# EE359-Multi-Graph-Matching

Python implementation of three algorithms in paper "Unifying Offline and Online Multi-graph Matching via Finding Shortest Paths on Supergraph". Homework of EE359, Prof. Junchi Yan.

# **EE359 HW Report**

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### 1. Overview of the HW

In this short project we're required to implement Python code of the three algorithms proposed in <u>Jiang</u>, <u>Z</u>., <u>Wang</u>, <u>T.</u>, <u>& Yan</u>, <u>J.</u> (2020). <u>Unifying Offline and Online Multi-graph Matching via Finding Shortest Paths on Supergraph. IEEE Transactions on Pattern Analysis and Machine Intelligence</u>, 14(8), 1–1.

As follows we'll illustrate how we reproduce the algorithms, the result of pass test, and some of our observations.

# 2. Implementation

#### Affinity Score

In the graph matching synthesis, affinity score is designed to measure two-graph matching, usually written as a quadratic assignment programming (QAP) problem which is also called Lawler's QAP:

$$J(\mathbf{X}) = \min_{\mathbf{X} \in \{0,1\}^{n_1 \times n_2}} \operatorname{vec}(\mathbf{X})^{\mathsf{T}} \mathbf{K} \operatorname{vec}(\mathbf{X})$$

where  $\mathbf{X}$  is a (partial) permutation matrix indicating the node correspondence, and  $\mathbf{K} \in \mathbb{R}^{n1n2 \times n1n2}$  is the affinity matrix whose diagonal (off-diagonal) encodes the node-to-node affinity (edge-to-edge affinity) between two graphs. The symbol  $\text{vec}(\cdot)$  here denotes the column-wise vectorization of the input matrix.

In our practice X is the matching result of multi graphs in shape  $(num\_graph, num\_graph, num\_node, num\_node)$ , where X in above formula is X[i,j]. Thus instead of calculating each pair of graphs, we can compute them in a bunch:

```
1
    def cal_affinity_score(X, K):
2
         :param X: matching results, (num_graph, num_graph, num_node, num_node)
3
         :param K: affinity matrix, (num_graph, num_graph, num_node^2, num_node^2)
4
         :return: normalized affinity score, (num_graph, num_graph)
5
6
        n, _, m, _ = X.shape
7
        vx = np.reshape(X.transpose((0, 1, 3, 2)), newshape=(n, n, -1, 1))
8
        vxT = vx.transpose((0, 1, 3, 2))
9
        affinity_score = np.matmul(np.matmul(vxT, K), vx) # in shape (n, n, 1, 1)
10
        normalized_affinity_score = affinity_score.reshape(n, n) / np.max(affinity_score)
11
        return normalized_affinity_score
12
```

Note that affinity score is normalized to range [(0,1]] to be consistent with pairwise consistency.

#### • Pairwise Consistency

In the proposed unified approaches, given  $\{G_k\}_{k=1}^N$  and matching configuration  $\mathbb{X}$ , for any pair  $G_i$  and  $G_j$ , the pairwise consistency is defined as:

$$C_p\left(\mathbf{X}_{ij}, \mathbb{X}\right) = 1 - \frac{\sum_{k=1}^{N} \|\mathbf{X}_{ij} - \mathbf{X}_{ik}\mathbf{X}_{kj}\|_F}{2nN} \in (0, 1]$$

Though it's defined in a for any way and k is traversed as  $\sum_{k=1}^{N}$ , we don't need to write the code with three for loop, since it's mutually independent to compute each pair  $G_i$  and  $G_j$ , as well as the summation of k.

Computation of  $C_p\left(\mathbf{X}_{ij}\right)$  is related to  $\mathbf{X}_{ik}\mathbf{X}_{kj}$  for k from 1 to N. This is similar to the form of matrix multiplication. However we want one step before: where  $\mathbf{X}_{ik}\mathbf{X}_{kj}$  haven't been summarized so that  $\|\mathbf{X}_{ij}-\mathbf{X}_{ik}\mathbf{X}_{kj}\|_F$  operation can be done. Thus we use broadcasting in numpy to align shapes with additional dimensions we add. Note that we need to swap the two axes with transpose to achieve it:

```
def cal_pairwise_consistency(X):
1
2
         :param X: matching results, (num_graph, num_graph, num_node, num_node)
3
         :return: pairwise_consistency: (num_graph, num_graph)
4
5
         n, _, m, _ = X.shape
6
         X_t = X.transpose((1, 0, 2, 3)) # so that <math>X_t[j,k] = X[k,j]
7
         pairwise_consistency = 1 - np.abs(X[:, :, None] - \
8
               np.matmul(X[:, None], X_t[None, ...]))sum((2, 3, 4)) / (2 * n * m)
9
         # X[:,None]*X t[None,...] is X[i,k]*X[k,j] (matmul)
10
         return pairwise_consistency
11
```

We've had questions about whether to use pointwise or matrix multiplication here, which will be pointed out later.

#### MGM-Floyd

MGM-Floyd is used for offline multiple graph matching. It's able to find the optimal composition path more efficiently with fewer comparisons and thus being more competitive. Pseudocode provided in the paper:

where  $S\left(\mathbf{X}_{ij}, \mathbb{X}\right) = \overbrace{(1-\lambda)J\left(\mathbf{X}_{ij}\right)}^{\text{pairwise consistency}} + \overbrace{\lambda C_p\left(\mathbf{X}_{ij}, \mathbb{X}\right)}^{\text{pairwise consistency}}$ . In practice we use the pc approximated version  $S_{pc}^{\mathbb{X}}\left(\mathbf{X}_{ij}, \mathbf{X}_{jk}\right) = (1-\lambda)J\left(\mathbf{X}_{ij}\mathbf{X}_{jk}\right) + \lambda\sqrt{C_p\left(\mathbf{X}_{ij}, \mathbb{X}\right)C_p\left(\mathbf{X}_{jk}, \mathbb{X}\right)}$ . In this way we don't need to calculate pairwise consistency of the multiplied matrix again, but just multiply their original pairwise consistency value.

There are two rounds of updating X, with each round traversing all graphs. In the first round  $\lambda$  is set to 0 for affinity based boosting. In the second round  $\lambda=0.3$ . Similar as acceleration of above, each pair of graphs are computated parallelly.

```
1
    def mgm_floyd(X, K, num_graph, num_node):
2
         :param X: matching results, (num_graph, num_graph, num_node, num_node)
3
         :param K: affinity matrix, (num_graph, num_graph, num_node^2, num_node^2)
4
         :param num_graph: number of graph, int
5
         :param num_node: number of node, int
6
         :return: matching results, (num graph, num graph, num node, num node)
7
8
        for k in range(num_graph):
9
            Xopt = np.matmul(X[:, None, k], X[None, k, :])
10
            Sorg = cal_affinity_score(X, K)
11
            Sopt = cal_affinity_score(Xopt, K)
12
             update = (Sopt > Sorg)[:, :, None, None]
13
            X = update * Xopt + (1 - update) * X
14
15
        for k in range(num_graph):
16
            pairwise consistency = cal pairwise consistency(X)
17
            Xopt = np.matmul(X[:, None, k], X[None, k, :])
18
            Sorg = (1 - LAMBDA) * cal_affinity_score(X, K) + \
19
                   LAMBDA * pairwise_consistency
20
            Sopt = (1 - LAMBDA) * cal_affinity_score(Xopt, K) + \
21
                   LAMBDA * np.sqrt(\ # sqrt pc for approximate
22
                 np.matmul(pairwise_consistency[:, k][:, None], \
23
                 pairwise_consistency[k, :][None, ...]))
24
            update = (Sopt > Sorg)[:, :, None, None]
25
            X = update * Xopt + (1 - update) * X
26
27
        return X
28
```

#### MGM-SPFA

MGM-SPFA is based on SPFA, a single-source shortest path algorithm. It helps solve online multiple graph matching, which aims at matching the arriving graph  $G_N$  to N-1 previous graphs which have already been matched. Two constraints added: force termination when number of updated nodes reaches  $m^2$ , and pairwise consistency is updated every time two nodes get updated.

#### Algorithm 2: MGM-SPFA (Online MGM)

```
Input: Affinity matrix \{\mathbf{K}_{ij}\}_{i,j=1}^{N}, \lambda, initial matching \mathbb{X}.
1 for each newly arriving graph G_N do
         use two-graph solver to obtain \mathbb{X}_{Ni}^{(0)} for G_N and others;
         initialize the graph queue Q = \{G_1, G_2 \cdots, G_{N-1}\};
         while Q is not empty do
              obtain G_x in \mathcal{Q} and remove it;
5
              for each graph G_y do
 6
                    set S_{org} = S(\mathbf{X}_{yN}) by Eq. 5 (or Eq. 7, Eq. 8);
 7
                    set S_{opt} = S(\mathbf{X}_{yx}\mathbf{X}_{xN}) by Eq. 5 (or Eq. 7,
 8
                     Eq. 8);
                    if \bar{S}_{org} < S_{opt} then
                         \mathbf{X}_{uN} \leftarrow \mathbf{X}_{ux}\mathbf{X}_{xN};
10
                         add G_u into \mathcal{Q};
11
         for each pair of graphs G_x, G_y in \mathcal{H}\setminus\{G_N\} do
12
              set S_{org} = S(\mathbf{X}_{xN}) by Eq. 5 (or Eq. 7, Eq. 8);
13
              set S_{opt} = S(\mathbf{X}_{xy}\mathbf{X}_{yN}) by Eq. 5 (or Eq. 7, Eq. 8);
14
15
              if S_{org} < S_{opt} then
                \mathbf{X}_{xy} \leftarrow \mathbf{X}_{xN} \mathbf{X}_{Ny};
   Output: optimized matching X.
```

```
def mgm_spfa(K, X, num_graph, num_node):
1
2
         :param K: affinity matrix, (num_graph, num_graph, num_node^2, num_node^2)
3
         :param X: matching results, X[:-1, :-1] is the matching results obtained by last i
4
                   X[num_graph,:] and X[:,num_graph] is obtained via two-graph matching sol
5
                   graph is the new coming graph. (num_graph, num_graph, num_node, num_node
6
         :param num_graph: number of graph, int
7
         :param num node: number of node, int
8
         :return: X, matching results, match graph_m to {graph_1, ..., graph_m-1)
9
10
        q = queue.Queue()
11
        outnumber = 0
12
         [q.put(i) for i in range(num_graph - 1)]
13
         pairwise_consistency = cal_pairwise_consistency(X)
14
        while not q.empty():
15
             Gx = q.get()
16
             outnumber += 1
17
18
             Xopt = np.matmul(X[:, Gx][:, None], X[Gx, :][None, ...])
19
             # X_opt[y,N]=X[y,x]·X[x,N]
20
             Sorg = (1 - LAMBDA) * cal affinity score(X, K) + \
21
                   LAMBDA * np.sqrt(pairwise_consistency) # sqrt for pc
22
             Sopt = (1 - LAMBDA) * cal_affinity_score(Xopt, K) + LAMBDA * np.sqrt(
23
                 np.matmul(pairwise_consistency[:, Gx][:, None], \
24
                 pairwise_consistency[Gx, :][None, ...]))
25
26
             Sorg = Sorg[:, num_graph - 1, None, None]
27
             Sopt = Sopt[:, num_graph - 1, None, None] # only consider the new added one
28
             update = (Sopt > Sorg)
29
             update[Gx] = False # skip Gx the graph itself
30
```

```
31
             X[:, num_graph - 1] = update * Xopt[:, num_graph - 1] + \
32
                   (1 - update) * X[:, num_graph - 1]
33
             X[num\_graph - 1, :] = update * Xopt[num\_graph - 1, :].transpose((0, 2, 1)) + 
34
35
                   (1 - update) * X[num_graph - 1, :]
36
37
             [q.put(y) for y in range(num_graph) if update[y]] # add Gy into Q
38
39
             if outnumber % 2 == 0:
                 pairwise_consistency = cal_pairwise_consistency(X)
40
             if outnumber > num_graph ** 2:
41
                 break
42
43
44
         Xopt = np.matmul(X[:, num_graph - 1][:, None], X[num_graph - 1, :][None, ...])
         # X_{\text{opt}}[x,y]=X[x,N]\cdot X[N,y]
45
         Sorg = (1 - LAMBDA) * cal_affinity_score(X, K) + \
46
               LAMBDA * np.sqrt(pairwise consistency) # sqrt for pc
47
         Sopt = (1 - LAMBDA) * cal affinity score(Xopt, K) + LAMBDA * np.sqrt(
48
49
             np.matmul(pairwise_consistency[:, num_graph - 1][:, None],\
             pairwise_consistency[num_graph - 1, :][None, ...]))
50
51
         update = (Sopt > Sorg)[:, :, None, None]
         update[num_graph - 1] = False
52
53
         update[:, num_graph - 1] = False #Gx, Gy in H\GN
54
         X = update * Xopt + (1 - update) * X
55
56
         return X
```

Here some redundancy is made: all the pairwise  $X_{\tt opt[i,j]}$  are calculated, while only  $X_{\tt opt[i,N]}$  is needed. However this may not downshift time complexity a lot, since it's parallelized computation. What inpacts most is to add Gy back into queue Q. If this line is commented time and accuracy both pass the test. But with it, time test fails.

#### FAST-SPFA

### 2. Question and Observation

```
Algorithm 1: MGM-Floyd (Offline MGM)

Input: affinity matrix \{K_{ij}\}_{i,j=1}^N, initial \mathbb{X}^{(0)}, \lambda.

1 Set consistency weight to 0 for affinity based boosting.

2 for each garph G_i do

3 | for each pair of graphs G_x, G_y do

4 | set S_{org} = S(X_{xy}) by Eq. 5 (or using approximate S_{yc} by Eq. 7, S_{uc} by Eq. 8 for speedup);

5 | set S_{org} = S(X_{xy}) by Eq. 5 (or Eq. 7, Eq. 8);

6 | if S_{yc} to the pairwise consistency is defined as:

C_p(X_{ij}, \mathbb{X}) = 1 - \frac{\sum_{k=1}^{N-1} \|X_{ij} - X_{ik}X_{kj}\|_{L^2}}{n \cdot N} = (0, 1].

8 | 8 Set consistency weight to \lambda > 0 and run Line 2-7 again;

Output: optimized matching \mathbb{X}.
```

We are curious about whether  $X_{ik}X_{ki}$  should be pointwise or matrix multiplication, for each of the cases

Author Jiang Zetian has kindly answered our question:

```
矩阵乘法, 举个例子吧
Xiv =
[[0, 1, 0]
[1, 0, 0]
[0, 0, 1]
Xvj =
[[0, 0, 1]
[1, 0, 0]
[0, 1, 0]
矩阵乘法乘起来表示 i 到 v 的匹配,再到 j 的匹配,结果还是一个置换矩阵
XivXvj =
[[1, 0, 0]
[0, 0, 1]
[0, 1, 0]]
但是 elementwise 的相乘的话,结果就不是置换矩阵了,这不符合匹配链组合的思路
Xiv * Xvj =
[[0, 0, 0]
[1, 0, 0]
[0, 0, 0]]
希望对你有帮助。
```

From the aspect of matching chain combination, it should be matmul here to maintain a permutation matrix. What we found interesting, however, is that if pointwise-mul is used in pairwise consistency computation rather than mat-mul, higher accuracy can be achieved (let alone speed). We would like to remain it here and research more thoroughly in the next big project.

## 3. Results Screenshots

Offline Floyd		Car	Motorbike	Face	Winebottle	Duck
Time Cost (s)	Required	4.384	4.227	4.220	4.339	4.209
	Ours	1.999	1.950	1.903	1.889	1.938
Accuracy (%)	Required	60.46	80.51	91.08	72.20	57.69
	Ours	82.56	92.27	95.34	91.24	76.93

Online SPFA		Car	Motorbike	Face	Winebottle	Duck
Time Cost (s)	Required	2.190	2.179	2.023	2.631	2.135
	Ours	0.828	0.815	0.857	0.821	0.850
Accuracy (%)	Required	63.32	83.43	91.41	75.23	59.05
	Ours	71.74	88.56	93.94	84.19	68.64

```
Test offline multi-graph matching on class Car iter: 1/5, init.acc: 0.4655, floyd.acc: 0.8599, init.time: 0.0004, floyd.time: 1.8562 iter: 1/5, init.acc: 0.4655, floyd.acc: 0.8179, init.time: 0.0003, floyd.time: 1.7932 iter: 3/5, init.acc: 0.4656, floyd.acc: 0.8187, init.time: 0.0003, floyd.time: 1.7932 iter: 3/5, init.acc: 0.4656, floyd.acc: 0.8187, init.time: 0.0003, floyd.time: 1.8903 iter: 4/5, init.acc: 0.4668, floyd.acc: 0.8597, init.time: 0.0003, floyd.time: 1.9977 Performance on class Car, accuracy: 0.8256, time: 1.8514

Test offline multi-graph matching on class Motorbike iter: 0/5, init.acc: 0.5966, floyd.acc: 0.9323, init.time: 0.0003, floyd.time: 1.9977 iter: 1/5, init.acc: 0.5936, floyd.acc: 0.9323, init.time: 0.0003, floyd.time: 1.9973 iter: 1/5, init.acc: 0.5157, floyd.acc: 0.9323, init.time: 0.0003, floyd.time: 1.9973 iter: 2/5, init.acc: 0.5157, floyd.acc: 0.9329, init.time: 0.0003, floyd.time: 2.0304 iter: 3/5, init.acc: 0.6483, floyd.acc: 0.9309, init.time: 0.0003, floyd.time: 2.0304 iter: 3/5, init.acc: 0.5769, floyd.acc: 0.9339, init.time: 0.0003, floyd.time: 1.9785 Performance on class Motorbike, accuracy: 0.927, time: 1.9900

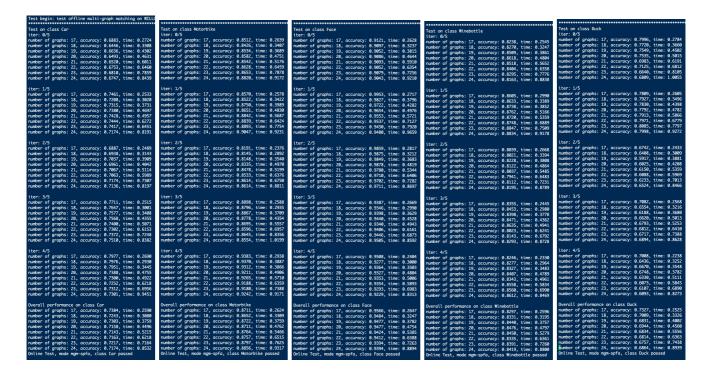
Test Motorbike passed

Test offline multi-graph matching on class face iter: 0/5, init.acc: 0.7845, floyd.acc: 0.9329, init.time: 0.0003, floyd.time: 1.9785 performance on class Motorbike, accuracy: 0.927, time: 1.9900

Test offline multi-graph matching on class Motorbike iter: 0/5, init.acc: 0.5903, floyd.acc: 0.9329, init.time: 0.0003, floyd.time: 1.9977 iter: 0/5, init.acc: 0.5903, floyd.acc: 0.9329, init.time: 0.0003, floyd.time: 1.9978 iter: 1/5, init.acc: 0.5769, floyd.acc: 0.9327, init.time: 0.0003, floyd.time: 1.9785 performance on class Motorbike, accuracy: 0.927, time: 1.9900

Test offline multi-graph matching on class Minebottle iter: 0/5, init.acc: 0.5769, floyd.acc: 0.9329, init.time: 0.0003, floyd.time: 1.9973 iter: 1/5, init.acc: 0.5769, floyd.acc: 0.9329, init.time: 0.0003, floyd.time: 1.9073 iter: 1.9973 iter: 1.9974 iter: 1.9974 iter: 1.9974 iter: 1
```

## Offline test using MGM-floyd passed



Online test using MGM-SPFA passed