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Melanoma Skin Cancer Segmentation with Image Region Growing Based on Fuzzy Clustering Mean

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Abstract **— Melanoma is the most common dangerous type of skin cancer. On the other hand, if found in an early stage, there is a high likelihood of cure. For that reason, various types of imaging techniques have been investigated. Dermoscopy is one non-invasive imaging technique for diagnosis. The accuracy of diagnosis using dermoscopy is very important and depends on the experience of dermatologists. Visual examination is a waste of time, so there is currently wide attention paid to the development of computer-aided diagnostic systems to aid the clinical evaluation of dermatologists. Image Segmentation is very important in digital-image processing and self-discovery, with an important role to play in solving many difficult problems, particularly those related to chronic diseases, such as skin cancer. Analysis of automatic dermoscopy images usually has three stages: a) feature selection and extraction, b) image segmentation, and c) feature classification.**

Keywords **— Melanoma Skin Cancer, Image region growing, Fuzzy C-mean**

I. INTRODUCTION

To achieve an active way to detect malignant melanoma early without doing unnecessary skin biopsies, digital image segmentation for skin lesions has been investigated. Among imaging techniques, dermoscopy is the most suitable for melanoma diagnosis. Image segmentation is very important in digital image processing and allows automatic discovery of the details of objects in important areas. This capability has an important role to play in solving many difficult problems, particularly problems related to many chronic diseases, such as skin cancer.

In [1] a prototype internet based melanoma screening system is improved because diagnostic accuracy is low in the hands of the dermatologist. 24-bits JPEG images are selected to use in diagnostic accuracy. These images are collected from four different university hospital and some criterias are omitted. Time consuming is not appropriate for this system. Dermatologist-like tumor area algorithm which is consisted with initial tumor area decision, region-realization, tumor area selection, region growing phases is used with the internet based system. Region growing is used especially to be big enough as dermatologist-drawn. The aim is to determine benign or malignant, and to find estimated malignant percentage. With this system, SE (malignant) and SP (benign) values are best for each ANN classifier (87-93.1%). Conventional algorithm is compared with dermatologist-like algorithm. Comparing the result, SE and SP values are better for this algorithm.

Color calibration and contrast are important for segmentation in dermoscopic images at border detection [2]. High contrast is appropriate for this purpose. When light is on the lesion, the accuracy of the segmentation is decreased. In preprocess, a normalized technique is named as automatic color equalization (ACE) is used to reduce different color pigments and increase the contrast. There is a difficult property by differing colors at the same image for segmentation. At the same time, low contrast occurred for poor segmentation. With the normalized technique, the contrast is improved in first stage of ACE. With the second part of the ACE, accuracy of brightness constant and color mapping increased. Actually, with the normalized technique (ACE), the improved image is closer to the accuracy of the lesion border and segmentation than original image by increasing contrast. In the red channel, the accuracy of border detection is better than blue or green. Lesion segmentation consists of two parts: iterative segmentation, co-operative neural network edge detection. These two technique is appropriate for different color images (RGB) and gray-tone images. In iterative segmentation, they used simple noise suppression method for decrease the effects of hairs, skin lines. After that,they applied an iterative to image segmention into N regions ,and they obtain the optimal threshold value. Pixels are seperated into regions by this value. With 3X3 pixels, we applied the second method on the regions and they achieved to remove unwanted things of image for segmentation. 5 edge is showed for example of second part of segmentation. As a result, three dermatologists drawn the segmentation by hands. When the error is wanted to find XOR is used for calculations by comparing automatic and handling drawn. They used firstly these two parts of segmentation and passing RGB color channels. The average error is shown by seperating and comparing these two methods with original image for accuracy. Iterative segmentation and co-operative neural network on RGB are better than the original image for segmentation in 100 dermoscopic images [2].

Thresholding method is compared using XOR for border detection and it achieved to be faster, higher accuracy than 9 state of the art methods [3]. Threshold is used to separate background and lesion in blue channel. To achieve this separation, statistical features are important for good performance. Different threshold methods are applied to

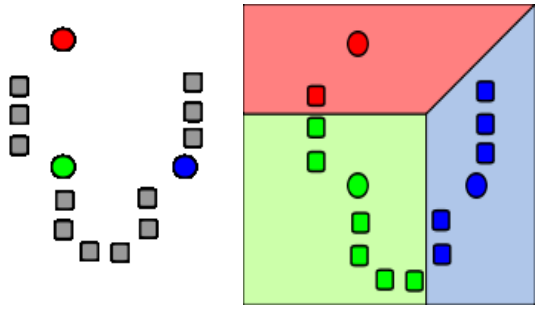
specific image and different accuracy is obtained. To solve this problem, an ensembles of thresholding methods are used in this article. To aim is here this thresholding methods must not good performance than the best thresholding method such as OTSU's method but must good for accuracy. Threshold fusion method is introduced. For fusion, energy functions are defined. For ensemble, 4 different threshold methods are used in fusion thresholding : Huang & Wang's fuzzy similarity method, Kapur et al.'s maximum entropy method, Kittler & Illingworth's minimum error thresholding method, Otsu's clustering based method. Using these threshold methods, thresholding set is obtained and spatial energy term is 0.1 here, initialize y by energy function for each pixel in fusion threshold method. By passing blue channel and filling output,removing bigger component, they obtained final fusion border region. Automated method is better than dermatologist-drawn to determine sharpest pigment changes. This method is applied on 90 images and 3 dermatologist are used. Dermatologist and this method are compared for good accuracy. This method may not be good performance in the presence of hair, skin lines.

II. MATERIALS AND METHODS

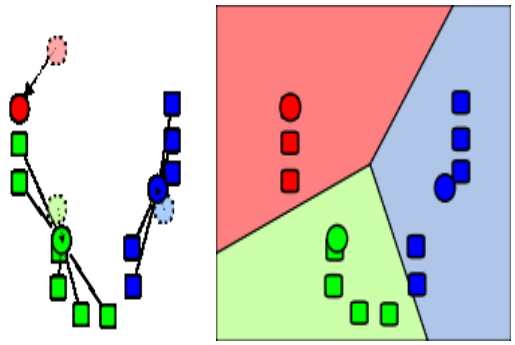
A. *Fuzzy clustering Mean*

In computer science, the Fuzzy C-Means algorithm is an unsupervised clustering algorithm that is an extension of the k-means clustering algorithm. In a generalized form he was introduced by Bezdek (1981)[4].

In c-Means clustering, the number of clusters C is initially determined (in k-Means clustering the number of clusters is denoted by k instead of C). In the first step random cluster centers vi (circles at the bottom of the graph) are defined. In the second step, each object (rectangle at the bottom of the graph) is assigned to the next cluster center. Then the (squared) distances between each object and its assigned cluster center are calculated and summed for all observations (J_{kmeans}). The goal is to make the value of J_{kmeans} as small as possible, i.e. find locations for the cluster centers so that the distance between each object and its associated cluster center is small. In the third step, the cluster centers are recalculated from the objects belonging to a cluster. In the fourth step, the next cluster center is assigned to each object. This method is iterated until a stable solution is found. As shown in figure 1, objects can be assigned to different clusters during the iteration process; Compare the graph to step 2 and step 4.



(a) (b)



(c) (d)

Figure 1. k-Means Clustering, (a) Step 1: Random choice of cluster centers, (b) Step 2: Assign the objects to a cluster center, (c) Step 3: Recalculation of cluster centers, (d) Step 4: Reassign the objects to a cluster center.

The disadvantage of k-means clustering is that each object is uniquely assigned to a cluster center in each step. This leads to the fact that the final solution can depend heavily on the choice of the location of the cluster centers at the beginning. Of course one is interested in a clear solution, as far as possible independent of the position of the cluster centers at the beginning.

In the fuzzy C-Means, therefore, each object is not uniquely assigned to a cluster center, but a set of weights (u_{1i}, …. ,u_{Ci}) is assigned to each object, which indicates how strongly the membership to a particular cluster is. For example, for the red object in step 2, the weights could be.

$u_{blue} = 0,1$ for the blue cluster

$u_{green} = 0,1$ for the green cluster and

$u_{red} = 0,8$ for the red cluster.

These weights are then also used to calculate the weighted distance to all cluster centers. Finally, objects close to a particular cluster center will have large weights for that cluster. The blue object near the blue cluster center in step 4 could have, for example, the weights $u_{blue} = 0.90$, $u_{green} = 0.05$ and $u_{red} = 0.05$. The two blue objects close to the boundary to the green cluster could then have, for example, the weights $u_{blue} = 0.5$, $u_{green} = 0.45$ and $u_{red} = 0.05$.

The weights (u_{1i}, …. ,u_{Ci}) for each object represent so-called fuzzy numbers. The weights also do not have to add to unity for each object (as has been made in this section for a better understanding). The name Fuzzy C-Means also derives from the derivation from k-Means clustering.

B. *Image region growing*

Image region growing is an approach that exploits spatial context by grouping adjacent pixels or small regions together into larger regions. Homogeneity is the main criterion for merging the regions. The parameters that distinguish different objects may include average gray level, texture, color, etc[5].

This technique starts with a pixel or a group of pixels, known as the seeds, which belong to the object of interest. These seeds can be either manually defined by the user or provided by an automatic seed finding procedure. In the next step, the neighboring pixels are examined one at a time and added to the growing region, if those pixels have properties similar to the seed (based on a homogeneity criterion). This process is applied iteratively until no more

pixels satisfy the homogeneity criterion for inclusion in the growing region. The segmented object is then represented by all pixels that have been merged during the growing procedure [6].

Region-growing methods often produce good segmentation results that correspond well to the visually apparent edges of objects in the image. Observing this procedure gives one the impression that regions in the interior of an object are growing and merging until their boundaries reach the edge of the object. Although region-growing algorithms are computationally more expensive than the simpler techniques, the methods are able to utilize several image parameters directly and simultaneously in determining the final boundary location [5, 7].

Region growing has the advantage of correctly segmenting regions that have the same properties and are spatially separated. Moreover, it generates connected regions. One of the main issues in region growing is the selection of a homogeneity criterion. When the homogeneity criterion is not properly chosen, the regions may leak out into adjoining areas or merge with regions that do not belong to the object of interest[8].

C. Dataset

The clinical database of Hospital Pedro Hispano (HPH) has over 4000 cases with dermoscopic images of various types of lesions, all of them obtained under the same conditions through Tuebinger Mole Analyzer system. A total of 100 dermoscopic images were selected randomly from the database along with the clinical diagnosis, being 35 melanocytic nevi (regular), 25 dysplasic nevi, and 30 melanomas. The images are in 24-bit RGB color, with 768 560 pixels. For each image a manual segmentation was performed in full sized printed images by Dr. Jorge Rozeira (an expert dermatologist with over 8 years of experience in dermoscopic image analysis). The set of manual segmentations were scanned and rectified. The contour of the lesions was identified on these digital images to produce a binary image for each lesion. Therefore the resulting reference binary database is a reliable ground truth in order to access the accuracy of each segmentation produced by the different methods under evaluation.

D. Algorithm evaluation parameters

There are several terms that are commonly used along with the description of sensitivity, specificity and accuracy. They are true positive (TP), true negative (TN), false negative (FN), and false positive (FP). In this paper we used three metrics for evaluating of our method. Accuracy, Sensitivity and Specificity are calculate as follows:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (1)$$

$$Sensitivity = \frac{TP}{TP + FN} \quad (2)$$

$$Specificity = \frac{TN}{TN + FP} \quad (3)$$

Sensitivity is the proportion of true positives that are correctly identified by a diagnostic test. It shows how good the test is at detecting a disease.

Specificity is the proportion of the true negatives correctly identified by a diagnostic test. It suggests how good the test is at identifying normal (negative) condition.

Accuracy is the proportion of true results, either true positive or true negative, in a population. It measures the degree of veracity of a diagnostic test on a condition.

The numerical values of sensitivity represents the probability of a diagnostic test identifies patients who do in fact have the disease. The higher the numerical value of sensitivity, the less likely diagnostic test returns false-positive results. For example, if sensitivity = 99%, it means: when we conduct a diagnostic test on a patient with certain disease, there is 99% of chance, this patient will be identified as positive. A test with high sensitivity tents to capture all possible positive conditions without missing anyone. Thus a test with high sensitivity is often used to screen for disease.

The numerical value of specificity represents the probability of a test diagnoses a particular disease without giving false-positive results. For example, if the specificity of a test is 99%. It means: when we conduct a diagnostic test on a patient without certain disease, there is 99% chance; this patient will be identified as negative.

A test can be very specific without being sensitive, or it can be very sensitive without being specific. Both factors are equally important. A good test is a one has both high sensitivity and specificity. A good example of a test with high sensitive and specificity is pregnancy test. A positive result of pregnancy test almost for sure suggests the subject who took the test is pregnant. A negative result almost certainly rules out the possibility of being pregnant.

In addition to the equation show above, accuracy can be determined from sensitivity and specificity, where prevalence is known.

The numerical value of accuracy represents the proportion of true positive results (both true positive and true negative) in the selected population. An accuracy of 99% of times the test result is accurate, regardless positive or negative. This stays correct for most of the cases. However, it worth mentioning, the equation of accuracy implies that even if both sensitivity and specificity are high, say 99%, it does not suggest that the accuracy of the test is equally high as well. In addition to sensitivity and specificity, the accuracy is also determined by how common the disease in the selected population. A diagnosis for rare conditions in the population of interest may result in high sensitivity and specificity, but low accuracy. Accuracy needs to be interpreted cautiously.

III. RESULTS

For quantitative evaluation of the proposed algorithm, we compared with seven segmentation methods, namely ASLM, K-means, JSEG, SRM, KPP, Level Set and Otsu which have been already considered for skin lesion images [9-11]. The result of proposed method is shown in table 1.

Table 1. Comparison between proposed method and other methods

Image	Accuracy	Specificity	Sensitivity
JSEG[12]	0.7591	0.9593	0.6746
SRM[13]	0.4148	0.7512	0.2234
KPP	0.4324	0.7623	0.2648
Otsu[14]	0.5524	0.4870	0.5971
Level Set[15]	0.7249	0.7015	0.7073
K-means	0.7313	0.7010	0.7141
ASLM[11]	0.6615	0.9597	0.5404
Proposed method	**0.9685**	**0.9829**	**0.9542**

The result for some images are shown in figure 4.

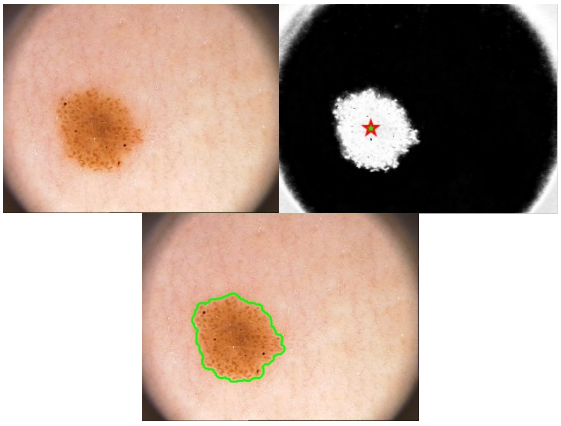
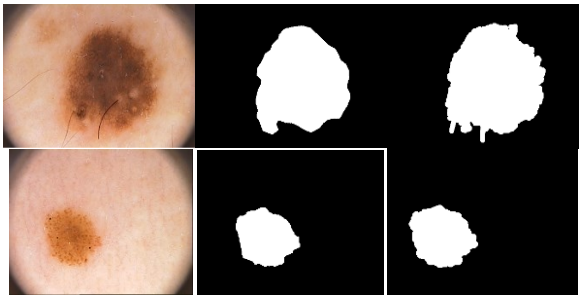


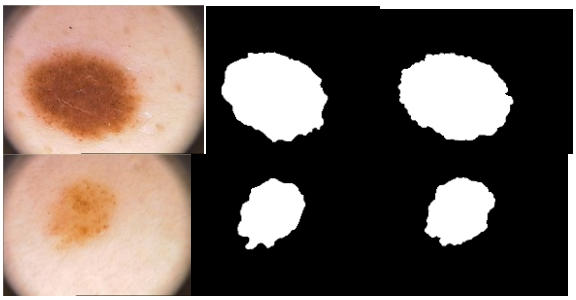
Figure 4. The result for sample melanoma image Best accuracy

Worst accuracy

Original image, Manualsegmentation, Segmentation result

Figure 5. Segmentation results for the PH2 dataset





(a) (b) (c)

Figure 6. Segmentation results for image 1, 57, 97, 104, a) Original image, b) Manual segmentation, c) Segmentation result

IV. Conclusion

Melanoma skin cancer is the most widely diagnosed type of cancer. As the number of cases grows each year, effective, quick, and early detection of melanoma is very important. If skin cancer is detected in early stages, it may be treated easily. The removal of skin-cancer lesions at last stages is expensive, while in early stages lesions are easy and economical to treat.

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