A General Multi-Graph Matching Approach via Graduated Consistency-regularized Boosting

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Abstract—This paper addresses the problem of matching \( N \) weighted graphs referring to an identical object or category. More specifically, matching the common node correspondences among graphs. This multi-graph matching problem involves two ingredients affecting the overall accuracy: i) the local pairwise matching affinity score among graphs; ii) the global matching consistency that measures the uniqueness of the pairwise matching results by different chaining orders. Previous studies typically either enforce the matching consistency constraints in the beginning of iterative optimization, which may propagate matching error both over iterations and across graph pairs; or separate affinity optimizing and consistency regularization in two steps. This paper is motivated by the observation that matching consistency can serve as a regularizer in the affinity objective function when the function is biased due to noises or inappropriate modeling. We propose multi-graph matching methods to incorporate the two aspects by boosting the affinity score, meanwhile gradually infusing the consistency as a regularizer. Furthermore, we propose a node-wise consistency/affinity-driven mechanism to elicit the common inlier nodes out of the irrelevant outliers. Extensive results on both synthetic and public image datasets demonstrate the competency of the proposed algorithms.

1 INTRODUCTION

Graph matching (GM) \cite{5}, \cite{6} has received extensive attentions over decades, and has found wide applications in various problems such as bioinformatics \cite{7}, data fusion \cite{8}, graphics \cite{9} and information retrieval \cite{10}, name a few. In particular, GM lies at the heart of a range computer vision tasks as diverse as object recognition, shape matching, object tracking, and image labeling among others, which require finding visual correspondences – refer to \cite{4} for more specific references. Different from the point based matching or registration methods such as RANSAC \cite{11} and Iterative Closet Point (ICP) \cite{12}, GM incorporates both the unary node-to-node, and the second-order edge-to-edge structural similarity. By encoding the geometrical information in the representation and matching process, GM methods are in general supposed to be more robust for solving the correspondence problems. Due to its well-known NP-complete nature, existing GM methods involve either finding approximate solutions \cite{13}, \cite{14}, \cite{15} or obtaining the global optima in polynomial time for a few types of graphs, including the planar graph \cite{16}, bounded valence graph \cite{17} and tree structure \cite{18}.

Most GM methods focus on establishing one-to-one correspondences (which is also the interest of this paper) between a pair of feature points \cite{19}, \cite{20}, \cite{14}, \cite{21}, \cite{22}. In general, the pairwise GM problem can be formulated as a quadratic assignment problem (QAP) that accounts for both individual node matches (unary terms) and pairs of matches (pairwise terms). The QAP formulations can be roughly divided into two subcategories \cite{13}: i) the Koopmans-Beckmann’s QAP \cite{23} \( \text{tr}(X^T A_1 X A_2) + \text{tr}(K_p X) \) where \( X \) refers to the assignment matrix between two graphs as will be introduced later in the paper. \( A_1, A_2 \) are the weighted adjacency matrices and \( K_p \) is the node-to-node similarity matrix between two graphs; ii) the more general Lawler’s QAP problem \cite{24} by \( \text{vec}(X)^T K \text{vec}(X) \) where \( K \) is the affinity matrix encoding unary and second-order edge affinities. The former can always be represented as a special case of the Lawler’s QAP by setting \( K = A_2 \otimes A_1 \).

Nevertheless, in many applications, visual objects do not appear in isolation or in pair, but more frequently in collections or families. Such collections provide a context and potentially allow for higher quality matching and analysis. Given a batch of graphs referring to an identical or related structure, it is required to find the global
matchings across all graphs. Due to the advance of modern imaging and scanning technologies, multi-graph matching is applied to infusing multi-source sensor data \[8\]. Graphic shape analysis and search often require to model objects by multi-view assembly \[25\]. And \[10\] applies multi-graph matching to the problem of multi-source topic alignment. It is also related to graph clustering, classification and indexing. Several multi-graph matching methods \[26\], \[27\], \[28\], \[29\], \[30\], \[31\] are proposed, which will be detailed in the next section.

2 Related Work and Models

Pairwise graph matching

The problem of pairwise GM involving two graphs has been extensively studied in the literature. It is beyond the scope of this paper for an exhaustive summary of these work. As will be detailed later in this paper, our methods and many other multi-graph matching methods \[29\], \[4\], \[2\], \[28\] build on top of pairwise matching solvers as a black-box, regardless the specific context in which these pairwise GM techniques are devised, such as machine learning based pairwise GM approaches \[19\], \[21\], \[31\], \[32\], \[33\], hyper-graph matching approaches \[31\], \[34\], \[35\], \[36\], \[37\] and the recent work \[3\] tailored for massive outliers.

Most pairwise GM methods \[38\], \[39\], \[40\], \[15\], \[14\], \[22\] are based on the Lawler’s QAP. Given two graphs \(G_1\) and \(G_2\) of node size \(n_1\) and \(n_2\), an affinity matrix \(K \in \mathbb{R}^{n_1 \times n_2}\) is defined such that its elements \(K_{ia;jb}\) measure the edge pair affinity \((v_i, v_j)\leftrightarrow(v_a, v_b)\) from two graphs. The diagonal term \(K_{ia;ia}\) describes the unary affinity of a node match \((v_i \leftrightarrow v_a)\) \(i,j=1,\ldots,n\). More rigorously, most existing graph matching work \[4\], \[14\], \[13\], \[1\] follow a convention for setting \(K\) such that the element \(K_{ia;jb}\) for the edge pair \((v_i, v_j)\leftrightarrow(v_a, v_b)\) is located at the \((a-1)n_1+i)\)-th row and \((b-1)n_2+j)\)-th column of \(K\).

We define the assignment matrix \(X \in \{0,1\}^{n_1 \times n_2}\) for two graphs which establishes the one-to-one node correspondence such that \(X_{ia} = 1\) if node \(v_i\) matches node \(v_a\) (0 otherwise). The problem of GM involves finding the optimal correspondence \(X\) such that the sum of the node and edge compatibility between two graphs is maximized. Without loss of generality, similar to \[14\], \[13\], by assuming \(n_1 \geq n_2\) for different sizes of graphs, it leads to the following widely used two-way constrained quadratic assignment problem (QAP) (e.g. \[14\], \[13\] and the references therein):

\[
X^* = \arg \max_X \vec{v}^T X K \vec{v}(X) \quad \text{s.t.} \quad X_{1n_2} \leq 1_{n_1} \quad i_1^{T} X_{1n_2} = 1_{n_2} \quad X \in \{0,1\}^{n_1 \times n_2}
\]

The constraints refer to the two-way one-to-one node mapping: a node from graph \(G_1\) can match at most one node in \(G_2\) and every node in \(G_2\) is corresponding to one node in \(G_1\). There is no (one/many)-to-many matching.

The above formulation is as general as it allows two graphs having unequal number of nodes \(n_1 \neq n_2\). A common protocol adopted by the previous studies \[38\], \[13\], \[4\] is converting \(X\) from an assignment matrix \((X_{1n_2} \leq 1_{n_1})\) to a permutation matrix \((X1_{n_2} = 1_{n_1})\) by adding dummy nodes to one graph (i.e. adding slack variables to the assignment matrix and augment the affinity matrix by zeros) in case \(n_1 \neq n_2\). This is a common technique from linear programming and is widely adopted by \[38\], \[13\] such that is supposed can handle superfluous nodes in a statistically robust manner (see the last paragraph of Sec.2.3 in \[38\]). By taking this step, the graphs are of equal sizes. This preprocessing also opens up the applicability of existing multi-graph methods \[30\], \[28\], \[41\] as they all assume that all graphs are of equal sizes. Therefore, the following formulation is derived which assumes \(n_1 = n_2 = n\).

\[
X_{12} = \arg \max X_{12}^T K_{12} X_{12} \quad \text{s.t.} \quad X_{1221} = 1_{n_1} \quad i_1^T X_{12} = 1_{n_2} \quad X_{12} \in \{0,1\}^{n_1 \times n_2}
\]

This is also coherent with the ideal case for the problem setting of this paper, matching the common inliers of equal sizes among graphs in the absence of outliers, or they are dismissed by a certain means.

We also mention several other threads for pairwise GM: i) learning the affinity over graphs \[21\], \[51\], \[19\], \[32\], \[33\]; ii) incorporating higher-order information \[31\], \[44\], \[45\], \[46\], \[47\]; iii) progressive matching \[42\] or combining feature detection and matching in an integrated system \[43\]. These methods focus on pairwise matching and are methodologically less relevant to this paper.

Multi-graph matching

Recently, matching a collection of related graphs becomes an emerging research topic with researchers from different communities including computer vision \[29\], \[4\], machine learning \[28\], \[2\], pattern recognition \[41\], \[24\], \[30\], graphics \[9\] and information retrieval \[10\], among others. We divide the state-of-the-arts into two categories concerning how the affinity and matching consistency are explored.

i) Affinity score-driven approaches \[30\], \[29\], \[4\], \[44\]: For these methods, usually first a compact set of basis pairwise matching variables are generated which can derive the matching solutions for each pair. Then an objective function regarding the overall pairwise matching affinity score is maximized by different algorithms. Solé-Ribalta et al. \[30\] extend the algorithm Graduated Assignment (GA) \[38\] for two-graph case to multi-graph. Each graph is associated with an assignment matrix mapping the nodes to a virtual node set. Then the variable set is updated in a deterministic annealing manner to maximize the overall affinity score. Yan et al. \[29\], \[4\] adaptively find a reference graph \(G_r\), which induces a compact basis matching variable set \(\{X_{ef}\}_{e=1,\neq r}^N\over N\) graphs. An alternating optimization framework is devised to update these basis variables in a rotating manner. The early work \[44\] by Gavril et al. selects a set of basis variables from the initial pairwise matching solutions via finding the maximum spanning tree on the super graph related to a maximized overall affinity score. In this sense, their work also falls into this category.

ii) Pairwise matching consistency-driven approaches \[41\], \[26\], \[28\], \[2\]: These methods usually are comprised of
two steps. First, a pairwise GM solver is employed to obtain the node mapping between all (or a portion of) pairs of graphs. Then, a spectrum smoothing technique is devised to enforce global matching consistency in the sense that two sequential pairwise matching in different chaining orders shall lead to the same solution. Specifically, in [41] and the journal version [26], Soile-Ribaltta et al. use a hyper-cube tensor to represent the \( N \)-node matching likelihood, each from \( N \) different graphs. Then a greedy method is used to binarize the final solutions satisfying the one-to-one two way constraints. Pachauri et al. [26] employ spectral analysis via eigenvector decomposition on the input pairwise matching solutions, and recover the consistent matching solutions. The success of this method lies on the assumption that the input pairwise matchings is corrupted by Gaussian-Wigner noise which is too ideal in reality. A more recent work proposed by Chen et al. [2] is suitable when only a part of nodes can find their correspondences in other graphs, which they term as ‘partial similarity’. They formulate the problem into a tractable convex programming problem solved by the popular first-order Alternating Direction Method of Multipliers (ADMM) method tailored for their semidefinite programming problem.

One observation to the above mentioned approaches is that they either enforce consistency early by using a compact set of basis variables for pairwise matchings [29], [4], [26], [41], which runs at the risk of propagating errors across iterations and graphs, or assume the initial pairwise matchings are obtained with corruptions by another method, and focus on improving the overall accuracy from the input pairwise matchings via spectral methods, however no affinity information is used in the procedure [41], [26], [28], [2].

In particular, a widely used multi-graph matching formulation [29], [4], [30] is as follows, under the implicit assumption of invertible pairwise matching relations i.e. \( X_{ij} = X_{ji}^T \), which meanwhile enforces matching consistency over all pairwise matchings:

\[
\begin{align*}
\{X_{ij}^{n-1,N}\}_{i=1,j=1}^{N} &= \arg \max_{X_{ij}} \sum_{i=1}^{N} \sum_{j=1}^{N} \text{vec}(X_{ij})^T K_{ij} \text{vec}(X_{ij}) \\
\text{s.t. } & I_{n}^{T} X_{ij} = I_{n}^{T} X_{ji} I_{n} = I_{n}, \quad X_{ij} = X_{ik}X_{kj} \in \{0,1\}^{n \times n} \quad k=1, \ldots, N \quad i \neq j
\end{align*}
\]

Note the above formulation assumes each graph shall contain and only contain the common inlier nodes, which does not hold in the presence of unmatchable outliers. Thus it calls for more flexible solutions.

In this paper, we adopt a flexible approximate affinity score boosting procedure, which is gradually regularized by the overall matching consistency. The key idea is that the affinity score is indicative to semantic matching accuracy in the early stage of iterative boosting, while it becomes less informative as the accuracy lifting saturates. Then, in the presence of a few outliers, consistency becomes a useful regularizer to avoid the degenerating case between the two local graphs due to the fact that affinity score is often biased to semantic accuracy when the two graphs are corrupted by arbitrary noises, in addition with the inherent difficulty in modeling the affinity matrix using a compact parametric model. In the presence of more outliers, we propose a node-consistency/affinity-driven mechanism to elicit the affinity score and consistency relevant to common inlier nodes. Extensive empirical results illustrate the efficacy of our methods which is further specified in our conclusive remarks in Sec.5.

### 3 Proposed Algorithms

Given the initial pairwise matching configuration \( X^{(0)} \) generated by a pairwise matching solver e.g. [14], [13], one can further derive a new pairwise matching \( X^{(1)} \) by the composition of a few ‘good’ matchings i.e. \( X^{(1)}_{ij} = X^{(0)}_{i,k_{1}}X^{(0)}_{k_{2},j} \cdots X^{(0)}_{k_{m-1},k_{m}} \) to replace the original \( X^{(0)} \) such that the matching accuracy can be improved or ideally maximized, by means of interpolating the sequence \( G_{i}, G_{k_{1}}, \ldots, G_{k_{m-1}}, G_{k_{m}}, G_{j} \). The problem of this dynamic-replacing framework is how to set up the appropriate compositional replacements. In case the original matching is best, the replacement set shall be empty.

This paper devises a mechanism for iteratively finding the appropriate new composition to replace the old one without knowing their true accuracy. We will start with a baseline ISB (Alg.1), and two variants ISB\(^{2nd}\), ISB\(^{est}\) for comparison. Then a graduated consistency-regularized method ISB-GC (Alg.2) is highlighted with two efficient variants ISB-GC-U/P (Alg.3). Before diving into the details, we first introduce several notations and definitions which help the exposition of our methods.

#### 3.1 Notations and definitions

Throughout the paper, \( \mathbb{R} \) denotes for the real number domain. Bold capital letters denote for a matrix \( X \), bold lower-case letters for a column vector \( x \) and hollow bold letters for a set \( \mathcal{X} \). All non-bold letters represent scalars. \( \mathcal{X}^T \) is the transpose of \( X \); vec\((X)\) is the column-wise vectorized matrix \( X \). \( \text{tr}(X) \) is the trace of matrix \( X \). \( I_{n} \in \mathbb{R}^{n \times n} \) is an identity matrix and the subscript \( n \) will be omitted when it can be inferred from context. \( 1_{m \times n}, 0_{m \times n} \in \mathbb{R}^{m \times n} \) is the matrix whose elements being all ones or zeros, respectively. \( 1_{n} \) is the abbreviation for \( 1_{n \times 1} \). \( |X| \) is the cardinality of the set \( X \), \( \|X\|_{F} = \text{tr}(X^{T}X) \) for the Frobenious norm and \( \| \cdot \|_{p} \) is the \( p \)-norm.

This paper intensively uses \( \mathcal{X} = \{X_{ij}\}_{i=1,j=1}^{N} \) to denote the set of pairwise matching matrices over \( N \) graphs \( \{c_{k}\}_{k=1}^{K} \), which is also termed as matching configuration, and \( \mathcal{K} = \{k_{i}\}_{i=1}^{N-1} \) is used for the affinity matrix set. In particular, we use \( \mathcal{X}_{c} \) to denote a solution set which is fully consistent (referred by the subscript ‘c’) as there is no contradictory pairwise matchings for \( \{X_{ij} \neq X_{k_{i}k_{j}}\}_{i,j,k=1}^{N} \). If not otherwise stated explicitly, we adopt the convention that uses \( N \) for the number of considered graphs, \( n \) and \( m \) for the number of nodes, and the number of edges in a graph, respectively.
So far we have not presented a formal definition regarding consistency, which has been widely used in [22, 4, 2, 26, 28] and mentioned earlier in this paper. Now we give the formal definitions regarding matching consistency induced by the initial pairwise matching \( \mathcal{X} \) from any pairwise matching solver. In addition, we also define two variants of the super graph and a concept related to matching composition. This paper does not claim the credit for the novelty of these definitions as similar definitions or concepts may appear in literature.

**Definition 1.** Given \( N \) graphs \( \{ \mathcal{G}_k \}_{k=1}^N \) and the pairwise matching configuration \( \mathcal{X} = (X_{ij})_{i=1,j=1}^{N-1,N} \), the unary consistency of graph \( \mathcal{G}_k \) is defined as \( C_u(k, \mathcal{X}) = 1 - \frac{\sum_{i=1}^N \sum_{j=1}^{N-1} \|X_{ij} - X_{ik}X_{kj}\|}{N(N-1)/2} \in (0, 1] \).

**Definition 2.** Given graphs \( \{ \mathcal{G}_k \}_{k=1}^N \) and matching configuration \( \mathcal{X} \), for any pair \( \mathcal{G}_i \) and \( \mathcal{G}_j \), the pairwise consistency is defined as \( C_p(\mathcal{X}_{ij}, \mathcal{X}) = 1 - \frac{\sum_{k=1}^N \|X_{ij} - X_{ik}X_{kj}\|}{N(N-1)/2} \in (0, 1] \).

**Definition 3.** Given \( N \) graphs \( \{ \mathcal{G}_k \}_{k=1}^N \) and \( \mathcal{X} \), we call \( \mathcal{X} \) is fully consistent if and only if \( \sum_{k=1}^N C_p(\mathcal{X}_{ij}, \mathcal{X}) = 1 \) and (or) \( \sum_{k=1}^N C_u(k, \mathcal{X}) = 1 \). The following equation always holds: \( \sum_{k=1}^N C_u(k, \mathcal{X}) = \sum_{k=1}^N C_p(\mathcal{X}_{ij}, \mathcal{X}) N(N-1)/2 \in (0, 1] \) where \( \mathcal{Y} = X_{kj} - X_{ki}X_{ij} \) and \( Y(\mathbf{u}, \mathcal{I}) \) is the \( \mathbf{u} \)th row of matrix \( \mathcal{Y} \).

**Definition 4.** Given \( \mathcal{G}_k \) and \( \mathcal{X} \), for node \( \{ \mathcal{X}_k \}_{k=1}^N \) in graph \( \mathcal{G}_k \), its consistency w.r.t. \( \mathcal{X} \) is defined by \( C_n(\mathcal{X}_k, \mathcal{X}) = 1 - \frac{\sum_{i=1}^N \sum_{j=1}^{N-1} \|\mathcal{W}(\mathbf{u}, \mathcal{I})\|}{N(N-1)/2} \in (0, 1] \) where \( \mathcal{Y} = X_{kj} - X_{ki}X_{ij} \) and \( Y(\mathbf{u}, \mathcal{I}) \) is the \( \mathbf{u} \)th row of matrix \( \mathcal{Y} \).

**Definition 5.** Given \( \mathcal{G}_k \) and \( \mathcal{X} \), for node \( \{ \mathcal{X}_k \}_{k=1}^N \) in \( \mathcal{G}_k \), its consistency w.r.t. \( \mathcal{X} \) is defined by \( S_n(u, \mathcal{X}) = \sum_{i=1}^N \sum_{j=1}^{N-1} vec(X_{ki})^T K_{ij} vec(X_{kj}) \) where \( X_{ki} \) denotes the matrix \( \mathcal{X} \) with zeros except for the \( \mathbf{u} \)th row as is.

**Definition 6.** Given \( \{ \mathcal{G}_k \}_{k=1}^N \) and \( \mathcal{X} \), the affinity-wise super graph \( \mathcal{G}^{sup} \) is defined as an undirected weighted graph s.t. each node \( k \) denotes \( \mathcal{G}_k \) and its weight \( \epsilon_{ij} \) is the affinity score \( \mathcal{J}_{ij}(\mathcal{X}_{ij}) = vec(X_{ij})^T K_{ij} vec(X_{ij}) \) induced by \( \mathcal{X} \).

**Definition 7.** Given \( \{ \mathcal{G}_k \}_{k=1}^N \) and \( \mathcal{X} \), the consistency-wise super graph \( \mathcal{G}^{sup} \) is defined as an undirected weighted graph s.t. each node \( k \) denotes \( \mathcal{G}_k \) and the weight of edge \( \epsilon_{ij} \) is the pairwise consistency \( C_p(\mathcal{X}_{ij}, \mathcal{X}) = 1 - \frac{\sum_{k=1}^N \|X_{ij} - X_{ik}X_{kj}\|}{N(N-1)/2} \in (0, 1] \).

**Definition 8.** The path \( Z_{ij}(k_1, k_2, \ldots, k_s) \) from \( \mathcal{G}_i \) to \( \mathcal{G}_j \) is defined as the chain \( \mathcal{G}_i \rightarrow \mathcal{G}_{k_1} \rightarrow \cdots \rightarrow \mathcal{G}_{k_{s-1}} \rightarrow \mathcal{G}_j \), which induces: \( Y_{ij}(k_1, k_2, \ldots, k_s) = X_{ik_1}X_{k_1k_2} \cdots X_{ks} \). Its order \( s_{ij} \) is the number of the intermediate graphs between \( \mathcal{G}_i, \mathcal{G}_j \). The path score is \( J_{ij}(k_1, k_2, \ldots, k_s) = vec(Y_{ij})^T K_{ij} vec(Y_{ij}) \).

We present several comments to the above definitions. The unary consistency \( C_u(k, \mathcal{X}) \) by Definition (1) is a function w.r.t. the graph index \( k \) and \( \mathcal{X} \). In contrast, the pairwise consistency \( C_p(\mathcal{X}_{ij}, \mathcal{X}) \) by Definition (2) is generalized to the one w.r.t. two variables of \( \mathcal{X}_{ij} \) and \( \mathcal{X} \) and the former one \( \mathcal{X}_{ij} \) does not necessarily belong to \( \mathcal{X} \). The pairwise consistency metric is symmetric such that \( C_p(\mathcal{X}_{ij}, \mathcal{X}) = C_p(\mathcal{X}_{ji}, \mathcal{X}) \), which derives Definition (3). Definition (4) and (5) break down to node level consistency/affinity similar to unary ones, and they will be used in the proposed inlier eliciting mechanism.

The super graph, either for affinity-wise \( \mathcal{G}^{sup}_a \) by Definition (6), or consistency-wise \( \mathcal{G}^{sup}_c \) by Definition (7), is a connected (not necessarily fully connected) graph as a portion of pairs are matched by a certain means, a maximum spanning tree (MST) [44] can be found with no less total weight of every other spanning tree.

Note Definition (1) and Definition (2) appeared in [4] in which they are used to identify the optimal alternating optimization sequence of variables. This paper utilize them differently to infuse the consistency along with the boosting procedure. The overall consistency for \( \mathcal{X} \) as by Definition (9), further tells the relation between unary consistency and pairwise consistency. A similar overall ‘inconsistency’ metric appears in [45], [50].

The affinity-wise super graph \( \mathcal{G}^{sup}_a \) by Definition (6) is similar to the one in [46], of which the author proposes to build a graph where each shape is a vertex, and edges between shapes are weighted by the cost of the best matching. We put it in the scenario for the problem of weighted multi-graph matching. Furthermore, we give a similar definition for a consistency variant \( \mathcal{G}^{sup}_c \) in terms of consistency-wise edge weights by Definition (7).

Finally, Definition (9) is related to the approximate path selection idea as used in our algorithms. Obviously, when \( \mathcal{X} \) is fully consistent, any two paths between two given graphs would induce the equal solution.

Based on the above definitions and discussion, we present our main approaches in the rest of this section.

### 3.2 Iterative affinity score/consistency boosting

Most GM methods aim to maximize an objective function regarding with affinity score [29, 4, 14, 13, 15], we also follow this methodology in this subsection. Our basic rationale is that the node matching regarding with the highest affinity score between two graphs can be found along a higher-order path, as related to Definition (8), instead of the direct (zero-order) pairwise matching. We formalize this idea as follows:

Without loss of generality, assume the affinity-wise super graph \( \mathcal{G}^{sup}_a \) is fully connected which is induced by the configuration \( \mathcal{X} \). Given \( \mathcal{G}_i, \mathcal{G}_j \), all loop-free matching paths on the super graph can form a set of loop-free paths \( Z_{ij} = \{Z_{ij}(k_1, \ldots, k_s)\}_{s=1}^{N-2} \), whose cardinality \( |Z_{ij}| = \sum_{s=1}^{N-2} s! \) is. Thus the overhead for finding the highest score solution is intractable since \( \sum_{s=1}^{N-2} s! \) times of compositions need be computed. Given the matching configuration \( \mathcal{X}^{(t-1)} \), one alternative is approximating the optimal \( Z_{ij} \) by a series of iterations involving the first-order paths. And the problem of finding the optimal
third-party graph $G_k$ in iteration $t$ becomes:

$$k^* = \arg \max_{k=1}^{n} J(X(t-1)^i_{ik}, X(kj)^{(t-1)})$$  \hspace{1cm} (4)$$

This can be regarded as approximately concatenating the iteratively generated piecewise paths, into a higher-order one that consists of multiple intermediate graphs.

The above idea is concretized into an iterative algorithm termed as **Iterative Score Boosting (ISB)** as described in the chart of Alg.1. In iteration $t$, every $X(t)^{ij}$ is updated by seeking the path with order $s = 1$ via maximizing the affinity score according to Eq.4. The efficacy of such a score-boosting strategy can be justified by an intuitive analysis: even matching graph $G_i$ and $G_j$ is inherently ambiguous when both are largely corrupted, it is still possible to improve matching accuracy by an order one that consists of multiple intermediate graphs.

The iteratively generated piecewise paths, into a higher-order path $X(t)$ that consists of multiple intermediate graphs. In fact, there can be other random search strategies aside from the first-order one described here, and these random search variants can be derived by our framework.

The first variant involves replacing the updating step $X(t)^{ij} = X(t-1)^{ij} \cdot X(t-1)^{(t-1)}$ using Eq.4 with the pairwise consistency in Definition (2), as formulated as follows:

$$k^* = \arg \max_{k=1}^{n} C_p(X(t-1)^{ij}, X(t-1)^{(t-1)})$$  \hspace{1cm} (5)$$

Unlike ISB, this consistency-driven variant ISB* (note superscript added) cannot ensure to converge to a stationary configuration. In particular, the consistency boosting mechanism at each round, can only guarantee $C_p(X(t)^{ij}, X(t-1)) \geq C_p(X(t-1)^{ij}, X(t-1))$ for any pair of $i, j$.

Moreover, in the ideal case when the ground truth is known, then we modify the method ISB by boosting the consistency constraint. These three methods are evaluated in Fig.1 together with Alg.2 (ISB-GC) as will be introduced later. Moreover, in the ideal case when the ground truth is known, then we modify the method ISB by boosting the consistency constraint. These three methods are evaluated in Fig.1 together with Alg.2 (ISB-GC) and its variant ISB-GC* which also both appear in Fig.1 to the next sub-section.

### 3.3 Graduated consistency-regularized boosting

Our key rationale is viewing the consistency constraint as a regularizer for affinity score maximization. Note that
Algorithm 1 Iterative Score boosting (ISB)

Input: \( \{K_{ij}\}_{i,j=1}^{N-1,N}; T_{\text{max}}, \delta, \gamma \in (0,1); \)
1. Perform pairwise matching to obtain initial \( X^{(0)} \);
2. Calculate \( J^{(0)} = \sum_{i=1,j=1}^{N-1,N} \text{vec}(X^{(0)}_t)K_{ij}\text{vec}(X^{(0)}_j) ; \)
3. for \( t = 1 : T_{\text{max}} \) do
4. for all \( i = 1, 2, \ldots, N-1; j = i+1, \ldots, N \) do
5. update \( X_{ij} = X_{ij}^{(t-1)}X_{ij}^{(t-1)} \) by solving Eq \( \ref{eq:4} \);
6. end for
7. if \( \sum_{i=1,j=1}^{N-1,N} \|X_{ij}^{(t-1)} - X_{ij}^{(t)}\|_2 < \delta, \) break;
8. end for
9. if \( C(X^{(t)}) = 1, \) return \( X^*_t = X^{(t)} ; \)
10. if \( C(X^{(t)}) < \gamma \) then
11. Build the super graph \( G^a_{\text{sup}} \) by pairwise affinity score \( J(X_{ij}^{(t)}) \) and find a maximum span tree to generate \( X^*_t ; \)
12. else
13. if \( n \geq N \) then
14. Build the super graph \( G^a_{\text{sup}} \) by \( C_p(X_{ij}^{(t)}, X^{(t)}) \) and find a maximum span tree to generate \( X^*_t ; \)
15. else
16. Perform the smoothing method \( \ref{eq:3} \) to obtain \( X^*_t ; \)
17. end if
18. end if

Algorithm 2 Graduated Consistency-regularized Iterative Score Boosting (ISB-GC)

Input: \( \{K_{ij}\}_{i,j=1}^{N-1,N}; T_{\text{max}}, \delta, \lambda(\tau_0) = \lambda(0), \delta, \gamma ; \)
1. Perform pairwise matching to obtain initial \( X^{(0)} ; \)
2. Calculate \( J^{(0)} = \sum_{i=1,j=1}^{N-1,N} \text{vec}(X^{(0)}_t)K_{ij}\text{vec}(X^{(0)}_j) ; \)
3. for \( t = 1 : T_0 \) do
4. for all \( i = 1, 2, \ldots, N-1; j = i+1, \ldots, N \) do
5. update \( X_{ij}^{(t)} = X_{ij}^{(t-1)}X_{ij}^{(t-1)} \) by solving Eq \( \ref{eq:4} \);
6. end for
7. if \( \sum_{i=1,j=1}^{N-1,N} \|X_{ij}^{(t-1)} - X_{ij}^{(t)}\|_2 < \delta, \) break;
8. end for
9. if \( t = T_0 + 1 : T_{\text{max}} \) do
10. for all \( i = 1, 2, \ldots, N-1; j = i+1, \ldots, N \) do
11. update \( X_{ij}^{(t)} = X_{ij}^{(t-1)}X_{ij}^{(t-1)} \) by solving Eq \( \ref{eq:8} \);
12. end for
13. \( \lambda^{(t)} = \min(1, \beta \lambda^{(t-1)}) ; \)
14. end for
15. Perform the same post-processing as in Alg \( \ref{alg:1} \) [10, 18].

maximizing pairwise matching score among all pairs cannot ensure the consistency constraint. Moreover, due to outliers, sparse edge sampling for efficiency, and local deformation as well as the difficulty in parameterizing the affinity matrix as already discussed in \[14\] and the references therein, there can be a case that for some pairs of graphs, the semantic ground truth matching configuration may not correspond to the highest affinity score. Thus purely maximizing the overall matching score is biased to accuracy, though maximizing overall score cannot ensure the consistency constraint. Moreover, due to over-fitting.

For the initial assignment matrix \( X^{(0)} \) obtained by the pairwise graph matching solver, its scores are more informative for the true accuracy; ii) After several rounds of iterations for score-boosting, affinity score becomes less discriminative and consistency becomes more indicative.

In this spirit, we infuse the matching consistency by a weighted term, whose weight \( \lambda \) is gradually increased. As a result, the evaluation function in each iteration is changed from Eq \( \ref{eq:4} \) to a weighted one between Eq \( \ref{eq:4} \) and Eq \( \ref{eq:5} \) by setting \( \lambda^{(0)}(1) = X^{(t-1)}_t \).

\[ k^* = \arg \max_{k=1}^N (1 - \lambda) J(Y_{ikj}^{(t-1)}) + \lambda C_p(Y_{ikj}^{(t-1)}, X^{(t-1)}) \] (7)

The similar post-processing that enforces full consistency in Alg \( \ref{alg:1} \) (ISB) can also be conducted here which will stop the score growing immediately. This method is detailed in the chart of Alg \( \ref{alg:2} \) Graduated Consistency-regularized Iterative Score Boosting (ISB-GC).

Similar to ISB\(^\text{est}\), ISB-GC in general cannot guarantee to converge to a stationary configuration, since the non-decreasing property of the sequence \( \{C_p(X_{ikj}^{(t)}, X^{(t)})\}_{t=0}^\infty \) cannot always hold. Our empirical tests show this method can often converge to a stationary \( X^*_t \) after 10 iterations or so. In our experiments, we stop it when the number of iterations arrives a certain threshold \( T_{\text{max}} \).

To make our study more comprehensive, like ISB\(^\text{est}\) to ISB, we further devise a counterpart to ISB-GC by swapping the role of consistency and affinity in this algorithm: the iterative updating is driven by choosing the anchor graph that lifts the pairwise consistency \( C_p(X_{ikj}^{(t)}, X^{(t)}) \) as denoted by Eq \( \ref{eq:5} \) for the method ISB\(^\text{inv}\). Meanwhile, the weight of the affinity score is gradually increased as the same as the consistency used in ISB-GC. Accordingly, the evaluation function becomes:

\[ k^* = \arg \max_{k=1}^N \lambda \frac{J(Y_{ikj}^{(t-1)})}{\lambda C_p(Y_{ikj}^{(t-1)}, X^{(t-1)})} + (1 - \lambda)C_p(Y_{ikj}^{(t-1)}, X^{(t-1)}) \] (8)

We call this algorithm ISB-GC\(^\text{inv}\) where the superscript denotes for ‘inverse’. The parameter settings \( \lambda_0 \) and \( \beta \) are identical to ISB-GC. We omit the algorithm chart for ISB-GC\(^\text{inv}\) since it is akin to ISB-GC. It is outperformed by ISB-GC as shown in Fig \( \ref{fig:1} \) which validates our idea.

### 3.4 Efficient consistency-regularized boosting

The step of computing \( C_p(X_{ikj}^{(t-1)}, X^{(t-1)}) \) in ISB-GC need be repeated for each new \( k \) because it depends on the dynamically generated candidate \( X_{ikj}^{(t-1)} \). As a result, its time complexity regarding the consistency is increased.

2. Note the affinity score is not directly comparable with either the unary or pairwise consistency as the latter fall in \([0,1]\) while the former is arbitrary depending on how the affinity matrix is set. In our implementation, the affinity score is further normalized by \( J(X_{ij}) = J(X_{ij}) / \max_{ij} J(X^{(0)}_{ij}) \) where the denominator is a constant. This convention is also used when \( J^v \) is introduced in Sec \( 3.5 \).


The merit of this metric is all \( \{C_u(k, X_{i,(l-1)})\}_{k=1}^N \) can be pre-computed in each iteration only for once. Alternatively, we devise another consistency estimator by first pre-computing all \( \{C_p(X_{i,(l-1)}, X_{j,(l-1)})\}_{i=1,j=1+1}^{N,N} \) in the beginning of each iteration \( t - 1 \), and then adopting Eq.\( 10 \) in the hope of approximating \( C_p(X_{i,k}, X_{j,k}) \) as reused in updating \( X_{i,(l)} \):

\[
k^* = \arg \max_{k=1}^{N} (1 - \lambda)J(X_{i,(l-1)}(k)X_{j,(l-1)}) + \lambda C_u(k, X_{j,(l-1)})
\]

We term the above two efficient variants as Unary/Pairwise Graduated Consistency-regularized Iterative Score Boosting as depicted in the chart of Alg.\( 3 \). In this paper, they are further abbreviated by ISB-GC-U and ISB-GC-P, where the last characters denote for ‘unary’ and ‘pairwise’ respectively. In particular, ISB-GC-U has a convergence property as stated in below.

**Proposition 2.** ISB-GC-U will converge to a stationary \( X^* \).

**Proof:** Given two graphs \( G_i, G_j \) of \( n \) nodes for each, first, define the set of score difference \( \{\Delta J_{ij}\} \) as \( \Delta J_{ij} = |\text{vec}(X)^T K_{ij} \text{vec}(X) - \text{vec}(Y)^T K_{ij} \text{vec}(Y)|, \forall X, Y, \) between any two assignment matrices \( X, Y \in \mathbb{R}^{n \times n} \) in the enumerable permutation space. Suppose the largest value of difference is \( \Delta J_{ij} \) which is constant given
Algorithm 3 Unary/Pairwise Graduated Consistency-
regularized Iterative Score Boosting (ISB-GC-U/P)

Input: \( \{ K_{ij} \}_{i,j=1,N}^{N-1,N}, T_{\text{max}}, \delta, \gamma, \lambda^{(0)} = \lambda^{(0)}, s, \) mode;
1: Perform pairwise matching to obtain initial \( X^{(0)} \);
2: Calculate \( J^{(0)} = \sum_{i=1,j=1}^{N-1,N} \text{vec}(X^{(0)})^T K_{ij} \text{vec}(X^{(0)}) \); 
3: Run line 2 in Alg. 2 for pure affinity score driven boosting;
4: for \( t = T_{\text{max}} + 1 \) do 
5: if mode='unary' then
6: Compute unary consistency \( \{ C_u(k, X^{(t-1)}) \}_{k=1}^{N} \);
7: else if mode='pairwise' then
8: Update pairwise metric \( \{ C_p(X^{(t-1)}, X^{(t-1)}) \}_{i,j=1}^{N-1,N} \);
9: end if
10: for all \( i = 1, 2, \ldots, N - 1; j = i + 1, \ldots, N \) do
11: if mode='unary' then
12: update \( X_{ij}^{(t)} = \chi_{ij}^{(t-1)} X_{ij}^{(t-1)} \) by solving Eq. 10;
13: else if mode='pairwise' then
14: update \( X_{ij}^{(t)} = \chi_{ij}^{(t-1)} X_{ij}^{(t-1)} \) by solving Eq. 10;
15: end if
16: end for
17: if \( \sum_{i=1,j=1}^{N-1,N} \| X_{ij}^{(t)} - X_{ij}^{(t)} \|_2 < \delta \), break;
18: \( \lambda^{(t)} = \min(1, \beta \lambda^{(t-1)}) \);
19: end for
20: Perform the same post-processing as in Alg. 1 (4-18).

**K_{ij}**: We further define the largest difference denoted by \( \Delta J_{ij} = \max \{ \Delta J_{ij} \}_{i,j=1,N}^{N-1,N} \) for all pairs in the graph.

For a certain iteration in ISB-GC-U, suppose the most consistent graph by Definition 1 is \( G_a \), and the second one is \( G_b \). In iteration \( t \) it will finally satisfy the condition: \( \Delta C_u = C_u(a, X^{(t)}) - C_u(b, X^{(t)}) > \frac{1}{1-\lambda} \Delta \tilde{J}_{ij} \) as \( \lambda^{(t)} \rightarrow 1 \) by \( \lambda^{(t)} = \min(\rho \lambda^{(t-1)}, 1) \). Then, the following inequality will hold for any \( k \neq a \) and \( \{ G_t \}_{i=1}^{N-1,N} \) of \( \{ G_t \}_{i=1}^{N-1,N} \) :

\[
(1 - \lambda) J(X_{ik}^{(t)} X_{kj}^{(t)}) + \lambda C_u(a, X^{(t-1)}) \\
= (1 - \lambda) J(X_{ik}^{(t-1)} X_{kj}^{(t-1)}) + \lambda C_u(k, X^{(t-1)}) + \lambda \Delta C_u^{(t)} \\
= (1 - \lambda) J(X_{ik}^{(t-1)} X_{kj}^{(t-1)}) - J(X_{ik}^{(t-1)} X_{kj}^{(t-1)}) + (1 - \lambda) J(X_{ik}^{(t-1)} X_{kj}^{(t-1)}) \\
+ \lambda C_u(k, X^{(t-1)}) + \lambda \Delta C_u^{(t)} \\
\geq \lambda \Delta C_u^{(t)} - \Delta \tilde{J}_{ij} + (1 - \lambda) J(X_{ik}^{(t-1)} X_{kj}^{(t-1)}) + \lambda C_u(k, X^{(t-1)}) \\
> (1 - \lambda) J(X_{ik}^{(t-1)} X_{kj}^{(t-1)}) + \lambda C_u(k, X^{(t-1)}) 
\]

As a result, all \( \{ X_{ij}^{(t+1)} \}_{i,j=1,N}^{N-1,N} \) will be updated by \( X_{ij}^{(t+1)} = \chi_{ij}^{(t)} X_{ij}^{(t)}. \) In fact, in iteration \( t, X^{(t)} \) becomes fully consistent by Definition 3 thus cannot be lifted by either affinity or consistency measures used in this paper.

The iterative procedure in ISB-GC-U may exceed the maximum iterating threshold \( T_{\text{max}} \) before reaching the above inequality holds when \( \lambda \) is assumed close to 1 enough. Thus a post-processing step is also needed in line with Alg. 1 (ISB) and Alg. 2 (ISB-GC) if necessary.

For the ‘pairwise’ version ISB-GC-P, this method in our experiments also often converges to a stationary \( X^* \) similar to ISB-GC, yet there is no theoretical guarantee.

Fig. 2 illustrates how the overall matching accuracy is lifted via the proposed algorithms, controlled by Table 2.

In case \( C_u(a, X^{(t)}) = C_u(b, X^{(t)}) \), without loss of generality, one can choose any of them as the largest one, and choose the next \( G_c \) as the second largest if \( C_u(a, X^{(t)}) > C_u(c, X^{(t)}) \).

### 3.5 Eliciting affinity and consistency for inliers

One limitation of many previous studies for both pairwise and multi-graph matching as mentioned in this paper, is that they enforce all nodes in one graph to have matchings from the other(s), either by explicitly using a permutation matrix imposing strict node-to-node correspondences [47], [13], or implicitly doing so by generating node-to-node matchings as many as possible such that the objective affinity score is optimized [32], [34], [35], [21], [20]. A common simplification when applying a pairwise GM method is assuming one of two graphs is a reference graph, such that each of its node can find a match from the other testing graph.

We are motivated to devise a general outlier-rejection mechanism not depending on the particular characters of the testing data in terms of the node distribution, weight attributes, noises type, and graph structure etc.

The Graduated Assignment method [20] attempts to handle outlier nodes by assigning them to additional slack variables. While in the presence of a majority of outliers, this approach is not widely adopted due to its sensitivity to parameters for the slack variables. The very recent work [3] proposes a general approach via a max-pooling mechanism suited for the scenario of matching two graphs with a majority of outliers. A less relevant work is by Torresani et al. [48] which also allows nodes to be assigned in an unmatchable status in an energy function induced on the Markov Random Field. However, its complex objective function is designed that account for various similarity measurements e.g. appearance descriptors, occlusions, spatial proximity etc. beyond the general setting of the affinity matrix considered in this paper. Moreover, the associated parameters need to be learned with labeled correspondence ground truth from a training dataset which impedes its applicability. Other pairwise GM methods [43], [12] integrate the point detection and matching in a synergic manner by an integrated system, while this paper assumes the graphs are given and specifically confined in visual problems.

As a building-block, all these pairwise GM methods can be used by our approaches and other state-of-the-arts [2], [29], [4], [28] to improve the initial \( X^{(0)} \). Nevertheless, the context of multiple graphs allows for a more robust mechanism for pruning outliers such that only the affinity and consistency relevant to common inliers are considered in our boosting framework.

We describe our ‘inlier nodes’ eliciting method using the node-wise consistency \( C_n(\vec{u}, X) \) by Definition 4. Another alternative is using the node-wise affinity \( S_n(\vec{u}, X, K) \) via Definition 3, which can be applied in a similar fashion thus its description is omitted here.

First, given the matching configuration \( X \), each node in one graph is scored by the node-wise consistency by Definition 4. Assume the number of common inliers i.e. \( n_i \) for all graphs is known, which is available when a reference template is given, or estimated by other means e.g. [2]. How to estimate \( n_i \) is not the focus of this paper.
TABLE 3: Description of the parameters for experiment settings in this paper.

|       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|
| graph | inlier | outlier | annotated | n_in | density | sensitivity | coverage | seed |
|       |       |       |       |       |       |       |     |      |

Then we make two revisions for all of our methods: i) the pairwise affinity term vec($X$)$^T \Lambda$vec($X$) is modified by keeping the rows of $X$ that correspond to the first $n_i$ (the number of inliers) nodes in descending order by their node-wise consistency score $C_p(u_i^k, X)$ in Definition [4], and zeroing the rest of rows. This is because the affinity or consistency between outliers is irrelevant to the semantic matching accuracy thus shall be excluded in the boosting procedure. For node-wise consistency, we use $\psi_i (X, X_i, n_i)$ (or $\psi_i (X, X_i, n_i)$ for node-wise affinity) to denote this ‘mask’ operation on $X$ as it is determined by both the input configuration $X$ and $n_i$ (also $n$ in case of the affinity metric). Then the affinity score is rewritten as $J(G_i) = \psi_i (X, X_i, n_i)$.

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The experiments are performed on both synthetic and real-image data. The synthetic test is controlled by varying the noise level of deformation, outlier, edge density and initial pairwise matching coverage. The real images are tested by varying viewing angles, scales, shapes etc. The matching accuracy over all graphs, is calculated by averaging all pairwise matching accuracy $\frac{\sum_{i=1}^{N} \sum_{j=1}^{N} Acc_{ij}}{N(N-1)/2}$. Each $Acc_{ij}$ computes the matches between $X_{ij}$ given by the ground truth $X_{ij}^{gt}$: $Acc_{ij} = \frac{\text{tr}(X_{ij}^{gt}X_{ij}^{gt})}{\text{tr}(X_{ij}X_{ij})}$. In line with [4], [13], we only calculate the accuracy for common inliers and ignore the correspondences between outliers. The above protocol is widely adopted by related work such as [13], [13].

If not otherwise specified, the parameters of our methods are universally set by: $T_0 = 2$, $T_{max} = 6$, $\mu(0) = 0.2$, $\gamma = 0.3$, $\beta = 1.1$. Note when $t \leq T_0$, only score boosting is performed without infusing consistency regularization. As a simple speed-up trick used in our methods, for the generated candidate solutions in the evaluation formulas $X_{ij}$ by Eq.4 and Eq.5, we compute their scores after excluding those duplicate ones.

**4 EXPERIMENTS AND DISCUSSION**

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**4.1 Dataset description and affinity setting**

**Synthetic random graph matching** The random graph test follows the widely used protocol of [29], [20], [14], [13], [40]. For each trial, a reference graph with $n_i$ nodes is created by assigning a random weight to its edge, uniformly sampled from the interval $[0, 1]$. Then the ‘perturbed’ graphs are created by adding a Gaussian deformation disturbance to the edge weight $q_{ij}$, which is sampled from $N(0, \varepsilon)$ i.e. $q_{ij} = q_{ij} + N(0, \varepsilon)$ where the superscript ‘p’ and ‘r’ denotes for ‘perturb’ and ‘reference’ respectively. Each ‘perturbed’ graph is further added by $n_o$ outliers, which can also be helpful to make the graphs of equal sizes when the input graphs are different sizes. Its edge density is controlled by the density parameter $\rho \in [0, 1]$ via random sampling. The edge affinity is computed by $K_{ia,jb} = \exp(-||q_{ij} - q_{oa}||^2/\sigma^2)$ where $\sigma^2$ is the edge similarity sensitivity parameter. No single-node feature is used and the unary affinity $K_{ia,ia}$ is set to zero, leaving the matching score entirely to the pairwise geometric information. In addition, we control the ‘coverage’ of the initial matching configuration $X$ by parameter $c \in [0, 1]$, which denotes the rate of matching pairs that are generated by the pairwise matching solver, and the rest $1 - c$ portion of pairs are assigned with a randomly generated matching solution. A description of these parameters is listed in Table 3.

**Synthetic random point set matching** The random point set matching is also explored as tested in [3], [59]. First, $n_i$ inliers $\{|p_k^{in}\}_{k=1}^{n_i}$ are randomly generated on the 2-D plane via Gaussian distribution $N(0, 1)$ as the reference point set. Then each point is copied with Gaussian noise $N(0, \varepsilon)$ to generate $N$ random point set by further adding $n_o$ outliers via $N(0, 1)$. The edge weight is set by the Euclidean distances $q_{ij} = ||p_i - p_j||$ for each graph. The subsequent steps are the same with the random graph matching case. This dataset is used for the synthetic testing in comparison with MPM [3] under a relatively large number of outliers. This is because the max-pooling method MPM is designed for geometric relation rather than arbitrary edge weights as in the random graph matching setting.

**CMU-POSE Sequence** This data contains four sequences. Two sequences are from the CMU house (30 landmarks, 101 frames), hotel (30 landmarks, 111 frames) sequence (http://vasc.ri.cmu.edu/~idb/html/motion/) which are commonly used in [29], [14], [21], [13], [52]. The other two sequences are sampled from the ‘VolvoC70’ and the ‘houseblack’ (both 19 landmarks, 225 frames) covering a range of 70 degrees of viewing angles from the POSE dataset [49]. We use this data for the ‘partial similarity’ test. We select $n_i=10$ landmarks out of all $n_{ant}$ annotated landmarks, and randomly choose $n_o=4$ nodes from the rest $n_{ant}-n_i$ nodes as ‘outliers’. The edge sampling follows the same way as [13] by constructing the sparse delaunay triangulation among the points (no distinction to inliers or outliers). The affinity matrix is set by $K_{ia,jb} = \exp((d_{ij}-d_{oa})^2)$ where $d_{ij}$, $d_{a}$ are the Euclidean distances between two points normalized to $[0, 1]$ by dividing the largest edge length. The diagonal is set to zero same as [13], [13].
4.2 Comparing methods and time complexity

The implementations of all comparing methods are the authors’ Matlab code and all tests run on a laptop (2.9G Intel Core i7 and 8G memory) with a single thread.

**Re-weighted Random Walk Matching (RRWM)** Since many existing multi-graph matching methods [29, 41] require a pairwise GM solver in different ways, we choose RRWM [14] due to its cost-effectiveness. We set its parameters $\alpha=0.2, \beta=30$.

**Max-Pooling Matching (MPM)** MPM [3] is an outlier-tolerant method computing the affinity score of each candidate match via maximal support from nearby matches. This method is tested in the presence of more outliers.

Several state-of-the-art multi-graph matching methods are evaluated together with our methods [4]. It shall be noted that all methods start with an initial matching configuration $X^{(0)}$ obtained from RRWM in this paper.

### Alternating optimization for multi-graph matching

**(MatchOpt)** MatchOpt [29, 41] transforms the multi-graph matching problem into a pairwise one by a star structure, whose root is the reference graph $G_\alpha$, and the leaf are the others $\{G_k\}_{k=1,\ldots,N}$. Then it sequentially updates each $X_u$ by fixing the rest $N-2$ basis variables. Both factorized and non-factorized models regarding the affinity matrix are devised in [4]. Only the non-factorized model MatchOpt is compared as it has been shown in [4] more cost-effective. We set its iteration threshold $T_{max}=4$ as it often converges quickly.

**Match lifting via convex relaxation (MatchLift)** MatchLift [2] adopts a first-order approximate algorithm for semi-definite programming. The main cost is computing the eigenvalues for iterative updating the dual variables as it often converges quickly.

**Permutation synchronization (MatchSync)** MatchSync [28] uses spectral analysis to the grouped ‘target matrix’ $T$ of size $n \times n \times N$ (Eq.7 in [28]) stacked by all initial $\{X_{ij}^{(0)}\}_{i,j=1}^N$. It involves a one-shot SVD to find the $n$ leading eigenvectors of ‘$T’ whose cost is $O(n^3N^2)$, and $N$ iterations of Hungarian method with cost $O(Nn^3)$. Thus the total cost except the initial pairwise matching step is $O(N^2n^3)$. Since MatchSync is applicable only when $n \leq N$, thus the Maximum Spanning Tree (MST) is used on the consistency-wise super graph $G^{sup}_n$ if $n > N$.

We consider the time complexity of our methods in several aspects as follows. The overall time complexity for all compared methods is summarized in Table 4.

| Method | Time Complexity |
|--------|-----------------|
| ISB (Alg1) | $O(N^2n^2 + N^2\tau_{pair})$ |
| ISB-GC-U, ISB-GC-P (Alg3) | $O(N^2n^2 + N^2\tau_{pair})$ |
| MatchOpt (non-factorized) | $O(N^2n^2 + N^2\tau_{pair})$ |
| MatchLift | $O(N^2n^2 + N^2\tau_{pair})$ |
| MatchSync | $O(N^2n^2 + N^2\tau_{pair})$ |
Finally, we consider the run-time overhead for the inlier-eliciting mask operation $\psi_c(\cdot, X, n_i)$ or $\psi_a(\cdot, X, X, n_i)$. For $\psi_c(\cdot, X, n_i)$, it is in fact concerning with computing the node-wise consistency $\{C_n(u^k, X, n_i)\}_{n=1,k=1}^{N}$. For each node in every graph, thus the total overhead in each iteration is $O(N^2n)$ at the unit cost of $O(N^2n)$ per graph. For $\psi_a(\cdot, X, X, n_i)$, the node-wise affinity by Definition 5 is $O(N^2n^3)$. Regardless $\psi_c$ or $\psi_a$ is used, the associated overhead can be absorbed in the overall complexity as shown in Table 4. We will evaluate these two inlier-eliciting metrics in the experiments.

### 4.3 Experimental results and discussion

For the ‘RRWM’ and ‘MPM’ curves in the plots, they are generated by applying the two methods on each pair of graphs independently. ‘ISB*’ denotes performing ISB without running the post step L10-18 in the chart of Alg. 1 and so for other methods. Fifty random trials are performed for all synthetic tests that generate the average results as plot in the figures. For real image data, 20 random trials are sampled from the image set for each setting. For clarity, standard deviations are not plot and they are found relatively homogenous over curves.

In case of few outliers Fig 1 gives a comparison with controlled noise level, for several putative methods in this paper besides the main algorithms: \{ISB, ISB\textsuperscript{cst}, ISB\textsuperscript{2nd}\} in Sec.3.2 and \{ISB-GC, ISB-GC\textsuperscript{inv}\} in Sec.3.3.
Fig. 2 shows the accuracy boosting behavior as a function of $T_{\text{max}}$ and based on this plot, we set $T_{\text{max}} = 6$. There is little noise regarding with the affinity function for the coverage test in Fig. 2(d), thus pure affinity-driven approaches outperform. In other cases, ISB and ISB$_2$nd under-perform and the latter even slightly degenerates as $T_{\text{max}}$ grows. Fig. 2(f) suggests the relation between the accuracy and the sampling rate $r$ for the $(N - 2) \times r$ graphs used from all graphs over the exhaustive searching space, to find the best anchor graph. Since our framework is applicable to other random search strategies, which might also depend on the specific applications, thus here we do not dwell on how to design an efficient random search technique. Our comments are as follows:

i) The proposed main method ISB-GC outperforms the baseline ISB and state-of-the-arts in most cases for both synthetic random graphs (Fig. 3) and real images (Fig. 4), except for the ‘coverage’ test (Fig. 3(d), Fig. 3(i)), in which many pairwise matchings in the initial $X_{(0)}$ are randomly generated and a consistent $X^*$ is biased to the true accuracy. Specifically, the methods utilizing affinity information including [4] and ours, outperform MatchLift [2] and MatchSync [28] that only use the initial matching configuration $X_{(0)}$ as input, when $X_{(0)}$
is largely corrupted as controlled by coverage rate $c$.  
ii) As shown in the bottom row of Fig.4 in addition with Fig.4, the accuracy in general increases as the number of graphs $N$ grows, though there is some fluctuations especially for the test on ‘car’ as shown in Fig.4. We think this is due to the inherent matching difficulty of the sampled images, which is evidenced by the baseline ‘RRWM’ whose performance also fluctuates. We find this phenomenon is more pronounced as shown in the bottom row of Fig.4 due to the larger viewing range when more frames are sampled. In fact the relative accuracy improvement against the RRWM baseline is increasing as $N$ grows. This is in line with the intuition that more graphs can help dismiss local ambiguity.

iii) For the ‘partial similarity’ CMU-POSE data test which is often the case in reality, as shown in the bottom row of Fig.4 without enforcing full consistency (dashed curve) is more effective than using this constraint (solid curve). It suggests the efficacy of our graduated consistency-regularized approach against the two-step hard synchronization methodology from another perspective.  

In case of more outliers Our methods are tailored to the presence of a majority of outliers as described in Sec. 3.3. The performance is depicted in Fig.5 and Fig.6 for the tests on synthetic point sets (inline with the setting for the compared method MPM [3]) and images, by varying the number of outliers, graphs and the estimated inliers. No post-synchronization is performed in the outlier tests. Discussions are presented as follows:

i) In Fig.6(o), we show an example of the hitting rate of the top $n_i$ nodes in descending order by the node-wise consistency (solid curve) and affinity (dashed curve) metrics against true inliers. Given such reasonable hitting rates ($> 0.8$), the suite of our inlier eliciting methods, i.e. the consistency-driven variant (marked by the superscript ‘cst’) and the affinity-driven one (marked by ‘sim’) in general outperform state-of-the-arts notably. Note in Fig.6(o) that the hitting rate for ‘face’ by the affinity-driven metric is robust against the number of outliers. This is because the landmarks on face form a very distinctive structure thus its affinity is more informative.

ii) The sensitive test w.r.t. the disturbance of $n_i$ is illustrated in Fig.5(d) and the bottom row of Fig.6 for synthetic data and real images respectively. The eliciting mechanism boosts the accuracy compared with our original algorithms which in fact set $n_i$ equal to $n = 20$ with no discrimination to outliers. Moreover, the accuracy decline is relatively smooth around the exact $n_i = 10$ in these plots which suggests the robustness of our methods given a rough estimation of $n_i$.

iii) Two run-time overhead examples are plot in Fig.6(o) for the synthetic test and in Fig.6(o) for the real image test. ISB-GC* is more costive as we find it converges slower and need more overhead in each iteration as discussed in the complexity analysis. Also, all the proposed algorithms can be parallelized more easily than other iterative methods like matchOpt, matchSync, because updating each $X_i^{(t-1)}$ can be done independently.

iv) MPM outperforms the baseline RRWM but does not perform as robustly as our methods. We think this is because MPM is suited under moderate noises in addition with the outliers. This is often not true in realistic scenarios and our settings – Table 5 and Table 7.

v) In the synthetic point data test for Fig.5(a) and Fig.5(b), the affinity-driven inlier eliciting variant outperforms the consistency-driven one given the deformation $\varepsilon < .05$. However, as shown in Fig.5(c) when $\varepsilon$ grows by fixing the number of outliers, the consistency-driven mechanism outperforms when $\varepsilon > .05$. This is consistent with the motivation of this paper: consistency becomes helpful in the existence of large noises given few outliers.

5 Conclusion  
In the paper, we propose general algorithms towards multi-graph matching by incorporating both affinity score and matching consistency in an iterative approximate boosting procedure. The outlier-tolerance variants are designed by eliciting the affinity and consistency associated with inliers. The experimental results suggest that i) the method Alg.2 (ISB-GC) in general achieves more competitive accuracy compared with state-of-the-arts; ii) the methods Alg.3 (ISB-GC-U/P) in general improve the cost-effectiveness of Alg.1 (ISB) especially on the real image data under arbitrary noises.

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