Gel image matching based on local homography constraints

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Abstract: - The paper discusses the 2DE gel image matching problem that occurs when define correspondence to detect spots position and their pairing correlations. It is expected that a proportion of these correspondences will in fact be mismatches. The feature description and matching method are used to find correspondences; these are refined by the algorithm that automatically computes a homography between two images. With the refined correspondences, the RANSAC is designed to deal with exactly this situation – to estimate 1) the homography and also 2) a set of inliers consistent with this estimate and 3) outliers. Experimental results show that the algorithm is efficient and it improves the robustness and accuracy of the automatic image matching.

Key-Words: gel matching, homography, point correspondence, RANSAC,

1 Introduction

Matching spots in gel images is a process defining the correspondences of spots from the same protein in different gel images. Gel matching results depend on the quality of the gel images that are being matched, and also the degree of similarity between the gels. Very similar gels maybe matched without setting any landmarks. The more dissimilar the gels are, the more landmarks are needed to start the matching process. If you have set corresponding landmarks in all gels you want to match, you may pair the spots associated to these landmarks using the Process-Match-Match-Landmarks option. Similarly, if you have assigned labels to given spots (for example, to spots corresponding to identified proteins), you can pair these spots using Process-Match-Match Labels. These pairs may then be used as starting pairs to improve and speed up the matching process greatly [11].

Therefore, a good point pattern matching approach is able to perform the geometrical quantities efficiently and matches well if the corresponding points are known. The geometrical transformation parameters (translation, rotation and scaling) can be found by using least-squares-error-minimization techniques.

Various methods have been proposed for point matching which define correspondences of spots. A brief description about a recently developed pattern matching program for detecting correspondences of spots between two images is given [2]. Spots are detected using standard image processing techniques. For two sets A and B of spots, they find a correspondence of spots between two sets by the following procedure. (1) A few pairs of matching spots (landmarks) are detected (manually or automatically). (2) In order to adjust distortion, B is transformed using a matrix derived by applying the least squares fitting method of landmarks. (3) A is divided into several rectangular regions. (4) For each rectangular region, a correspondence between spots in this region and spots in B is computed using bipartite graph matching. Moreover, this correspondence is refined via iterative improvement using least squares fitting and bipartite graph matching. (5) A correspondence between the entire regions is refined using bipartite graph matching.

When strong variations between corresponding sets of spots are expected, the completion task of individual spot matching and gel registration is more complex. A one-to-one mapping is expected between the two images, however missing spots (spots without correspondence) may exist on both images. This problem can be solved by a new distance measure together with a correspondence estimation algorithm based on graph matching which takes into account the structural information between the detected spots. Each image is represented by a graph and the task is to find an isomorphism between subgraphs [9]. Finding correspondences of two image spots prepared from different conditions is a critical image interpretation tool for high level matching process.

The goal of this paper is to propose a probabilistic approach to match spots segments in the images for estimating their homography transformation. A good proportion of these correspondences should be correct, but the aim is not perfect matching, since RANSAC will later be used to eliminate the mismatches. The simulation results on synthetic images validate the proposed method.

The outline of this paper is as follows. In section 2, probabilistic matching of point segments is described introducing RANSAC algorithm estimates the fundamental matrix robustly and the more accurate correspondences with less outliers are gotten. We
present experimental result of the proposed method in Section 3. Finally, section 4 presents some conclusions and suggests directions for further investigation.

2 Probabilistic Matching

In matching process definition of highest neighborhood cross correlation is not easy to satisfy. The two examined points should be closed enough to be considered as candidate for matched pairs. The criterion is the similarity of their local neighborhood configuration. The local neighborhood configuration is the skeleton shape that is formed by connecting the neighboring spot together, in the most experiments.

If we can find correctly and effectively find the exact protein spot central locations and its boundary, we could define perfect matched spots in all regions those revealed in Fig.1, (a) and (b) show a local list of spots in which the spots in the reference gel have the similar configuration with the spots in the matched gel. However, for big single protein spot that has more than one local minimum, the detection may yields many spots in the region, defining of correct similar configuration is difficult to perform.

An algorithm we proposed to automatically compute a homography between two images is described in this section. The input to the algorithm is simply the images, with the information required any other a priori and the output is estimated homography together with a set of interest points in correspondence. The idea is first to obtain by some means a set of putative point correspondences. It is expected that a proportion of these correspondences will in fact be mismatches. RANSAC is designed to deal with exactly this situation estimate the homography and also a set of inliers consistent with this estimate (the true correspondences), and outliers (the mismatches), example is shown in Fig.2. The putative correspondences are obtained by detecting interest points independently in each image, and then matching these interest points using a combination of proximity and similarity of intensity neighborhoods as follows. For each corner at \((x, y)\) in image 1 the match with highest neighborhood cross correlation in image 2 is selected within a square search region centered on \((x, y)\). Symmetrically, for each corner in image 2 the match is sought in image 1.

Fig.2. Precaution of dense matches in images needed to obtain a reliable estimate

In Fig 2, points A, B, C, and D define a square patch \(P_1\) in image 1. A sparse subset of the dense matching within is labeled from 1 to 11. The matches 1, 2, 3 and 4 (selected by a RANSAC trial) are respectively in the small framed neighborhood of vertices A, B, C and D. They are used to accurately define a planar homography \(H\), which maps the square patch \(P_1\) in image 1 to the distorted square patch \(P_2\) defined by transformed points \(H(A), H(B), H(C)\) and \(H(D)\) in image 2. All matches (except 9) are compatible with \(H\).

The sample size four correspondences determine a homography. In this case distance measure has to be defined. In transforming the point coordinates before applying the Direct Linear Transform (DLT) algorithm by centering them about the centroid

\[
\hat{x}_i = \frac{1}{N} \sum_{i=1}^{N} x_i
\]

and then scaling them so that their average distance from the origin is approximately equal to a small constant equal to \(\sqrt{2}\). This can be done by computing the average distance:

\[
\frac{1}{N} \sum_{i=1}^{N} x_i
\]
A desirable property of the algorithm used to estimate the parameters of the homographic transformation is to be invariant with respect to certain class of transformations of the point correspondences. More specially consider two linear transformations are in projective space, such that:
\[ p = Tp \]
\[ p' = T'p' \]
and suppose that the points \( p \) and \( p' \) are related via an homography: \( p \sqsubset Hp \). It follows immediately that the transformed points are related via a new homography \( H' \):
\[ p' \sqsubset T^{-1}H'T^{-1}p \]

The aim of robust mean maximum likelihood estimation and guided matching is having two parts: first to obtain an improved estimate of the homography by using all the inliers in the estimation, second, to obtain more inlying matches from the putative correspondence set because a more accurate homography is available.

### Algorithm

1. **Interest points**: Compute interest points in each gel image
2. **Correspondences**: Compute a set of interest point matches based on proximity and similarity of their intensity neighborhood
3. **RANSAC robust estimation**: Repeat for \( N \) samples, where \( N \) is determined adaptively.
   - (a) Select a random sample of 4 correspondences and compute the homography \( H \)
   - (b) Calculate the distance \( d_{av} \) for each correspondence
   - (c) Compute the number of inliers consistent with \( H \)

Choose the \( H \) with the largest number of inliers.

4. **Optimal estimation**: re-estimate \( H \) from all correspondences classified as inliers, by minimizing the ML cost function

5. **Guided matching**: Further interest point correspondences are now determined using the estimated \( H \) to define a search region about the transferred point position

### Results

<table>
<thead>
<tr>
<th>Results:</th>
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<tbody>
<tr>
<td>Minimal set dimension</td>
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<tr>
<td>Gaussian noise, for sigma</td>
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<tr>
<td>Inliers</td>
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<tr>
<td>Final number of inliers</td>
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<td>Converged on iterations</td>
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Table.1. Experimental results

### 4 Conclusions

In this paper, we present a new efficient image matching approach which can be applied to any local homography descriptions. The experimental results show that the guided matching based on local homography and RANSAC technique can not only find accurate correspondences, but also match them more efficiently.
Fig. 4. Experimental results.

References


