Clique-graph Matching by Preserving Global & Local Structure

Wei-Zhi Nie[1], An-An Liu[1*], Zan Gao[2], Yu-Ting Su[1]
1School of Electronics Information Engineering, Tianjin University, China.
2School of Computer & Communication Engineering, Tianjin University of Technology, China.

Graph matching is very essential in the fields of computer vision and pattern recognition. Previous methods mainly focus on node-to-node mapping by leveraging the first & second order attributes [3]. Since this node-wise mapping can not well preserve both global and local structure, many researchers developed the hyper-graph matching methods [1]. Different from the classic graph or hyper-graph, we originally propose the concept of clique-graph and further present a clique-graph matching method by preserving global and local structure. The main contributions are summarized as follows: 1) Clique-graph can be considered as the generalized form of both graph and hyper-graph since individual clique can convey arbitrary order attributes to represent the local structure; 2) The proposed clique-graph matching method can benefit simplifying the hyper-edge correspondence into the formulation only with clique-wise correspondence; 3) The proposed method can easily impose the one-to-one constraint for clique-graph matching; 4) The local similarity measure is unique.

The proposed method contains two consecutive steps, clique-graph generation and matching, as shown in Fig.1.

• **Clique-graph generation**: Different from classic graph/hyper-graph matching which considers each node as the basic unit, we propose to regard each clique as the basic unit for matching, which consists of several neighbor nodes in the feature space and can implicitly convey arbitrary order attributes with the specific structure. Consequently, we originally propose the concept of clique-graph. As shown in Fig.1, a clique-graph $\tilde{G}=\{\tilde{V},\tilde{A}\}$ is composed of two kinds of elements, the clique set $\tilde{V}$ and the attribute set $\tilde{A}$ associated with individual cliques. Each clique $\tilde{V}_i \in \tilde{V}$ can be represented by the star model, $\tilde{V}_i=\{\tilde{c}_i,\{\tilde{l}_{ij}\}_{j=1}^k,\{\tilde{e}_{ij}\}_{j=1}^k\}$, where $\tilde{c}_i$ denotes the center of the clique, $\{\tilde{l}_{ij}\}_{j=1}^k$ denotes k leaf nodes of the clique, $\{\tilde{e}_{ij}\}_{j=1}^k$ denotes k edges linking the center node and k leaf nodes. The order of one clique, $\delta(\tilde{V}_i)$, equals to the number of the nodes in it. $\tilde{A}_i \in \tilde{A}$ is the attribute for the i^{th} clique, which represents the importance of this clique in the entire clique-graph and can be calculated based on the term frequency by dividing the total frequency of the nodes in $\tilde{V}_i$ by the produce of the clique number and the node number in each clique. Since each clique implicitly convey the compact local structure information, the edge between two cliques can be ignored by assuming the relation between two cliques is too weak. This simplification will benefit directly imposing the one-to-one constraint for clique-graph matching.

• **Clique-graph matching**: Given two clique-graphs, $\tilde{G}^p=\{\tilde{V}^p,\tilde{A}^p\}$ and $\tilde{G}^q=\{\tilde{V}^q,\tilde{A}^q\}$, clique-graph matching aims to discover the clique-to-clique correspondence with one-to-one constraint. Thus, the original graph matching can be realized by achieving the correspondences between each pair of centers, which is consistent with the discovered clique-to-clique correspondence. By denoting the similarity between $\tilde{V}_i \in \tilde{G}^p$ and $\tilde{V}_m \in \tilde{G}^q$ as $S_{i,m}$, $S=\{S_{i,m}\}_{i=1,\ldots,N^p,m=1,\ldots,N^q} \in R^{N^pN^q\times 1}$, where N^p and N^q respectively denotes the clique numbers in $\tilde{G}^p$ and $\tilde{G}^q$, can be used to represent the similarities between all pairwise cliques. We define the solution of clique-graph matching as a binary indicator matrix $\bar{X} \in \{0,1\}^{N^p\times N^q}$. If $\tilde{V}_i \in \tilde{G}^p$ is matched to $\tilde{V}_m \in \tilde{G}^q$, $X_{i,m}=1$. Otherwise, $X_{i,m}=0$. For a convenient representation, we use X to represent the vectorized version of $\bar{X}$. The problem of clique-graph matching can be formulated as an integer linear programming to discover the indicator vector X^* that maximizes the following objective function:

$$(X,\tilde{G}^p,\tilde{G}^q)^* = \arg\max_{X,\tilde{G}^p,\tilde{G}^q}(S^\top \cdot X),$$
$$s.t.\ \ \bar{X}\cdot 1_{N^q\times 1} \le 1_{N^p\times 1}, \quad \bar{X}^\top \cdot 1_{N^p\times 1} \le 1_{N^q\times 1} \tag{1}$$

Till now, we have converted clique-graph matching into the optimization of the objective function above. However, it is non-trivial to optimize Eq.1 directly since both the clique structure information in individual clique-graph and the similarity measure of pairwise cliques from different clique-graphs are latent variables. We will detail the solution of both as follows. After achieving the clique-to-clique similarity, the objective function in Eq.1 can be easily solved by integral linear programming.

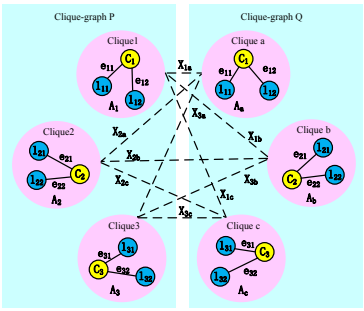

Figure 1: Framework of clique-graph matching.

1) Clique discovery We consider individual node of one clique-graph as the center of one clique. We well adapt the sparse representation method to discover the neighbor nodes of individual center by selecting those with the highest k weights for sparse reconstruction of the center. Each compact clique can be constructed with the center and its neighbors and consequently convey the specific local structure.

2) Clique-wise similarity measure We convert the problem of clique-wise similarity measure into the problem of graph matching. Since the structure of each clique is extremely simpler comparing against the structure of the original graph, the clique-wise similarity measure can be formulated only with the unary and pairwise correspondences, which can simplify the complicated high-order correspondence with the low-order correspondence and consequently benefit avoiding the high computational complexity. In our work, we utilized the cosine distance for node-wise similarity measure and utilized the Euclidean distance for edge-wise similarity measure. With both unary and pairwise similarity, the similarity between pairwise cliques, $S_{i,m}$, can be formulated in the quadratic form and solved by the Rayleigh quotients maximization method as [2].

The proposed method is validated in three scenarios: 1) varying the clique size to evaluate its effect on the performance; 2) testing on the synthetic point set to evaluate the effects of the deformation noise, the outlier number and the edge density on the performances; 3) testing on Caltech+MSRC and Car+Motor datasets to show its performances on the real application. To show the superiority, we compare it against several representative methods, including SM, HGM, RRWM, RRWHM, TM, FGM, and IPFP. The extensive comparison experiments show that the proposed method can outperform the competing methods in terms of accuracy and time on both synthetic and real datasets by preserving global and local structure.

Acknowledgement: This work was supported in part by the National Natural Science Foundation of China (61472275, 61170239,61202168), the Tianjin Research Program of Application Foundation and Advanced Technology, the grant of Elite Scholar Program of Tianjin University.

[1] Jungmin Lee, Minsu Cho, and Kyoung Mu Lee. Hyper-graph matching via reweighted random walks. In *CVPR*, pages 1633–1640, 2011.

[2] T.Cour, P.Srinivasan, and J.Shi. Balanced graph matching. In *NIPS*, 2006.

[3] Barend J. van Wyk and Michaël A. van Wyk. A pocs-based graph matching algorithm. *IEEE Trans. Pattern Anal. Mach. Intell.*, 26(11): 1526–1530, 2004.