Improving Feature Extraction Accuracy for Skin Analysis

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***Abstract*— In this paper, we revise our skin feature extraction method based on cell segmentation to improve the accuracy and efficiency of skin feature analysis. Accurate skin feature extraction is critical for the evaluation of skin conditions. In order to improve the accuracy of analyzing skin features, we use the contrast limited adaptive histogram equalization (CLAHE) method for contrast enhancement. Also, we use the extended-minima transform in order to enhance the depth of wrinkles on the skin. After conducting watershed transform for cell segmentation, we utilize the labeled information of skin cells to extract skin features. We consider two types of skin features that are important for estimating the skin age of users. They are cell features and wrinkle features. To evaluate the performance of our revised method, we collected diverse images using two types of microscopy cameras and estimated the skin age based on their skin features. Through various experiments, we show that our revised method achieves 11% increase in analysis accuracy and 53% decrease in feature extraction time compared to our previous work.**

Keywords- Skin analysis; Feature extraction; Wrinkle feature; Contrast stretching; Microscopy image.

I. INTRODUCTION

Various factors, such as exposure to sunlight or pollution, smoking and excessive drinking are known to accelerate the normal skin aging process and eventually lead to premature skin aging. Usually, the degree of skin aging has been evaluated by dermatologists based on their personal experience or knowledge. This is because there is no standard method for quantitative and objective evaluation. If such method was available, then users would get consistent and quantitative information about their skin condition, and hence perform suitable treatment for their skin more effectively and conveniently.

In our previous work, we proposed a scheme for skin texture aging trend analysis based on diverse skin texture features. To extract such features, we cropped microscopy skin image, carried out histogram equalization, removed noise and then binarized the image using the Otsu threshold. After that, we segmented the skin texture into cells by using the watershed algorithm and calculated their features [1][2].

In this paper, we modify some of the preprocessing steps and segmentation method in the previous work to improve feature extraction accuracy and reduce processing time. Figure 1 shows the overall steps to do that, which consist of preprocessing, cell segmentation and feature extraction. In the preprocessing, the original image is cropped to reduce the effect of vignetting. Then, contrast stretching is applied in order to enhance the intensity between skin and wrinkle. Denoising filters are applied to the image. In the cell segmentation, extended-minima transform and watershed algorithm are used for cell-based segmentation. Each cell cluster is labeled, and the labeled information is utilized for calculating skin features. We extract five features from the skin image to analyze the skin condition. In Figure 1, modified modules are represented by double line rectangles.

The remainder of this paper is organized as follows. In Section 2, we introduce several related works for skin analysis. Detailed techniques for skin segmentation method are described in Section 3 and skin feature extraction method is described in Section 4. We explain our experiment and conclude this paper in Section 5.

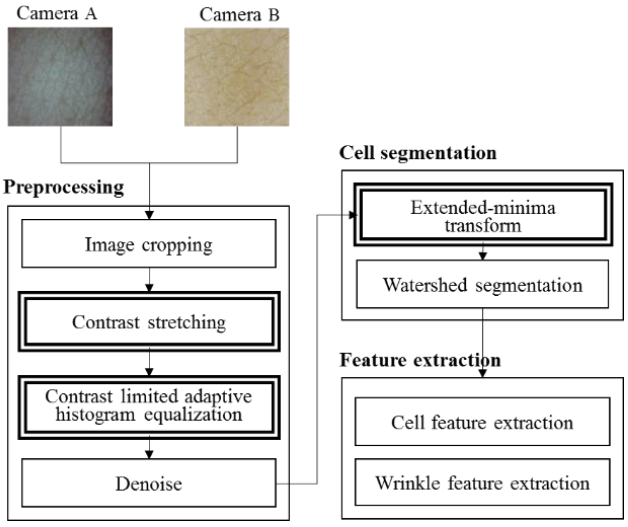

Figure 1. Overall scheme of skin feature extraction

II. RELATED WORKS

So far, medical analysis and diagnosis based on biometric images have been performed in the various domains. Skin analysis is one of the most popular and interesting tasks, since skin is the outermost part of the human body. Various methods have been proposed for evaluating skin condition quantitatively using skin images.

As an effort to detect skin wrinkles, H. Tanaka et al. applied a cross-binarization method to digital skin image to

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get its binary image, and then, the short straight line matching method to detect wrinkles from the binary image and measure their length [3]. More specifically, for each base line in the cross-binarized image, if more than 70% of its pixels are marked black, then the line is considered a wrinkle. After that, they continue from the end of current base line to create a new base line. This repeats until the end of the wrinkle or the end of the image is reached. J. Ute et al. measured the topography of skin surface using an optical 3D device and showed that there is a significant dependency between skin surface topography and the age [4]. On the other hand, G. O. Cula et al. developed the automatic facial wrinkles detection algorithm based on estimating the orientation and frequency of the elongated spatial feature, captured via digital image filtering [5]. Recently Yow. Ai Ping et al. proposed the ASHIMA system framework and showed how to process HD-OCT (High-Definition Optical Coherence Tomography) skin images automatically to measure the epidermal thickness and skin surface topography [6].

III. SKIN SEGMENTATION METHOD

A. Preprocessing

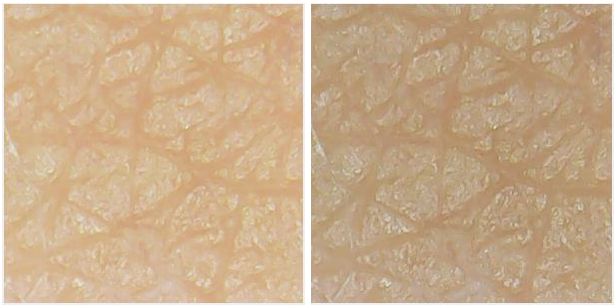
Direct image processing on microscope image or captured image might face several problems if the image is in RGB (Red-Green-Blue) form. Usually, dealing with RGB image shows less accuracy than dealing with gray image. Other typical factors to decrease the accuracy are vignetting effect and noises. To avoid these problems, original images need to be converted into binary images through preprocessing. In this work, pre-processing consists of three steps. First, the original image is cropped to reduce the effect of vignetting. Second, contrast stretching [7] is applied to make brightness difference between skin and wrinkle bigger. Then, adaptive histogram equalization is applied to the image.

1) Cropping

Due to the limitations of the camera and the interference of the light source, captured images may have noise and vignetting. Vignetting is a phenomenon where the outer edges of the images are dark due to the reduction of light at the periphery of camera lens, and hence causing the captured images to have different color histogram distributions. In order to avoid the problem, we cropped 300 by 300 pixels in the center of the image, which has the concentrated luminous source of the image.

2) Contrast stretching

Correct detection of skin wrinkles is critical in the skin analysis and its accuracy can be improved by clearly separating skin and wrinkle pixels in the image. However, original images often lack sufficient contrast due to diverse variations in the environment such as light source and shooting area. Insufficient contrast could make certain areas in the image have similar contrast even though they must be distinguished. This problem can be moderated by contrast stretching. Contrast stretching expands the dynamic range of the intensity levels so that it spans the color distance between skin and wrinkle. Figure 2 illustrates the effect of contrast stretching.



(a) Original image (b) After contrast stretching

Figure 2. Example of contrast stretching

In the figure, we can see that the intensity of the scalp pixels is reduced and the color distinction between skin and winkle becomes more prominent.

3) Contrast limited adaptive histogram equalization

Skin wrinkles can be detected using the watershed algorithm [8]. However, we observed that some of the wrinkles were missing during the detection due to the lack of contrast. Hence, before we use the watershed algorithm to the skin image, we apply the contrast limited adaptive histogram equalization (CLAHE) method to the image to enhance the intensity of winkles [9]. Histogram equalization is a gray scale transformation used for contrast enhancement. The aim is to get an image with uniformly distributed intensity levels over the whole intensity scale. The result of histogram equalization might be worse compared to the original image since the histogram of the resulting image becomes approximately flat. For instance, when high peaks in the histogram are caused by an uninteresting area, histogram equalization results in enhanced visibility of unwanted image area. This means that the local contrast requirement is not satisfied, and as a result, minor contrast differences are entirely ignored when the number of pixels falling in a particular gray range is relatively small.

An adaptive method to avoid this drawback is block-based processing of histogram equalization [10]. In this method, an image is divided into sub-images or blocks, and histogram equalization is performed on each sub-images or blocks. Then, blocking artifacts among neighboring blocks are minimized by filtering or bilinear interpolation.

The CLAHE method uses a clip limit to overcome the noise problem. That is, the amplification is limited by clipping the histogram at a predefined value before computing the Cumulative Distribution Function (CDF). The value at which the histogram is clipped, the so-called clip limit, depends on the normalization of the histogram and thereby on the size of the neighborhood region. The redistribution will push some bins over the clip limit again, resulting in an effective clip limit that is larger than the prescribed limit and the exact value of which depends on the image.

In our work, we need to remove hairs from the gray image. Hairs can be mistaken for wrinkles and hence they are the

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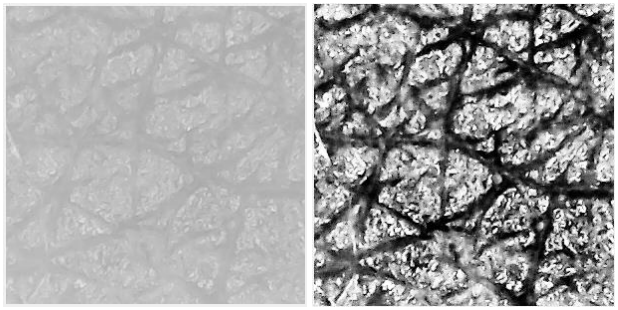
most critical noise in the wrinkle detection. Skin hairs are easily removed by a simple threshold filter.



(a) After hair removal (b) After CLAHE

Figure 3. Example of CLAHE

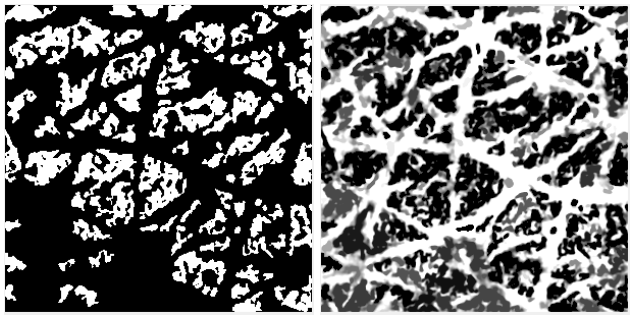
Figures 3 (a) and (b) show images after hair removal and after CLAHE method, respectively.

B. Segmentation processing

In this section, we describe how to segment a skin image into wrinkle cells using the extended-minima transform [11] and watershed transform. Watershed transform is one of the most widely used image segmentation techniques in image processing and we use it for segmentation into wrinkle cells. Especially, we perform the extended-minima transform before the watershed transform in order to increase the accuracy of finding wrinkle cells.

1) Extended-minima transform

Even though watershed transform is widely used for image segmentation, it often suffers from the over-segmentation problem since regional minima or ultimate eroded points are employed for segmenting cells directly. One of the main factors that determines the accuracy of segmenting skin image by wrinkle cells is how much the minima points are extended. In this paper, we revise the extended-minima transform, which is the regional minima of the H-minima transform. Regional minima are connected components of pixels with a constant intensity value, and whose external boundary pixels have higher value.



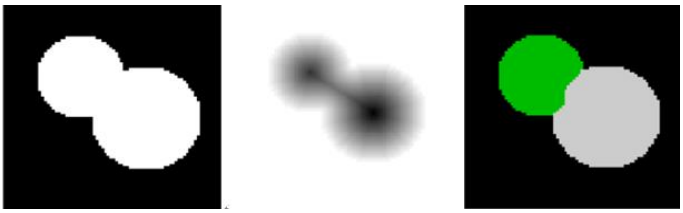
(a) Extended-minima extraction (b) Imposed minima image

Figure 4. Example of extended-minima transform

In other words, the result of h-minimum operator is linked to the depth of the minima. In a skin image, wrinkle cells consist of some minima and maxima. Minima correspond to parts of low depth points and maxima correspond to high depth points. Therefore, using the extended-minima transform, we can increase the depth between wrinkle cell clusters. It can help the watershed transform to cluster the wrinkle cells. Figure 4 shows an example of the extended-minima transform. First, we extract minima from an image and extend the depth of the points. The extended minima are shown in Figure 4 (a). Figure 4 (b) shows the result after imposing the extended minima to original gray scale image.

2) Watershed segmentation

Image segmentation is a computer analysis of image objects to decide which pixel of the image belongs to which object. Basically, this is the process of separating objects from background, as well as from each other. Watershed transform is a powerful and well-known tool for performing image segmentation.



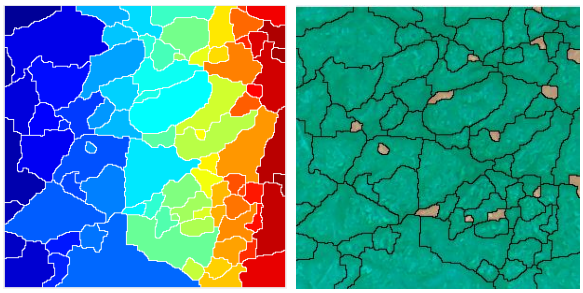
(a) Overlapping objects (b) Distances (c) Separated objects

Figure 5. Segmentation using watershed transform

Figure 5 shows how to segment two overlapping circles using the watershed transform. To segment them, an image distance to the background is computed. The maxima of the distance (i.e., the minima of the opposite of the distance) are chosen as markers, and the flooding of basins from such markers separates the two circles along a watershed line. We adapt these steps to our skin image, so that pixels of each wrinkle cell are clustered.

3) Cell labelling

Wrinkle cell labelling can be easily done by applying the watershed transform to the skin image.



(a) Labeled image (b) Filtered image with valid cells

Figure 6. Labelling process

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From the result of watershed transform, we can get a set of wrinkle cells. Each cell contains the positions of pixels in the cell which belong to same cluster. Sometimes, the segmentation result contains unexpected cells with very small size, which are usually noise or moles. Since they are not the regular wrinkle cell, they should be removed. In Figure 6 (a), we can see an example of labelling wrinkle cells. Each cell is labeled using a different color. Figure 6 (b) shows the noise cells that have to be removed. The brown cells need to be removed by merging into a neighboring cell. Currently, we decide the size of noise cells empirically.

IV. SKIN FEATURE EXTRACTION

A. Defining skin features

We have developed algorithms for extracting various features from microscopy images. Our feature extraction method is based on the labeled image described previously. Before defining these features, we made the assumptions presented in Table 1 based on common knowledge of skin [1].

TABLE 1. ASSUMPTIONS BASED ON COMMON KNOWLEDGE OF SKIN

1. Total wrinkle length decreases with age.
2. Wrinkle width increases with age.
3. Wrinkle depth increases with age.
4. Wrinkle cell area increases with age.
5. The number of cells decreases with age.
6. Diameter ratio of inscribed circle and circumscribed circle of a cell decreases with age.
7. Total length of lines connecting cross points of a cell increases with age.

In this paper, we define five features which are critical in the evaluation of aging skin. The five features are cell count, average cell area, average cell gradient, total wrinkle length, and average wrinkle width. Cell count indicates how many cell clusters are in the skin image. Average cell area indicates the average area of cell clusters in the skin image. Every wrinkle cell has its own shape, and the distortion of the shape is relevant to the degree of skin aging. So, it is useful to know how much a skin cell is distorted for skin aging estimation. For this purpose, we consider the slope of principal horizontal axis as distortion of a cell.

The wrinkle itself is also very important clue for estimating the degree of skin aging. We use two wrinkle features in this work; the total wrinkle length and the average wrinkle width.

B. Calculating skin features

In this section, we describe how to calculate those five features. We first estimate the number of cells by counting the number of labeled cells while excluding cells with a size under some threshold.

The average cell area is quite simple to calculate. We can get this feature by just dividing the total number of pixels in the labeled cells by the number of cells which we just described.

Total wrinkle length can be calculated using the line sieving method. This method first counts the pixels on the horizontal and vertical texture lines. It then counts the pixels along the diagonal line, and estimates the actual wrinkle length considering its slope. In the case of single pixel islands on the image, we simply count these islands and add the number to the total length.

We can get wrinkle width using Principal Component Analysis (PCA) analysis [12]. PCA algorithm is a method of calculating Eigen value and Eigen vector by using all data's covariance and average. The result of segmented line (extracted skeleton) is a set of 1×1 points. These pixels have specific direction, thus we can calculate each point's direction. In order to calculate the direction, we used PCA algorithm. When all of points on the skeleton's direction are calculated, we can get a perpendicular line for each point. Figure 7 shows how to calculate average wrinkle thickness. In the figure, each white '×' is skeleton point, and the line passing the skeleton point is a normal line. The red circles indicate the intersection of line and wrinkle contour. The length between these two intersection points is the wrinkle thickness at that point.

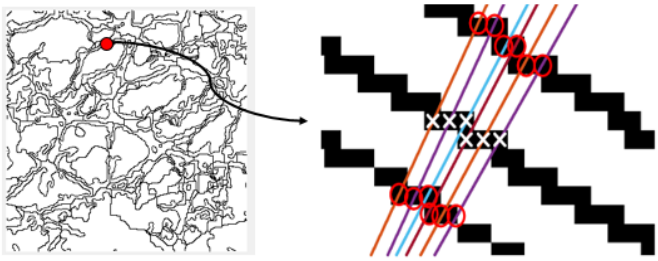

Figure 7. Calculating wrinkle width

Cell gradient is calculated for estimating how irregular a cell is due to skin aging. In order to measure the cell gradient, we used the regionprops function [13] which calculates a set of features for each labeled region. One of the major features in the result of regionprops is a scalar angle value for each labeled region.

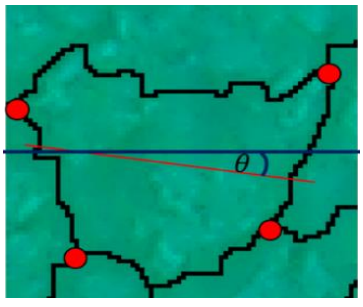

Figure 8. Example of calculating angle

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It can be obtained by calculating the angle between the x-axis and the major axis of the ellipse that has the same second-moment as the region. Figure 8 illustrates how to calculate the angle.

V. EXPERIMENTS

In order to evaluate the performance of our revised scheme, we performed several experiments based on the Matlab R2016a. The test images were prepared using microscopy cameras compatible with smartphone. We constructed a dataset of skin images using two cameras shown in Figure 9.

(a) Camera A (b) Camera B

Figure 9. Microscopy cameras compatible with smartphone

One camera has a scale of 50X to 500X, and the other camera has a scale of 25X to 400X. We got approximately 300 skin images from face and 50 skin images from hand using the two cameras.

1) *Detection accuracy*

Figure 10 depicts the segmentation result after watershed transform. The pixels on the segmented lines are matched to the pixels on the wrinkles in the binarized image. The binarized image can be obtained using the Otsu's method [14]. A skin image is composed of multiple wrinkle cells with different shape and size.

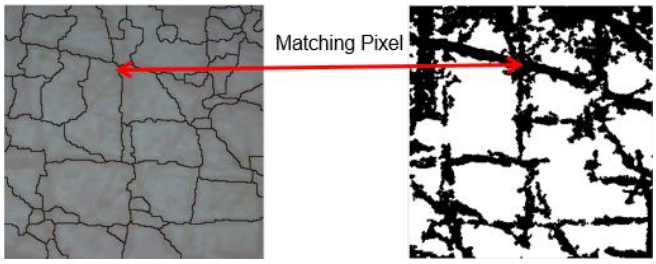

Figure 10. Comparison of cell segmentation and binarized image

We can compute the accuracy of wrinkle cell detection by the matching rate of segmented pixels as shown in Eq. (1). Basically, the equation counts how many matched pixels exist on both images, and then they are divided by the total number of pixels on the cell contour lines in Figure 10.

$$Accuracy = \frac{Cell\_contour\_pixels \cap Wrinkle\_pixels}{Cell\_contour\_pixels} \times 100 \quad (1)$$

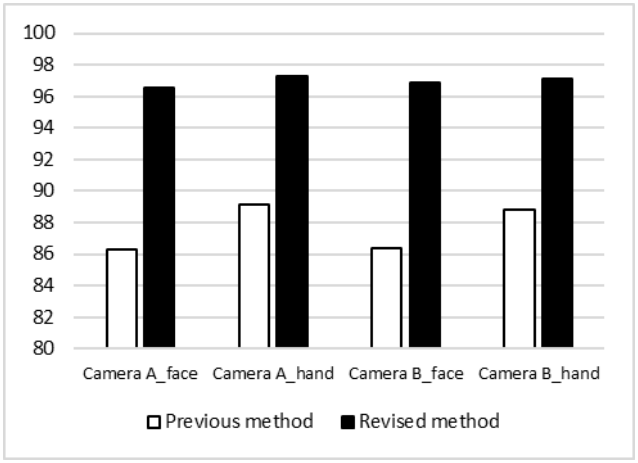

Figure 11. Comparison of detection accuracy

Figure 11 depicts the result. Accuracies of the previous method are under 90 percent. On the other hand, we can see that accuracies of our revised method are over 95 percent. Overall, our revised method achieved about 10 percent improvement over the previous method for each dataset.

B. *Execution time*

Next, we compared the execution time of our previous method and revised method for cell detection. Here, the execution time includes all the steps for the preprocessing and segmentation. In the case of feature extraction, both methods show little difference.

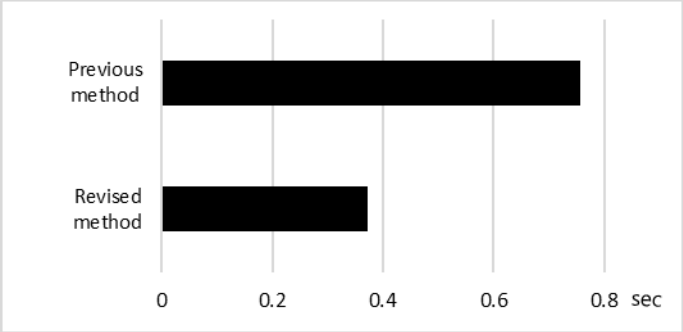

Figure 12. Comparison of excution time

Figure 12 compares the execution time of previous method and revised method taken for analyzing one skin image. As shown in the figure, the execution time of our revised method was about half that of the previous method.

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VI. CONCLUSION

In this paper, we revised our previous scheme for skin feature extraction to improve accuracy and reduce cell detection time. To improve the accuracy of skin cell detection, we used the contrast stretching and CLAHE filter for contrast enhancement, and the extend-minima transform to the skin image for cell segmentation. We performed several experiments to evaluate the accuracy and execution time of our revised method.

Consequently, our revised method improves the accuracy of cell detection by about 10 percent for all the image data set. Also, the total execution time for cell detection was reduced by half compared to our previous work.

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