2006 IEEE International Conference on
Systems, Man, and Cybernetics
October 8-11, 2006, Taipei, Taiwan

Spectral Multiplicity Tolerant Inexact Graph Matching

Wei Feng and Zhi-Qiang Liu

***Abstract*— A graph can be exactly specified by the spectrum and corresponding eigenvectors of its adjacency matrix. This provides a solid foundation for spectrum based graph matching. However, most previous methods ignore the spectral multiplicity, which may significantly affect the matching accuracy. In this paper, we address the problem of minimizing the matching error when graph spectral multiplicity is involved. We first model spectral multiplicity by the sub-eigenspace rotation matrix R, and integrate R into the spectrum based graph matching model. We then focus on the exact graph matching problem, and show how to establish the vertex-to-vertex correspondence by iteratively optimizing the sub-eigenspace rotation matrix R and the permutation matrix P. A reliable matching initialization method is proposed to make this process converge rapidly. Finally, we extend the approach to the inexact graph matching problem by optimally warping two graphs to the same size. The proposed approach is robust and efficient. We support our approach with numerical experiments and demonstrate its effectiveness in the practical application of uncaliberated stereo matching.**

I. Introduction

In computer vision, structural description is regarded as the most general model to describe an object. By representing an object in terms of its parts, the properties of these parts and their relations, the structural description inherently possesses a graph nature. This makes graph matching become a core problem for many applications.

Briefly, graph matching is to seek an optimal vertex-to-vertex correspondence between two graphs, which is usually not easy due to the problem's combinatorial nature. As for this problem, many methods can be found in the literature, which can be broadly divided into two categories. The first category is based on global optimization by constructing a state space within which some statistical or heuristic schemes are used to search the optimum. For instance, Lin et al. modeled the problem as the maximum likelihood estimation of the correspondence indicators and solved it using the EM algorithm [1]. Generally speaking, the global optimization based methods are robust to structural errors and inexactness. But they always converge slowly and are sensitive to initialization. The second category is spectrum based graph matching. The importance of graph spectrum has been recognized early in [2]. Recently, many spectrum based graph matching methods have been proposed, such as the eigendecomposition algorithm [3], the linear programming method [4], graph edit distance, and the eigenspace projection clustering (EPC) algorithm [5] etc. In general, spectrum based methods are efficient and effective in many cases. But for most spectrum based methods, their matching accuracy may be significantly affected by the nonuniqueness of eigenvectors and the existence of multi-eigenvalues (namely the spectral multiplicity as a whole).

In this paper, we propose a spectral multiplicity tolerant (SMT) graph matching approach. We model the spectral multiplicity by the sub-eigenspace rotation matrix R. Its impact on exact graph matching is minimized by an iterative process, whose convergence is fast based on the proposed reliable initialization method. Additionally, we present a graph warping approach to incorporate the inexact graph matching problem in the same framework.

In the following, we briefly review the concept of graph matching and introduce our SMT model in Section 2. Section 3 focuses on the SMT exact graph matching algorithm. We then extend the proposed method to inexact graph matching in Section 4. Experimental results are presented in Section 5 followed by conclusion in Section 6.

II. SMT Graph Matching

A graph G can be expressed as an ordered pair (V, w), where V is its vertex set, and the weight w is a nonnegative real value which denotes the fuzzy connectivity of each edge (v_i, v_j). The vertices number of G is $n = |V|$. The adjacency matrix A_G is defined by an $n \times n$ matrix, where a_{ij} denotes the corresponding weight $w(v_i, v_j)$. G is *undirected* if and only if A_G is symmetric. A_G is an equivalent representation of G. For simplicity, we do not distinguish a graph and its adjacency matrix, and use G to represent both.

Let $G = (V_G, w_G)$ and $H = (V_H, w_H)$ be two graphs with n and m vertices respectively. Graph matching is to find a unique vertex-to-vertex correspondence which minimize the structural difference between G and H. Without loss of generality, we assume $n \leq m$ and regard G as the *reference graph* and H the *duplicate graph*. If $n = m$, it is an *exact graph matching* (EGM) problem; otherwise an *inexact graph matching* (IGM) problem. H is rigidly matched to G if there exist an $m \times n$ permutation matrix P such that $PGP^T = H$. The relationship may be more realistic if H is expressed as

$$H = PGP^T + \epsilon N, \tag{1}$$

where N is an $m \times m$ zero-mean noise matrix, and ϵ controls the noise magnitude. Thus, a general graph distance measure can be defined as

$$L(G, H) = \min_P \|PGP^T - H\|_F, \tag{2}$$

where $\|\cdot\|_F$ is the Frobenius norm. From (2), we can model the graph matching problem as the following optimization

Wei Feng and Zhi-Qiang Liu are with Group of Media Computing, School of Creative Media, City University of Hong Kong, Kowloon Tong, Hong Kong SAR, China w.feng@student.cityu.edu.hk, zq.liu@cityu.edu.hk

problem:

$$\hat{P} = \arg\min_{P} \tilde{L}(P, G, H), \tag{3}$$

where $\tilde{L}(P, G, H)$ is the graph matching error under P. Note that the isomorphism problem is a special case of (3) with $n = m$ and $\epsilon = 0$. Because the searching space of $\hat{P}$ is of combinatorial size, additional clues must be used.

Since an undirected graph G has a real symmetric adjacency matrix, its eigenvalues must be real and can be ordered as a sequence $d_1 \geq d_2 \geq \cdots \geq d_p$. This ordered sequence is called the *spectrum* of G [2]. Graph spectrum has been widely used to reduce the matching complexity. Note that G can be exactly specified by its spectrum and the corresponding eigenvectors. Thus, if H matches G strictly, we have

$$\begin{aligned} H &= PGP^T = PUDU^TP^T \\ &= (PU)D(PU)^T = VDV^T, \end{aligned} \tag{4}$$

where D is a diagonal matrix of their spectrum in descending order and U, V are corresponding eigenvectors of G and H respectively. This means that two strictly matched graphs have the same spectrum and the corresponding eigenvectors preserve their vertex permutation exactly. This leads to the spectrum based graph distance measure:

$$L(G, H) = \min_{P} \|PU - V\|_F, \tag{5}$$

which has been widely used in EGM [3], [4].

In general, spectrum based graph matching methods are quite efficient. But most of them ignore the graph spectral multiplicity or simplify the problem by imposing additional constraints. Indeed, even when H strictly matches G, their matching error measured by (5) may be quite large affected by the nonuniqueness of eigenvectors of G and H. The nonuniqueness of eigenvectors is a common property of all matrices. This may have a significant impact on the matching accuracy, especially when there exist multi-eigenvalues. Although this fact has been recognized, many spectrum based graph matching methods cannot tolerate the spectral multiplicity as expected.

We model the spectral multiplicity by a sub-eigenspace rotation matrix R:

$$R = \begin{bmatrix} R'_1 & & \\ & \ddots & \\ & & R'_q \end{bmatrix},$$

where R'_i is a rotation matrix in the ith sub-eigenspace of graph G. For a simple eigenvalue d_i, its eigenvector may be uncertain in the direction. So its corresponding sub-matrix in R, i.e., R'_i, is a single value and can be set as ± 1 to represent the possible rotations in 1D sub-eigenspace. Generally, a multiple eigenvalue d_j corresponds to multiple sets of orthogonal eigenvectors, which can be aligned by rotating some angle in the associated sub-eigenspace. Hence we use the sub-matrix R'_j in R to represent this rotation involved. If we integrate the spectral description R in (4), the relationship between G and H becomes:

$$V = PUR. \tag{6}$$

Because a graph can be exactly specified by its spectrum and the associated eigenvectors, we can use the projection in the eigenspace to fully represent a graph. Thus, a spectral multiplicity tolerant graph distance can be defined as

$$L(G, H) = \min_{P,R} \|PUD_GR - VD_H\|_F. \tag{7}$$

We use $L(G, H)$ to denote the SMT graph distance defined in (7) and its equivalent form in the rest of this paper. In addition, considering the constraints of real applications, we make the following two basic assumptions:

1) For each vertex in the reference graph G, i.e., the graph with less vertices, there is at least one matching vertex in the counterpart; and
2) For each vertex in the duplicate graph H, i.e., the graph with more vertices, there exists one and only one matching vertex in the counterpart.

The definition of SMT graph distance in (7) is a general model and can be easily extended to attribute graph matching problems. In this paper, we restrict our attention to undirected inexact graph matching. We firstly analyze a simpler case, i.e., the EGM problem. For a pair of graphs of the same size, we present a greedy iterative algorithm to efficiently optimize the sub-eigenspace rotation matrix R and the permutation matrix P. Then we show how to convert an IGM problem to an EGM problem by the method of graph warping. Fig. 1 shows the algorithmic structure of the proposed approach.

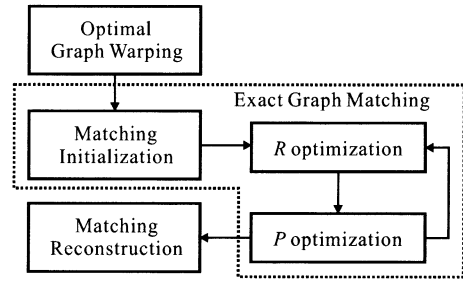


Fig. 1. Algorithmic structure of the proposed approach.

III. Case I: Exact Graph Matching

We start with the exact graph matching problem. When $n = m$, the vertex permutation matrix P is square and of full rank. The SMT graph distance defined in (7) can be further deduced to

$$\begin{aligned} &L(G, H) = \min_{P,R} \tilde{L}(P, R, G', H') \\ &\tilde{L}(P, R, G', H') = \|G'R - P^{-1}H'\|_F \\ &G' = UD'_G, \quad H' = VD'_H \end{aligned}, \tag{8}$$

where $\tilde{L}(P, R, G', H')$ is the matching error of G and H under P and R, G' and H' are the projections in the joint eigenspace of G and H, D'_G and D'_H are diagonal matrix composed of the normalized eigenvalues in descending order. To compare the structural similarity of two different graphs, it is very important to introduce a normalization process since the absolute magnitude difference may introduce matching bias. To remove the magnitude bias, we consider only the angle between eigenvectors and the relative magnitude between

the spectra of G and H. Thus in (8), we use the normalized graph spectrum D' and unit eigenvectors. In other words, we represent a graph by a polar mapping point set in a unit hypersphere, i.e., the normalized spectrum for the length and corresponding eigenvectors for the direction. The eigenspace normalization is also used by the EPC method [5]. However, our approach is different because we do not make any dimensionality reduction and the eigenvector correspondence is exactly preserved.

Note that in (8), G' and H' are independently computable and all spectrum scaled eigenvectors are compared with each other in an n-dimensional Euclidean hypersphere. Therefore, it is possible to minimize the graph matching error by the following iterative optimization process:

$$\begin{cases} \hat{R}_{(i)} = \arg\min_{R} \|G'R - \hat{P}^{-1}_{(i-1)}H'\|_F \\ \hat{P}_{(i)} = \arg\min_{P} \|G'\hat{R}_{(i)} - P^{-1}H'\|_F \end{cases}, \tag{9}$$

given a good matching initialization $\hat{P}_{(0)}$. Note that in this paper we use $\hat{R}_{(i)}$ to represent the estimation of $\hat{R}$ after i iterations, $\hat{R}_{*i}$ denotes the ith column vector of $\hat{R}$, and $\hat{R}_{i*}$ for the ith row vector.

A. Matching Initialization

A good initialization is crucial for iterative optimization processes. Thanks to the Perron-Frobenius theorem, we can derive a simple yet effective method to initialize the permutation matrix $\hat{P}_{(0)}$.

Theorem 1: If G is a connected graph with n vertices ($n \geq 2$). Then,

1) Its largest eigenvalue d_1 is the spectral radius of G, i.e., for any other eigenvalue d_i, ($i \neq 1$), $d_i \in [-d_1, d_1)$;
2) To d_1 there corresponds an positive eigenvector u_1;
3) The increase or decrease of any edge weight will cause d_1 increase or decrease accordingly;
4) d_1 is a simple eigenvalue.

Theorem 1 is the direct result of applying the Perron-Frobenius theorem to the graph spectrum. For detailed information, please refer to [2].

Recalling (7) and (8), the graph distance $L(G, H)$ may be corrupted by the spectral multiplicity of G. From Theorem 1, however, we can see that $d_1(G)$ and $d_1(H)$ are simple eigenvalues and that the nonuniqueness of corresponding eigenvectors can be removed by simply checking the positiveness of u_1 and v_1. Thus, we can initialize P_0 by

$$\begin{aligned} \hat{P}_{(0)} &= \arg\min_{P} \tilde{L}_0(P, G', H') \\ &= \arg\min_{P} \|u_1 - P^{-1}v_1\|_F, \end{aligned} \tag{10}$$

where $\tilde{L}_0(P, G', H')$ is derived from the largest eigenvalues and corresponding eigenvectors and can be viewed as a pseudo graph matching error of G and H under P. The computation of $\hat{P}_{(0)}$ is a typical minimum cost assignment problem that can be solved efficiently by the Hungarian algorithm.

Using (10) to initialize $\hat{P}_{(0)}$ is efficient and robust to the spectral multiplicity. In addition, when there exists no multi-eigenvalues, it is also possible to estimate $\hat{P}_{(0)}$ directly based on (9) by assuming $\hat{R}_{(0)}$ as an identity matrix. Hence, in real applications, we can try these two methods and choose a better one as the matching initialization.

B. Optimizing Rotation Matrix $\hat{R}_i$

When $\hat{P}_{(i-1)}$ is available, H' can be relabelled as $H'_{(i-1)} = \hat{P}^{-1}_{(i-1)}H'$ to match the reference graph. Then, we can obtain $G'_{(i)}$ by optimizing the sub-eigenspace rotation matrix:

$$\begin{cases} \hat{R}_{(i)} = \arg\min_{R} \|G'_{(i-1)}R - H'_{(i-1)}\|_F \\ G'_{(i)} = G'_{(i-1)}\hat{R}_{(i)} \end{cases}, \tag{11}$$

where $G'_{(0)} = G'$.

In fact, it is unnecessary to optimize $R_{(i)}$ explicitly. We can do this by adjusting $G'_{(i-1)}$ to minimize the matching error under the *sub-eigenspace constraints*: For the jth sub-eigenspace of $G'_{(i-1)}$ (i.e., $G'_{(i-1)j}$), the corresponding eigenvectors $(u_{j1}, \cdots, u_{jk})$, can be rotated only by a k-dimensional rotation matrix R'_j in the same subspace; and the length of each eigenvector should remain unchanged.

In other words, we can optimize $R_{(i)}$ by seeking an optimal rotation matrix $\hat{R}'_{(i)j}$ for each sub-eigenspace independently. In current iteration, let $g = G'_{(i-1)j}$ represent the point set $\{(d'_j, u_{j1}), \cdots, (d'_j, u_{jk})\}$ corresponding to the jth sub-eigenspace. Its counterpart h ($h = H'_{(i-1)j}$) can act as the target point set of g to minimize the matching error. We then use the following greedy method to adjust g for each sub-eigenspace independently:

$$\begin{cases} g := \Phi\big(g + \alpha\nabla g\big), \\ \nabla g = gg^T h - g, \end{cases} \tag{12}$$

where $\Phi(X)$ is a normalization function that normalizes each column vector of X, and α ($0 \leq \alpha \leq 1$) is the adjusting factor. In (12), we use the difference between g and the target point set h to minimize the matching error for each sub-eigenspace. To make the method satisfy the sub-eigenspace constraints, we project h into the corresponding subspace of g and rescale it accordingly.

C. Optimizing Permutation Matrix $\hat{P}_i$

Referring to (9), the impact of G's spectral multiplicity can be compensated when $\hat{R}_{(i)}$ is known. Thus, we can optimize $P_{(i)}$ by

$$\hat{P}_{(i)} = \arg\min_{P} \|G'_{(i)} - P^{-1}H'\|_F. \tag{13}$$

This becomes a standard EGM problem without spectral multiplicity. Many methods are able to solve it [4], [5], [3]. Here, we model (13) as a minimum cost assignment problem and solve it by the Hungarian algorithm. The cost matrix $C = c_{pq}$ is defined as follows:

$$c_{pq} = \|G'_{(i)p*} - H'_{q*}\|_2, \tag{14}$$

where $G'_{(i)p*}$ is the pth row vector of $G'_{(i)}$ and H'_{q*} is the qth row vector of H'.

Now we have developed a complete SMT algorithm to solve the EGM problem. Based on a reliable initialization

process, the proposed iterative process converges fast. In worst cases, the complexity of our method is $O(n^3 + q)$, where n is the graph size and q is the spectrum length of G.

Algorithm 1: SMT Graph Warping

initialize M as an $n \times m$ zero matrix, M' as an $m \times m$ zero matrix, and the $m \times 1$ flag vector f as 'unmerged';
compute vertex distance matrix $Z = \{z_{kl}\}$ according to (18);
for $i = 1; i \leq m - n; i{+}{+}$ **do**
  find the minimum distance $z_{kl} = z_{lk}$ in Z;
  $\iota := \min(l, k)$; $\kappa := \max(l, k)$;
  $H'_{\iota *} := \frac{H'_{\iota *} + H'_{\kappa *}}{2}$;
  for $j = 1; j \leq m; j{+}{+}$ **do**
    if $j \neq \iota$ *and* $j \neq \kappa$ *and* $f_j \neq$ 'merged_deleted' **then**
      $z_{\iota j} := \left\| H'_{\iota *} - H'_{j *} \right\|_2$; $z_{j\iota} := z_{\iota j}$;
    $z_{\kappa j} := \infty$; $z_{j\kappa} := z_{\kappa j}$;
  switch f_ι **do**
    case 'unmerged'
      if $f_\kappa =$ 'unmerged' **then**
        $M'_{\iota\kappa} := 1$; $M'_{\iota\iota} := 1$;
      if $f_\kappa =$ 'merged_reserved' **then**
        $M'_{\iota\iota} := 1$; $M'_{\iota *} := M'_{\kappa *}$; $M'_{\kappa *} := 0$;
      $f_\iota :=$ 'merged_reserved';
    case 'merged_reserved'
      if $f_\kappa =$ 'unmerged' **then**
        $M'_{\iota\kappa} := 1$;
      if $f_\kappa =$ 'merged_reserved' **then**
        $M'_{\iota *} := M'_{\iota *} + M'_{\kappa *}$; $M'_{\kappa *} := 0$;
  $f_\kappa :=$ 'merged_deleted';
$v := 0$;
for $i = 1; i \leq m; i{+}{+}$ **do**
  if $sum(M'_{i*}) > 0$ **then**
    $v{+}{+}$; $M_{v*} := M'_{i*}$;
$Y := find(f =$ 'unmerged'$)$; // Y is the index set of 'unmerged' elements in f
for $i = 1; i \leq n - v; i{+}{+}$ **do**
  if $sum(M'_{i*}) > 0$ **then**
    $v{+}{+}$; $M_{vY_i} := 1$;
normalize each row of M to get $\hat{M}$;

IV. Case II: Inexact Graph Matching

The SMT graph distance defined in (8) is still applicable to inexact graph matching problems if replacing P^{-1} with the pseudoinverse P^+. Although the iterative framework for exact graph matching can also be extended to inexact graph matching problems, this is not a wise choice. Note that in (8) only the spectral multiplicity of G may affect the matching error, and the sub-eigenspaces of H remain invariant in the iterative matching process. Thus, it is possible to separate the problem of size difference (i.e., the inexactness) from the graph matching process.

For convenience, we first introduce the concept of merging matrix.

Definition 1 (Merging matrix): An $n \times m$ ($n < m$) matrix M is a merging matrix if and only if

1) M is nonnegative;
2) The sum of each row of M equals to 1;
3) For each column of M, there exists one and only one positive element;
4) $M_{ij} = M_{ik}$, if $M_{ij} \neq 0$ and $M_{ik} \neq 0$.

If G and H have different size, i.e., $n < m$, $\hat{P}$ is an $m \times n$ matrix with rank n. Due to the two basic assumptions of graph matching, $\hat{P}$ can be represented by the combination of an $n \times m$ merging matrix $\hat{M}$ and an $n \times n$ permutation matrix $\hat{P}'$:

$$\hat{P} = \hat{M}^+ \hat{\hat{P}}. \tag{15}$$

Hence, we can solve an inexact graph matching problem in two steps: optimally warping H to $\bar{H}$ of the same size with G by $\hat{M}$, and optimally matching $\bar{H}$ to G by $\hat{\hat{P}}$.

A. Graph Warping

Given a merging matrix M, H is warped to $\bar{H}$ by,

$$\bar{H} = MHM^T \tag{16}$$

with warping error $\bar{L}(M, H)$:

$$\bar{L}(M, H) = \| M^+ \bar{H} M^{+T} - H \|_F, \tag{17}$$

where the existence of M^+ is guaranteed by the two basic assumptions of graph matching. To find an optimal $\hat{M}$ minimizing the warping error, we need a vertex distance measure and a vertex merging rule.

Theorem 2 (Multiplicity Invariance): The distance defined in (18) is invariant to the spectral multiplicity of H; thus can be used as the vertex distance measure:

$$z_{kl} = \begin{cases} \left\| H'_{k*} - H'_{l*} \right\|_2, & k \neq l, \\ \infty, & k = l. \end{cases} \tag{18}$$

Proof: Since we have

$$z_{kl} = \begin{cases} \frac{1}{\rho(H)} \left\| (T_{k*} - T_{l*}) C_H \right\|_2, & k \neq l, \\ \infty, & k = l, \end{cases}$$

where $T = HV$. Supposing $e_{kl} = T_{k*} - T_{l*}$, then $z_{kl}^2 = \frac{1}{\rho^2(H)} \left\| e_{kl} C_H \right\|_2^2 = \frac{1}{\rho^2(H)} Tr(e_{kl} C_H C_H^T e_{kl}^T)$ when $k \neq l$. Thus, we have $z_{kl}^2 = \frac{1}{\rho^2(H)} Tr(e_{kl} e_{kl}^T)$ because of the orthogonality nature of C_H, that is, C_H is irrelevant in (18). □

Since the vertex distance ordering is spectral multiplicity invariant, we can derive a multiplicity invariant graph warping method based on the nearest-first-merging rule: for each time we find the two vertices with the shortest length and merge them together. The detailed process of the proposed graph warping (i.e., the computation of $\hat{M}$) is given in Algorithm 1. Note that the proposed graph warping method is not restricted to our SMT approach. It can be be incorporated with any EGM method to solve IGM problems.

B. Matching Reconstruction

After graph warping, the optimal matching $\hat{\hat{P}}$ from $\bar{H}$ to G can be obtained by the proposed SMT-EGM algorithm proposed in Section 3. Accordingly, the optimal matching $\hat{P}$ from H to G can then be reconstructed by $\hat{\hat{P}}$ and $\hat{M}$ according to (15).

Since the complexity of graph warping is $\sigma O(m^2)$, the worst case complexity of our SMT-IGM method is $O(n^3 + q + \sigma m^2)$, where σ is the graph size difference and q is spectrum length of the reference graph. Note that the graph difference is not large in many cases. Thus the worse complexity of our approach is close to $O(n^3)$.

V. Experimental Results

In order to evaluate the performance, we compared our SMT approach with the eigendecomposition (ED) method [3] and the EPC method [5] on a large set of synthesized data. The proposed approach was also used in uncalibrated stereo matching to demonstrate its practical effectiveness.

A. Numerical Experiments

In our experiments, the following procedure was used to generate the reference graph G and its duplicate H. Firstly, we used the method developed by Ide et al. to generate a connected polytree [6], within which we randomly selected υ vertex pairs and added an edge to any selected vertex pair, if unconnected. Then the edge weight of G was set randomly between 0 and κ according to the uniform distribution. The duplicate graph H was derived by relabelling the vertices of G with a randomly permutation matrix P. To test the performance for inexact graph matching, the structural noise was introduced by randomly selecting a vertex of H and appending an additional one on it for τ iterations. Finally, we added an independent weight noise (uniformly distributed on $[-1/2, 1/2]$ with magnitude ϵ) to H. In particular, $\|PGP^T - H\|_F$ was used to measure the matching error, and we fixed $\upsilon = 10$, $\kappa = 5$.

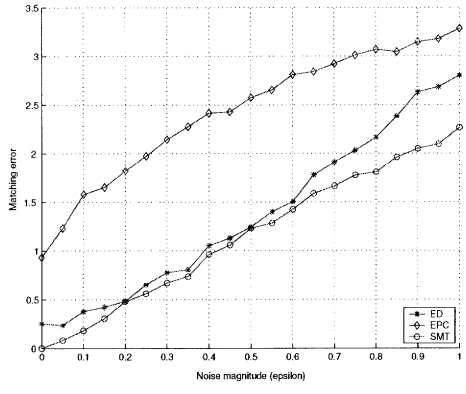


Fig. 2. EGM without spectral multiplicity: matching error versus noise magnitude ϵ.

Sensitivity to noise. Fig. 2 presents the curve of matching error vs. noise magnitude for EGM without spectral multiplicity. When $\epsilon < 0.5$, the performance curves of the SMT and ED are close and well separated from that of the EPC method. But the SMT approach is more robust to noises when ϵ is larger.

Fig. 3 shows the results for EGM with spectral multiplicity. The performance of the EPC method seems to be zigzag upwards for EGM with spectral multiplicity. And the advantage of the SMT approach becomes apparent.

Fig. 4 displays the results for IGM with spectral multiplicity. We extend the ED method to IGM by combining with our graph warping process. In this experiment, all three curves are well spaced and the SMT approach outperforms the other two. The performance of the EPC method is stable and it outperforms the "ED+Graph Warping" method when $\epsilon > 0.6$.

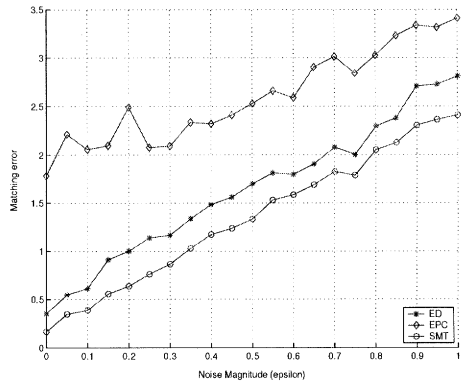


Fig. 3. EGM with spectral multiplicity: matching error versus noise magnitude ϵ.

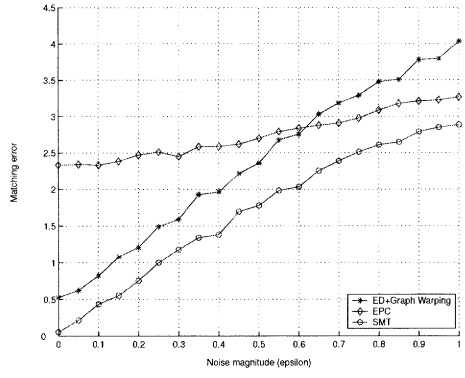


Fig. 4. IGM with spectral multiplicity: matching error versus noise magnitude ϵ.

Sensitivity to spectral multiplicity. In this experiment, the reference graph G was generated by explicitly setting its second eigenvalue to be k-multiple and other eigenvalues to be simple. Thus the max multiplicity ratio k/n can be used to measure the degree of spectral multiplicity. G's duplicate graph H was generated by setting $\tau = 5$ and $\epsilon = 0$. To evaluate the robustness to spectral multiplicity, we generated 200 graph pairs covering the max multiplicity ratio from 0.1 to 0.6 and calculated the average matching error accordingly. The results shown in Fig. 5 demonstrate our approach's robustness to the spectral multiplicity.

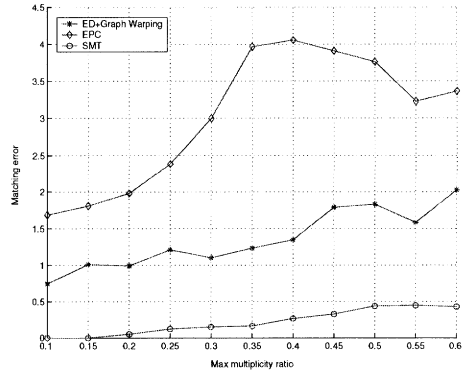


Fig. 5. Matching error versus max multiplicity ratio k/n.

Discussion. The numerical experiments indicate that, compared with other spectrum based graph matching methods, the SMT approach is more robust to the independent and

structural noise, especially more robust to the spectral multiplicity. This is attributed to the iterative process of optimizing the sub-eigenspace rotation matrix R and the permutation matrix P alternatively.

Except for robustness, the SMT approach is comparable to other spectrum based graph matching methods in terms of complexity. Table 1 lists the worst case complexity of some graph matching algorithms, within which L denotes the size of the linear programming problem, σ is the size difference, q is spectrum length of the reference graph G, and n is G's vertex number.

TABLE I

ALGORITHM COMPLEXITY

Method	Worst Case Complexity
Linear programming [4]	$O(Ln^6)$
Eigendecomposition [3]	$O(n^3)$
proposed SMT approach	$O(n^3 + \sigma m^2 + q)$

B. Uncalibrated Stereo Matching

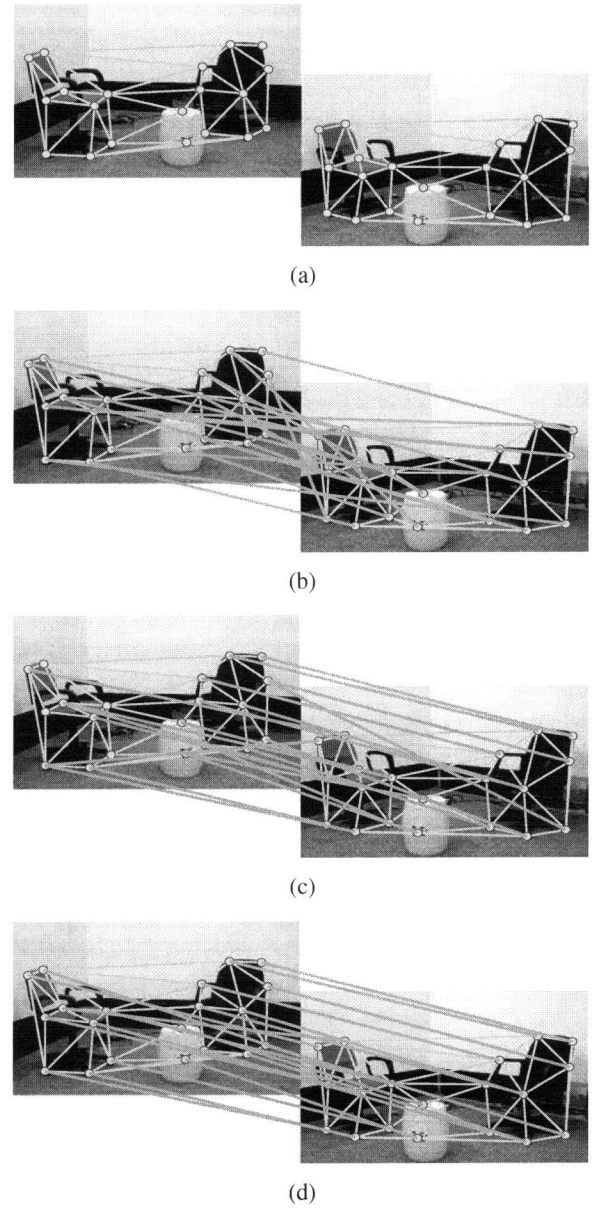
In order to demonstrate the effectiveness of the proposed approach for real-world images, we carried out experiments on uncalibrated stereo matching. Without an accurate calibration, stereo matching becomes more difficult. Inexact graph matching can be used to tolerate the unknown geometric deformation and to recover the correspondence.

The feature graph was generated by Delaunay triangulating the feature points in the left and right view images. We used a semi-automatic process to extract the feature points. We then used the triangulation feature graphs to determine the optimal stereo matching. Fig. 6 shows the matching results with comparison of the ED algorithm [3] and EPC method [5].

VI. CONCLUSION

In this paper, we have presented a robust inexact graph matching algorithm based on iteratively optimizing the sub-eigenspace and the vertex permutation. We use an efficient matching initialization method to make the iterative process converge fast. Based on the same framework, we then propose an optimal graph warping method to convert the IGM to EGM. The proposed approach overcomes a common limitation of previous spectrum based graph matching methods and has comparable complexity.

Our method is designed for undirected inexact weighted graph matching. But it can be easily extended to attributed graphs by inducing a set of vertex attribute diagonal matrix and edge attribute matrices. In this case, the normalized eigenspace of all attribute matrices can be concatenated together, and the proposed approach is still applicable. Our approach can also be extended to directed graph matching when applied to the Hermitian matrices derived from the adjacency matrix [3]. Additionally, the graph warping method has potential use as a preprocessing to enable an EGM method to solve IGM problems. In some applications, the graph warping method can also be used to decrease the vertex number leading to reduced complexity.



(a) (b) (c) (d)

Fig. 6. Stereo matching for the lab scene: (a) feature graphs of left view and right view; (b) matching result of the ED algorithm (matching error 2.3174); (c) matching result of the EPC method (matching error 1.4796); (d) matching result of the proposed SMT approach (matching error 0.8249).

REFERENCES

[1] B. Luo and E. Hancock, "Structural graph matching using the em algorithm and singular value decomposition," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 23, no. 10, pp. 1120–1136, Oct. 2001.

[2] A. Schwenk and R. Wilson, "On the eigenvalues of a graph," in *Seletcted Topics in Graph Theory*, L. Beineke and R. Wilson, Eds. Academic Press, 1978, pp. 307–336.

[3] S. Umeyama, "An eigendecomposition approach to weighted graph matching problems," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 10, no. 5, pp. 695–703, Sep. 1988.

[4] H. Almohamad and S. Duffuaa, "A linear programming approach for the weighted graph matching problem," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 15, no. 5, pp. 522–525, May. 1993.

[5] T. Caelli and S. Kosinov, "An eigenspace projection clustering method for inexact graph matching," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 26, no. 4, pp. 515–519, Apr. 2004.

[6] J. Ide and F. Cozman, "Generating random bayesian networks," in *Proc. Brazillian Symp. AI*, Oct. 2002, pp. 234–241.