Automatic Surveying of Cutaneous Hemangiomas*

Sebastian Zambanini[1], Georg Langs[1,2], Robert Sablatnig[1], Peter Donath[3], Harald Maier[3†]

[1]Pattern Recognition and Image Processing Group, Vienna University of Technology, Austria
[2]Institute for Computer Graphics and Vision, Graz University of Technology, Austria
[3]Division of Special and Environmental Dermatology, Medical University of Vienna, Austria
{zambanis, langs, sab}@prip.tuwien.ac.at, harald.maier@meduniwien.ac.at

Abstract

This paper presents a method for the fully automatic surveying of cutaneous hemangiomas by means of a hemangioma segmentation and a ruler visible in the images. The algorithm computes the spatial resolution of an image. Hemangioma segmentation is accomplished by a single-layer perceptron classification by means of pixel color features. The algorithm was evaluated on a set of 120 images. It achieves satisfactory results on images with clearly visible, saturated hemangiomas.

1 Introduction

Cutaneous hemangiomas are the most common benign vascular tumors in infancy with a frequency of about 10 %. Due to their potency of rapid proliferation they may threaten vital structures by tumor compression or tumor obstruction and/or may impair vital functions such as breathing, vision, hearing, ingestion or excretion. Lesions occurring in the face or neck may cause psychological problems in the little patients and their parents [1]. Safe and effective treatment modalities at the earliest time possible can stop further proliferation, induce regression and prevent complications [6]. Until now the natural course of hemangiomas or their response to a certain therapy was assessed only by clinical examination and simple measurement of the diameters of the lesion. The affected area / area reduction, however, was very difficult to measure. In order to make the area assessment faster and more precise than a manual procedure, an automated method is highly desirable. By automated image segmentation the area measurement would become clinically practicable and could highly improve the quality of any investigations on the efficacy of hemangioma treatment.

This paper presents an automated method for surveying cutaneous hemangiomas that were photographed along with a ruler to determine the scale of the image. The task is divided in two main parts. First, the scale of the images is determined by means of the ruler visible in the image, and second, the skin area belonging to the hemangioma is segmented.

The paper is organized as follows: Sec. 2 explains the algorithm used for scale estimation. In Sec. 3 a description of the segmentation process is given. In Sec. 4 experiments performed on the data are presented and discussed. A conclusion is finally given in Sec. 5.

2 Computing the Scale of the Images

All images show a ruler close to the hemangioma. The ruler has 4 bold lines in 1 cm distance steps. The task of the algorithm is to compute the Euclidean distance between two lines to obtain the spatial resolution of the images. The area of the hemangioma can then be estimated after image pixels have been segmented w.r.t. the hemangioma. The error due to the fact that both hemangioma and ruler are not situated on a planar surface parallel to the image plane is neglected (see Sec. 4 for an evaluation of the resulting decrease of precision). The algorithm consists of two main steps:

1. Segmentation of the ruler: Since all rulers are white and differ clearly from the rest of the image, this can simply be done by global thresholding with the H and V channel of the HSV color model. Sometimes small regions not belonging to the ruler remain, so only the largest region in the computed mask is considered.

2. Scanlining: After segmentation the distance between two marks is measured along the major axis of the ruler region. For robustness we use three scanlines to determine the number of pixels between two marks: one on the midpoint between the top and bottom of

*This research has been supported by the Austrian Science Fund (FWF) under the grant P17083-N04 (AAMIR).

†Senior co-author

(a) (b)

Figure 1. Example for determining the scale of an image.

the ruler and another two 10 pixels above and below, respectively. To ensure the most precise measurement possible the maximum number of pixels between two marks in all of the three scanlines is used. It can happen that some marks are not recognized in the scanline (e.g. when the ruler has a strong curvature), hence too large distances with more than 200 pixels between two marks are rejected (in all images no greater distance than 155 pixels could be found). An example for determining the scale of an image can be seen in Fig. 1: After segmenting the ruler of Fig. 1a, three scanlines are used to find the maximum distance between two marks (Fig. 1b).

3 Segmentation of Hemangiomas

The segmentation determines the regions in an image belonging to the hemangioma. For the special problem of skin lesion segmentation various methods have been proposed. A thresholding operation is often used for the segmentation of melanomas [2], [10]. Round et al's work on segmentation of skin lesions is an application of the split-and-merge algorithm [7]. Schmid et al. present a region-based approach working with two-dimensional histogram analysis and fuzzy c-means clustering [8]. Hance et al. [4] compare six different color segmentation algorithms for the special application of finding skin tumor borders with the conclusion, that the best results can be achieved by adaptive thresholding and the PCT/median cut algorithm or by combining different methods. Other methods for skin lesion segmentation include radial search [11] and DBSCAN-Clustering [3].

For the segmentation of hemangiomas a different approach has to be applied. This is due to the low contrast between skin and hemangioma regions, since hemangiomas mainly appear in bright red [9]. Furthermore, the problem of all color segmentation algorithms is to determine which of the segmented regions are hemangioma regions. Making use of specific a priori knowledge about the general appearance of hemangiomas is difficult because hemangiomas can come in a variety of shapes and sizes.

Due to this difficulties we use a classifier for segmenting the images that classifies each pixel in the image as hemangioma or non hemangioma on the basis of features extracted from the pixel. For a simple and fast classification a single-layer perceptron is used. Multilayer perceptrons were tested but were abandoned since they did not provide significant improvement. Better image acquisition techniques are crucial in order to distinguish between skin colors which are hard to discern even for the medical expert.

In the following our segmentation method is described in detail, divided into preprocessing (Sec. 3.1) and classification (Sec. 3.2).

3.1 Preprocessing

Before classification the images have to be preprocessed to improve the accuracy of the perceptron classifier and to reduce computation time. To remove noise a 5x5 median filter is applied on the images. Furthermore, image regions containing no skin are masked out and the images are normalized in such a way that skin has nearly the same color values in all images:

Non skin masking: After the median filtering a simple test for masking out non skin regions is used to exclude regions that likely are not part of the skin or the hemangioma (e.g. the ruler). That step is necessary for a robust skin color normalization. Our method is based on a heuristic proposed in [4] but substantially simpler. We only check for each pixel, if the red color value is smaller than the green and blue color value. If one of these conditions is complied with, the particular pixel is marked as non skin. This test makes use of the fact that skin has usually a reddish color and therefore shows a greater red portion than green and blue portion. By applying this test on all 120 images we got an almost perfect result for 96 images (classification error less than 1%). The rest shows an average classification error of about 5%.

Skin color normalization: To achieve more accurate classification results a normalization with the skin color has to be performed on the images. We have to determine the color value of the skin in an image and subtract these value from all pixels with the aim of having nearly the same color value of (0,0,0) for skin pixels in all images. For that purpose a 3D histogram of the RGB color channels is created and the maximum RGB value, which has a brightness greater than 120, is taken as skin color (the threshold of 120 was decided for by empirical tests). This method makes use of the fact that after non skin masking the majority of the remaining pixels in an image represents skin. Tests have shown that a manual normalization (by choosing three 3x3 windows near the border of the hemangioma and taking the mean color value of all windows as skin color) does not induce better classification results than the histogram normalization.

Figure 2. The intensity images of the four features (a) G, (b) H, (c) a and (d) $abdist$ of a particular hemangioma image.

3.2 Classification of Hemangiomas

Our segmentation method is based on a single perceptron that classifies all pixels in the images based on 4 color features. In order to eliminate interference with natural features (e.g. lips) a rectangular region of interest is defined coarsely encompassing the hemangioma. In the following the features are described and a final postprocessing step eliminating highlight artifacts is explained.

Feature selection: For classification we have to define a set of features showing a big difference between skin and hemangioma pixels. Possible features for the classification are the color channels of the color spaces RGB, HSV and CIE 1976 L*a*b* [5]. G from RGB, H from HSV and a^* from L*a*b* proved to be usable for our purpose by achieving the best results with a perceptron classification of our images. Additionally we use a 4^{th} feature *abdist*. As can be seen in Fig. 2, each of these features has a rather big difference between pixels belonging to the hemangioma and pixels belonging to the skin.

The feature *abdist*: The feature *abdist* stands for the Euclidean distance between the skin and the hemangioma in the $L^*a^*b^*$ color space without consideration of the luminance L^* and intensification of the a^* component. This feature is adopted from [10]. In this paper the proposed method works on an intensity image describing the Euclidean distance between the skin and the lesion.

If a_s, b_s denotes the a^* and b^* values of the skin (obtained from the normalization step) and a_p, b_p that from a particular pixel, its *abdist* is computed as $\sqrt{(2a_s - 2a_p)^2 + (b_s - b_p)^2}$. The difference of the a^* channel is multiplied with the factor 2, because the a^* value differs more between hemangioma and skin pixels than the b^* value.

Treatment of highlights: Highlights on the hemangioma are normally erroneously detected as healthy skin by the classifier. This is corrected by closing all holes occurring in the masked region. Since hemangiomas with large holes of normal skin could not be found in the data, they seem to be very rare and a possible error resulting from that operation can be neglected.

4 Experiments

Setup: Experiments were performed on a set of 120 images gathered during clinical examinations. 30 images were used for training and the remaining 90 images served as test set. For all images the relative ground truth was obtained by a manual segmentation in a region of interest under the supervision of a medical expert. To evaluate the accuracy of the segmentation for every image the following error metrics were applied:

- error rate $= \frac{\text{number of misclassified pixels}}{\text{total number of pixels}}$
- false positives rate $= \frac{\text{nr. of false positive pixels}}{\text{nr. of negative pixels}}$
- false negatives rate $= \frac{\text{nr. of false negative pixels}}{\text{nr. of positive pixels}}$
- absolute area difference $= |Area(A) - Area(M)|$
- border error $= \frac{Area(A \cup M) - Area(A \cap M)}{Area(M)}$

where A and M are the regions obtained by the automatic segmentation and the manual segmentation, respectively. The proposed formula for the border error (adopted from [4]) is the most significant error metric because it is independent of both the hemangioma and region of interest size.

To assess the precision of the entire procedure the hemangioma area on 19 pairs of images, depicting the same hemangioma and taken within a few minutes were measured. Absolute area difference and variation coefficient are reported.

Results: The average border error on the 90 test images is 32.1 %, as can be seen in Table 1 where the average errors of all 90 test images are shown.

Error Rate	False Pos. Rate	False Neg. Rate	Absolute Area Difference	Border Error
6.8 %	**5.5 %**	**11.6 %**	**0.0965** cm^2	**32.1 %**

Table 1. Mean errors on 90 test images.

The average error made in the surveying of the hemangiomas lies at 0.0965 cm^2, where the average hemangioma size is 0.6132 cm^2. Generally the errors made are hardly influenced by very bad segmentation results on particular images. The distribution of the different border errors of all 90 images shows that the majority of the images (54 of 90) could be segmented with a border error less than 20 %, for 21 images the error lies between 20 % and 50 % and only 15 images yield an error of more than 50 %.

In Fig. 3 some results are depicted. Fig. 3a-c belongs to the best segmentation results with border errors of 3.6 %, 5.7 % and 6.8%, respectively. Fig. 3d-f belongs

Figure 3. Automatic segmentation (white) and ground truth (black) of 6 images.

to the worst segmentation results with border errors of 247.7 %, 137.5 % and 141.2 %, respectively. Especially declining hemangiomas pose a challenge under difficult lighting conditions. Their correct segmentation is subject of ongoing research.

For the image pairs the average difference of hemangioma area is 0.082 cm^2 while the average variation coefficient is 10.1 %. This error is mainly caused by variations in the image acquisition procedure. Reference measurements with manual segmentation and scale computing leads to an average difference of 0.056 cm^2 and an average variation coefficient of 5.7 %.

5 Conclusion

Experimental results show that the segmentation is accurate on the majority of images. Hemangiomas with regressing, slightly reddish parts (e.g. Fig. 3e), where it is even difficult for a medical expert to distinguish between hemangiomas and healthy skin, pose a problem to the algorithm. Here more sophisticated classifiers like multi-layer perceptrons are expected to improve performance in conjunction with more training data. In general the image acquisition process is crucial to the quality of the results. Inaccuracies in computing the hemangioma area are mainly caused by a less than optimal position of the ruler and hemangioma during acquisition. An improvement of camera position, ruler placement and adequate illumination could contribute considerably to a more precise quantification.

Although the average error of the area calculation (variation coefficient of 10.1 %) seems to be rather high, in most cases the presented automatic method outperforms manual surveying of the images. Thus clinical trials can be improved by a more consistent evaluation of the effect of therapies.

References

[1] B. Drolet, N. Esterly, and I. Frieden. Hemangiomas in children. *New Eng. J. Med.*, 341:173–181, 1999.

[2] H. Ganster, P. Pinz, R. Rohrer, E. Wildling, M. Binder, and H. Kittler. Automated melanoma recognition. *IEEE TMI*, 20(3):233–239, 2001.

[3] W. Guo and Y. Alp Aslandogan. Mining skin lesion images with spatial data mining methods. Technical Report CSE-2003-19, Dep. of Computer Science and Engineering, University of Texas at Arlington, 2003.

[4] G. Hance, S. Umbaugh, R. Moss, and W. Stoecker. Unsupervised color image segmentation with application to skin tumor borders. *IEEE Engineering in Medicine and Biology*, 15(1):104–111, 1996.

[5] J. Kasson and W. Plouffe. An analysis of selected computer interchange color spaces. *ACM Transactions on Graphics*, 11(4):373–405, 1992.

[6] H. Maier and R. Neumann. Treatment of strawberry marks with flashlamp-pumped pulsed dye laser in infancy. *Lancet*, 347:131–132, 1996.

[7] A. Round, A. Duller, and P. Fish. Colour segmentation for lesion classification. *Proc. of the Engineering in Medicine and Biology Society*, 2:582–585, 1997.

[8] P. Schmid and S. Fischer. Colour segmentation for the analysis of pigmented skin lesions. *Proc. of the 6th International Conference on Image Processing and its Applications*, 2:688–692, July 1997.

[9] F. Wirth and M. Lowitt. Diagnosis and treatment of cutaneous vascular lesions. *American Family Physician*, 57(4):765–773, 1998.

[10] L. Xu, M. Jackowski, A. Goshtasby, D. Roseman, S. Bines, C. Yu, A. Dhawan, and A. Huntley. Segmentation of skin cancer images. *Image and Vision Computing*, 17(1):65–74, 1999.

[11] Z. Zhang, W. Stoecker, and R. Moss. Border detection on digitized skin tumor images. *IEEE TMI*, 19(11):1128–1143, 2000.