2021 International Conference on Computational Performance Evaluation (ComPE),
North-Eastern Hill University, Shillong, Meghalaya, India. Dec 1–3, 2021

2021 International Conference on Computational Performance Evaluation (ComPE) | 978-1-6654-3656-4/21/$31.00 ©2021 IEEE | DOI: 10.1109/ComPE53109.2021.9752441

Handling Uncertainty with Fuzzy Lesion Segmentation Improves the Classification Accuracy of Skin Diseases using Deep Convolutional Networks

Dasari Anantha Reddy
Department of Information Technology
National Institute of Technology
Raipur, India
ananth.dasari@gmail.com

Swarup Roy*
Department of Computer Applications
Sikkim University
, Gangtok, India
sroy01@cus.ac.in

Rakesh Tripathi
Department of Information Technology
National Institute of Technology
Raipur,India
rtripathi.it@nitrr.ac.in

Sanjay Kumar
Department of Information Technology
National Institute of Technology
City, Country
skumar.it@nitrr.ac.in

Abhishek De
Department of Dermatology
Calcutta National Medical College
Kolkata,India
dr_abhishek_de@yahoo.co.in

Sourav Dutta
IQVIA
Bangaluru,India
Sourav.dutta@in.imshealth.com

***Abstract*—Often skin disease classification models suffer from confusion due to similar lesion regions with background skin. It has been observed that disease lesions are sometimes non-distinguishable due to similar structure and texture with skin, which leads to misclassification. Segmentation of lesions may help to improve the accuracy of prediction by extracting the region of interest. However, exclusive clustering-based segmentation methods limited handling uncertainty in the lesion regions. Fuzzy clustering methods are built to handle such uncertain homogeneous regions.**

In this work, we employ Fuzzy C-Means (FCM) segmentation to extract lesion from the diseased skin images. Segmented images are then fed into Deep Convolutional Neural Network (DCNN) for skin disease classification. The comparative analysis over the traditional segmentation techniques demonstrates that the FCM segmentation enhances the performance of DCNN in classifying skin diseases with improved accuracy.

***Index Terms*—Skin Disease Classification, Segmentation, Deep Convolutional Neural Network, Fuzzy C-Means, Lesion segmentation**

I. Introduction

The skin diseases are infectious, inflammatory, malignant and affect people of different age groups leads to severe consequences like damage to internal organs, and death (say, due to melanoma) [1]. Further, it also causes mental illness that leads to suicide, depression, as well as isolation. The skin diseases must be treated earlier for minimizing the related morbidity and mortality rate. Looking into the variability of disease types practitioners always find it challenging to diagnose visually with bare eyes. The manual skin disease diagnosis needs more human effort and is considered time-consuming and subjective. Hence, it is required to propose a computer-aided system that can diagnose skin diseases in an automatic format [2]. Computer vision and pattern recognition techniques are popular aids and alternatives for near accurate diagnosis of diseased lesions. The AI-based expert system relies primarily on the distinguishable features inherent in the diseased lesions. The hand-crafted features are ineffective for skin disease classification categories [3]. Especially, diseases that are non-distinguishable from each other. Any good feature extraction algorithm is always not effective due to the above reason. Other than feature engineering, this conflict can be handled by feature learning for choosing the necessary features using the machine.

The conventional machine-learning models such as Artificial Neural Network (ANN), Support Vector Machine (SVM), gradient boosting, and many are used for skin lesion diagnosis [2] for the last few decades. More recently deep neural networks like convolution neural network (CNN) models were established to be more accurate in the classification of disease [4] due to their inherent feature engineering layers. Though the traditional deep CNN are better than the existing techniques, their performance relies on input images too. Sometimes deep classifiers too become confused due to similar lesion features with background skin. In computer vision, image segmentation is generally considered an intermediate step. It helps any classifiers to perform better by feeding region of interest (ROI) to the classifiers. Traditional exclusive segmentation methods deterministically segregate lesion and skin pixels. If the lesion pixels are not well differential from normal skins, exclusive clustering-based segmentation may categorise them wrongly to either of these regions leads to distortion or misrepresentation of the lesions. As a result, even the best classifier is unable to perform at its best due to such confusion.

978-1-6654-3656-4/21/$31.00 ©2021 IEEE

In this work, we try to segment skin lesions using fuzzy c mean clustering that may handle better the overlapping regions that creates uncertainty. We used the segmented image for the classification of diseases using one of the recent deep classification models, deep CNN.

II. Prior Researches

In present days deep networks have become the obvious choice of researchers in the automatic diagnosis of diseased skin lesions. In particular, CNN has used more rigorously image-based classification due to its inbuilt feature engineering capabilities.

In 2017, Esteva et al. [5] have used CNN for getting the superior skin disease classification rate as 72.10% with the ImageNet dataset. In 2019, Tschandl et al. [2] have proposed a Skin Cancer Diagnosis model through gathering the skin cancer clinic in Queensland, Australia, between January 1, 2008, and July 13, 2017. It was performed by combined CNN and scored 95% accuracy. Melbin and Raj [6] have proposed a dragonfly optimization-based DNN for getting a 98% accuracy rate, which has also used a level set approach for segmentation. Gu et al. [7] have proposed a method named cycle consistent adversarial networks (cycle-GAN), which was experimented on HAM, MoleMap, MoleMap+HAM. This model has attained an accuracy of 90%. Pham et al. [8] have developed a Deep CNN that was evaluated on the HAM10000 dataset and attained the accuracy of 89.97%. Hameed et al. [9] have used ANN for classifying the skin diseases on open-access dermatology repositories. Open-access dermatology repositories include the International Skin Imaging Collaboration (ISIC) Dermoscopic Archive [3] and the PH2, which has segmented the images through K-means clustering, Otsu's thresholding and morphological erosion operation. This model has attained an accuracy rate as 96.50%

Adegun and Viriri [10]have proposed an automatic skin cancer segmentation using FCN for the efficient training and residual learning scheme. The next stage has used a new FCN-oriented DenseNet framework for detection that has been implemented using the HAM10000 dataset and obtained 98%accuracy. Ahmad et al. [11] have used a total of 12000 skin disease images for skin disease classification through deep CNN using triplet loss function, which has attained 87.42%.

The existing research works either skipping the important steps like segmentation or did not give due importance to similar lesion colour and texture with skin leads to inappropriate segmentation followed by misclassification and relatively inferior accuracy. To overcome the above issue we try to experiment with fuzzy segmentation followed by classification using deep CNN. We discuss the steps in detail, next.

TABLE I: Features and challenges of state of the art skin diseases classification methods

Author [citation	**Segmentation**	**Classification**	**challenges**
Pham *et al.* [8]		Deep CNN	It cannot be applied to the imbalanced data sets and the various medical image analyses
Ahmad *et al* [11]		Deep CNN	It does not model a data set using a dermatologist for the visually organized taxonomy.
Victor*et al.* (year) [12]	active contour method.	SVM	An Neural Network based classification approach is needed.
Nazia Hameed*et al.* [9]	Otsu threshold	SVM with quadratic kernel	Few images are produced the same features which deteriorate the system performance adversely.
Muhammad Qasim Khan*et al.* [13]	K-Means Clustering	SVM	Computational complexity is high due to it works in real time environment.

III. FCM Segmentation guided Skin Disease Classification

In this section, we describe our experimental scheme with the objective of whether simple fuzzy-based segmentation can improve the performance of a deep learning network for detecting skin diseases.

The workflow of the proposed experimental setup is illustrated in Figure 1. At first lesion, images are improvised before being fed into deep CNN. The preprocessed images are then segmented using FCM. Finally, segmented images are used to train DCNN. We discuss each step in detail below.

A. Pre-processing

The pre-processing is used for improving the quality of the images from the collected dataset. Here, the pre-processing of gathered images is done using the RGB to grey conversion, morphological close operation, and contrast enhancement methods. Consider the input images from the dataset asY_s^{IN}, in which$s = 1, 2, \cdots, S$, were S defines the total number of images collected from the two datasets.

RGB to grayscale conversion: The RGB images are converted into grayscale level images by measuring the chrominance and luminance and also adjusted the RGB approximation. Several linear, as well as non-linear approaches, are employed for the grayscale conversion. The RGB to grayscale conversion of an input image is shown by Y_s^{GS}.

Morphological close operation: It represents a combination of erosion as well as dilation that is changed from the opening operation. The closing of grayscale converted images $Y_s^{GS}$is shown on the basis of the structuring element SEas in Eq. (1).

$$Y_s^{MC} = Y_s^{GS} \cdot SE = \left(Y_s^{IN} \oplus SE\right) \otimes se \tag{1}$$

It defines the correlation between the dilation as well as erosion via the closing operation, where the result is eroded through the structuring elementSE. It is used to blend the

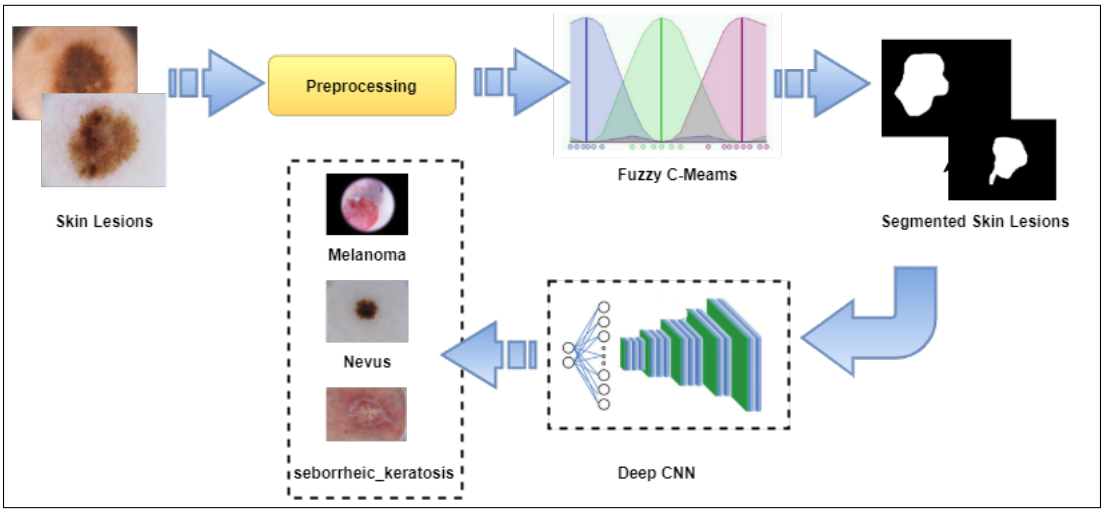


Fig. 1: Workflow of proposed skin disease classification scheme

narrow breaks as well as the thin gaps present in the images and to smoothen the contours. Here, this operation is used to remove the hair present in the grayscale converted images and it is shown by Y_s^{MC}.

Contrast enhancement: The contrast enhancement [14] is mostly employed for the image processing for attaining a broader dynamic range. Histogram modification-oriented algorithm is the familiar technique for attaining a broad dynamic range. The histogram-oriented approaches equalize the histogram and also improve the dynamic range. A digital image is considered with gray levels in the range of$[0, LT-1]$. The Probability Distribution Function (PDF) is shown in Eq. (2).

$$PT\left(rt_{kt}\right) = \frac{nt_{kt}}{NT} \quad kt = 0, \cdots, LT-1 \tag{2}$$

Here, the gray level is given by $rt_{kt}$and the pixel count is given by nt_{kt}respectively. The Cumulative Distribution Function (CDF) is also measured as in Eq. (3)

$$\begin{aligned} &CT\left(rt_{kt}\right) = \textstyle\sum_{it=0}^{it=kt} PT\left(rt_{it}\right) \\ &kt = 0, \cdots, LT-1, \;\; 0 \leq CT\left(rt_{kt}\right) \leq 1 \end{aligned} \tag{3}$$

The gray level $ST_{kt}$is evaluated to the gray level rt_{kt}as in Eq. (4).

$$ST_{kt} = (LT-1) \times CT\left(rt_{kt}\right) \tag{4}$$

The changes in the gray level $ST_{kt}$is measured in the typical histogram equalization technique as in Eq. (5).

$$\Delta ST_{kt} = (LT-1) \times PT\left(rt_{kt}\right) \tag{5}$$

The final pre-processed image is given by Y_s^{pre}.

B. Lesion Segmentation

The segmentation partitions the pre-processed image into multiple segments for positioning the region of interest (lesions). Here, the segmentation of lesions is done by the Fuzzy C-means segmentation technique.

Fuzzy C-Means segmentation: The fuzzy c-means [15] provides the partial membership value to every pixel present in the image. There does not exist any abrupt transition among the non-membership and full membership. These are the major features included in the membership function characterization. The core represents a complete fuzzy set member. The support represents a non-membership value present in the set.

The FCM is the clustering algorithm that permits a single data piece to be a member of multiple clusters. It is dependent on minimizing the function as in Eq. (6).

$$RQ_{jq} = \frac{\sum_{iq=1}^{NQ} xq_{iq} \cdot MQ_{iqjq}^{mq}}{\sum_{iq=1}^{NQ} MQ_{iqjq}^{mq}} \tag{6}$$

In the above equation, the clusters are shown byRQ, the membership is shown byMQ_{iqjq}^{mq}, the dqdimension center of the cluster is shown byRQ_{jq}, the data computed in dqdimensional is shown byxq_{iq}, the degree of membership of XQin the cluster $jq$is shown by MQ_{iqjq}, and real number more than 1 is shown by mqrespectively. This technique ends when it reaches$\max_{iqjq}\left\{\left|MQ_{iqjq}^{(kq+1)} - MQ_{iqjq}^{(kq)}\right|\right\} < \delta$. Here, the iteration count is shown bykq, and the constant or termination value among 0 and 1 is shown by δrespectively. Hence, the final FCM segmented image is shown byY_s^{FCM}.

C. Deep Classification

The classification represents a technique of labelling and categorizing the groups of vectors or pixels inside an image based on particular rules. Here, the classification of the skin diseases is done by Deep CNN.Deep CNN [16] describes the feedforward networks. It is composed of pooling as well as convolutional layers. The pooling layers are clustered in the module format. The class label is produced by the final fully connected layer and it denotes the output.

Convolutional Layers: It behaves in the form of feature extractors. The neurons are arranged in the feature map format. Each neuron consists of a receptive field. The results are transferred through a nonlinear activation function. The neuron is assumed to contain equal weights. Each feature map is

composed of varied weights. Therefore, several features can be extracted at each location. The km^{th} output feature map YM_{km} is computed as given in Eq. (7).

$$YM_{km} = f\left(WM_{km} * Y_s^{FCM}\right) \tag{7}$$

In the above equation, the multiplication sign gives the 2D convolutional operator; the input image is shown byY_s^{FCM}, the convolutional filter is shown byWM_{km}, and the non-linear activation function is shown by $f(\cdot)$respectively. The nonlinear activation functions extract the nonlinear features. The traditional techniques utilized the sigmoid as well as the hyperbolic tangent functions. The Rectified Linear Units (ReLUs) are mostly dependent these days.

Pooling Layers: The spatial resolutions related with the component maps are limited here. The largest element is selected in every receptive field as given in Eq. (8).

$$YM_{kmimjm} = \max_{(pm,qm)\in\Re_{imjm}} xm_{kmpmqm} \tag{8}$$

Here, the pooling operation output is given byYM_{kmimjm}, and the element at location $(pm, qm)$is given by xm_{kmpmqm}respectively.

Fully Connected Layers: The abstract features are extracted by stacking the pooling and the convolutional layers one above the other. The high-level reasoning function is also performed here. Here, the features are extracted from the pooling layer and finally, the image is classified using the fully connected layer.

Next, we experimentally evaluate the performance of FCM supported DCNN based skin classification.

IV. Results and Discussion

At first, we report the quality of segmentation by different candidate segmentation methods. A comparative performance improvement of DCNN over different segmentation methods are also reported to show that FCM is superior in improving the classification accuracy of DCNN in comparison to other segmentation methods. We also show that skin disease classification using segmented images is better than considering direct input images without any segmentation.

A. Sources of lesion images

We used the following two lesion image sources for our experimentation.

PH^2: It[1] contains 40 melanomas, 80 atypical nevi, and 80 common nevi. It is composed of the medical annotation of the entire images such as assessment of various dermoscopic criteria, histological and clinical diagnosis, as well as medical lesion segmentation. The assessment of every parameter was done by an expert dermatologist.

HAM 10000[2]: It represents a vast collection of multi-source dermatoscopic images. It comprises of 10015 pictures with multi-source dermatoscopic pictures of pigmented sores. It is a benchmark dataset can be used for Machine learning ,Deep learning and for comparisons with human specialists.It contains diverse infection types like Actinic keratoses(Solar Keratoses), intraepithelial carcinoma/Bowen's illness (akiec), basal cell carcinoma (bcc), amiable keratosis-like injuries (sun powered lentigines/seborrheic keratoses and lichen-planus like keratoses, bkl), dermatofibroma (df), melanoma (mel), melanocytic nevi (nv) and vascular sores (angiomas, angiokeratomas, pyogenic granulomas and discharge, vasc).

B. Experimental setup

The proposed deep CNN-based skin disease classification model was implemented in Python, and the results were analyzed. The Deep CNN consists of an input layer, convolutional layer (5 times), max-pooling layer (5 times), fully connected layer, dropout layer, softmax layer, regression and output layer. As mentioned Deep CNN includes 5 convolution layers, in which each layer contains hidden neurons with different ranges. The 1st layer of convolution has 32, the 2nd layer includes 64, the 3rd layer consists of 128, the 4th layer has 64 neurons and the 5th layer includes 32 neurons, respectively. The python package version Pycharm version 3.7.0 was used and the package was downloaded from [17].

C. Comparative Segmentation Results

We compared performance of FCM with four (04) different popularly used segmentation methods such as Active contour [18], Watershed [19], Otsu [20], k-means [21] . Few qualitative assessments of segmentation outcomes for the candidate datasets are reported in Table II and III.

The overall performance of segmentation techniques is assessed based on images from skin data sets, Ph2 and HAM10000. From the results, we observed that FCM achieved better segmentation accuracy while comparing with ground truth for both data sources. It further indicates that overlapping pixels exist in the diseased lesion that is not well differentiated from skin colour and texture. Since FCM use fuzzy membership during clustering pixel values, it can handle such uncertainty of skin lesions with membership scores.

D. Performance analysis of Deep CNN for different segmentation methods

The performance of deep CNN on classifying skin diseases based on different candidates segmentation algorithms such as K-Means, active contour, watershed, Otsu, and FCM is reported in IV and V. We evaluated the performance in terms of assessment measures such as accuracy(ACC), sensitivity(SEN), specificity(SPF), Precision,Negative Predictive Value (NPV), F1 Score(F1), Mathews Correlation Coefficient (MCC), False Positive rate (FPR), False Negative Rate (FNR), and False Discovery Rate (FDR).

From the tables, it can be observed that for Ph2 and HAM10000 data sets, Ph2, the performance of DCNN improves while using FCM as a segmentation analysis. The

[1]https://www.fc.up.pt/addi/ph2%20database.html

[2]https://www.kaggle.com/kmader/skin-cancer-mnist-ham10000?select=HAM10000_images_part_1

TABLE II: Sample segmented images with different techniques for Ph$^2 Dataset$

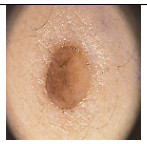
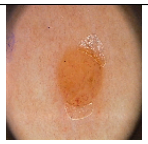
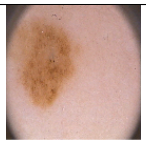
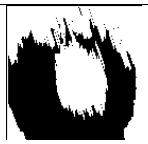
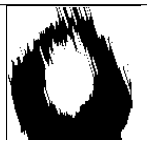
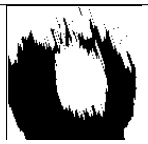
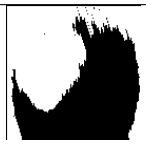
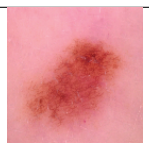
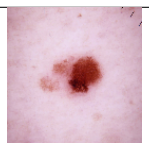
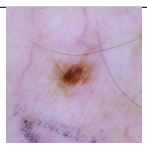
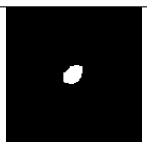
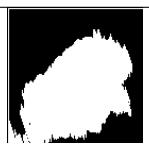
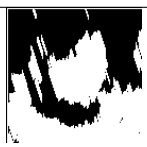
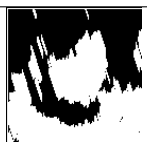
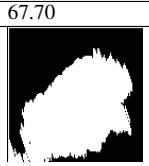
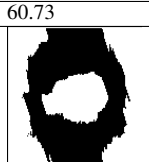
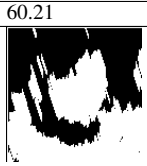
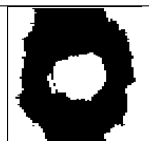
Dataset1:ph^2			
Sample images	Image 1	Image 2	Image 3
Original image			
Ground truth image			
Active contour			
Accuracy	61.93	60.39	70.56
Watershed			
Accuracy	67.18	66.87	76.63
Otsu Thresolding-			
Accuracy	60.76	59.97	70.34
K-means			
Accuracy	68.89	70.50	78.54
FCM			
Accuracy	**71.46**	**71.98**	**80.10**

TABLE III: Sample segmented images with different techniques for HAM10000 Data set

Dataset2:HAM10000			
Sample images	Image 1	Image 2	Image 3
Original image			
Ground truth image			
Active contour			
Accuracy	62.03	54.18	51.54
Watershed			
Accuracy	67.70	60.73	60.21
Otsu Thresold-ding			
Accuracy	62.12	53.22	51.54
K-means			
Accuracy	69.44	63.97	64.52
FCM			
Accuracy	**70.42**	**65.10**	**64.06**

segmentation analysis on the deep CNN for the skin disease classification using several forms of segmentation algorithms such as K-Means CNN, active contour CNN, watershed CNN, Otsu CNN, and FCM CNN are displayed in Table IV and V respectively. From table IV, for dataset 1, the segmentation analysis of the FCM-CNN in terms of accuracy is 5.49%, 5.74%, 6.35%, and 5.01% better than Otsu Thresholding-CNN, watershed-CNN, active contour-CNN, and K-Means-CNN, respectively. On considering Table V, for HAM10000, the accuracy of the FCM-CNN in terms of segmentation analysis is 4.27%, 5.91%, 6.27%, and 7% superior to Otsu Thresholding-CNN, watershed-CNN, active contour-CNN, and K-Means-CNN respectively. Overall, the FCM-CNN gets a 91.8% accuracy rate on ph and a 93.6% accuracy rate for HAM10000. Thus, the segmentation analysis on deep CNN is better with the FCM-CNN than the existing algorithms for both datasets for the skin disease classification. For every measure, the suggested Deep CNN gets higher

values for positive measures and less value for negative measures. Thus, the overall classification analysis holds superior results with the proposed method than all the state-of-the-art algorithms for the two target datasets.

TABLE IV: Overall Segmentation analysis of Deep CNN for the proposed and existing algorithms in terms of $Ph^2 dataset$

Performance measures	K-means + DCNN	Active Contour + DCNN	Watershed + DCNN	OTSU + DCNN	FCM + DCNN	DCNN Without Segmentation
ACC	0.875	0.864	0.869	0.871	**0.918**	0.885
SEN	0.888	0.875	0.882	0.883	**0.937**	0.895
SPF	0.514	0.515	0.468	0.527	0.531	0.5
Precision	0.98	0.981	0.98	0.98	**0.976**	0.985
FPR	0.485	0.484	0.531	0.472	**0.468**	0.5
FNR	0.111	0.124	0.117	0.116	**0.062**	0.104
NPV	0.514	0.515	0.468	0.527	0.531	0.5
FDR	0.019	0.018	0.019	0.019	0.023	0.014
F1 Score	0.932	0.925	0.928	0.929	**0.956**	0.938
MCC	0.222	0.203	0.184	0.227	0.355	0.197

TABLE V: Overall Segmentation analysis of Deep CNN for the proposed and existing algorithms in terms of HAM10000 data set

Performance measures	K-means + DCNN	Active Contour + DCNN	Watershed + DCNN	OTSU + DCNN	FCM + DCNN	DCNN Without Segmentation
ACC	0.875	0.881	0.884	0.897	**0.936**	0.902
SEN	0.886	0.894	0.897	0.912	**0.957**	0.912
SPF	0.531	0.527	0.484	0.457	0.5	0.518
Precision	0.982	0.98	0.98	0.978	**0.975**	0.985
FPR	0.468	0.472	0.515	0.542	0.5	0.481
FNR	0.113	0.105	0.102	0.087	**0.042**	0.087
NPV	0.531	0.527	0.484	0.457	0.5	0.518
FDR	0.017	0.019	0.019	0.021	0.024	0.014
F1	0.932	0.935	0.937	0.944	**0.966**	0.947
MCC	0.22	0.241	0.214	0.226	0.393	0.233

V. Conclusion

This paper has demonstrated the utility of FCM for skin disease classification with DCNN. FCM-DCNN achieved a superior accuracy in comparison to other contemporary CNN based methods for PH2 and HAM10000 skin images. Our work established further that segmentation is an important step while classifying skin lesions. Moreover, due to the similar texture of lesions with background skin, classifiers get confused with different types of lesions leads to misclassification. Work is on to perform similar experiments on samples collected from indian patients where skin tones are different from European patients (samples used in this work).

References

[1] M. Chen, P. Zhou, D. Wu, L. Hu, M. M. Hassan, and A. Alamri, "Ai-skin: Skin disease recognition based on self-learning and wide data collection through a closed-loop framework," *Information Fusion*, vol. 54, pp. 1–9, 2020.

[2] P. Tschandl, C. Rosendahl, B. N. Akay, G. Argenziano, A. Blum, R. P. Braun, H. Cabo, J.-Y. Gourhant, J. Kreusch, A. Lallas *et al.*, "Expert-level diagnosis of nonpigmented skin cancer by combined convolutional neural networks," *JAMA dermatology*, vol. 155, no. 1, pp. 58–65, 2019.

[3] C. Barata, M. E. Celebi, and J. S. Marques, "A survey of feature extraction in dermoscopy image analysis of skin cancer," *IEEE journal of biomedical and health informatics*, vol. 23, no. 3, pp. 1096–1109, 2018.

[4] N. Gessert, T. Sentker, F. Madesta, R. Schmitz, H. Kniep, I. Baltruschat, R. Werner, and A. Schlaefer, "Skin lesion classification using cnns with patch-based attention and diagnosis-guided loss weighting," *IEEE Transactions on Biomedical Engineering*, vol. 67, no. 2, pp. 495–503, 2019.

[5] A. Esteva, B. Kuprel, R. A. Novoa, J. Ko, S. M. Swetter, H. M. Blau, and S. Thrun, "Dermatologist-level classification of skin cancer with deep neural networks," *nature*, vol. 542, no. 7639, pp. 115–118, 2017.

[6] K. Melbin and Y. J. V. Raj, "An enhanced model for skin disease detection using dragonfly optimization based deep neural network," in *2019 Third International conference on I-SMAC (IoT in Social, Mobile, Analytics and Cloud)(I-SMAC)*. IEEE, 2019, pp. 346–351.

[7] Y. Gu, Z. Ge, C. P. Bonnington, and J. Zhou, "Progressive transfer learning and adversarial domain adaptation for cross-domain skin disease classification," *IEEE journal of biomedical and health informatics*, vol. 24, no. 5, pp. 1379–1393, 2019.

[8] T.-C. Pham, A. Doucet, C.-M. Luong, C.-T. Tran, and V.-D. Hoang, "Improving skin-disease classification based on customized loss function combined with balanced mini-batch logic and real-time image augmentation," *IEEE Access*, vol. 8, pp. 150 725–150 737, 2020.

[9] N. Hameed, A. M. Shabut, M. K. Ghosh, and M. A. Hossain, "Multi-class multi-level classification algorithm for skin lesions classification using machine learning techniques," *Expert Systems with Applications*, vol. 141, p. 112961, 2020.

[10] A. A. Adegun and S. Viriri, "Fcn-based densenet framework for automated detection and classification of skin lesions in dermoscopy images," *IEEE Access*, vol. 8, pp. 150 377–150 396, 2020.

[11] B. Ahmad, M. Usama, C.-M. Huang, K. Hwang, M. S. Hossain, and G. Muhammad, "Discriminative feature learning for skin disease classification using deep convolutional neural network," *IEEE Access*, vol. 8, pp. 39 025–39 033, 2020.

[12] A. Victor and M. R. Ghalib, "A hybrid segmentation approach for detection and classification of skin cancer." *Biomedical Research (0970-938X)*, vol. 28, no. 16, 2017.

[13] M. Q. Khan, A. Hussain, S. U. Rehman, U. Khan, M. Maqsood, K. Mehmood, and M. A. Khan, "Classification of melanoma and nevus in digital images for diagnosis of skin cancer," *IEEE Access*, vol. 7, pp. 90 132–90 144, 2019.

[14] H. Yeganeh, A. Ziaei, and A. Rezaie, "A novel approach for contrast enhancement based on histogram equalization," in *2008 International Conference on Computer and Communication Engineering*. IEEE, 2008, pp. 256–260.

[15] A. Jose, S. Ravi, and M. Sambath, "Brain tumor segmentation using k-means clustering and fuzzy c-means algorithms and its area calculation," *International Journal of Innovative Research in Computer and Communication Engineering*, vol. 2, no. 3, 2014.

[16] W. Rawat and Z. Wang, "Deep convolutional neural networks for image classification: A comprehensive review," *Neural computation*, vol. 29, no. 9, pp. 2352–2449, 2017.

[17] "Jetbrains pycharm description," accessed: 2021-07-24.

[18] R. Hemalatha, T. Thamizhvani, A. J. A. Dhivya, J. E. Joseph, B. Babu, and R. Chandrasekaran, "Active contour based segmentation techniques for medical image analysis," *Medical and Biological Image Analysis*, vol. 4, p. 17, 2018.

[19] L. J. Belaid and W. Mourou, "Image segmentation: a watershed transformation algorithm," *Image Analysis & Stereology*, vol. 28, no. 2, pp. 93–102, 2009.

[20] A. B. Patil and J. Shaikh, "Otsu thresholding method for flower image segmentation," *International Journal of Computational Engineering Research (IJCER)*, vol. 6, no. 05, 2016.

[21] P. Panwar, G. Gopal, and R. Kumar, "Image segmentation using k-means clustering and thresholding," *Image*, vol. 3, no. 05, pp. 1787–1793, 2016.