3D Point Correspondence by Minimum Description Length with 2DPCA

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Abstract— **Finding point correspondences plays an important role in automatically building statistical shape models from a training set of 3D surfaces. Davies et al. assumed the projected coefficients have a multivariate Gaussian distributions and derived an objective function for the point correspondence problem that uses minimum description length to balance the training errors and generalization ability.**

Recently, two-dimensional principal component analysis has been shown to achieve better performance than PCA in face recognition. Motivated by the better performance of 2DPCA, we generalize the MDL-based objective function to 2DPCA in this paper. We propose a gradient descent approach to minimize the objective function. We evaluate the generalization abilities of the proposed and original methods in terms of reconstruction errors. From our experimental results on different sets of 3D shapes of different human body organs, the proposed method performs significantly better than the original method.

I. INTRODUCTION

Finding point correspondence is essential for automatically building statistical shape models [1] from a training set of 3D surfaces. Statistical shape models are widely used in model-based image segmentation and tracking [1]. Davies *et al.* [2] assumed the projected coefficients have multivariate Gaussian distributions and derived an objective function for point correspondence problems that uses minimum description length (MDL) to balance the training errors and generalization ability. A recent evaluation study [3] that compares several well known 3D point correspondence methods for modeling purposes shows that the MDL-based approach [2] is the best method.

Recently, two-dimensional principal component analysis (2DPCA) [4] has been shown to achieve better performance than PCA in face recognition [4]. In contrast to the conventional method of using a vector to represent a shape, 2DPCA represent a shape by a two-dimensional matrix.

In this paper, we generalize the MDL-based objective function [2] to 2DPCA. We propose a gradient descent approach to minimize the objective function. We compare the generalized MDL objective function for 2DPCA with the original one and evaluate their abilities in terms of reconstruction errors. From our experimental results on different sets of 3D shapes of different organs, the proposed method performs significantly better than the original method.

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II. RELATED WORK

Assume that we have a training set of N 3D shapes and each shape is represented by M 3D landmarks points. Conventionally, we can represent each such shape by a vector $\mathbf{x}$ whose dimension is $3M \times 1$ and let $\Omega_t = \{\mathbf{x}_i | i = 1, \ldots, N\}$ denote the training set of N 3D shapes.

A. PCA

PCA is a common approach to model the shape variations of a given training set of 3D shapes. Given Ω_t, the total scatter matrix $\mathbf{S}$ is defined as

$$\mathbf{S} = \sum_{i=1}^{N} (\mathbf{x}_i - \bar{\mathbf{x}})^t (\mathbf{x}_i - \bar{\mathbf{x}}) \tag{1}$$

where $\bar{\mathbf{x}}$ is the mean shape vector as defined below.

$$\bar{\mathbf{x}} = \frac{\sum_{i=1}^{N} \mathbf{x}_i}{N} \tag{2}$$

PCA finds a projection axis $\mathbf{b}$ that maximizes $\mathbf{b}^t \mathbf{S} \mathbf{b}$. Intuitively, the total scatter of the projected samples is maximized after the projection of the samples onto $\mathbf{b}$. The optimal K projection axes $\mathbf{b}_k, k = 1, \ldots, K$ that maximize the above criterion are the eigenvectors of $\mathbf{S}$ corresponding to the largest K eigenvalues, $\{\lambda_k | k = 1, \ldots, K\}$. The reconstruction $\tilde{\mathbf{x}}$ of shape vector $\mathbf{x}$ can be used to approximate it.

$$\tilde{\mathbf{x}} = \bar{\mathbf{x}} + \sum_{k=1}^{K} c_k \mathbf{b}_k \tag{3}$$

where $c_k = (\mathbf{x} - \bar{\mathbf{x}})^t \mathbf{b}_k$.

B. Correspondence by Minimizing Description Length

Davies *et al.* [2] proposed a MDL-based objective function to quantize the quality of the correspondence. In this paper, we use the simplified version of the MDL, F, proposed by Thodberg [5] as defined below.

$$F = \sum_{k=1}^{N} L_k \text{ with } L_k = \begin{cases} 1 + \log(\lambda_k/\lambda_{cut}), & \text{if } \lambda_k \geq \lambda_{cut} \\ \lambda_k/\lambda_{cut}, & \text{otherwise} \end{cases} \tag{4}$$

Given a set of shapes and a set of known correspondences, PCA is computed on the set of shapes and the computed eigenvalues, $\{\lambda_k | k = 1, \ldots, N\}$, are used to calculate F in eqn. (4). λ_{cut} is a parameter that represents the expected noise in the training data and its value is manually determined.

Given the above MDL-based objective function, an efficient method for manipulating correspondences and an

optimization algorithm that minimizes the objective function are required in order to find optimal correspondences [1]. Typically, manipulating correspondences is treated as parameterizing and then re-parameterizing the surfaces. A parameterization assigns every point on the surface of the mesh to a unique point on the unit sphere, although parameterizations may not exist for arbitrary surfaces. In this paper, we assume that the 3D shapes are closed two-manifolds of genus 0 (e.g., a sphere). We use a conformal mapping as a parameterization and a reparameterization that modifies the parameterization based on kernels with strictly local effects, as developed in [6].

We assume that the parameterization of the ith shape is controlled by some parameter vector α_i, for which the individual parameters are given by $\{\alpha_{i,a} | a = 1, \ldots, A\}$. The gradient descent approach is used to minimize F with respect to a parameter vector α_i. The Jacobian matrix for the gradient of the objective function is defined as

$$\frac{\partial F}{\partial \alpha_{i,a}} = \sum_{k=1}^{N} \frac{\partial L_k}{\partial \lambda_k} \frac{\partial \lambda_k}{\partial \alpha_{i,a}} \quad (5)$$

It is easy to compute $\frac{\partial L_k}{\partial \lambda_k}$ and so we focus on $\frac{\partial \lambda_k}{\partial \alpha_{i,a}}$ in the following discussions. $\frac{\partial \lambda_k}{\partial \alpha_{i,a}}$ can be computed by using the following chain rule for derivatives.

$$\frac{\partial \lambda_k}{\partial \alpha_{i,a}} = \frac{\partial \lambda_k}{\partial \mathbf{x}_i}^t \frac{\partial \mathbf{x}_i}{\partial \alpha_{i,a}} \quad (6)$$

While $\frac{\partial \mathbf{x}_i}{\partial \alpha_{i,a}}$ is typically computed by using finite differences, the following analytic form for $\frac{\partial \lambda_k}{\partial \mathbf{x}_i}$ exists.

$$\frac{\partial \lambda_k}{\partial x_i} = 2 c_{i,k} \mathbf{b}_k \quad (7)$$

where $c_{i,k}$ is the projection coefficient of the i-th shape vector $\mathbf{x}_i$ onto the k-th eigenvector $\mathbf{b}_k$.

C. 2DPCA

The idea behind [4] is to project a $3 \times M$ shape matrix $\mathbf{X}$ onto an $M \times 1$ vector $\mathbf{b}$ by the linear transformation.

$$\mathbf{c} = \mathbf{X}\mathbf{b} \quad (8)$$

The 2DPCA scatter matrix $\mathbf{G}$ is defined as

$$\mathbf{G} = \sum_{i=1}^{N} (\mathbf{X}_i - \bar{\mathbf{X}})^t (\mathbf{X}_i - \bar{\mathbf{X}}) \quad (9)$$

where

$$\bar{\mathbf{X}} = \frac{\sum_{i=1}^{N} \mathbf{X}_i}{N} \quad (10)$$

Similar to PCA, the goal of 2DPCA is to find a projection axis that maximizes $\mathbf{b}^t \mathbf{G} \mathbf{b}$. The optimal K projection axes $\mathbf{b}_k, k = 1, \ldots, K$ that maximize the above criterion are the eigenvectors of $\mathbf{G}$ corresponding to the largest K eigenvalues. For a shape matrix $\mathbf{X}$, its reconstruction $\tilde{\mathbf{X}}$, defined below, can be used to approximate it.

$$\tilde{\mathbf{X}} = \bar{\mathbf{X}} + \sum_{k=1}^{K} \mathbf{c}_l \mathbf{b}_l{}^t \quad (11)$$

where $\mathbf{c}_k = (\mathbf{X} - \bar{\mathbf{X}})\mathbf{b}_k$.

III. THE PROPOSED METHOD

We extend the MDL-based objective function, eqn. (4), to 2DPCA. In other words, instead of using the eigenvalues computed by PCA, we propose to use those computed by 2DPCA. We propose a gradient descent approach to minimize the objective function based on the ideas in subsection II.B. to compute the Jacobian matrix for the gradient of the objective function. In order to reuse eqn. (5) and eqn. (6), eqn. (7) must be extended to 2DPCA. Let the eigendecomposition of $\mathbf{G}$ be defined by

$$\mathbf{D} = \mathbf{U}^T \mathbf{G} \mathbf{U} \quad (12)$$

where $\mathbf{D}$ is the diagonal matrix composed of the eigenvalues of $\mathbf{G}$, and $\mathbf{U}$ is a matrix composed of eigenvectors of $\mathbf{G}$. The extension of eqn. (7) to 2DPCA is defined by The extension of eqn. (7) to 2DPCA is approximated by

$$\frac{\partial \mathbf{D}}{\partial \mathbf{X}_i(j,k)} \approx \mathbf{U}^t (2(\mathbf{X}_i - \bar{\mathbf{X}})^t \mathbf{J}_{jk}) \mathbf{U} \quad (13)$$

where $\mathbf{J}_{jk}$ is a binary matrix all of whose elements are zeros, except the element at position (j,k), which is one.

IV. EXPERIMENTS

We have 3D triangular mesh models of 20 livers, 17 left kidneys, 15 right kidneys, and 18 spleens as shown in Figure 1. All 3D meshes are constructed from CT scans of different patients and the 3D point correspondence problems among different 3D mesh models of the organs are solved[1]. Our implementation is built on top of [7][6] that implements the ideas described in subsection II.B. All the mesh models of the same organ have the same number of vertices (2563) and the same number of faces (5120), and all vertices are used as landmarks to represent the shapes.

We follow a standard procedure extensively used in [2][1][3][6] to compare different point correspondence methods when the ground truth correspondences among different shapes are not available. Given the correspondences computed by different correspondence methods, the standard procedure is to measure the difference between an unknown shape and its reconstruction. Leave-one-out cross validation is used to determine how accurately an algorithm will be able to predict data that it was not trained on. In order to reflect different definitions of shape similarities, the Euclidean distance (i.e, the sum of the distances between all pairs of corresponding landmarks) and Hausdorff distance[2] are used to measure the shape difference between two shapes.

[1]We constructs the shape of an organ from manual segmentation of CT scans of a patient by using marching cubes in ITK-SNAP

[2]Given a pair of two 3D point sets, A and B, the Hausdorff distance between A and B is given by:

$$H(A,B) = \max\{\min_{p \in A} \min_{q \in B} d(p,q), \min_{q \in B} \min_{p \in A} d(p,q)\} \quad (14)$$

where $d(p,q)$ is the Euclidean distance between two 3D points, p and q. To compare a pair of two shapes, the Hausdorff distance between the two vertex sets of this given pair of shapes is computed.

Even though different correspondence methods use different kinds of criteria [1][3] to find the correspondences, the standard procedure [2][1][3][6] uses PCA to model the variations of the shapes whose correspondences are estimated. A potential problem here is that using PCA is biased to the MDL objective function, because the sum of eigenvalues is a good indicator for estimating the reconstruction errors and the computation of the MDL objective function [2] involves the eigenvalues of PCA. To avoid this potential problem and to be more fair, the original MDL method uses PCA to model shapes, while our extension uses 2DPCA to model shapes.

Figures 2 and 3 show the average leave-one-out reconstruction errors for different organs. From these two figures, it is clear that the combination of the proposed MDL for 2DPCA and reconstruction using 2DPCA is better than the combination of MDL for PCA and reconstruction using PCA in all test data sets. In addition, as the number of eigenvectors in use increases, the reconstruction error decreases, due to the use of more variables to encode the shape variations. However, as the number of eigenvectors in use increases, the differences between the reconstruction errors of these two methods decreases (Figure 2), while as the numbers of eigenvectors in use increases, the difference between the reconstruction errors of these two methods can increase accordingly (Figure 3). One possible explanation is that the MDL objective functions and the error measures being minimized are all related, to some degree, to Euclidean distances, and so their performances may potentially converge to similar reconstruction errors in terms of Euclidean distance if there is infinite training data. However, their performances may not converge to similar reconstruction errors in terms of Hausdorff distance.

V. Conclusions and Future Work

In this paper, we generalize the MDL-based objective function to 2DPCA and propose a gradient descent approach to minimize the objective function. From our experimental results on different sets of 3D shapes of different organs, the combination of the proposed MDL for 2DPCA and reconstruction using 2DPCA is significantly better than the combination of MDL for PCA and reconstruction using PCA.

Instead of using the reconstruction errors, which depend on the particular reconstruction methods, to compare different correspondence methods, we plan to use some datasets whose ground truth correspondences are known to directly compare the proposed method with other existing methods. In addition, many different methods [8][9][10] for modeling shapes have been shown to have better potential than PCA. How to generalize MDL-based objective functions to these different approaches is an important direction we will pursue. Furthermore, we would like to relax the assumptions Davies *et al.* made in [2]. One such assumption is that the projected coefficients in different eigenvectors are independent. However, this assumption may not hold in 2DPCA or the general case.
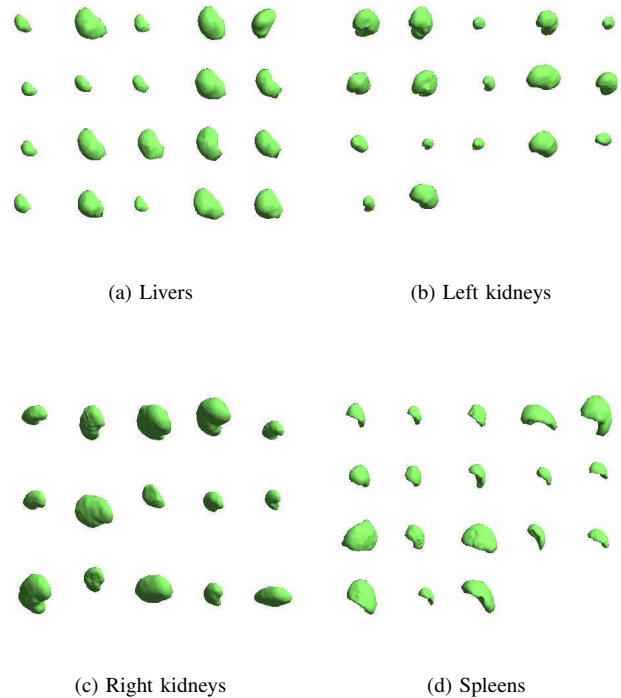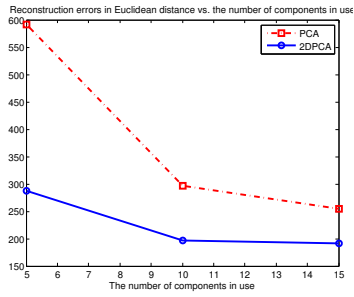

(a) Livers   (b) Left kidneys

(c) Right kidneys   (d) Spleens

Fig. 1: The 3D triangular meshes of different organs we use in the experiments.

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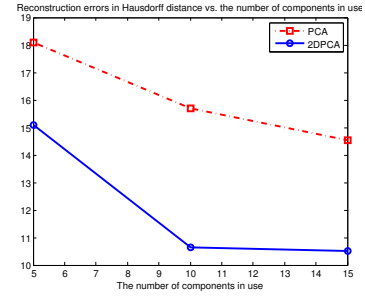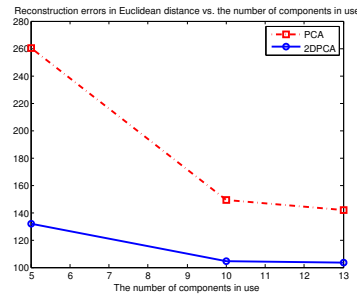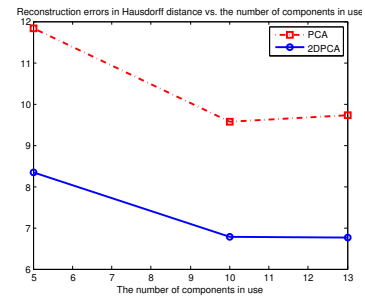
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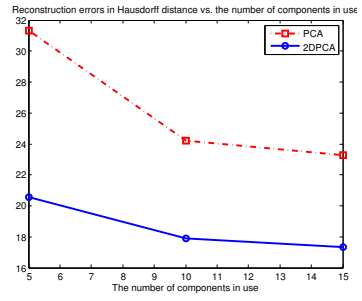
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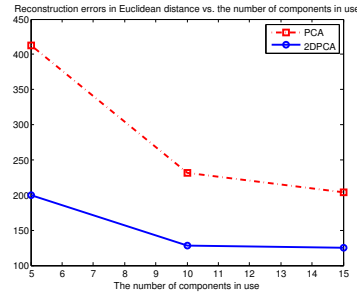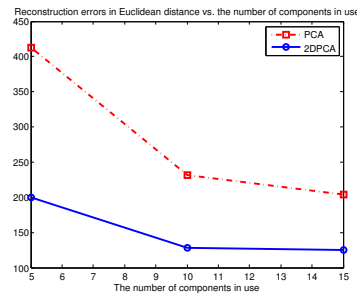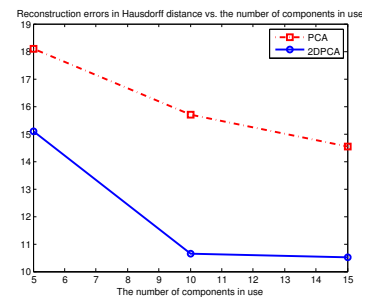

(b) Left kidneys

(b) Left kidneys

(c) Right kidneys

(c) Right kidneys

(d) Spleens

(d) Spleens

Fig. 2: Generalization ability comparisons in terms of Euclidean distance in different datasets.

Fig. 3: Generalization ability comparisons in terms of Hausdorff distance in different datasets.