Robust point correspondence matching and similarity measuring for 3D models by relative angle-context distributions

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Abstract

Robust solutions for correspondence matching of deformable objects are prerequisite for many applications, particularly for analyzing and comparing soft tissue organs in the medical domain. However, this has proved very difficult for 3D model surfaces, especially for approximate symmetric organs such as the liver, the stomach and the head. In this paper, we propose a novel approach to establish the 3D point-correspondence for polygonal free-form models based on an analysis of the relative angle distribution around each vertex with respect to relative reference frame calculated from principal component analysis (PCA). Two kinds of distributions, the Relative Angle-Context Distribution (RACD) and the Neighborhood Relative Angle-Context Distribution (NRACD) have been defined respectively from the probability mass function of relative angles context. RACD describes the global geometric features while NRACD provides a hierarchical local to global shape description. The experiments and evaluation of adopting these features for the human head and liver models show that both distributions are capable of building robust point correspondence while the NRACD gives better performance because it contains additional information on the spatial relationship among vertices and has the ability to provide an effective neighborhood shape description. Furthermore, we propose a similarity measure between correspondence ready models based on relative angle-context distribution factors. The experimental results demonstrate that this approach is very promising for model analysis, 3D model retrieval and classification.
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1. Introduction

The ability to establish robust correspondence between 2D images and more recently, 3D objects is frequently a central issue in many image analysis paradigms, such as structure-from-motion [1], stereoposis [2], optical flow analysis [3], and deformable or morphable models [4,5], etc. This is particularly true in the medical and biological domains where robust solutions to the correspondence problem is vital to many applications such as organ growth measurement [4], histological section alignment [6], aesthetic surgical planning [7]. Recently, correspondence algorithms are becoming the fundamental building block for object segmentation techniques that make use of the classical as well as statistical deformable models [8–12] and for the construction of point distribution models [13]. A recent survey shows that solving the correspondence problem continues to be the central issue in many medical image registration algorithms [14].

With the increasing availability of large collections of 3D graphical models for a variety of applications, tech-

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niques that have been developed for image analysis, classification and content-based retrieval of 2D images are being extended for 3D models. This makes 3-dimensional morphological analysis [15], model classification [16], 3D graphical model indexing and retrieval [17] fast growing areas of active research. Among the many research issues that have been brought forth by these new topics, 3D correspondence problems have been identified as a major challenge and a prerequisite for many applications. For the last decade, researchers in the medical domain have been investigating robust techniques for 3D point correspondence matching of organs or anatomical structures. One of the most common approaches to determine the correspondence between sets of 3D model data is to match distinctive local features such as local geometric invariants. As a general method, one of the advantages of local invariants such as corners or curvature is that they are insensitive to occlusion [9,18]. Such features, however, are very sensitive to noise, although a multi-scale framework could alleviate this problem [19]. Usually for most applications the amount of local information is insufficient for robust matching, especially in 3D space. Modal matching was introduced in 1995 to find feature correspondence and perform object recognition [20,21]. They described objects in terms of generalized symmetries, which were defined by the object's eigenmodes. Since eigenmodes could provide a global to local ordering of shape deformation, point correspondence between two surfaces can be reliably determined by comparing their trajectories in this modal space. However, the technique that requires the calculation of eigenmodes and their interpolation for 3D points-set mass is computationally very expensive. Recently, Walkers et al. [22] tried to determine a globally consistent set of correspondences across all of the face images in a set using the transformation of a grid. However, the algorithm could not handle significant changes in scale and orientation, which are inevitably present for many medical applications.

In this paper, we focus on the problem of searching for the correspondence between the same classes of 3D graphical models that differ from each other through some form of non-linear deformation. Such models frequently occur in medical applications as the results of soft-tissue organ segmentation. The challenge posed by such soft-tissue organ models is that it is frequently difficult to define landmarks or to obtain salient geometric features from the model surfaces. To overcome this problem, we propose an intuitively simple but very effective and robust feature for 3D point correspondence matching. The feature is based on the distribution of Relative Angles (RAngs) in the vertex set. We introduce a vertex context descriptor, which is called Relative Angle-Context (RAC), to describe the shape of the surface around a vertex. We show that RAC is able to capture the global geometric information of the model from the point of view of any vertex as well as its local structures by associating each vertex of the model with a probability distribution of angles between vectors linking pairs of vertices. The correspondence between points or vertices in a pair of models can

then be cast as a problem of searching for a pair of points or vertices in the two matching models which have the most similar distribution. The experimental results indicate that our technique could establish robust point correspondence for 3D medical objects even for near spherical, as well as approximately symmetric organs such as livers and human heads, which have been shown to be very difficult for many local-invariant based algorithms. More importantly, since the algorithm is based on the distributions of the global and local relative angles context, it possesses the general qualities of statistical methods such as computational efficiency and robustness (insensitivity to noise). The other advantage of our method is that, for the surface points which have no truly 'accurate' correspondences, it could locate to correspondence region within a small neighborhood of the points. We show that the resulting point correspondence could be used to (i) construct active shape models (ASM) which requires knowledge of one to one point correspondence between all the sample models, and (ii) to compute the similarity between models of organs.

2. Literature review of statistical based geometric point correspondence matching

In the following, we will focus our review on previous approaches to point correspondence matching and model classification based on statistical analysis of geometric features. As a traditional but still very popular statistical approach, histograms have been widely investigated for representing, analyzing and characterizing 2D and 3D shapes. Unlike other feature representation, a histogram representation possesses an inherent structure which is governed by the probability density distribution of the underlying random variable. The most important advantages of histograms include computational efficiency, robustness to noise, invariance to image transformation and significant data reduction. There exist some techniques that construct histograms from shape attributes. For example, Evans et al. [23] proposed a two dimensional histogram of pair wise attributes for each line segment in the images to recognize objects. This approach was extended by DiMauro [24] by restricting the histogram binning only to segment pairs located in a region of interest. Huet et al. [25] proposed the construction of two-dimensional histograms based on relative angles and positions of directed segments in an image and found they were very effective and robust in 2D shape indexing and retrieval. A similar idea has been used by Belongie et al. [26] who used the distribution of relative coordinates of the vectors originating from a point as the shape context to solve for correspondence between similar 2D shapes.

Histogram-based retrieval has also been shown to operate effectively for indexing 3D volumetric or polygonal data, when the histogram is computed from surface normal information [27]. Recently, our group proposed an optimal classification representation of 3D head models based on surface normal orientation statistics [16]. In this work, the distribution of the surface normals are mapped to the