An automatic feature extraction technique from the images of granular parakeratosis disease

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Abstract *– The largest and most vital part of the human body is skin and any change in the features of skin is termed as a skin lesion. The paper considers granular parakeratosis lesion that is an epidermal reaction occurring due to the disorder of keratinization, and mainly seen in intertriginous areas. The manual inspection of the lesion features is a bit cumbersome due to which an automated system is proposed in this paper. The main goal is to determine the size and depth of granular parakeratosis lesions using the proposed ensemble algorithm, partition clustering and region properties method. As a flow of the proposed model, segmentation is done using U-net with binary cross entropy, features are extracted using partition clustering and region properties method, and classification is done using SVM 10-fold model. The proposed feature extraction method estimates the depth and absolute size of K lesions in each image by predicting the absolute height and width of the lesion in terms of pixel square. After extracting the features, classification is done, thereby obtaining an accuracy of 95%, sensitivity and specificity of 100%. The proposed model provides better performance compared to state-of-the-art models. The main application of this automated system is in dermatology field where some skin lesions have same features which makes the experts to diagnose the disease incorrectly. If the proposed system is incorporated, diagnosis can be done in an effective manner considering all the relevant features.*

Keywords*: U-net with Binary Cross Entropy, Partition Clustering, Region Properties, Depth and Absolute Size, SVM 10-fold*

1. INTRODUCTION

Granular parakeratosis appears as red or brown hyperkeratotic papules or plaques in intertriginous areas. Patients of various ages have been diagnosed with the illness, and is more common in women than in men [1]. Granular parakeratosis was once assumed to be a contact dermatitis caused by hygiene products like deodorants and antiperspirants; however, cases have been documented even without the application of any personal hygiene products in the affected areas, ruling out contact dermatitis as the cause [2]. Other intertriginous and non-intertriginous body parts, such as the face, have also been reported to develop granular parakeratosis.

As described above, Granular parakeratosis is a type of skin disease. For the diagnosis of such type of diseases, most of the dermatologists rely on traditional methods. Though these methods have shown improved performance, they are still not feasible for a variety of factors such as a large number of patients, infrastructure, technical equipment, etc. Further, granular parakeratosis shares many of the characteristics of benign lesions in its early stages, making it difficult to distinguish. Experts find it difficult to detect the disease with the naked eye. Also, the diagnosis process is quite challenging as the analysis depends on the clinical expertise of the experts.

To overcome this problem, there is a requirement of an automated system that can adapt to technological advancements in the discipline of dermoscopy and assist specialists in detecting lesions accurately and giving a better path to diagnosis. Computer-aided diagnosis (CAD) systems use a variety of machine learning techniques for extracting the features from a given lesion dataset. Several texture analysis techniques like Principal Component Analysis (PCA) and Gray-Level Co-Occurrence Matrix (GLCM) have recently been presented in this arena, and their models have gained widespread acceptance for feature extraction, resulting in enhanced classification [3]. These techniques adopt dermoscopic images and are able to detect the most required features of the affected area.

"The malignant and benign lesions are classified using several feature extraction algorithms such as the ABCD rule, the seven-point checklist method, three-point checklist, and CASH algorithm. The ABCDE rule (Asymmetry, Border, Color, Diameter, Evolve), the 7-point checklist, and the Menzies technique are three clinical diagnosis methods used by dermatologists to distinguish melanoma from nevus [4]. These feature extraction techniques are dependent on lesion color, shape, geometry, texture, and structure [5]. An important screening tool for the detection of melanoma with accurate sensitivity and specificity is ABCD [6]".

Feature extraction is regarded as a necessary tool for properly analysing an image. Many authors explored a variety of features for classification as explained above; however none of them properly distinguish benign and malignant lesions. Several lesion extraction techniques have been developed in the past to aid specialists in finding the lesions automatically. However, due to variations in shapes and sizes, extracting the features from dermoscopic lesions is a hard task since it results in inaccurate extraction and increases the computational time. To tackle the aforementioned hurdles for more accurate lesion extraction, a new technique for extracting the features from lesion is created.

The novelty of the proposed work lies in feature extraction that is described as follows:

- In this paper, different digital images of parakeratosis have been analyzed.
- Initially, U-net with binary cross entropy technique is applied to segment the dataset, followed by which features (size and depth) of the segmented lesion are extracted using the region properties method, and finally classification of the lesion into starting or later stage is done using the SVM 10-fold validation model.
- Following that, a thorough discussion based on the findings is presented.

The paper comprises four sections, starting with the literature review, where a brief overview of the existing literature is presented. Next, the proposed methodology section describes the system architecture and the method implemented. The results and discussion section gives the results obtained from the experiments and discussions on them, and eventually, the final section concludes the paper.

2. LITERATURE REVIEW

Feature selection is a technique used in both machine learning and statistical pattern recognition. This is crucial in a variety of applications, including classification. Many methods for detecting melanoma have been reported in the last decade [7], [8]. Some of these attempts were to imitate dermatologists' performance by extracting and detecting most dermoscopic structures, such as pigment networks, irregular streaks, granularities, blotches, etc. Many studies utilised global approaches to classify skin lesions, whereas others employed local ones [9]. Several feature extraction techniques for various types of skin lesions investigated so far are described.

Features, which are retrieved using local, global, or local–global scenarios, play an important part in classification. For melanoma detection using dermoscopic pictures, Barata et al. [10] used a local–global technique. Local methods were employed to extract features using bag-of-words, whereas global methods were studied for skin lesions categorization in terms of higher sensitivity and specificity, with encouraging results.

The author of [11] suggested an entropy-controlled neighbourhood component analysis paradigm for most discriminant feature selection and dimensionality reduction (ECNCA). A model for lesion classification is also proposed that leverages deep feature information to build the best discriminant feature vector. The ECNCA framework improves fused characteristics by removing the duplicate and superfluous data and selecting the most important components. After the application of the proposed feature framework, the classification is done by testing on four datasets: PH2, ISIC MSK, ISIC UDA, and ISBI-2017, leading to an accuracy of 98.8%, 99.2%, 97.1%, and 95.9%, respectively. The drawback of the method is that it is applicable only to a limited dataset.

The article [12] proposed a diagnosis guided feature fusion (DGFF) that uses lesion information from the melanoma to improve skin lesion segmentation pixel-wise classification performance. It creates feature representations that distinguish between melanoma and non-melanoma lesions and also improves the network's ability to recognise various sorts of skin lesions using dermoscopic images. The extracted features are fed into the pixel-wise classification task, leading to an accuracy of 88.2%, a sensitivity of 63.3%, and a specificity of 94.2%. This method has the limitation of not considering some of the dermoscopic images that contain redness around the lesion area and black spots in an image.

The framework of [13] proposes the Self-supervised Topology Clustering Network (STCN) to segment the skin images automatically. The STCN consists of a transformation-invariant network that comprises a feature extraction function, a self-expression function, and a self-supervision deep topology clustering algorithm. The main goal is to determine the appearance characteristics and keep them consistent across multiple variations. These features will further be automatically partitioned into groups using the Deep Topology Clustering (DTC) algorithm, which will be used to construct pseudo labels for skin images. Finally, the DTC module is used as the self-supervision component to train a classification network using the estimated annotations. But the model is unable to use hand-craft features due to which the required information will be ignored.

To investigate the textural complexity of a skin lesion, a fractal-based regional texture analysis (FRTA) technique was created. FRTA separated the lesion area into smaller subregions based on textural complexity. Successful feature extraction from dermoscopic images has been achieved using a fractal-based border irregularity measurement and regional texture analysis technique. The performance of classification is increased when the Support Vector Machine (SVM) recursive feature elimination (RFE) technique is applied before each stage of the layered structured model [14], but the difficult cases present in an image cannot be classified correctly.

The labels are defined as a method of grouping items into clusters in which objects in one cluster are almost identical and objects in other clusters are significantly different. Clustering's main purpose is to extract sets of patterns, points, or objects from natural groupings [15]. Clusters of various forms and densities are determined using the MDCUT algorithm (Multi-Density ClUsTering) [16]. It is a density based clustering algorithm that can handle noisy data and discover neighbouring and imbricated clusters. The drawback is that only a few preprocessing methods are applied to the dataset.

Trabelsi et al. [17] used a variety of clustering techniques, including fuzzy c-means, modified fuzzy c-means, and K-means, to segment a skin disease with an 83% true positive rate. The clustering algorithms depend on the identification of a centroid that can generalise a cluster of data. However, the performance of these algorithms degrades with the presence of noisy data and outliers.

Table 1.: Overview of the literature

Method	Major contributions	Limitations
ECNCA	Improves fused characteristics	Works only for Small dataset
DGFF	Improves pixel-wise classification performance	Doesn't consider black spots in an image
STCN	Determines the appearance characteristics	Ignores the required information
FRTA	Improves the performance	Difficult cases are ignored

According to literature, there are various problems with successful feature extraction. The proposed integrated system plays a significant role in overcoming the obstacles of accurate disease diagnosis based on visual and simulated evaluation by measuring the effective features and diagnosing the disease with a higher degree of accuracy. The proposed method employs the conjunction of clustering and region properties methods to overcome these. The suggested approach extracts the size and depth of lesions in an image by applying several morphological functions to the given dataset.

3. PROPOSED METHODOLOGY

3.1. FEATURE EXTRACTION

"Relevant information for accomplishing the computing tasks associated with a certain application" is defined as a feature. There are two types of features: local ones and global ones [18]. In order to build a classification rule, a collection of numerical criteria that describe the object or phenomena seen (supervised or not) is described. Several feature extraction algorithms have been developed, each with their own set of principles [19]. Here, a feed-form method of partition clustering and the region properties method are proposed.

3.2 SYSTEM ARCHITECTURE

The architecture of the proposed system is shown in figure 1. To begin, 224x224 lesion images are acquired, segmentation is performed using the U-net method, followed by watershed-based separation of lesions (formation of clusters), then, extracting the features using regionprop and finally, classification is done using SVM 10-fold model.

If features extracted from the lesion are efficient, it can lead to a better classification of granular parakeratosis. Here, the parakeratosis image consists of several lesions that can be easily identified by labeling the lesions and then determine the width, height, and depth of a lesion. The detailed steps of pre-processing and feature extraction using clustering and region properties are shown in figure 2. Some transformations like thresholding and morphology are applied to the clustered lesion to extract the most descriptive set of features. Using the regionprops approach, the size and depth of the clustered lesions obtained in figure 1 are extracted.

The proposed feature extraction method, being an unsupervised one, extracts the size and depth of a lesion in the following manner:

- Morphology pre-processing techniques remove any small objects and holes in the image.
- The touching cells in an image can be effectively separated using distance transform and thresholding. Thus, leading to the separation of lesions and non-lesions, followed by which a number of clusters of lesions are created.

- Different lesions in the clusters are labeled, after which watershed filling is applied. For each label, the size and depth of the lesion is extracted using the regionprops method of skimage.

3.3 CLUSTERING

One of the most prominent approaches for skin disease segmentation and classification is the clustering algorithm. Clustering, often known as cluster analysis, is a machine learning technique for organizing unlabeled data. It is defined as "***grouping similar data points into different clusters***". Clustering is a form of unsupervised learning that works with unlabeled data. The advantage of clustering algorithms is that they are flexible, easy to implement, and can generalize features having a similar statistical variance. *Here, lesions in a group have possible similarities and have fewer or no similarities with another group*.

Partition Clustering

It's a type of clustering in which data is split into non-hierarchical groups. This strategy is also known as the centroid-based method [20]. In this type, the dataset is divided into K groups, with K denoting the number of pre-defined groups. The cluster centre is designed in such a way that the distance between one cluster data point is the smallest when compared to the cluster centroid of the other cluster.

The type of clustering used in the implementation is partitioning clustering. The patterns like size and depth of lesions are considered, and the data points having the same size and depth are formed into a cluster (group). After the application of the clustering technique, each cluster is provided with a cluster ID (or label id) and the area and depth of each cluster (lesion) are found.

Mathematical analysis involved in the partition clustering

An image can be partitioned into K clusters such that the total of Manhattan distances (L1) between locations and the cluster's centre is kept to a minimum. Then, the sum of L1 absolute errors (SAE) can be minimised by using the following equation 1.

$$SAE = \sum_{i=1}^{K} \sum_{x \in C_i} dist_{L_1}(c_i, x) \quad (1)$$

where $dist_{L_1}$ is L_1 distance, C_i is the i^{th} cluster, x is a point in C_i, and c_i is the i^{th} cluster average.

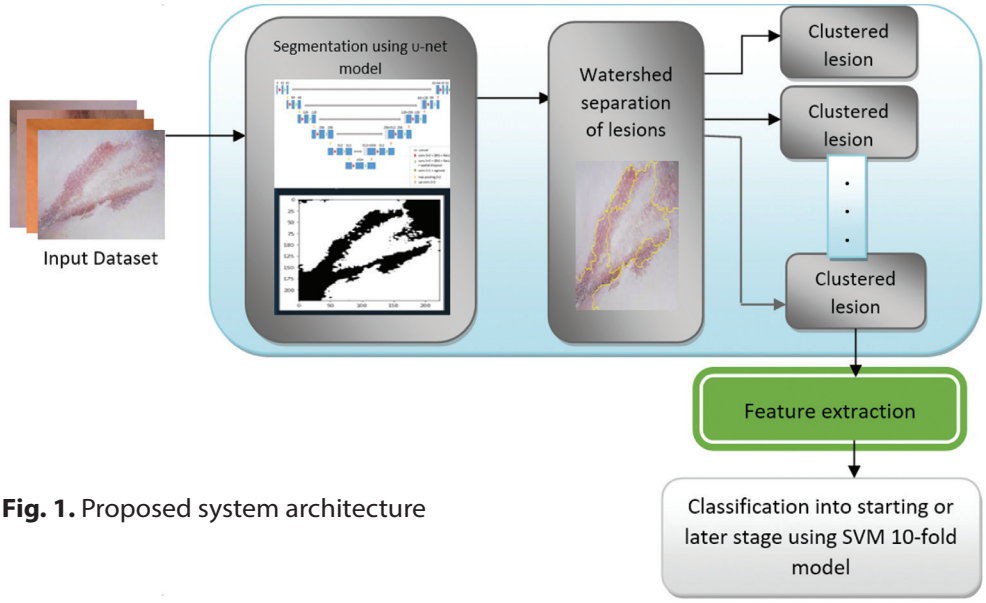

Fig. 1. Proposed system architecture

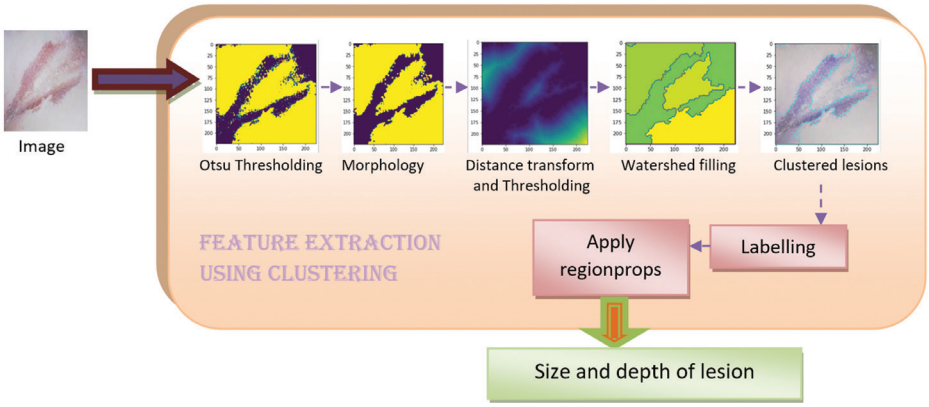

Fig. 2. Feature extraction using clustering

3.4 Dataset

To test the proposed methodology, publicly available DermnetNZ and DermIS datasets are chosen [21], [22]. These datasets consist of several RGB images of granular parakeratosis and is partitioned into two classes, starting stage and later stage wherein 79 samples are considered for each class. For the implementation of size and depth features, the OpenCV library and the python machine learning package, Scikit-learn library, are adapted. All the experiments are run on a Windows 10 system with an i5 processor. Figure 3 shows some of the sample images of granular parakeratosis.

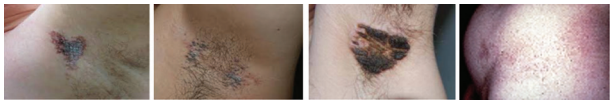

Fig. 3. Samples of granular parakeratosis

3.5 Implementation

The given skin image undergoes several steps like normalization, clustering (form the clusters of skin lesion), extract the size and depth features, and pass them to the classification model.

In this section, the implementation of the distance transform, watershed, and clustering algorithms for extracting the features from the granular parakeratosis dataset is described. The model is trained on 79 dermoscopy images.

The below mentioned algorithm describes the generalised steps incorporated by the proposed model:

Step 1: Initially, import the libraries required for feature extraction

Step 2: Then, read an image by defining pixel size

Step 3: Perform segmentation using the U-net model. The result of the U-net model is transformed to binary image (threshold image to separate lesion boundaries) using Otsu thresholding

Step 4: Watershed based separation of lesions: Apply morphological functions to enhance the boundaries and create a mask

Step 5: Label the lesions in an image

Step 6: Extract the size and depth of each lesion using regionprops method

Step 7: Output results into a csv file

A detailed description of the flow of the implementation is as follows:

1. Initially, segmentation is done using the encoder-decoder process of the U-net model with binary cross entropy as a loss function. The main aim of choosing binary cross entropy is to minimise the loss so as to improve performance of the model. A 224x224 image is passed into the network for which 32 filters are applied. Then, it gets converted into 112x112x64, 56x56x128, 28x28x256, 14x14x512, and 7x7x1024 as it passes through different levels of the network. In the decoder path, each level concatenates with the corresponding level in the encoder path, leading to a 7x7x1024, 14x14x512, 28x28x256, 56x56x128, 112x112x64, and 224x224x32 image. To this image, the last layer with a filter of size 1x1 and a sigmoid activation function is applied, generating 224x224x1 segmented-image.

2. Otsu thresholding: It is an auto-thresholding technique that automatically calculates a threshold value for a binary image. The flags cv2.THRESH_BINARY & cv2.THRESH_OTSU are passed as parameters to the cv2.threshold() function with the threshold value set as zero. The main goal of Otsu's approach is to minimise the variance by choosing the correct value for the threshold. If it is chosen wrong, the variance of one or more classes will be significant. Thus, to get the total variance, add all the within-class and between-class variances together as shown in equation

$$\sigma_T^2 = \sigma_w^2(t) + \sigma_b^2(t) \tag{2}$$

where $\sigma_w^2(t) = w_1(t)\sigma_1^2(t) + w_2(t)\sigma_2^2(t)$ and

$$\sigma_b^2(t) = w_1(t)w_2(t)[\mu_1(t) - \mu_2(t)]^2$$

$w_1(t)\ and\ w_2(t)$ → probabilities of the classes divided by threshold t (0-255)

μ_i → class i^{th} mean

3. Morphological transformations are straightforward operations that are usually applied to binary images. OpenCV's morphologyEx() function is as follows:

- Morphological transformations are simple procedures done on images depending on their shape to remove noise, small holes in foreground objects, and so on. Erosion, dilation, opening, and closing are some of the morphological operations. In implementation part, after otsu thresholding, opening morphology is done. To execute opening morphological procedures on a given image, the MORPH_OPEN operation in the morphologyEx() method is used.

4. To extract the exact lesion in an image, a distance transform followed by a threshold is applied [23]. The distance transform function calculates the approximate distance from every pixel in the image to the zero pixel. For zero pixels, it will be zero. Out of several distance types available, DIST_L2 is chosen which runs the linear-time algorithm. This algorithm makes use of squared Euclidean (or quadratic) distance described as follows. Let G stand for regular grid and $f:G \rightarrow R$ be

a grid function where R is the range of distance function d. The distance transform of f is defined by equation 3.

$$D_f(p) = \min_{q \in G}\big(d(p,q) + f(q)\big) \quad (3)$$

where $d(p, q)$ is a distance measure between p and q. A point q that is close to p and with a small f(q) is discovered for each point p.

Let $G = \{0, \ldots, n-1\}$ be a one dimensional grid, and $f : G \rightarrow R$ an arbitrary grid function. The squared Euclidean (or quadratic) distance transform of f is described by equation 4.

$$D_f(p) = \min_{q \in G}\big((p-q)^2 + f(q)\big) \quad (4)$$

5. The non-lesion area can be found by applying dilation to the result obtained in the previous step. To determine the area which is not sure of a lesion or non-lesion (also called boundaries or border of lesion, where lesion and non-lesion touch each other), watershed algorithm is applied.

6. A *watershed* is a transition defined on a grayscale image. This technique aids in the detection of touching and overlapping lesions in an image. The watershed algorithm extracts the completely lesion area and the completely non-lesion area, leading to the creation of clusters. Several clusters of lesions are identified and then markers are applied to detect the exact boundaries (labeling). These markers assign positive numbers to completely lesion and non-lesion areas and zero to the area that is not sure to be lesion or non-lesion **using cv2.connectedComponents()**. Finally, after labelling the regions, apply the watershed algorithm for filling.

7. After identifying labelled lesions in an image, the features of these lesions can be determined using the regionprops() module of the skimage library. The size and depth of lesions in an image are calculated by measuring the cluster's height and width in pixel square.

8. The features obtained are then given as an input to the SVM 10 fold cross validation model. The reason for chosing SVM is that it finds the best separator to differentiate the classes. Thus, SVM serves as a binary classifier. Here, it classifies the lesions into starting stage or later stage. In SVM 10 fold model, 224x224 images from which the features extracted using the region properties technique are input into the SVM classifier with hinge loss and linear activation function. Hinge loss is a function that is mainly used to train the SVM classifier. The linear activation function decides the output of the model and when associated with neurons, it decides whether a neuron should be activated or not depending on the input provided. The output of this SVM classifier is then fed into the 10 fold validation model wherein the model is trained on one partition and evaluated on other nine partitions, thereby increasing an accuracy to 95%, sensitivity to 100% and specificity to 100%. The output of classification is shown in figure 4.

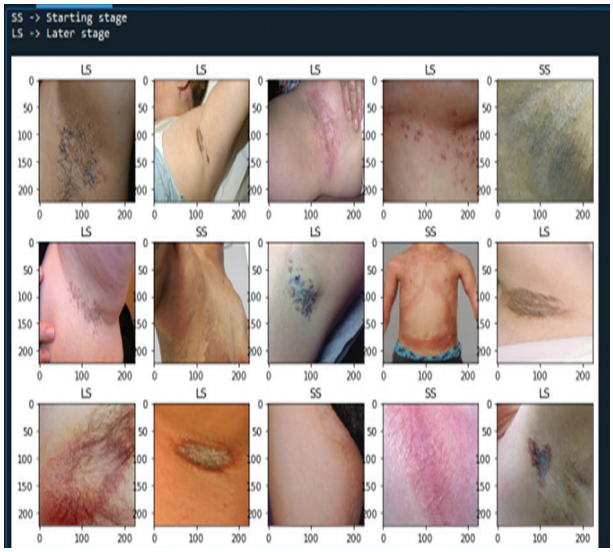

Fig. 4. Classification of granular parakeratosis into starting or later stage

4. RESULTS AND DISCUSSION

4.1 QUANTITATIVE EVALUATION

The model is evaluated quantitatively using accuracy, sensitivity, and specificity metrics. This is computed as

$$\text{Accuracy} = \frac{TP+TN}{TP+FN+TN+FP}$$

$$\text{Sensitivity} = \frac{TP}{TP+FN}$$

$$\text{Specificity} = \frac{TN}{TN+FP}$$

Abbreviations: TP - True Positive, TN - True Negative, FP -False Positive and FN - False Negative

4.2 ANALYSIS

The size and depth of the lesion (segmented object) are determined in the model. Figure 5 shows the samples of original image, an overlay on the original image, a segmented image, and the size and depth extracted from the lesions of sample images. The results obtained for other images are shown in Table 2. The table shows that for each image, different lesions are identified and labeled with a unique number. For each label, the area and depth of the lesion are found. For example, the first four rows (excluding the heading) of the table correspond to an image, images.bmp. This image consists of four lesions identified by lesion numbers 1, 2, 3, and 4 (second column). For each of these lesions, an area and depth are computed. The same thing is repeated for the other images in the dataset (from the fifth row).

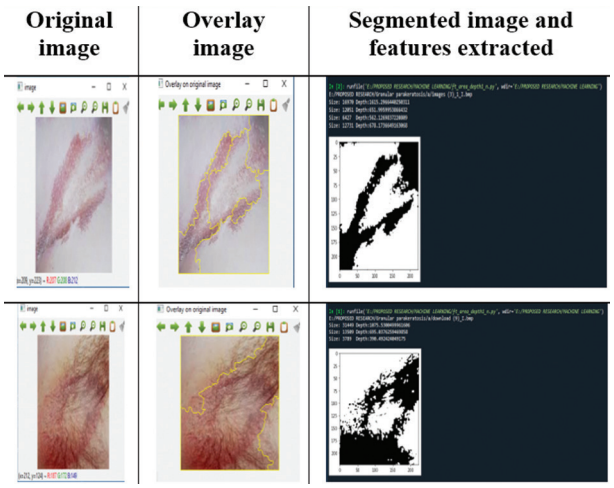

Fig. 5. Original image, overlay image, segmented image and features extracted

Table 2. Simulation results of the model

Image Name	Lesion#	Area	Depth
images.bmp	1	4242.5	1615.297
images.bmp	2	3012.75	651.996
images.bmp	3	1606.75	562.127
images.bmp	4	3182.75	678.1737
download.bmp	1	7862.25	1075.53
download.bmp	2	3377.25	695.0376
download.bmp	3	947.25	390.4924
Axillary Granulary Parakeratosis.bmp	1	2846.5465	1207.022
Axillary Granulary Parakeratosis.bmp	2	8344	1199.578
Axillary Granulary Parakeratosis.bmp	3	934.5	313.2203
Axillary-Granular-Parakeratosis-1.bmp	1	6636.25	1308.71
Axillary-Granular-Parakeratosis-1.bmp	2	1522.75	479.2031
Axillary-Granular-Parakeratosis-1.bmp	3	1146	419.2386
Axillary-Granular-Parakeratosis-1.bmp	4	111.25	89.25483
Axillary-Granular-Parakeratosis-1.bmp	5	101.25	114.1604
Axillary-Granular-Parakeratosis-1.bmp	6	91	104.332
Axillary-Granular-Parakeratosis-1.bmp	7	140.75	119.1665
Axillary-Granular-Parakeratosis-1.bmp	8	41.25	59.35534
Axillary-Granular-Parakeratosis-1.bmp	9	280.5	171.3797
Axillary-Granular-Parakeratosis-1.bmp	10	26	47.83452
Axillary-Granular-Parakeratosis-1.bmp	11	172.25	137.3026
Axillary-Granular-Parakeratosis-1.bmp	12	136.5	121.3026
Axillary-Granular-Parakeratosis-1.bmp	13	53.75	95.01219
Axillary-Granular-Parakeratosis-1.bmp	14	67.25	73.39697
Axillary-Granular-Parakeratosis-1.bmp	15	207.25	144.6518
Axillary-Granular-Parakeratosis-1.bmp	16	16.5	33.14214
Axillary-Granular-Parakeratosis-1.bmp	17	270.5	196.5097

Experiment shows that the proposed strategy produces good results. The performance of the proposed model provides a better result compared to the state-of-art methods. After the application of the partition clustering and region properties method to the given dataset, the output is fed to SVM 10-fold model that achieved an accuracy of 95%, a sensitivity of 100% and a specificity of 100%. The performance of each fold in 10-fold model is presented in table 3.

Table 3. Fold-wise performance of 10-fold

Fold	Accuracy	Sensitiviy	Specificity
1	95	99.99	99.99
2	94.99	99.99	100
3	94.99	99.98	99.98
4	95	100	99.99
5	94.99	100	100
6	95	99.99	100
7	94.99	100	99.99
8	95	100	100
9	95	100	100
10	95	100	100
Average	94.99	99.99	99.99

Table 4 shows the performance of the existing models and compares them with the proposed model after feature extraction.

Table 4. Comparison of the proposed method to state-of-the-art techniques in terms of classification performance

Model	Feature extracted	Accuracy	Sensitivity	Specificity
Morphological geodesic active contour [24]	Color	94.59	91.72	97.99
Fuzzy clustering [25]	Area, perimeter, and centroid	97.6	96.82	96.94
Scattered Wavelet Transform[26]	Hand-crafted features	93.14	-	-
Stationary Wavelet Transform[27]	Entropy	91.5	90	93
RESNET-50 [28]	Contrast	89.8	-	-
Proposed model	**Size and depth**	**95**	**100**	**100**

The model proposed by salih et al. achieved an accuracy of 97.6 which is bit higher than the proposed model. Though this model achieved higher accuracy, it didn't work well with few of the skin lesions and couldn't achieve higher sensitivity and specificity. Thus, the proposed hybrid model can be used for parakeratosis feature extraction that not only works well with all of the training samples but also achieved better performance metrics, including accuracy, sensitivity, and specificity.

Figure 6 shows the graphical representation of the performance comparison of proposed and existing models.

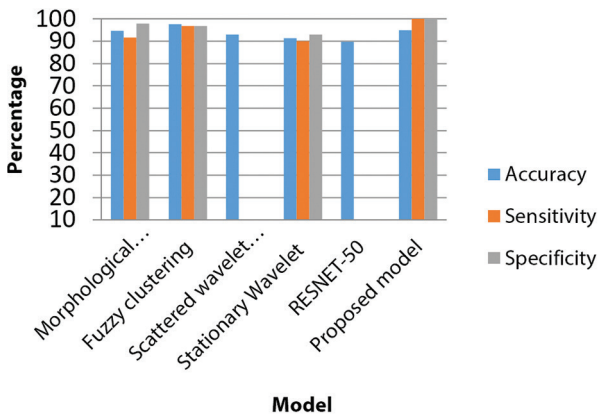

Fig. 6. Performance comparison

5. CONCLUSION

An estimation of the features of lesions in an image is an important application of medical image processing. The paper proposes an automatic method for size and depth extraction using partition clustering and the region properties method. The model performs the segmentation of the given dataset using U-net with binary cross entropy technique, extracts the features using partition clustering and region properties methods, and finally classify into starting or later using SVM cross validation model. The proposed method estimates the depth and absolute size of K lesions in each image by predicting the absolute height and width of the lesion in terms of pixel square. After extracting the size and depth, classification is performed using SVM 10-fold model. The experiment results demonstrate that the proposed model provides a better performance compared to the other models.

The model has the limitation that it works well only for the limited number of samples. As a future work, the model can be improvized in such a way that it works well even for a large dataset.

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