TREE-STRUCTURE BASED FRAMEWORK FOR AUTOMATED SKIN LESION ANALYSIS

by

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a Thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in the School of Computing Science

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Abstract

Cutaneous malignant melanoma is one of the most frequent types of cancer in the world but if a malignant lesion is detected early, it can be cured without complication. Automated skin lesion analysis attempts to accomplish early detection of malignancy using digital dermoscopic images.

We address two challenging applications in automated analysis of dermoscopic skin lesion images: lesion segmentation and lesion diagnosis, both of which use a novel tree structure based framework to model the radial and the vertical growth pattern of the skin lesion. To construct the tree, the pixels are repeatedly clustered into sub-images based on color information and spatial constraints. This framework allows us to extract features by looking at the tree from a graphical aspect, or a textural/geometrical aspect on the nodes.

The features are used in supervised learning algorithms on datasets containing 116 challenging images for segmentation, and 410 images for diagnosis. Our method outperforms many other published results.
To my lovely wife and our families for all their support
“Imagination is more important than knowledge.”

ALBERT EINSTEIN, 1879-1955
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Chapter 1

Introduction

Cutaneous malignant melanoma is one of the most frequent types of cancer in the world. In recent decades, the annual rate of its incidence has been increasing by 3%-7% in fair-skinned populations [37, 20]. It is increasing faster than any other cancer in the world, and in 2008, melanoma was the sixth most common malignancy in men and the seventh in women [20]. Despite the lethality of the disease, if the malignant lesion is detected early, it can be cured without complication. Hence, there is a growing demand for computer-aided-diagnosis of melanoma to improve the diagnostic accuracy.

In this thesis, a new framework for automated segmentation and diagnosis of skin lesions is introduced. It is a novel approach inspired by the analysis of the growth pattern of skin lesions. In this approach, a tree-structure is constructed based on the growth of the skin lesion and distribution of the colors over the skin lesion. The tree is constructed by repeatedly clustering the pixels into sub-images based on their color components and spatial information.

A malignant lesion is often identified with two growth phases: radial and vertical [14]. Both malignant and benign lesions start growing radially. In this phase, a pigmented lesion is formed by nests of melanocytes, which synthesize a brown pigmentation called melanin. This phase happens in the epidermis, the outer layer of the skin. Invasive melanoma forms in the vertical phase when malignant melanocytes start penetrating into the dermis (see Fig. 1.1 and Fig. 1.2). In this phase, an invasive melanoma tends to show multiple colors due to the position of melanin in different skin layers, formation of blood vessels, and regression of the lesion.

There are several different modalities to obtain images of skin lesions. One reliable
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Figure 1.1: The radial and vertical growth phase of pigmented skin lesion over time. Skin lesion is simultaneously growing radially and vertically over the time. Malignant melanocytes penetrate into dermis and change the coloration of the lesion starting from the 3rd time slice in this figure. (©2001 by Med-Art http://www.med-ars.it)

way to screen skin lesions is to use a dermoscope [8], a non-invasive hand-held device which captures magnified digital skin images using either polarized light or oil immersion to render the outermost layer of the skin, called the epidermis, translucent. In dermoscopic images, different coloration is caused by different absorbance of light in different layers of skin. This 3-dimensional information can be captured in a magnified 2-dimensional digital image using dermoscopy. The idea of using this spatial information of the growth pattern for the skin lesion segmentation was provided previously by Zhou et al. [58]. In this thesis we use this information in different ways to decompose the image, and to extract features for lesion segmentation and diagnosis.

The rest of the thesis is as follows. Chapter 2 reviews the existing methods for the segmentation and diagnosis of skin lesions. Chapter 3 describes our method of segmentation of the skin lesion. In Chapter 4, we discuss our method of malignancy diagnosis for skin lesions. Chapter 5 concludes the thesis.
Figure 1.2: The melanin appears as different colors in different depths. The dark brown and the dark blue coloration mainly appear in deeper layers. The red color appears where the blood vessels exist in deeper layers. Dermoscopy can capture and provide the information in both radial and vertical dimensions. (Image is taken from http://www.basicdermoscopy.blogspot.com)
Chapter 2

Background

2.1 Image Acquisition

There are several different modalities to obtain images of skin lesions. Up until 1995 pigmented lesions were mainly examined by naked eye, therefore early automated skin lesion analysis methods were performed on these simple camera-captured images, the so-called 'clinical' images, which record the surface characteristics of a skin lesion [15]. Around 1995, dermoscopy (aka: dermatoscopy, epiluminescence microscopy (ELM), skin surface microscopy, incident light microscopy) became available and automated skin lesion analysis methods began using dermoscopic images for analysis. Today, most research in automated skin lesion analysis and diagnosis uses dermoscopic images [15].

Dermoscopes enable dermatologists to recognize the subsurface structures that are associated with malignancy. Therefore, image processing algorithms can be developed for dermoscopic images to facilitate the diagnosis.

2.2 Lesion Segmentation

Lesion segmentation is defined as an assignment of binary labels from the label set $L = \{\text{'lesion'}, \text{'background'}\}$ to the pixels in the image. However, segmentation can also be defined as assigning a probability of belonging to 'lesion' or 'background' for every pixel [53]. The probability can easily be transformed to the binary version of segmentation by utilizing thresholding techniques and morphological operations.
Skin lesion segmentation is a crucial step in automated skin lesion analysis. The quality of the extracted lesion border plays an important role in the output quality of some methods \cite{7, 31} as these methods directly use the border for the feature extraction. Other methods may use segmentation to determine the region of interest (ROI) in the lesion for feature extraction \cite{35, 45}.

In some studies, segmentation is performed manually \cite{16, 19, 48}.

Most segmentation methods are histogram based methods \cite{17, 13, 23, 26, 47, 56, 57}. The main technique in the histogram based segmentation is to use gray level or color level (in different color spaces) intensity thresholding. In some of these methods, user interaction is also used to increase the quality of segmentation \cite{23}.

Active contours and vector flow snakes have been applied to segment skin lesions \cite{50, 21, 46}. Behavior of the active contour model (snake) is governed by minimizing the energy function that contains internal terms (smoothness/tension) and image terms (gradient flow around the boundary).

Statistical region merging (SRM) is another approach which is used to segment the skin lesion in dermoscopic images \cite{12}.

The combination of some of these methods in association with the supervised or unsupervised machine learning methods provided interesting results. Iyatomi et al. described a method called the dermatologist-like tumor extraction algorithm (DTEA) \cite{28} which is based on thresholding followed by iterative region growing. In the J-image segmentation algorithm (JSEG) \cite{10} which is provided by Celebi et al., the computational time is reduced by incorporating approximate lesion localization and searching the border neighborhood rather than the whole image. A multiscale region-growing method is then used to merge the resulting $J$-images into a final segmentation. Zhou et al. added a spatial constraint as a feature into cluster analysis of pixels and used k-means++ algorithm (KPP) \cite{5} for segmenting the image \cite{58}. The threshold fusion algorithm (FSN) \cite{11} takes the results of several thresholding algorithms and fuses them using a Markov model to arrive at a final segmentation. Recently, Wighton et al. employed a supervised learning model to segment the lesion by learning the model parameters and computing the maximum likelihood over the pixels in the unseen images \cite{53, 52}. Random walker algorithm \cite{54} is also employed to segment the skin lesion in dermoscopic images. In this method, the seed point properties for lesion and background pixels are learnt and used to fully automate the random walker algorithm for skin lesion segmentation. Tenenhaus et al. \cite{51} used intensity values at multiple
scales and logistic regression to segment images. They achieve an accuracy of 75%.

Some methods involve artificial intelligence and heuristic methods to improve the segmentation procedure. Donadey et al. [18] used heuristic methods to select points within the lesion and create intensity profiles to train a neural network for border prediction on unseen images. They do not report any quantitative or comparative results. Maglogiannis et al. [34] used thresholding in association with heuristic methods to segment and characterize the skin lesions. Roberts et al. [43] employ many standard image processing primitives (morphological operations, logical operations, thresholding, edge filtering, etc.) and genetic programming to evolve the segmentation algorithms. Quantitative results are reported graphically, but it appears that approximately 60% of the lesions are segmented with a sensitivity and specificity greater than 90%.

2.3 Lesion Diagnosis

For the conventional use of dermoscopy without computer assistance, dermoscopists have proposed different scoring methods that facilitate the diagnostic process. These methods demonstrate how experts diagnose the skin conditions. Some of the research in automated skin lesion diagnosis attempts to automate these procedures.

The methods described below are developed for skin lesion diagnosis [3]. These methods are intended to be performed with a dermoscope, except the clinical ABCD rule which is applied on clinical images, which are skin lesion images captured by a still or video camera.

2.3.1 Scoring methods

- The (clinical and dermoscopy) ABCD rule: The clinical ABCD rule is the most well-known and easy to perform method provided by Friedman et al. [22] in 1985. It was designed to increase the self-awareness of melanoma amongst the general population as well as promote self-examinations. In this method four main clinical characteristics of the skin lesion are evaluated: (a)symmetry, (b)order irregularity, (c)olor variegation, and (d)iameger. The ABCD rule of dermoscopy [49] is a similar approach which uses dermoscopic images and can only be applied on melanocytic lesions. Four similar criteria for this method are: (a)symmetry, abrupt cutoff of the pigment pattern at the (b)order, differential (c)olors, and differential (d)ermoscopic structures. Some computer-aided diagnosis researchers have taken advantage of this method in order to
automate the diagnosis procedure. Lee et al. [31] developed a method for measuring the irregularity of the border of the lesion. In [59] the irregularity index is calculated by introducing a centroid distance diagram (CCD). This is done by connecting the centroid of the lesion to the boundary and drawing a centroid distance curve based on the length of lines connecting centroid to the boundary of the lesion; then features are extracted by characterizing the curve. Ng et al. [39] studied asymmetry measurement over the fuzzy borders. The circular index or compactness index (CI) [9] is one of the most popular and easy to compute border irregularity descriptors. Manousaki et al. [36] have used color texture information for skin lesion analysis.

- **7-point checklist:** In the 7-point checklist method [2], seven dermoscopic structures are used to evaluate the skin lesion, although, the weights assigned to the features are different. These features are based on the shape and the texture of the pigmented lesion. Three major criteria (*atypical pigment network*, *gray-blue areas* and *atypical vascular pattern*) and four minor criteria (*streaks*, *blotches*, *irregular dots and globules* and *regression pattern*) are defined and are scored as absent or present. If present the major criteria are multiplied by two and the minor criteria is multiplied by one. The final score is defined as the summation of these points. If this score is greater than or equal to three, the lesion is classified as melanoma. Betta et al. [7] extracted some of these patterns and use the 7-point checklist to classify the lesion.

Table 2.1 summarizes the scoring methods and the weights assigned to every feature.

### 2.3.2 Pattern recognition methods

- **Pattern analysis:** Pattern analysis [29] is the first dermoscopic algorithm for dermatologists presented in 1987. It provides the initial definitions of specific patterns, however, these definitions have been modified since that time. These patterns can be global or local. The global patterns are: *reticular*, *globular*, *cobblestone*, *homogeneous*, *starburst*, *parallel*, *multicomponent*, and *non-specific*. The local patterns are: *pigment network*, *dots/globules*, *streaks*, *blue-whitish veils*, *regression structures*, *hypopigmentation*, *blotches*, and *vascular structures*. Fig. 2.1 shows two images highlighting examples of these local structures. Sadeghi et al. [45] model the pigment network pattern over the skin lesion using graphs and finding cyclic subgraphs in the extracted graphs. Wighton et al. [53, 52] propose a supervised learning method in which the color-based
features for pigment network are used to train a maximum a posteriori (MAP) model.

This model is then used to detect the existence of the pigment network pattern in unseen images. Betta et al. [7] measure streaks and pigment network pattern features in two parallel pipelines for lesion diagnosis. In order to detect the presence of streaks pattern over the lesion, they extract the border of the lesion and measure the irregularity of the border. The drawback of this method is the sensitivity to the quality of the extracted lesion border. They also characterize the pigment network using chromatic information over the image in HSI color space.

• **Menzies’ method:** In the Menzies’ method [38] features are divided to negative and positive categories. The negative features are *symmetry of pigmentation pattern* and *presence of only a single color*. Nine positive features are also defined as *blue-white veil, multiple brown dots, pseudopods, radial streaming, scarlike depigmentation, peripheral black dots/globules, multiple colors, multiple blue-gray dots*, and *broad pigment network*. If a lesion has neither of the negative features and at least one of the positive features, then the lesion is classified as melanoma. This method is an attempt
Figure 2.1: Two dermoscopic images of melanoma illustrating the local patterns (dermoscopic structures). The points assigned to structures in these images are using 7-point check-list method for scoring. Images taken from [3].

to simplify the pattern analysis method [29].

- **Texture analysis:** The texture can be labeled as 'fine', 'rough' and 'irregular'. Texture analysis is an attempt to measure these notions. In [42] an example of using wavelet transform to extract texture characteristics is provided. In this method a tree structure is constructed by decomposing the image using wavelet transform. The decision for further decomposition is done based on an energy function at every node of the tree.

All the methods discussed above are explained and compared quantitatively in [35].
Chapter 3

Lesion Segmentation

Skin lesion segmentation is an essential preprocessing step in most Automated Skin Lesion Diagnostic (ASLD) systems. In some diagnostic methods such as clinical and dermoscopic ABCD rules, the extracted border is used to compute some features such as asymmetry, border irregularity and diameter of the lesion. In other applications, by segmenting the lesion, we can be assured that the image processing algorithm is only considering the lesion for feature extraction.

We hypothesize that the quality of the segmentation of the skin lesion can be increased significantly if the growth pattern of the lesion is modeled and incorporated properly.

In our method, the spatial constraint provided by the growth pattern of the lesion is used in two parallel pipelines as demonstrated in Fig. 3.1. In the upper pipeline the spatial constraint is used to extract spatial features that will directly be added to the feature set to segment the lesion. In the lower pipeline the spatial constraint is used to decompose the image to construct a tree structure that will be employed to extract color based features.

3.1 Feature Extraction

As the spatial feature is used in both pipelines in Fig. 3.1, first the upper pipeline will be explained; then this will be used to describe the steps for the tree structure construction and color based feature extraction in the lower pipeline.
Figure 3.1: Overview of feature extraction procedure. Color based and space based features are extracted simultaneously and used in the segmentation algorithm.

### 3.1.1 Extraction of Spatial Features

The distribution of the melanin over the skin layers and the resulting color variety in dermoscopic images provides the possibility of incorporating spatial information to the segmentation procedure.

**Extraction of Weighted Center of Dark Pixels**

In contrast to Zhou et al. [58] who make the assumption that the center of the lesion is the same as the center of the image, we provide a more general statement: the lesion center should be calculated with respect to the position of the dark spots in the lesion. This is calculated by taking a specific number of dark pixels in the image and calculating a weighted average of coordinates of these pixels. The center obtained in this way can be interpreted as the center of the growth of the lesion. Fig. 3.2 illustrates the overview of our method for extracting lesion center point.

In order to calculate the position of the center point, the dermoscopic sRGB image is converted to gray-scale image using the following equation [1]:

\[ I = 0.2989 \times R + 0.5870 \times G + 0.1140 \times B \]  

Then \( I \) is normalized between 0 and 1 and the darker pixels with \( I \leq I_d \) are extracted (see Section 3.3 for the details about the parameter settings). As a result, \( X \) and \( Y \) which are two sets of coordinates of darker pixels are defined as follows:

\[ (X, Y) = \{(x, y) | I_{x,y} \leq I_d \} \]  

(3.2)
Then, \((x_C, y_C)\) the coordinates of the center point are calculated as follows:

\[
x_C = \frac{1}{N} \times \sum_{i=1}^{N} x_i \quad \text{and} \quad y_C = \frac{1}{N} \times \sum_{i=1}^{N} y_i
\]

(3.3)

where \(N = |X| = |Y|\). Simply, \((x_C, y_C)\) is the centroid of the dark pixels.

### Computing Radial Distance

The radial distance \(D_{x,y}\) is computed for every pixel in the image by calculating the Euclidean distance between pixels and the extracted center, where

\[
D_{x,y} = \sqrt{(x - x_C)^2 + (y - y_C)^2}
\]

(3.4)

Consequently, all the pixels on the same circle centered on the extracted center point, will have the same radial distance. The goal is to include this distance as a feature for segmentation and also in the clustering stage described in next section. This will lead to layered clusters of pixels which represent the growth pattern of the spot centered on the point that is the weighted average over the dark pixels.

#### 3.1.2 Image Decomposition and Extraction of Color Based Features

Extraction of the color based features is done on a multi-scale tree-structured model of the lesion growth pattern. We build this model by performing three steps as presented in Fig. 3.3. These three steps are repeated four times resulting in a tree-structure with four layers. The first two steps are similar to the steps described in section 3.1.1, although, these steps are repeated for every resulting sub-cluster. In other words, for every sub-image, a new center point is extracted and new values of radial distance are assigned to pixels.

### Clustering stage

In the first iteration there is only one cluster containing all pixels of the image. Color features for the clustering stage are set to green and blue channel from RGB color-space. The red channel is eliminated in order to reduce the effect of the blood vessels in the clustering stage. Therefore, by adding radial distance \((D)\) to the feature set in the clustering stage, the feature set \(\{G, B, D\}\) is obtained. These features are used in the well-known \(k−\)means [33] clustering algorithm to cluster pixels to two (dark and light) clusters at every iteration.
CHAPTER 3. LESION SEGMENTATION

In the next iteration, every cluster is re-clustered to dark and light clusters independently. This is repeated three times. At every iteration, features are normalized and multiplied by different weights separately. The weights are assigned empirically to reduce the effect of the spatial features, as assigning high values to spatial features will lead to unnaturally rounded clusters in lower layers of the tree. The details about parameter settings and normalization are provided in section 3.3.

In this stage, for every disjoint cluster we add a corresponding node to the tree structure. Thus, the root in the tree corresponds to a cluster containing all pixels of the image. The second layer contains two groups of nodes corresponding to light and dark clusters. This structure is retained through four layers of the tree.
CHAPTER 3. LESION SEGMENTATION

This tree structure has two important properties: i) summation of the pixels at every layer of the tree is equal to the number of pixels in the image, and ii) every pixel belongs to exactly one cluster at every layer of the tree. These two properties of the tree lead to a novel approach in extraction of the features for the lesion segmentation task. Decomposing the image into such a tree-structure provides a rich description over which many salient features can be extracted.

Feature extraction

We use some simple, but powerful features for lesion segmentation task. First, the average of red, green, and blue intensity channels is calculated over the pixels in every cluster as shown in Fig. 3.4(b). To remove noise artifacts, in the next step, mean values are blurred by a $15 \times 15$ Gaussian filter with $\sigma = 5$ as seen in Fig. 3.4(c). For every pixel, the corresponding values from every color channel in every layer of the tree is extracted and used to construct the feature vector of length 12.

3.2 Supervised Learning Based Segmentation

So far we have obtained 12 color features (mean over red, green and blue over four layers) and one spatial feature (radial distance). Gathering them all in one feature vector results in a vector of length 13 for every pixel in the image. Extracted feature vectors are used to segment the skin lesion using a general supervised learning model for ASLD [53], where the label set for the segmentation task in this model is $L = \{\text{'lesion'}, \text{'background'}\}$.

In our method features are assigned based on the clusters that contain information about neighboring pixels in the same cluster. In addition, smoothing the features after the clustering stage helps the pixels lying around border of the clusters to share the information with the pixels in the neighboring clusters. Therefore, all relevant dependencies are captured. Consequently, maximum a posteriori estimation model is a proper model for our purpose.

The first stage in the supervised learning model is the training stage in which parameters for the multivariate Gaussian distribution are estimated for the labeling phase. The posterior probabilities $P(p|l_i)$ (i.e. probability of a pixel $p$ given the label $l_i$ in the label set $L$) are modeled as multivariate Gaussian distribution. In the second stage which is the labeling stage, labels are assigned to the pixels of previously unseen images using maximum likelihood
Figure 3.4: (a) the original dermoscopic image. (b) the mean values over three color channels in four layers of the decomposition tree, and (c) the smoothed mean values.
estimation

\[ l^* = \arg \max_{l_i \in L} (\log P(p|l_i) + \log P(l_i)) \] (3.5)

As in this case there are two classes \( l_1 = \text{lesion} \) and \( l_2 = \text{background} \), the following constraint is considered:

\[ P(l_1) + P(l_2) = 1 \] (3.6)

The ROC curve is obtained by varying the values of \( P(l_1) \) and \( P(l_2) \) according to constraint in equation above. Equivalently, the ROC curve could be generated using a simple threshold method over the pixel probability map obtained using the following equation:

\[ \ell_i(p) = \frac{P(p|l_i)}{P(p|l_1) + P(p|l_2)} \] (3.7)

where \( \ell_i(p) \) is the likelihood of each label [53].

Ten-fold cross-validation is used to validate the method.

### 3.3 Implementation Details

This method is implemented in MATLAB and its image processing toolbox is employed to facilitate the implementation. The parameters in the implementation are empirically chosen based on trial and error; however, the provided method is not significantly sensitive to these parameters’ values. The threshold value \( I_d \) for the center extraction and the spatial feature extraction step is set to 0.25. Incorporating lighter pixels to this process by increasing this threshold value will lead to a slight change in the resulting center point. This change will affect the values of the radial distance and finally the clusters. As this change is trivial, the final color features which are obtained by taking the average over the pixel intensities in the clusters will not vary effectively. This confirms the robustness of our provided algorithm.

During the decomposition of the image, we normalize the values of the color components and radial distance between 0 and 255. In addition, in order to avoid artificially rounded borders of the clusters, we assign less weight to the radial distance feature \( D \) than the chromatic features. The weights assigned to color components (green and blue) is set to 2 and the weight of radial distance \( D \) is set to 1. The lower weight assigned to the radial distance also increase the robustness to the extracted center at the image decomposition stage.
CHAPTER 3. LESION SEGMENTATION

Based on the experiments executed on different depths (described in section 3.5.4), the depth of the tree is set to four to simultaneously keep the complexity and running time low and the accuracy of the method high.

3.4 Material

A dataset containing 116 images of which 100 were considered challenging from dermoscopic atlases [4, 3] is used. An image is considered challenging if at least one of the following conditions are true [53]:

i) the contrast between skin and lesion is low,

ii) there is significant occlusion by oil or hair,

iii) the entire lesion is not visible (partial lesion),

iv) the lesion contains variegated colors,

v) the lesion border is not clearly defined.

Each image is segmented by a dermatologist to provide the ground truth, and pixels are labeled from the set $L = \{ \text{lesion'}, \text{background'} \}$.

3.5 Results and Discussion

3.5.1 Comparison with other methods

We present our segmentation results and compare them to six other skin lesion segmentation techniques: G-LoG/LDA [53], KPP [58], JSEG [10], DTEA [28], SRM [12], and FSN [11]. We have used the authors’ implementation of their methods on the same dataset to evaluate results.

Examples of segmentation results from our method are provided in Fig. 3.5. In this figure the first row is an easy image to segment and the next six rows are challenging images containing lesions occluded with hair, partial lesions and low contrast borders of the lesions. Some of the artifacts such as hair and noise can be removed using existing algorithms [32, 40, 41, 47, 55]. This might help to improve the segmentation results, although, our method performs gracefully on such images.

Similar to G-LoG/LDA, the output of our method is a probability map of the pixels. Consequently, by changing the threshold of the segmentation over this probability map the ROC curves are obtained (see Fig. 3.6). The output of other five methods is binary segmentation of lesions; therefore, we use the nearest point on the ROC curve to compare the sensitivity/specificity pairs (see Table 3.1). In this table, $\Delta$Sens. and $\Delta$Spec. show the difference between the sensitivity/specificity of methods with the closest pair on ROC.
## Chapter 3. Lesion Segmentation

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Our method</td>
<td>0.954</td>
<td>0.881</td>
<td>0.903</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>G-LoG/LDA</td>
<td>0.948</td>
<td>0.880</td>
<td>0.887</td>
<td>0.006</td>
<td>0.001</td>
<td>0.016</td>
</tr>
<tr>
<td>KPP</td>
<td>N/A</td>
<td>0.717</td>
<td>0.790</td>
<td>N/A</td>
<td>0.164</td>
<td>0.025</td>
</tr>
<tr>
<td>DTEA</td>
<td>N/A</td>
<td>0.641</td>
<td>0.987</td>
<td>N/A</td>
<td>0.035</td>
<td>-0.001</td>
</tr>
<tr>
<td>SRM</td>
<td>N/A</td>
<td>0.770</td>
<td>0.946</td>
<td>N/A</td>
<td>0.002</td>
<td>0.024</td>
</tr>
<tr>
<td>JSEG</td>
<td>N/A</td>
<td>0.678</td>
<td>0.986</td>
<td>N/A</td>
<td>-0.002</td>
<td>-0.001</td>
</tr>
<tr>
<td>FSN</td>
<td>N/A</td>
<td>0.812</td>
<td>0.935</td>
<td>N/A</td>
<td>0.012</td>
<td>0.017</td>
</tr>
</tbody>
</table>

Table 3.1: Comparison of results of our method with other six methods.

The area under the curve is only used to compare our method with G-LoG/LDA in the column ∆AUC. The sensitivity/specificity reported in the table for our method and for G-LoG/LDA is the closest point to (0, 1) on the ROC curve.

Our method outperforms G-LoG/LDA, KPP, DTEA, SRM, and FSN, and is comparable to JSEG’s performance.

### 3.5.2 Use of different color spaces

In Section 3.1.2, we stated that \{G, B, D\} is used for clustering pixels into sub-clusters. We have also done further analysis of the method using different color spaces. The following feature sets were evaluated: \{L*, a*, b*, D\}, \{H, S, I, D\} and \{G, B, L*, a*, b*, H, S, I, D\} (all the color components).

We used the code provided in [44] to convert the RGB color space to L*a*b* color space. RGB is converted to HSI using the formulae provided in [25]:

\[
H = \begin{cases} 
\vartheta & \text{if } B \leq G \\
360 - \vartheta & \text{if } B > G 
\end{cases} \quad (3.8)
\]

where

\[
\vartheta = \cos^{-1} \left\{ \frac{\frac{1}{2}[(R - G) + (R - B)]}{[(R - G)^2 + (R - B)(G - B)]^{1/2}} \right\} \quad (3.9)
\]

\[
S = 1 - \frac{1}{R + G + B} \min R, G, B \quad (3.10)
\]
\[
I = \frac{1}{3}(R + G + B) \quad (3.11)
\]
Figure 3.5: Example of easy (first row) and challenging (second to seventh row) images for segmentation. Images in first column are original dermoscopic images, second column demonstrates resulting probability maps obtained using the learning model, our segmentation results are provided in third column, and it is compared with the ground-truth segmentations (red dashed lines).
CHAPTER 3. LESION SEGMENTATION

Figure 3.6: ROC curve demonstrating our method’s segmentation results compared with six other methods: G-LoG/LDA [53], KPP [58], JSEG [10], DTEA [28], SRM [12], and FSN [11].

Results are provided in Fig. 3.7 and Table 3.2. The best result is obtained using all color components, although we reported the results of using \{G, B, D\} in Fig. 3.6 to keep the feature set simple.

3.5.3 Use of different feature sets

For further analysis of the strength of the feature set that is used to segment the lesion, the features are tested separately. Fig. 3.8 provides the ROC curve for the segmentation using two different feature sets: non-smoothed color features without incorporating spatial features, smoothed color features without incorporating spatial features. Table 3.3 shows the performance of these two feature sets compared with the final results provided in top row of Table 3.1.

It is seen that incorporating radial distance into the feature sets provides a more accurate segmentation, likely because of including the lesion shape prior in the procedure that also leads to reducing the effect of occluding hair and artifacts.
3.5.4 Use of different depths in the tree

In all the results reported so far, the depth of the tree structure was set to 4 as mentioned in Section 3.3. We evaluated the results of lesion segmentation using different depths for the tree structure in the image decomposition stage.

Fig. 3.9 and Table 3.4 shows that the quality of lesion segmentation increases when using higher depths of the tree. As these changes are not linear, there is no significant change in the AUC of ROC curve when using depths of 4, 5, 6 and 7. On the other hand, the complexity of the tree (i.e. number of nodes of the tree) increases exponentially by increasing the depth of the tree. Therefore, choosing 4 as the depth of the tree for our method is a reasonable choice.

3.6 Summary

In this chapter we have developed a skin lesion segmentation method in dermoscopic images which is inspired by the biology of the skin and its growth pattern. The implicit
<table>
<thead>
<tr>
<th>Feature set</th>
<th>AUC</th>
<th>Sens.</th>
<th>Spec.</th>
</tr>
</thead>
<tbody>
<tr>
<td>All Features</td>
<td>0.956</td>
<td>0.890</td>
<td>0.901</td>
</tr>
<tr>
<td>G and B</td>
<td>0.954</td>
<td>0.881</td>
<td>0.903</td>
</tr>
<tr>
<td>L<em>a</em>b*</td>
<td>0.949</td>
<td>0.867</td>
<td>0.897</td>
</tr>
<tr>
<td>HSI</td>
<td>0.952</td>
<td>0.877</td>
<td>0.900</td>
</tr>
</tbody>
</table>

Table 3.2: Comparison of results of our method using different color spaces in the clustering stage.

<table>
<thead>
<tr>
<th>Feature Configuration</th>
<th>AUC</th>
<th>Sens.</th>
<th>Spec.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Smoothed Mean + D</td>
<td>0.954</td>
<td>0.881</td>
<td>0.903</td>
</tr>
<tr>
<td>Smoothed Mean</td>
<td>0.943</td>
<td>0.871</td>
<td>0.895</td>
</tr>
<tr>
<td>Non-smoothed Mean</td>
<td>0.934</td>
<td>0.860</td>
<td>0.884</td>
</tr>
</tbody>
</table>

Table 3.3: Comparison of results of our method using different configuration of the features.

<table>
<thead>
<tr>
<th>Depth of the tree</th>
<th>AUC</th>
<th>Sens.</th>
<th>Spec.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>0.932</td>
<td>0.856</td>
<td>0.868</td>
</tr>
<tr>
<td>3</td>
<td>0.950</td>
<td>0.885</td>
<td>0.886</td>
</tr>
<tr>
<td>4</td>
<td>0.954</td>
<td>0.881</td>
<td>0.903</td>
</tr>
<tr>
<td>5</td>
<td>0.956</td>
<td>0.884</td>
<td>0.906</td>
</tr>
<tr>
<td>6</td>
<td>0.956</td>
<td>0.889</td>
<td>0.903</td>
</tr>
<tr>
<td>7</td>
<td>0.956</td>
<td>0.888</td>
<td>0.904</td>
</tr>
</tbody>
</table>

Table 3.4: Comparison of results of our method using different depths in the tree.
Figure 3.8: ROC curve demonstrating our method’s segmentation using different configuration of features.

rough segmentation of sub-images during the spatially-constrained, growth-pattern-based, decomposition of the image, leads to the proper feature extraction framework. The results show that our proposed segmentation method outperforms four state of the art skin lesion segmentation methods and performs competitively with another method.

The strength of our method is the robustness to artifacts such as noise and hair; however, removing these artifacts might improve the segmentation accuracy.

As a future work, we will examine different decomposing features as well as segmentation features. The extracted tree structure provides a framework in which various features can be incorporated from different aspects. In this work, we used simple features to convey the strength of our tree-structured framework.
Figure 3.9: Area Under Curve (AUC) of ROC curve using different depths in the tree.
Chapter 4

Lesion Diagnosis

We hypothesize that the growth pattern of the skin lesion can also be used to diagnose the malignancy of the lesion, as the irregularity of the distribution of dark colors over the lesion can reflect the irregularity of the growth of the lesion. Therefore, distribution can be used as a feature to diagnose the lesion type. We use a multi-level tree structure model in a different way than for lesion segmentation. The tree structure can model the growth in reverse from the center of dark spots. This framework allows us to study: i) the radial growth pattern of the individual dark spots, and ii) the irregularity of distribution of the dark spots over the lesion, that will be reflected in the complexity of the tree structure.

4.1 Constructing the Tree Structure

Our diagnosis method takes a top-down approach in which every skin lesion image is repeatedly sub-divided into sub-images through a clustering procedure over the pixels similar to procedure described in Section 3.1.2. At every iteration of the sub-division, the color features and a spatial coordinate feature for all pixels in the sub-image are rescaled and clustered into two clusters representing light and dark pixels. Similar to the segmentation method, we are constructing a multi-scale tree structure such that every sub-image corresponds to a node in the tree and its children are obtained by rescaling the image features, and re-clustering pixels. In contrast to the method described for lesion segmentation, for diagnosis we keep only the darkest clusters of pixels and create a new sub-image. Therefore, in this diagnosis tree we shrink the image clusters by pruning the light pixels. The process
4.1.1 Preprocessing

As for segmentation, one of the main artifacts that significantly affects our lesion diagnosis method is the presence of occluding dark hairs over the lesion shown in Fig. 3.5. This can mislead the cluster centers and consequently the clustering procedure. Therefore, as a preprocessing step, we removed dark hairs using Dullrazor® [32]. Fig. 4.2 demonstrates some examples of the images with hairs occluding the lesion and the results of hair removal using Dullrazor®.

4.1.2 Extraction of Weighted Center of Dark Pixels

This section of the procedure is exactly the same as the method provided in section 3.1.1 for lesion segmentation. First, the RGB image is converted to a gray-scale image using the same provided equation; then the darker pixels with intensities less than 0.25 are taken, and the center point is calculated based on the selected pixels’ coordinates.

4.1.3 Computing Radial Distance

Radial distance is computed in exactly the same way as provided in section 3.1.1 for segmentation. This is a simple Euclidean distance from the extracted center point to every pixel on the image.
CHAPTER 4. LESION DIAGNOSIS

4.1.4 Clustering and Shrinking

In the first iteration, we have the original image as the first sub-image. Therefore, the first sub-set of pixels contains all pixels in the image. This sub-set is clustered into two clusters using the k-means [33] clustering algorithm. In the clustering stage, a four-dimensional normalized feature set containing three color components and the previously computed radial distance is fed to the algorithm with different weights assigned. Empirically, we chose Hue-Saturation-Intensity (HSI) color space to build the feature set. Results of diagnosis using different color spaces are also provided in results section.

First, the RGB color space is converted to HSI color space using equations given in [25] (see equations (3.8),(3.9),(3.10), and (3.11)). Thus, for pixel \((x,y)\) the feature set is \(\{H_{x,y},S_{x,y},I_{x,y},D_{x,y}\}\). After obtaining two clusters, the darker cluster is characterized and kept by looking for the highest \(I\) value in the resulting clusters’ color-map. The new sub-set of pixels in the dark cluster delimits regions over the image. These regions undergo hole filling and opening morphological operations and define our final sub-images. Every sub-image obtained so far will be entered in the loop independently and all aforementioned three steps will be repeated for them and for their descendant sub-images.
4.1.5 Termination Conditions

In order to terminate the procedure above, we use 4 termination conditions, and sub-image decomposition ends when at least one of these four conditions is true: i) number of pixels in the obtained sub-image is less than a constant value, ii) color variance over the blue and green intensity channels in a sub-image is less than a threshold, iii) descendant of a sub-image has not significantly changed in comparison to its parent, or iv) the depth of the implicitly constructed tree is more than a limit.

The termination condition parameters are discussed in section 4.3 as implementation details.

4.1.6 Tree Structure Construction

The above process can be interpreted as a depth first search (DFS) over a tree. When a sub-image breaks into multiple sub-images, each sub-image is traversed until termination, then the next sub-image is traversed and so on. Hence, the main image corresponds to the root of the tree; its sub-images form its children in the second layer; the third layer consists of sub-images of the second layer; and so forth. Fig. 4.3 illustrates samples of the extracted tree structure, for a benign and a malignant lesion.

In contrast with the tree structure for segmentation, the length of the different paths from root of the tree to the leaves are not necessarily equal. Based on the definition of the termination conditions, this length could reflect the size of the sub-image, variation of color intensities, and tendency of pixels of a sub-image to stay together in one cluster rather than breaking into two clusters.

Our hypothesis is that if the complexity of the tree structure is high, the probability of malignancy is also high. Complexity can be defined as the number of nodes and the degree at every node. This can be seen in examples provided in Fig. 4.3.

4.2 Feature Extraction

The tree structure framework allows us to extract a variety of features, based on the tree itself (graphical aspect) or the sub-images at each node of the tree (textural and geometrical aspect). In this study some preliminary features are extracted and examined separately and together to illustrate the strength of each aspect.
Figure 4.3: (a) and (c) illustrate decomposition of a malignant and benign lesions respectively. Their corresponding tree structures are shown in (b) and (d). The number of branches and leaves in the benign lesion is less than that of malignant lesion.

4.2.1 Tree complexity

The number of nodes and leaves in the tree, and the depth of the tree are very basic graphical features that can be used in a classification procedure. As can be seen in Fig. 4.3, these features reflect the complexity of the tree structure to some extent.

4.2.2 Border features

Compactness index [24] is chosen as a geometrical feature which reflects the irregularity of the border of the sub-image. It is calculated as follows

\[ CI = \frac{P^2}{4\pi A} \]  

(4.1)

where \( P \) is the perimeter of the object and \( A \) is the object area. The extracted compactness index is stored in an array, where element \( i \) of the array corresponds to depth \( i + 1 \) of the tree. The \( CI \) is calculated for all the nodes in depth \( i \) and is summed up and multiplied by \( \frac{N-i}{N-1} \) which is proportional to the depth where depth limit is \( N \). Borders of sub-images which are placed close to the root of the tree are more similar to the border of the lesion in
the main image. As a result, they are more reliable and their corresponding nodes should be
given more weight than nodes close to leaves. The results of using these features separately
are discussed in Section 4.5. The CI is not calculated for the root as it is the main image
with square border. Thus, the length of the array should be one less than the maximum
possible depth of the tree which is defined in the loop termination conditions. Other features
such as border irregularity index [31] can be extracted and used instead of CI; however,
their time cost is higher than calculating CI.

4.3 Implementation Details

We implemented the algorithm using the MATLAB’s image processing toolbox. In this thesis,
thresholds and parameters of the algorithm are experimentally chosen, as the algorithm
is not very sensitive to these values. As for segmentation, extracting the center point as
the first step in every iteration of the loop, is not sensitive to the threshold chosen for the
gray-scale image intensities. This threshold \( I_d \) is set to 0.25. Increasing this value will
cause incorporation of more pixels over the image and change the center point slightly. This
change will affect the value of \( D_{x,y} \). As the number of clusters in the clustering stage is
set to two, we are assured that the darker cluster includes all the dark regions that we are
interested in. Consequently, the final tree structure will have a similar shape. This is an
advantage of our algorithm.

The weights assigned to the H, S, and I are set to 2 and the weight of radial distance
\( D \) is set to 1 in the clustering stage. Higher weighting on \( D \) results in rounded borders of
sub-images in the nodes close to the leaves. The low weighting on \( D \) and higher weighting
on color components reduce the sensitivity to the threshold value for center extraction step.

Values of parameters and thresholds for termination conditions are as follows: \( i) \) area
of sub-images should be more than 500 pixels, \( ii) \) the variance over the both blue and green
channels should be greater than 40 when the blue and green channel values are between
0 and 255, \( iii) \) difference in area between two consecutive nodes should be more than 50
pixels, and \( iv) \) the maximum allowed depth is set to 10.
CHAPTER 4. LESION DIAGNOSIS

4.4 Materials

In order to evaluate the extracted features, a dataset of 410 images randomly taken from [4, 3] is created and used. These images were picked out of 763 images to provide sufficient malignant lesions in the data set for machine learning algorithms. This was done without visual inspection and only by looking at the diagnosis of lesions ordered randomly. In this dataset, we have 112 malignant lesion images (containing melanoma and pigmented basal cell carcinoma (BCC)), and 298 benign lesion images (containing atypical, congenital, compound, dermal, Spitz, and blue nevi; seborrheic keratosis; and dermatofibroma). Our ground truth is based on dermatologists’ diagnosis provided in [4, 3].

4.5 Results

The goal is to classify the lesions to either malignant or benign classes. WEKA [27] which is a machine learning tool is used to classify the images. 3-layer perceptron and AdaBoost are chosen as classifiers. The parameters for 3-layer perceptron are set as follows: learning rate is set to 0.3, momentum is set to 0.2, training time is set to 500 and validation threshold is set to 20. The parameters of AdaBoost are set as follows: the number of iterations is set to 10, the seed is randomly generated and the weight threshold is set to 100.

Four different approaches for evaluating the method are employed.

4.5.1 Comparison with other feature sets

In the first approach, all the features which are computed in the feature extraction section are gathered in a 12-dimensional feature set (number of nodes, number of leaves, depth, and 9 CI components) and the resulting set is fed into the classifiers. The second evaluation is done by just using the graphical feature set (number of nodes, number of leaves, depth). In the third and fourth approaches, CI1 to CI3 and CI4 to CI9 are evaluated respectively to validate the weighting assignment to different layers in the method. In all these approaches, the validation method is set to ten-fold cross validation. The malignant and benign images are randomly chosen from separate classes and uniformly merged and distributed over the folds. Table 4.1 illustrates the classification results between malignant and benign classes for our dataset using two different classifiers and four different approaches. Fig. 4.4 and Fig. 4.5 provide the ROC curves of two methods obtained using 3-layer perceptron and
### Table 4.1: Results of classifying the data-set of 410 images using graphical and geometrical features in different layers of the tree.

<table>
<thead>
<tr>
<th>Feature set</th>
<th>Classifier</th>
<th>Precision</th>
<th>Recall</th>
<th>F-Measure</th>
<th>AUC of ROC</th>
</tr>
</thead>
<tbody>
<tr>
<td>All Features</td>
<td>3-layer perceptron</td>
<td>0.855</td>
<td>0.849</td>
<td>0.834</td>
<td>0.786</td>
</tr>
<tr>
<td>Graphical Features</td>
<td>3-layer perceptron</td>
<td>0.848</td>
<td>0.841</td>
<td>0.824</td>
<td>0.787</td>
</tr>
<tr>
<td>CI1 to CI3</td>
<td>3-layer perceptron</td>
<td>0.639</td>
<td>0.712</td>
<td>0.641</td>
<td>0.617</td>
</tr>
<tr>
<td>CI4 to CI9</td>
<td>3-layer perceptron</td>
<td>0.713</td>
<td>0.729</td>
<td>0.622</td>
<td>0.494</td>
</tr>
<tr>
<td>All Features</td>
<td>AdaBoost</td>
<td>0.829</td>
<td>0.832</td>
<td>0.817</td>
<td>0.745</td>
</tr>
<tr>
<td>Graphical Features</td>
<td>AdaBoost</td>
<td>0.835</td>
<td>0.837</td>
<td>0.823</td>
<td>0.776</td>
</tr>
<tr>
<td>CI1 to CI3</td>
<td>AdaBoost</td>
<td>0.692</td>
<td>0.732</td>
<td>0.685</td>
<td>0.637</td>
</tr>
<tr>
<td>CI4 to CI9</td>
<td>AdaBoost</td>
<td>0.596</td>
<td>0.722</td>
<td>0.614</td>
<td>0.490</td>
</tr>
</tbody>
</table>

These results explain the reason for assigning higher weights to CI at higher levels of the tree. Interestingly, the graphical features alone are performing almost as well as using all features together when using 3-layer perceptron classifier and performing better when using AdaBoost classifier. This illustrates the strength of the tree structure over the other methods that are only based on textural/geometrical features.

The ROC curves in this study are obtained using WEKA [27] machine learning software. Likely, the reason behind the more jagged ROC curve for AdaBoost is the low density of the grid search over the parameters of the classifier. The denser grid for the 3-layer perceptron classifier results in the smoother curves.

#### 4.5.2 Comparison with another method

The results obtained using all features is also compared to Betta et al.’s diagnostic method based on the streaks features [7]. We reimplemented this method in MATLAB and evaluated using the same dataset. In Betta’s method, the image is subdivided into 16 equal rectangular blocks and, like our method, the dark brown color is examined in HSI color space, though Betta uses it for detecting streaks. However, Betta’s method is very sensitive to the segmentation of the lesion. The results of comparison are provided in Table 4.2. The values reported for Precision, Recall, and F-measure are weighted average values based on the size of the class. Fig. 4.6 and Fig. 4.7 provide the ROC curves of two methods obtained using 3-layer perceptron and AdaBoost respectively. As before, the ROC curve for AdaBoost is
Figure 4.4: Receiver Operating Characteristic (ROC) curve of classification by employing different features using 3-layer perceptron classifier.
Figure 4.5: Receiver Operating Characteristic (ROC) curve of classification by employing different features using AdaBoost classifier.
Table 4.2: Results of classifying the dataset into malignant and benign classes using 12 features.

<table>
<thead>
<tr>
<th>Method</th>
<th>Classifier</th>
<th>Precision</th>
<th>Recall</th>
<th>F-Measure</th>
<th>AUC of ROC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Our Method</td>
<td>3-layer perceptron</td>
<td>0.855</td>
<td>0.849</td>
<td>0.834</td>
<td>0.786</td>
</tr>
<tr>
<td>Streaks Detection</td>
<td>3-layer perceptron</td>
<td>0.689</td>
<td>0.732</td>
<td>0.656</td>
<td>0.648</td>
</tr>
<tr>
<td>Our Method</td>
<td>AdaBoost</td>
<td>0.829</td>
<td>0.832</td>
<td>0.817</td>
<td>0.745</td>
</tr>
<tr>
<td>Streaks Detection</td>
<td>AdaBoost</td>
<td>0.639</td>
<td>0.724</td>
<td>0.619</td>
<td>0.642</td>
</tr>
</tbody>
</table>

Our method outperforms streaks detection method significantly using both classifiers. The weak results of the Betta et al.’s method may be because of the lack of precision of extracted borders using a simple thresholding method. In addition, our data set is a challenging data set for segmenting; therefore, methods that depend on the quality of the segmentation will fail to perform properly. Consequently, one important property of our diagnosis method is that there is no need for explicitly segmenting the lesions.

4.5.3 Comparison with different color spaces

Different color spaces are used to construct the tree structure and the results are compared to the result of using HSI color space. Table 4.3 provides the quantitative results of diagnosis using different color spaces. The ROC curves are also provided in Fig. 4.8 and Fig. 4.9. In these experiments, the red channel was ignored to reduce the effect of blood vessels in the lesion. For converting the RGB to the L*a*b* color space, the MATLAB code provided in [44] is employed.

4.6 Summary

This work is accepted and will be presented in second international workshop on Machine Learning in Medical Imaging (MLMI) in conjunction with MICCAI [30].

In this chapter we presented a novel approach in skin lesion diagnosis using the dermoscopic images inspired by the biology of the skin growth. The spatial constraints obtained from the growth pattern of the skin lesion are incorporated in the top-down iterative procedure of the clustering of the image pixels. This procedure provided a model of the growth
CHAPTER 4. LESION DIAGNOSIS

Figure 4.6: Receiver Operating Characteristic (ROC) curve of classification using our method and streaks detection method [7] using 3-layer perceptron classifier.

<table>
<thead>
<tr>
<th>Color space</th>
<th>Classifier</th>
<th>Precision</th>
<th>Recall</th>
<th>F-Measure</th>
<th>AUC of ROC</th>
</tr>
</thead>
<tbody>
<tr>
<td>HSI</td>
<td>3-layer perceptron</td>
<td>0.855</td>
<td>0.849</td>
<td>0.834</td>
<td>0.786</td>
</tr>
<tr>
<td>GB</td>
<td>3-layer perceptron</td>
<td>0.711</td>
<td>0.739</td>
<td>0.712</td>
<td>0.654</td>
</tr>
<tr>
<td>L<em>a</em>b*</td>
<td>3-layer perceptron</td>
<td>0.735</td>
<td>0.756</td>
<td>0.736</td>
<td>0.677</td>
</tr>
<tr>
<td>HSI</td>
<td>AdaBoost</td>
<td>0.829</td>
<td>0.832</td>
<td>0.817</td>
<td>0.745</td>
</tr>
<tr>
<td>GB</td>
<td>AdaBoost</td>
<td>0.675</td>
<td>0.722</td>
<td>0.673</td>
<td>0.608</td>
</tr>
<tr>
<td>L<em>a</em>b*</td>
<td>AdaBoost</td>
<td>0.714</td>
<td>0.744</td>
<td>0.704</td>
<td>0.654</td>
</tr>
</tbody>
</table>

Table 4.3: Table of results of classifying the dataset into malignant and benign classes using different color spaces in the clustering stage.
Figure 4.7: Receiver Operating Characteristic (ROC) curve of classification using our method and streaks detection method [7] using AdaBoost classifier.
Figure 4.8: Receiver Operating Characteristic (ROC) curve of classification using different color spaces in the clustering stage. The classifier is the 3-layer perceptron.
Figure 4.9: Receiver Operating Characteristic (ROC) curve of classification using different color spaces in the clustering stage. The classifier is the AdaBoost.
pattern. This model can be directly used to extract wide variety of features from different aspects in order to diagnose the skin lesion. In this work simple features were used and the promising results were obtained.

One of the strengths of our method is the ability to classify the lesion without explicitly segmenting the lesion. In most of the existing diagnostic methods, the lesion segmentation is a crucial step. Additionally, some methods are extremely sensitive to the quality of the extracted boundary.
Chapter 5

Conclusion

In this thesis we proposed a novel tree structure based framework inspired by the skin lesion growth pattern. The tree structure based framework is employed in two important tasks on the dermoscopic skin lesion image analysis with minor differences in the procedure of constructing tree structures between the segmentation method and the diagnosis method.

5.1 Skin lesion segmentation

In Chapter 3, we provided a new feature extraction framework for skin lesion segmentation. My contributions to this area of research are:

- The confirmation that incorporating the growth pattern of the skin lesion in the segmentation task in a proper way resulted in the improved quality of the lesion segmentation over other available methods.
- The attainment of a robustness to some preprocessing steps by including the spatial constraints to the procedure.

5.2 Skin lesion diagnosis

In Chapter 4, we designed and developed a new method for diagnostic feature extraction. My contributions are [30]:

- The design and development of a growth pattern model that provides useful diagnostic features.
• The proposal and evaluation of the fact that the irregularity of distribution of dark spots is a useful feature for diagnosis. We have shown that the complexity of the tree structured model reflects this distribution of dark spots, and evaluated this complexity to show it is a significant diagnostic feature.

5.3 Future work

The limitation of our proposed method is that it requires several parameters; although we have shown that the method is not significantly sensitive to the parameter tuning. In future work, these parameters can be learnt via a machine learning procedure.

The extracted tree structure provides a framework in which various features can be incorporated from different aspects. In this work, we used simple features to convey the strength of the provided model. Another avenue to explore in future, will be to examine different decomposing features as well as segmentation features.
Bibliography


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