Modelling of edge profiles in pigmented skin lesions

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Abstract. The sharpness of the lesion boundary and the contrast between the lesion and the surrounding skin provide important diagnostic information in the assessment of pigmented skin lesions. This paper presents a new method for computing these parameters by employing an edge model based on a sigmoid function. For each radial profile of the lesion, optimal parameters are found by using an iterative least-squares method. The level and nature of variability of these parameters along the boundary will be correlated with lesion diagnosis in a future study. The method also returns the location equivalent to "zero-crossing" for each profile, thus producing a lesion outline. Additionally, the spread of the pigment beyond the zero-crossing point is computed, thus showing the lesion extent.

Introduction

In clinical and dermatoscopic assessment of pigmented skin lesions the region of transition between the body of the lesion and the surrounding normal skin is considered to carry a number of important diagnostic clues [1]. For example, a sharp transition and high contrast may indicate a particular type of melanoma; a gradual transition over a small section of an otherwise sharp periphery may also indicate malignancy. Humans, in general, are not very good at discriminating between subtle variations in contrast or blur [2] and this may partially explain the relatively poor clinical performance of even experienced clinicians [3]. These problems have been recognised and a number of groups have been working on the development of computer-based objective methods for characterising the periphery of lesions [4]. A common approach is to obtain first an outline of a lesion and then proceed along the consecutive radial profiles carrying out computations. Contrast is usually computed as a difference between brightness of the skin and the lesion. The sharpness of the transition is normally computed as the gradient of the transition. Typically these computations are carried out on a grey-level representation of the lesion's luminance.

We propose an alternative approach where all the parameters characterising the transition are computed simultaneously. We chose to represent the edge profile using a particular functional model and the derived parameters are optimal (in a least-squares sense) with respect to this model. In contrast with existing methods, this approach also makes it much simpler to evaluate the results as this is done via an objective function rather than using subjective judgement. The method proceeds as follows:

- Determine the location of the "body" of the lesion and find a rough location of its boundary;
- Decompose the lesion into a number of profiles perpendicular to the lesion boundary found above;
- For each profile compute the contrast, the slope and the edge midpoint (equivalent to the location of the zero crossing);
- Compute the error of fit and remove from further processing the profiles for which the error is too large.

The computation is carried out on "parametric maps" showing the total melanin content at a given skin location. Parametric maps are lesion representations which show separately the magnitudes of skin components, namely blood, dermal and epidermal melanin, and collagen. They are computed from colour and near-infrared images using a physical model of skin optics. The limited space here prevents description of the method of computing the parametric maps, interested readers are referred to [5]. The proposed edge modelling method is suitable for any edge profiles. In its application to pigmented skin lesions described here the parametric maps for melanin are used because it is the nature of melanin spread and its levels that are important in the diagnosis of melanomas

Methods

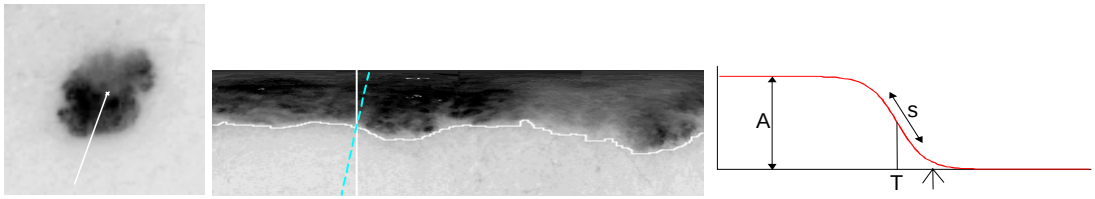
Finding the lesion and its boundary

In order to make the process fully automatic, it is necessary first to find the region in the image which approximately corresponds to the body of a lesion. This binary region will be subsequently used to compute the (approximate) centre of the lesion and the boundary coordinates, both required for the radial decomposition.

There has been much work on lesion segmentation (e.g. [4]). Variability in the appearance of pigmented skin lesions is such that a single method usually does not work for more than half the lesions in a sample set. In this

work we have adopted a modified "fusion" method originally proposed by Ganster *et al* [6]. In outline, several histogram-based segmentation methods are applied, yielding a set of segmented binary images. Those which are over-fragmented, under-segmented, or contain regions adjacent to the image boundary are rejected. The remaining images are "fused" by the logical OR function and smoothed using morphological closing. On a set of 300 lesions, 96% of the segmentations were of a quality acceptable for the subsequent edge modelling.

The method of edge parameter recovery takes values along lesion profiles (see Figure 1). In a simple approach the profiles are computed along lines all originating in the lesion centre. However, for non-circular lesions such profiles lead to under-estimation of edge sharpness. In order to avoid this problem, the profiles should be in a direction locally normal to the lesion boundary. This is achieved in two steps. First, the lesion is decomposed into a set of profiles by using a polar coordinate transform with origin in the centre of the binary region computed above. Using the same transformation, the *(x,y)* coordinates of the region's outline are also converted to polar representation. The coordinates are lightly smoothed to further remove small irregularities in the contour. For each point *k* on this provisional boundary, a new profile is computed, normal to the boundary at point *k*. Finally, value $E_k = min($ profile $k)$ is subtracted from each profile *k*.



(a) (b) (c)

Figure 1: (a) A lesion with a radial profile overlaid; (b) Radial decomposition of the lesion with a provisional boundary overlaid. Solid vertical line shows a radial profile, dashed line shows a profile normal to the provisional boundary; (c) Model of the edge profile showing graphically the interpretation of parameters A, T and s. The arrow shows the "lesion extent".

Edge modelling

The key edge characteristics sought in pigmented skin lesions are the contrast, the edge sharpness and the extent of the melanin spread. Preliminary analysis of lesion edge profiles showed that they can be usefully modelled using a sigmoid function of the form

$$p(r, A, T, s) = \frac{A}{1 + s^{(r - T)}}$$

where *A* corresponds to the amplitude, *s* corresponds to the sharpness and *T* is the location of the edge midpoint (see Figure 1(c)). Given the image values *P* along a single profile of length *m*,

$$y_i = P(r_i),\ i=1, ..., m$$

the parameters *A*, *T* and *s* can be recovered by nonlinear least squares fitting.

If *p()* is taken to be a function of a known analytic form which depends on parameters *r*, *A*, *T* and *s*, we can construct a set of *m* equations, to be solved with respect to *A*, *T* and *s*:

$$y_1 = p(r_1, A, T, s) = p(r_1, \alpha)$$
$$\cdots$$
$$y_m = p(r_m, A, T, s) = p(r_m, \alpha)$$

where, for simplicity of notation, $\alpha = [\ A\ \ T\ \ s\ ] = [\ \alpha_1\ \ \alpha_2\ \ \alpha_3\ ]$ is a vector of the parameters. If *m* is greater than the number of parameters, this system is overdetermined and least squares fitting methods can be used to solve it. We shall use an iterative method [7].

At initialisation the parameters in $\alpha^{(0)}$ are assigned a set of values which can be arbitrary, but preferably are chosen to be a reasonable approximation to the parameters sought. We follow the latter scheme and derive the initial parameters $\alpha^{(0)} = [\ A^{(0)}\ \ T^{(0)}\ \ s^{(0)}\ ] = [\ \alpha_1^{(0)}, \alpha_2^{(0)}, \alpha_3^{(0)}\ ]$ by applying the least squares fitting procedure to the average of all the profiles. We define residuals $R_i = y_i - p(r_i, \alpha)$, $i = 1, ..., m$, and seek to compute a vector of changes, $\delta = [\delta_1, ..., \delta_m]$, such that the sum of squared residuals is minimised. A linearised estimate of R_i is

$$R_i = \sum_{j=1}^{3} \frac{\partial p}{\partial \alpha_j}(r_i,\alpha)\delta_j\ ,\ \ i = 1, ..., m$$

which can be expressed in matrix notation as $R_i = M\delta_j$, where M is a matrix

$$M = \begin{bmatrix} \frac{\partial p}{\partial \alpha_1}(r_{1,}\alpha) & \frac{\partial p}{\partial \alpha_2}(r_{1,}\alpha) & \frac{\partial p}{\partial \alpha_3}(r_{1,}\alpha) \\ \frac{\partial p}{\partial \alpha_1}(r_{2,}\alpha) & \frac{\partial p}{\partial \alpha_2}(r_{2,}\alpha) & \frac{\partial p}{\partial \alpha_3}(r_{2,}\alpha) \\ \cdots & \cdots & \cdots \\ \frac{\partial p}{\partial \alpha_1}(r_{m,}\alpha) & \frac{\partial p}{\partial \alpha_2}(r_{m,}\alpha) & \frac{\partial p}{\partial \alpha_3}(r_{m,}\alpha) \end{bmatrix} \quad \text{and} \quad \frac{\partial p}{\partial \alpha_1} = \frac{\partial p}{\partial A}, \quad \frac{\partial p}{\partial \alpha_2} = \frac{\partial p}{\partial T} \quad \text{and} \quad \frac{\partial p}{\partial \alpha_3} = \frac{\partial p}{\partial s}$$

The entire system of equations then becomes, $\boldsymbol{R} = M\delta$, and after multiplication by M^T:

$$M^T\boldsymbol{R} = (M^TM)\,\delta$$

As M and **R** are known, this matrix equation can be solved with respect to δ - a vector of changes which generates a new vector, $\alpha^{(1)}$, of approximate solutions. New residuals are computed using $\alpha = \alpha^{(1)}$ and iteration continues until the least squares error of residuals does not change by more than a pre-defined limit. This procedure is applied to each profile to compute its parametrisation in terms of A, T and s which characterise, respectively, elevation, edge midpoint and slope.

Although the parameters derived above are optimal, this does not mean that they always generate parametric profiles which fit well the real lesion profiles. Problems occur in low contrast and / or highly textured lesions. Such lesions have a proportion of poorly fitted profiles which should not be used in subsequent analysis. The error of fit is computed by comparing real profiles with the profiles reconstructed using the derived parameters:

$$\varepsilon = \frac{1}{m}\sqrt{\sum_{i=0}^{m} [\,P(r_i) - (E + \frac{A}{1 + s^{(r_i - T)}})]^2 \cdot w_i}$$

The profiles for which the error ε is excessive are excluded from further analysis. In the above equation w_i is a vector of weights which emphasises those locations on the profile which were found to be most important for the profile parametrisation: namely both ends (being the minimum and maximum of elevation values) and the central part, from which the slope is determined. The use of w_i can possibly be avoided by formulating ε as a chi-square estimator with variable σ_i [10].

Results

Experiments were carried out on images of 94 pigmented lesions selected so that they represented a variety of appearances. The analysis was applied to parametric maps showing total melanin because it is the nature of melanin spread on the periphery that is of diagnostic interest. All together about 20,000 profiles were examined, of which 76% had excellent fit ($\varepsilon < 0.33$), and 88% had acceptable fit ($\varepsilon < 0.5$). Profiles with $\varepsilon > 0.5$ were rejected. Only 1.8% profiles had $\varepsilon > 1$. Most rejected profiles were in lesions having poor contrast.

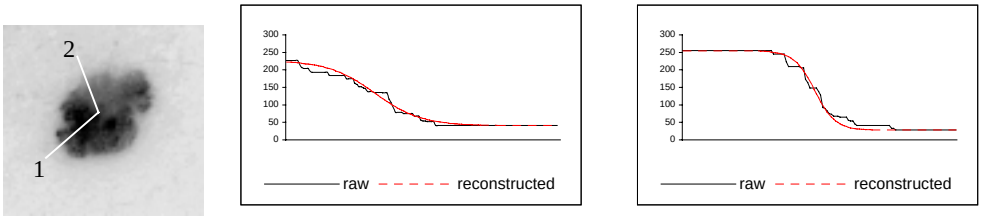


Figure 2: A pigmented skin lesion and examples of two lesion profiles together with their reconstructed sigmoid models.

By way of subjective evaluation, two further (non-quantitative) tests were carried out. In the first, the real profiles were displayed alongside the reconstructed profiles in a polar coordinate view. In the second, the location of the edge midpoint was displayed overlaying the lesion, to observe the correctness of the border placement. Both tests confirmed satisfactory performance.

Discussion

Modelling of edge profiles using a sigmoid function worked well for pigmented skin lesions. The model used in our previous work was a step edge convolved with a Gaussian, $p(r, A, T, \sigma) = A \cdot H(x-T) * G(r,\sigma)$ [8], where $H(x)$ is the Heaviside function, A is the amplitude, T is the location of discontinuity and σ the Gaussian standard

deviation. Parameters *A* and *T* were derived directly from the edge profile, thus defining the step function $A \cdot H(x-T)$, and parameter σ was obtained by deconvolving the lesion profile with the step function derived above. Although the results were satisfactory, that method was not as robust as the one presented here. Firstly, *A* and *T* were not necessarily optimal as they had to be computed directly from edge profiles. Secondly, profiles with a large amount of variability required the use of heuristics to correctly identify the amplitude. Problems were also arising due to the use of de-convolution, which sometimes generated large errors caused by small denominator values in frequency domain division. The current method does not suffer from these problems. The use of a least squares method guarantees that the results are optimal.

The use of an edge modelling approach enables us to derive simultaneously two diagnostically important parameters: one related to the lesion contrast and the other to the sharpness of the boundary. One intended use is to investigate the variability of these parameters along the lesion periphery. Figure 3 shows graphs characterising the boundary of the lesion in Figure 4. Our earlier work on feature perception [9] strongly indicated that it is not the *magnitude* (of contrast or sharpness), but the level and nature of *variability* of these features that correlate with lesion diagnosis. We have begun a separate study to test this hypothesis.

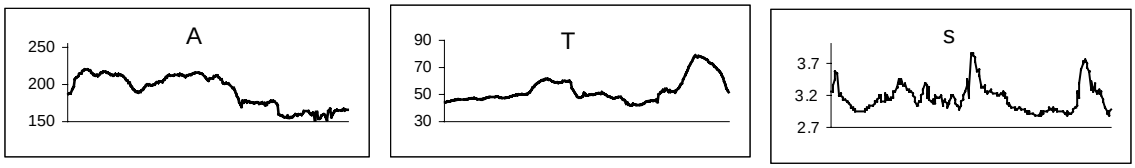


Figure 3: Graphs showing magnitude of parameters *A*, *T* and *s* along periphery of the lesion in Figure 4.

Parameter *T* indicates the position on a lesion profile which is equivalent to the commonly used zero crossing. By linking these positions for all the profiles we obtain a lesion boundary. "A boundary" is used deliberately here; we have previously argued (e.g. [8]) that the zero crossing and similar approaches may not be the best choice for boundary localisation in medical images which involve a degree of translucency or spread. Such boundaries are placed in the *middle* of the spread rather than at its *periphery*. We compute two boundary locations: one showing the zero crossing equivalent, and the other the "lesion extent". The latter is placed at the point of the highest curvature on the reconstructed sigmoid profile and should be a better indicator of the real extent of a lesion (see Figure 1(c), the position marked with an arrow and an outline shown in Figure 4 on the right).

Figure 4: The outline in the image on the left is equivalent of "zero crossing"; outline on the right shows the "lesion extent".

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