Topology Preserving Graph Matching

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Abstract

We describe an algorithm for graph matching which preserves global topological structure using an homology preserving graph matching. We show that for simplicial homology, graph matching is equivalent to finding an optimal simplicial chain map, which can be posed as a linear program satisfying boundary commutativity, simplex face intersection and assignment constraints. The homology preserving matching provides (i) globally consistent matching with higher order simplex weights, (ii) match verification using topological invariants, and (iii) topological constraints to improve any geometric matching approach. Vision applications require 'topologically rich' graphs, so we describe a general simplicial complex construction such that salient image structures correspond to homology groups. Finally, we evaluate performance on random graphs and demonstrate use of homology preserving subgraph matching for object matching applications.

1. Introduction

Graph matching is the problem of finding correspondences between graphs such that relational structure is preserved. This is a fundamental problem in computer vision, machine learning and pattern recognition since structured data in widespread in such forms as part based object recognition, image grammars, structured prediction, and shape representations. For recent surveys of graph matching, see [1, 2].

Many structure preserving correspondence problems in vision can be posed a weighted graph matching problem. Given two attributed graphs $G = (V, E, \alpha)$, $G' = (V', E', \alpha')$, let X be an $|V| \times |V'|$ permutation matrix, such that $X(i, i') = 1$ if nodes (i, i') are matched and zero otherwise. Let W be an $|V||V'| \times |V||V'|$ weight matrix determined from attributes (α, α') such that $w_{ii',jj'} \in \mathbb{R}$ encodes the compatibility of matching (i, i') and (j, j'). Let x be an an $|V||V'| \times 1$ columwise vector representation of

X such that $x_{ij} = X(i, j)$ and x_i^T is the ith row and x_j is the jth column. Then,

$$
\begin{aligned}
x_{QAP}^* = \arg\max \quad & x^T W x \\
\text{s.t.} \quad & \mathbb{1}^T x_j = 1 \\
& x_i^T \mathbb{1} = 1 \\
& x_{ij} \in \{0, 1\}
\end{aligned}
\tag{1}
$$

The optimization in (1) is an instance of a quadratic assignment problem, such that x_{QAP}^* is a maximum weight edge preserving matching where $(u, v) \in E \Leftrightarrow (X(u), X(v)) \in E'$ [3].

The optimization in (1) is an integer quadratic program which is NP-complete, so approximate solutions are necessary. Approximation algorithms that have been explored in the literature include combinatorial search [3], graduated assignment [7], spectral [9, 6], semidefinite programming [8], and graph edit distance [4]. These approaches require a construction of the quadratic objective weights W which is quadratic in the size $|V||V'|$. Robust performance has been demonstrated [7, 6], but practical problem sizes are limited to hundreds of nodes due to the quadratic objective, and weights are limited to pairwise interactions.

Recent work has focused on geometry preserving linearizations [11, 13, 12] of the quadratic objective in (1). Similarity invariant matching [13] solves for the optimal permutation matrix X and linearized similarity transformation parameters θ to minimize an assignment cost and an $L1$-norm linear deformation cost. Locally affine invariant matching [12] solves for the optimal assignment X given $L1$-norm barycentric coordinate preservation costs for each node, where barycentric coordinates are locally affine invariant and defined in terms of neighboring graph nodes. Both approaches use an $L1$-norm in the objective, and exhibit linear constraints ([13] includes a linearization of the similarity constraints) resulting in a linear programming relaxation.

These geometric approaches provide fast and efficient matching, but they can suffer from ambiguity when the input graph does not satisfy the assumptions of the geomet-

ric transform model, such as cases of non-similarity transformations or degenerate triangulations. Furthermore, assignment weights are limited to node assignment weights only, ignoring informative assignment weights for edges and other higher order structures [10]. Finally, these methods must discretize X to a final binary permutation matrix for valid and invalid matches. Poor geometric alignments with large deformation costs may still be valid (e.g. articulated objects), and good geometric alignments with small deformations may be invalid. We would like a "certification" for good and bad matches to handle such ambiguity.

In this work, we focus on *topology preserving* graph matching to address these observations. Topology can be described as qualitative geometry [15], which is focused on issues of "connectedness" rather than metric properties. We pose the problem of structure preserving graph matching as topological structure preserving graph matching, where topological structure is defined in terms of simplicial homology. Therefore, our goal is to determine an optimal assignment X that preserves *homologies*. Results from algebraic topology show that a *chain map* is a such an assignment that induces a globally consistent map on homologies, and can be used to compute global topological properties of the final match. Basically, a valid match must preserve topological invariants of the source graph.

The primary contributions of this work are:

1. **Globally consistent matching using multiple higher order simplexes**. Simplicial homology is defined in terms of k-simplexes, the higher dimensional analogue of nodes and edges. Each simplex ($\leq k$) has an independent weight for assignment, and constraints handle consistency between simplexes of different dimension.

2. **Match verification using topological invariants.** Topological constraints on boundary commutativity and face intersection allow for computation of topological invariants such as Betti number on the final assignment X. Invalid matches do not preserve topological invariants of the source graph.

3. **Geometrically extensible.** Any geometric method can be augmented with the topological constraints for improved performance.

4. **Linear programming implementation**. All topological constraints can be posed as a constrained linear assignment problem satisfying boundary commutativity, simplex face intersection and assignment constraints.

2. Homology Preserving Graph Matching

In this section, we first provide a brief introduction to those definitions and results in simplicial homology necessary to introduce the homology preserving graph matching in section 2.3. For detailed discussion of homology and algebraic topology, see [15, 19, 20].

2.1. Simplicial Homology

We begin with general definitions. Practical vision applications are typically limited to dimension ≤ 3, however we introduce general definitions for completeness. The reader is referred to section 2.2 for a discussion on examples and intuition for these concepts in the context of graph theory.

Definition 2.1. A p-dimensional simplex or p-simplex is the convex hull of $p + 1$ affinely independent vertices $v \in \mathbb{R}^D$

Definition 2.2. A *face* of a p-simplex σ is a non-empty subset of vertices of σ.

Definition 2.3. A simplicial complex K is a set of simplices that satisfies the following closure conditions

(i) Any face of a simplex in K is a simplex in K

(ii) The intersection of any two simplexes $\sigma_i, \sigma_j \in K$ is a face of both σ_i, σ_j

Let K be a finite simplicial complex of dimension p, such that all simplexes $\sigma \in K$ have dimension at most p. A simplicial k-chain is a finite formal sum of k-simplices

$$\sum_{i=1}^{N} c_i \sigma_i, \ c_i \in \mathbb{R}, \ \sigma_i \in K \qquad (2)$$

where c_i are real valued coefficients. For each $k \geq 0$, k-chains along with the addition operator form the *chain group* $C_k(K)$.

Definition 2.4. The boundary operator $\partial_k \colon C_k \to C_{k-1}$ is a homomorphism between chain groups such that

$$\partial_k(\sigma) = \sum_{i=0}^{k} (-1)^i \langle v^0, \ldots, v^{i-1}, \hat{v^i}, v^{i+1}, \ldots, v^k \rangle \quad (3)$$

The notation $\hat{v^i}$ denotes that the vertex should be dropped. The boundary homomorphism is a linear operator and commutes with addition $\partial_k(c_1 + c_2) = \partial_k(c_1) + \partial_k(c_2) \forall c_1, c_2 \in C_k(K)$ Observe that $\partial_k(\sigma) = \sum c_i \partial_k(\sigma_i)$, and the boundary homomorphism is a map from k-simplexes to a sum of its $(k+1)$ faces.

The boundary homomorphism has a unique matrix representation with respect to a choice of basis. Let $\{\sigma_i\}$ and $\{\tau_j\}$ be the sets of k-simplexes and $(k-1)$-simplexes of size $|M - 1|$ and $|N - 1|$ that represent the elementary chain bases for C_k and C_{k-1}. Then, ∂_k is represented as an MxN boundary matrix with entries $a_{ij} \in \{-1, 0, 1\}$, such that $|a_{ij}| = 1$ if $i \in \tau$ is a face of $j \in \sigma$ with sign determined from (3), and zero otherwise.

Definition 2.5. The chain complex

$$C_k \xrightarrow{\partial_k} C_{k-1} \xrightarrow{\partial_{k-1}} C_{k-2} \ldots C_0 \xrightarrow{\partial_0} 0$$

is a sequence of chain groups connected by boundary homomorphisms.

The boundary homomorphism has several useful properties, which we state but do not prove [15].

Lemma 2.6. *Given a boundary homomorphism ∂,*

(i) The boundary of a boundary is zero, $\partial_k \partial_{k+1} d = 0$, for every integer k and every $(k + 1)$-chain d.

(ii) A k-cycle c is a k-chain with zero boundary $\partial_k c = 0$

(iii) The boundary of every 0-simplex is zero.

(iv) The cycle group $Z_k = ker(\partial_k) = \{x \in C_k(K) : \partial_k x = 0$

(v) The boundary group $B_k = im(\partial_{k+1}) = \{x \in C_k(K) : \exists\, y \; s.t. \; x = \partial_{k+1} y.$

Elements of the cycle group Z_k are k-chains called k-cycles, elements of the boundary group B_k are k-chains which called k-boundaries, which are boundaries of a $(k + 1)$-chain and are also cycles ($B_k \subset Z_k$).

Definition 2.7. The *homology group* $H_k(K) = Z_k/B_k$ is a quotient group, with elements such that $\{z|z = z_0 + \partial_{k+1} c, c \in C_{k+1}(K)\}$ for a fixed representative cycle z_0.

Cycles of the same homology class are *homologous* and denoted $c \sim c'$.

Definition 2.8. The kth betti number

$$\beta_k = rank(H_k(K)) = rank(L_k) L_k = \partial_k^T \partial_k + \partial_{k+1} \partial_{k+1}^T$$

is the rank of the kth homology group or equivalently the rank of the kth combinatorial laplacian L_k [17].

Definition 2.9. A chain map $M_k \colon K \to K'$ is a homomorphism mapping k-simplexes of simplicial complexes K and K'. The chain map must satisfy boundary commutativity.

$$\partial'_k \circ M_k = M_{k-1} \circ \partial_k$$

This requirement follows from the requirement $\partial_k \circ \partial_{k+1} = 0$. A chain map between chain complexes maps boundaries to boundaries and cycles to cycles, and induces homomorphisms between homology groups of the two complexes [15]. This fundamental property of the chain map is the foundation for the homology preserving graph matching.

2.2. Discussion and Examples

The definitions for simplicial homology were introduced in general for k-simplexes, however these concepts have intuitive low dimensional interpretations in the context of graph theory. Given a graph $G = (V, E)$, a 0-simplex is a vertex in V, a 1-simplex is an edge in E, a 2-simplex

is a triangle which forms a three node clique, a 3-simplex as a tetrahedron or four node clique, and so on. The faces of a edge (1-simplex) are the two incident vertex endpoints (0-simplexes), and trivially the edge itself. The faces of a triangle (2-simplex) are the triangle itself (trivially), three edges (1-simplexes) and three nodes (0-simplexes).

The simplicial complex closure constraints in (2.3) states intuitively that if two edges are incident on a common vertex, then both edges must contain the vertex as a face. A 1-chain (2) is any subset of edges, not necessarily connected. The boundary map ∂_1 (3) is the oriented node-edge incidence matrix, and the boundary map ∂_2 is the edge-triangle incidence matrix. For node-edge incidence only, the combinatorial laplacian $L = \partial_1 \partial_1^T = D - W$, which is the classic graph laplacian for unit weights W. Betti numbers β_1 (2.3) capture the number of "holes" in the graph, and the homology group H_1 contains equivalence classes such that each homology class is the set of all cycles that differ by a boundary from a cycle surrounding this hole. Finally, traditional graph matching is an estimation of $\hat{M}_0$, the permutation matrix between graph nodes (0-simplexes) that preserves edges (1-simplex intersections).

2.3. Constrained Linear Assignment

Homology preserving graph matching is the estimation of chain maps $M_i \colon K_i \to K'_i$ for all $i \leq p$ subject to boundary commutativity, simplex intersection and assignment constraints. This can be reformulated as constrained integer linear assignment problem, which can be relaxed to a linear programming optimization.

Given two simplicial complexes K and K' of dimension p, let $X = \{X_0, \ldots, X_p\}$ be a set of permutation matrices, such that X_k encodes the chain map M_k. Assume that for notational simplicity all $i \leq p$, $|K_i| \leq |K'_i|$. Let W_k be a weight matrix for the chain map X_k, such that w_{ij} is the weight of matching $\sigma_i \in K_k$ and $\sigma_j \in K'_k$. Let $\bar{W}_k = diag(W_k^T \mathbb{1})$ be a diagonal matrix of rowsums of W_k, where $\mathbb{1}$ is vector of ones. Let boundary maps $\partial = \{\partial_1, \ldots, \partial_p\}$ for K and $\partial' = \{\partial'_1, \ldots, \partial'_p\}$ for K'. Then, the optimal homology preserving graph matching X^* is the constrained linear assignment problem:

$$X^* = \arg\max_{X_0,\ldots,X_p} \sum_{k=0}^{p} tr(\bar{W}_{k+1} W_k^T X_k) \quad (4)$$

s.t. $\quad \forall k \leq p$
$$\partial'_k X_k - X_{k-1} \partial_k = 0$$
$$x_k^{ij} \leq \sum_n x_{k-1}^{mn} \; ; \forall (m, n) \in \partial_k(i) \times \partial'_k(j)$$
$$\mathbb{1}^T X_k = \mathbb{1} \quad (5)$$
$$X_k^T \mathbb{1} \leq \mathbb{1}$$
$$X_k \geq 0.$$

This linear program our primary contribution.

The objective (4) is a sum of the traces of the form $tr(W^T X)$. This objective is linear in X, and can be reformulated to a vector $x = [col(X_0)\ldots col(X_p)]^T$ by columnwise expansion of matrices X_i, and a vector $c = [col(W_0),\ldots,col(W_p)]^T$. Then it is clear that $c^T x$ is equivalent to the objective (4). We maintain matrix unknowns for readability, similar to [12, 13].

Lemma 2.10. $tr(\bar{W}_1 W_0^T X) = \hat{w}^T x$ *is a linear approximation to the quadratic objective* $x^T Q x$ *in* (1) *for* $\hat{w}_i = \sum_j w_1(i,j) w_0(i)$.

Proof. Consider a first order Taylor series approximation

$$x^T Q x = \sum_{i=0}^{N} \sum_{j=0}^{M} x_i q_{ij} x_j = \sum_{i=0}^{N} \sum_{j=0}^{M} f(x_i, x_j)$$

$$f(x,y) = \alpha x y$$
$$\simeq f(a,b) + (x-a) f_x(x,y) + (y-b) f_y(x,y)$$
$$f(x,y) \simeq \alpha x + \alpha y - \alpha$$

$$x^T Q x \simeq \sum_{i=0}^{N} \sum_{j=0}^{M} q_{ij} x_i + q_{ij} x_j - q_{ij}$$

for x, y in the small range $[0, 1]$. Entries q_{nm} in the quadratic objective Q denote the compatibility matching nodes (n', n'') and (m', m''). This is equivalent to the weights in W_1 which denonote the compatibility of matching edges, which is defined as the compatibility of matching pairs of nodes. Therefore,

$$x^T Q x \simeq \sum_{i=0}^{N} (q_{i1} + q_{i2} + \ldots + q_{iM}) x_i$$
$$x^T Q x \simeq \hat{w}^T x$$
$$\hat{w}_i = \sum_j w_1(ij) w_0(i)$$

where the weights w_0 are node weights equivalent to the on-diagonal elements of Q. We introduce this as a product instead of a sum, however the linearization still holds. □

Observe that the objective (4) is "intertwined" with weights from simplexes of increasing dimension, just as the boundary commutativity is intertwined. We have shown this for the dimension 0 and 1 case, but this holds by induction for higher dimensions as well since in general simplexes σ_k and σ_{k-1} intersect in at most one face.

The constraints (5) are boundary commutativity, face intersection, assignment and positivity. The notation $\mathbb{1}$ is a vector of ones, $X_k \geq 0$ denotes elementwise positivity, and x_k^{ij} is the ijth element of X_k. The assignment constraint $\mathbb{1}^T X_k = 1$ requires that columns of X_k sum to one, and that $X_k^T \mathbb{1} \leq 1$ row sums are upper bounded by one. Since

by assumption X_k is a permutation from $K_k \rightarrow K'_k$ and $|K|$ is smaller, then this assignment constraint results in a surjection. The elementwise positivity constraint $X_k \geq 0$ is a relaxation of the integer linear programming constraint $x_k^{ij} \in \{0, 1\}$.

Lemma 2.11. *The boundary commutativity constraint* $\partial'_k X_k = X_{k-1} \partial_k$ *is equivalent to the nullspace constraint* $Vx = 0$ *for* $V = ker(A)$ *such that*

$$A = \begin{bmatrix} \partial' & 0 & 0 & -B_1 \\ 0 & \ddots & 0 & \vdots \\ 0 & 0 & \partial' & -B_M \end{bmatrix} \quad B_i = \begin{bmatrix} (\partial_i)^T & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & (\partial_i)^T \end{bmatrix}$$

where ∂_i is the ith column of ∂.

Proof. This follows from straightforward algebraic manipulations of $\partial'_k X_k - X_{k-1} \partial_k = 0$, vectorizing matrix X_k columnwise and X_{k-1} rowwise, then collecting terms. The nullspace constraint results is many fewer constraints than the corresponding equality constraints. □

Lemma 2.12. *If* $x_k^{ij} \leq \sum_n x_{k-1}^{mn}$ *for all* $(m,n) \in \partial_k(i) \times \partial'_k(j)$ *then face intersection is preserved.*

Proof (sketch). If two k-simplexes (i,j) are matched, then $x_k^{ij} = 1$. A k-simplex σ_i has $k-1$ faces. The faces of σ_i are $\partial_k(i)$ and the faces of σ_j are $\partial'_k(j)$. We abuse notation $(\partial_k(i) \times \partial'_k(j))$ to refer to all pairwise matches of $k-1$ faces of σ_i to $k-1$ faces of σ_j. Each element of this subset is (m,n) to refer to the matching of face m of σ_i to face n of σ_j. The sum $\sum_n x_{k-1}^{mn}$ refers to the sum over all faces of σ_j matched to one face m of σ_i. Therefore, there are $k-1$ constraints, one for each face m of σ_i, such that if $x_k^{ij} = 1$ then every face of σ_i must match to at least one face of σ_j. □

Theorem 2.13. *The constrained linear assignment problem in* (4) *is homology preserving.*

Proof (sketch). The optimal assignment X^* is a homomorphism $X^* = \{X_0, \ldots, X_k\}$ such that $X_k : K \rightarrow K'$. By the previous lemma, the optimization is closed under face intersection, so X is a homomorphism that preserves face intersection, and the range of X satisfies the definition of a simplicial complex (2.3). Furthermore, by construction, the optimization satisfies boundary commutativity. Therefore, X^* is a homomorphism between simplicial complexes that exhibits boundary commutativity, and is a chain map (2.9). □

The optimization in (4) requires as inputs the weights W and unoriented boundary maps $|\partial|, |\partial'|$, and provides output X^*. For $p = 1$, this results in inputs $\partial_1 \in \mathbb{Z}^{nxm}$ (n nodes, m edges), $\partial'_1 \in \mathbb{Z}^{NxM}$ (N nodes, M edges), $W_0 \in \mathbb{R}^{Nxn}$, $W_1 \in \mathbb{R}^{Mxm}$ and outputs $X_0 \in \mathbb{R}^{Nxn}$,

$X_1 \in \mathbb{R}^{Mxm}$. In the case $p = 1$, the total number of variables is $O(Nn + Mm)$ and the total number of constraints is $O(Mm + Nm)$, where the constraints are dominanted by the face intersection and boundary commutativity conditions.

2.4. Topological Invariants

Homology preserving graph matching attempts to find a best match that preserves homology. However, for some matches, homology is so different that is cannot be preserved. In this case, we would like to have a measure for invalid match, that is invariant to geometric deformations.

Homology preserving graph matching provides this in the form of Betti numbers. Betti numbers are topological invariants defined in (2.8) that are preserved under homeomorphisms. Given the assignment matrices X_k, X_{k-1} and X_{k-2} determined from HPGM, and since HPGM is homology preserving, observe that:

$$\hat{L}_k = X_{k-1}^T \partial_{k-1}'^T X_{k-2} \partial_{k-1} + X_{k-1}^T \partial_k' X_k \partial_k^T \quad (6)$$

where L_k is the kth combinatorial laplacian defined in (2.8), and $\hat{L}_k$ is an estimated combinatorial laplacian by mapping between simplicial complexes $K \to K' \to K$ using the estimated assignment matrices. If the homologies are preserved correctly, then this mapping through K' a should not change the topological invariant, and $\beta_k = rank(L_k) = \hat{\beta}_k = rank(\hat{L}_k)$. The dimension of the nullspace of $\hat{L}$ can be determined by singular value decomposition $\hat{L}_k = UDV^T$, such that the rank is the number of zero singular values of D. $\hat{L}$ is positive semidefinite, and singular values will be positive. Therefore, a measure of invalid match invariant to geometric deformations is

$$\tau = \sum_{k=0}^{p} (\sigma_k - \hat{\sigma}_k)^2$$

where $\sigma_k = diag(D_k)$ is a vector of the singular values of L_k in increasing order, less than a given maximum value. This measure can be used as a feature for classification or used directly as a certification of valid topology preserving matching.

2.5. Rips Complex

Vision applications of the homology preserving graph matching requires an appropriate construction of a simplicial complex from images such that homology classes correspond to salient image features. In this section, we describe one such construction using a Rips complex [18] to construct "topologically rich" (e.g. $\beta_1 >> 0$) simplicial complex for homology class H_1. This is a generalization of the contour grouping construction of Zhu et al [22], which we refer the reader for references.

Given an image, threshold the output of an edge detector such as global Pb to obtain a discrete set of edgels S. The Vietoris-Rips complex $V_\epsilon(S)$ of S at scale ϵ is defined as [18]: :

$$V_\epsilon(S) = \{\sigma \subseteq S | d(u,v) \leq \epsilon, \forall u \neq v \in \sigma\}$$

for Euclidean distance d. Each simplex $\sigma \in V_\epsilon(S)$ has vertices that are pairwise within distance ϵ. The scale parameter ϵ defines a neighborhood in which nodes are connected. The complex $V_\epsilon(S)$ is a simplicial complex, of dimension equal to the largest clique of radius ϵ in S. Given a maximum dimension d, $V_{\epsilon,d}(S) \subseteq V_\epsilon(S)$ such that $\sigma \ in V_{\epsilon,d}(S)$ has at most dimension d, which in this construction we limit to one. Attributes for 1-simplexes are defined by the construction in [22], and attributes for 0-simplexes are defined by a local feature descriptor (such as SIFT).

An example of the Vietoris-Rips complex $V_\epsilon(S)$ is shown in figure 3. In this construction, the elements in the homology group H_1 correspond to sets of non-bounding cycles for each dominant closed contour in an image. As a final note, we observe that not all objects contain multiple dominant closed contours. If this is the case, then Betti numbers for these images *given this construction* are not a good invariant for verification. However, consider a different simplicial complex construction that (for example) adds additional nodes at dominant corners, then connects these new nodes with edges or triangles. This introduces homology classes defined by salient contours connected by corners, and Betti numbers for this construction are likely to be valid.

3. Experimental Results

We evaluate on a set of random graphs and on real images for an object matching application. For all experiments, we limited the maximum dimension of the simplicial complex to $p = 1$, so that the constrained linear assignment objective of (4) has the form $X^* = \arg\max_{X_0, X_1} tr(W_1^T X_1) + tr(W_0^T X_0)$, with the corresponding constraints for $k \leq 1$. In this form, X_0 is an assignment matrix for nodes and X_1 for edges. For all experiments, we create rips complexes K and K' using the approach in section 2.5 for a source graph, and a target or scene graph respectively. We construct boundary matrices ∂_1 and ∂_1' from eq. 3. We then specify a subgraph of K as an object or model within the source. Weight matrices W_0 and W_1 are defined with entries $w_{ij} = exp(-(\alpha_i - \alpha_j)^2)$ for edge or node attribute similarity. Finally, we run the linear program (4) using the multithreaded MOSEK interior point solver, and final node match is the argmax over columns of $X_0 + \partial_1' X_1 \partial_1$, with an experimentally set threshold for invalid matches. Graph matching experiments on the order of hundreds of nodes and edges in the source matched to thou-

sands of nodes and edges in the target typically run in about fifteen minutes on current hardware.

3.1. Random Graphs

Figure 1 shows results on matching performance for perturbed random graphs, comparing performance of homology preserving graph matching (HPGM), balanced graph matching (BGM) [6] and bipartite matching. We chose these comparisons to show performance of HPGM against a quadratic objective (BGM) and a linear objective without constraints (bipartite). For all experiments, unless otherwise stated, the graph K is constructed with $|K_0| = 32$ nodes and $\beta_1 = 8$, then perturbed according to the experiment to create K'. Examples of these homology rich graphs are shown in the figure. Performance evaluation is mean error rate ($\#_{correct}/\#_{total}$) for node matching X_0 vs. the true perturbation.

First, we perturbed weights W_0 and W_1 by adding Gaussian random noise with $\sigma \in [0, 2]$. Results show that HPGM significant outperforms the others. Next, we performed the same experiment, but on Erdos-Renyi random graphs ($\beta_1 = 0$) with edge probability $p = 0.5$, and results show that even without significant non-trivial homology classes, the HPGM still outperforms due the large number of node-edge intersections. Next, we randomly deleted nodes from the source graph at a constant noise level ($\sigma = 0.5$), and we show that HPGM is approximately equivalent in performance to BGM. Next, we increased Betti numbers for a constant noise level ($\sigma = 0.5$), and showed that HPGM decreases in error as the Betti number is increased. Next, we randomly inserted nodes with edge probability $p = 0.05$ with noise level $\sigma = 0.5$ and again with noise level $\sigma = 0.1$. This is the most critical result for subgraph matching, as this demonstrates accuracy for subgraph matching as clutter is added to the target. Results show that if the noise on the weights is not too large, then matching for HPGM does not depend on the number of nodes in the target (at least up to 2x node addition). This result highlights how important accurate node and edge weights are to matching performance.

3.2. Subgraph Matching

Figure 2 shows subgraph matching results on a subset of the affine covariant features dataset [21]. We chose this dataset to investigate performance using a graph construction consistent with geometric graph matching results in the literature. We constructed simplicial complexes using SIFT keypoints and delaunay triangulation, where node attributes are sift descriptors and edge attributes are the relative dominant orientation between nodes. The matchings are stable, however results are sensitive to missing keypoints in the target graph. These missing nodes result in a large number of changes in edges from the Delaunay triangulation, which causes the source nodes to be (correctly) not

matched. This can be seen in the third image with only two matches. The matching is also sensitive to errors in SIFT descriptor weights (as expected from random graph evaluation), causing some nodes to be rejected such as in the wall sequence (bottom). These experiments show that a different graph construction is needed for robust topological invariance, which motivates the Rips complex construction from section 2.5.

Next we evaluated subgraph matching for the Rips complex construction. Figure 3 shows a matching result. This construction is less sensitive to missing nodes as additional edges can preserve the topology, and global Pb is more stable to viewpoint deformations. Unfortunately, the Rips complex introduces an order of magnitude more nodes and edges, resulting in an LP with on the ordero of millions of constraints and variables. As a result, even for 128x128 images, the runtime for this construction is impractical ($\sim$12 hours). While the construction looks promising, due to runtime limitations we show only a single subgraph to subgraph matching result as proof of concept.

4. Conclusions

We have described an algorithm for homology preserving graph matching that provides a global topological match between graphs. We have shown that this matching is robust to random graph perturbations, and that it can be used for subgraph alignment of real imagery with geometric deformation. Results are promising, however more evaluations are needed on real imagery to determine robustness. Performance is sensitive to the graph construction, and while the Rips complex construction results in a prohibitively large linear program, the "intertwined" nature of the homologies suggests an iterative approximation of this LP, where simplexes are matched dimension by dimension, preserving homology constraints and reducing the total number of possible matches as the dimension is increased. We leave such extensions to future work. Finally, we observe that the topology preserving matching can also enable new vision applications of tools from computational topology literature. Optimal homologous cycle detection [16] could be used for part matching and persistent homology [19] can be used for shape descriptors in clutter.

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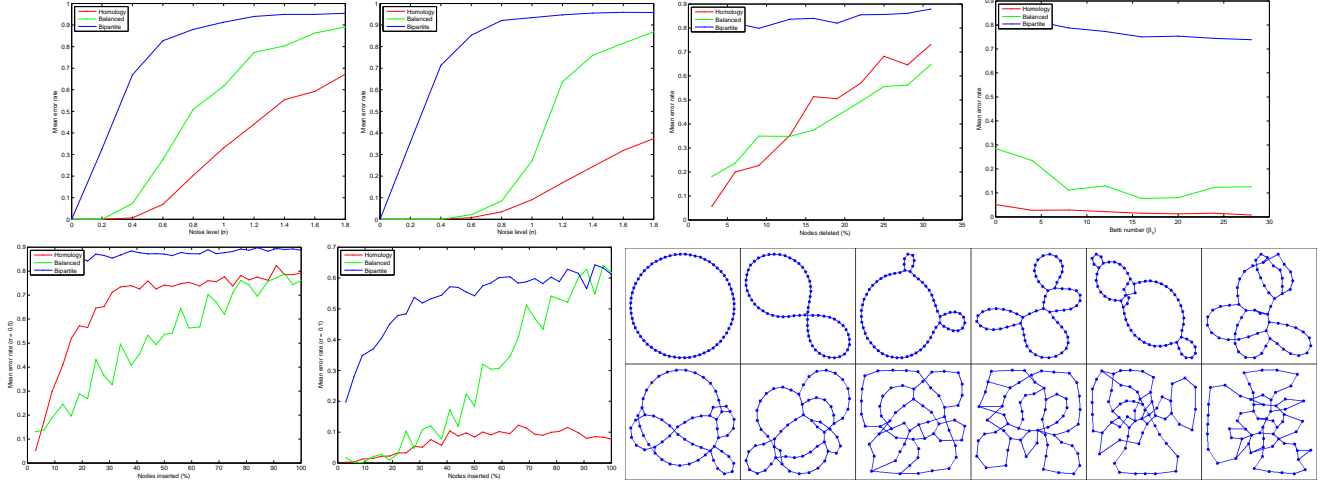[3] J. R. Ullman, An algorithm for subgraph isomorphism, J. Assoc. Comput. Mach. 23 (1976) 31(42).; 1

Figure 1. Evaluation on random graphs (left to right, by rows). (i) Increasing noise level $\sigma \in [0, 2]$ for homology rich graphs ($\beta_1 = 8$) (ii) Increasing noise level on Erdos-Renyi random graphs (p=0.5) (iii) Deleted nodes (iv) Increasing Betti number (v) Nodes inserted ($\sigma = 0.5$) (vi) Nodes inserted ($\sigma = 0.1$). (vii) Examples of homology rich graphs used in these experiments with increasing Betti number $\beta_1 \in \{1, 2, \ldots, 12\}$

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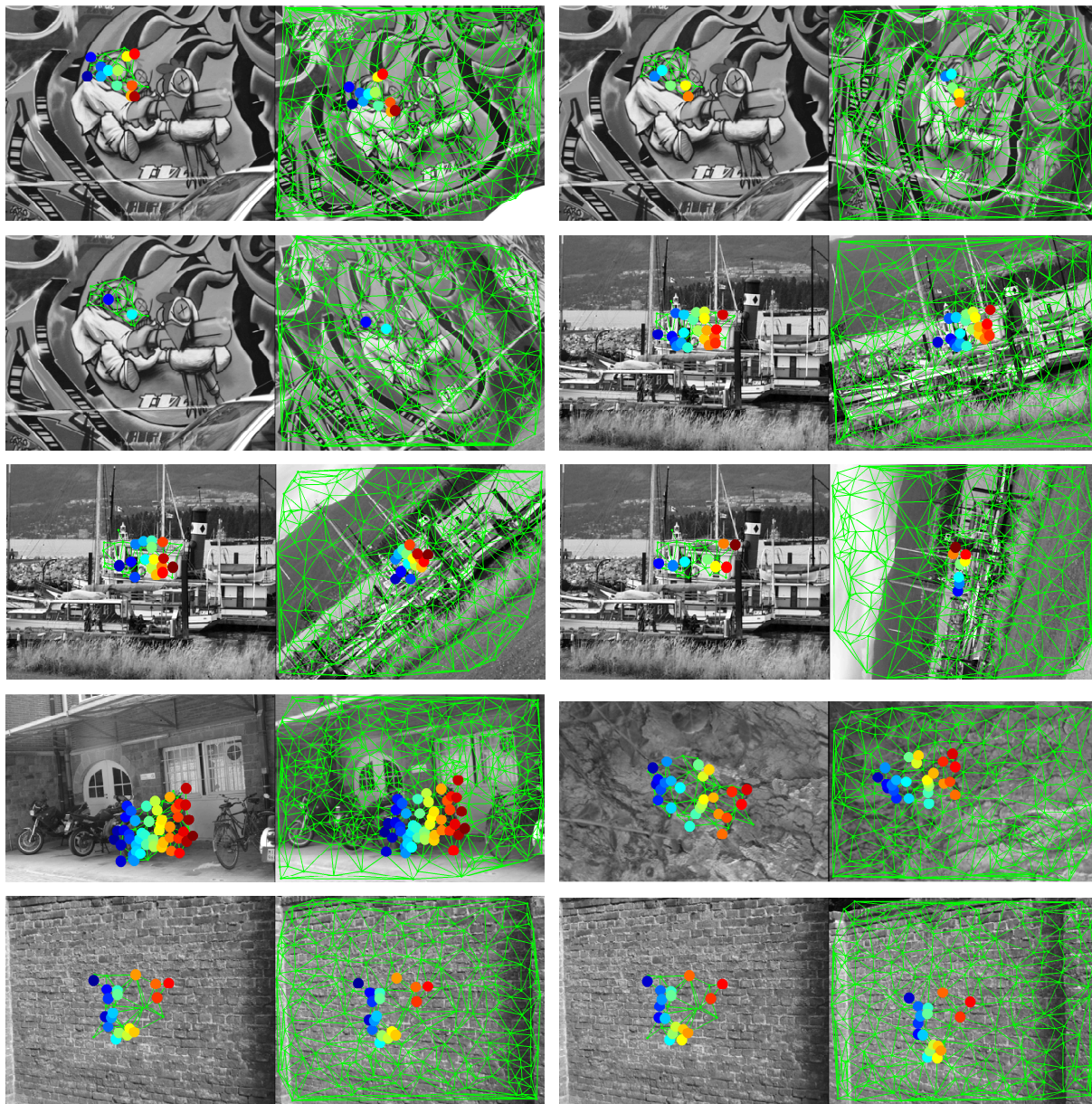
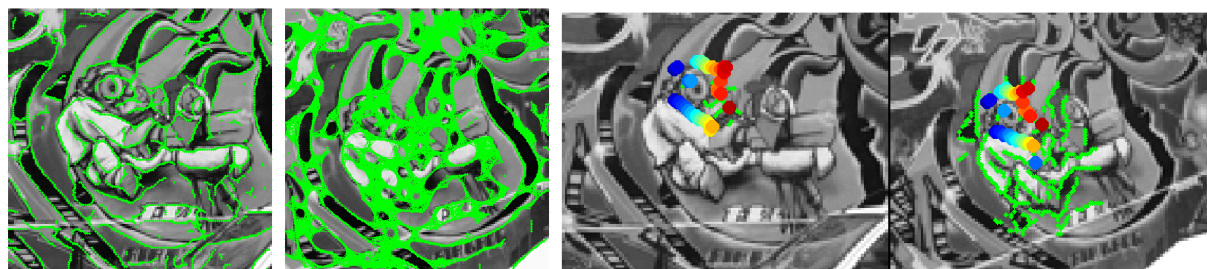Figure 2. Homology preserving subgraph matching using delaunay triangulation

Figure 3. Vietoris-Rips complex construction (section 2.5) (left) $\epsilon = 2$, (middle) $\epsilon = 4$, (right) subgraph to subgraph matching example ($\epsilon = 2$)