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Deep Neural Networks For Accurate Skin Disease Segmentation And Classification

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Abstract—
In recent years, the skin disease detection and classification are considered as the essential topic to identify the affected people. In literature review, cycle-consistent Generative Adversarial Network (cycle-GAN) is analyzed with the consideration of two step progressive transfer learning and domain adaptation. This cycle-GAN is mainly utilized to pre-trained the images by fully supervised Deep Convolutional Neural Network (DCNN) which is utilized to skin disease classification. This DCNN is not an efficient method for skin images. In this paper, modified SegNet is developed to segment the images during training period and it is augmented with the consideration of cycle-GAN method. This method operates the dilated convolution operation in its place of general convolution to normally extract the multi-scale contextual features without considering resolution. This extracted feature of multi-scale high resolution is encoded with the assistance of encoder and send to the decoder model. After that, the dropout layer with the addition of Dynamic Conditional Random Fields (DCRFs) to reduce the overfitting issue. Additionally, the dropout layer is defined as the segmented skin images. This segmented image is sent to the ResNet18 to type classification of skin diseases. Hence, this proposed model is defined as segmentation and classification (SegClassNet) model. At lase, the outcomes show that the projected technique attains the mean accuracy of 91.28% for HAM image dataset contrasted to different conventional classification methods.
Keywords—Skin diseases classification, Deep transfer learning, Deep convolutional neural network, Cycle-GAN, SegNet, Conditional random fields, Dilated convolution

I. INTRODUCTION

Skin or dermatological illnesses are the foremost complicated subfields of science because of its difficulties in the treatment of syndromes and their variations in different environments. Skin sicknesses are usual among many illnesses, especially prone to expand and may verify to be fatal providing to skin tumor if not treated in its prior periods. In recent days, the fraction of skin sicknesses is increasing drastically compared to the fraction of other categories of sicknesses [1-2]. Analysis encourages which one-fifth of the human can be likely to be pretentious through the skin sicknesses in their lifestyle in addition therefore creating the aforementioned taxonomy highly difficult. As a result, automated categorization of these sicknesses emerges into the primary role by considering different visual symptoms such as the skin lesion morphology, the human skin dimension distribution, arrangement of lesions, scaling and color. Through evaluating every human skin features separately, the classification complexity is raised in addition the normal feature extraction cannot apt aimed at categorization [3]. The major techniques developed for the categorization of skin sicknesses is transfer learning which may be used to train the DNNs. In transfer learning, a pre-trained network model is employed through adjusting its weight via recurrent backpropagation rather than learning the network with the aid of randomly initialized variables [4]. There are many open pre-trained DCNN models accessible to implement certain task [5]. These design structures are ResNet, VGGNet and GoogleNet. These remain also known as transfer learning such that the variable training aimed at an unknown problem is not beginning after scrape in addition may employ the pre-trained CNN towards rapidly train the proper variable. From this perspective, Gu et al. [6] designed a new cross-domain skin disease identification framework using fully supervised ResNet152 design with the consideration of two step progressive transfer learning on ImageNet by changing network design on the specific set. After that, cycle-GAN training is adopted as a domain version strategy to achieve skin imaging features translation from source to the final domain. However, it achieves better accuracy,

the image understanding of DCNN is not effective aimed at skin like images. Towards solve these problem, segmentation of skin images using SegNet model is considered with the DCNN. SegNet is defined as deep decoder and encoder design which provide results are troublesome since it can be fast and operate efficient [7]. But, this SegNet nose-dives to optimal polishing the limits among the ROIs in the skin image. In this paper, modified SegNet is developed to segment the images during training period and it is augmented with the consideration of cycle-GAN method. This method operates the dilated convolution operation in its place of general convolution to normally extract the multi-scale contextual features without considering resolution. This extracted feature of multi-scale high resolution is encoded with the assistance of encoder and send to the decoder model. After that, the dropout layer with the addition of Dynamic Conditional Random Fields (DCRFs) to reduce the overfitting issue. Additionally, the dropout layer is defined as the segmented skin images. This segmented image is sent to the ResNet18 to type classification of skin diseases. Hence, this proposed model is defined as segmentation and classification (SegClassNet) model. The rest of the article is organized as follows: Section II presents the previous articles related to the skin diseases classification. Section III explains the technique of SegClassNet design and Section IV shows its experimental results. Section V concludes this work in addition suggests the future scope.

II. RELATED WORKS

An ensemble technique [8] has been developed which fuses the deep learning with standard machine learning schemes for segmenting skin lesions and analyzing the detected region and surrounding tissue for melanoma identification. In this method, Support Vector Machines (SVMs), sparse coding, hand coded feature extraction were combined with recent machine learning methods including deep residual networks and fully CNN for recognizing the melanoma and segmenting dermoscopy images. This method consists of three phases such as lesion classification, dermoscopic feature extraction and lesion segmentation. lesion segmentation, lesion dermoscopic feature extraction and lesion classification. But, collected database was prejudiced in addition not complete labels were signified positively. An enhanced identification technique [9] has been designed to categorize the skin syndromes into herpes, dermatitis and psoriasis. Initially, different skin images were preprocessed to remove the noise and unwanted details by filtering and conversion. Then, the Grey-Level Co-occurrence Matrix (GLCM) can be applied to segment the texture and color features from the given images. Further, SVM was applied to identify the skin syndrome categories. However, it does not consider various diseases caused by similar category of skin syndromes. An enhanced technique [10] has been suggested to categorize the skin lesions. First, improved codebook training algorithm depending on Feature Similarity Measurement (FSM) was performed to estimate the feature relevance to classify the melanomas. Also, Scale-Invariant Feature Transform (SIFT), color histogram fusion in addition the Bag-of-Features (BoFs) were accounted to lessen the difficulty of codebook training. Moreover, the merged BoF histograms were fed to the SVM classifier to obtain the final outcome. But it was not able to train the most significant high-level features effectively. An image processing-based scheme [11] has been recommended to recognize the skin syndromes. First, a color image can be given as an input to the pre-processing method for resizing the images and take out the features via pre-trained CNN. Then, a multiclass SVM can be used for categorizing the features and recognizing the categories of skin syndromes with their progress in addition harshness. But, it was not able to categorize all the skin syndromes. Also, its efficiency was not validated for large-scale dataset. A robotic skin lesion is created using learning to move order [12] and a pre-made deep neural network (DNN). Here, transfer learning was used in Alexnet in different ways: i) changing the system weights, ii) changing the classification layer by Softmax and iii) extending the database through constant and spontaneous improvements. Softmax was used to classify shadow image lesions in melanoma, seborrheic keratosis, and nevus. Again, it is less capable of finite scope image databases. ResNet50-based DCNN model [13] has been developed to predict the acute Lyme syndrome from erythema migrans images under varied circumstances. In this scheme, a cross-sectional image database was taken into consider to learn the DCNN and categorize the erythema migrans versus other skin syndromes like tinea corporis and

herpes zoster and ordinary non-pathogenic skin. But, its efficiency may be affected by classifying irrelevant images.

The ResNet50-based DCNN model [13] was developed to detect severe Lyme disorder from erythema microns images under a variety of conditions. In this project, the cross-sectional image database can be considered for acquaintance with DCNN in addition for ordering erythema microns against fungal carburization and other skin diseases such as herpes zoster in addition non-normal pathogenic skin. However, its productivity can be affected by the rendering of meaningless images. The DNN has been trained [14] on the largest publicly accessible skin image datasets for increasing the classification efficiency. But, non-visual metadata was not usually accessible with most of the medical image datasets. A new dynamic graph cut algorithm has been designed [15] for segmenting skin lesion and a naive Bayes classifier has been used for categorizing for skin syndromes. But, its accuracy was not effective.

III. Proposed System Model

In this portion, SegClassNet model can be briefly explained. The overall diagram of skin diseases detection by means of SegClassNet model can be shown in Figure 1.

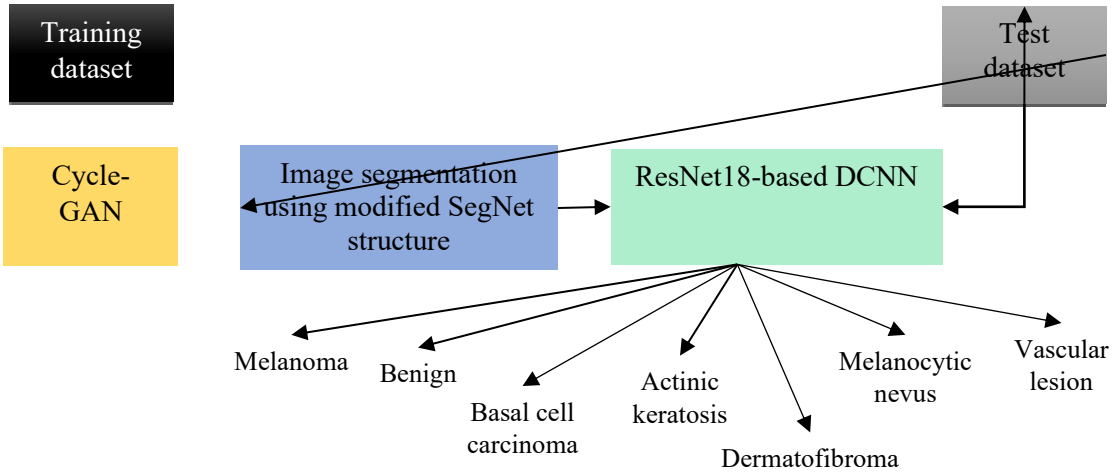


Figure 1. Proposed System Model

3.1 Image Acquisition

Skin images are derived from the HAM database [16] which is the largest direct open skin database collected from the ISIC document. This database can be accessed at https://isic-archive.com/. It includes 10015 dermoscopic images of 7 types, for example, 5 benign and 2 malignant types, namely melanoma and basal cell carcinoma. Images have long been collected from Australia and Austria. This includes only dermoscopic images of 505 lesions examined pathologically. The epidemiology of this database is recorded in Table 1.

Table 1. information about HAM10000 Dataset

Name of Diseases	Ratio between Micro Images/Macro Images	% of Total	Number of Samples
Vascular lesion	1	1.42	142
Melanocytic nevus	1	66.95	6705
Melanoma	1	11.11	1113
Dermatofibroma	1	1.15	115
Benign keratosis	1	10.97	1099
Basal cell carcinoma	1	5.13	514
Actinic keratosis	1	3.27	327

3.2 Multi-domain Adaptation using Cycle-GAN

First, cycle-GAN can be a pixel-wise image synthesizing version used to chart the skin image features with the consideration of source domain (ImageNet) and it is considered as the target domain (HAM) [6]. It uses a cycle-consistent loss instead of generative adversarial loss which militaries the collected images to be same if they can be transformed spinal to the actual source system. The design of GAN contains of 2 major structure such as a discriminator (D) and generator (G). The generator is utilized towards map an image feature from the ImageNet (S) towards the HAM (T) and vice versa. The discriminator can be trained to differentiate the original HAM images from unnaturally created fake images from ImageNet. So, the artificial HAM lesion images are generated in addition inconsistency is introduced through regulating the tag deliveries. Also, it develops a sequence loss towards preserve cycle constancy, hence for slightly image example, the produced example which is mapped to T is transformed back to the S and vice versa. Figure 2 portrays a domain adaptation using cycle-GAN.

First, m images are randomly chosen from the ImageNet and HAM datasets towards learn the cycle-GAN design in that a minor portion of the ImageNet images can be manufactured into the HAM images. The count of manufactured HAM images can be connected to the scope of actual HAM dataset n that can be $p\%n$. At last, these $p\%n$ manufactured images can be mutual with the actual n HAM images to create the learning set for the classification structure.

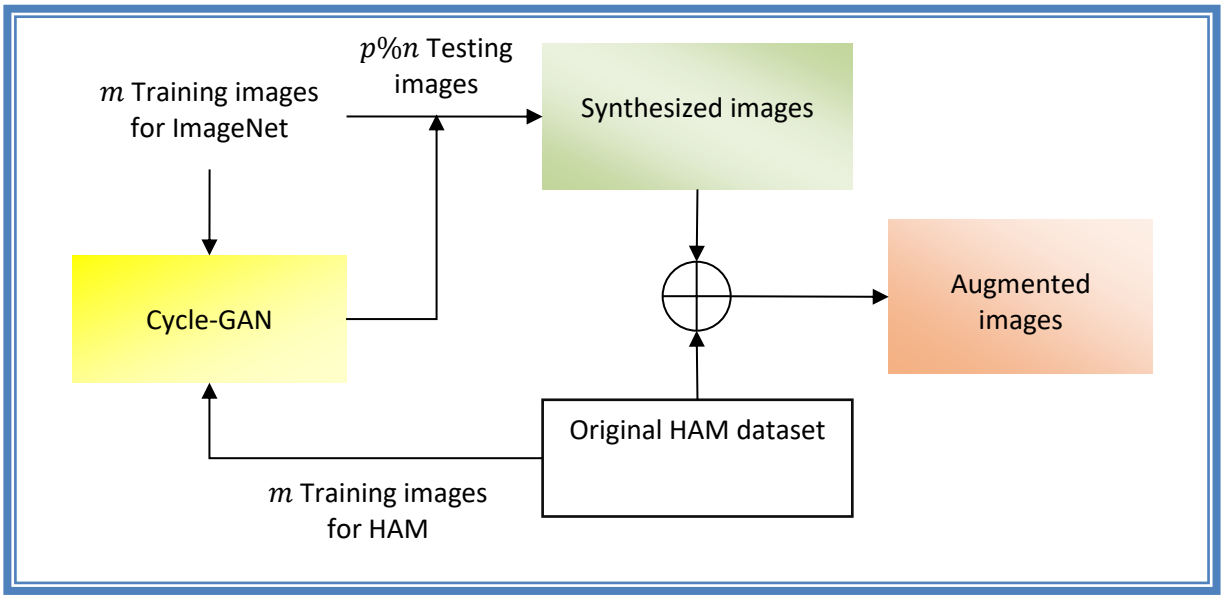


Figure 2. Domain Adaptation based on Cycle-GAN

3.3 Modified SegNet Structure for Skin Images Segmentation

In this modified SegNet, the encoder is used in light of the design of the VGG16, which is known to provide an excellent high level and low-resolution feature maps. Similarly, the decoder generates multiple features per pixel from the low-resolution map. That is, what is of interest to the SegNet's is that Decoder creates high-target maps directly through non-samples, using max-pooling encoders, which are then expanded with teachable channels. SegClassNet, based on this modified SegNet design shown in Figure 3, is triggered by the idea that extended curves support dramatically extending responsive fields without losing target. In Figure 3, graphs are included in the comparator decoders for moving high-resolution features from the encoder system to the decoder system. The encoder consists of four large scale layers: 1) expanded convolution layers with channels of sizes 64, 128, 256 and 512, 2) cluster standardization layers, 3) rectified linear units (ReLU) and maximum-pooling. Each decoder implements a model of its feedback feature map. The only significant difference between SegNet and the modified SegNet is that SegNet uses only the maximum pooling lists, although SegNet moves the aggregate element wizard of the individual encoder to a separate encoder and elevates the map. The decoder network system is similar to the SegNet system.

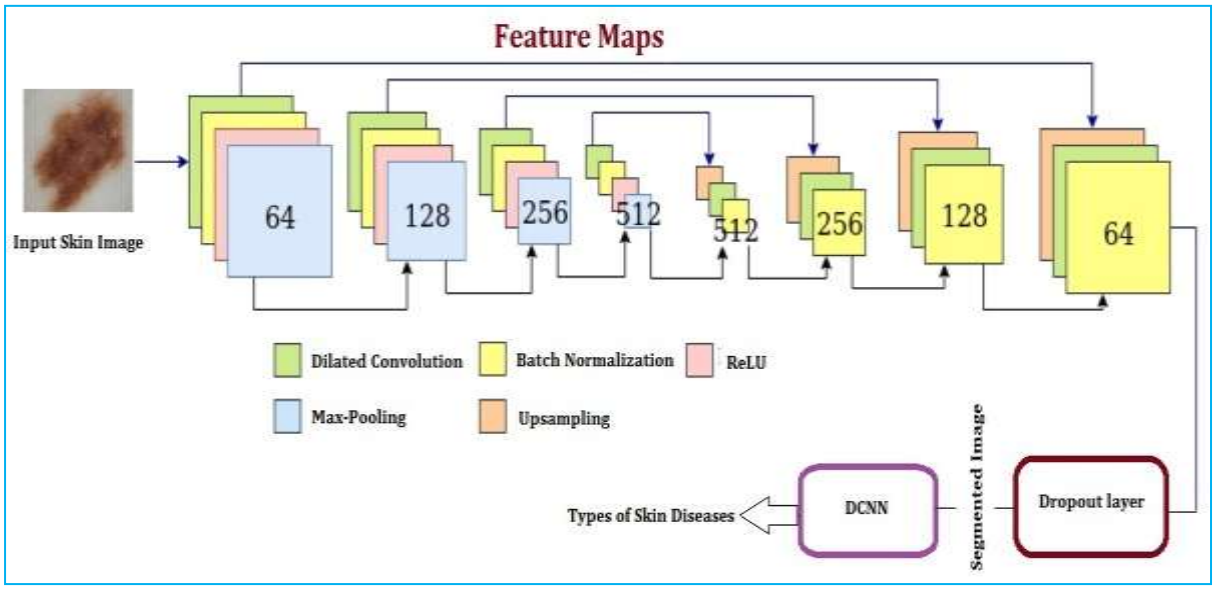


Figure 3. Architecture of SegClassNet using Modified SegNet for Skin Diseases Classification

Consider $F_0, F_1, \dots, F_{n-1}: \mathbb{Z}^2 \to \mathbb{R}$ are the discrete functions and $k_0, k_1, \dots, k_{n-1}: \Omega_1 \to \mathbb{R}$ are the discrete 3×3 filters. Assume using the filters with exponentially increasing dilation:

$$F_{i+1} = F_i *_{2^i} k_i, for\ i = 0,1, \dots, n-2 \quad (1)$$

In Eq. (1), $*_{2^i}$ denotes the 2^i-dilated convolution and 2^i denotes the dilation factor. Identify the receptive field of a factor p in F_{i+1} as the group of factors in F_0 which alters the value of $F_{i+1}(p)$. Consider the size of the receptive field of p in F_{i+1} is the number of these factors. It is simple to observe that the size of the receptive field of every factor in F_{i+1} is $\left(2^{i+2}-1\right) \times \left(2^{i+2}-1\right)$. The receptive field is a square of exponentially increasing size.

The ability of dilated convolutions is leveraged for adding global context without losing significant regional features via stacking dilated convolutions of increasing width. The non-local features are added into every pixel's representation via feeding the outputs of every dilated convolution as the input to the next. Executing a dilation-1 convolution in the primary layer guarantees that no pixels within the effective input width of any pixel are omitted. Through doubling the dilated width at every layer, the dimension of an effective input width increases exponentially when the amount of parameters increases linearly with the amount of layers. Thus, a pixel representation quickly adds rich global features from a whole skin image. Additionally, it introduces a dropout layer using DCRF to prevent overfitting and reduce the error rate. The easiest method to use CRF for increasing the accuracy of SegNet is to apply a stand-alone CRF framework as a step after decoding. But, since CRF is not integrated with the remaining network, the enhancement in accuracy may not be statistically essential. But, it must be provided a prior knowledge which is difficult for complex correlations among skin diseases labels.

Therefore, this issue is solved by using a DCRF model which generalizes both linear CRFs and highly complicated patterns. It considers a factorial CRF consisting of linear label sequences including relations among cotemporal labels. Consider a factorial CRF along L chains where $Y_{l,t}$ is a factor in l at period t. The DCRF's group indexes are $\{(0,l),(1,l)\}$ for each within-chain boundaries and $\{(0,l),(0,l+1)\}$ for each between-chain boundaries. The factorial CRF G defines a possibility over hidden states as:

$$\mathcal{P}(y|x) = \frac{1}{\mathcal{Z}(x)}\left(\prod_{t=1}^{T-1}\prod_{l=1}^{L}\phi_l\left(y_{l,t}, y_{l,t+1}, x_t\right)\right)\left(\prod_{t=1}^{T}\prod_{l=1}^{L-1}\psi_l\left(y_{l,t}, y_{l+1,t}, x_t\right)\right) \quad (2)$$

In Eq. (2), $\{\phi_l\}$ and $\{\psi_l\}$ are the likelihoods over within-chain and between-chain boundaries and $\mathcal{Z}(x)$is a partition parameter. A graphical version of factorial CRFs is shown in Figure 4.

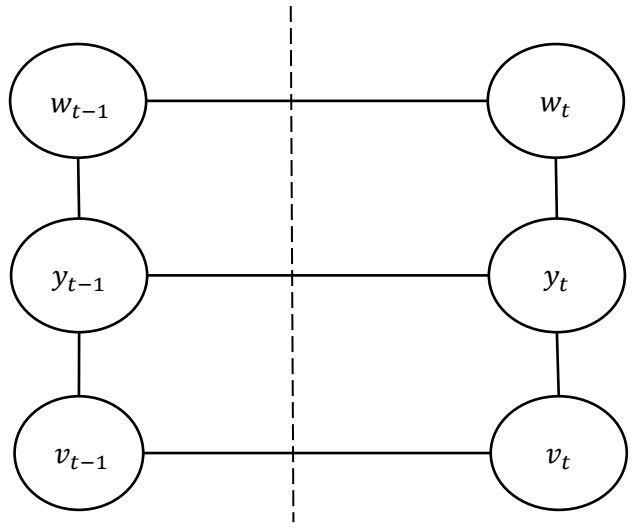


Figure 4. Graphical Version of Factorial CRFs (the dashed line represent the boundary between time slots)

The potentials factorize depend on the features $\{f_k\}$ and weights $\{\lambda_k\}$ of G as:

$$\phi_l(y_{l,t}, y_{l,t+1}, x_t) = e^{\{\sum_k \lambda_k f_k(y_{l,t}, y_{l,t+1}, x_t)\}} \quad (3)$$

$$\psi_l(y_{l,t}, y_{l+1,t}, x_t) = e^{\{\sum_k \lambda_k f_k(y_{l,t}, y_{l+1,t}, x_t)\}} \quad (4)$$

Also, more complicated features are promising where the state shift chances rely on how long the chain is in its ongoing stage. Thus, this factorized structure employs many factors compared to the state space of cross-product. Also, it solves two hypotheses for an unlabeled skin image x such as calculating the marginal $\mathcal{P}(y_{t,c}|x)$ in every set $y_{t,c}$ and the Viterbi decoding $y^* = \underset{y}{argmax}\, \mathcal{P}(y|x)$.

It is used to label an unrecognized skin image and marginal calculation is used for computing the factors. Because marginal calculation is needed for learning, hypothesis must be efficient so that large-scale training datasets are taken into account even if there are multiple classes. In this model, an approximate hypothesis is represented through Belief Propagation (BP) which iteratively update a vector $i_t = (m_u(i_v))$ of contextual features between $i_u$and i_v. The update from i_u to $i_v$is as:

$$m_u(i_v) \leftarrow \sum_{i_u} \phi(i_u, i_v) \prod_{i_t \neq i_v} m_v(i_u) \quad (5)$$

In Eq. (5), $\phi(i_u, i_v)$is the potential factorize on the margin (i_u, i_v). An approximate marginal for i_t is calculated as:

$$\mathcal{P}(i_u, i_v) \leftarrow \kappa\phi(i_u, i_v) \prod_{i_t \neq i_v} m_v(i_u) \prod_{i_w \neq i_u} m_w(i_v) \quad (6)$$

In Eq. (6), κ is a regularization factor. At each iteration of BP, contextual features are transferred using tree-based in addition haphazard strategies. The tree-related strategy transfers contextual features along the set of cross-cutting spanning trees of the real graph. In every iteration process of this strategy, a spanning tree $\mathcal{T}^{(i)} \in \Upsilon$ is decided in addition contextual features can be transferred in an end-to-end with every margin $\mathcal{T}^{(i)}$for obtaining precise hypothesis on $\mathcal{T}^{(i)}$.

The random way simply transfers contextual features across every margin arbitrarily. To improve convergence, each margin $e_i = (s_i, t_i)$ and every contextual feature $m_{s_i}(t_i)$ are sorted in a random way before any feature $m_{t_i}(s_i)$. Besides, a set of factors $\zeta = \{\lambda_k\}$ in training image dataset $\mathcal{D} = \{x_i, y_i\}_{i=1}^N$ is acquired via optimizing the conditional log-chance as:

$$\mathcal{L}(\zeta) = \sum_i log\, \mathcal{P}_\zeta(y_i|x_i) \quad (7)$$

The derivative of $\mathcal{L}(\zeta)$ with regards λ_k associated with the set index c is as:

$$\frac{\partial \mathcal{L}}{\partial \lambda_k} = \sum_i \sum_t f_k(\vec{y}_{i,t,c}, x_i, t) - \sum_i \sum_t \sum_{\vec{y}_{t,c}} \mathcal{P}_\zeta(\vec{y}_{t,c}|x_i) f_k(\vec{y}_{t,c}, x_i, t) \quad (8)$$

In Eq. (8), $\vec{y}_{i,t,c}$ is the distribution of $y_{t,c}$ in y_i and $\vec{y}_{t,c}$ differs over distributions to $y_{t,c}$. Observe that it is the factor $\mathcal{P}_\zeta(\vec{y}_{t,c}|x_i)$ which requests to calculate marginal chances in the unfolded DCRFs. A prior $\mathcal{P}(\zeta)$ is defined over factors and $log\, \mathcal{P}(\zeta|\mathcal{D}) = \mathcal{L}(\zeta) + log\, \mathcal{P}(\zeta)$ is tuned for preventing overfitting.

A spherical Gaussian prior is applied with average $\mu = 0$ in addition covariance matrix $\Sigma = \sigma^2 x$, therefore a gradient considers:

$$\frac{\partial \mathcal{P}(\zeta|\mathcal{D})}{\partial \lambda_k} = \frac{\partial \mathcal{L}}{\partial \lambda_k} - \frac{\lambda_k}{\sigma^2} \quad (9)$$

Thus, DCRF is used in dropout layer to prevent overfitting problem and minimize the error rate for classification. Further, the output of this modified SegNet i.e., segmented skin images are passed to the ResNet18 related DCNN towards categorize the categories of skin diseases.

3.4 ResNet18 based DCNN for Skin Diseases Classification

For classification, ResNet18-based DCNN is used in this work. Because the classifier uses the segmented skin images, ResNet-18 is satisfactory whereas increasing the layers cause an unnecessary training complexity. This network consists of 5 convolutional layers, 1 average pooling and a fully connected layer with a softmax. This network is trained using an ADAM optimizer [17]. The learning rate begins at 0.001 and anneals over the course of learning via dropping by a decay factor of 10 for each epoch in a total of 50 epochs. So, the trained SegClassNet is used to classify the test image samples into the 7 various types such as vascular lesion, melanocytic nevus, melanoma, dermatofibroma, benign keratosis, basal cell carcinoma, actinic keratosis and different categories.

Process of the proposed model is presented as follows

Input: ImageNet and HAM image dataset

Output: Skin disease classification

Start

Collect the features of skin images from the source domain (ImageNet) to the final domain (HAM10000) using cycle-GAN;

Collected the augmented images

for $(each\ input\ skin\ image)$

Learning process of proposed SegNet

Obtain the segmented skin images;

Achieve the segmented images to the DCNN classifier based ResNet18

Skin disease classification;

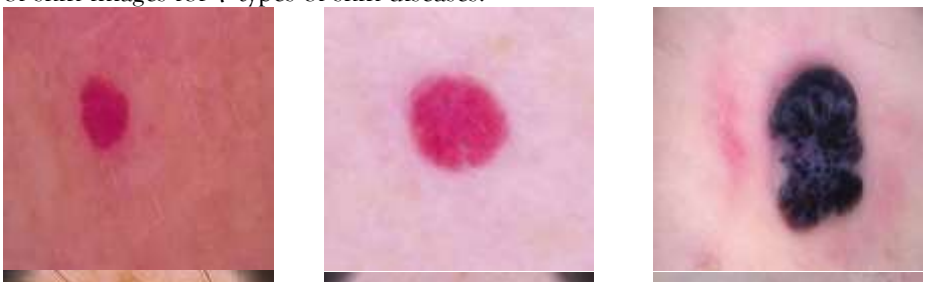
end for

End

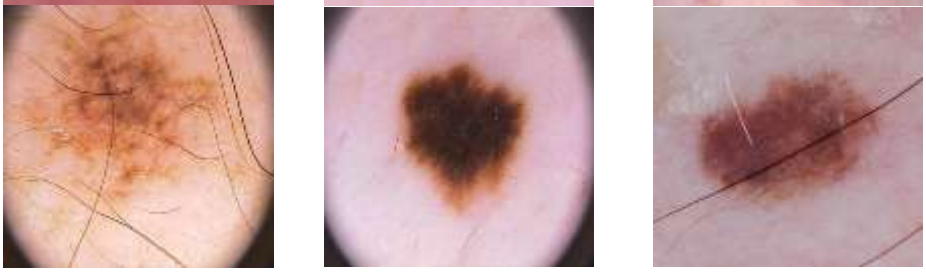
IV. Outcome Evaluation

In this portion, the performance of SegClassNet design is analyzed through implementing it in Python 3.7.8 using HAM10000 dataset and ImageNet. For training, 70% of HAM images in every class are selected arbitrarily. The remaining 30% of HAM images in every class are used aimed at testing. Also, its effectiveness is compared with the AlexNet [12], ResNet50 [13] and ResNet152 [6] in parameters of accuracy, f-measure, recall and precision to know its improvement on classification of skin diseases. Figure 5 depicts the samples of skin images for 7 types of skin diseases.

Vascular Lesion



Melanocytic Nevus



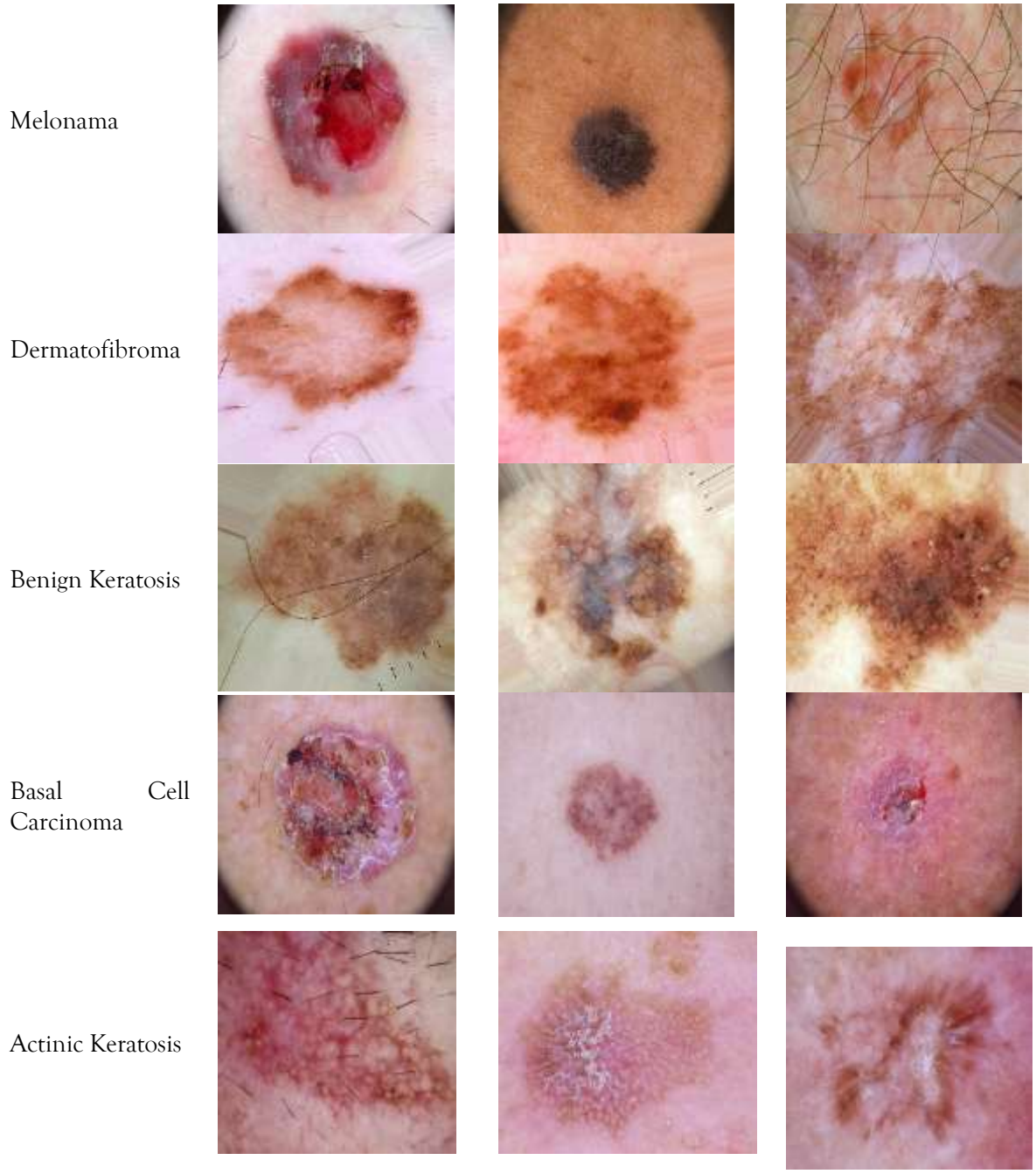


Figure 5. Samples of Skin Images for various Skin Diseases

Precision can be calculated through,

$$Precision = \frac{No.of\ perfectly\ classified\ melanoma/cancer\ cases}{No.of\ perfectly\ classified\ melanoma/cancer\ cases + No.of\ imperfectly\ classified\ melanoma/cancer\ cases} \quad (11)$$

Recall is calculated by,

$$Recall = \frac{No.of\ perfectly\ classified\ melanoma/cancer\ cases}{\text{No.of perfectly classified melanoma/cancer cases+No.of imperfectly classified benign cases}} \quad (12)$$

F-measure is calculated as:

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

Accuracy can be calculated through,

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

Table 1. Outcomes of Implemented Skin Disease detection structures on HAM Dataset

Performance Metrics	AlexNet	ResNet-50	ResNet-152 (DCNN)	SegClassNet
Precision (%)	83.28	86.10	88.40	90.94
Recall (%)	83.45	86.51	88.68	91.22
F-measure (%)	83.38	86.30	88.56	91.04
Accuracy (%)	83.54	86.52	88.78	91.28

The comparative results of AlexNet, ResNet-50, ResNet-152 and SegClassNet implemented on HAM dataset in terms of accuracy, f-measure, recall and precision which presented in table 1 and presented in figure 6.

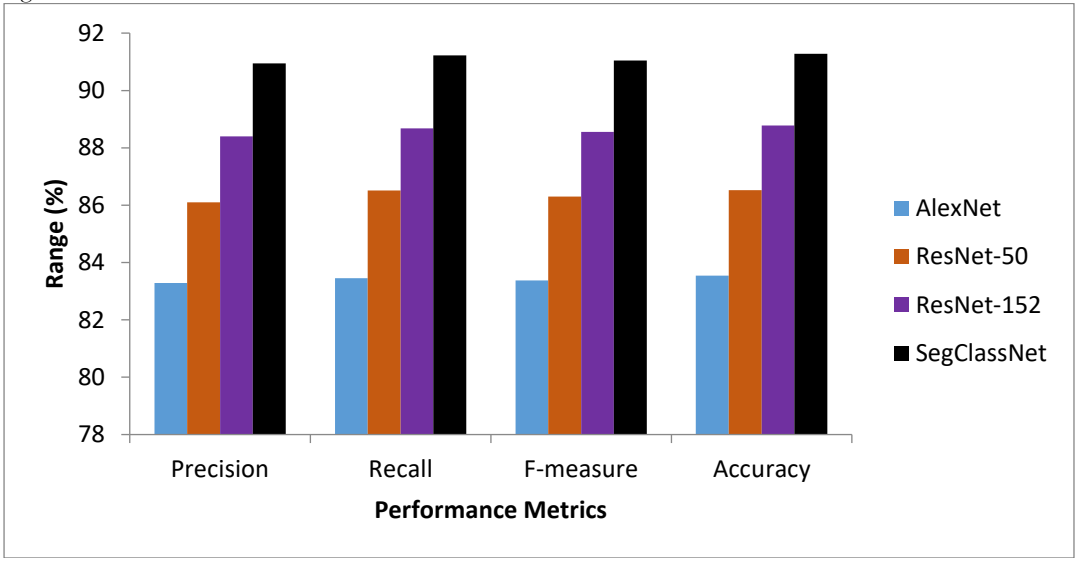


Figure 6. Comparison analysis

A similar investigation demonstrates that the SegClassNet-based order model offers a better efficiency when contrasted with different models. All things considered, the SegClassNet model is precisely the most effective in skin disease prediction.

V. CONCLUSION

In this paper, a SegClassNet model is designed to classify the categories of skin syndromes. First, cycle-GAN model is executed to map the skin images in the ImageNet to the HAM10000 dataset and obtain the augmented images. Then, these images are fed to the modified SegNet which performs dilated convolutions to extract features of multi-scale high-resolution. After, these features can be transferred from the decoder and encoder structure. After decoder, a dropout layer is added utilizing DCRFs for preventing overfitting and acquiring the segmented images. Further, these segmented images from the dropout layer are passed towards the ResNet18 design-based DCNN towards categorize the categories of skin syndromes accurately. At last, the validation results showed that the SegClassNet model attains a optimal accuracy of 91.28% aimed at HAM dataset while the mean accuracy of AlexNet, ResNet50 and ResNet152 are 83.54%, 86.52% and 88.78%, respectively. On the other hand, this DCNN uses the classical loss functions that limit this model to train discriminative features from the skin image. In future research, this work will be considering on resolving the learning of discriminative features from the skin images using new loss functions.

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