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Melanoma detection using a mobile phone app

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ABSTRACT

Mobile phones have had their processing power greatly increased since their invention a few decades ago. As a direct result of Moore's Law, this improvement has made available several applications that were impossible before. The aim of this project is to develop a mobile phone app, integrated with its camera coupled to an amplifying lens, to help distinguish melanoma. The proposed device has the capability of processing skin mole images and suggesting, using a score system, if it is a case of melanoma or not. This score system is based on the ABCDE signs of melanoma, and takes into account the area, the perimeter and the colors present in the nevus. It was calibrated and tested using images from the PH2 Dermoscopic Image Database from Pedro Hispano Hospital. The results show that the system created can be useful, with an accuracy of up to 100% for malign cases and 80% for benign cases (including common and atypical moles), when used in the test group.

Keywords: Melanoma detection, mobile phone app, image processing, mobile phone microscopy

1. INTRODUCTION

According to the American Cancer Society[1], the number of melanoma cases has greatly increased in the last 30 years. Despite accounting for less than 2% of all skin cancer cases, it is responsible for most of the skin cancer deaths and, in 2015, it is estimated that it will cause 9,940 deaths and 73,870 new cases will be diagnosed in the USA. With other types of cancer, the efficiency of the treatment and the survivability is heavily dependent on the stage it is discovered,. (with the 5-year survival rate falling from 98% in localized cases to 63% in regional stage and 16% in distant stage. Therefore, detecting the melanoma in early stages is essential to make the treatment effective.

Melanoma originates from mutated melanocytes and is generally related to sun exposure and sunbeds, the skin type (people with fairer skin have higher risk of developing melanoma) and even family history[2]. It is usually present as an asymmetrical, irregular mole, with more than one color and a diameter greater than 6mm. Despite its most precise diagnosis being made through biopsy, the use of the ABCDE signs (asymmetry, border irregularity, color, diameter and evolution) can be very helpful in detecting and treating malign moles. Even with their recognition depending heavily on subjective patterns, a computer can be used to detect them, and establish if these signs are indicating whether the mole is malign or not. As mentioned in [3], several studies already have been trying this through diverse methods, including fractal geometry, Fourier descriptors and Gabor filters. Some recent works[4] obtained good results, with an accuracy of approximately 95%. However, they rely on a remote server processing the images for the smartphone, which creates a restriction for the app usage.

The aim of this project is to create a lightweight and portable Android app able to identify melanoma signs and help doctors in isolated areas, with no access to sophisticated equipment, to diagnosis this disease or, at least, indicate that further examinations are required. The program created was adjusted and tested using an image database from the Pedro Hispano Hospital, containing 200 images of benign and malign melanocytic lesions[5].

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2. SOFTWARE BACKGROUND

2.1 Related Projects

Computerized analysis of images in general is a growing research field, with many possible applications. As expected, there are already a considerable number of research projects in the area of pigmented skin lesions (PSL). According to [3], the first papers summarizing progress in this area were published in 1995.

A recent work [6] is composed by an app developed for iOS, installed in an iPhone 4/4S integrated with a microscope of 60x zoom capability. Basically, this app makes a color transformation from Red-Green-Blue (RGB) color space to a Hue Saturation Value color space, with a further transformation of the image to binary. The region of interest is then extracted, as well as its geometry (area size, perimeter, equivalent diameter and Shape Index), texture and color features (Haralick`s texture features and Gabor wavelets). For the classification process, the mentioned system uses Support Vector Machines from a built-in library. This system is clearly portable and uses complex descriptors to obtain a diagnosis. However it was tested only with 12 images, identifying 11 cases correctly. Also, it was developed for iOS only, which is specific to Apple products only.

Another app [4] was also developed for iOS and is based on Support Vector Machines, but, differently from the other, its image processing is made on a remote server, so internet connection is required. It analyses ten different features: 2-D Fast Fourier Transform, 2-D Discrete Cosine Transform, complexity, color, pigment network, lesion shape, lesion orientation, lesion margin, lesion intensity and lesion variation pattern. The Support Vector Machines used was trained and tested using the database provided by [5], with an accuracy of over 90%. These results are quite impressive, but the fact that the app depends on a connection with a remote server removes the advantage of portability.

Another work analyzed was [7]. It presents a color analysis technique for melanoma detection, with recognition rates varying from 65% to 85%, depending on some parameters. It also used a database composed by a considerable number of images, and, despite the relatively low accuracy compared to [4], parts of the methodology applied are interesting and adaptable to a mobile phone app. Its results show that color analysis can be a great tool for melanoma detection, but other analyses are necessary if a higher accuracy is desired. Neither the hardware nor the used operational system were specified on the mentioned article, so it was supposedly tested on a computer.

Another project related to the area is [8]. It also developed a melanoma detection app for iOS based on Support Vector Machines, but totally independent from a computer or remote server. A comparison between three segmentation techniques (ISODATA, Fuzzy c-Means and Active Contour) was also made, with Active Contour obtaining the best results, and Fuzzy c-Means obtaining the worst. A dataset of 1300 skin images was used in training and testing the software, obtaining 80.76% sensitivity and 85.57% specificity. The execution time was also quite good, with a mean time of approximately 5 seconds.

All the mentioned works have made contributions to the area, indicating that this is an area with many potential improvements. However, limitations related to accuracy, portability and availability to other operational systems may reduce their usability and should be worked.

2.2 Definition of the software

The app developed in this research project should be able to take photos, save them in the mobile phone and make a dermoscopy analysis, indicating if the mole photographed is a melanoma or not with a reasonable accuracy. The app must also allow storing the results on the mobile phone, so the case can be monitored. It must not depend on a connection with remote servers, as it should be usable in regions with few resources available. Finally, it was decided that the software should be available for Android-based systems, as it is a popular, open source operational systems, compatible with many devices.

2.3 Development environment and hardware specifications

The Eclipse IDE (Integrated Development Environment), version Luna (4.4.2), was used to program the app, as well as the program used to calibrate the weights of the score system. The language used in the app is Android Java, with minimum supported Application Programming Interface (API) version 11 (Android Honeycomb, version 3.0), and target API version 22 (Android Lollipop, version 5.1). The language used in the program created to calibrate the score system weights is Java, with JavaSE version 1.8. The app was tested on a Motorola Moto G, 2014, Android version 5.1, with a quad-core processor Qualcomm Snapdragon of 1.2GHz, a graphical processing unit Adreno 305 and 1 GB of RAM.

2.4 Training and test sample

To adjust the weights of the score system and test its accuracy, the PH2 image database, from Pedro Hispano Hospital, was used. It contains 200 dermoscopic images, with 80 common nevi, 80 atypical nevi and 40 melanomas, in JPEG and BITMAP format, and is open for researchers. These images have a resolution of 768x560 pixels approximately (as it may vary in some images) and are 8-bit RGB color. For each case, 75% of the images (the "training" sample) were separated to calibrate the score system and the other 25% (the test group) were used to test the accuracy.

According to the authors of the database, "the skin colors represented in the PH2 database may vary from white to cream white", which are skin types at increased risk of developing a melanoma[2]. Fig.1 shows an example of image from the database.

Figure 1. Example of malign melanoma (taken from PH2 image database[5])

2.5 Camera and lens

The mobile phone in which this app was tested has a camera resolution of 2592x1944 pixels, considerably higher than the images from the database. As its camera only has a 4x zoom, a magnifying lens was necessary. This magnifying lens (shown in Fig. 2) has 60x zoom capability, auxiliary LED lights and a universal detachable clip, which makes it adaptable to almost every phone. The quality of the images obtained with this apparatus is good, as demonstrated in Fig. 3.

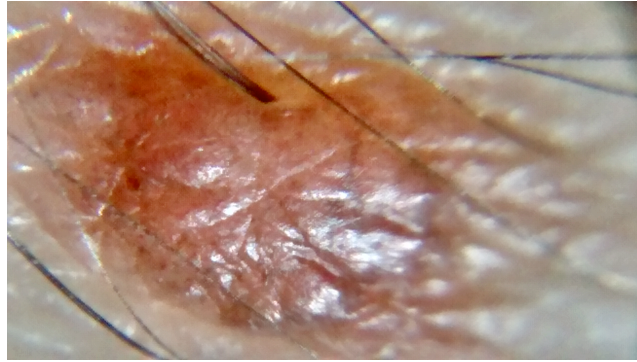Figure 2. Amplifying lens attachable to the phone

Figure 3. Photo of a mole taken with the amplifying lens

This system is considered low-cost, as even cheaper mobile phones could be used, and the attachable microscope cost only £8, approximately. The microscope is also easily obtainable through websites such as Amazon[9]. Therefore, it can be used in large scale without needing huge amounts of investments.

2.6 Software framework

The app developed was based on the software created by Kermit Sibindi[10] and improved by Su Yonghuai[11]. It offers the layout (shown in Fig. 4 and Fig. 5) and some routines that were adapted for the new functionality of the app.
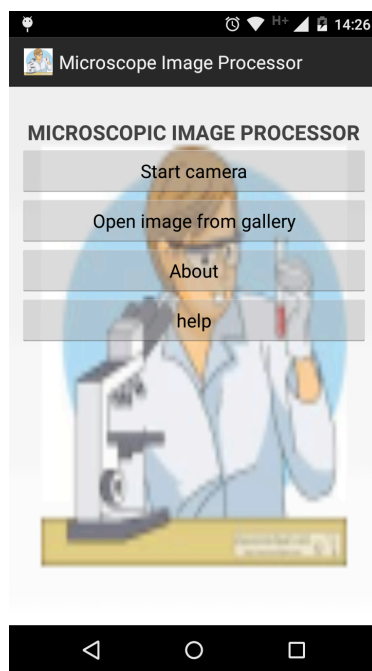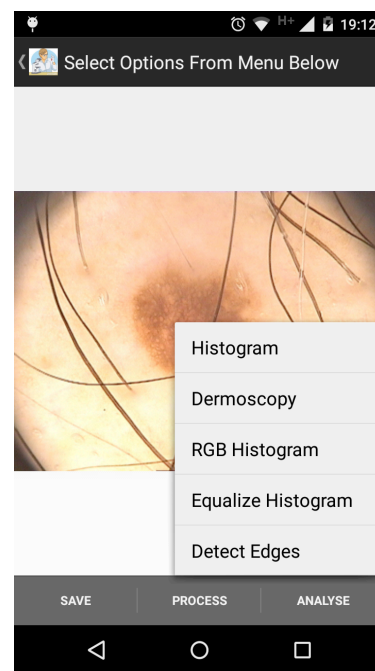

Figure 4. Application main menu

Figure 5. Application image analysis menu

3.   IMAGE PRE-PROCESSING

In order to analyze the mole, the first step is to properly prepare the image, eliminating information that could cause the system to work improperly. It is expected that the image may have some noises that can change drastically the results of the analysis made by the software. The pre-processing stages are fundamental in reducing these noises to an acceptable

level, as well as making any necessary modifications in the image, without demanding too much processing power. All these stages and the image analysis routines are integrated and used in sequence automatically by the program, without needing intervention from the user.

3.1 Related projects

The first action that the app does when the image is selected and the "Dermoscopy" function activated is distinguishing the mole from the skin. For this, it creates a histogram of the whole image in a vector with 256 positions, in which the index of each position is the simple average of the RGB value and the number it stores is the number of pixels that have this corresponding value. The RGB value threshold is then obtained through an isodata algorithm based on ImageJ[12]. Inspired on [13], this algorithm "divides the image into objects and background by taking an initial threshold, then the averages of the pixels at or below the threshold and pixels above are computed. The averages of those two values are computed, the threshold is incremented and the process is repeated until the threshold is larger than the composite average". Pixels with RGB value above this threshold are considered part of the object, being set to black in an output binary image, and the rest is considered as background (skin), being set to white.

One observation to be made is that when comparing results obtained when running equivalent codes in the computer and in the mobile phone is that depending on the image compression used the threshold value may vary slightly with the system used. This happens because each operational system has its own libraries for decompressing images in different formats to bitmap, which is the format used for pixel reading. As this happens in the first stage, cumulative differences may rise in the rest of the program. After systematic simulations, it was concluded that these differences only create a divergence of diagnosis in one case of the final test group, from a total of 50 cases, meaning they are not very significant. The observed differences were considerably small, and similar variations can be caused even by the use of different cameras, which can register slightly different RGB values for each pixel depending on its quality. However, it is strongly recommended to only compare results obtained using the same device.

3.2 Lens edges

The use of a magnifying lens on a camera generates shadows on the edges of the picture taken, which can cause the algorithm to detect it as a mole. The solution devised for this problem was to use an elliptical mask, with semi-axis equal to a half of the image's width and height: the pixels out of this mask were not considered. A small margin was taken out of each image also, to eliminate possible borders from it. Fig. 6 and Fig. 7 show how this process works.

Figure 6. Photo of a malign melanoma, with marks of the lens edges (taken from PH2 image database[5])

It is important to note that, in some images of the database, parts of the mole were taken out or edges of the lens were not totally removed by the mask (as shown in Fig. 7). In some situations, the mole is "touching" the edges of the lens, thus making it hard to remove the marks without removing parts of the mole. To avoid this problem, it is recommended to take photos with the mole in the center of the lens.

Figure 7. Binary image of figure 6, after the application of the elyptical mask

3.3 Hair removal

Depending on the thickness of the hair around the mole, it can appear quite clearly in the resulting binary image from the last two procedures. This fact could modify the result of the analysis made by the software, detecting different colors and calculating an area or perimeter bigger than the real value. To avoid this, a type of filter was created to remove the hair from the image. Basically, it is an algorithm that checks pixels nearby black pixels in the binary image: it divides adjacent pixels in four axes and, in case a set of equidistant pixels from the black pixel in two perpendicular axes are white, this black pixel is considered as hair and set to white.

This procedure reduced considerably the amount of hair in the output binary image, as shown in Fig. 8 and Fig. 9. However it is important to note that the hair may not be totally filtered, especially if it is too thick.

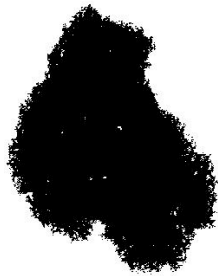Figure 8. Example of a common mole with hairs (taken from PH2 image database[5])

Figure 9. Binary output image of figure 8, after the application of the elyptical mask and the hair filter

4. IMAGE ANALYSIS

Once the image pre-processing is finished, the app starts analyzing the output image and compares the data from the original image with patterns obtained in the "training" sample. To avoid reading pixels from the source image repeatedly, some procedures were mixed with the pre-processing stage, without compromising the results.

As explained previously, this app functions based on a score system, whose criteria are colors present, mole size, perimeter and shape factor. These criteria are based on the ABCDE signs of melanoma, with the perimeter and shape factor representing the border irregularity and the area representing the diameter. This information is obtained in this step.

4.1 Color extraction

Melanomas usually have different colors than benign moles, including, but not limited to, blue and black tones. Detecting and associating colors to benign and malign moles can be a good way to characterize it.

There are two main difficulties with color extraction: the first is that variations in the environment in which the photo was taken (e.g. light) can cause the camera to identify different colors; the second is that, using the RGB space, the software will have to manipulate and compare cubic arrays with a dimension of 256x256x256 integers, demanding much of the processor and the memory. As suggested by [7], the definitions of relative color and quantized histogram were used to avoid these problems

The relative color consists in comparing each pixel of the mole with an average background color. The procedure is quite simple: first, the red, green and blue average values are calculated for the background pixels only (hair pixels are not included). These values are then subtracted from each pixel`s red, green and blue components, and, to avoid negative numbers, they are added to 255, generating a new color space, with size 511x511x511. Only colors that are present in more than 0.125% of the mole area are considered and therefore reducing the effects of possible noises.

As the new color space demands even more memory than the original one, its components are divided by four (according to [14], this value preserves color features) and grouping similar colors into cubic bins. This drastically reduces the requirements of the app, making it more lightweight and portable, as well as makes the color recognition more efficient.

Using these two definitions described, the quantized relative color histogram of the mole is created, and will be later converted to a score component.

4.2 Area

The area calculation is a simple pixel counter, which counts the number of black pixels in the output binary image. This information is displayed in the output binary image mainly to help monitoring the case, as it may be affected by hair pixels that were not filtered and the mole border detection algorithm (which can behave slightly differently in some devices, or can be different from a specialist's analysis). Therefore, its reduced precision should be considered whenever using the app. However, this influence should not affect drastically the results.

It is important to note that the photos should be always taken with the lens touching the mole, and with a constant zoom. As it is impossible for the app to know the size of the area photographed, it will always consider it as constant, and it may generate wrong results when this is not the situation.

4.3 Perimeter

The perimeter calculation is also a pixel counting method, with no complexity involved. It analyses the four pixels near a black pixel in the binary output image and decides its contribution to the perimeter. If all four pixels are black, the pixel is considered internal, so it does not change the perimeter. If three pixels are black, or if three pixels are white, the perimeter is increased by 1. If two pixels are white, and they are at opposite sides of the black pixel, the perimeter is increased by 2. If two pixels are white and they are not opposite, the perimeter is increased by 1.414. If all four near pixels are white, the black pixel is considered a noise, and does not contribute to the perimeter.

The same observations made for the area calculation should be applied for the perimeter: its value may change when using different devices, and photos should be taken with the lens touching the mole. Also, the user must remember this information should not be considered alone, due to the amount of variables involved.

4.4 Shape factor

The shape factor is a mathematical method to analyse border irregularity, which compares area and perimeter: for a constant area, irregular shapes will have a higher perimeter than regular ones.

This project takes an approach to shape factor similar to [15], with the formula

$$Shape\ factor = \frac{L}{\sqrt{A}} \tag{1}$$

where L is the perimeter and A is the area of the mole. The square root was used in this formula to avoid influence of the area, as it is already considered by the score system. In a circumference, the value of the shape factor would be $2\sqrt{\pi}$, indicating that all circles have this same shape factor, regardless of its diameter.

4.5 Score calculation

The last part of the analysis is the final score calculation, made by a simple linear equation, which adds the weighted value of the color score, area score, perimeter score and shape factor score. The malign, atypical and common score are then calculated, and if the malign score is the highest, the software indicates a melanoma case; otherwise, it indicates a benign case.

Before adjusting the weights of the equation, it was necessary to adjust the parameters of reference. A simple java program was created to obtain the quantized relative color histogram, area, perimeter and shape factor of all the images from the "training sample". This training sample is composed by 150 mole images (divided into 60 common, 60 atypical and 30 malign moles), obtained from [5].

Using the training sample, the average and standard deviation for area, perimeter and shape factor were obtained for each case, and chosen as parameters for the score equation. To calculate the score generated by each of these variables, they are compared to these reference parameters (if the difference is greater than the standard deviation, they will not contribute to the related score, except when it is greater than the value for malign cases), and the score is inversely proportional to the difference. As expected, the averages were the highest in the malign group, so if there are values greater than it, they will be considered indicatives of a possible melanoma.

The color parameters were obtained in a different way than the dimension ones. First, the quantized relative color histogram was generated for all the 150 images of the training sample (it is important to remember that colors must be present in more than 0.125% of the area of the mole to be considered). The histograms were then grouped by diagnosis and each of its components was compared. If a color component was proportionally more present in a case than in the other two, then it was considered related to that case. Finally, colors observed in less than 10% of the cases were disregarded. The resulting group of expected colors were then added to the score equation and normalized.

Figure 10. Output binary image from the analysis of Figure 1

With all these parameters adjusted, the score equation was made, adding individual scores and multiplying them by different weights to increase or decrease its participation. These weights were selected manually after empirical analysis, trying to maximise the accuracy of the software. When applied to the training sample, the software was able to identify 46 atypical cases as benign (76% accuracy), 53 common cases as benign (88% accuracy) and 27 malign cases as malign (90% accuracy).

4.6 Displaying results

After all analysis is made, the results are shown in the mobile phone screen. The output binary image is displayed, and the area, the perimeter and the source path of the image are written in red on it. In case the app detects the mole as melanoma, the message "High risk of melanoma detected by the camera" will also be registered in red. Otherwise, the message "Low risk of melanoma detected by the camera" will be registered in blue. The highest score (which is also the one responsible for the diagnosis) is displayed too, but it is important to note that it does not mean anything by itself, as the results are always relative.

Area: 44521
Perimeter: 2632
Low risk of melanoma detected by the camera.
Source:/storage/sdcard1/Benign/IMD384.jpg
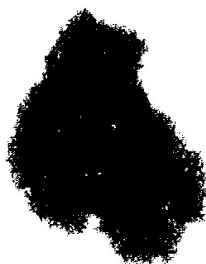Score:Common:0.1213633

Figure 11. Output binary image from the analysis of Figure 8

As the result is a comparative analysis between the malign score, the common score, and the atypical score, comparing separate scores from different images may lead to wrong interpretations. Fig. 10 and Fig. 11 show examples of the results screen.

5. RESULTS

The test mentioned in the last session with the images used to adjust the software cannot be used to validate it, as expected. For this purpose, 50 images (25%) of the database were previously separated to calculate the accuracy of the app with a random sample. Considering the atypical group, 16 images (80%) were correctly identified as benign; the same number applies for the common group, and for the malign group 10 images (100%) were correctly identified as malign. Therefore, the true-positive rate (TPR or sensitivity) is 1 and the false-positive rate (FPR or specificity) is 0.2.

These results are adequate if the classification is considered binary. However, if the diagnosis is divided into three cases, like the database was divided, the overall accuracy of the app falls drastically: only 6 images (30%) of the atypical group were diagnosed as atypical; 9 images (45%) of the common group were considered common; and all images of the malign group were considered malign, as expected.

Each analysis did not take more than 20 seconds to be totally processed by the mobile phone, indicating that the objective of making a lightweight and portable app was accomplished. It should be able to run in almost every modern smartphone, with only small variations on its performance (higher resolution images will take much more time to be processed, as pixel reading is the process that demands most processing time).

6. CONCLUSION AND FUTURE WORK

The app has an acceptable accuracy to distinguish malign moles from benign moles, despite not being able to properly classify each mole into one of the three subgroups mentioned. However, it was able to correctly identify all malign cases

and 80% of the benign cases. It is important to note that it does not use a lot of processing power, and actually need only two components, the mobile phone and the lens, to properly work. These are the two main advantages over some works released about the subject, which rely on a server and, consequently, an internet connection to analyze each case.

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