Skin Lesion Matching using Jacobian based Descriptors for Topology Preservation

Hengameh Mirzaalian¹, Tim K. Lee^{1,2,3}, Ghassan Hamarneh¹

¹Medical Image Analysis Lab, Simon Fraser University.

²Cancer Control Research, BC Cancer Agency. ³Department of Dermatology and Skin Science, University of British Columbia.

ABSTRACT

Developing an automatic system for tracking pigmented skin lesions (PSL) is important for early skin cancer detection. PSL tracking is typically formulated as finding correspondences in an optimization framework. When lesions are close to each other, it becomes likely to mis-correspond a PSL with nearby ones. To alleviate this problem, we introduce a novel topology-preservation concept based on which we derive different energy terms for the PSL matching objective function. Given two graph-represented sets of PSLs to correspond, in addition to unary and binary energy terms, we quantify topological-preservation using a Jacobian-like matrix capturing how triplets of vertices in one graph match another triplet in the other graph. We validate the goodness of our proposed descriptors on 97 pairs of human back digital color images. The results indicate that our new descriptors improve the PSL matching accuracy by over 9%.

Index Terms— PSL matching; graph matching; topology preservation; Jacobian descriptors.

1. INTRODUCTION

One of the most well-documented risk factors for malignant melanoma cancer is the presence of a large number of pigmented skin lesions (PSLs), which can be detected in their early stages using *total body photography* [1, 2]. Regular screening of the skin can help identify newly-appearing, disappearing, and changing PSLs by tracking them in 2D digital color images collected during examinations [1].

Until recently, PSL screening and matching have been done completely manually; a subjective, tedious, and error prone process that suffers from inter- and intra-operator variability. In the past few years, a few works have been proposed towards automatic PSL tracking to free up dermatologists' time from manually locating and corresponding dozens of PSLs [1, 2, 3, 4]. As digital photography is becoming more prevalent in dermatology clinics and even by regular users via mobile devices, computerized methods are increasingly being proposed to analyze PSLs.

PSL tracking is typically formulated as finding correspondences within an optimization framework (Section 2). In

Method	Order	Node descriptor
[3]	U	Voronoi area of the PSLs
[6, 7]	U+B	2DSC
[4]	U+B	2DSNC [1]
[2]	U+B+T	2DSNC [1]

Table 1. Key existing works on PSL matching in terms of the different energy terms, unary (U), binary (B), and ternary (T), and the type of the node descriptor in the optimization objective.

Table 1, we summarize key existing works on PSL matching in terms of: i) the order of different energy terms in the optimization objective, which measure unary (U), binary (B), and ternary (T) compatibilities between the two graph-represented sets of PSLs; and ii) the type of the node descriptor used to compute the compatibilities. In this table¹, 2DSC denotes 2D spatial coordinates of the PSLs in the image domain, whereas 2DSNC represents spatially normalized coordinates of the PSLs, which are computed by warping the PSL coordinates in the image domain to a human back template [1].

It has been shown that including higher order terms, e.g. ternary, into the objective function increases the matching robustness [5]. Further, considering 2DSNC improves the PSL matching accuracy compared to the non-normalized coordinates (2DSC). However, when PSLs are close to each other, the previous methods are prone to mis-correspond a PSL with nearby ones. These matching errors become obvious when one examines how groups of nearby PSLs are ordered. In Figure 1, two sample matchings are shown; one preserves order and the other does not. In Figure 1(c), the order of the vertices of two “PSL-triangles” is not preserved: one of them is clockwise, while the other is counter-clockwise.

A similar situation may occur when registering images that causes image folding and non-invertible transformations. This has prompted the development of image registration methods with topology-preservation, e.g. [8]. In this work, we borrow and adapt the topology preservation idea for the PSL matching problem. Given two graph-represented sets of PSLs to correspond, we quantify topological-preservation using Jacobian-like matrices and use them to measure different terms of the PSL matching objective function (Section 3). We

¹Note that *image*-based descriptors are not listed here as such descriptors are used for *locating* PSLs (as in [1, 2]); a step that precedes the graph-based PSL *matching* examined here.

Fig. 1. (a) Examples of back images of the same subject at different times [9] overlaid with the PSLs (circles) and a set of anatomical landmarks (crosses). (b) Representation of the unary, binary, and ternary compatibilities of the PSL matching objective function in Eq. 1, which are computed between two nodes (one node per graph used to compute unary compatibilities), four nodes (two nodes per graph for binary), and six nodes (three nodes per graph for ternary). (c-d) Sample PSL matchings with different (c) and similar (d) ordering. In (c), the ordering on the left is clockwise and the other is counter-clockwise. In (d), both are clockwise.

validate the goodness of our proposed descriptors on 97 pairs of human back digital color images. The results indicate that our method improves the PSL matching accuracy by over 9% (Section 4).

2. PSL MATCHING FORMULATION

Let us denote the PSLs configuration in the first image by a graph $\mathcal{G}(\mathcal{V}, \mathcal{E}, \mathcal{C})$ consisting of a set of nodes $\mathcal{V}$, edges $\mathcal{E}$, and cliques $\mathcal{C}$ (a third order clique or triplet). We adopt a similar notations for the second image but including the prime symbol, i.e. $\mathcal{G}'(\mathcal{V}', \mathcal{E}', \mathcal{C}')$. Our goal in PSL matching, is finding a matrix $\mathcal{X}$, which encodes the mapping between $\mathcal{V}_i$ and $\mathcal{V}'_{i'}$, i.e. $\mathcal{X}_{ii'} = 1$ if $\mathcal{V}_i$ is a correct mapping to $\mathcal{V}'_{i'}$ and $\mathcal{X}_{ii'} = 0$ otherwise. To find $\mathcal{X}$, we define our PSL matching energy as:

$$\hat{\mathcal{X}}(\mathcal{G}, \mathcal{G}') = \arg \min_{\mathcal{X}} \mathbf{w}_u^T \phi_u(\mathcal{X}, \mathcal{G}, \mathcal{G}') + \mathbf{w}_b^T \phi_b(\mathcal{X}, \mathcal{G}, \mathcal{G}') + \mathbf{w}_t^T \phi_t(\mathcal{X}, \mathcal{G}, \mathcal{G}') \quad (1)$$

with:

$$\begin{aligned} \phi_u(\mathcal{X}, \mathcal{V}, \mathcal{V}') &= \sum_{ii'} \mathcal{X}_{ii'} \text{abs}(\mathcal{V}_i - \mathcal{V}'_{i'}), \\ \phi_b(\mathcal{X}, \mathcal{E}, \mathcal{E}') &= \sum_{ii'} \sum_{jj'} \mathcal{X}_{ii'} \mathcal{X}_{jj'} \text{abs}(\mathcal{E}_{ij} - \mathcal{E}'_{i'j'}), \\ \phi_t(\mathcal{X}, \mathcal{C}, \mathcal{C}') &= \sum_{ii'} \sum_{jj'} \sum_{kk'} \mathcal{X}_{ii'} \mathcal{X}_{jj'} \mathcal{X}_{kk'} \text{abs}(\mathcal{C}_{ijk} - \mathcal{C}'_{i'j'k'}), \\ \{\phi_u, \mathbf{w}_u, \mathcal{V}_i, \mathcal{V}'_{i'}\} &\in \mathbb{R}^u \\ \{\phi_b, \mathbf{w}_b, \mathcal{E}_{ij}, \mathcal{E}'_{i'j'}\} &\in \mathbb{R}^b \\ \{\phi_t, \mathbf{w}_t, \mathcal{C}_{ijk}, \mathcal{C}'_{i'j'k'}\} &\in \mathbb{R}^t \end{aligned}$$

where $\mathcal{V}_i$ represents features² of the i^{th} node of the graph (similarly $\mathcal{V}'_{i'}$ for the second graph); $\mathcal{E}_{ij}$ and $\mathcal{C}_{ijk}$ represent edge and clique features connecting $\{i, j\}$ and $\{i, j, k\}$ nodes, respectively; ϕ_u , ϕ_b , and ϕ_t measure matching compatibilities between the nodes, edges, and cliques (Figure 1(b)); $\{\mathbf{w}_u, \mathbf{w}_b, \mathbf{w}_t\}$ are a set of weight vectors. In the next section, we will see how the compatibilities in Eq. 1 will be derived based on the newly proposed Jacobian descriptors, which enforce topology preservation.

3. JACOBIAN BASED FEATURES

As stated in Section 1, our descriptor is inspired by the image registration method in [10], which has been proposed to enforce topology preservation into a given deformation field. We adopt a similar concept to enforce topology preservation into our PSL matching. In this section, we, first, summarize the main concept of topology-preservation for a continuous deformation. Then, we explain our extension to the point matching problem.

Let $h = (f, g) : \Omega \subset \mathbb{Z}^2 \mapsto \mathbb{R}^2$ be a deformation defined over a discrete rectangular grid, i.e. a point (x, y) is mapped to $(f(x, y), g(x, y)) \in \mathbb{R}^2$. It has been shown that the deformed grid preserves topology if its Jacobian determinants are positive everywhere on the grid [10]. For each point of the 2D grid, depending on its forward and backward neighbouring points, four possible approximations of the Jacobians are defined $\{J^{ff}, J^{bb}, J^{fb}, J^{bf}\}$ [10]. For example, J^{ff} is computed based on the forward-forward (ff) partial derivatives of the deformation field $h = (f, g)$, considering ff neighbors of (x, y) , which are $(x, y + 1)$ and $(x + 1, y)$ (Figure 2):

$$J^{ff}(x, y) = \begin{pmatrix} f_x^f(x, y) & f_y^f(x, y) \\ g_x^f(x, y) & g_y^f(x, y) \end{pmatrix}. \quad (2)$$

$\{J^{bb}, J^{fb}, J^{bf}\}$ are computed similar to Eq. 2. The forward and backward partial derivatives of f and g at (x, y) can be approximated by:

$$\begin{aligned} f_x^f(x, y) &= f(x + 1, y) - f(x, y), \\ f_y^f(x, y) &= f(x, y + 1) - f(x, y), \\ f_x^b(x, y) &= f(x, y) - f(x - 1, y), \\ f_y^b(x, y) &= f(x, y) - f(x, y - 1). \end{aligned}$$

similar derivatives are defined for the g component.

The above J s are computed among three neighbouring nodes of the image grid. Adopting a similar idea for our graph-based PSL matching problem, we compute a variant of these Jacobian matrices for a set of corresponding cliques between the two graphs. Given three points $\{i, j, k\}$ in the

²For clarity, we abuse the notation slightly by using $\mathcal{V}$ to denote both the vertices and their features, similarly for $\mathcal{E}$ and $\mathcal{C}$.

Fig. 2. Visualisation of the forward and backward neighboring points of (x, y) , which are considered in computing different forward and backward Jacobians defined in Eq. 2. For example, J^{ff} is computed based on the forward-forward (ff) partial derivatives of the deformation h considering ff neighbors of (x, y) , which are $(x, y + 1)$ and $(x + 1, y)$.

Fig. 3. Triplets defined over the unary, binary, and ternary terms in our PSL matching formulation. Landmarks are visualized as white circles and PSLs as diamonds. For the unary term (a) and binary term (b), we introduce several triplets using $\{1 \text{ PSL and } 2 \text{ landmarks}\}$ and $\{2 \text{ PSLs and } 1 \text{ landmark}\}$, respectively. For the ternary term (c), we simply compute the Jacobian for a triplet introduced by the three PSLs. (d) shows $N=8$ ordered triplets utilizing the 8 anatomical landmarks: left/right neck, shoulder, armpit, and hip points shown overlaid on a skin back image in the middle.

first graph corresponding to $\{i', j', k'\}$ in the second graph, we define:

$$J(ijk) = \begin{pmatrix} x(i) - x(j) & x(i) - x(k) \\ y(i) - y(j) & y(i) - y(k) \end{pmatrix},$$

$$J(i'j'k') = \begin{pmatrix} x(i') - x(j') & x(i') - x(k') \\ y(i') - y(j') & y(i') - y(k') \end{pmatrix} \quad (3)$$

where $x(\cdot)$ and $y(\cdot)$ represent the x and y coordinates of the points. Our underlying assumption is that if $\{i, j, k\}$ and $\{i', j', k'\}$ are correct mappings to each other, we expect them to have similar Jacobian matrices computed as in Eq. 3.

Given a set of points (i.e. landmarks or seeds) with known correspondences (as in [1, 2, 4]) denoted by $\mathcal{L}_1 \dots \mathcal{L}_N \in \mathcal{L}$ and $\mathcal{L}'_1 \dots \mathcal{L}'_N \in \mathcal{L}'$, if node i of the first graph is a correct mapping of node i' of the second graph, as mentioned in the above paragraph, we expect similar Jacobian matrices for the triplets introduced by $\{i\mathcal{L}_p\mathcal{L}_q\}$ and $\{i'\mathcal{L}'_p\mathcal{L}'_q\}$, where $\{\mathcal{L}_p, \mathcal{L}_q\} \in \mathcal{L}$ and $\{\mathcal{L}'_p, \mathcal{L}'_q\} \in \mathcal{L}'$ are two corresponding landmarks. Therefore, we define node compatibilities in Eq. 1 as the difference between $\text{abs}(\det(J(i\mathcal{L}_p\mathcal{L}_q)) - \det(J(i'\mathcal{L}'_p\mathcal{L}'_q)))$. The Jacobian differences can be computed for any possible pairwise combinations of the landmarks, i.e. $\binom{N}{2} = \frac{(N)!}{(N-2)!2!}$, where N is the total number of the landmarks. However, assuming that we randomly order the points in $\mathcal{L}$ as shown in Figure 3(d), it

can be shown that:

$$\det(J(\mathcal{L}_k o \mathcal{L}_i)) = \det(J(\mathcal{L}_j o \mathcal{L}_i)) + \det(J(\mathcal{L}_k o \mathcal{L}_j)) - \det(J(\mathcal{L}_k \mathcal{L}_i \mathcal{L}_j)) \quad (4)$$

which indicates that $\det(J(\mathcal{L}_k o \mathcal{L}_i))$ is a linear combination of $\det(J(\mathcal{L}_j o \mathcal{L}_i))$ and $\det(J(\mathcal{L}_k o \mathcal{L}_j))$. Therefore, given $\mathcal{L}$, the minimum number of independent J s is equal to N . Using only N components in our framework, we set the node compatibilities in Eq. 1 to (Figure 3):

$$(\mathcal{V}_i - \mathcal{V}'_{i'}) = \begin{pmatrix} \frac{\det(J(i\mathcal{L}_1\mathcal{L}_2))}{Z} - \frac{\det(J(i'\mathcal{L}'_1\mathcal{L}'_2))}{Z'} \\ \vdots \\ \frac{\det(J(i\mathcal{L}_{N-1}\mathcal{L}_N))}{Z} - \frac{\det(J(i'\mathcal{L}'_{N-1}\mathcal{L}'_N))}{Z'} \\ \frac{\det(J(i\mathcal{L}_N\mathcal{L}_1))}{Z} - \frac{\det(J(i'\mathcal{L}'_N\mathcal{L}'_1))}{Z'} \end{pmatrix} \quad (5)$$

Similarly, using one of the landmarks, we compute the difference of the Jacobian determinants of triplets introduced by $\{ij\mathcal{A}_p\}$ and $\{i'j'\mathcal{A}'_p\}$ to set the edge compatibilities:

$$(\mathcal{E}_{ij} - \mathcal{E}'_{i'j'}) = \begin{pmatrix} \frac{\det(J(ij\mathcal{L}_1))}{Z} - \frac{\det(J(i'j'\mathcal{L}'_1))}{Z'} \\ \vdots \\ \frac{\det(J(ij\mathcal{L}_{N-1}))}{Z} - \frac{\det(J(i'j'\mathcal{L}'_{N-1}))}{Z'} \\ \frac{\det(J(ij\mathcal{L}_N))}{Z} - \frac{\det(J(i'j'\mathcal{L}'_N))}{Z'} \end{pmatrix} \quad (6)$$

and we set the clique compatibilities to:

$$(\mathcal{C}_{ijk} - \mathcal{C}'_{i'j'k'}) = \left(\frac{\det(J(ijk))}{Z} - \frac{\det(J(i'j'k'))}{Z'} \right) \quad (7)$$

where $\{Z, Z'\}$ are normalization factors:

$$Z = \sum_{i=1}^N \|\det(J(p\mathcal{L}_i\mathcal{L}_{i+1}))\|_2, \quad (8)$$

and $\mathcal{L}_{N+1} = \mathcal{L}_1$. With these compatibilities defined in Eq. 5-Eq. 7, we optimize Eq. 1 using different optimization techniques mentioned in Section 4.

Note that in our application, we have eight landmarks ($|N| = 8$) defined as the left and right: neck, shoulder, armpits, and hip-points Figure 1(a)) [1, 2, 4].

4. RESULTS

We evaluate our method on 194 images (97 pairs) of human back digital color images with isotropic resolution of 0.25 mm/pixel [9]. The number of PSLs varied between 2 and 30 (9 ± 8). We perform ten-fold cross validation to learn the free parameters in our framework ($\{\mathbf{w}_u, \mathbf{w}_b, \mathbf{w}_t\}$ in Eq. 1).

First, we evaluate our assumption that indeed correct (or ground truth) matchings preserve topology. For that, we compute Jacobian determinants (Eq. 3) for a set of third order cliques of the graphs in our dataset with known correct and

Fig. 4. Similarity and dissimilarity of the Jacobian matrices of the corresponding and non-corresponding triplets of the two graphs, respectively. x and y axes represent $\det(J(ijk))$ and $\det(J(i'j'k'))$ of $\{i, j, k\}$ and $\{i', j', k'\}$ triplets of the graphs with correct (a) and incorrect (b) mappings.

Fig. 5. PSL matching error when using 2DSC (green) [6, 7], 2DSNC (gray) [2, 4], and our proposed (yellow) node descriptors. It can be seen that using the proposed node descriptors, the accuracy of the PSL matching is improved regardless of the matching algorithm employed.

(intentionally) incorrect mappings. The results are reported in Figure 4. It can be seen that for the correct ones, the points in Figure 4(a) are spread along the diagonal, which indicates that the signs and magnitudes of the $\det(J(ijk))$ and $\det(J(i'j'k'))$ are close to each other. In other words, when triplet of vertices (forming a triangle) correctly map to each other, they would have similar Jacobian based features.

Next, we verify the effectiveness of the proposed Jacobian based descriptors (Section 3) compared with using PSL spatial coordinates (2DSC) [6, 7] and spatially-normalized PSL coordinates (2DSNC) [2, 4] resulting from the back template [1]. We apply different matching algorithms including: coherent point drift (PAMI10) [11], spectral graph matching (ICCV05) [12], hypergraph matching (CVPR08) [5], tensor based graph matching (PAMI11) [13], and our self-learning based method (MICCAI12) using different node descriptors. Figure 5 shows the PSL matching errors defined as:

$$\Delta_M(\hat{\mathcal{X}}, \mathcal{X}^*) = \|\hat{\mathcal{X}} - \mathcal{X}^*\|_2 \quad (9)$$

where $\mathcal{X}^*$ and $\hat{\mathcal{X}}$ are the ground truth and the estimated matchings, respectively. As evident from Figure 5, the best performance is achieved by the proposed Jacobian based descriptors.

5. CONCLUSION

We proposed a new set of Jacobian based graph descriptors, which enforce topology preservation into the graph matching problem. We showed that considering our new descriptors when performing PSL tracking improves the matching accuracy. As future work, we consider extending and applying our method to 3D graph matching.

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