EE359 HW Report

戴昊悦 李竞宇

517030910{288,318}

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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 Jiang, Z., Wang, T., & Yan, J. (2020). Unifying Offline and Online Multi-graph Matching via Finding Shortest Paths on Supergraph. IEEE Transactions on Pattern Analysis and Machine Intelligence, 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:

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

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 $\mathrm{vec}(\cdot)$ 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 $\mathbf{X}$ in above formula is `X[i,j]`. Thus instead of calculating each pair of graphs, we can compute them in a bunch:

```python
def cal_affinity_score(X, K):
    """
    :param X: matching results, (num_graph, num_graph, num_node, num_node)
    :param K: affinity matrix, (num_graph, num_graph, num_node^2, num_node^2)
    :return: normalized affinity score, (num_graph, num_graph)
    """
    n, _, m, _ = X.shape
    # UPDATE: this is column vectorize
    XT = X.transpose((0, 1, 3, 2))
    vx = np.reshape(XT, newshape=(n, n, -1, 1))
    vxT = vx.transpose((0, 1, 3, 2))
    affinity_score = np.matmul(np.matmul(vxT, K), vx)  # in shape (n, n, 1, 1)
    normalized_affinity_score = affinity_score.reshape(n, n) / X0
    return normalized_affinity_score
```

Note that affinity score is normalized to range `(0,1]` to be consistent with pairwise consistency. We use the normalization factor `X0` to be the maximal affinity score of the raw input X, as proposed in CAO.

- **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:

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

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 $\left\|\mathbf{X}_{ij} - \mathbf{X}_{ik}\mathbf{X}_{kj}\right\|_F$ 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:

```python
def cal_pairwise_consistency(X):
    """
    :param X: matching results, (num_graph, num_graph, num_node, num_node)
    :return: pairwise_consistency: (num_graph, num_graph)
    """
    n, _, m, _ = X.shape
    X_t = X.transpose((1, 0, 2, 3)) # so that X_t[j,k] = X[k,j]
    pairwise_consistency = 1 - np.abs(X[:, :, None] - \
          np.matmul(X[:, None], X_t[None, ...])).sum((2, 3, 4)) / (2 * n * m)
    # X[:,None]*X_t[None,...] is X[i,k]*X[k,j] (matmul)
    return pairwise_consistency
```

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:

Algorithm 1: MGM-Floyd (Offline MGM)

Input: affinity matrix $\{\mathbf{K}_{ij}\}_{i,j=1}^{N}$, initial $\mathbb{X}^{(0)}$, λ.
1 Set consistency weight to 0 for affinity based boosting.
2 **for** *each graph* G_v **do**
3 **for** *each pair of graphs* G_x, G_y **do**
4 set $S_{org} = S(\mathbf{X}_{xy})$ by Eq. 5 (or using approximate $S_{pc}^{\mathbb{X}}$ by Eq. 7, $S_{uc}^{\mathbb{X}}$ by Eq. 8 for speedup);
5 set $S_{opt} = S(\mathbf{X}_{xv}\mathbf{X}_{vy})$ by Eq. 5 (or Eq. 7, Eq. 8);
6 **if** $S_{org} < S_{opt}$ **then**
7 $\mathbf{X}_{xy} \leftarrow \mathbf{X}_{xv}\mathbf{X}_{vy}$;
8 Set consistency weight to $\lambda > 0$ and run Line 2-7 again;
Output: optimized matching $\mathbb{X}$.

where $S\left(\mathbf{X}_{ij}, \mathbb{X}\right) = \overbrace{(1-\lambda)J\left(\mathbf{X}_{ij}\right)}^{\text{affinity score}} + \overbrace{\lambda C_p\left(\mathbf{X}_{ij}, \mathbb{X}\right)}^{\text{pairwise consistency}}$. 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 $\mathbf{X}$, with each round traversing all graphs. In the first round λ 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.

```
def mgm_floyd(X, K, num_graph, num_node):
    """
    :param X: matching results, (num_graph, num_graph, num_node, num_node)
    :param K: affinity matrix, (num_graph, num_graph, num_node^2, num_node^2)
    :param num_graph: number of graph, int
    :param num_node: number of node, int
    :return: matching results, (num_graph, num_graph, num_node, num_node)
    """
    for k in range(num_graph):
        Xopt = np.matmul(X[:, None, k], X[None, k, :])
        Sorg = cal_affinity_score(X, K)
        Sopt = cal_affinity_score(Xopt, K)
        update = (Sopt > Sorg)[:, :, None, None]
        for i in range(num_graph):
          update[i, i] = False
        X = update * Xopt + (1 - update) * X

    for k in range(num_graph):
        pairwise_consistency = cal_pairwise_consistency(X)
        Xopt = np.matmul(X[:, None, k], X[None, k, :])
        Sorg = (1 - LAMBDA) * cal_affinity_score(X, K) + \
               LAMBDA * pairwise_consistency
        Sopt = (1 - LAMBDA) * cal_affinity_score(Xopt, K) + \
               LAMBDA * np.sqrt(\  # sqrt pc for approximate
            np.matmul(pairwise_consistency[:, k][:, None], \
            pairwise_consistency[k, :][None, ...]))
        update = (Sopt > Sorg)[:, :, None, None]
        update[np.diag_indices(num_graph)] = False
        X = update * Xopt + (1 - update) * X

    return X
```

We find that when using update in the matrix form would bring undesired update of self-assignment (i.e. X_{ii}), which should always be unit matrix. So we do not update these entries.

- **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.

Algorithm 2: MGM-SPFA (Online MGM)

Input: Affinity matrix $\{\mathbf{K}_{ij}\}_{i,j=1}^{N}$, λ, initial matching $\mathbb{X}$.

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 $\mathcal{Q} = \{G_1, G_2 \cdots, G_{N-1}\}$;
  while $\mathcal{Q}$ *is not empty* **do**
    obtain G_x in $\mathcal{Q}$ and remove it;
    for *each graph* G_y **do**
      set $S_{org} = S(\mathbf{X}_{yN})$ by Eq. 5 (or Eq. 7, Eq. 8);
      set $S_{opt} = S(\mathbf{X}_{yx}\mathbf{X}_{xN})$ by Eq. 5 (or Eq. 7, Eq. 8);
      if $S_{org} < S_{opt}$ **then**
        $\mathbf{X}_{yN} \leftarrow \mathbf{X}_{yx}\mathbf{X}_{xN}$;
        add G_y into $\mathcal{Q}$;
  for *each pair of graphs* G_x, G_y *in* $\mathcal{H}\backslash\{G_N\}$ **do**
    set $S_{org} = S(\mathbf{X}_{xN})$ by Eq. 5 (or Eq. 7, Eq. 8);
    set $S_{opt} = S(\mathbf{X}_{xy}\mathbf{X}_{yN})$ by Eq. 5 (or Eq. 7, Eq. 8);
    if $S_{org} < S_{opt}$ **then**
      $\mathbf{X}_{xy} \leftarrow \mathbf{X}_{xN}\mathbf{X}_{Ny}$;

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

```python
def mgm_spfa(K, X, num_graph, num_node):
    """
    :param K: affinity matrix, (num_graph, num_graph, num_node^2, num_node^2)
    :param X: matching results, X[:-1, :-1] is the matching results obtained by last iterat
              X[num_graph,:] and X[:,num_graph] is obtained via two-graph matching solver(R
              graph is the new coming graph. (num_graph, num_graph, num_node, num_node)
    :param num_graph: number of graph, int
    :param num_node: number of node, int
    :return: X, matching results, match graph_m to {graph_1, ... , graph_m-1)
    """

    q = [i for i in range(num_graph - 1)]
    outnumber = 0
    while len(q) > 0:
        Gx = q[0]
        del q[0]
        outnumber += 1
        Xopt = np.matmul(X[:, Gx, None], X[Gx, None, :])  # X_opt[y,N]=X[y,x]·X[x,N]
        for y in range(num_graph - 1):
            if y == Gx:
                continue
            Sorg = (1 - LAMBDA_SPFA) * cal_affinity_score_single(X[y, -1], K[y, -1]) + \
                   LAMBDA_SPFA * cal_pairwise_consistency_single(X, y, -1)
            Sopt = (1 - LAMBDA_SPFA) * cal_affinity_score_single(Xopt[y, -1], K[y, -1]) + \
                   LAMBDA_SPFA * cal_pairwise_consistency_single(Xopt, y, -1)
            if Sorg < Sopt:
                X[y, -1] = Xopt[y, -1]
                if y not in q:
                    q.append(y)
        if outnumber > num_graph ** 2:
            break

    pairwise_consistency = cal_pairwise_consistency(X)
    Xopt = np.matmul(X[:, num_graph - 1][:, None], X[num_graph - 1, :][None, ...])  # X_opt
    Sorg = (1 - LAMBDA_SPFA) * cal_affinity_score(X, K) + LAMBDA_SPFA * pairwise_consistenc
    Sopt = (1 - LAMBDA_SPFA) * cal_affinity_score(Xopt, K) + LAMBDA_SPFA * np.sqrt(
        np.matmul(pairwise_consistency[:, num_graph - 1][:, None], pairwise_consistency[num_
    update = (Sopt > Sorg)[:, :, None, None]
    update[num_graph - 1] = False
    update[:, num_graph - 1] = False  # Gx, Gy in H\GN
    update[np.diag_indices(num_graph)] = False
    X = update * Xopt + (1 - update) * X

    return X
```

Here we use iteration instead of matrix operation to update the matches, because matrix operation has some redundancies: all the pairwise `X_opt[i,j]` are calculated, while only `X_opt[i,N]` is needed.

Through experiments, we find that using iteration is more efficient than matrix operation in mgm-spfa.

- **FAST-SPFA**

Fast-SPFA is based on MGM-SPFA. But instead of doing MGM-SPFA on all of the graphs, Fast-SPFA randomly partition the graphs into several clusters and doing MGM-SPFA-like update on each clusters instead. In this part, all clusters updates match information by the newly arrived graph. Then in the second part, all graph updates their match to each other (regardless of clusters) given the newly arrived graph.

Algorithm 3: FastSPFA (Online Fast MGM)

Input: Affinity matrix $\{\mathbf{K}_{ij}\}_{i,j=1}^{N}$, λ, C_{min}, initial $\mathbb{X}$.
1 **for** *each newly arriving graph* G_N **do**
2 calculate the cluster number $M = \max(1, N/C_{min})$.
3 partition $\mathcal{H}\backslash\{G_N\}$ into M clusters randomly.
4 **for** *each cluster* C_i **do**
5 generate the sub-supergraph $\mathcal{H}_i$ by $C_i \cup \{G_N\}$.
6 apply Line 1 to 16 in Alg. 2 to obtain the edges between G_N and other vertices on $\mathcal{H}_i$: $\{\mathbb{X}_{Nh}\}_{h=1}^{N-1}$.
7 perform the same post-processing Line 12 to 16 in Alg. 2 to optimize all pairwise matchings $\mathbf{X}_{uv}$ in $\mathcal{H}\backslash\{G_N\}$: i.e. use $\mathbf{X}_{uN}\mathbf{X}_{Nv}$ to update $\mathbf{X}_{uv}$ via G_N for each pair.
Output: optimized matching $\mathbb{X}$.

```python
def fast_spfa(K, X, num_graph, num_node):
    """
    :param K: affinity matrix, (num_graph, num_graph, num_node^2, num_node^2)
    :param X: matching results, X[:-1, :-1] is the matching results obtained by last iterat
              X[num_graph,:] and X[:,num_graph] is obtained via two-graph matching solver(RI
              graph is the new coming graph. (num_graph, num_graph, num_node, num_node)
    :param num_graph: number of graph, int
    :param num_node: number of node, int
    :return: X, matching results, match graph_m to {graph_1, ... , graph_m-1)
    """
    M = max(1, num_graph // CMIN)

    for k in range(num_graph):
        Xopt = np.matmul(X[:, k, None], X[k, None, :])
        Sorg = cal_affinity_score(X, K)
        Sopt = cal_affinity_score(Xopt, K)

        update = (Sopt > Sorg)[:, :, None, None]
        update[np.diag_indices(num_graph)] = False
        X = update * Xopt + (1 - update) * X

    for ci in range(M):
        if ci < M - 1:
            coord = [i for i in range(ci * CMIN, (ci + 1) * CMIN)]
            if num_graph - 1 not in coord:
                coord.append(num_graph - 1)
        else:
```

```
            coord = [i for i in range(ci * CMIN, num_graph)]
        Xc = X[coord, ...][:, coord]
        Kc = K[coord, ...][:, coord]

        q = [i for i in range(len(coord) - 1)]
        outnumber = 0
        while len(q) > 0:
            Gx = q[0]
            del q[0]
            outnumber += 1
            Xopt = np.matmul(Xc[:, Gx, None], Xc[Gx, None, :])  # X_opt[y,N]=X[y,x]·X[x,N]
            for y in range(len(coord) - 1):
                if y == Gx:
                    continue
                Sorg = (1 - LAMBDA_FAST) * cal_affinity_score_single(Xc[y, -1], Kc[y, -1]) +
                       LAMBDA_FAST * cal_pairwise_consistency_single(Xc, y, -1)
                Sopt = (1 - LAMBDA_FAST) * cal_affinity_score_single(Xopt[y, -1], Kc[y, -1]
                       LAMBDA_FAST * cal_pairwise_consistency_single(Xopt, y, -1)
                if Sorg < Sopt:
                    Xc[y, -1] = Xopt[y, -1]
                    if y not in q:
                        q.append(y)
            if outnumber > CMIN ** 2:
                break

    pairwise_consistency = cal_pairwise_consistency(X)
    Xopt = np.matmul(X[:, num_graph - 1][:, None], X[num_graph - 1, :][None, ...])  # X_opt
    Sorg = (1 - LAMBDA_FAST) * cal_affinity_score(X, K) + LAMBDA_FAST * pairwise_consistency
    Sopt = (1 - LAMBDA_SPFA) * cal_affinity_score(Xopt, K) + LAMBDA_SPFA * np.sqrt(
        np.matmul(pairwise_consistency[:, num_graph - 1][:, None], pairwise_consistency[num_
    update = (Sopt > Sorg)[:, :, None, None]
    update[num_graph - 1] = False
    update[:, num_graph - 1] = False  # Gx, Gy in H\GN
    update[np.diag_indices(num_graph)] = False
    X = update * Xopt + (1 - update) * X

    return X
```

---

2. Question and Observation

Definition 2. **[4]** *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:*

$$C_p(\mathbf{X}_{ij}, \mathbb{X}) = 1 - \frac{\sum_{k=1}^{N} \|\mathbf{X}_{ij} - \mathbf{X}_{ik}\mathbf{X}_{kj}\|_F^2}{nN} \in (0, 1]. \quad (3)$$

Algorithm 1: MGM-Floyd (Offline MGM)

Input: affinity matrix $\{\mathbf{K}_{ij}\}_{i,j=1}^N$, initial $\mathbb{X}^{(0)}$, λ.
1 Set consistency weight to 0 for affinity based boosting.
2 **for** *each graph* G_v **do**
3 **for** *each pair of graphs* G_x, G_y **do**
4 set $S_{org} = S(\mathbf{X}_{xy})$ by Eq. 5 (or using approximate $S_{pc}^{\mathbb{X}}$ by Eq. 7, $S_{uc}^{\mathbb{X}}$ by Eq. 8 for speedup);
5 set $S_{opt} = S(\mathbf{X}_{xv}\mathbf{X}_{vy})$ by Eq. 5 (or Eq. 7, Eq. 8);
6 **if** $S_{org} < S_{opt}$ **then**
7 $\mathbf{X}_{xy} \leftarrow \mathbf{X}_{xv}\mathbf{X}_{vy}$;
8 Set consistency weight to $\lambda > 0$ and run Line 2-7 again;
Output: optimized matching $\mathbb{X}$.

We are curious about whether $X_{ik}X_{kj}$ 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).

Another observation is that, when adding affinity boost step before both MGM-SPFA and Fast-SPFA, the accuracy would be increased dramatically while using little extra time.

We would like to keep the above two here and research more thoroughly in the next big project.

---

3. Results Screenshots

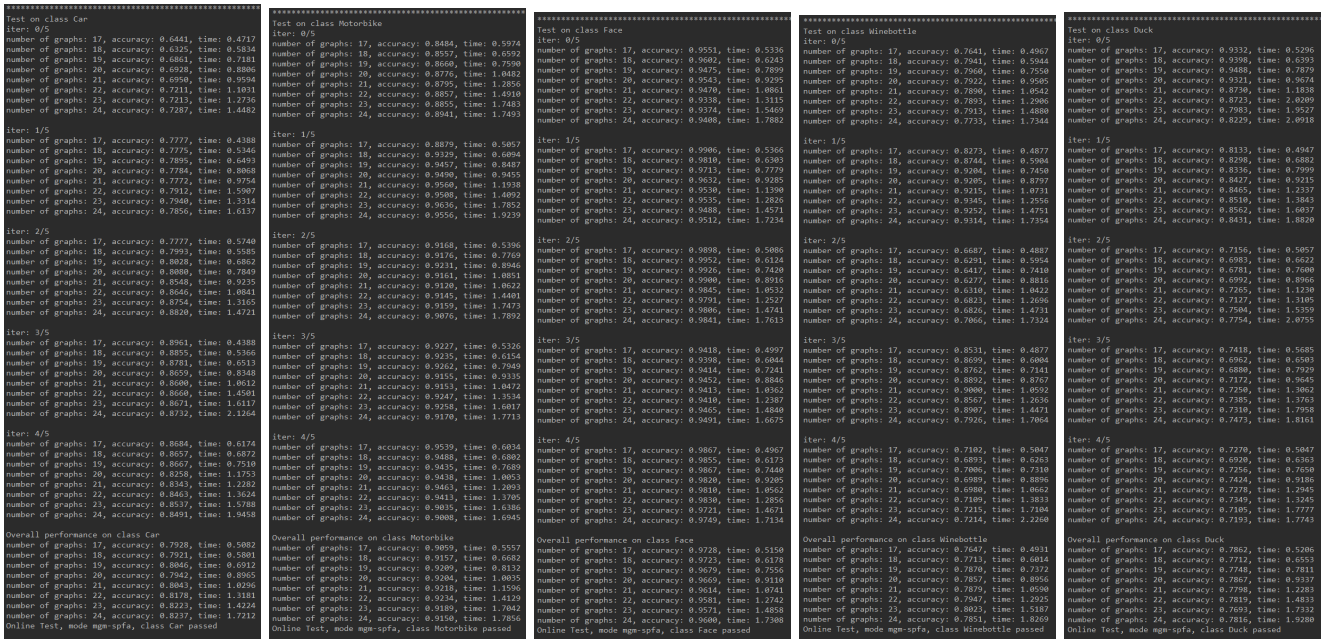
Offline Floyd		Car	Motorbike	Face	Winebottle	Duck
Time Cost (s)	Required	4.384	4.227	4.220	4.339	4.209
	Ours	2.3236	2.1036	2.4006	2.2967	2.2574
Accuracy (%)	Required	60.46	80.51	91.08	72.20	57.69
	Ours	82.16	90.89	95.77	77.07	75.20

Online MGM-SPFA		Car	Motorbike	Face	Winebottle	Duck
Time Cost (s)	Required	2.190	2.179	2.023	2.631	2.135
	Ours	1.021	1.138	1.046	1.053	1.158
Accuracy (%)	Required	63.32	83.43	91.41	75.23	59.05
	Ours	80.65	91.78	96.46	78.48	77.89

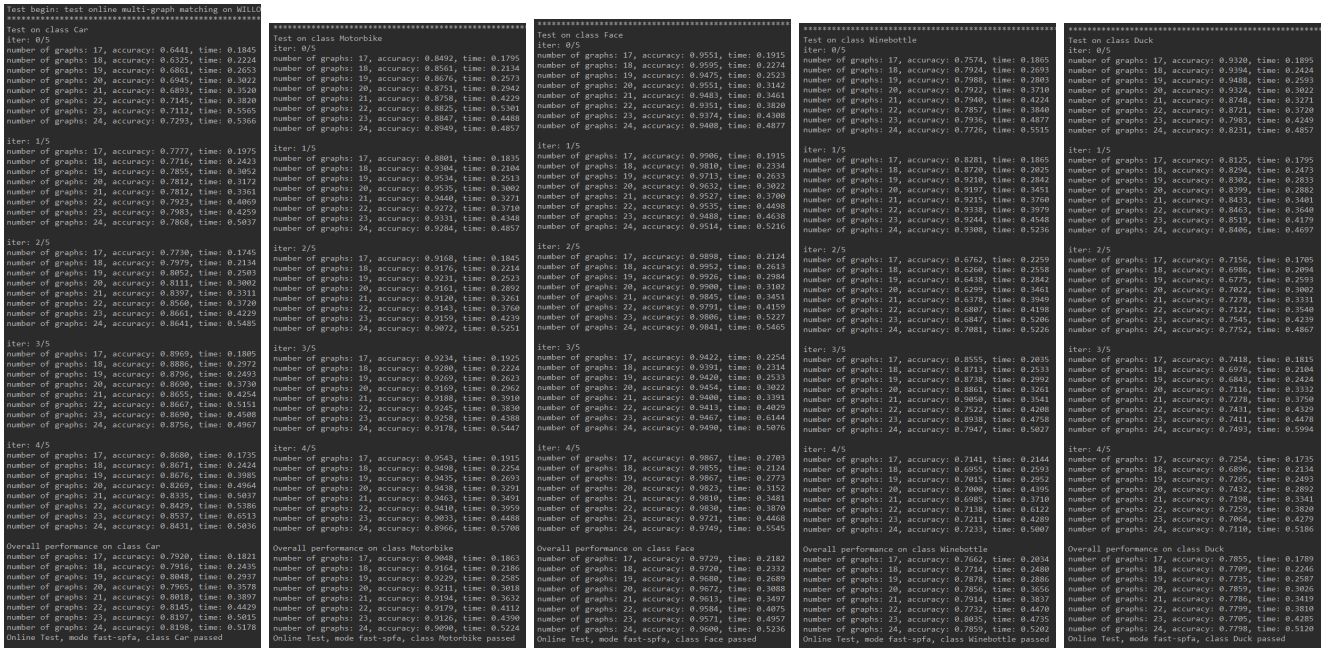
Online Fast-SPFA		Car	Motorbike	Face	Winebottle	Duck
Time Cost (s)	Required	0.7323	0.7586	0.8077	0.7993	0.7591
	Ours	0.3661	0.3376	0.3507	0.3663	0.3285
Accuracy (%)	Required	61.87	82.90	91.45	73.57	57.82
	Ours	80.51	91.55	96.46	78.31	77.81

```
Test begin: test offline multi-graph matching on WILLOW-ObjectClass
**********************************************************************
Test online multi-graph matching on class Car
iter: 0/5, init_acc: 0.4175, floyd_acc: 0.7528, init_time: 0.0010, floyd_time: 2.3118
iter: 1/5, init_acc: 0.4665, floyd_acc: 0.8240, init_time: 0.0010, floyd_time: 2.5990
iter: 2/5, init_acc: 0.4887, floyd_acc: 0.8523, init_time: 0.0010, floyd_time: 2.4624
iter: 3/5, init_acc: 0.5092, floyd_acc: 0.8903, init_time: 0.0000, floyd_time: 2.1901
iter: 4/5, init_acc: 0.4868, floyd_acc: 0.7885, init_time: 0.0010, floyd_time: 2.0585
Performance on class Car, accuracy: 0.8216, time: 2.3236
Test Car passed

**********************************************************************
Test online multi-graph matching on class Motorbike
iter: 0/5, init_acc: 0.5986, floyd_acc: 0.9175, init_time: 0.0010, floyd_time: 2.0306
iter: 1/5, init_acc: 0.6135, floyd_acc: 0.9033, init_time: 0.0010, floyd_time: 2.0236
iter: 2/5, init_acc: 0.6373, floyd_acc: 0.9151, init_time: 0.0010, floyd_time: 2.1483
iter: 3/5, init_acc: 0.6483, floyd_acc: 0.9153, init_time: 0.0000, floyd_time: 2.0615
iter: 4/5, init_acc: 0.6778, floyd_acc: 0.8934, init_time: 0.0010, floyd_time: 2.2580
Performance on class Motorbike, accuracy: 0.9089, time: 2.1036
Test Motorbike passed

**********************************************************************
Test online multi-graph matching on class Face
iter: 0/5, init_acc: 0.7328, floyd_acc: 0.9219, init_time: 0.0010, floyd_time: 2.4505
iter: 1/5, init_acc: 0.8497, floyd_acc: 0.9559, init_time: 0.0010, floyd_time: 2.2859
iter: 2/5, init_acc: 0.7840, floyd_acc: 0.9767, init_time: 0.0010, floyd_time: 2.3417
iter: 3/5, init_acc: 0.7845, floyd_acc: 0.9573, init_time: 0.0010, floyd_time: 2.4016
iter: 4/5, init_acc: 0.7832, floyd_acc: 0.9767, init_time: 0.0000, floyd_time: 2.5272
Performance on class Face, accuracy: 0.9577, time: 2.4006
Test Face passed

**********************************************************************
Test online multi-graph matching on class Winebottle
iter: 0/5, init_acc: 0.5510, floyd_acc: 0.8083, init_time: 0.0010, floyd_time: 2.2031
iter: 1/5, init_acc: 0.5655, floyd_acc: 0.8672, init_time: 0.0010, floyd_time: 2.4435
iter: 2/5, init_acc: 0.4969, floyd_acc: 0.7293, init_time: 0.0010, floyd_time: 2.3108
iter: 3/5, init_acc: 0.5903, floyd_acc: 0.7049, init_time: 0.0000, floyd_time: 2.3228
iter: 4/5, init_acc: 0.5769, floyd_acc: 0.7436, init_time: 0.0000, floyd_time: 2.2061
Performance on class Winebottle, accuracy: 0.7707, time: 2.2967
Test Winebottle passed

**********************************************************************
Test online multi-graph matching on class Duck
iter: 0/5, init_acc: 0.4632, floyd_acc: 0.8167, init_time: 0.0010, floyd_time: 2.2979
iter: 1/5, init_acc: 0.5264, floyd_acc: 0.8377, init_time: 0.0000, floyd_time: 2.2799
iter: 2/5, init_acc: 0.4319, floyd_acc: 0.6618, init_time: 0.0000, floyd_time: 2.2460
iter: 3/5, init_acc: 0.4743, floyd_acc: 0.7863, init_time: 0.0000, floyd_time: 2.2270
iter: 4/5, init_acc: 0.4156, floyd_acc: 0.6576, init_time: 0.0000, floyd_time: 2.2370
Performance on class Duck, accuracy: 0.7520, time: 2.2574
Test Duck passed
```

Offline test using MGM-floyd passed



Online test using MGM-SPFA passed



Online test using Fast-SPFA passed

P.S. Our experiments is run on Intel® Core™ i7-8565U CPU @ 1.80GHz 1.99GHz, 16GB RAM.