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Skin lesion tracking using structured graphical models

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ABSTRACT

An automatic pigmented skin lesions tracking system, which is important for early skin cancer detection, is proposed in this work. The input to the system is a pair of skin back images of the same subject captured at different times. The output is the correspondence (matching) between the detected lesions and the identification of newly appearing and disappearing ones. First, a set of anatomical landmarks are detected using a pictorial structure algorithm. The lesions that are located within the polygon defined by the landmarks are identified and their anatomical spatial contexts are encoded by the landmarks. Then, these lesions are matched by labeling an association graph using a tensor-based algorithm. A structured support vector machine is employed to learn all free parameters in the aforementioned steps. An adaptive learning approach (on-the-fly vs offline learning) is applied to set the parameters of the matching objective function using the estimated error of the detected landmarks. The effectiveness of the different steps in our framework is validated on 194 skin back images (97 pairs).

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1. Introduction

1.1. Background

Malignant melanoma (MM) is one of the common cancers among the white population (American Cancer Society, 2009). It has been shown that the presence of a large number of pigmented skin lesions (PSLs) is an important risk factor for MM (Gallagher & McLean, 1995). For early detection of MM, dermatologists advocate *total body photography* for high-risk patients. Regular examination and comparison of the skin using 2D digital pictures collected at different times can help identify newly-appearing, disappearing, and changing PSLs (Gachon et al., 2005). However, tracking PSLs in skin images is time consuming and error prone with large inter- and intra-rater variability. Recently, a few works have been proposed towards an automatic system for tracking PSLs (Huang & Bergstresser, 2007; Mirzaalian et al., 2009; 2012), which mostly focused on the PSL matching task, where the positions of the PSLs and a set of anatomical landmarks (LNDs) are assumed to be known. In order to develop an end-to-end PSL tracking system, we need to detect the PSLs and LNDs automatically as well as perform PSL matching. In the remaining of the introduction section, we review the steps required for building such an automatic PSL tracking system.

1.1.1. LND detection

There exist many techniques for automatic LND detection based on feature points (Perakis et al., 2010; Potesil et al., 2011; Segundo et al., 2007; Xiea et al., 2014). In general, these methods consider a set of appearance models of the LNDs and their geometric relations to regularize the final detected LNDs. To the best of our knowledge, no work has been done on automatic LND detection on skin back images.

1.1.2. PSL detection

A notable number of methods have been proposed for PSL segmentation on *dermoscopic* images, which show *close-ups* on lesions, but not for skin back images in total-body photography, which are two different problems. The following are the key existing works on PSL detection on wide-area skin images. Sang et al. (2007) detected potential PSL candidates on skin images of human arms by using feature vectors of steerable filter responses as input to a support vector machine (SVM) classifier. Pierrard and Vetter (2007) applied Laplacian of Gaussian filter to enhance PSLs and then defined a saliency measurement to select the potential enhanced structures on face skin images. The most closely related PSL detection method for our application (i.e. back images) is the one by Lee et al. (2005), in which they, first, applied thresholding to the output of an image enhanced by an adaptive Gaussian kernel. Then, they detected potential PSL candidates in the thresholded binary image based on geometric feature (e.g. area and elongation).

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1.1.3. PSL matching

Finding the mapping between the PSLs in a pair of images can be formulated as a graph matching problem. There exists extensive research on point matching as a graph labeling problem. In general, these methods construct a matching cost function including unary, binary, and ternary terms to measure matching compatibilities between the single, pair-wise, and triplet-wise correspondences. A common basic constraint is that each vertex in one graph be mapped to at most one point in the other one, and vice versa. To search for a crisp solution or a fuzzy solution different optimization approaches have been applied to minimize the matching cost function, e.g. dual decomposition, spectral and tensor-based formulation, successive projections to find marginalization-matrix, gradient descent on Taylor expansion, genetic algorithm, and expectation-maximization. In Table 1, we compare the state-of-the-art point matching algorithms in terms of the order of the cost function (single, pair-wise, and triplet-wise) and the optimization approach.

Despite extensive research on graph matching, only a few works specifically focus on PSL matching. Huang and Bergstresser (2007) developed a PSL matching algorithm using a PSL-based Voronoi decomposition of the image space. However, the Voronoi decomposition changes dramatically when one or more PSLs appear or disappear causing the matching to fail. To normalize PSL coordinates prior to PSL matching, we previously proposed a landmark-based non-rigid warping of the back images to a unit-square template (Mirzaalian et al., 2009; 2012). However, this approach suffers from the following weaknesses: it requires an accurate segmentation of the back silhouette; the warping is influenced by all landmarks equally, even when certain landmarks are clearly more stable than others; and undesired distortions may occur for subjects requiring large warps.

Another observation on the existing point matching algorithms is that only a few papers propose a solution for learning the optimal set of parameters for graph matching. Leordeanu et al. (2011a); 2011b) applied gradient descent to minimize the error of their non-convex spectral-based formulation. Caetano et al. Caetano et al. (2009) applied a max-margin structured estimation technique to learn the parameters of quadratic assignment relaxation problems.

1.2. Our contributions

We formulate all the aforementioned steps (LND detection, PSL localization, and PSL matching) as optimization problems. *Our first contribution* is parts-based graphical models (Felzenszwalb & Huttenlocher, 2005) for detecting the LNDs. The detected LNDs serve two purposes: they restrict the search space to a polygon during lesion localization and encode the anatomical spatial context of lesions (Section 2.1). The latter encoding is a novel PSL descriptor that we leverage for PSL matching.

Our second contribution is to improve PSL-detection approaches by using a new set of Hessian-based descriptors (Section 2.3). Applying a random forest (RF) classifier, we compute a likelihood map for the presence of PSLs. Then, only the pixels inside the aforementioned polygon having a large likelihood value and belonging to a large enough connected component, are used in the subsequent PSL matching (Section 2.3).

As *our third contribution*, we devise a new landmark-based PSL descriptor that encodes uncertainty in the automatically detected LNDs and does not rely on any warping (Section 2.4). This descriptor is reminiscent of shape context (Belongie et al., 2002), with the key conceptual difference that we capture spatial context with respect to the anatomical landmarks without constructing any histogram.

Similar to many medical image analysis problems, our formulations require setting objective functions with hyperparameters. In the *fourth contribution*, we apply structured support vector machine (SSVM) (Joachims et al., 2009) to learn the free parameters (Sections 2.2). Thus, the proposed system is called the structured skin lesion tracking system.

Because of the dependence of the PSL descriptors on the detected LNDs, in *our final contribution*, we propose an adaptive system that, first, predicts the error in the detected LNDs and, then leverages the measured error to adapt (on-the-fly vs offline learning) the PSL matching (Section 2.6).

In contrast to the earlier works on graph matching (Table 1), our PSL matching technique uses the three terms (unary, binary, ternary) together using a spectral-based optimization algorithm. We learn the hyperparameters of our objective function using SSVM.

In Table 2, we compare existing works on automatic lesion tracking systems. In contrast to the previous works on skin lesion tracking, the three tasks of LND detection, PSL detection, and PSL matching are performed automatically. Further, our method is unique in including parameter learning and consideration of uncertainty and predicted-error.

We evaluate the effectiveness of the different steps in our framework on 194 skin back color images (97 pairs). The results are presented in Section 3, followed by concluding remarks in Section 4.

2. Method

A summary of our framework is presented in Fig. 1. Given two 2D color skin images $\mathcal{I}$ and $\mathcal{I}'$, the goal is to detect PSLs in these two images and match (correspond) them. Let $\mathcal{V}$ represent the set of PSLs in $\mathcal{I}$ (similarly for $\mathcal{V}'$ in $\mathcal{I}'$). We define a matching matrix $\mathcal{X}$, such that if $\mathcal{V}_i \in \mathcal{V}$ matches (corresponds to) $\mathcal{V}'_j \in \mathcal{V}'$ then $\mathcal{X}_{ij} = 1$

Table 1
Comparison between different point matching methods in terms of the order of the energy terms in the cost function (unary, binary, and ternary), the optimization approach, and the hyperparameter learning.

Reference	Unary	Binary	Ternary	Optimization approach	Learning
Huang and Bergstresser (2007)	✓	×	×	Dynamic programming	×
Berg et al. (2005); Gold and Rangarajan (1996)	✓	✓	×	Taylor expansion and Gradient descent	×
Leordeanu et al. (2011b)	✓	✓	✓	Taylor expansion and Gradient descent	✓
Torresani et al. (2008)	✓	✓	×	Dual decomposition	×
Zeng et al. (2010)	✓	✓	✓	Dual decomposition	×
Ansari et al. (1990), Tico and Rusu (1998), Zhang et al. (2010), Xing et al. (2011)	✓	×	×	Genetic algorithm	×
Zhang (1994)	✓	×	×	Expectation-maximization	×
Myronenko et al. (2007), Gold et al. (1998), Jian and Vemuri (2005), Belongie et al. (2002), Zheng and Doermann (2006), Chui and Rangarajan (2003), Escolano et al. (2011)	✓	✓	×	Expectation-maximization	×
Wyk and Wyk (2004)	✓	✓	×	Marginalization	×
Zass and Shashua (2008)	✓	✓	✓	Marginalization	×
Leordeanu and Hebert (2005), Cour et al. (2006), Mirzaalian et al. (2009)	✓	✓	×	Spectral based	×
Leordeanu et al. (2011a), Caetano et al. (2009)	✓	✓	×	Spectral based	✓
Duchenne et al. (2011), Chertok and Keller (2010), Mirzaalian et al. (2012)	✓	✓	✓	Spectral based	×
Proposed	✓	✓	✓	Spectral based	✓

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