A software platform for the analysis of dermatology images

Maria Vlassi, Vlasios Mavraganis, Panteleimon Asvestas
Department of Biomedical Engineering, Technological Educational Institution of Athens, Agioy Spyridonos, 122 43, Greece

E-mail: maria_vlassi@outlook.com, vlasisvv@gmail.com

Abstract. The purpose of this paper is to present a software platform developed in Python programming environment that can be used for the processing and analysis of dermatology images. The platform provides the capability for reading a file that contains a dermatology image. The platform supports image formats such as Windows bitmaps, JPEG, JPEG2000, portable network graphics, TIFF. Furthermore, it provides suitable tools for selecting, either manually or automatically, a region of interest (ROI) on the image. The automated selection of a ROI includes filtering for smoothing the image and thresholding. The proposed software platform has a friendly and clear graphical user interface and could be a useful second-opinion tool to a dermatologist. Furthermore, it could be used to classify images including from other anatomical parts such as breast or lung, after proper re-training of the classification algorithms.

1. Introduction
Melanoma is one of the deadliest forms of skin cancer. Therefore, massive effort has been put into the development of diagnosis methods for this disease [1]. The malignant tumours develop when damage to skin cells triggers mutations that can cause rapid multiplication of the skin cells. These tumours originate in the pigment, producing melanocytes on the epidermis. The main cause of malignant melanoma is the exposure to ultraviolet light. In case melanoma is diagnosed and treated early, the curability can be indubitable [2]. Otherwise, it might be spread to other body parts and lead to fatality.

Diagnosis of the skin lesions can be performed automatically. The higher incidence of malignant melanoma makes the automated diagnosis of skin lesions a main concern. In automated diagnosis of skin lesions, feature design is based on the ABCDE-melanolytic algorithm represents asymmetry, border, colour, diameter and evolving of the mole over time. Melanoma lesions often have asymmetrical shape, whereas benign moles are usually symmetrical [4]. Unhealthy moles have irregular borders while benign moles have even borders. Additionally, a warning sign of melanoma can be the variety of colours. Benign moles regularly have a single shade of brown. In regards to the factor of diameter, the benign moles usually have a smaller diameter than the malignant lesions. Alternative algorithms apart from the ABCDE rule are the Menzies Scoring method and 7-Point Checklist [3].

The determination of the mole type (benign or malignant) is relied on observation by a dermatologist. Many dermatologists use a technique called dermatoscopy to observe spots on the skin. During this process, the doctor uses a magnifying lens and light source held near the skin. Another skin medical test is called skin biopsy, where a part of the affected area will be removed and looked under a microscope. In both cases, the doctor might take a photo of the affected spot.
The determination of the mole type is a time-consuming process. Developing a platform which can be used by dermatologists in order to reduce the duration of the process, can be considered as a useful second-opinion tool in medicine. This paper presents a platform developed in Python environment which relies on image processing of the moles samples and could be used to assist the classification of images depending on their features.

2. System architecture

An ongoing effort across the medical and scientific communities has begun to implement standardized evaluation criteria of pigmented lesions that can be performed by automated analysis systems, in order to improve melanoma diagnosis [5]. This platform is used for the classification of benign or malignant samples depending on their features.

Initially, the platform loads all the necessary libraries, such as OpenCV and PyLab. OpenCV library is mainly used for loading images and converting them to different colour channels as needed for each process. Additionally, thresholding filters implement the tool of OpenCV library. Thereafter, the user selects an image to upload into the platform. The user can crop the image in order to focus on the structure of interest (malignant or benign mole). Then, the region of the mole is extracted using one of the following two methods: manual and automatic. During the manual method, the user selects the region of interest by using the mouse and left clicks on the image. The automated method is a process where the mask occurs with a thresholding filter (Otsu or Binary). The automated method is based on the object detection analysis. The process of object detection analysis is to determine the location, number, size and position of the objects in the loaded image. Object detection is basically the concept for tracking and recognition of objects [6]. The image is converted from BGR to RGB colour channels. This process is important because OpenCV only recognises the RGB colour channels while PyLab recognises both channels. Thus, the libraries have to work on the same channels to avoid confusion. Subsequently, the user chooses the region of interest of the mole sample. The chosen structure has to be precise in order to achieve pragmatic mask results. Thereafter, the platform presents the automatic method of the extraction of the mole region. A thresholding filter must be used for this purpose; either Otsu or Binary thresholding. These filters work properly only for 2-dimensional images. Consequently, the image is converted into grayscale colour channels in order for the filters to work. Afterwards, the original image, the mask of the mole region and the histogram of the mask are displayed in one frame with the same dimensions. This can be achieved by using PyLab library which includes a number of options for creating a plot such as the colour, the subplots in it and the titles of each subplot. Furthermore PyLab is used for showing the results and not processing them at any way.

As for future work, the mole samples will be classified into two different categories; benign or malignant. This will be achieved by using classifiers (e.g. Neural Networks). The classifiers must be trained in order to categorize each sample properly. This training method will be based on a database with two pre-labeled categories including healthy moles and melanomas. Each category will contain a sufficient number of dermatology images of each case. Thus, the classifier will be able to recognize every new loaded image and provide a percentage which will reflect the possibility that corresponds to each category. The final percentage depends on the amount of images that will be classified; the more samples we provide, the higher result will be obtained.

![Figure 1. Architecture of the proposed platform](image-url)
3. Results

Figure 2a shows the original image as loaded into the platform, before the modification. The second result is presented in Figure 2b which reflects the part of the manual ROI selection process by the user. The user selected the region of interest (red line) on the approximate limits of the mole for the mask creation. Thereafter, Figure 2c presents the mask of the selected ROI. The limits cannot be precise as in this case the ROI was selected manually by the user. The final results of the automatic method of defining the mole region are presented in Figure 3 and Figure 4. Specifically, Figure 3 contains the original image, the automatic ROI selection, with the addition of the mask histogram by using the filter of Otsu Thresholding. In Figure 4, the same process is followed, by using Binary Thresholding.

![Figure 2a](image1.png)  ![Figure 2b](image2.png)  ![Figure 2c](image3.png)

**Figure 2.** (a) display of the original image, (b) display of the ROI, (c) display of the manual mask

![Figure 3](image4.png)

**Figure 3.** Display of the final results with the automatic ROI selection with Otsu Thresholding

![Figure 4](image5.png)

**Figure 4.** Display of the final results with the automatic ROI selection with Binary Thresholding
Conclusion
The suggested platform can be used by dermatologists in order to provide a second opinion during the process of the moles examination. The user can keep the platform on their personal computer where all the dermatology samples are kept, alongside with the Python program.

As for future work, there will be the classification of the images in two categories: benign and malignant. This can be processed by creating a database for the two different mole types. This will be achieved by training the platform after loading as many dermatology images as possible in order to obtain maximum accuracy. With the help of a classifier, the platform will be able to foresee the possible correct category of a new image after proper training. Furthermore, this platform can be developed to classify images including other anatomical parts, after proper re-training of the classification algorithms.

References
[1] Barata C, Ruela M, Francisco M, Mendonça T and Marques J. S. 2014 IEEE System J. 8 965
[2] Westerhoff K, McCarthy W H and Menzies S W 2000 Clin. Exp. Dermatol. 143 1016
[3] Johr R. H. 2002 Clin. Dermatol. 20 240
[4] Ganster H, Pinz P, Röhrer R, Wildling E, Binder M and Kittler H 2001 IEEE Tran. Med. Imaging 20 233
[5] Gareau, D S, Correa da Rosa J, Yagerman, S, Carucci J A, Gulati N, Hueto F, DeFazio J L, Suárez-Fariñas M, Marghoob A and Krueger J G 2017 Exp. Dermatol. 26 615
[6] Gupta B, Chaube A, Negi A and Goel U 2017 Int. J. Comput. Appl. 162 17