Building dynamic population graph for accurate correspondence detection

Shaoyi Du [a,b], Yanrong Guo [b], Gerard Sanroma [b], Dong Ni [c,*], Guorong Wu [b], Dinggang Shen [b,d,*]

[a] *Institute of Artificial Intelligence and Robotics, Xi'an Jiaotong University, Xi'an, Shaanxi 710049, China*
[b] *Department of Radiology and Biomedical Research Imaging Center, University of North Carolina, Chapel Hill, NC 27599, USA*
[c] *The Guangdong Key Laboratory for Biomedical Measurements and Ultrasound Imaging, Department of Biomedical Engineering, Shenzhen University, Shenzhen 518060, China*
[d] *Department of Brain and Cognitive Engineering, Korea University, Seoul 02841, Republic of Korea*

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ABSTRACT

In medical imaging studies, there is an increasing trend for discovering the intrinsic anatomical difference across individual subjects in a dataset, such as hand images for skeletal bone age estimation. Pair-wise matching is often used to detect correspondences between each individual subject and a pre-selected model image with manually-placed landmarks. However, the large anatomical variability across individual subjects can easily compromise such pair-wise matching step. In this paper, we present a new framework to simultaneously detect correspondences among a population of individual subjects, by propagating all manually-placed landmarks from a small set of model images through a dynamically constructed image graph. Specifically, we first establish graph links between models and individual subjects according to pair-wise shape similarity (called as *forward step*). Next, we detect correspondences for the individual subjects with direct links to any of model images, which is achieved by a new multi-model correspondence detection approach based on our recently-published sparse point matching method. To correct those inaccurate correspondences, we further apply an error detection mechanism to automatically detect wrong correspondences and then update the image graph accordingly (called as *backward step*). After that, all subject images with detected correspondences are included into the set of model images, and the above two steps of *graph expansion* and *error correction* are repeated until accurate correspondences for all subject images are established. Evaluations on real hand X-ray images demonstrate that our proposed method using a dynamic graph construction approach can achieve much higher accuracy and robustness, when compared with the state-of-the-art pair-wise correspondence detection methods as well as a similar method but using static population graph.

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1. Introduction

Correspondence detection (Shen et al., 1999) is a fundamental problem in medical image analysis with a wide range of applications, such as skeletal bone age estimation (BAE) (Martin-Fernandez et al., 2003; Thangam et al., 2012), medical image registration (Xue et al., 2006; Yang et al., 2008; Heimann and Meinzer, 2009; Tang et al., 2009; Wu et al., 2011), and organ detection and segmentation (Zhan et al., 2008; Shi et al., 2010; Zheng et al., 2010). For the case of computational anatomy, robust correspondence detection is a key step to allow the quantitative measurement of anatomical difference across individuals. However, it is still challenging for accurate correspondence detection, especially between the subjects with very large anatomical differences.

Given a set of landmarks in the model images (delineated either manually (Styner et al., 2003; Murphy et al., 2008; Castillo et al., 2009) or automatically (Criminisi et al., 2010; Ou et al., 2010; Paganelli et al., 2012)), the goal of correspondence detection is to determine the corresponding location of each landmark in the subject images. The existing pairwise correspondence detection methods can be roughly classified into two categories, according to the correspondence relationship and the expression of geometric transformation. The **first** category of methods determines point-to-point correspondences and geometric transformation simultaneously, such as iterative closest point algorithm (ICP) (Besl and McKay, 1992), thin plate spline–robust point match (TPS-RPM) (Chui and Rangarajan, 2003), etc. These methods mostly focus on point-to-point correspondences and model the whole transformation between the two point sets explicitly. The **second** category of methods takes into account

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* Corresponding authors at: Department of Radiology and Biomedical Research Imaging Center, University of North Carolina, Chapel Hill, NC 27599, USA; and Department of Biomedical Engineering, Shenzhen University, Shenzhen 518060, China.
    E-mail address: dgshen@med.unc.edu (D. Shen).

pair-to-pair relationship. They mostly represent the geometric transformation implicitly, but focus on the correspondence searching, such as using graph-based methods. Graph-based methods have shown their potential in medical imaging applications by modeling *not only* the point-to-point correspondence (Zhang and Lu, 2004; Jiang et al., 2007) *but also* the pair-to-pair consistency (Leordeanu and Hebert, 2005; Zass and Shashua, 2008). Many scholars have developed various graph-based methods (Duchenne et al., 2011; Sanromà et al., 2012; Sanromà et al., 2012). Guo et al. (Guo et al., 2013) introduced a sparsity constraint into the conventional graph matching method for more accurate and robust correspondence detection.

Apart from these pairwise correspondence detection methods, some scholars also studied various groupwise models for correspondence detection. Donner et al. (Donner et al., 2009) proposed a MRF model for groupwise model learning. Adeshina and Cootes (2010a, 2010b) and Zhang et al. (Zhang et al., 2012; Zhang and Cootes, 2012) proposed parts-based methods for initializing groupwise registration. Although these matching methods have been successfully used for correspondence detection, they still have limitations in detecting correspondences between images with large anatomical difference, such as in medical studies that often involve a large amount of images with variable anatomical shapes.

In the past, some methods have been proposed for addressing the above challenges. For example, in the case of image segmentation, Wolza et al. (Wolza et al., 2010) proposed the learning embeddings for atlas propagation (LEAP), which uses an intensity-based similarity to build a population graph for linking similar images in the neighboring nodes first. Then, they decomposed the task of segmenting all subjects into a series of easy segmentation tasks, i.e., (1) segmenting images with similar anatomical structures and (2) propagating segmentations forward to other nearby images, thus avoiding segmenting images with large structural discrepancies. However, the population graph built by LEAP does not prevent the propagation errors, since it is fixed throughout the whole segmentation procedure. Thus, this will lead to possible accumulation of segmentation errors due to the use of spurious graph links, since no mechanism is used to re-evaluate the population graph and then improve the segmentation results. More critically, the similarity measure used for building the population graph is simply computed with image intensity difference, which unfortunately has no direct relation with the shape of anatomical structure.

To address all the above issues, we propose using *dynamic population graph* for detecting correspondences among a set of individual images. Our method includes two steps, *forward step* and *backward step*, which are repeated until completion. In the **forward step**, we investigate shape discrepancies between any pair of images, instead of simply using the traditional image intensity similarity. Then, we build a *population graph* with the *nodes* representing (model or subject) images and the *edges* linking pairs of *model-subject* images with small shape differences. Note that we here establish correspondences only for the subject images with direct links to any of the model images. For the case that one subject image is linked to multiple model images, we propose a *multiple model selection and fusion method* for correspondence detection. In the **backward step**, we update the population graph according to the current correspondences just established, after removing correspondence detection errors in the *forward step* by using our proposed *error detection mechanism* which is built based on the shape similarity and the spatial relationship of all landmarks. As the result of this *backward step*, the inaccurate correspondence detection results are removed and also the set of model images is updated by including the subject images with their newly established correspondences. We repeat the above two steps until correspondences for all subject images are determined.

We comprehensively evaluate our proposed correspondence detection method on the real hand X-ray images. Compared with the state-of-the-art methods, our correspondence detection method (based on the *dynamic population graph*) achieves significant improvement, in terms of both accuracy and robustness.

The rest of this paper is organized as follows. In Section 2, we present our proposed method. In Section 3, we compare our method with the state-of-the-art methods. Finally, we draw the conclusion in Section 4.

2. Method

2.1. Overview of our proposed method

Conventional methods often detect correspondences independently between each subject image and the pre-defined model image. Thus, their performances are limited when subject and model images have large structural discrepancies. To address this issue, we propose a novel correspondence detection method by dynamically updating the *population graph* during the iterative correspondence detection procedure. The framework of our proposed method is depicted in Fig. 1.

Specifically, each image is regarded as a node in the population graph. In the **forward step**, we first build a population graph by linking between model images and their most similar subject images. Here, we use a novel shape similarity measurement, instead of simple image intensity similarity, as described in Section 2.2 for measuring the similarity of two images. Then, we determine correspondences for each subject image that is linked to any of model images by using the model image(s) linked to this subject image, as detailed in Section 2.3.1. For the case that a subject is linked to multiple model
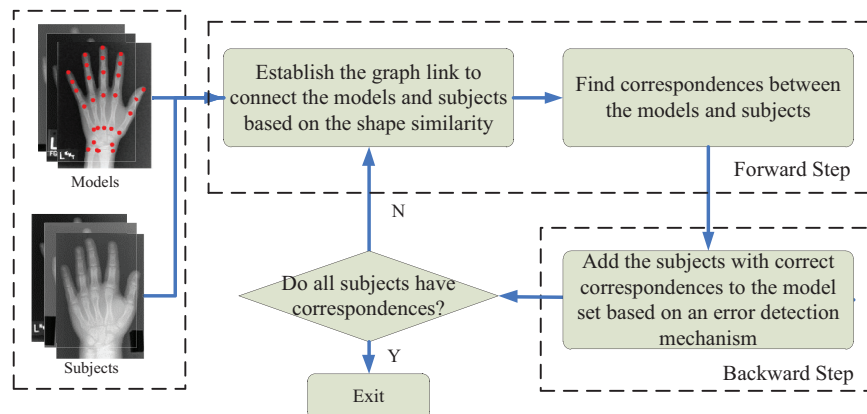

Fig. 1. Correspondence detection based on a dynamic population graph.