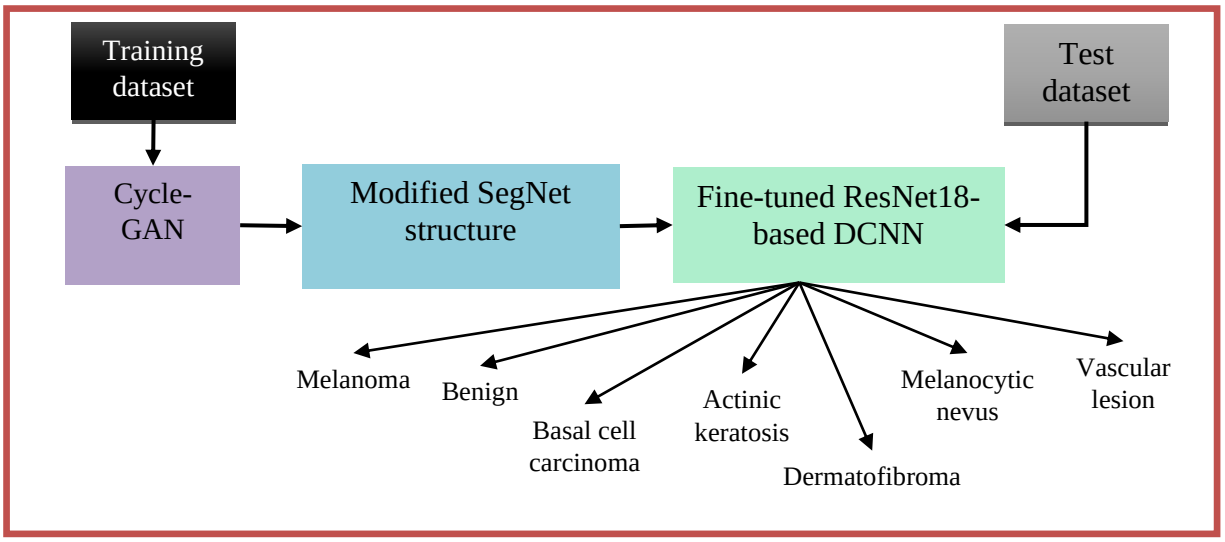

Figure 1. Block Diagram of Skin Diseases Classification using F-SegClassNet Model

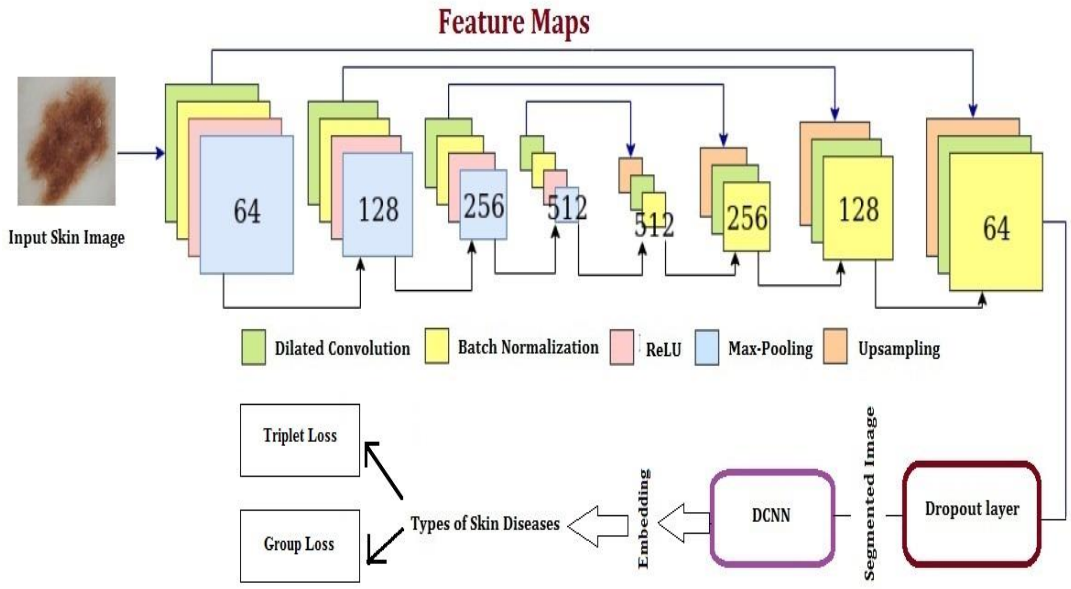

Figure 2. Architecture of F-SegClassNet for Skin Diseases Classification

3.1 Determination of Triplet Loss Function

The DCNN using a combined triplet loss and group loss functions can learn a dense embedding to solve the classification issues efficiently. Because this combined loss function learns better embeddings $f(I^i)$ of a skin lesion image I^i into d-dimensional Euclidean space R^d i.e., $f(I^i) \in R^d$. Also, it guarantees that a specified skin image I_a (anchor) is nearer to each image from similar label I_p^i (positive) than images from varied labels I_n^i (negative). Therefore, the objective is defined as:

$$\left\|f(I_a) - f\left(I_p^i\right)\right\|_2^2 + \alpha_t < \left\|f(I_a) - f(I_n^i)\right\|_2^2, \forall f(I_a), f\left(I_p^i\right), f(I_n^i) \qquad (1)$$

In Eq. (1), $f(I_a), f\left(I_p^i\right)$ and $f(I_n^i)$ indicate the embedding of a triplet $\left(I_a, I_p^i, I_n^i\right)$ from a group of each potential triplets T in training set with major N and threshold α_t denotes the predefined boundary that

exploits between skin images from different classes. The Euclidean distance reduces the triplet loss is described as:

$$L_t = \sum \left[\left\| f(I_a) - f\left(I_p^i\right) \right\|_2^2 - \left\| f(I_a) - f(I_n^i) \right\|_2^2 + \alpha_t \right] \quad (2)$$

Such triplets will not be active during training in slower convergence. Therefore, it is necessary to choose complex triplets which are activated in training for increasing the efficiency of the model.

3.2 Selection of Triplets

To guarantee quick convergence, triplet selection is necessary that choose the triplets to violate triplet restraint by producing the bias in selection. Because triplet selection needs to modify the trade-off between complex triplets to produce bias rather than choosing triplet accurately that imbalance the trade-off, the bias is directly reduced for avoiding this issue. Specifically, an identical contribution of each promising triplet is formulated in an unbiased condition. Then, $\text{argmax}\left\| f(I_a) - f\left(I_p^i\right) \right\|_2^2$ and $\text{argmin}\left\| f(I_a) - f(I_n^i) \right\|_2^2$ are determined, where $\left(I_p^i\right)$ and (I_n^i) are complex positive and complex negative for a given skin image (I_a), respectively. Besides, the less quality images would dominate the complex positives, complex negatives and mislabeled that can be caused by poor training. To solve this problem, triplets are generated through online and mini-batch of some input samples is generated for determining argmax and argmin within mini-batch.

To maintain a remarkable representation for a positive L_2 distance, a mini-batch of the minimum number of input images from separate class is needed to be generated. If uncertain outcomes are obtained because of creating the triplets for small mini-batch, then selecting the complex negative leads to worse local minima at the primary phase of training, particularly for a poor network i.e., $f(I) = 0$. So, this issue is minimized by choosing I_n^i such that

$$\left\| f(I_a) - f\left(I_p^i\right) \right\|_2^2 - \left\| f(I_a) - f(I_n^i) \right\|_2^2 \quad (3)$$

The distance of anchor from a negative image is larger than the positive image whereas L_2 distance is nearer to anchor positive distance. So, it is called semi-complex to these negative images and the range of these images is under the value of predefined boundary α_t. To enhance the convergence rate, it needs to consider a small mini-batch.

This network model can be applied to classify the skin diseases types where the absolute class label is not available; but, only relative label is available. So, in the presence of both relative and absolute labels, a group loss function is also combined with the triplet loss which enhances the classification efficiency.

3.3 Determination of Group Loss Function

For a mini-batch $\mathfrak{B}$ comprising n images, assume the issue of allocating the class label $\lambda \in \Lambda = \{1, \dots, m\}$ to every image in $\mathfrak{B}$. Let $X = (x_{i\lambda})$ be a $n \times m$ (non-negative) matrix of image-class soft

allocations. In contrast, every row of X is a probability distribution over the class set $\Lambda(\sum_{\lambda} x_{i\lambda} = 1, \forall i = 1, \dots, n)$. The determination of group loss function involves different steps which are:

Initialization:

The primary allocation matrix represented $X(0)$ obtains from the softmax output of the DCNN. Few primary allocations in matrix X are replaced with one-hot labelings of those samples. These randomly selected samples are called as anchors since their allocations do not alter during the iterative task and so they do not directly impact the loss factor. But, they direct rest of the samples towards their perfect class by using their accurate class rather than the predicted class.

Additionally, a similarity measure is calculated among each pair of embeddings (determined through a DCNN) in $\mathfrak{B}$ for creating a similarity matrix $W \in \mathbb{R}^{n \times n}$. The similarity measure is computed by the Pearson's correlation coefficient as:

$$w(i,j) = \frac{Cov[\Phi(I_i), \Phi(I_j)]}{\sqrt{var[\Phi(I_i)] var[\Phi(I_j)]}}, for\ i \neq j \tag{4}$$

It state that the linear correlation measure among features provides a better similarity measure is defined by the fact that the extracted features are normally a highly non-linear function of the inputs. So, the linear correlation among the embeddings can capture a non-linear relationship among the actual images.

Refinement:

In this step, the primary allocation matrix $X(0)$ is refined in an iterative way considering the similarity data provided by matrix W. After that, X is updated according to smoothness hypothesis which recommends that similar objects must distribute the same class. The support matrix $\Pi = (\pi_{i\lambda}) \in \mathbb{R}^{n \times m}$ and its (i, λ)-element are defined as:

$$\Pi = WX \tag{5}$$

$$\pi_{i\lambda} = \sum_{j=1}^{n} w_{ij}\, x_{j\lambda} \tag{6}$$

It indicates the support that the current mini-batch gives to the hypothesis that the i^{th} image in $\mathfrak{B}$ belongs to label λ. In compliance to the smoothness theory, $\pi_{i\lambda}$ is predicted to be high if images similar to i are likely to belong to label λ.

For a primary allocation matrix $X(0)$, this algorithm refines it using the below update principle:

$$x_{i\lambda}(t+1) = \frac{x_{i\lambda}(t)\pi_{i\lambda}(t)}{\sum_{\mu=1}^{m} x_{i\mu}(t)\pi_{i\mu}(t)} \tag{7}$$

In Eq. (7), the denominator indicates a normalization factor which ensures that the rows of the updated matrix sum up to 1. This is called as multi-population replicator dynamics in evolutionary game theory

and is similar to non-linear relaxation labeling tasks. In matrix notation, the update principle is written as:

$$X(t+1) = Q^{-1}(t)[X(t) \odot \Pi(t)] \quad (8)$$

$$\text{Where } Q(t) = diag([X(t) \odot \Pi(t)]\mathbb{1}) \quad (9)$$

In Eq. (9), $\mathbb{1}$ is the all-one m-dimensional vector, $\Pi(t)$ is defined in Eq. (5) and $\odot$ is the Hadamard (element-wise) matrix product. In contrast, the diagonal elements of $Q(t)$ denote the normalization factors in Eq. (7) which is also be interpreted as the mean support that object i acquires from the current mini-batch at iteration t. Normally, the idea behind this update principle is that at every step of the refinement task, for every skin image i, a class λ can increase its probability $x_{i\lambda}$ if and only if its support $\pi_{i\lambda}$ is larger than the mean support among each competing class hypothesis Q_{ii}.

Loss Determination:

After converge the labeling allocations, the cross-entropy loss is used to measuring the classification error and back-propagating the gradients. By using Eq. (8), it is shown that it is consisted of completely differentiable functions and so it is simply combined within backpropagation. Though the refining task has no parameters for learning, its gradients are back-propagated to the preceding layers of the DCNN generating better embeddings to determine the similarity. Thus, a group loss is computed using different tasks. Further, both loss functions are combined to get a unified loss function as:

$$L_{total} = Triplet\ loss + Group\ loss \quad (10)$$

3.3 Classification

In this work, the feature vectors of 7 different classes of input skin images are classified. After interpreting the features, an ensemble triplet and group loss function with ResNet18-based DCNN is employed to learn better embeddings. Also, L_2 distance between each input image into d-dimensional Euclidean space is calculated which directly relates to the image similarity. The L_2 distance between same label images is small whereas high for varied label images. The distance between each image is independent of various imaging factors. Thus, the pre-learned network i.e., ResNet18 is optimized by the novel loss function used for learning and classifying the skin lesion images.

Algorithm for F-SegClassNet Model:

Input: HAM image dataset and ImageNet

Output: Classified categories of skin diseases

Begin

Map the skin image features from the ImageNet (source domain) to the HAM (target domain) by cycle-GAN;

Acquire the augmented skin images for training;

$\boldsymbol{for}(every\ skin\ image\ input)$

Train the modified SegNet in end-to-end manner;

Segment the skin lesion regions;

Transfer the segmented images to the ResNet18-based DCNN classifier;

Train the ResNet18;

Determine the triplet loss function using Eq. (2);

Choose the appropriate triplets using Eq. (3);

Calculate the similarity measure using Eq. (4);

Define support matrix and its (i, λ)-element by Eqns. (5)-(6);

Refine the labeling task using update principle in Eqns. (7)-(8);

Compute the cross-entropy loss and total loss;

Classify the types of skin diseases;

$\boldsymbol{end\ for}$

End

IV. EXPERIMENTAL RESULTS

This section evaluates the efficiency of F-SegClassNet model by executing it in Python 3.7.8. For analysis, HAM10000 dataset [17] is obtained from ISIC archive also available in https://isic-archive.com/. It consists of 10015 skin images in 7 different categories and includes only skin images with 505 of lesions being confirmed by pathology. The 7 different categories are actinic keratosis, basal cell carcinoma, benign keratosis, dermatofibroma, melanoma, melanocytic nevus and vascular lesion. In this analysis, 70% of skin lesion images from every class are applied for training whereas 30% of skin lesion images from every class are applied for testing. The efficiency is measured and compared with existing models based on precision, recall, f-measure and accuracy. Figure 3 displays the sample skin images for 7 different categories of skin disorders.

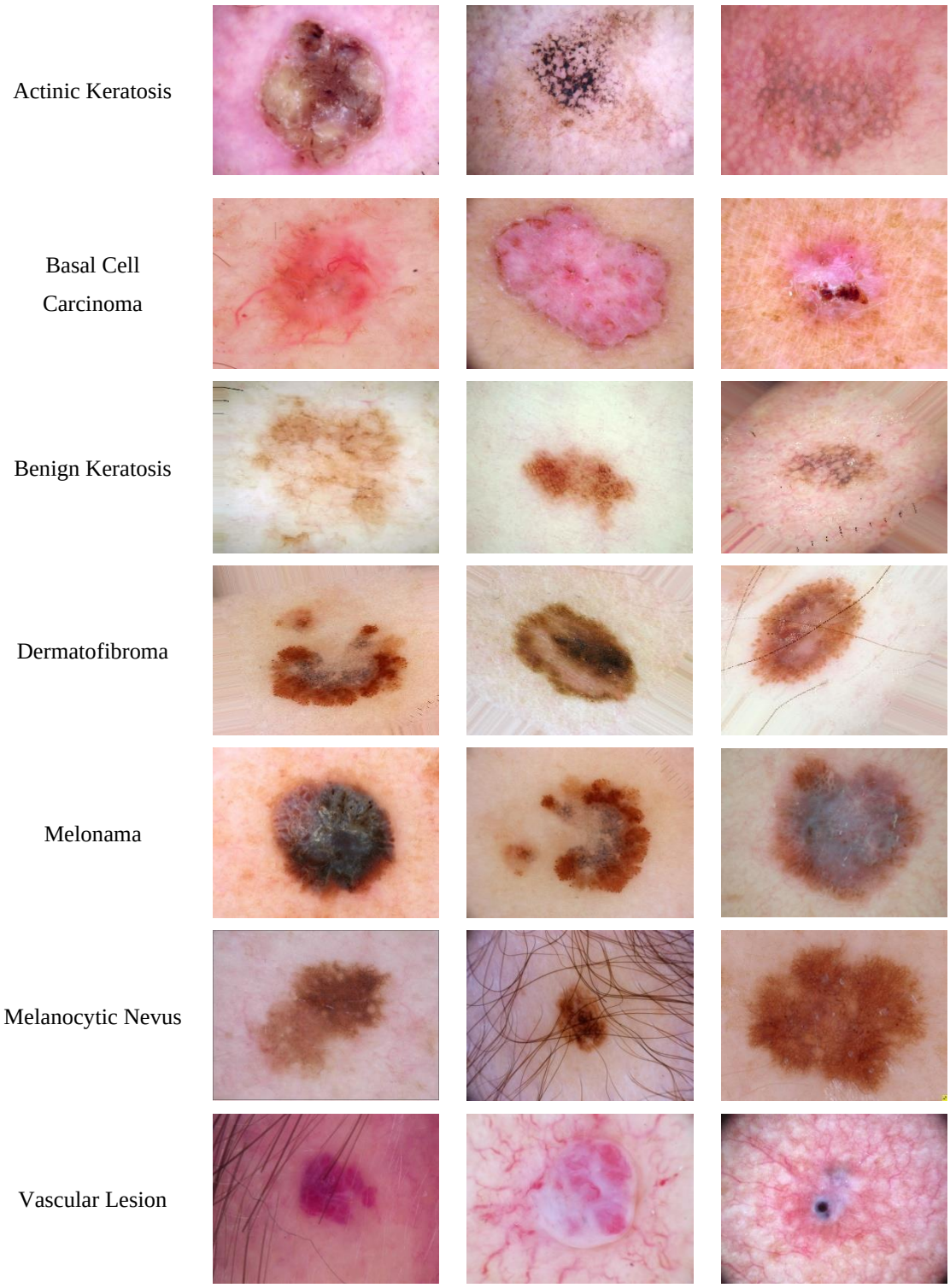

Figure 3. Sample Skin Images for Different Categories Skin Disorders

Precision is determined by

$$Precision = \frac{No.of\ correctly\ categorized\ melanoma/benign\ images}{No.of\ correctly\ categorized\ melanoma/benign\ images + No.of\ incorrectly\ categorized\ melanoma/benign\ images} \quad (11)$$

Recall is determined by

$$Recall = \frac{No.of\ correctly\ categorized\ melanoma/benign\ images}{No.of\ correctly\ categorized\ melanoma/benign\ images+No.of\ incorrectly\ categorized\ benign\ images} \quad (12)$$

F-measure is determined as:

$$F - measure = 2 \times \frac{Precision \cdot Recall}{Precision+Recall} \quad (13)$$

Accuracy is determined by

$$Accuracy = \frac{TP+True\ Negative\ (TN)}{TP+TN+FP+FN} \quad (14)$$

The comparative results of ResNet-152 [6], RCNN [12], SegClassNet [8], YOLOv3 [15] and F-SegClassNet executed on HAM dataset in accordance with the precision, recall, f-measure and accuracy are presented in Table 1 and displayed in Figure 4.

Table 1. Results of Different Skin Disease Classification Models on HAM Dataset

Performance Metrics	ResNet-152 (DCNN)	RCNN	SegClassNet	YOLOv3	F-SegClassNet
Precision (%)	88.40	89.11	90.94	92.05	93.26
Recall (%)	88.68	89.26	91.22	92.14	93.31
F-measure (%)	88.56	89.18	91.04	92.10	93.28
Accuracy (%)	88.78	89.33	91.28	92.21	93.37

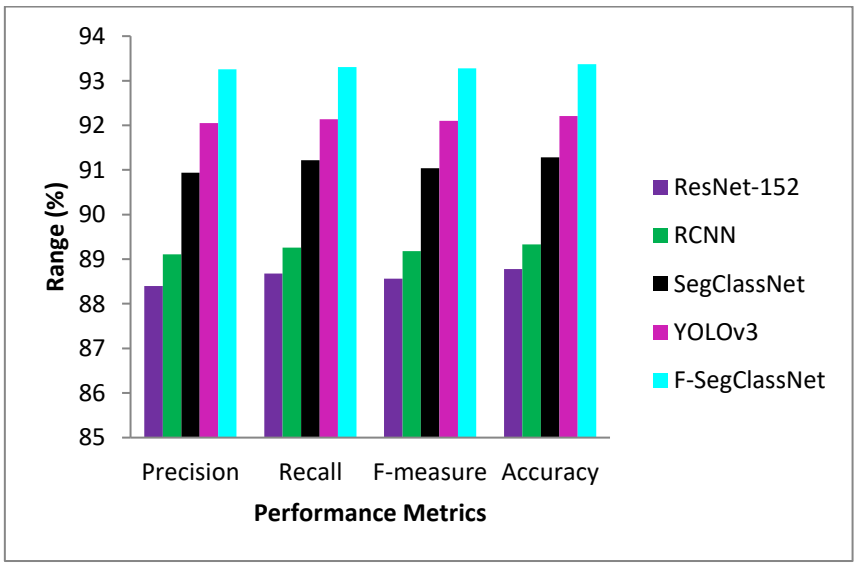

Figure 4. Comparison of Performance Metrics on HAM10000 Dataset

The comparative analysis indicates that the F-SegClassNet-based classification model yields a better efficiency when compared to other models. As far as the skin disease classification model is concerned, the F-SegClassNet model is more efficient in terms of accuracy.

V. CONCLUSION

In this article, an F-SegClassNet was proposed based on the fine-tuning of ResNet18 layers using a combined triplet and group loss. Initially, the skin lesion images were segmented by the modified SegNet. After, the embedding from segmented images was learned into the Euclidean space by using ResNet-18 model. In this model, l_2 distance was calculated among corresponding segmented images from Euclidean space for learning discriminative features of skin disease images using combined triplet and group loss function. By using this model, the types of skin diseases were classified with reduced false rates. To end, the experimental outcomes proved that the F-SegClassNet achieves a mean accuracy of 93.37% for HAM dataset whereas the mean accuracy of ResNet152, RCNN, SegClassNet and YOLOv3 are 88.78%, 89.33%, 91.28% and 92.21%, accordingly. Though it applies domain adaptation to skin disease imaging dataset, this model is not suitable for the imbalanced training datasets. So, the future work will focus on solving the imbalanced training image dataset by an integration of bootstrapping strategy in DCNN.

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