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# Computer-Aided Detection of Melanoma, A Case Study

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***Abstract*—Melanoma is the most dangerous form of skin cancer, and its detection at an early stage can allow timely treatment and prevention of fatal consequences. In this paper we present a case study of computer-aided diagnostics of melanoma using images of patients moles. The initial study was performed on two datasets: a benchmark dataset which is publicly available and a second one, containing images that were taken in hospitals in Macedonia. We present the obtained results and a short discussion of further directions for research. The results on the initial dataset were promising and showed 83% accuracy in the detection of the melanoma on the benchmark dataset. However, the same approach applied on the Macedonian dataset, the results could not be reproduced due to the low number of positive examples. The results showed that the performance of the classifiers did not benefit from under-sampling or oversampling techniques, nor did from feature selection. We can conclude that to build a reliable system for melanoma detection, a datasets of hundreds of images is not enough to train a machine-learning based model.**

## I. Introduction

Skin cancer is found in various types, such as melanoma, basal and squamous cell carcinoma, among which melanoma is the most unpredictable and most dangerous form of skin cancer. It is known that ultraviolet radiation from sunshine or tanning beds can trigger DNA mutations leading to rapidly multiplication of skin cells and forming malignant tumors. These tumors originate in the pigment-producing melanocytes in the basal layer of the epidermis, and they often resemble moles. The majority of melanomas are black or brown, but they can also be skin-colored, pink, red, purple, blue or white. There were around 55,500 deaths from malignant melanoma worldwide in 2012 (0.7% of total cancer deaths) [1]. According to American Cancer Society [2], melanoma is most commonly diagnosed in non-Hispanic whites (25 per 100,000), then in Hispanics (4 per 100,000) and it is not so common in African Americans (1 per 100,000). Ten percent of all people with melanoma have a family history of melanoma. Early melanoma diagnostics and proper treatment is almost always successful, but late melanoma detection advances to cancer, spreading to other parts of the body, where it becomes hard to treat and can be fatal.

Normal and abnormal skin tissues visually differ in smoothness; the first are smooth and even, the second are irregular, complex and odd. In dermatology many systems and algorithms for improved diagnostics of melanoma skin cancer can be found [3] (seven-point checklist [4], ABCD rule, and the Menzies method [5]). Even when the dermatology expert uses the dermoscopy for diagnosis, the accuracy of melanoma diagnosis is estimated to be about 75-84% [6]. On the other hand, computer algorithms for image analysis can be found faster and more accurate than human visual perception in extraction of some visual information, like color variation, asymmetry, and texture features. Therefore computer aided methods and techniques should be applied for leveraging the melanoma diagnosis process.

In the last few decades, availability of new technologies, devices and equipment combined with computer vision played an important role in the medicine, providing better diagnosis, treatment and prediction of diseases. Computer vision can exploit texture, shape, contour and prior knowledge along with contextual information from image sequence, resulting in much needed multidimensional quantitative information not easily available by trained human specialists. The very first description of a computer system for analysis of skin lesions [7] was published in 1984, and since then, computer technology have made a giant leap forward.

In the field of skin cancer detection, we can find a plenty of researchers that have applied computer vision approaches for melanoma detection. In general, all of these approaches are based on the following key steps: (1) image acquisition and preprocessing, (2) skin lesion segmentation, (3) feature extraction and (4) classification of the provided features.

In the preprocessing step the main issue is the hair removal. Most of the techniques apply morphological closing operation [8] [9] to identify long, thin, straight shapes, and the curvature of the resulting pixels in the hair mask [10]. Then, the hair artifacts are removed from the image, by using linear interpolation [8], masked median filtering [9] or auto-regressive as well as band-limited techniques [11].

Image segmentation should result in separation of the skin lesion from the surrounding skin region. This process could be supervised or unsupervised. Supervised segmentation methods require input from the user, such as examples of skin and

lesion pixels, a rough approximation of the lesion borders to be optimised, or a final refinement of a proposed solution [12] [13].

Conversely, unsupervised segmentation methods (called automatic segmentation methods) attempt to find the lesion borders without any user intervention. Most common border detection techniques rely on histogram thresholding [14] [15], where most commonly RGB information is mapped to an optimaly determined number of color channels and hybrid thresholding is performed for lesion borders detection. Other approaches apply global thresholding on optimised colour channels followed by morphological operations [12], region-based techniques [16] [17], segmentation fusion techniques [18], wavelets [19]. When the contrast between the skin lesion and the surrounding skin is low, the segmentation can be very obscure [20].

The feature extraction step generates lesion features that will be used as input during the classification process. The extracted features can mimic some dermatoscopic features that rely on the conventional dermatoscopy ABCD-rule algorithm, or they can be dermatoscopic independent. The overview and categorization of the features according to the clinical ABCDE-rule, dermatoscopic ABCD-rule, and pattern analysis is given by Korotkov and Garcia [21]. Altough these features are easy to extract and have high correlation with the dermatoscopic features, the dermatoscopic independent features provide a broad possibilities for experimentation. While constructing these features, the researches can choose between features that apply the analysis of variance for the lesion border [22], colour [23], shape and textures [24], some geometric features, and so on. Fractal features [25] can be also used, but there are different advantages and disadvantages in the process of calculating the fractal dimension, which should be taken into consideration in order to avoid misreading of the results[26].

After determining the set of features, the last step is to distinguish the malignant structures from their counterparts. For diagnosis purposes, we can distinguish two groups of studies: (1) statistical test on the features [27] to examine if there is a significant difference between the value of at least one particular feature for different classes; and (2) machine learning algorithms that learn from the provided features how to distinguish the different classes. In this paper we will treat the machine learning approach. Here the most applied algorithms are the neural networks [28] [29], support vector machines [30], logistic regression [31], decision trees [32], k-nearest neighborhood algorithm [33]. There are numerous other classifiers that can also be explored for classification.

In this paper we will stress the potential of computer image analysis and classification as a valuable diagnostic aid that could enable dermatologists to make highly sensitive and specific diagnoses of early, curable melanoma.

## II. Datasets

For this case study we used two datasets. The first dataset is consisted of 100 images which were labeled by experts [34], [17], [35], [36]. From the 100 images, 32 were diagnosed as melanoma and the rest 68 images were non-melanoma. This dataset is used to examine which descriptors would give the best classification for melanoma detection. We used texture, contour and fractal descriptors for this purpose.

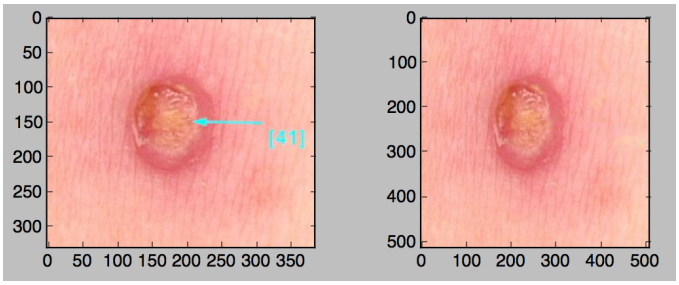


Fig. 1. Mole image before and after preprocessing for removal of diagnostic arrows

The second dataset is consisted of 138 images that are taken from patients in the Republic of Macedonia. The dataset is marked with diagnosis arrows that needed to be removed from the images. For this purpose, the images were initially preprocessed and the drawn arrows from the diagnostics were removed using the in-painting method of OpenCV[37]. After this, the mole regions were cropped and resized to 512×512 pixels. An example of the images before and after pre-proecssing is depicted in Fig. 1.

## III. Feature extraction

For both datasets we took the whole image when calculating the texture descriptor. We did this to incorporate both the area inside the mole and the mole shape characteristics in the texture. To extract the texture characteristics we used one of the best descriptors for texture classifications available, the Complete local binary pattern descriptor (CLBP) [38]. CLBP is a variation of the Local binary pattern descriptor (LBP). The CLBP descriptor is calculated by comparing pixels of the image around a central pixel. There are 2 parameters that need to be set prior to the calculation: the radius and the number of points in the circle around the pixels. If the pixel intensity is higher than the central pixel, a value of 1 is set and if the pixel is lower than the central pixel, a value of 0 is set. These values are then concatenated and further transformation is performed so that the cases that are very rare are ignored and they are shifted to the right until the first 1 is on the least significant bit so that a rotation invariance is obtained. The CLBP descriptor also includes the magnitude and the sign of the pixels which increases the dimensionality but is shown [38] that it improves the classification performance. For the first dataset we used only radius 3 and selected 24 points around the central point. For the second dataset we used multiple combinations

The fractal descriptor is consisted of 5 fractal characteristics of the mole image. To compute these characteristics we use the fractal computation box counting method described in [39].

The contour descriptor is used to describe the contour of the mole. We first segment the mole from the image using OTSU thresholding [40]. From the binary image obtained trough thresholding, we take only the contour pixels, as a set of points in counter clockwise order. After that we calculate the TSLA contour descriptor [41], [42]. We generate the TSLA descriptor by taking 100 equidistant points from the contour

of the mole. For each point a triangle is generated with 5 pairs of points on distances of 1 point, 2 points, 4 points etc. In this way we generate a triangular representation for 5 scales of the contour. We then generate all the descriptors for each image and we use K-means clustering to obtain 100 cluster centroids. These centroids are used as dictionary. Based on the dictionary we generate a bag of words descriptor for each image. The bag of words descriptor gives information about how many of each of the "words" in the dictionary are present in the contour of the mole.

## IV. Classification and results

To generate the classification model for the mole images, we used a combination of texture descriptor, fractal descriptor and contour descriptor for the first dataset. We first fuse the three descriptors and then form a single descriptor of the image. The images are separated in two classes: melanoma and non-melanoma as described in II. The problem now is to train a two class classifier that would be capable of distinguishing between the two types of images.

Prior to training the classifier, we use feature selection to reduce the feature dimensions. We use the approach described in [43], [44]. The used approach automatically selects the most informative features that have the potential to lead to a better classification model. We noted that the most important features that were selected from the full set of features (LBP, Fractal and TSLA) all belonged to the LBP feature. This could mean that the texture of the mole images is the most important factor when classifying the images.

For the classification algorithms we used the WEKA [45] package and the implementation of SVM, and we used scikit-learn Python package [46] for the Extra trees and Random Forest algorithms. All of the algorithms were evaluated using 10-fold cross validation and grid search for the classification algorithms parameter space. The best results were obtained using SVM with Gaussian kernel and parameters C=1 and gamma = 0.001. The confusion matrix for the best results is presented in Table I. The best classification algorithm used the top 205 features and achieved 83% accuracy.

TABLE I. **Confusion matrix for melanoma detection using the first dataset**

| Actual ↓ | Predicted | |
|---|---|---|
| | **Melanoma** | **Non-melanoma** |
| Melanoma | 25 | 7 |
| Non-melanoma | 10 | 58 |

Motivated by the initial successful classification of the used approach, we used the CLBP descriptor algorithm only to obtain descriptors for 138 images that were taken from clinics in Macedonia and diagnosed by experts. The mole region was extracted using OTSU thresholding and the CLBP was generated only for the segmented region. Furthermore we tried to improve the approach by calculating the descriptor not only from the L channel but also from the H and S image channels. We also used both radius 1 and 8 points and radius 3 and 24 points to calculate the descriptor.

Based on this we obtained a high dimension descriptor that was reduced using the above mentioned feature selection approach to 36 descriptors. Due to the high imbalance of the data (only 15 images diagnosed with melanoma), in spite of the feature selection and multiple algorithms for machine learning with wide variety of parameters, the testing accuracy was very low. This showed that the same approach that was used on one dataset could not be applied on another dataset of melanoma images. The results using different classification techniques are shown on Table II.

TABLE II. **Confusion matrices for melanoma detection using the second dataset**

| Classifier | Actual ↓ | Predicted | |
|---|---|---|---|
| | | **Melanoma** | **Non-melanoma** |
| Naive Bayes classifier | Melanoma | 1 | 14 |
| | Non-melanoma | 13 | 104 |
| SVM | Melanoma | 0 | 15 |
| | Non-melanoma | 0 | 117 |
| Random Forest | Melanoma | 0 | 15 |
| | Non-melanoma | 0 | 117 |

Sub-sampling or super-sampling the data has lead to similar results. One of the reasons for this is that there was a wide varieties in the melanoma images and the diagnosis is not always performed based on the visual presentation of the mole but also based on its 3D characteristics which are not available in the images. This could lead to a doctors mistake when the labeling is performed based on a single image of the mole.

## V. Discussion

In this paper we have discussed the usage of the CLBP descriptor in combination of the TSLA descriptors and the Fractal descriptors for melanoma detection from images. Based on the initial findings, the CLBP descriptor gave the most informing features and the SVM classifier gave the best accuracy. We applied this descriptor on different set of images but didn't manage to obtain good classification model due to the high imbalance of the data after experimenting with the same classifiers and with wide variety of parameters.

Overall the number of images that we had to experiment with is very low and a lot more images would be needed to give a conclusion about the performance of the descriptors and classification algorithms. For the initial experiment we obtained the best results using SVMs, however in the second set of images the best algorithm was Random Forest which outperformed the other algorithms. Even tough techniques for feature selection and re-sampling of the data to try to balance the dataset[47] were used, a model could not be build that would successfully distinguish between melanoma and non-melanoma images on the second dataset.

Additional images are needed to obtain a good classification model. Based on the current state of the art, more than 100.000 images were used to obtain an expert quality deep learning model. The challenge of using smaller datasets to obtain a good model is yet to be overcome.

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