Image Matching Using Photometric Information

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Abstract

Image matching is an essential task in many computer vision applications. It is obvious that thorough utilization of all available information is critical for the success of matching algorithms. However most popular matching methods do not incorporate effectively photometric data. Some algorithms are based on geometric, color invariant features, thus completely neglecting available photometric information. Others assume that color does not differ significantly in the two images; that assumption may be wrong when the images are not taken at the same time, for example when a recently taken image is compared with a database. This paper introduces a method for using color information in image matching tasks. Initially the images are segmented using an off-the-shelf segmentation process (EDISON). No assumptions are made on the quality of the segmentation. Then the algorithm employs a model for natural illumination change to define the probability of two segments to originate from the same surface. When additional information is supplied (for example suspected corresponding point features in both images), the probabilities are updated. We show that the probabilities can easily be utilized in any existing image matching system. We propose a technique to make use of them in a SIFT-based algorithm. The technique's capabilities are demonstrated on real images, where it causes a significant improvement in comparison with the original SIFT results in the percentage of correct matches found.

1. Introduction

Image matching, or finding corresponding features in different images of a scene is an essential step in most computer vision tasks (3D reconstruction, object recognition, tracking, image mosaicing, to name a few). Features of various forms - points, edges, contours and regions - have been used for this purpose, see Zitova and Flusser [18] for a survey. In this work we concentrate on point features, as they have the widest usage, but our results can easily be expanded to work with other feature types.

The accuracy of matching algorithms depends on their ability to reliably extract all available information from the neighborhood of the feature. While the geometric properties of the object are relatively stable, its color may vary significantly with the time of day, cloud cover and other atmospheric conditions, Judd *et al.* [9]. See Fig. 1 for illumination influence on object colors. With respect to the usage



Figure 1. Four Macbeth cells under different natural illuminants morning, noon and afternoon light of a cloudy day. (a) A row is the same cell under different three illuminants. A column has four cells with the same illuminant. (b) The values of the cells in the normalized $R / \sum (RGB), B / \sum (RGB)$ format. Every cell has a mark in appropriate color. Note that colors of different surfaces are sometimes closer than the colors of the same surface (the upper green mark is closer to grey than to the other green marks).

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of color, point feature correspondence algorithms can be divided into three main groups. The first group consists of methods relying entirely on geometric features: Lowe [10], Schmid and Mohr [14], Beardsley [2]. The neglect of photometric information by these methods can hurt their performance and can even cause failures when the geometric information is insufficient. The methods of the second group assume that the illumination color is constant in all images. They can use correlation - Smith et al. [16], wavelets - Sebe et al. [15], affine invariant regions - Georgescu and Meer [7], or a combination of point and region data - Matas et al. [11] and Tuytelaars and Van Gool [17]. The disadvantage of these methods is their inability to work with images taken at different times. For example when real-time data should be compared with an image database prepared in advance. The third group employs color constancy techniques (see Barnard [1]) to model the possible illumination change, such as the diagonal model - Montesinos et al. [12]. These methods are better suited for handling illumination changes. Still the diagonal model cannot cope with significant illumination changes or wide-band camera sensors. An additional drawback of many algorithms of the second and the third group is that the color is examined around salient points. Salient points are typically formed on surface discontinuities - corners, edges and so on. Finite pixel sizes and camera de-focus often cause colors from neighboring surfaces to merge and to create spurious colors near salient locations.

The above difficulties raise the following questions:

- What is the probability that two colors originate from the same surface? We are not concerned with the actual surface and illumination properties, but only with the relationships of various colors.
- *How to combine those probabilities with geometric features?* Geometric feature matching has been extensively researched and many good quality applications exist. We search for a way to associate the data extracted from those applications with photometric correspondence probabilities. Schaffalitzky and Zisserman [13] suggest an analogous approach for texture-based region descriptors. They match regions and then match features from the corresponding regions only.

We propose a method that answers these questions. Initially we segment the image using an off-the-shelf segmentation application: EDISON by Christoudias *et al.* [3]. Segments allow for more stable results, whereas the color of a single pixel is noisy and tends to be affected by its neighbors, especially on the borders between several surfaces. Nothing is assumed on the quality of the segmentation.

We employ the natural illumination model suggested by Finlayson *et al.* [5] to calculate the probability that two colors belong to the same surface. Given a surface color, the model allows us to estimate the range of colors that the surface can obtain under any natural illumination conditions. Any two colors that lie within this predefined range of each other will get a high probability to originate from the same source surface. When we are given two colors that are considered to belong to the same surface, the illumination change can be calculated.

The main difference between our method and Finlayson's *et al.* [5] method is that we take into account in our analysis the magnitude of the illumination change together with its direction. The accuracy of the segment probabilities to match each other is improved by comparing the immediate neighbors of the segments. Only when enough neighbors can match each other, and the illumination change is the same for the whole group, the probability remains high. The robustness to segmentation flaws is ensured by allowing a certain fraction of the neighbors of the segment not to abide by these rules.

The probabilities can easily be utilized in any existing image matching system. They can be used as a false matches removing factor, additional weights in matching process or serve for validation purposes. We present a more sophisticated method that uses the segment correspondence probabilities to aid the feature matching process. Initially, the segment probabilities are updated according to the feature matching results using a Bayesian approach. Afterwards, the feature matchings are influenced by the correspondence of the segments they belong to.

The main innovations of our method are:

- Full exploitation of the illumination change between the two images.
- Probabilistic, color based approach to segment matching that exploits the segment neighborhood structure.
- A Bayesian method for integrating point features and segment correspondence information.

The algorithm contribution is demonstrated with an offthe-shelf implementation of the SIFT feature detection and matching method by Lowe [10]. Our method was tested on real images and showed significant improvements in comparison with the original SIFT results in the percentage of correct matches found. Given the same absolute number of inliers, the inlier rate of our method is at least twice as large as in SIFT. The method also works successfully for the special case of images taken at the same time.

The paper continues as follows. Section 2 describes the illumination change model. Our segment matching method is described in Section 3. Section 4 provides an example of the successful combination of our algorithm with the SIFT feature matching application. Finally experimental results are presented in Section 5.

2. Color path model

This section presents the model that estimates the probability that two colors originated from the same surface. The basic idea of the method is inspired by the work of Finlayson *et al.* [5]. They defined a 2D rb color space:

$$r_k = \log(p_k/p_g) = \log(s_k/s_g) + (e_k - e_g)/T,$$
 (1)

where p_k are pixel values, $k = R, G, B, s_k$ are constants that depend on the observed surface and the camera, e_k depend only on the camera and T is the temperature in Planck's law approximation of the illumination spectrum.

As the temperature (in other words illumination) changes, the 2D vectors r_k will form a straight line - termed *color paths* - in the 2D color space. All the lines will have the same direction. Thus, all possible colors of the same surface will lie on one color path under any illumination change.

We observed that the natural extension of the above conclusion is that the length of vectors r_k depends only on the temperature change and not on the color itself (as e_k and e_g are constant). Therefore when the same scene is shot at different illumination conditions, all colors r_k of the scene will travel the same distance along their color paths. This observation allows us to estimate the probabilities that various colors of two images match each other.

We use the same log-log color space, only replacing p_g by the geometric mean of all colors $p_m = \sqrt[3]{p_r p_g p_b}$, because it gives more stable results. So our color coordinates:

$$r_k = \log(p_k/p_m) = \log(s_k/s_m) + (e_k - e_m)/T,$$
 (2)

where $s_m = \sqrt[3]{s_r s_g s_b}$ and $e_m = \frac{1}{3}(e_r + e_g + e_b)$. The modification does not change the basic principles. It only alters the color path directions and distances.

2.1. Color paths construction

Macbeth Chart cells data and color paths



Figure 2. Colors of Macbeth Checker cells under various natural illumination in the $\log(R/\sqrt[3]{RGB}), \log(B/\sqrt[3]{RGB})$ domain with estimated lines (see text).

To obtain the color paths we followed the calibration method suggested by Finlayson *et al.* [5]. Fig. 2 displays the colors of Macbeth Chart cells in the log-log color space under various illumination conditions throughout the day. The colors are marked by red stars, and the color paths (estimated using SVD for every cell) are blue lines. It can be easily observed the color path behavior deviates from the theory: the color paths do not have the same lengths and slopes, and cell colors do not lie exactly on the path but are scattered around it. The errors are likely to be caused by the inaccuracy of the model assumptions: narrowness of the sensors, illumination approximation and other reasons. Random noise is not considered to be a source of significant errors, as Macbeth Chart colors represent an average over large (100×100 pixels) image regions.

The meaning of the errors in our model is that even in ideal conditions we cannot expect the colors to behave according to the theory and that slight deviations from the model (that are estimated experimentally) must either be taken into account by the algorithms (see Section 3.1) or incorporated into the model itself.

The lengths and and directions of the color paths vary along the color space. The dependency between the lengths and the color path locations was expressed with a second degree polynomial. The direction variations seem to have a random nature. They were approximated by the average direction.

We observed that despite variation in the lengths, the relative distances that the colors move are approximately the same. For example, if one color moves a distance equal to half its color path length under illumination change T, other colors will also move half their color path length under illumination change T. To neutralize the influence of color path lengths we represent each pair of colors ab from two images A and B in a normalized coordinate frame, where the x axis is the projection of the vector ab on a's color path divided by a's color path length, and the y axis is the projection of ab on a vector perpendicular to a's color path divided by NR (see Fig. 3(b)). As a and b may have different color path lengths, we use their average in order to guarantee identical representation of ab and ba.

3. Photometric Image Matching - PIM

The rather theoretical term *color* used in the definition of the color path model is usually replaced by pixels. Most segmentation methods unite pixels into segments, mainly because of two reasons: noise sensitivity and complexity. The pixels are usually combined according to two parameters (constant or adaptive): spatial and color distance. The only assumption on the segmentation quality that we make is that those parameters have reasonable values. In our experiments we use the off-the-shelf segmentation application EDISON by Christoudias *et al.* [3]. Additional assumption used throughout the paper is that illumination changes slowly in the image, or in other words that the illumination is constant in the segment's neighborhood. The assumption is justified for most segments, except those lying on a shadow border. However the robust nature of our algorithm enables us to deal with cases in which these assumptions are violated.

3.1. Probability distribution function

At first we add a few definitions:

- G_K segment K and its immediate geometrical neighbors. K_i means i member of K.
- T_d the illumination (temperature) change that cause segments to move distance d along the color path along the x axis of the normalized coordinates.
- $\begin{array}{l} d_{AB} \ \text{-the signed distance between segments } A \ \text{and } B \ \text{on} \\ \text{the } x \ \text{axis of the normalized coordinates. In Fig. 3(b):} \\ d_{A_1B_1} \approx 0.9, \quad d_{A_2B_2} \approx 0.95, \\ d_{A_3B_3} \approx 0.85, \quad d_{A_2B_3} \approx -0.5. \end{array}$



Figure 3. (a) - Three surfaces from two images. The first color of a pair (marked by blue circle) is from the first image, and the second (marked by red star) is from the second image. The black arrows are the projections of the vectors between pairs of colors onto normalized coordinates. Light brown lines (partly covered by the black arrows) are the color paths calculated in the first color. NR is the solid green line. The dotted green line represents ENRin the direction perpendicular to the color path and m from Eq. 6 in the direction of the color path. The second color of the pair 3 can belong to both color paths 2 and 3, it is in their NR. The projection of a wrong pair (pair 2 in the first image with pair 3 in the second image) is represented by the blue arrows. (b) - The movement vectors of the above pairs presented in normalized coordinates. See text.

In Section 2.1 we saw that the possible range of object colors in an image can be estimated from its color in another image. Given two images of the same scene, we define the probability density function of a segment A of the first image to have color a, when the image B of the second image has color b and the segments cover (at least partly) the same surface:

$$p(A = a|B = b, S(A) \approx S(B)) \equiv p(a|b, A \approx B).$$
(3)

We assume that the above density function can be decomposed into two independent perpendicular components:

$$p(a|b, A \approx B) = p_p(a|b, A \approx B) \cdot p_c(a|b, A \approx B).$$
(4)

The first component $p_p(a|b, A \approx B)$ arises due to the model errors and random noise. It reflects the distance of A from B's color path. Two thresholds were defined to approximate the probability. The first one, *noise range* (NR) is the maximal distance of a color from a path that does not result in any penalty to the color's probability to belong to that path. The second one, *extended noise range* (ENR) represents the maximal possible distance of a "real world" color to its color path. If the distance is larger, the tested color cannot belong to that color path. The penalty changes linearly if the distance is between NR and ENR. NR is computed from the Macbeth Chart data as the maximal distance of a point to its color path, ENR was experimentally set to $2 \cdot NR$. See Fig. 3.

The second component $p_c(a|b, A \approx B)$ corresponds to the deviations along the color path. In addition to model errors and random noise it depends on the variations in the illumination. Therefore we include T_d into its definition:

$$p_c(a|b, A \approx B) = \int_{-1}^1 p_c(a|b, A \approx B, T_d) P(T_d) dT_d.$$
(5)

 $P(T_d)$ indicates our prior knowledge about T_d variation (it is equal to $u_1(T_d)$ if no such knowledge is accessible). It is assumed that:

$$p_c(a|b, A \approx B, T_d) = u_m(a - b - T_d), \tag{6}$$

where

$$u_k(x) = \begin{cases} \frac{1}{2k} & \|x\| \le k\\ 0 & \text{otherwise} \end{cases},$$
(7)

and a - b is calculated along the color path. Comparing colors of segments that underwent the same illumination change we set m to 0.2.

When no information about T_d is available substituting Eq. 6 into Eq. 5 gives:

$$p_c(a|b, A \approx B) = \int_{-1}^{1} u_{0.2}(a - b - T_d)u_1(T_d)dT_d.$$
 (8)

To continue we want to precisely define the term *match* as its apparently straightforward meaning has diverse interpretations. We say that segment A matches segment B if the physical area covered by segment A is covered at least partly by segment B and fully by B's neighbors B_i . The definition is much more robust to segmentation flaws. Formally we write:

$$A \to B \text{ if } (A \subseteq [B \cup B_1 \cup \ldots \cup B_n]) \land (A \cap B \neq \emptyset).$$
(9)

Occasionally we may omit \rightarrow for simplification. Note that Eq. 9 implies that: $A \rightarrow B \Rightarrow B \rightarrow A$.

The definition of matching allows us to reformulate Eq. 4 for segment neighborhoods:

$$p'(G_A = g_a | G_B = g_b, AB) = p'_p(g_a | g_b, AB) \cdot p'_c(g_a | g_b, AB),$$
(10)

where g_k represents colors of G_K .

We assume that $A \rightarrow B$ implies that for every segment in G_A there is a segment in G_B that (at least partly) originates from the same surface. Formally:

$$A \subseteq [B \cup B_1 \cup \ldots \cup B_n] \Rightarrow \forall j \exists i_j : A_j \cap B_{i_j} \neq \emptyset.$$
(11)

Assuming that the segments in G_A are independent we obtain:

$$p'_{p}(g_{a}|g_{b}, AB) = p_{p}(a|b, AB) \prod_{G_{A}-A} p_{p}(a_{i}|b_{1}(a_{i}), A_{i}B_{1}(A_{i}))$$

$$p'_{c}(g_{a}|g_{b}, AB) = \int_{-1}^{1} p_{c}(a|b, AB, T_{d})$$

$$\cdot \prod_{G_{A}-A} p_{c}(a_{i}|b_{2}(a_{i}), A_{i}B_{2}(A_{i}), T_{d})P(T_{d})dT_{d}.$$
(12)

where $B_1(A_i)$ is the neighbor of B that maximizes

$$p_p(a_i|b(a_i), A_iB(A_i)),$$

and $B_2(A_i)$ maximizes

$$\int_{-1}^{1} p_c(a_i|b(a_i), A_i B(A_i), T_d) P(T_d) dT_d.$$

To make the algorithm more robust we do not calculate the product in Eq. 12 for all A_i , but only for a predefined percent of the neighbors (called *minimal number of inliers*) that provide the highest probabilities.

Moreover, substituting $T_d = a - b$ in Eq. 12 instead of calculating the integral over $T \in [-1, 1]$ significantly speeds up the algorithm without hurting its performance.

3.2. Matching probability definition

We are interested in the probability of segment A of the first image to match segments B_i of the second image (the segments of the two images are examined independently). We assume that a segment can match only one segment of another image, but in turn can be matched by any number of segments. According to the Probability law:

$$P(AB_{\emptyset}|g_a) + \sum_{B_i \in \text{Image 2}} P(AB_i|g_a, g_{b_i}) = 1, \quad (13)$$

where $P(AB_{\emptyset}|g_a)$ is the probability of A to represent an object that is not in the second image. We set this number to a constant for all segments.

From Bayes law:

$$P(AB_i|g_a, g_{b_i}) = \frac{p(g_a|g_{b_i}, AB_i)P(AB_i|g_{b_i})}{p(g_a|g_{b_i})}.$$
 (14)

If no prior information is available to prefer B_k over other segments, $P(AB_i|g_{b_i})$ are equal for all *i* and can be removed. $p(g_a|g_{b_i}) = \sum_{B_i} p(g_a|g_{b_i}, AB_i)P(AB_i|g_{b_i})$ is the normalizing coefficient. Thus Eq. 14 can easily be calculated from Eq. 12 and Eq. 10.

4. SIFT-based PIM

In the previous section we showed how to calculate the probability of two segments to match each other. However bare segment-to-segment matching cannot provide enough information for many subsequent computer vision tasks (for example 3D reconstruction algorithms require point correspondences). As a variety of successful techniques has been proposed for point correspondences, we search for a method to improve the point correspondence quality by combining segment-to-segment matching probabilities with the point features provided by them.

Our experiments demonstrated that even a simple, intuitive approach to reject point features that do not reside in matchable segments, can cause significant increase in correct matches percent. To achieve even better results, we suggest a more sophisticated method that incorporates point and segment probabilities in a process whose purpose is to separate correct and spurious matches.

Our method is suitable for any point feature correspondence algorithm that is able to provide correctness probability for a match or at least an overall inlier rate (percent of correct matches). We selected Lowe's SIFT algorithm [10] to present the method's capabilities.

Several new definitions are used in the following sections:

- j_k member of keypoint pair j that resides in image k.
- S locations of all keypoint pairs.
- S_i locations of keypoint pair j.
- S_A locations of all keypoint pairs that have a member in segment A.
- $\rho_j \equiv P(C_j)$ probability that the keypoint pair j is a correct match.

Our algorithm is summarized as follows:

- 1. Calculate probabilities P(AB) using Eq. 14.
- 2. Obtain initial probability ρ_i from SIFT.
- 3. Update segment-to-segment matching probabilities given the spreading of keypoints and their correspondence probabilities P(AB|S, P(C)).

4. Recalculate keypoint correspondence probabilities using the spreading of keypoints and segment-tosegment probabilities - $P(C_j|S, P(AB))$.

The algorithm can iteratively repeat steps 3 and 4.

4.1. Probability of SIFT correspondences

Lowe showed in [10] the dependency of the probability distribution functions for correct and incorrect matches $(PDF_{corr} \text{ and } PDF_{incorr} \text{ accordingly})$ on the ratio of distances from the closest neighbor to the second closest. The probability that keypoint *j* with *best to second* ratio *r* is correct can be calculated by:

$$\rho_j = \frac{PDF_{corr}(r)(1-\epsilon)}{PDF_{corr}(r)(1-\epsilon) + PDF_{incorr}(r)(\epsilon)},$$
 (15)

where ϵ is the assumed outlier rate. Our experiments showed that the value of ϵ does not have a significant impact on the results. It does modify the absolute values of final correspondence probabilities, but their relative values remain the same. Note that ρ_j is defined separately for both keypoints of a match. We use their average value for the final probability. Eq. 15 can be extended to a 2D probability distribution that includes the ratios of both points.

4.2. Update of segment-to-segment probabilities

We search for $P(AB_i|S, P(C))$. We will omit P(C) for a simpler notation. As it was mentioned previously, $P(AB_i|S)$ is independent of other segments in the first image, therefore only feature pairs with a point in $A(S_A)$ can influence $P(AB_i|S)$. Using Bayes' rule we formalize:

$$P(AB_i|S) = P(AB_i|S_A) = \frac{P(S_A|AB_i)P(AB_i)}{P(S_A)},$$
(16)

where $P(S_A)$ is the normalizing coefficient. As the correspondences are independent:

$$P(S_A|AB_i) = \prod_{S_j \in S_A} P(S_j|AB_i).$$
(17)

Given a member of a correspondence j inside A we look at the second member of the correspondence as a random variable. If the correspondence is correct (with probability ρ_j), it must reside inside G_{B_i} according to our definition of matching (Eq. 9). If the correspondence is incorrect, its location is chosen randomly among segments in the second image. Its chance to fall inside a segment can be set to the same constant $\beta \approx \frac{10}{\text{Number of segments}}$ for all segments or be proportional to the segment area / number of keypoints in the segment.

The formal description of the above is:

$$P(S_j|AB_i) = 1 \cdot \rho_j + (1 - \rho_j) \cdot \beta, \text{ if } S_j \in G_{B_i}, \quad (18)$$

$$P(S_j|AB_i) = 0 \cdot \rho_j + (1 - \rho_j) \cdot \beta, \text{ if } S_j \notin G_{B_i}.$$

4.3. Update of keypoint correspondence probabilities

We want to calculate $P(C_j|S, P(AB))$. We will omit P(AB) for a simpler notation. Using Bayes' rule we write:

$$P(C_j|S) = \frac{P(S|C_j)P(C_j)}{P(S)},$$
(19)

where $P(S) = P(S|C_j)P(C_j) + P(S|\neg C_j)P(\neg C_j)$.

Though ρ_j is the correctness probability of a pair j, our definition of matching forces us to calculate it separately for each member of the pair. Similar to the approach we chose for the calculation of the probability of feature pairs in the original SIFT, the pair probability is set to the average of its members. The formulas are presented only for one direction, i.e. $P(C_j)$ is the probability that j_1 has a correct match. The second direction is symmetric.

If j_1 is inside segment A, it is obvious that $P(C_j)$ is independent of the keypoint pairs that do not have members in A. Therefore $P(C_j|S) = P(C_j|S_A)$.

Incorporating the knowledge of segment matching probabilities and assuming that the keypoints are independent we obtain:

$$P(S_A|C_j) = \sum_{\forall B_i} \prod_{S_m \in S_A} P(S_m|C_j, AB_i) P(AB_i),$$
$$P(S_A|\neg C_j) = \sum_{\forall B_i} \prod_{S_m \in S_A} P(S_m|\neg C_j, AB_i) P(AB_i),$$
(20)

where $P(S_m|C_j, AB_i)$ is the probability of the location of m_2 given that the pair j is correct and A matches B_i . $P(S_m|C_j, AB_i)$ and $P(S_m|\neg C_j, AB_i)$ are defined in a manner similar to Eq. 18:

$$P(S_{m}|\neg C_{j}, AB_{i}) = \begin{cases} \beta & m = j \\ \rho_{m} + (1 - \rho_{m})\beta & m \neq j, m_{2} \in G_{B_{i}} \\ (1 - \rho_{m})\beta & m \neq j, m_{2} \notin G_{B_{i}} \end{cases}$$

$$P(S_{m}|C_{i}, AB_{i}) = \begin{cases} 0 & m = j, m_{2} \notin G_{B_{i}} \\ 1 & m = j, m_{2} \in G_{B_{i}} \end{cases}$$

$$P(S_m | C_j, AB_i) = \begin{cases} 1 & m = j, m_2 \in G_{B_i} \\ \rho_m + (1 - \rho_m)\beta & m \neq j, m_2 \in G_{B_i} \\ (1 - \rho_m)\beta & m \neq j, m_2 \notin G_{B_i} \end{cases}$$
(21)

The fact that $P(S_m|C_j, AB_i) = 0$ when m = j and $m_2 \notin G_{B_i}$ allows us to reduce Eq. 20 to

$$P(S_A|C_j) = \sum_{B_i \in G_B(j_2)} \prod_{S_m \in S_A} P(S_m|C_j, AB_i) P(AB_i),$$
(22)

where j_2 resides in $B(j_2)$. Eq. 19 is computed using Eq. 20, Eq. 21 and Eq. 22.

We have shown an effective method to combine segment and point feature correspondences into one probabilistic approach. The method can significantly improve performance



Figure 4. The probability densities of inlier and outlier matching probabilities of keypoint pairs of house image pair in Fig. 6(a) estimated with *ksdensity* MATLAB function. The inlier is solid blue and outlier is dotted red. (a) - original SIFT, (b) - our method.

of existing matching algorithms. The possible objective of further research can be removing the current restriction to images taken with the same photometrically calibrated camera.

5. Experimental results

Our method has two distinct, though interconnected goals - segment matching and enhancement of correct point correspondences. Initially we demonstrate the quality of segment matching. Fig. 6(a) shows two images of a house taken at different times and from different locations. We chose a segment S in the first image - the grey region in Fig. 5(a). Fig. 5(b) shows the value of the probability density function (Eq. 4) for segment S and segments of the second image. The higher the correspondence probability, the darker is the color. Segment S was intentionally chosen so that 90% if the segments of the second image have higher probability than its correct correspondence. Fig. 5(c) displays the matching probabilities of S (probability to match segments from the other image given the segments neighborhood, Eq. 14). Only 15% of segments have better correspondence probability than the correct segment. Finally Fig. 5(d) displays the updated probabilities (Eq. 16). The correct segment is the best and only correspondence. The improvement is obvious.

To show the influence of our algorithm on point feature correspondences, we compare the densities of inlier and outlier probabilities. The probability separation is important since these probabilities are used to guide the RANSAC [6] step of the subsequent algorithms (e.g. Chum and Matas [4], Goshen and Shimshoni [8]). Evidently, the ability of the algorithm to separate the histograms is its main achievement.

Figure 4 presents the zoomed in versions of the probability density of inlier and outlier matching probabilities of the keypoint pairs from the images in Fig. 6(a). The inlier probability density function has a peak at one (the probability density graph of the inliers reaches 120 at 1). The meaning of this is that many inliers were detected with high probability. Both density functions have a peak at zero causing rejection of many outliers but also rejection of several inliers that do not conform to our model. Still, as many more inliers are detected with high probability, they be used in subsequent steps. The improvement in separation of histograms is observable even more clearly in Tbl. 1. The table shows the values of the cumulative sum of the histogram the number and percent of true inliers above a given probability. The values are presented for all images of Fig. 6. As can be easily observed our method obtains many more inliers for a given inlier rate or vice versa - a better inlier rate given the required inlier number. For example, consider the columns of the dolls image pair in Table 1. For the same inlier rate (61%), our method obtains twice as many inliers as the SIFT. The contribution of PIM is even more important when there are few matches in the images. Moreover, in the house image pair SIFT results seem insufficient for successful fundamental matrix estimation, while our method provides enough inliers with good inlier rate.

In addition to improving the quality of image matching in different illumination conditions, our algorithm can be used when the images are taken at the same time. In this case we do not calculate the integral in Eq. 12 for $T \in [-1, 1]$ but only for $T \in [-m, m]$ (*m* is taken from Eq. 6), thus making the algorithm faster and more accurate. An example of such an image pair is shown in Fig. 6(d) improving significantly the number of inliers detected with high probability.

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Figure 5. An example of segment matching results. (a) - The contours of the segments of the first image. The chosen segment S is marked in grey. (b) - The value of probability density function (Eq. 4) for segment S and segments of the second image. (c) - The matching probabilities of S (Eq. 14). (d) - The updated matching probabilities of S. See text for further explanation.

(a) - House image pair







(b) - Dolls image pair



(d) - Identical illumination image pair (c) - Sculpture image pair Figure 6. Some of the images on which the algorithm was tested. Several images were resized to fit the window.

Probability	(a) - SIFT	(a) - PIM	(b) - SIFT	(b) - PIM	(c) - SIFT	(c) - PIM	(d) - SIFT	(d) - PIM
0.8	0,100%	12,100%	20,100%	52,98%	2,100%	8,100%	3,100%	11,100%
0.6	3,100%	27,71%	26,96%	69,88%	3,75%	12,75%	5,83%	17,85%
0.4	7,88%	36,50%	41,83%	97,74%	7,58%	20,51%	10,45%	30,75%
0.2	9,69%	45,42%	53,62%	109,61%	14,31%	36,27%	21,40%	49,55%
0	88,13%	88,13%	223,25%	223,25%	70,12%	70,12%	172,15%	172,15%

Table 1. The cumulative histogram of correspondence probabilities of the original SIFT and PIM method for the images in Fig. 6. The two numbers in the 2nd-9th columns represent the number and the percent of inliers with probability larger than the number in the first column. Every image has two columns, one for the SIFT method and one for the PIM method.

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