Automatic Robust Registration of Cutaneous Hemangiomas for Follow-up Examinations [1)]

Sebastian Zambanini[1], *Georg Langs*[1,2], *Robert Sablatnig*[1], *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
{zamba, langs, sab}@prip.tuwien.ac.at, harald.maier@meduniwien.ac.at

Abstract:

This paper presents an automatic method for registering follow-up hemangioma images taken during clinical trials in specific time intervals. The registration is a prerequisite for the analysis of subtle surface changes on the hemangioma, that requires knowledge about the previous state of local appearance to determine the development of the disease. The registration method has to handle the partially changing shape of the hemangioma during its healing process, while typically no surrounding landmarks are available to aid the registration process. The method finds interest points in two images and matches corresponding interest points using SIFT features to determine a homography between the two images by means of RANSAC. Experimental evaluation of the robust registration are reported for image pairs acquired at the same time point and during follow-up.

1 Introduction

Cutaneous hemangiomas are benign vascular tumors made up of newly-formed blood vessels in the skin. They are a common disease in infancy with a frequency of about 10 % [3]. Until now the natural course of hemangiomas or their response to a certain therapy was assessed only by clinical examination. Dermatologists usually make scorings where they try to estimate the degree of regression or enlargement of the lesion. In the case of hemangiomas regressions are indicated by a "graying" of the hemangioma or parts of it. An automatic system for the detection of such grayish regions based on photos taken of a specific hemangioma in given intervals would be useful to support the physician detecting and quantifiying the changes of a hemangioma in an objective manner. A necessary prerequisite of such a system is the registration of consecutive images to detect local color changes of the hemangioma. This paper presents an automatic method for registering images of partially changing hemangioma taken during clinical trials.

State of the art: Several approaches for the registration of dermatological images were proposed in the past dealing mainly with images of skin lesions representing melanoma or

[1)]This research has been partly supported by the FWF under the grant P17083-N04 (AAMIR) and by a grant of the Anniversary Fund of the Oesterreichische Nationalbank.

psoriasis. Maglogiannis [7] and Pavlopoulos [9] both propose a similar hybrid method using the log-polar transformation for estimating scaling and rotation parameters and a sign change similarity criterion in combination with a hill-climbing optimization scheme for translation estimation. Ersbøll et al. [8] work with statistical shape analysis after lesion segmentation to do a first rigid alignment under the assumption of image scale constancy. Afterwards small internal displacements are corrected by a combined registration and alignment scheme. The SHARP-algorithm presented in [2] segments the lesions in the images and uses the first and second order moments of the resulting binary images to determine the rotation and translation parameters. These methods are not capable to handle certain properties of typical hemangioma follow-up images: differences of view point during image acquisition typically exceed a range that can be accounted for by 2D rotation and translation in the image plane. Hemangiomas change appearance during the period of follow-up examinations, thus a robust approach is necessary. In Fig. 1 these cases are illustrated: Fig. 1(a) and Fig. 1(b) show a pair for which reliable matching is only possible for a small part of the hemangioma due to the healing process between examinations and Fig. 1(c) and Fig. 1(d) show a pair of images where the viewpoint change is high.

Our contribution: Our approach is based on the detection and matching of a sparse set of interest points by means of local features. It can deal with partially changing hemangioma shape by employing a robust homography estimation that registers the images. To obtain reliable matches of interest points we use SIFT features [6] for their description. Under the assumption that hemangiomas are planar, the transformation between images is defined as a homography which is estimated by the detected point correspondences using RANSAC.

The method has several advantages over existing approaches for dealing with hemangioma data: SIFT is a rotation and scale-invariant descriptor which allows the reliable matching of points under different views, the modeling of the transformation between images with a homography can represent any projective relation between the images, and finally RANSAC can cope with partially incorrect or missing matches between interest points caused by changed hemangioma appearances.

The feature-based image registration method can be divided into four main steps [11]. They also roughly set the structure of this paper: **1. Feature detection:** Interest Points are detected in both images (Section 2). **2. Feature matching:** Interest points are matched by means of their feature descriptions (Section 3). **3. Transform model estimation:** Matched interest points are used to compute the parameters of the mapping function which is in our case a homography (Section 4). **4. Image resampling and transformation:** The image is finally transformed using the computed mapping function and usually bilinearly interpolated. In Section 5 several experiments performed on the data gathered with the algorithm proposed are presented and discussed. A conclusion is finally given in Section 6.

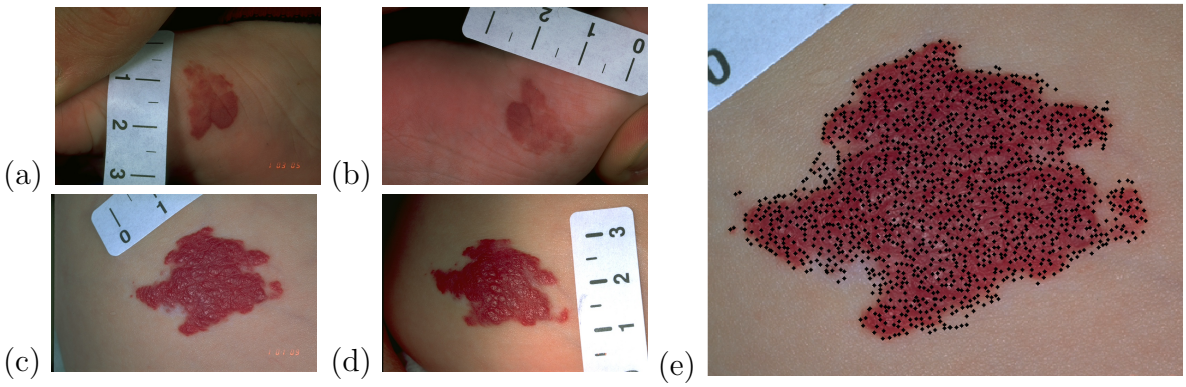


Figure 1: (a)-(d) Two image pairs representing images of the same hemangioma taken at different time points, (e) detected interests point in image (c).

2 Interest Points in Hemangioma Images using SIFT

The first task is to find distinctive interest points in the images to be registered. To detect interest points the standard SIFT method was modified on some points, to account for the specific nature of the image data. The interest point detection is constrained to a region covering the hemangioma, only the green color component of the images is taken into account, and Canny edges are used for the interest point localization.

Constraining interest points to the hemangioma region: The analysis is constrained to a region of interest, including the hemangioma. Segmentation of the hemangioma region is done by a pixel-wise classification method proposed in [10]. Once the image has been segmented, only interest points inside or near the hemangioma region are accepted. This accounts for a better chance of reliable matches in the close vicinity of the hemangioma and reduces computational costs. We perform the SIFT method on normalized green channel images, since they provide more distinctive texture of the hemangioma [10]. **Interest point localization:** The DoG interest points employed in the standard SIFT approach tend to have more extrema at intensity variations inside the hemangioma than at the exact hemangioma border. Therefore they are sensitive to the typical appearance of regressing hemangioma, impeding the use for reliable correspondences. Our method uses Canny edges [1] and interest points are finally localized at edge pixels showing the highest gradient magnitude in a local neighborhood. Although edge-based interest points have the disadvantage that they can not be localized unambiguously, location errors of corresponding interest points can be avoided by a large number of densely located interest points. The improvement achieved by this method is evaluated in Section 5. In Fig. 1(e) the detected interest points (totally 1441) of the image of Fig. 1(c) are shown as black spots.

3 Matching of Interest Points in Two Hemangioma Images

Once the interest points have been localized, their SIFT description has to be computed and they have to be matched in a robust way. For the SIFT description the scale of all interest points is constantly set to the empirically determined value of 3.2 since no scale information

is given by the edge-based interest point localization. The task of the matching step is to find for every interest point of the first image (the *sensed* image) the corresponding interest point of the second image (the *reference* image). We determine the initial matches between the interest points similar to [6]. Although RANSAC is capable of handling a large portion of incorrect matches, a preselection of the matches with highest confidence can improve the stability. Therefore, matches are sorted in terms of the distance between the nearest and the second nearest neighbor in the feature space, and only the best n matches are accepted. The value n is determined by $n = 2\sqrt{m_{si}}$, rounded to the nearest integer value, where m_{si} is the number of interest points detected in the sensed image. This value has been shown to perform well in empirical tests. In the provided images m_{si} can vary from about 50 up to about 1500, corresponding to a n-value of 14 to 77.

4 Robust Homography Estimation Based on Interest Point Matches

The final step in the image registration procedure is the robust computation of the homography that maps the two images onto each other. The planarity assumption is a reasonable simplification since only small patches of skin with an average size of $\sim 0.7\ cm^2$ are registered.

An evaluation of the error made by this assumption and the possible use of more flexible transformation models is subject of ongoing research.

The initial match of interest points results in false matches (e.g. due to changing hemangioma appearance during follow-up) that have to be detected and discarded. Since every match is equally considered for homography computation by the Direct Linear Transform (DLT) algorithm [5], that estimates a homography from more then the necessary 4 point pairs, it is not robust against outliers. Therefore, a necessary requirement of the final homography estimation method is a robust detection of inliers and outliers in the present interest point matches. The RANSAC (RANdom SAmple Consensus) [4] scheme is applied on the interest point matches to obtain outlier-tolerant homography estimations. The underlying idea is to randomly and repeatedly choose four matches out of the set of putative matches, compute a homography for each set of four matches and finally take the homography H that has the largest number of inliers in the remaining set. An inlier in this case is defined as a match where the interest point in the sensed image is located within a given distance to the matching interest point in the reference image after a transformation with H.

On our images best results were achieved by iterating 2000 times and allowing a maximum distance of 5 pixels for the inlier decision (in a typical image 5 pixels correspond to $\sim$ 0.375mm). To increase robustness only homographies with an absolute value of the determinant in the range of 0.1 to 10 are allowed. If the determinant of a homography or its inverse is close to zero, it corresponds to a degenerated case.

In Fig. 2 the final results for the images Fig. 1(c) and Fig. 1(d) are shown. Fig. 2(a) shows the detected initial matches, and Fig. 2(b) the remaining inliers, determined by RANSAC, of the

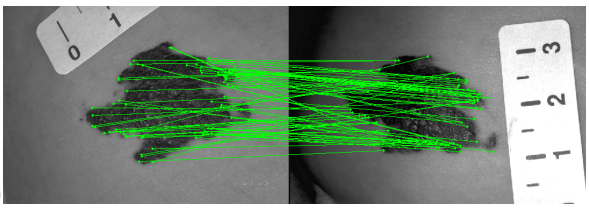
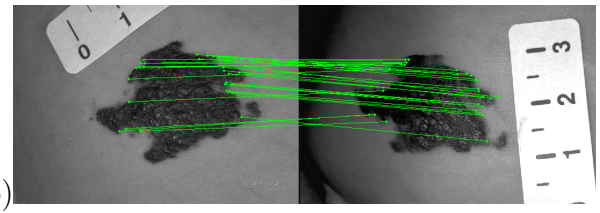
(a)  (b) 

Figure 2: (a) Initial matches between sensed image (left) and reference image (right),(b) detected inliers.

initial matches (Fig.2(a)). In this example 31 of the 76 initial matches are classified as inliers.

5 Experiments

For experiments in total 63 different images taken at the *Vienna General Hospital* using an analog photo camera and digitalized with a scanner were available. All images have a resolution of 512x768 pixels and a bit depth of 8 bits per color channel.

At first, an comparative evaluation of Canny edge interest points and standard DoG interest points is given. For an evaluation of the image registration method under "perfect" conditions with unchanged hemangioma appearances experiments were conducted on a set of 20 image pairs, each pair showing the same hemangioma at the same time, i.e. only a few seconds between image acquisitions. In order to assess the amount of deterioration for registrations of consecutive images, finally tests on four image series are reported.

Comparison of DoG interest points and canny edge interest points: As described in Section 2 interest points are detected at Canny edge points having a local maximum of gradient magnitudes. In this section the improvement achieved by this method compared to the original DoG localization is demonstrated by a simple test where we have compared the number of correct matches of three image pairs of consecutive hemangioma images. For every image pair the best 40 matches having the lowest euclidean distance are determined and the correct matches are counted for both methods by visual inspection. With our localization method 49 ($\sim$41 %) of the total 120 matches are rated as correct whereas with the DoG localization method (using the standard parameter values defined in [6]) only 19 ($\sim$16 %) are rated as correct. As a conclusion, on our images Canny interest points are much more stable than DoG interest points.

Precision of the image registration method on hemangioma images taken at the same time point: In order to increase reliability two or more images of a hemangioma during an examination are taken. 20 of such image pairs are used for testing the precision of the proposed image registration method. The error of a registration is measured using two metrics. The *Distance Error of Inliers* is the average pixel distance of transformed inliers to the real points of the matches classified as inliers. For the *Distance Error of 5 Test Points* for each image pair 5 matches are manually placed and the average pixel distance achieved with the estimated homography is measured. Additionally, the average number of detected interest points (IPs) in the sensed and reference images, the resultant number of initial matches and

IPs sensed image	389.8	Initial Matches	36.7	Distance Error of Inliers	1.61 px
IPs reference image	407.5	Inliers	35.3	Distance Error of 5 Test Points	2.31 px

Table 1: Average results of the proposed image registration method on 20 image pairs, each pair showing the same hemangioma at the same time.

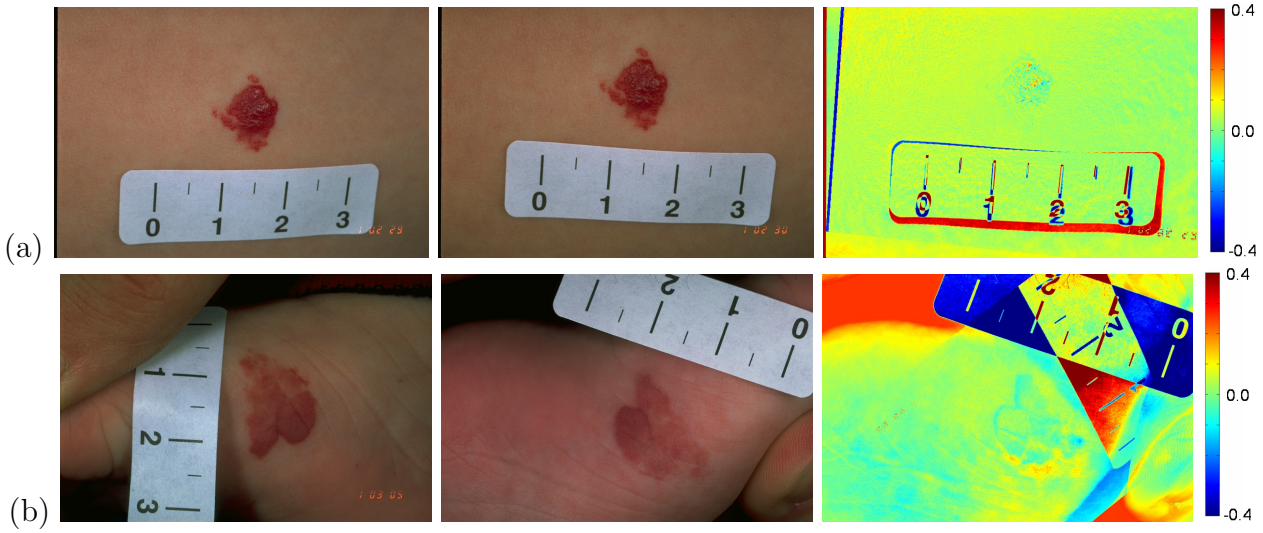


Figure 3: Difference images after registration of two image pairs. (a) shows a hemangioma at the same time point, (b) a hemangioma at different time points.

the fraction of these matches classified as inliers is reported.

The average results for the 20 image pairs are listed in Tab. 1. The average distance error of the 5 test points lies at 2.31 pixels ($\sim$ 0.175mm) which is not a large increase compared to the distance error of the inliers (1.61 pixels or $\sim$ 0.125mm). Another indication of accuracy is the fraction of the initial matches classified as inliers. On average 35.3 of the 36.7 initial matches are classified as inliers which corresponds to a percentage of $\sim$96 %.

In Fig. 3 exemplarily for a registration the sensed image, the reference image and the difference image between the transformed sensed and the reference image is shown. It can be seen that the difference image of Fig. 3(a) shows small disparities in the range of $\sim$0.1 inside and around the hemangioma region (note that larger local differences are caused by highlights on the hemangiomas). This registration shows an average distance error of the 5 test points of 2.41 pixels.

Precision of the image registration method on hemangioma images taken at different time points: To assess the accuracy of the proposed method on consecutive images of the same hemangioma taken at increasing intervals from 4 weeks up to 6 months we applied our algorithm on four different image series. Each image series consists of four or five images, resulting in a total of 13 registrations marked by two characters, patient (1,2,3,4) and position in the sequence of registrations (A,B,C,D). For instance, 2C indicates the registration of the images from the third and the fourth examination of patient 2. The same error metrics as in the previous test are measured and listed in Tab. 2. Additionally, a further error metric

Registration	Interest Points Sensed Image	Interest Points Reference Image	Initial Matches	Inliers	Average Distance Error of Inliers	Average Distance Error of 5 Test Points	Average Reference Points Displacement
1A	500	590	45	17	3.03 px	7.96 px	2.41 px
1B	590	671	49	28	2.79 px	3.96 px	8.67 px
1C	671	664	52	31	2.90 px	6.45 px	5.79 px
2A	1441	945	76	30	3.30 px	7.39 px	2.00 px
2B	945	1350	61	15	2.77 px	8.77 px	5.42 px
2C	1350	1497	73	35	2.41 px	12.94 px	5.67 px
2D	1497	187	77	7	1.41 px	354.84 px	440.38 px
3A	393	266	40	12	3.61 px	3.95 px	3.60 px
3B	266	191	33	18	2.57 px	4.92 px	3.76 px
3C	191	550	28	16	2.70 px	5.21 px	
4A	363	477	38	8	3.33 px	10.08 px	11.50 px
4B	477	213	44	11	3.97 px	4.69 px	
4C	213	767	29	6	0.94 px	196.43 px	
Average	684.38	643.69	49.62	18.00	2.75 px	48.27 px	48.92 px
Average(w/o 2D,4C)	653.36	674.00	49.00	20.09	**3.03 px**	**6.94 px**	**5.43 px**

Table 2: Results of the image registration method on 4 image series with overall 13 registrations.

measuring the consistency of three circularly concatenated registrations is used: in this experiment two images from examination 1 (Image A and Image A') and one from the subsequent examination 2 (Image B) are taken. The three homographies H_{AB}, $H_{BA'}$ and $H_{A'A}$ between the images are computed and the composite homography $H = H_{AB}H_{BA'}H_{A'A}$ is build. In the absence of error, H is the identity matrix and every point in Image A is not displaced by a transformation with it. Inevitably, there is an error which can be measured by the average displacement of points in Image A. Therefore, a set of reference points is equally placed in 10 pixel distances inside the hemangioma region of Image A and transformed by the composite homography H. The error is computed as the average Euclidean distance between reference points and their corresponding transformed points, listed as *Average Reference Points Displacement* in Tab. 2. This error is not stated for the registrations 3C, 4B and 4C because in this cases only one image from examination 1 is available.

Not surprisingly, the results are worse than for the image pairs taken at the same time point since the content of the images changes from one time to another. Nevertheless, the registrations results are satisfactory with the exception of the registrations 2D and 4C. In this two cases the hemangiomas have changed too much to obtain reliable matches and a meaningful homography. By excluding these two very bad results we achieve an average reference points displacement of 5.43 pixels ($\sim$ 0.4mm). The results of the match detection deteriorate as well, indicated by a lower fraction of initial matches finally classified as inliers ($\sim$41 %).

In Fig. 3(b) the difference image of registration 1C is shown. Here differences occur at the regressing regions of the reference image.

The accuracy of the registrations is expected to be adequate for an automatic analysis of hemangioma changes over time which is part of future work. The potential to improve the registration result by local non-rigid refinements, and the involved risk of *over registration* if changes of the hemangioma are large, is subject of ongoing research.

6 Conclusion

The paper proposes a method to robustly register hemangioma follow-up images. It deals with the changing appearance of the hemangioma during the healing process, and allows for a subsequent analysis of subtle surface alterations. Experimental results show that the majority of the images can be registered without considerable errors. The average reference point displacement of $\sim 0.4\ mm$ accumulated by three subsequent registrations is acceptable with an average hemangioma diameter of $\sim 14\ mm$. Nevertheless, the conducted tests have also shown that registrations on image pairs containing strongly changed hemangiomas sometimes result in a failure of the registration. The visual control of registration results by a human expert is inevitable to detect such erroneous registrations. However, these infrequent cases could be manually registered by user-defined matches between the two images. The proposed method can be applied to other types of lesions as well (e.g. melanoma or psoriasis). Future work will focus on the development of an automatic system for change detection supporting the dermatologist in the analysis of hemangioma changes in follow-up studies. For this purpose, the proposed automatic registration of hemangioma images is an essential prerequisite. The improvement of registration results by local refinements at hemangioma borders and by the use of more flexible transformation models is subject of ongoing research.

References

[1] J. Canny. A computational approach to edge detection. *PAMI*, 8(6):679–698, 1986.

[2] D. Delgado, B. K. Ersbøll, and J. M. Carstensen. S.H.A.R.P: A smart hierarchical algorithm to register psoriasis. In *Proc. of Int. Workshop on Systems, Signals and Image Processing*, pages 43–46, 2004.

[3] B.A. Drolet, N.B. Esterly, and I.J. Frieden. Hemangiomas in children. *New England Journal of Medicine*, 341:173–181, 1999.

[4] M.A. Fischler and R.C. Bolles. Random sample consensus: A paradigm for model fitting with applications to image analysis and automated cartography. *Communications of the ACM*, 24(6):381–395, 1981.

[5] R.I. Hartley and A. Zisserman. *Multiple View Geometry in Computer Vision*. Cambridge University Press, ISBN: 0521540518, second edition, 2004.

[6] D. G. Lowe. Distinctive image features from scale-invariant keypoints. *IJCV*, 60(2):91–110, 2004.

[7] I. Maglogiannis. Automated segmentation and registration of dermatological images. *Journal of Mathematical Modelling and Algorithms*, 2(3):277–294, 2003.

[8] G. Maletti, B. K. Ersbøll, and K. Conradsen. A combined alignment and registration scheme of lesions with psoriasis. *Information Sciences*, 175(3):141–159, 2005.

[9] S.A. Pavlopoulos. New hybrid stochastic-deterministic technique for fast registration of dermatological images. *Medical & Biological Engineering & Computing*, 42(6):777–786, 2004.

[10] S. Zambanini, G. Langs, R. Sablatnig, P. Donath, and H. Maier. Automatic surveying of cutaneous hemangiomas. In *Proc. of ICPR 2006*, volume 1, pages 1022–1025.

[11] B. Zitova and J. Flusser. Image registration methods: a survey. *IVC*, 21(11):977–1000, 2003.