

Learning Correspondence Structures for Person Re-Identification

Weiyao Lin, Yang Shen, Junchi Yan, Mingliang Xu, Jianxin Wu, Jingdong Wang, and Ke Lu

Abstract—This paper addresses the problem of handling spatial misalignments due to camera-view changes or human-pose variations in person re-identification. We first introduce a boosting-based approach to learn a correspondence structure, which indicates the patchwise matching probabilities between images from a target camera pair. The learned correspondence structure can not only capture the spatial correspondence pattern between cameras but also handle the viewpoint or human-pose variation in individual images. We further introduce a global constraint-based matching process. It integrates a global matching constraint over the learned correspondence structure to exclude cross-view misalignments during the image patch matching process, hence achieving a more reliable matching score between images. Finally, we also extend our approach by introducing a multi-structure scheme, which learns a set of local correspondence structures to capture the spatial correspondence sub-patterns between a camera pair, so as to handle the spatial misalignments between individual images in a more precise way. Experimental results on various data sets demonstrate the effectiveness of our approach.

Index Terms—Person re-identification, correspondence structure learning, spatial misalignment.

I. INTRODUCTION

PERSON re-identification (Re-ID) is of increasing importance in visual surveillance. The goal of person Re-ID is to identify a specific person indicated by a probe image from a set of gallery images captured from cross-view cameras (i.e., cameras that are non-overlapping and different from the probe image's camera) [2]–[4]. It remains challenging due to the large appearance changes in different camera views and the interferences from background or object occlusion.

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W. Lin and Y. Shen are with the Department of Electronic Engineering, Shanghai Jiao Tong University, Shanghai, China (e-mail: wylin@sjtu.edu.cn; shenyang1715@sjtu.edu.cn).

J. Yan is with the Software Engineering Institute, East China Normal University, Shanghai, China (e-mail: jcyan@sei.ecnu.edu.cn).

M. Xu is with the School of Information Engineering, Zhengzhou University, Zhengzhou, China (e-mail: iexumingliang@zzu.edu.cn).

J. Wu is with the National Key Laboratory for Novel Software Technology, Nanjing University, Nanjing, China (e-mail: wujx2001@nju.edu.cn).

J. Wang is with Microsoft Research, Beijing, China (e-mail: jingdw@microsoft.com).

K. Lu is with the College of Computer and Information Technology, China Three Gorges University, Yichang, China, and also with the University of Chinese Academy of Sciences, Beijing, China (e-mail: luk@ucas.ac.cn).

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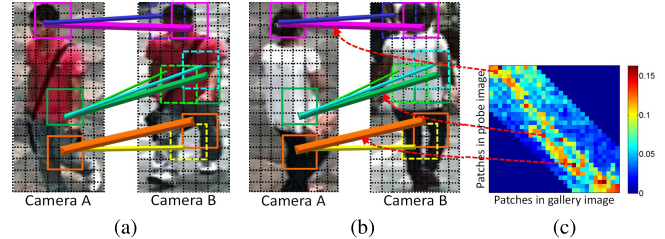


Fig. 1. (a) and (b): Two examples of using a correspondence structure to handle spatial misalignments between images from a camera pair. Images are obtained from the same camera pair: *A* and *B*. The colored squares represent sample patches in each image while the lines between images indicate the matching probability between patches (line width is proportional to the probability values). (c): The correspondence structure matrix including all patch matching probabilities between *A* and *B* (the matrix is down-sampled for a clearer illustration). (Best viewed in color).

One major challenge for person Re-ID is the uncontrolled spatial misalignment between images due to camera-view changes or human-pose variations. For example, in Fig. 1a, the green patch located in the lower part in camera *A*'s image corresponds to patches from the upper part in camera *B*'s image. However, most existing works [2]–[11] focus on handling the overall appearance variations between images, while the spatial misalignment among images' local patches is not addressed. Although some patch-based methods [12]–[15] address the spatial misalignment problem by decomposing images into patches and performing an online patch-level matching, their performances are often restrained by the online matching process which is easily affected by the mismatched patches due to similar appearance or occlusion.

In this paper, we argue that due to the stable setting of most cameras (e.g., fixed camera angle or location), each camera has a stable constraint on the spatial configuration of its captured images. For example, images in Fig. 1a and 1b are obtained from the same camera pair: *A* and *B*. Due to the constraint from camera angle difference, body parts in camera *A*'s images are located at lower places than those in camera *B*, implying a lower-to-upper correspondence pattern between them. Meanwhile, constraints from camera locations can also be observed. Camera *A* (which monitors an exit region) includes more side-view images, while camera *B* (monitoring a road) shows more front or back-view images. This further results in a high probability of side-to-front/back correspondence pattern.

Based on this intuition, we propose to learn a correspondence structure (i.e., a matrix including *all* patch-wise matching probabilities between a camera pair, as Fig. 1c) to

encode the spatial correspondence pattern constrained by a camera pair, and utilize it to guide the patch matching and matching score calculation processes between images. With this correspondence structure, spatial misalignments can be suitably handled and patch matching results are less interfered by the confusion from appearance or occlusion. In order to model human-pose variations or local viewpoint changes inside a camera view, the correspondence structure for each patch is described by a one-to-many graph whose weights indicate the matching probabilities between patches, as in Fig. 1. Besides, a global constraint is also integrated during the patch matching process, so as to achieve a more reliable matching score between images.

Moreover, since people often show different poses inside a camera view, the spatial correspondence pattern between a camera pair may be further divided and modeled by a set of sub-patterns according to these pose variations (e.g., Fig. 1 can be divided into a left-to-front correspondence sub-pattern (a) and a right-to-back correspondence sub-pattern (b)). Therefore, we further extend our approach by introducing a set of local correspondence structures to capture various correspondence sub-patterns between a camera pair. In this way, the spatial misalignments between individual images can be modeled and handled in a more precise way.

In summary, our contributions to Re-ID are four folds.

- 1) We introduce a correspondence structure to encode cross-view correspondence pattern between cameras, and develop a global constraint-based matching process by combining a global constraint with the correspondence structure to exclude spatial misalignments between images. These two components establish a novel framework for addressing the Re-ID problem.
- 2) Under this framework, we propose a boosting-based approach to learn a suitable correspondence structure between a camera pair. The learned correspondence structure can not only capture the spatial correspondence pattern between cameras but also handle the viewpoint or human-pose variation in individual images.
- 3) We further extend our approach by introducing a multi-structure scheme, which first learns a set of local correspondence structures to capture the spatial correspondence sub-patterns between a camera pair, and then adaptively selects suitable correspondence structures to handle the spatial misalignments between individual images. Thus, image-wise spatial misalignments can be modeled and excluded in a more precise way.
- 4) We release a new and challenging benchmark ROAD DATASET for person Re-ID which includes large variation of human pose and camera angle.

The rest of this paper is organized as follows. Section II reviews related works. Section III describes the framework of the proposed approach. Sections IV to V describe the details of our proposed global constraint-based matching process and boosting-based learning approach, respectively. Section VI describes the details of extending our approach with multi-structure scheme. Section VII shows the experimental results and Section VIII concludes the paper.

II. RELATED WORKS

Many person re-identification methods have been proposed. Most of them focus on developing suitable feature representations about humans' appearance [2]–[5], [16], or finding proper metrics to measure the cross-view appearance similarity between images [6]–[9], [17]–[19]. Recently, due to the effectiveness of deep neural networks in learning discriminative features, many deep Re-ID methods are proposed which utilize deep neural networks to enhance the reliability of feature representations or similarity metrics [20]–[27]. Since most of these works do not effectively model the spatial misalignment among local patches inside images, their performances are still impacted by the interferences from viewpoint or human-pose changes.

In order to address the spatial misalignment problem, some patch-based methods are proposed [12]–[15], [28]–[33] which decompose images into patches and perform an online patch-level matching to exclude patch-wise misalignments. In [28], [30], [32], a human body in an image is first parsed into semantic parts (e.g., head and torso) or patch clusters. Then, similarity matching is performed between the corresponding semantic parts or patch clusters. Since these methods are highly dependent on the accuracy of body parser or patch clustering, they have limitations in scenarios where the body parser does not work reliably or the patch clustering results are less satisfactory.

Oreifej *et al.* [12], divide images into patches according to appearance consistencies and utilize the Earth Movers Distance (EMD) to measure the overall similarity among the extracted patches. However, since the spatial correlation among patches are ignored during similarity calculation, the method is easily affected by the mismatched patches with similar appearance. Although Ma *et al.* [13] introduce a body prior constraint to avoid mismatching between distant patches, the problem is still not well addressed, especially for the mismatching between closely located patches.

To reduce the effect of patch-wise mismatching, some saliency-based approaches [14], [29], [33], [34] are recently proposed, which estimate the saliency distribution relationship between images and utilize it to control the patch-wise matching process. Following the similar line, Bak and Carr [33] introduce a deformable model to obtain a set of weights to guide the patch matching process. Bak *et al.* [34] further introduce a hand-crafted Epanechnikov kernel to determine the weight distribution of patches. Although these methods consider the correspondence constraint between patches, our approach differs from them in: (1) our approach focuses on constructing a correspondence structure where patch-wise matching parameters are jointly decided by both matched patches. Comparatively, the matching weights in most of the saliency-based approaches [29], [33] are only controlled by patches in the probe-image (probe patch). (2) Our approach models patch-wise correspondence by a one-to-many graph such that each probe patch will trigger multiple matches during the patch matching process. In contrast, the saliency-based approaches only select one best-matched patch for each probe patch. (3) Our approach introduces a global constraint to control the patch-wise matching result while the patch

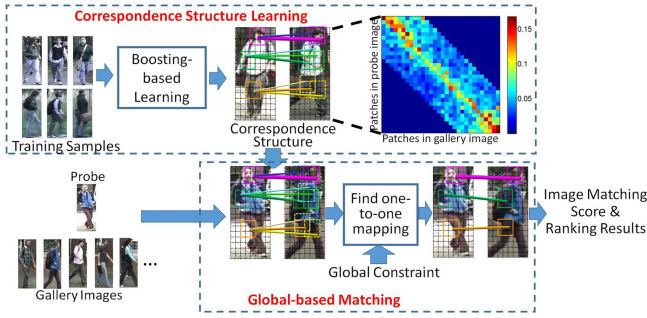


Fig. 2. Framework of the proposed approach.

matching result in saliency-based methods is locally decided by choosing the best matched within a neighborhood set.

Besides patch-based approaches, some other methods are also proposed which aim to simultaneously find discriminative features and handle the spatial misalignment problem. In [35], the correspondence relationship between images is captured by a hierarchical matching process integrated in an end-to-end deep learning framework. In [36], [37], image-wise similarities are measured by kernelized visual word co-occurrence matrices where a latent spatial kernel is integrated to handle spatial displacements. Since these methods give more weights on small displacements and less weights on large displacements, they are more suitable to handle spatial misalignments with relatively small displacements and may have limitations for very large displacements.

III. OVERVIEW OF THE APPROACH

The framework of our approach is shown in Fig. 2. During the training process, which is detailed in Section V, we present a boosting-based process to learn the correspondence structure between the target camera pair. During the prediction stage, which is detailed in Section IV, given a probe image and a set of gallery images, we use the correspondence structure to evaluate the patch correlations between the probe image and each gallery image, and find the optimal one-to-one mapping between patches, and accordingly the matching score. The Re-ID result is achieved by ranking gallery images according to their matching scores.

IV. PERSON RE-ID VIA CORRESPONDENCE STRUCTURE

This section introduces the concept of correspondence structure, show the scheme of computing the patch correlation using the correspondence structure, and finally present the patch-wise mapping method to compute the matching score between the probe image and a gallery image.

A. Correspondence Structure

The correspondence structure, $\Theta_{A,B}$, encodes the spatial correspondence distribution between a pair of cameras, A and B . In our problem, we adopt a discrete distribution, which is a set of patch-wise matching probabilities, $\Theta_{A,B} = \{P_{i,B}\}_{i=1}^{N_A}$, where N_A is the number of patches of an image in camera A . $P_{i,B} = \{P_{i1}, P_{i2}, \dots, P_{iN_B}\}$ describes the correspondence distribution in an image from camera B for

the i th patch x_i of an image captured from camera A , where N_B is the number of patches of an image in B . The illustrations of the correspondence distribution are shown on the top-right of Fig. 2.

The definition of the matching probabilities in the correspondence structure only depends on a camera pair and are independent of specific images. In the correspondence structure, it is possible that one patch in camera A is highly correlated to multiple patches in camera B , so as to handle human-pose variations and local viewpoint changes.

B. Patch Correlation

Given a probe image U in camera A and a gallery image V in camera B , the patch-wise correlation between U and V , $C(x_i, y_j)$ ($x_i \in U$, $y_j \in V$), is computed from both the correspondence structure between two cameras and the visual features:

$$C(x_i, y_j) = \lambda_{T_c}(P_{ij}) \cdot \log \Phi(\mathbf{f}_{x_i}, \mathbf{f}_{y_j}; x_i, y_j). \quad (1)$$

Here x_i and y_j are i th and j th patch in images U and V ; \mathbf{f}_{x_i} and \mathbf{f}_{y_j} are the feature vectors for x_i and y_j , respectively. P_{ij} is the correspondence structure between U and V . $\lambda_{T_c}(P_{ij}) = 1$, if $P_{ij} > T_c$, and 0 otherwise, and $T_c = 0.05$ is a threshold. $\Phi(\mathbf{f}_{x_i}, \mathbf{f}_{y_j}; x_i, y_j)$ is the correspondence-structure-controlled similarity between x_i and y_j ,

$$\Phi(\mathbf{f}_{x_i}, \mathbf{f}_{y_j}; x_i, y_j) = \Phi_{ij}(\mathbf{f}_{x_i}, \mathbf{f}_{y_j})P_{ij}, \quad (2)$$

where $\Phi_{ij}(\mathbf{f}_{x_i}, \mathbf{f}_{y_j})$ is the similarity between x_i and y_j .

The correspondence structure P_{ij} in Equations 1 and 2 is used to adjust the appearance similarity $\Phi_{ij}(\mathbf{f}_{x_i}, \mathbf{f}_{y_j})$ such that a more reliable patch-wise correlation strength can be achieved. The thresholding term $\lambda_{T_c}(P_{ij})$ is introduced to exclude the patch-wise correlation with a low correspondence probability, which effectively reduces the interferences from mismatched patches with similar appearance.

The patch-wise appearance similarity $\Phi_{ij}(\mathbf{f}_{x_i}, \mathbf{f}_{y_j})$ in Eq. 2 can be achieved by many off-the-shelf methods [14], [29], [38]. In this paper, we extract Dense SIFT and Dense Color Histogram [14] from each patch and utilize the KISSME metric [7] as the basic distance metric to compute $\Phi_{ij}(\mathbf{f}_{x_i}, \mathbf{f}_{y_j})$. Note that in order to achieve better performance [33], we learn multiple metrics so as to adaptively model the local patch-wise correlations at different locations. Specifically, we train an independent KISSME metric Φ_{ij} for each set of patch-pair locations $\{x_i, y_j\}$. Besides, it should also be noted that both the feature extraction and distance metric learning parts can be replaced by other state-of-the-art methods. For example, in the experiments in Section VII, we also show the results by replacing KISSME with the kLFDA [8] and KMFA- R_{χ^2} [39] metrics to demonstrate the effectiveness of our approach.

C. Patch-Wise Mapping

After obtaining the alignment-enhanced correlation strength $C(x_i, y_j)$, we can find a best-matched patch in image V for each patch in U and herein calculate the final image matching score. To compute $C(x_i, y_j)$ of testing image pairs, we only consider the potential matching patches within a searching

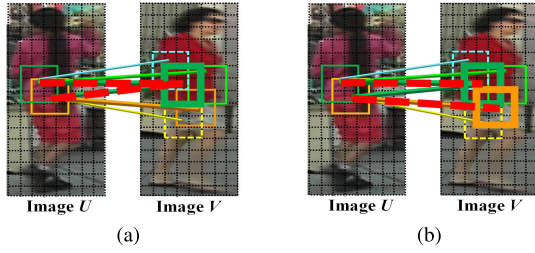


Fig. 3. Patch matching result (a) by locally finding the largest correlation strength $C(x_i, y_j)$ for each patch and (b) by using a global constraint. The red dashed lines indicate the final patch matching results and the colored solid lines are the matching probabilities in the correspondence structure. (Best viewed in color).

range $\mathbf{R}(x_i)$ around the chosen probe patch x_i . That is, $\mathbf{R}(x_i) = \{y_j | d(y_i, y_j) < T_d\}$, where y_i is x_i 's co-located patch in camera B , $d(y_i, y_j)$ is the distance between patches y_i and y_j (cf. Eq. 6), and $T_d = 32$ in this paper. However, locally finding the largest $C(x_i, y_j)$ may still create mismatches among patch pairs with high matching probabilities. For example, Fig. 3a shows an image pair U and V containing different people. When locally searching for the largest $C(x_i, y_j)$, the yellow patch in U will be mismatched to the bold-green patch in V since they have both large appearance similarity and high matching probability. This mismatch unsuitably increases the matching score between U and V .

To address this problem, we introduce a global one-to-one mapping constraint and solve the resulting linear assignment task [40] to find the best matching:

$$\Omega_{U,V}^* = \arg \max_{\Omega_{U,V}} \sum_{\{x_i, y_j\} \in \Omega_{U,V}} C(x_i, y_j) \quad (3)$$

s.t. $x_i \neq x_s, y_j \neq y_t \quad \forall \{x_i, y_j\}, \{x_s, y_t\} \in \Omega_{U,V}$

where $\Omega_{U,V}^*$ is the set of the best patch matching result between images U and V . $\{x_i, y_j\}$ and $\{x_s, y_t\}$ are two matched patch pairs in Ω . According to Eq. 3, we want to find the best patch matching result $\Omega_{U,V}^*$ that maximizes the total image matching score

$$\psi_{U,V} = \sum_{\{x_i, y_j\} \in \Omega_{U,V}} C(x_i, y_j), \quad (4)$$

given that each patch in U can only be matched to one patch in V and vice versa.

Eq. 3 can be solved by the Hungarian method [40]. Fig. 3b shows an example of the patch matching result by Eq. 3. From Fig. 3b, it is clear that by the inclusion of a global constraint, local mismatches can be effectively reduced and a more reliable image matching score can be achieved. Based on the above process, we can calculate the image matching scores ψ between a probe image and all gallery images in a cross-view camera, and rank the gallery images accordingly to achieve the final Re-ID result [13].

V. CORRESPONDENCE STRUCTURE LEARNING

A. Objective Function

Given a set of probe images $\{U_\alpha\}$ from camera A and their corresponding cross-view images $\{V_\beta\}$ from camera B in the

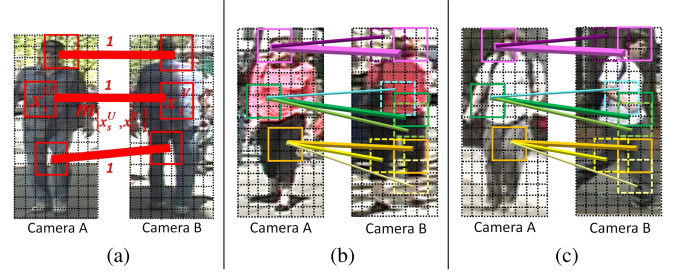


Fig. 4. (a): An example of binary mapping structure (the red lines with weight 1 indicate that the corresponding patches are connected). (b)-(c): Examples of the correspondence structures learned by our approach for the VIPeR [41] data. The line widths in (b)-(c) are proportional to the patch-wise probability values. (Best viewed in color).

training set, we learn the optimal correspondence structure $\Theta_{A,B}^*$ between cameras A and B so that the correct match image is ranked before the incorrect match images in terms of the matching scores. The formulation is:

$$\min_{\Theta_{A,B}} \sum_{U_\alpha} R(V_{\alpha'}; \psi_{U_\alpha, V_{\alpha'}}(\Theta_{A,B}), \Psi_{U_\alpha, V_{\beta \neq \alpha'}}(\Theta_{A,B})), \quad (5)$$

in which $V_{\alpha'}$ is the correct match gallery image of the probe image U_α . $\psi_{U_\alpha, V_{\alpha'}}(\Theta_{A,B})$ (as computed from Eq. 4) is the matching score between U_α and $V_{\alpha'}$ and $\Psi_{U_\alpha, V_{\beta \neq \alpha'}}(\Theta_{A,B})$ is the set of matching scores of all incorrect matches. $R(V_{\alpha'}; \psi_{U_\alpha, V_{\alpha'}}(\Theta_{A,B}), \Psi_{U_\alpha, V_{\beta \neq \alpha'}}(\Theta_{A,B}))$ is the rank of $V_{\alpha'}$ among all the gallery images according to the matching scores. Intuitively, the penalty is the smallest if the rank is 1, i.e., the matching score of $V_{\alpha'}$ is the greatest.

According to Eq. 5, the correspondence structure that can achieve the best Re-ID result on the training set will be selected as the optimal correspondence structure. However, the optimization is not easy as the matching score (Eq. 4) is complicated. We present an approximate solution, a boosting-based process, to solve this problem, which utilizes an iterative update process to gradually search for better correspondence structures fitting Eq. 5.

B. Boosting-Based Learning

The boosting-based approach utilizes a progressive way to find the best correspondence structure with the help of *binary mapping structures*. A binary mapping structure is similar to the correspondence structure except that it simply uses 0 or 1 instead of matching probabilities to indicate the connectivity or linkage between patches, cf. Fig. 4a. It can be viewed as a simplified version of the correspondence structure which includes rough information about the cross-view correspondence pattern.

Since binary mapping structures only include simple connectivity information among patches, their optimal solutions are tractable for individual probe images. Therefore, by searching for the optimal binary mapping structures for different probe images and using them to progressively update the correspondence structure, suitable cross-view correspondence patterns can be achieved.

The entire boosting-based learning process can be describe by the following steps, which are summarized in Algorithm 1.

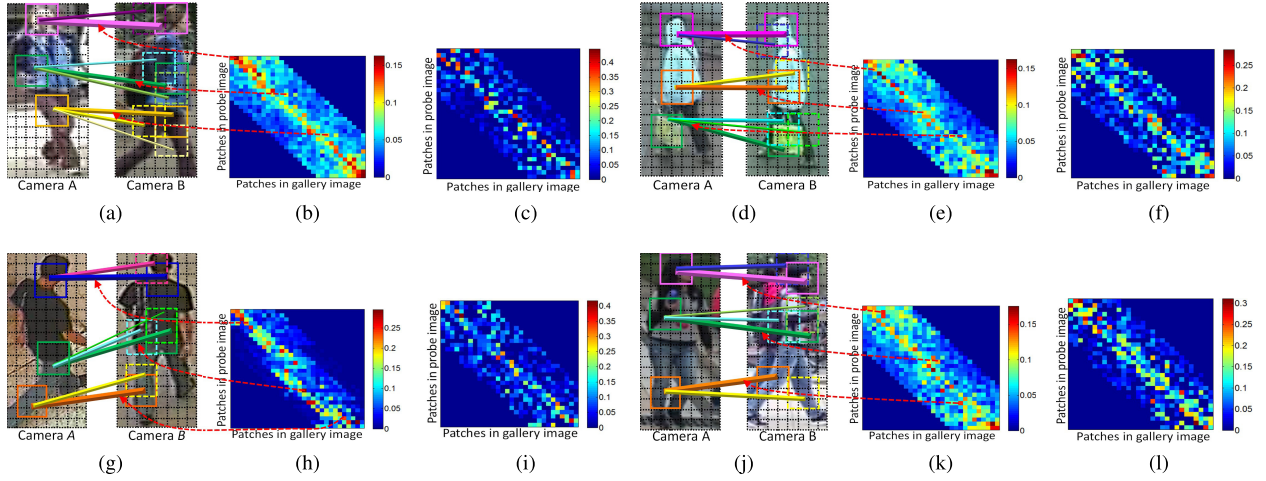


Fig. 5. The learned correspondence structures for various datasets. (a, d, g, j): The correspondence structures learned by our approach (with the KISSME metric) for the VIPeR [41], PRID 450S [9], 3DPeS [43], and SYSU-sReID [44] datasets, respectively (the correspondence structure for our ROAD dataset is shown in Figure 1). The line widths are proportional to the patch-wise probability values. (b, e, h, k): The complete correspondence structure matrices of (a, d, g, j) learned by our approach. (c, f, i, l): The correspondence structure matrices of (a, d, g, j)’s dataset obtained by the simple-average method. (Patches in (b, e, h, k) and (c, f, i, l) are organized by a row-first scanning order. All the correspondence structure matrices are down-sampled for a clearer illustration of the correspondence pattern). (Best viewed in color).

Algorithm 1 Boosting-Based Learning Process

Input: A set of training probe images $\{U_\alpha\}$ from camera A and their corresponding cross-view images $\{V_\beta\}$ from camera B

Output: $\Theta_{A,B} = \{P_{ij}\}$, the correspondence structure between $\{U_\alpha\}$ and $\{V_\beta\}$

- 1: Find an optimal binary mapping structure M_α for each probe image U_α , as described in Sec V-B
- 2: Set $k = 1$. Initialize P_{ij}^0 by Eq. 6.
- 3: Use the previous correspondence structure $\{P_{ij}^{k-1}\}$ to perform Re-ID on $\{U_\alpha\}$ and $\{V_\beta\}$, and select 20 binary mapping structures M_α based on the Re-ID result, as described in Sec V-B
- 4: Compute updated matching probability \hat{P}_{ij}^k by Eq. 7
- 5: Compute new candidate correspondence structure $\{\tilde{P}_{ij}^k\}$ by Eq. 13
- 6: Use $\{\tilde{P}_{ij}^k\}$ to calculate the Re-ID result on the training set by Eq. 5, and compare it with the result of the previous structure $\{P_{ij}^{k-1}\}$
- 7: If $\{\tilde{P}_{ij}^k\}$ has better Re-ID result than $\{P_{ij}^{k-1}\}$, set $\{P_{ij}^k\} = \{\tilde{P}_{ij}^k\}$; Otherwise, $\{P_{ij}^k\} = \{P_{ij}^{k-1}\}$
- 8: Set $k = k + 1$ and go back to step 3 if not converged or not reaching the maximum iteration number
- 9: Output $\{P_{ij}\}$

1) *Finding the Optimal Binary Mapping Structure:* For each training probe image U_α , we aim to find the optimal binary mapping structure M_α such that the rank order of U_α ’s correct match image $V_{\alpha'}$ is minimized under M_α . In order to reduce the computation complexity of finding M_α , we introduce an approximate strategy. Specifically, we first create multiple candidate binary mapping structures under different searching ranges (from 26 to 32) by adjacency-constrained search [14], and then select the one which minimizes the rank order of $V_{\alpha'}$ and use it as the approximated optimal binary mapping structure M_α . Note that we find one optimal binary mapping structure for each probe image such that the obtained binary mapping structures can include local cross-view correspondence clues in different training samples.

2) *Correspondence Structure Initialization:* In this paper, patch-wise matching probabilities P_{ij} in the correspondence structure are initialized by:

$$P_{ij}^0 \propto \begin{cases} 0, & \text{if } d(y_i, y_j) \geq T_d \\ \frac{1}{d(y_i, y_j) + 1}, & \text{otherwise,} \end{cases} \quad (6)$$

where y_i is x_i ’s co-located patch in camera B , such as the two blue patches in Fig. 5g. $d(y_i, y_j)$ is the distance between patches y_i and y_j which is used to measure the distance between patches x_i and y_j from two different images. The distance $d(y_i, y_j)$ is defined as the number of strides to move from y_i to y_j (i.e., the ℓ_1 distance). We use $d(y_i, y_j) + 1$ to avoid dividing by zero. T_d is a threshold which is set to be 32 in this paper. According to Eq. 6, a patch pair whose patches are located close to each other (i.e., small $d(y_i, y_j)$) will be initialized with a large P_{ij}^0 value. On the contrary, patch pairs with large patch-wise distances will be initialized with small P_{ij}^0 values. Moreover, if patches in a patch pair have extremely large distance (i.e., $d(y_i, y_j) \geq T_d$), we will simply set their corresponding matching probability to be 0.

3) *Binary Mapping Structure Selection:* During each iteration k in the learning process, we first apply correspondence structure $\Theta_{A,B}^{k-1} = \{P_{ij}^{k-1}\}$ from the previous iteration to calculate the rank orders of all correct match images $V_{\alpha'}$ in the training set. Then, we randomly select 20 $V_{\alpha'}$ where half of them are ranked among top 50% (implying better Re-ID results) and another half are ranked among the last 50% (implying worse Re-ID results). Finally, we extract binary mapping structures corresponding to these selected images and use them to update and boost the correspondence structure.

Note that we select binary mapping structures for both high- and low-ranked images in order to include a variety of local patch-wise correspondence patterns. In this way, the final obtained correspondence structure can suitably handle the variations in human-pose or local viewpoints.

4) *Calculating the Updated Matching Probability*: With the introduction of the binary mapping structure \mathbf{M}_α , we can model the updated matching probability in the correspondence structure by combining the estimated matching probabilities from multiple binary mapping structures:

$$\hat{P}_{ij}^k = \sum_{\mathbf{M}_\alpha \in \Gamma^k} \hat{P}(x_i, y_j | \mathbf{M}_\alpha) \cdot P(\mathbf{M}_\alpha), \quad (7)$$

where \hat{P}_{ij}^k is the updated matching probability between patches x_i and y_j in the k -th iteration. $\hat{P}(x_i, y_j | \mathbf{M}_\alpha)$ is the estimated matching probability between x_i and y_j when including the local correspondence pattern information of binary mapping structure \mathbf{M}_α . Γ^k is the set of binary mapping structures selected in the k -th iteration. $P(\mathbf{M}_\alpha) = \frac{\tilde{\mathcal{R}}_n(\mathbf{M}_\alpha)}{\sum_{\mathbf{M}_y \in \Gamma^k} \tilde{\mathcal{R}}_n(\mathbf{M}_y)}$ is the prior probability for binary mapping structure \mathbf{M}_α , where $\tilde{\mathcal{R}}_n(\mathbf{M}_\alpha)$ is the CMC score at rank n [42] when using \mathbf{M}_α as the correspondence structure to perform person Re-ID over the training images. n is set to be 5 in our experiments. Similar to $C(x_i, y_j)$, when calculating matching probabilities, we only consider patch pairs whose distances are within a range (cf. Eq. 6), while probabilities for other patch pairs are simply set to 0.

According to Eq. 7, the updated matching probability \hat{P}_{ij}^k is calculated by integrating the estimated matching probability under different binary mapping structures (i.e., $\hat{P}(x_i, y_j | \mathbf{M}_\alpha)$). Moreover, binary mapping structures that have better Re-ID performances (i.e., larger $P(\mathbf{M}_\alpha)$) will have more impacts on the updated matching probability result.

$\hat{P}(x_i, y_j | \mathbf{M}_\alpha)$ in Eq. 7 is further calculated by combining a correspondence strength term and a patch importance term:

$$\hat{P}(x_i, y_j | \mathbf{M}_\alpha) = \hat{P}(y_j | x_i, \mathbf{M}_\alpha) \cdot \hat{P}(x_i | \mathbf{M}_\alpha), \quad (8)$$

in which $\hat{P}(y_j | x_i, \mathbf{M}_\alpha)$ is the correspondence strength term reflecting the correspondence strength from x_i to y_j when including \mathbf{M}_α . $\hat{P}(x_i | \mathbf{M}_\alpha)$ is the patch importance term reflecting the impact of \mathbf{M}_α to patch x_i . $\hat{P}(y_j | x_i, \mathbf{M}_\alpha)$ is calculated as

$$\hat{P}(y_j | x_i, \mathbf{M}_\alpha) \propto \begin{cases} 1, & \text{if } m_{ij} \in \mathbf{M}_\alpha \\ \tilde{\mathcal{A}}_{y_j | x_i, \mathbf{M}_\alpha}, & \text{otherwise,} \end{cases} \quad (9)$$

in which m_{ij} is a patch-wise link connecting x_i and y_j . $\tilde{\mathcal{A}}_{y_j | x_i, \mathbf{M}_\alpha} = \frac{\bar{\Phi}_{ij}(x_i, y_j)}{\sum_{y_t, m_{it} \in \mathbf{M}_\alpha} \bar{\Phi}_{it}(x_i, y_t)}$, where $\bar{\Phi}_{ij}(x_i, y_j)$ is the average appearance similarity [7], [14] between patches x_i and y_j over all correct match image pairs in the training set. y_t is a patch that is connected to x_i in the binary mapping structure \mathbf{M}_α .

According to Eq. 8, given a specific binary mapping structure \mathbf{M}_α , the estimated matching probability $\hat{P}(x_i, y_j | \mathbf{M}_\alpha)$ between a probe patch x_i and a gallery patch y_j is calculated by jointly considering the importance of the probe patch x_i under \mathbf{M}_α (i.e., $\hat{P}(x_i | \mathbf{M}_\alpha)$) and the correspondence strength from the probe patch x_i to the gallery patch y_j under \mathbf{M}_α (i.e., $\hat{P}(y_j | x_i, \mathbf{M}_\alpha)$).

Moreover, from Eq. 9, $\hat{P}(y_j | x_i, \mathbf{M}_\alpha)$ is mainly decided by the relative appearance similarity strength between patch

pair $\{x_i, y_j\}$ and all patch pairs which are connected to x_i in the binary mapping structure \mathbf{M}_α . This enables patch pairs with larger appearance similarities to have stronger correspondences. Besides, we also include a constraint that $\hat{P}(y_j | x_i, \mathbf{M}_\alpha)$'s value will be the largest (equal to 1) if the binary mapping structure \mathbf{M}_α includes a link between x_i and y_j . In this way, we are able to bring \mathbf{M}_α 's impact into full play when estimating the matching probabilities under it.

Furthermore, the probe patch importance probability $\hat{P}(x_i | \mathbf{M}_\alpha)$ in Eq. 8 can be further calculated by accumulating the impact of each individual link in \mathbf{M}_α on patch x_i :

$$\hat{P}(x_i | \mathbf{M}_\alpha) = \sum_{m_{st} \in \mathbf{M}_\alpha} \hat{P}(x_i | m_{st}, \mathbf{M}_\alpha) \cdot \hat{P}(m_{st} | \mathbf{M}_\alpha), \quad (10)$$

where m_{st} is a patch-wise link in \mathbf{M}_α , as the red lines in Fig. 4a. $\hat{P}(m_{st} | \mathbf{M}_\alpha)$ is the importance probability of link m_{st} which is defined similar to $P(\mathbf{M}_\alpha)$:

$$\hat{P}(m_{st} | \mathbf{M}_\alpha) = \frac{\tilde{\mathcal{R}}_n(m_{st})}{\sum_{m_{hg} \in \mathbf{M}_\alpha} \tilde{\mathcal{R}}_n(m_{hg})}, \quad (11)$$

where $\tilde{\mathcal{R}}_n(m_{st})$ is the rank- n CMC score [42] when only using a single link m_{st} as the correspondence structure to perform Re-ID. $\hat{P}(x_i | m_{st}, \mathbf{M}_\alpha)$ in Eq. 10 is the impact probability from link m_{st} to patch x_i , defined as:

$$\hat{P}(x_i | m_{st}, \mathbf{M}_\alpha) \propto \begin{cases} 0, & \text{if } d(x_i, x_s) \geq T_d \\ \frac{1}{d(x_i, x_s) + 1}, & \text{otherwise} \end{cases} \quad (12)$$

where x_s is link m_{st} 's end patch in camera A. $d(\cdot)$ and T_d are the same as in Eq. 6.

According to Eq. 10, a probe patch x_i 's importance probability $\hat{P}(x_i | \mathbf{M}_\alpha)$ under \mathbf{M}_α is calculated by integrating the impact probability $\hat{P}(x_i | m_{st}, \mathbf{M}_\alpha)$ from each individual link in \mathbf{M}_α to x_i . Since $\hat{P}(x_i | m_{st}, \mathbf{M}_\alpha)$ is modeled by the distance between link m_{st} and x_i (cf. Eq. 12), it enables patches that are closer to the links in \mathbf{M}_α to have larger importance probabilities. Moreover, Eq. 11 further guarantees links with better Re-ID performances (i.e., larger $\hat{P}(m_{st} | \mathbf{M}_\alpha)$) to have more impacts on the calculated importance probability $\hat{P}(x_i | \mathbf{M}_\alpha)$.

5) *Correspondence Structure Update*: After obtaining the updated matching probability \hat{P}_{ij}^k in Eq. 7, we can calculate matching probabilities of the new candidate correspondence structure $\{\tilde{P}_{ij}^k\}$ by:

$$\tilde{P}_{ij}^k = (1 - \varepsilon)P_{ij}^{k-1} + \varepsilon\hat{P}_{ij}^k, \quad (13)$$

where P_{ij}^{k-1} is the matching probability in iteration $k - 1$. ε is the update rate which is set 0.2 in our paper.

In order to guarantee that the boosting-based learning approach keeps optimizing Eq. 5 during the iteration process, an evaluation module is further included to decide whether to accept the new candidate correspondence structure $\{\tilde{P}_{ij}^k\}$. Specifically, we use $\{\tilde{P}_{ij}^k\}$ to calculate the Re-ID result on the training set by Eq. 5, and compare it with the Re-ID result of the previous structure $\{P_{ij}^{k-1}\}$. If $\{\tilde{P}_{ij}^k\}$ has better Re-ID result than $\{P_{ij}^{k-1}\}$, we will select $\{\tilde{P}_{ij}^k\}$ as the correspondence

structure in the k -th iteration (i.e., $\{P_{ij}^k\} = \{\tilde{P}_{ij}^k\}$); Otherwise, we will still keep the correspondence structure in the previous iteration (i.e., $\{P_{ij}^k\} = \{P_{ij}^{k-1}\}$).

From Equations 7–13, our update process integrates multiple variables (i.e., binary mapping structure, individual links, patch-link correlation) into a unified probability framework. In this way, various information cues that affect the objective function in Equation 5 (such as appearances, ranking results, and patch-wise correspondence patterns) can be effectively included, such that suitable candidate correspondence structures for the objective function can be created during the iterative model updating process. Therefore, by selecting the best structure among these candidate structures (with the evaluation module), a satisfactory correspondence structure can be obtained.

Figures 1, 4, and 5 show some examples of the correspondence structures learned from different cross-view datasets. From these figures, we can see that the correspondence structures learned by our approach can suitably indicate the matching correspondence between spatial misaligned patches. For example, in Figures 5g–5h, the large lower-to-upper misalignment between cameras is effectively captured. Besides, the matching probability values in the correspondence structure also indicate the correlation strengths between patch pairs, which are displayed as the colored blocks in Figures 5b, 5e, 5h and 5k.

Furthermore, comparing Figures 1a and 1b, we can see that human-pose variation is also suitably handled by the learned correspondence structure. More specifically, although images in Fig. 1 have different human poses, patches of camera A in both figures can correctly find their corresponding patches in camera B since the one-to-many matching probability graphs in the correspondence structure suitably embed the local correspondence variation between cameras. Similar observations can also be obtained from Figures 4b and 4c.

VI. EXTENDING THE APPROACH WITH MULTIPLE CORRESPONDENCE STRUCTURES

As mentioned before, since people often show different poses inside a camera view, the spatial correspondence pattern between a camera pair can be further divided and modeled by a set of sub-patterns according to these pose variations. Therefore, we extend our approach by introducing a multi-structure scheme, which first learns a set of local correspondence structures to capture various spatial correspondence sub-patterns between a camera pair, and then adaptively selects suitable correspondence structures to handle the spatial misalignments between individual images.

Fig. 6 shows our extended person Re-ID framework with multiple correspondence structures. During the training stage, we first divide images in each camera into different pose groups, where images in each pose group includes people with similar poses. Then, we construct a set of pose-group pairs. Each pose-group pair is composed of two pose groups from different cameras and reflects one spatial correspondence sub-pattern between cameras. Finally, we apply our boosting-based learning process over the constructed pose-group pairs

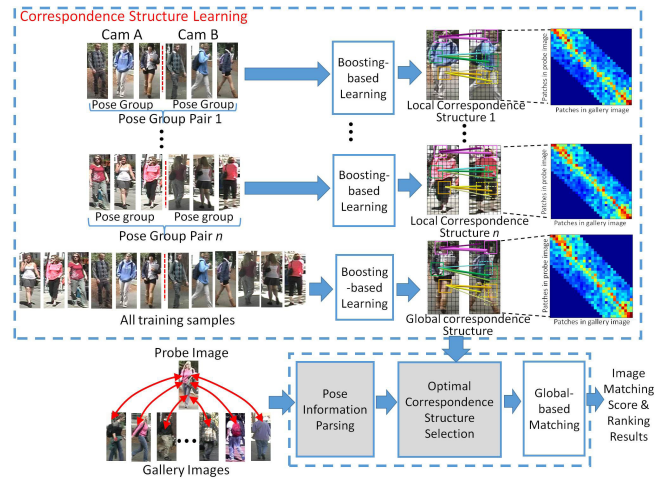


Fig. 6. Framework of the proposed approach with multiple correspondence structures.

and obtain a set of local correspondence structures to capture the correspondence sub-patterns between a camera pair.

During the prediction stage, we parse the human pose information for each pair of images being matched, and adaptively select the optimal correspondence structure to calculate the image-wise matching score for person Re-ID. More specifically, for a pair of test images (a probe image and a gallery image), we first parse the human pose information for both images [45] and classify them into their closest pose groups, respectively. Then, we are able to identify the pose-group pair for the test images and use its corresponding correspondence structure as the optimal structure for image matching.

Moreover, the following settings need to be mentioned about our multi-structure scheme in Fig. 6.

- 1) During the prediction stage, since we only need to obtain a rough estimation of human poses (e.g., differentiate front pose, side pose, or back pose), we utilize a simple but effective method which parses human pose from his/her head orientations. Specifically, we first utilize semantic region parsing [45] to obtain head and hair regions from a test image. Then, we construct a feature vector including the size and relative location information of head and hair regions, and apply a linear SVM [46] to classify this feature vector into one of the pose groups. According to our experiments, this method can achieve satisfactory (over 90%) pose classification accuracy on the datasets in our experiments. Note that our framework is general, and in practice, more sophisticated pose estimation methods [34], [47], [48] can be included to handle pose information parsing under more complicated scenarios.
- 2) During the training stage, we utilize two ways to divide pose groups & pose group pairs: (1) Defining and dividing pose groups & pose group pairs manually; (2) Dividing pose groups & pose group pairs automatically, where we first cluster training images [49] in each camera into a set of pose groups (using the same feature vector as described in point 1), and then form camera-wise pose group pairs based on the pose group set

including the largest number of pose groups. Note that in order to automatically decide the number of clusters, we utilize a spectral clustering scheme [49] which is able to find the optimal cluster number by integrating a clustering-coherency metric to evaluate the results under different cluster numbers. Since the automatic pose group pair division scheme can properly catch the major pose correspondence patterns between a camera pair, it can also achieve satisfactory performances. Experimental results show that methods with this automatic pose group pair division scheme can achieve similar Re-ID results to the ones with manual pose group pair division (cf. Section VII-C).

- 3) Note that in Fig. 6, besides the *local* correspondence structures learned from pose-group pairs, we also construct a *global* correspondence structure learned from all training images (cf. Fig. 2). Thus, if a test image pair cannot find suitable local correspondence structure (e.g., a test image cannot be confidently classified into any pose group, or the correspondence structure of a specific pose-group pair is not constructed due to limited training samples), this global correspondence structure will be applied to calculate the matching score of this test image pair.

VII. EXPERIMENTAL RESULTS

A. Datasets and Experimental Settings

We perform experiments on the following five datasets:

1) *VIPeR*: The VIPeR dataset [41] is a commonly used dataset which contains 632 image pairs for 632 pedestrians, as in Figures 4a-4c and 8d. It is one of the most challenging datasets which includes large differences in viewpoint, pose, and illumination between two camera views. Images from camera *A* are mainly captured from 0 to 90 degree while camera *B* mainly from 90 to 180 degree.

2) *PRID 450S*: The PRID 450S dataset [9] consists of 450 person image pairs from two non-overlapping camera views. Some example images in PRID 450S dataset are shown in Fig. 5d. It is also challenging due to low image qualities and viewpoint changes.

3) *3DPeS*: The 3DPeS dataset [43] is comprised of 1012 images from 193 pedestrians captured by eight cameras, where each person has 2 to 26 images, as in Figures 5g and 8a. Note that since there are eight cameras with significantly different views in the dataset, in our experiments, we group cameras with similar views together and form three camera groups. Then, we train a correspondence structure between each pair of camera groups. Finally, three correspondence structures are achieved and utilized to calculate Re-ID performance between different camera groups. For images from the same camera group, we simply utilize adjacency-constrained search [14] to find patch-wise mapping and calculate the image matching score accordingly.

4) *Road*: The Road dataset is our own constructed dataset which includes 416 image pairs taken by two cameras with camera *A* monitoring an exit region and camera *B* monitoring

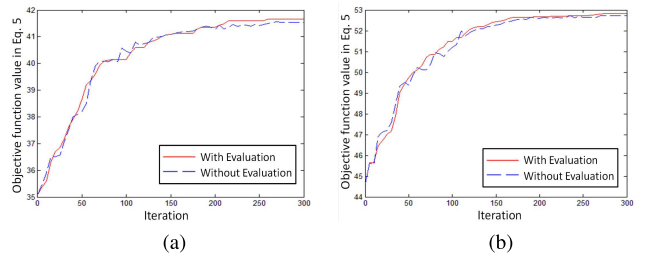


Fig. 7. The convergence curves when using our learning approach to find the correspondence structure in the VIPeR and SYSU datasets. (y-axis: the value of the objective function in Eq. 5 when using the correspondence structure in a certain iteration; x-axis: the iteration number. Red solid curve: our learning approach with the evaluation module; Blue dashed curve: our learning approach without the evaluation module) (Best viewed in color). (a) VIPeR dataset. (b) SYSU dataset.

a road region, as in Figures 1 and 8g.¹ This dataset has large variation of human pose and camera angle. Images in this dataset are taken from a realistic crowd road scene.

5) *SYSU-sReID*: The SYSU-sReID dataset [44] contains 502 individual pairs taken by two disjoint cameras in a campus environment, as in Fig. 5k. This dataset includes more cross-camera pose correspondence patterns.

For all of the above datasets, we follow previous methods [2], [5], [8] and perform experiments under 50%-training and 50%-testing. All images are scaled to 128×48 . The patch size in our approach is 24×18 . The stride size between neighboring patches is 6 horizontally and 8 vertically for probe images, and 3 horizontally and 4 vertically for gallery images. Note that we use smaller stride size in gallery images in order to obtain more patches. In this way, we can have more flexibilities during patch-wise matching.

Furthermore, in order to save computation complexity, we make the following simplifications on the learning process during our experiments:

- 1) The global constraint in Eq. 3 is not applied in the training stage (cf. step 3 in Algorithm 1). Our experiments show that skipping the global constraint in training does not affect the final Re-ID results too much.
- 2) The evaluation module (cf. step 7 in Algorithm 1) is also skipped in the training stage, i.e., we directly use $\{\tilde{P}_{ij}^k\}$ in Eq. 13 to be the correspondence structure in the k -th iteration without evaluating whether it is better than $\{P_{ij}^{k-1}\}$. Our experiments show that our learning process without the evaluation module can achieve similar Re-ID results to the one including the evaluation module while still obtaining stable correspondence structures within 300 iterations. For example, Fig. 7 shows the convergence curves when using our learning approach to find the correspondence structure in the VIPeR and SYSU datasets. We can see that our learning approach without the evaluation module (the blue dashed curves) can achieve stable results after 270 iterations, which is similar to the one including the evaluation module (the red solid curves).

¹Available at <http://wylin2.drivehq.com>



Fig. 8. Comparison of different patch mapping methods. Left column: the adjacency-constrained method; Middle column: the simple-average method; Last column: our approach (with the KISSME metric). The solid lines represent matching probabilities in a correspondence structure and the red-dashed lines represent patch matching results. Note that the image pair in (a)-(c) includes the same person (i.e., correct match) while the image pairs in (d)-(l) include different people (i.e., wrong match). (Best viewed in color).

B. Results of Using a Single Correspondence Structure

We first evaluate the performance of our approach by using a single correspondence structure to handle the spatial misalignments between a camera pair (cf. Fig. 2). Note that although multiple correspondence structures are used to handle the view differences among the 8 cameras in the 3DPeS dataset (cf. Section VII-A), we only use one correspondence structure for each camera pair. Therefore, it also belongs to the situation of using a single correspondence structure.

1) *Patch Matching Performances*: We compare the patch matching performance of three methods: (1) The adjacency-constrained search method [14], [15], [29] which finds a best matched patch for each patch in a probe image (probe patch) by searching a fixed neighborhood region around the probe patch's co-located patch in a gallery image (*Adjacency-constrained*). (2) The simple-average method which simply averages the binary mapping structures for different probe images (as in Fig. 4a) to be the correspondence structure and combines it with a global constraint to find the best one-to-one patch matching result (*Simple-average*). (3) Our approach which employs a boosting-based process to learn the correspondence structure and combines it with a global constraint to find the best one-to-one patch matching result.

Fig. 8 shows the patch mapping results of different methods, where solid lines represent matching probabilities in

a correspondence structure and red-dashed lines represent patch matching results. Besides, Figures 5b, 5e, 5h, 5k and Figures 5c, 5f, 5i, 5l also show the correspondence structure matrices obtained by our approach and the simple-average method, respectively. From Figures 5 and 8, we can observe:

- 1) Since the adjacency-constrained method searches a fixed neighborhood region without considering the correspondence pattern between cameras, it may easily be interfered by wrong patches with similar appearances in the neighborhood (cf. Figures 8d, 8g, 8j). Comparatively, with the indicative matching probability information in the correspondence structure, the interference from mismatched patches can be effectively reduced (cf. Figures 8f, 8i, 8l).
- 2) When there are large misalignments between cameras, the adjacency-constrained method may fail to find proper patches as the correct patches may be located outside the neighborhood region, as in Fig. 8a. Comparatively, the large misalignment pattern between cameras can be properly captured by our correspondence structure, resulting in a more accurate patch matching result (cf. Fig. 8c).
- 3) Comparing Figures 5b, 5e, 5h, 5k and Figures 5c, 5f, 5i, 5l with the last two columns in Fig. 8, it is obvious that the correspondence structures by our approach is better than the simple average method. Specifically, the correspondence structures by the simple average method include many unsuitable matching probabilities which may easily result in wrong patch matches. In contrast, the correspondence structures by our approach are more coherent with the actual spatial correspondence pattern between cameras. This implies that reliable correspondence structure cannot be easily achieved without suitably integrating the information cues between cameras.

Moreover, in order to further evaluate the effectiveness of our correspondence structure learning process, we also show the learned correspondence structures when using different distance metrics (KISSME [7], kLFDA [8], and KMFA- R_{χ^2} [39]) to measure the patch-wise similarity (cf. Eq. 2), as in Fig. 9. From Fig. 9, we see that our approach can effectively capture the overall spatial correspondence patterns under different distance metrics (e.g., the large lower-to-upper misalignments between cameras are properly captured by all the correspondence structures in Fig. 9).

2) *Performances of Person Re-ID*: We evaluate person Re-ID results by the standard Cumulated Matching Characteristic (CMC) curve [42] which measures the correct match rates within different Re-ID rank ranges. The evaluation protocols are the same as [5]. That is, for each dataset, we perform 10 randomly-partitioned 50%-training and 50%-testing experiments and average the results.

To verify the effectiveness of each module of our approach, we compare results of four methods: (1) Not applying correspondence structure and directly using the appearance similarity between co-located patches for person Re-ID, (*Non-structure*); (2) Simply averaging the binary mapping structures for different probe images as the correspondence structure

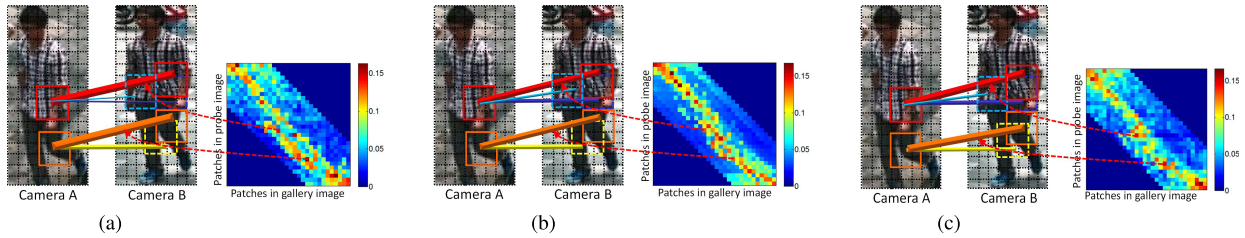


Fig. 9. Comparison of correspondence structures for the Road dataset when using different distance metrics (KISSME [7], kLFDA [8] and $KMFA-R_{\chi^2}$ [39]) to measure the patch-wise similarity. The line widths are proportional to the patch-wise probability values. (Best viewed in color). (a) the KISSME metric. (b) the kLFDA metric. (c) the $KMFA-R_{\chi^2}$ metric.

and utilizing it for Re-ID (*Simple-average*); (3) Using a correspondence structure where the correspondence probabilities for all neighboring patch-wise pairs are set as 1 (i.e., $P_{ij} = 1$, if $d(y_i, y_j) < T_d$ and $P_{ij} = 0$ otherwise, cf. Eq. 6), and applying a global constraint as Section IV-C to calculate image-wise similarity (*AC+global*); (4) Using the correspondence structure learned by our approach, but do not include global constraint when performing Re-ID (*Non-global*); (5) Our approach (*Proposed (Single)*).

Tables I–V show the CMC results of different methods under three distance metrics: KISSME [7], kLFDA [8], and $KMFA-R_{\chi^2}$ [39] (note that we use Dense SIFT and Dense Color Histogram features [14] for KISSME & kLFDA metrics, and use RGB, HSV, YCbCr, Lab, YIQ, 16 Gabor texture features [39] for $KMFA-R_{\chi^2}$ metric). From Tables I–V, we notice that:

- 1) Our approach has obviously improved results than the non-structure method. This indicates that proper correspondence structures can effectively improve Re-ID performances by reducing patch-wise misalignments.
- 2) The simple-average method has similar performance to the no-structure method. This implies that an inappropriate correspondence structure reduces the Re-ID performance.
- 3) The AC+global method can be viewed as an extended version of the adjacency-constrained search method [14], [15], [29] plus a global constraint. Compared with the AC+global method, our approach still achieves obviously better performance. This indicates that our correspondence structure has stronger capability in handling spatial misalignments than the adjacency-constrained search methods.
- 4) The non-global method has improved Re-ID performances than the non-structure method. This further demonstrates the effectiveness of the correspondence structure learned by our approach. Meanwhile, our approach also has superior performance than the non-global method. This demonstrates the usefulness of introducing global constraint in patch matching process.
- 5) The improvement of our approach is coherent on different distance metrics (KISSME [7], kLFDA [8], and $KMFA-R_{\chi^2}$ [39]). This indicates the robustness of our approach in handling spatial misalignments. In practice, our proposed correspondence structure can also be combined with other features or distance metrics to further improve Re-ID performances.

TABLE I
CMC RESULTS WITH DIFFERENT DISTANCE METRICS ON VIPeR DATASET

Rank (with KISSME)	1	5	10	20	30
Non-structure	27.5	57.0	73.7	83.9	87.7
Simple-average	28.5	57.9	74.1	84.2	88.3
AC+global	28.3	57.5	74.3	84.7	88.7
Non-global	30.8	62.7	77.5	88.9	91.7
Proposed (single)	34.8	68.7	82.3	91.8	94.9
Proposed (multi-manu)	35.3	69.8	83.8	92.2	94.5
Proposed (multi-auto)	35.1	69.5	83.5	92.2	95.1
Proposed (multi-GT)	35.5	70.3	84.3	92.7	95.3
Rank (with kLFDA)	1	5	10	20	30
Non-structure	31.5	64.9	79.4	89.2	92.4
Simple-average	30.3	64.4	77.3	89.4	91.7
AC+global	32.1	69.1	83.2	91.4	94.1
Non-global	33.8	69.3	81.5	90.3	93.2
Proposed (single)	35.2	69.7	83.5	91.9	94.5
Proposed (multi-manu)	36.4	71.4	84.5	92.2	94.8
Proposed (multi-auto)	36.1	71.2	84.2	92.0	94.5
Proposed (multi-GT)	36.4	71.7	84.2	91.7	94.1
Rank (with $KMFA-R_{\chi^2}$)	1	5	10	20	30
Non-structure	40.3	74.1	85.3	90.0	95.2
Simple-average	39.5	73.7	84.4	89.8	95.7
AC+global	40.8	74.8	86.1	90.8	96.3
Non-global	42.6	76.5	87.4	92.4	97.3
Proposed (single)	43.3	77.4	88.2	92.7	97.8
Proposed (multi-manu)	44.8	78.5	89.8	93.4	97.2
Proposed (multi-auto)	44.6	78.2	89.4	93.8	97.6
Proposed (multi-GT)	45.0	79.2	90.3	93.5	97.4

- 6) If comparing our approach (*proposed+single*) with the non-structure method, we can see that the improvement of our approach is the most significant on the Road dataset (cf. Table IV). This is because the Road dataset includes a large number of image pairs with significant spatial misalignments, and the effectiveness of our approach is particularly pronounced in this scenario.

C. Results of Using Multiple Correspondence Structures

We further evaluate the performance of our approach by using multiple structures to handle spatial misalignments (i.e., the multi-structure strategy described by Fig. 6). Note that since the number of pedestrians for each pose is small in the 3DPeS [43] dataset, which is insufficient to construct reliable local correspondences, we focus on evaluating our multi-structure strategy on the other four datasets: VIPeR [41], PRID 450S [9], Road, and SYSU-sReID [44].

1) *Results for Correspondence Structure Learning*: In this section, we evaluate the results of multiple correspondence

TABLE II
CMC RESULTS WITH DIFFERENT DISTANCE
METRICS ON PRID 450S DATASET

Rank (with KISSME)	1	5	10	20	30
No-structure	39.6	64.9	76.0	85.3	89.3
Simple-average	38.2	63.6	75.1	84.9	88.9
AC+global	40.5	66.3	76.3	87.8	90.4
No-global	42.7	69.3	78.2	87.4	91.1
Proposed (single)	44.4	71.6	82.2	89.8	93.3
Proposed (multi-manu)	45.8	72.8	82.8	90.3	93.4
Proposed (multi-auto)	45.6	72.5	82.4	90.3	93.5
Proposed (multi-GT)	46.1	73.3	83.3	90.7	93.8
Rank (with kLFDA)	1	5	10	20	30
No-structure	46.5	74.5	82.2	88.1	92.7
Simple-average	44.7	73.7	81.4	87.4	91.6
AC+global	47.7	75.4	82.7	88.9	92.5
No-global	49.3	76.5	84.3	89.6	93.3
Proposed (single)	51.1	77.7	85.1	91.2	94.4
Proposed (multi-manu)	52.9	79.3	86.2	92.2	95.0
Proposed (multi-auto)	52.7	78.8	85.7	91.8	94.8
Proposed (multi-GT)	53.2	79.0	86.9	92.7	95.6
Rank (with KMFA- $R_{\chi^2_2}$)	1	5	10	20	30
No-structure	57.8	79.0	87.3	92.8	96.2
Simple-average	57.3	78.5	86.7	92.6	95.8
AC+global	58.2	79.5	88.2	93.4	96.7
No-global	61.5	80.4	89.7	94.2	96.9
Proposed (single)	63.2	82.7	90.5	94.8	97.3
Proposed (multi-manu)	65.1	84.9	91.2	95.4	97.7
Proposed (multi-auto)	65.3	84.9	91.4	95.1	97.4
Proposed (multi-GT)	65.7	84.6	91.8	95.8	96.9

TABLE III
CMC RESULTS WITH DIFFERENT DISTANCE
METRICS ON 3DPeS DATASET

Rank (with KISSME)	1	5	10	15	20	30
No-structure	51.6	75.8	84.2	88.4	90.5	92.6
Simple-average	50.5	74.7	83.2	87.4	89.5	92.6
AC+global	52.4	76.0	85.3	88.7	90.8	92.4
No-global	54.7	77.9	87.4	90.5	91.6	93.7
Proposed (single)	57.9	81.1	89.5	92.6	93.7	94.7
Rank (with kLFDA)	1	5	10	15	20	30
No-structure	54.8	75.6	85.3	89.8	92.1	93.1
Simple-average	53.6	76.1	84.7	88.1	91.4	92.4
AC+global	55.5	76.3	85.8	90.1	92.4	93.3
No-global	57.6	78.3	87.4	91.4	92.9	93.8
Proposed (single)	60.3	82.4	89.3	92.3	93.6	94.3
Rank (with KMFA- $R_{\chi^2_2}$)	1	5	10	15	20	30
No-structure	56.6	78.5	86.2	90.4	92.2	93.3
Simple-average	55.7	77.8	85.8	90.2	92.4	93.1
AC+global	57.2	79.0	87.8	91.3	92.7	93.8
No-global	59.8	82.6	89.6	92.3	93.8	94.6
Proposed (single)	61.4	84.2	90.7	92.7	94.2	94.9

structure learning based on the manually divided pose group pairs. Similar results can be observed when automatic pose group pair division (cf. Section VI) is applied.

Since each of the VIPeR, PRID 450S, and Road dataset includes two major cross-view pose correspondences (e.g., front-to-right and front-to-back for VIPeR, and left-to-left and right-to-right for PRID 450S), we divide the training images in each dataset into two pose group pairs and construct two local correspondence structures from these pose group pairs. Comparatively, since more major cross-view pose correspondences are included in the SYSU-sReID dataset (i.e., left-to-left, right-to-right, front-to-side, and back-to-side), we further divide the training images in this dataset into four pose group pairs and construct four local correspondence structures accordingly.

TABLE IV
CMC RESULTS WITH DIFFERENT DISTANCE METRICS ON ROAD DATASET

Rank (with KISSME)	1	5	10	15	20	30
No-structure	50.5	80.3	87.0	91.3	94.2	95.7
Simple-average	49.0	81.7	90.4	92.8	95.7	96.2
AC+global	53.1	82.4	89.1	94.4	95.3	96.4
No-global	58.2	85.6	94.2	97.1	98.1	98.6
Proposed (single)	61.5	91.8	95.2	98.1	98.6	99.0
Proposed (multi-manu)	63.1	92.2	95.2	98.2	98.8	99.2
Proposed (multi-auto)	62.8	92.0	95.4	98.4	98.6	99.3
Proposed (multi-GT)	63.6	92.6	95.8	98.4	98.6	99.2
Rank (with kLFDA)	1	5	10	15	20	30
No-structure	58.6	87.6	92.4	94.8	96.7	97.4
Simple-average	56.9	85.8	91.8	93.6	95.4	96.2
AC+global	60.3	88.4	92.8	95.3	97.3	97.7
No-global	63.3	90.7	93.7	96.2	97.8	98.4
Proposed (single)	66.8	91.5	94.8	97.7	98.4	99.2
Proposed (multi-manu)	68.2	92.8	96.2	98.1	98.6	99.4
Proposed (multi-auto)	68.3	92.6	95.9	97.7	98.6	99.2
Proposed (multi-GT)	68.6	93.4	96.8	98.3	98.8	99.5
Rank (with KMFA- $R_{\chi^2_2}$)	1	5	10	15	20	30
No-structure	65.4	90.4	92.7	94.8	96.1	96.6
Simple-average	63.9	89.6	92.2	94.3	95.7	96.8
AC+global	66.0	91.2	93.4	95.2	96.4	96.8
No-global	68.1	92.1	94.3	95.9	96.7	97.2
Proposed (single)	71.4	92.5	95.6	96.3	97.1	97.8
Proposed (multi-manu)	73.1	92.8	96.4	97.2	97.8	98.6
Proposed (multi-auto)	72.8	92.8	96.0	96.8	97.4	98.3
Proposed (multi-GT)	73.5	93.3	96.8	97.5	98.2	99.0

TABLE V
CMC RESULTS WITH DIFFERENT DISTANCE
METRICS ON SYSU-sReID DATASET

Rank (with KISSME)	1	5	10	15	20	30
No-structure	33.5	70.1	80.0	83.4	88.8	92.8
Simple-average	32.3	68.9	78.9	82.6	87.6	91.2
AC+global	33.9	69.3	78.1	83.8	88.9	91.8
No-global	36.7	71.7	81.7	84.3	88.4	92.4
Proposed (single)	38.6	73.1	83.7	85.2	90.4	92.7
Proposed (multi-manu)	43.3	76.2	83.9	86.1	90.7	93.4
Proposed (multi-auto)	43.0	75.7	83.5	86.3	90.4	92.8
Proposed (multi-GT)	43.8	76.8	84.2	86.9	90.7	93.2
Rank (with kLFDA)	1	5	10	15	20	30
No-structure	35.8	70.5	83.7	87.9	92.0	95.6
Simple-average	36.0	69.7	81.7	86.4	91.6	96.1
AC+global	36.8	70.9	83.4	87.3	91.6	95.4
No-global	39.0	71.9	84.3	88.6	92.8	95.6
Proposed (single)	41.2	73.6	84.8	89.2	93.2	96.3
Proposed (multi-manu)	45.4	75.8	86.7	91.4	94.6	96.5
Proposed (multi-auto)	45.1	75.5	86.5	91.6	95.0	97.2
Proposed (multi-GT)	45.8	76.3	87.2	92.3	94.3	96.8
Rank (with KMFA- $R_{\chi^2_2}$)	1	5	10	15	20	30
No-structure	42.3	71.3	84.5	88.5	91.8	95.2
Simple-average	41.5	71.0	84.3	88.2	92.1	95.7
AC+global	42.7	72.6	84.8	88.8	92.4	96.3
No-global	44.5	74.3	85.6	89.7	93.3	96.0
Proposed (single)	46.2	76.4	87.2	90.8	94.2	96.7
Proposed (multi-manu)	49.3	77.9	88.1	92.7	94.7	97.4
Proposed (multi-auto)	49.1	77.5	87.7	92.3	95.0	97.2
Proposed (multi-GT)	49.6	78.6	88.9	93.5	95.4	97.8

Fig. 10 shows the multiple correspondence structure learning results of our approach. In Fig. 10, the left and middle columns show the two local correspondence structures learned for each dataset, and the right column shows the absolute difference matrices between the local correspondence structures in left and middle columns. Note that since the SYSU-sReID dataset includes four local correspondence structures which can form six difference matrices, we only show two local

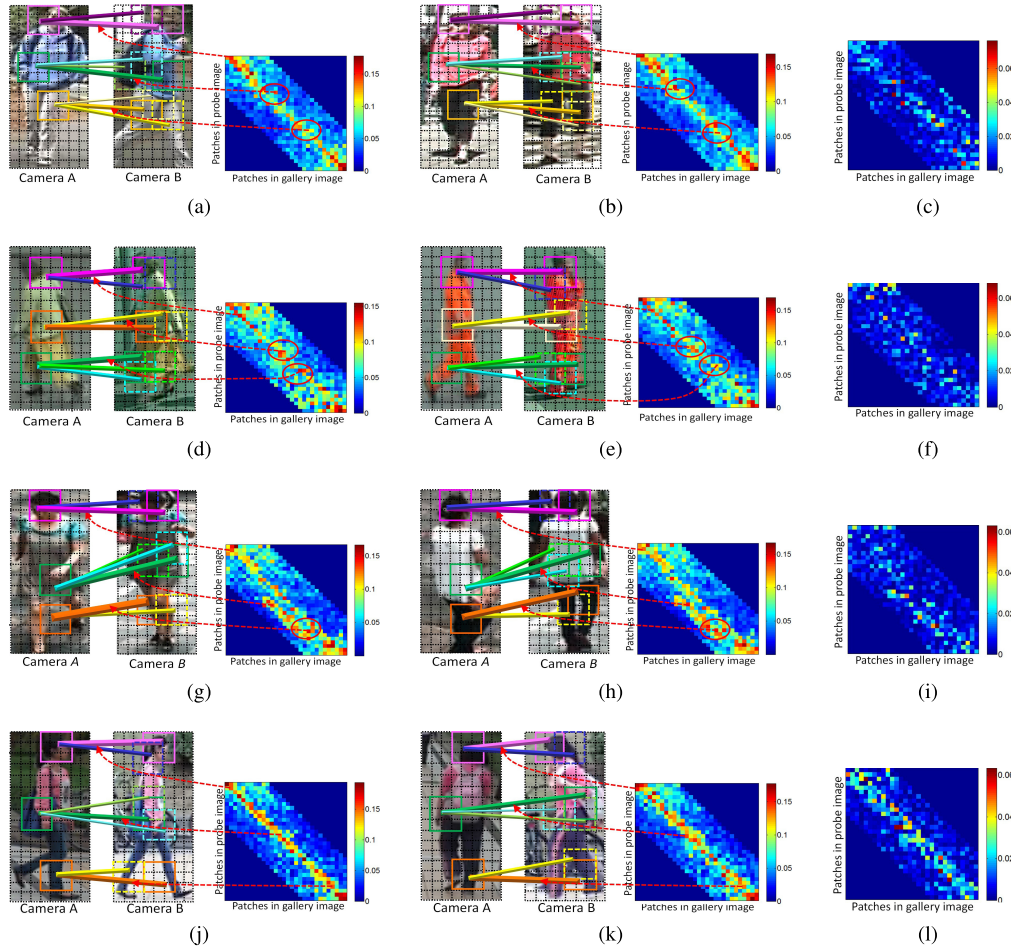


Fig. 10. Multiple correspondence structures learned for VIPeR (a, b, c), PRID 450S (d, e, f), Road (g, h, i), SYSU-sReID (j, k, l) datasets (learned with the KISSME metric). Left and middle columns: the two local correspondence structures learned for each dataset (line width is proportional to the probability values). Right column: the absolute difference matrices between the local correspondence structures in left and middle columns. (Best viewed in color).

correspondence structures and their corresponding difference matrix to save space (cf. Figs 10j, 10k, 10l).

Fig. 10 indicates that by introducing multiple correspondence structures, the spatial correspondence pattern between cameras can be modeled in a more precise way. Specifically:

- 1) The spatial correspondence pattern between a camera pair can be jointly described by a set of local correspondence structures, where each local correspondence structure captures a sub-pattern inside the global correspondence pattern. For example, the local correspondence structure in Fig. 10a can properly emphasize the large spatial displacement due to the cross-view pose translation in the front-to-side correspondence sub-pattern. At the same time, the local correspondence structure in Fig. 10b also properly captures the front-to-back correspondence sub-pattern. In this way, our approach can have stronger capability to handle spatial misalignments with large variations.
- 2) Due to the effectiveness of our correspondence structure learning process, the learned local correspondence structures can properly differentiate and highlight the subtle differences among different spatial correspondence sub-patterns. For example, the absolute difference matrix in Fig. 10c shows large values in the middle and

downright corner. This implies that the major difference between the front-to-side and front-to-back correspondence sub-patterns in Figs. 10a and 10b is around the torso and leg regions. Similarly, large difference values appear in the top left and bottom right corners in Fig. 10f, indicating that the major difference between the left-to-left and right-to-right correspondence sub-patterns in Figs. 10d and 10e is around the head and leg regions.

2) *Performances of Person Re-ID*: We further perform person Re-ID experiments by using the multiple correspondence structures in Fig. 10. Note that besides the local correspondence structures in Fig. 10, the global correspondence structure learned over all training samples is also included (cf. Fig. 6).

Tables I, II, IV, and V show the CMC results of our approach with multiple correspondence structures where *proposed+multi-manu* and *proposed+multi-auto* represent the results of our approach under manually and automatically divided pose group pairs, respectively (cf. Section VI). Moreover, in order to evaluate the impact of pose classification error, we also include the results by using the ground-truth pose classification label² to select the optimal correspondence

²The ground-truth labels are defined based on the manually divided pose group pairs.

structure during person Re-ID (i.e., *proposed+multi-GT* in Tables I, II, IV, and V).

From Tables I, II, IV, and V, we can observe:

- 1) Our approach with multiple correspondence structures (*proposed+multi-manu* and *proposed+multi-auto*) can achieve better results than using a single correspondence structure (*proposed+single*). This further demonstrates that our multi-structure strategy can model the cross-view spatial correspondence in a more precise way, and spatial misalignments can be more effectively handled and excluded by multiple correspondence structures.
- 2) Our approach, which uses automatic pose classification to select the optimal correspondence structure (*proposed+multi-manu*), can achieve similar results to the method that uses the ground-truth pose classification label for correspondence structure selection (*proposed+multi-GT*). This implies that the pose classification method used in our approach can provide sufficient classification accuracy to guarantee satisfactory Re-ID performances.
- 3) Our approach under automatically obtained pose group pairs (*proposed+multi-auto*) can achieve similar performances to the one under manually divided pose group pairs (*proposed+multi-manu*). This implies that if we can find proper features to describe human poses, automatic pose grouping can also obtain proper pose group pairs and achieve satisfactory Re-ID results.
- 4) The improvement of multiple correspondence structures (*proposed+multi-manu* and *proposed+multi-auto*) is the most obvious on the SYSU-sReID dataset. This is because the SYSU-sReID dataset includes more cross-view pose correspondence patterns. Thus, by introducing more local correspondence structures to handle these pose correspondence patterns, the cross-view spatial misalignments can be more precisely captured, leading to more obvious improvements.

D. Comparing With the State-of-Art Methods

We also compare our results with the state-of-the-art methods on different datasets: RankBoost [3], LF [4], JLCF [4], KISSME [9], SalMatch [29], DSVR FSA [15], svmml [50], ELS [18], kLFDA [8], MFA [8], IDLA [23], JLR [20], PRISM [37], DG-Dropout [26], DPML [33], LOMO [19], Mirror-KMFA(R_{χ^2}) [39], DCSL [35], deCPPs [32], MCP-CNN [25], and FNN [27] on the VIPeR dataset; KISSME [9], EIML [6], SCNCD [2], SCNCDFinal [2], svmml [50], MFA [8], kLFDA [8], Mirror-KMFA(R_{χ^2}) [39], and FNN [27] on the PRID 450S dataset; PCCA [51], rPCCA [8], svmml [50], MFA [8], and kLFDA [8] on the 3DPeS dataset; eSDC-knn [14], svmml [50], MFA [8], and kLFDA [8] on the Road dataset; and eSDC-knn [14], svmml [50], MFA [8], kLFDA [8], MLACM [44], and TA+W [34] on the SYSU-sReID dataset.

Note that since the rotation and orientation parameters used in the TA+W method [34] are derived from camera calibration and human motion information which is not available on SYSU-sReID dataset, we manually label these parameters so

TABLE VI

CMC RESULTS ON THE VIPeR DATASET (PROPOSED(SINGLE-KMFA) AND PROPOSED(MULTI-MANU-KMFA) INDICATES OUR APPROACH USING A SINGLE AND MULTIPLE CORRESPONDENCE STRUCTURES WITH KMFA- R_{χ^2} METRIC)

Rank	1	5	10	20	30
RankBoost [3]	23.9	45.6	56.2	68.7	-
JLCF [4]	26.3	51.9	67.1	-	-
KISSME [9]	27	-	70	83	-
SalMatch [29]	28.1	52.3	-	-	-
DSVR FSA [15]	29.4	50.7	61.9	74.9	-
svmml [50]	30.1	63.2	77.4	88.1	-
ELS [18]	31.3	62.1	75.3	86.7	-
kLFDA [8]	32.3	65.8	79.7	90.9	-
MFA [8]	32.2	66.0	79.7	-	90.6
IDLA [23]	34.8	64.5	-	-	-
JLR [20]	35.8	68.0	-	-	-
PRISM [37]	36.7	66.1	79.1	90.2	-
JLCF-fusing [4]	38.0	70.3	81.0	-	-
DG-Dropout [26]	38.6	-	-	-	-
DPML [33]	41.5	-	80.9	90.5	-
LOMO [19]	42.3	71.5	82.9	92.1	-
Mirror-KMFA(R_{χ^2}) [39]	43.0	75.8	87.3	94.8	-
DCSL [35]	44.6	73.4	82.6	-	-
svmml+SalMatch [29]	44.6	73.4	-	-	-
deCPPs [32]	44.6	75.1	86.8	-	-
deCPPs+MER [32]	47.5	75.3	86.8	-	-
MCP-CNN [25]	47.8	74.7	84.8	91.1	94.3
FNN [27]	51.1	81.0	91.4	96.9	-
LOMO-fusing [19]	51.2	82.1	90.5	95.9	-
Proposed (single-KMFA)	43.3	77.4	88.2	92.7	97.8
Proposed (multi-manu-KMFA)	44.8	78.5	89.8	93.4	97.2
Proposed (multi-manu-KMFA)-fusing	51.4	82.5	91.2	96.0	98.1

TABLE VII

CMC RESULTS ON THE PRID 450S DATASET

Rank	1	5	10	20	30
KISSME [9]	33	-	71	79	-
EIML [6]	35	-	68	77	-
SCNCD [2]	41.5	66.6	75.9	84.4	88.4
SCNCDFinal [2]	41.6	68.9	79.4	87.8	91.8
svmml [50]	42.8	69.7	79.2	86.6	91.2
MFA [8]	44.7	71.9	80.2	86.9	91.9
kLFDA [8]	46.9	73.1	81.7	87.2	91.4
Mirror-KMFA(R_{χ^2}) [39]	55.4	79.3	87.8	93.9	-
FNN [27]	66.6	86.8	92.8	96.9	-
Proposed (single-KMFA)	63.2	82.7	90.5	94.8	97.3
Proposed (multi-manu-KMFA)	65.1	84.9	91.2	95.4	97.7

TABLE VIII

CMC RESULTS ON THE 3DPeS DATASET

Rank	1	5	10	20	30
svmml [50]	34.7	66.4	78.8	88.5	-
PCCA [51]	41.6	70.5	81.3	90.4	-
rPCCA [8]	47.3	75.0	84.5	91.9	-
MFA [8]	48.4	72.4	81.5	89.8	-
kLFDA [8]	54.0	77.7	85.9	92.4	-
DG-Dropout [26]	56.0	-	-	-	-
Proposed (single-KMFA)	61.4	84.2	90.7	94.2	94.9

as to have a fair comparison with our approach (i.e., guarantee that [34]'s performance will not be degraded due to improper rotation and orientation parameters).

The CMC results of different methods are shown in Tables VI–X. Moreover, since many works also reported fusion results on the VIPeR dataset (i.e., adding multiple Re-ID results together to achieve a higher

TABLE IX
CMC RESULTS ON THE ROAD DATASET

Rank	1	5	10	20	30
eSDC-knn [14]	52.4	74.5	83.7	89.9	91.8
svmm1 [50]	57.2	85.2	92.1	96.1	97.6
MFA [8]	58.3	85.5	92.4	96.2	97.3
kLFDA [8]	59.1	86.5	91.8	95.8	98.1
Proposed (single-KMFA)	71.4	92.5	95.6	97.1	97.8
Proposed (multi-manu-KMFA)	73.1	92.8	96.4	97.8	98.6

TABLE X
CMC RESULTS ON THE SYSU-sReID DATASET (NOTE: THE TA-W METHOD USES THE SAME FEATURE AND DISTANCE METRIC AS THE PROPOSED (SINGLE-KMFA) METHOD)

Rank	1	5	10	20	30
KISSME [9]	28.6	62.0	72.8	82.4	85.0
svmm1 [50]	30.8	63.5	74.9	84.2	88.3
MFA [8]	32.4	65.2	75.4	85.7	89.4
kLFDA [8]	33.4	65.9	76.3	86.3	90.0
MLACM [44]	32.5	57.7	68.3	78.2	—
TA-W [34]	43.0	73.1	85.3	92.2	96.1
Proposed (single-KMFA)	46.2	76.4	87.2	94.2	96.7
Proposed (multi-manu-KMFA)	49.3	77.9	88.1	94.7	97.4

Re-ID result) [4], [14], [29], we also show a fusion result of our approach (*svmm1+Proposed+multi-manu-KMFA*) and compare it with the other fusion results in Table VI. Tables VI–X show that:

- 1) Our approach has better Re-ID performances than most of the state-of-the-art methods. This further demonstrates the effectiveness of our approach.
- 2) Our approach also achieves similar or better results than some deep-neural-network-based methods (e.g., IDLA [23], JLR [20], and DG-Dropout [26] in Table VI). This implies that spatial misalignment is indeed a significant factor affecting the performance of person Re-ID. If the spatial misalignment problem can be properly handled, satisfactory results can be achieved with relatively simple hand-crafted features. Moreover, since our approach is independent of the specific features used for Re-ID, it can easily accommodate future advances by combining with the deep-neural-network-based features (such as [27]) without changing the core protocols.
- 3) Since the TA+W method [34] creates multiple weight matrices for pedestrians with different orientations, it can be viewed as another version of using multiple matching structures. However, our approach (*proposed+multi-manu*) still outperforms the TA+W method [34] (cf. Table X). This further indicates that our multi-structure scheme is effective in modeling the cross-view spatial correspondence.

E. Time Complexity & Effects of Different Parameter Values

1) *Time Complexity*: We also evaluate the running time of training & testing excluding dense feature extraction in Table XI. Testing process with (*Test+Proposed*) and without (*Test+Non-global*) Hungarian method are both evaluated. Moreover, for the testing process, we list two time complexity

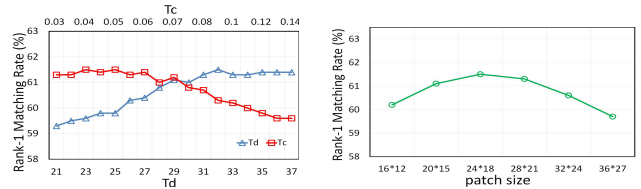


Fig. 11. The effect of different parameter values (The results are evaluated by the rank-1 CMC score on the Road dataset using KISSME distance metric). (a) Results with different T_c & T_d . (b) Results with different patch sizes.

values: (1) the running time for the entire process (*Test-all image pairs*), and (2) the average running time for computing the similarity of a single image pair (*Test-per image pair*).

We can notice that the running time of both training and testing are acceptable. Table XI also reveals that Hungarian method takes the major time cost of testing. This implies that our testing process can be further optimized by replacing Hungarian method with other more efficient algorithms [52].

2) *Effect of Different Parameter Values*: Finally, we evaluate the effect of three parameters: (1) T_c which is the threshold of keeping the learned matching probability value P_{ij} (cf. Eq. 1); (2) T_d which is the search range of handling spatial displacement (cf. Eq. 6); and (3) Patch size which is the size of the basic element for calculating image-wise similarity.

Figures 12a to 12b show the rank-1 CMC scores [42] of our approach under different T_c , T_d , and patch size values on the Road dataset. Moreover, Fig. 12 further shows the learned correspondence structures under different search ranges T_d . Figures 11 and 12 show that:

- 1) Basically, T_c should be kept small since a large T_c will exclude many useful matching probabilities in the correspondence structure and lead to decreased Re-ID results. However, when T_c becomes extremely small, the Re-ID performance may also be slightly affected since some noisy matching probabilities may be included in the correspondence structure. According to our experiments, 0.03—0.07 is a proper range for T_c and we use $T_c = 0.05$ throughout our experiments.
- 2) T_d normally should be set large enough in order to handle large spatial misalignments. However, a large T_d will also increase the complexity of person Re-ID. According to our experiments, satisfactory results can be achieved when T_d is larger than 32. Therefore, in our experiments, we set $T_d = 32$ to guarantee performance while minimizing computation complexity.
- 3) The patch size should not be too small or too large. If the patch size is too small, the visual information included in each patch becomes very limited. This may reduce the reliability of patch matching results. On the other hand, if the patch size is too large, the number of patches in an image will be obviously reduced. This will affect the flexibility of our approach to handle spatial misalignments. According to our experiments, 20×15 — 28×21 is a proper patch size range for images with 128×48 sizes.

VIII. CONCLUSION

In this paper, we propose a novel framework for addressing the problem of cross-view spatial misalignments in person

TABLE XI

RUNNING TIME ON FIVE DATASETS (EVALUATED ON A PC WITH 4-CORE CPU AND 2G RAM; *hr, min, sec, ms* REFER TO *hour, minute, second* AND *millisecond*, RESPECTIVELY)

Datasets	ViPeR	PRID 450S	3DPeS	Road	SYSU-sReID
Train-all image pairs	2.06 hr	1.22 hr	0.89 hr	1.07 hr	1.43 hr
Test-all image pairs (Non-global)	57.97 sec	34.64 sec	24.87 sec	29.45 sec	39.06 sec
Test-per image pair (Non-global)	0.58 ms	0.68 ms	0.52 ms	0.68 ms	0.62 ms
Test-all image pairs (Proposed)	6.64 min	3.49 min	2.61 min	3.03 min	4.28 min
Test-per image pair (Proposed)	3.99 ms	4.14 ms	3.26 ms	4.20 ms	4.08 ms

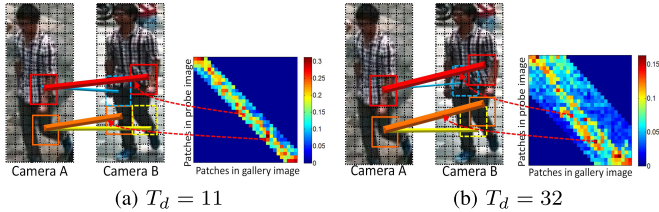


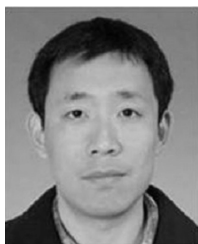
Fig. 12. Comparison of correspondence structures of the Road dataset with different search ranges T_d . (The correspondence structures are learned with the KISSME metric. Best viewed in color). (a) $T_d = 11$. (b) $T_d = 32$.

Re-ID. Our framework introduces the idea of correspondence structure and learns this structure via a novel boosting method to properly handle the spatial misalignment among arbitrary cameras. Extensive experimental results demonstrate the effectiveness of our approach.

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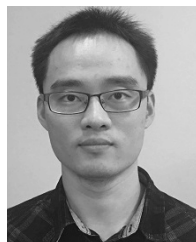
Weiyao Lin received the B.E. and M.E. degrees from Shanghai Jiao Tong University, China, in 2003 and 2005, respectively, and the Ph.D. degree from the University of Washington, Seattle, USA, in 2010.

He is currently an Associate Professor with the Department of Electronic Engineering, Shanghai Jiao Tong University. His research interests include image/video processing, video surveillance, and computer vision.



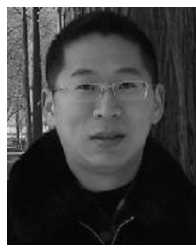
Yang Shen received the B.E. degree from Shanghai Jiao Tong University, China, in 2014.

He is currently pursuing the master's degree with the Department of Electronic Engineering, Shanghai Jiao Tong University. His research interests include image processing and computer vision.

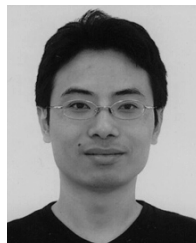


Junchi Yan received the M.S. and Ph.D. degrees from Shanghai Jiao Tong University, China. He is currently a Research Staff Member and a Master Inventor with IBM. He is also a post-doc researcher with Software Engineering Institute, East China Normal University, China.

His research interests are computer vision and machine learning applications. He was a recipient of the IBM Research Accomplishment Award in 2013 and the Outstanding Accomplishment Award in 2014.

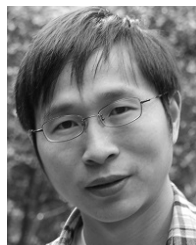


Mingliang Xu received the B.E. and M.E. degrees from Zhengzhou University, China, in 2005 and 2008, respectively, and the Ph.D. degree from the State Key Laboratory of CAD & CG, Zhejiang University, China, in 2012, all in computer science. He is currently an Associate Professor with the School of Information Engineering, Zhengzhou University. His research interests include computer graphics and computer vision.



Jianxin Wu received the B.S. and M.S. degrees from Nanjing University, China, and the Ph.D. degree from the Georgia Institute of Technology, all in computer science.

He was an Assistant Professor with Nanyang Technological University, Singapore. He is currently a Professor with Nanjing University. His research interests are computer vision and machine learning.



Jingdong Wang received the Ph.D. degree in computer science from the Department of Computer Science and Engineering, The Hong Kong University of Science and Technology, Hong Kong. He is currently a Lead Researcher with the Visual Computing Group, Microsoft Research Asia.

His areas of interest include computer vision, multimedia, and machine learning.



Ke Lu received the Ph.D. degree from the Department of Computer Science, Northwest University, Xi'an, China, in 2003. He was a Post-Doctoral Fellow with the Institute of Automation, Chinese Academy of Sciences, Beijing, China, from 2003 to 2005. He is currently a Professor with the University of the Chinese Academy of Sciences, Beijing. He is also a ChuTian Scholar-Professor with the College of Computer and Information Technology, China Three Gorges University, Yichang, China.

His research focuses on curve matching, 3-D image reconstruction, and computer graphics.