Genetic Recognition of Changes in Melanocytic Lesions

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Abstract—**Because of the higher incidence of malignant melanoma, researchers are concerned more and more with the automated diagnosis of skin lesions. We investigate in this paper the application of genetic algorithms for recognizing the images of the same melanocytic nevus taken at different moments of time. The idea is that a novel view of an object can be recognized by simply matching it to combinations of known views of the same object. The main difficulty in implementing this idea is determining the parameters of the combination of views. The space of parameters is very large and we propose a genetic approach to search this space efficiently. The effectiveness of this approach is shown on a set of real images captured with a camera and a video capture board under different angles of view.**

Index Terms—**Biomedical image processing, genetic algorithms image matching, medical diagnosis**

I. Introduction

MALIGNANT melanoma is nowadays one of the leading cancers among many white-skinned populations around the world. Change of recreational behavior together with the increase in ultraviolet radiation cause a dramatic increase in the number of melanomas diagnosed. The curability of this type of skin cancer (about 70%) depends of early enough recognition and surgically treatment. Because of the higher incidence of malignant melanoma, researchers are concerned more and more with the automated diagnosis of skin lesions. Many publications report on isolated efforts into the direction of automated melanoma recognition by image processing, but complete integrated dermatological image analysis systems are hardly found in clinical use [2].

Clinical features of melanoma are summarized as what's called ABCD: Asymmetry, Border irregularity, Colour variegation and Diameter greater than 6mm. Early recognition of changes of lesion in terms of the above features provides important diagnostic and prognostic information. On the other hand, the seven-point checklist, advocated by a group of dermatologists from Glasgow, emphasizes the progression of the symptoms. This checklist consists of three major features (change in size, shape and colour) and four minor features (inflammation, crusting or bleeding, sensory change, and diameter greater than 7mm). When any of the major features is detected in a melanocytic lesion, immediate help from health professionals is recommended. The presence of any minor features is advised to be monitored regularly [4].

We have focused on the detection of any modification in the border irregularity of the lesion, by comparing two different images: one of them is an older reference view of the lesion, and the other one is a more recent view of the same lesion. If the novel view of the lesion is able to match the reference view, modified by a 2D affine transformation eventually, then the size and shape of the lesion is not modified. A genetic algorithm searchs the parameters of the transformation.

Image segmentation plays an important role in identifying borders of the lesion because accurate description and measurement of image features cannot be achieved without accurate image segmentation. A wide range of algorithms have been used for image segmentation, broadly categorized as pixel-based segmentation, region-based segmentation and edge detection. An efficient algorithm from data mining perspective by applying a clustering technique was proposed in [3].

In the Fig. 1, we can see two different images of the same skin lesion. Before these lesion images can be used for border shape analysis, they have to be processed by two programs. First, the dark thick hairs of the skin images are removed by the software program called DullRazor, a program implemented in [4], which consists of three basic steps: identifying the dark hair locations, replacing the hair pixels with the nearby non-hair pixels, and smoothing the final result.

The images from the Fig. 2 are obtained with a simple segmentation program. Our goal in this paper is to find as more as matches between some significant points of the first border shape and the contour of the second shape.

The remainder of this paper is organized as follows. Section II presents an overview of the theory of Algebraic Functions of Views. The methodology used to estimate the best values for the parameters of the combination scheme, including the genetic search, is described in Section III. Section IV includes our experimental results and finally, our conclusions are given in Section V.

II. Background on Algebraic Functions of Views

A short introduction in the theory of Algebraic Function of Views is presented in [1]. This concept provides a powerful foundation for tackling variations in the appearance of an object's shape due to viewpoint changes. According to this theory, the variety of two-dimensional views depicting an 2D or 3D object can be expressed as a combination of a small

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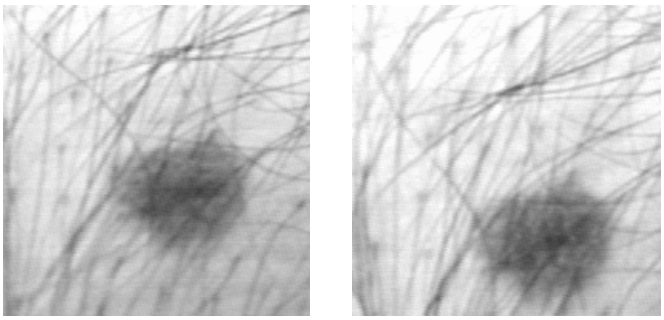

Fig. 1. Two different images of the same skin lesion

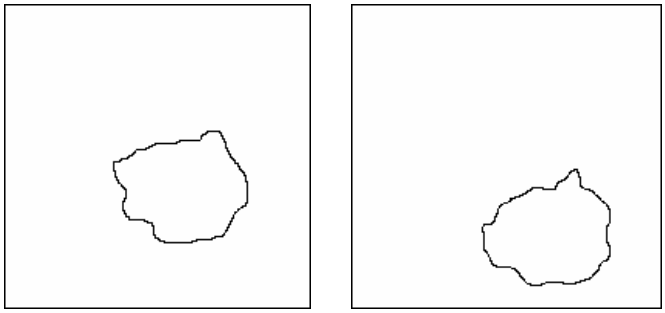

Fig. 2. The above images, after DullRazor and segmentation

number of 2D views of the object. In the case of 2D objects, the combination scheme is equivalent to an affine transformation of the image coordinates from the known view. It was shown that if we let an object undergo 3D rigid transformations, (i.e., rotations and translations in space), and we assume that the images of an object are obtained by orthographic projection followed by a uniform scaling, then any novel view of the object can be expressed as a linear combination of three other views of the same object. If we have three corresponding points, with coordinates (x', y'), (x'', y'') and (x''', y'''), one from each reference view of the object, then the coordinates (x, y) of the corresponding point from a novel view of the same object, obtained by applying a different rigid transformation is as the following:

$$x = a_1 x' + a_2 x'' + a_3 x''' + a_4 \quad (1)$$

$$y = b_1 y' + b_2 y'' + b_3 y''' + b_4 \quad (2)$$

where the parameters $a_j, b_j, j = \overline{1,4}$ are the same for all the points that are in correspondence across the four views. These parameters can be recovered by solving a linear system of equations, given that we know at least four point correspondences across the views.

Although it was not explicitly discussed in the literature, algebraic functions of views also exist in the case of 2D objects, and is sufficient a single reference view. This is because in the case of planar objects, scaled orthographic projection is equivalent to a 2D affine transformation. Given a novel view and a point with coordinates (x, y) that is in correspondence with the point with coordinates (x', y') in a reference view, then the coordinates of the corresponding point from the novel view are:

$$x = a_1 x' + a_2 y' + a_3 \quad (3)$$

$$y = b_1 x' + b_2 y' + b_3 \quad (4)$$

In this paper, we have used (3) and (4) for a number of N selected points from the border of the first lesion. Given the point correspondences across the reference and new view, the following system of equations should be satisfied:

$$\begin{bmatrix} x_1' & y_1' & 1 \\ x_2' & y_2' & 1 \\ \dots & \dots & \dots \\ x_N' & y_N' & 1 \end{bmatrix} \cdot \begin{bmatrix} a_1 & b_1 \\ a_2 & b_2 \\ a_3 & b_3 \end{bmatrix} = \begin{bmatrix} x_1 & y_1 \\ x_2 & y_2 \\ \dots & \dots \\ x_N & y_N \end{bmatrix} \quad (5)$$

where (x_1', y_1'), (x_2', y_2'), … (x_N', y_N') are the coordinates of the points in the reference image, and (x_1, y_1), (x_2, y_2), … (x_N, y_N) are the coordinates of the points in the new view.

A very important problem consists in determining the range of values for $a_i, b_i, i = 1,2,3$. Splitting the above system into two subsystems, we have:

$$P \cdot c_1 = p_x \quad (6)$$

$$P \cdot c_2 = p_y \quad (7)$$

where the columns of the P matrix are shown in (5), c_1 and c_2 are vectors corresponding to the parameters of the combination scheme a_i and b_i, and p_x, p_y are vectors corresponding to the x and y coordinates of the new view. The P matrix can be factorized as $P = U_P \cdot W_P \cdot V_P^T$, where both U_P and V_P are orthonormal matrices, while W_P is a diagonal matrix whose elements w_{ii}^P are always nonnegative. The solutions of the above two systems are $c_1 = P^+ \cdot p_x$ and $c_2 = P^+ \cdot p_y$, where P^+ is the pseudoinverse of P. Assuming that P has been factorized, its pseudoinverse is $P^+ = V_P \cdot W_P^+ \cdot U_P^T$, where W_P^+ is also a diagonal matrix with elements $1/w_{ii}^P$ if w_{ii}^P is greater than zero and zero otherwise. The solutions of (6) and (7) are given by the following:

$$c_1 = \sum_{i=1}^{k} \left(\frac{u_i^P \cdot p_x}{w_{ii}^P} \right) \cdot v_i^P \quad (8)$$

$$c_2 = \sum_{i=1}^{k} \left(\frac{u_i^P \cdot p_y}{w_{ii}^P} \right) \cdot v_i^P \quad (9)$$

where u_i^P is the ith column of matrix U_P, v_i^P is the ith column of matrix V_P, and k = 3. To determine the range of values for c_1 and c_2, we assume that the x and y coordinates belong within a specific interval.

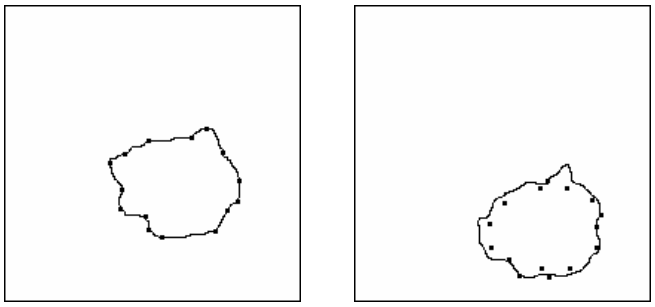

Fig. 3. An example of matching between the model and the scene by evolution.

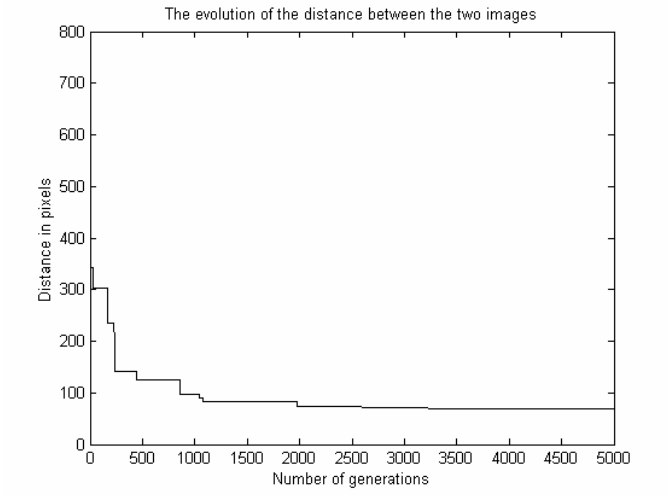

Fig. 4. Evolution of the fitness of the best chromosome for the above example.

This scaling can be done, e.g., by mapping the views to the unit square. In this way, its *x* and *y* image coordinates will be mapped to the interval [0,1]. To determine the range of values for c_1 and c_2, we need to consider all possible solutions of (6) and (7), assuming that p_x and p_y belong to [0,1]. This problem is solved by Interval Analysis in [1]. It should be mentioned that since the matrix *P* and the intervals for p_x, p_y are all the same, the interval solutions for c_1^I and c_2^I will be the same (the superscript *I* denotes an interval vector). The range of values calculated in [1] are: [-0.408, 0.408] for a_1, b_1, [-0.391, 0.391] for a_2, b_2, and [0.0, 1.0] for a_3, b_3.

III. GENETIC SEARCH

We have used a genetic algorithm to search the space of all possible transformations in order to find a transformation which would bring a large number of model points into alignment with the scene. We consider the reference view as a model, and the novel view as a scene.

Each chromosome contains six fields, with each field corresponding to one of the six parameters $a_i, b_i, i = 1,2,3$. Each parameter is encoded on the seven bits, and the precision of encoding is better than 1%. The total length of each chromosome is 42 bits.

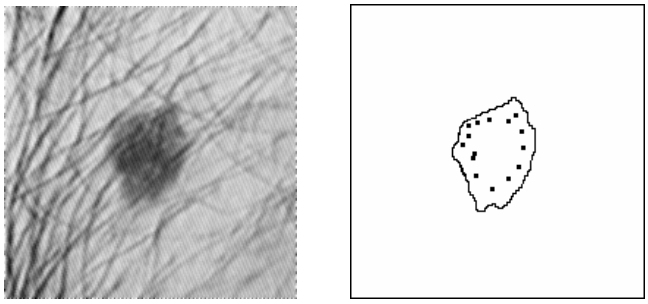

Fig. 5. An example of matching between the same model as in Fig. 3 and the scene, which consists of the same lesion as in Fig. 1, but from a completely different angle of view.

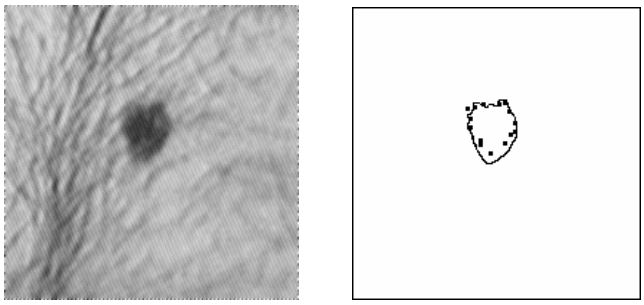

Fig. 6. Another example of matching between the model in Fig. 3 and a new scene, which consists of the same lesion as in Fig. 1, but from a different angle of view (a greater distance from the camera).

The fitness of individuals is estimated by computing the back-projection error between the model and the scene. To compute this error, for every model point, we find the closest scene point and then compute the distance between these two points. The overall back-projection error, that is the total distance in pixels, is the sum of all these partial distances.

The genetic algorithm is a standard one, with a two point crossover and fitness-proportionate selection by roulette-wheel sampling. The population size is 100 and 40 of these chromosomes are changed each generation. We have usually used in our experiments a crossover probability of 100% and a mutation probability of 5%. The stop criterion of the algorithm is the number of generations. A fast and reliable result is obtained after 1000 generations, but for the simulations presented in this paper we have used a number of 5000 generations.

IV. EXPERIMENTS AND RESULTS

We have selected in the model from the Fig. 3 a number of $N = 15$ representative points. These fiducial points are matched with the second contour, and, as we can see in the Fig. 4, the maximum back-projection error between the model and the scene, after an evolution of 5000 generations, is less than 100 pixels. The two images are represented with a resolution of 200×200 pixels. Our experiments show that the best results are obtained with small populations (between 50 and 100 chromosomes) and a sufficient great number of generations. We can see that the performance plot from the

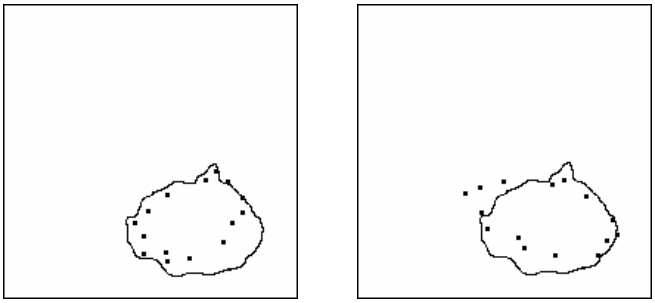

Fig. 7. The scene differs from the model given in the Fig. 3. The surface of the lesion is greater than in the first case. This fact is explained by an assumed growing of the lesion in the right-down side.

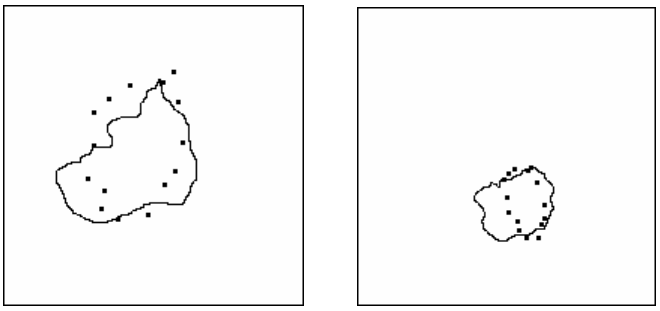

Fig. 8. The scene differs from the model given in the Fig. 3. There is no connection between the model and these two scenes, obtained by segmentation of two different lesions.

Fig. 4 indicates that the genetic algorithm very quickly predicts roughly the correct appearance of the model in the scene and then spends most of its time making little progress.

In the Figs. 5 and 6, we have presented another two different images of the same lesion. The angles of view are completely different than in the first case. This fact explains maybe some errors in the process of matching between the model and the scene. However, it's easy to see that the approximate matching is a precious indication that all these images are obtained from the same lesion. We suggest, for a final decision, to take different images from the same lesion, with different angles of view, and compare them, as we did in the Figs 3, 5 and 6.

In the Figs. 7 and 8, we have shown the matching of the model in modified scenes, coresponding to segmented images of the different lesions. In the Fig. 7, we can see a modified scene by growing in the surface of the lesion with about 10%. In the image from the left side of the figure, we can see even the direction of growing in the lesion, but this result is only a lucky event. In the image from the right side of the figure, we can see that it is possible the matching with the new points of the scene, others than those from the original image. These images from the Fig. 7 have been obtained with two different runnings of the same genetic algorithm.

In the Fig. 8, we have two completely different scenes, without any conection with the original model from the Fig. 3. The contours of these images can not be matched with the original model, and this figure shows two possible best results of attempting to match between the model and the scenes. It is sufficiently clear that the matching in these cases is not possible, and the decision is that these two lesions are completely different from the model discussed. Obviously, in a melanoma screening program, we are interested on the evolution of suspicious lesions in time and the results shown in the Fig. 7 are much more concludent than those presented in the Fig. 8.

V. CONCLUSION

In this paper, we considered using a genetic algorithm to recognize some contours of the skin lesions. This idea is useful in the screening of the suspicious skin lesions. Two different images of the same lesion are taken at different moments of time, under different angles of view, and we must decide if the borders of the lesion are modified or not. The recognition strategy used was based on the theory of Algebraic Functions of Views. Our goal was only the matching between the model and the scene. The problems of removing the hair and segmentation of the image have been solved in another works.

We have observed in our experiments that, even if the back-projection error is big in some cases, the shape of the model looks like the shape of the scene, if we discuss about the same lesion. If the borders of the lesion are modified, we must easy observe this modification. Near-exact matches are useful in the sense that can actually reduce the search space of the parameters to a limited domain. Then, a local optimization technique can be used for finding an exact match. The preliminary stage of rough alignment may help preventing such methods from reaching a local minimum instead of the global one.

The most important step in this process of recognition is automatic segmentation of the images. This task is not trivial, because the software approach to hair removal affects some pixel values underneath the hairs, and these values cannot be reconstructed accurately by a single view. On the other hand, some lesions have fuzzy borders, and these borders may depend on angle of view, light of the scene, the distance between the camera and the skin, and so on. Our segmentation algorithm introduces some errors, but we think that they are not very important for our results. For future research, we plan to solve better the problem of segmentation, to increase the number of fiducial points on the contour and to establish some useful rules for the construction of a robust genetic algorithm.

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