Statistical Texture Modeling for Medical Volume Using Generalized N-Dimensional Principal Component Analysis Method and 3D Volume Morphing

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Abstract

In this paper, a statistical texture modeling method is proposed for medical volumes. As the shapes of the human organ are very different from one case to another, 3D volume morphing is applied to normalize all the volume datasets to a same shape for removing shape variations. In order to deal with the problems of high-dimension and small number of medial samples, we propose an effective image compression method named Generalized N-dimensional Principal Component Analysis (GND-PCA) to construct a statistical model. Experiments applied on liver volumes show good performance on generalization using our method. A simple experiment is employed to show that the features extracted by the statistical texture model have capability of discrimination for different types of data, such as normal and abnormal.

1. Introduction

In order to interpret of images of structures and variations for the internal organs of human body, it is important to construct a statistical model for organs.

Statistical modeling [1] is one kind of modeling technique and is a hot topic in recent research. According to the different type of target information, statistical model can be classified into statistical shape model and statistical appearance model [2]. Statistical shape model is focus on the shape information, such as feature points and volume surface. It is a useful tool to study variation in anatomical shape and have been wildly used in medical image analysis, for example, medical image segmentation [3] and shape registration [4]. Statistical appearance model is focus on both shape and texture (pixel intensity) information.

For medical diagnosis, texture conveys more useful diagnostic information. Radiologists are mainly depending on the intensity variations of organs on medical images to make a diagnostic decision. There is little report concerned with texture modeling in application of medical analysis because there are several problems need to deal with: (1) **High-dimensional data**. For example, Computed Tomography scan (CT-scan) can be seen as 3-dimensional (3D) data; (2) **Small samples of medial volumes**. It is difficult to access a large number of volume datasets; (3) **Individual shape differences**. Organ shapes are different from one case to another.

In this paper, we propose an approach for constructing a statistical texture modeling for medical organ volumes. Our method is based on our previously proposed tensor-based Generalized N-dimensional Principal Component Analysis (GND-PCA) [5]. Experiments on both MR brain volumes and CT lung volumes show that GND-PCA method has good performance on generalization of high-dimensional data even though the training samples are quite few. But in our previous work, the GND-PCA based statistical models describe a mixed variation of shape and texture. In order to apply the statistical modeling technique to computer aided diagnostics (CAD), we have to describe the shape variation and the texture (pixel intensity) variation separately. So we propose to use a 3D volume morphing technique to normalize all the volume datasets to a same shape in order to remove shape variations. The morphed datasets just contain the texture variations. Then we use them to construct the statistical texture model by GND-PCA method. Our proposed method is applied on liver volumes. Reconstruction results show good performance on generalization by using our method. We also did a
simple experiment to classify different type of data, such as normal and abnormal.

2. Statistical Texture Modeling

Our proposed methodological framework for statistical texture modeling consists of two parts: (1) employ a non-rigid transformation for 3D liver morphing; (2) apply GND-PCA method for statistical modeling.

2.1. 3D Volume Morphing

In order to remove shape variations, we apply a non-rigid transformation based on mathematical forms for morphing all the datasets to a same shape. This is because that the mathematical non-rigid transformations are simpler and they can make the registration faster. Additionally, we do not need to assume the physical parameters which are difficult to be guessed in practice. Hence, we adopt the mathematical non-rigid transformations in our research.

Here, we applied rigid transformation for global transformation and B-spline transformation for local transformation. The combination of global and local transformations can be represented by:

\[ T(x) = T_{\text{Global}}(x) + T_{\text{Local}}(x) \]  

where \( x = [x, y, z]^T \) is the coordinate of a 3D point.

A rigid transformation is expressed by

\[ T_{\text{Global}}(x) = Rx + t \]  

where \( R \) is the rotation matrix which can be calculated from the rotation angles \( \theta = [\theta_x, \theta_y, \theta_z]^T \) around each axis. \( t \) is the translation vector \( t = [t_x, t_y, t_z]^T \) along each axis. There are 6 parameters should be estimated.

The local motion is described by a cubic B-spline based free form deformation (FFD) modeling [6]. FFD is based on locally controlled functions such as B-spline and has been successfully applied for image registration. The basic idea of FFD is to deform an object by manipulating an underlying mesh of control points. B-spline transformation is defined on a regular mesh of control points with uniform spacing. Let \( \rho = [\rho_x, \rho_y, \rho_z]^T \) to be the spacing of the control points along each axis, the coordinate of a control point can be expressed by

\[ \phi_{ij} = \phi_{ijk, x, y, z} = [i \rho_x, j \rho_y, k \rho_z]^T, \]

where \( i, j, k \) are the sequence number of the control points. Given the coefficients (translations) of the control points denoted as \( \lambda_{ijk} = [\lambda_{ijk, x}, \lambda_{ijk, y}, \lambda_{ijk, z}]^T \), the B-spline transformation of a point \( x \) can be expressed by

\[ T_{\text{Local}}(x) = \sum_{ijk} \lambda_{ijk} \beta^3 \left( \frac{x - \phi_{ijk, x}}{\rho_x} \right) \beta^3 \left( \frac{y - \phi_{ijk, y}}{\rho_y} \right) \beta^3 \left( \frac{z - \phi_{ijk, z}}{\rho_z} \right) \]  

where \( \beta^3(a) \) is the third order cubic B-spline kernel. The coefficients of the control points, \( \lambda_{ijk} \), are the parameters of B-spline transformation.

The parameters of global and local transformation are optimized separately.

2.2. GND-PCA Method

Inspired from the framework of Generalized 2-Dimensional Principal Component Analysis [7] and N-Dimensional Principal Component Analysis [8], we proposed a method called GND-PCA. The high-dimensional data is treated as a series of higher-order tensors and the optimal subspace on each mode are simultaneously calculated by minimizing the square error between the original tensor and the reconstructed tensor based on the subspace with an iteration algorithm.

GND-PCA is formalized as follows: Given a series of the N-order tensors with zero-means \( \mathcal{A}_i \in \mathbb{R}^{l_i \times d_i \times d_i \times d_i} \), \( i = 1, 2, \ldots, M \), where \( M \) is the number of samples. We hope to get another series of low rank \((J_1, J_2, \ldots, J_N)\) tensors \( \mathcal{A}_i^* \) which accurately approximate the original tensors, where \( J_n \leq l_n \). The new series is decomposed by the matrices \( \mathbf{U}^{(n)} \in \mathbb{R}^{l_n \times J_n} \) with orthogonal columns according to Tucker Model [9] which is shown by

\[ \mathcal{A}_i^* = \mathbf{b}_i \mathbf{x}_i \mathbf{U}^{(1)} \times_1 \mathbf{U}^{(2)} \times_2 \cdots \times_n \mathbf{U}^{(n)} \times_n \mathbf{U}^{(N)} \]  

where \( \mathbf{b}_i \in \mathbb{R}^{J_1 \times J_2 \times \cdots \times J_N} \) are core tensors. The illustration of reconstructing a third order tensor by three orthogonal bases is shown in Fig.1.

The orthogonal matrices \( \mathbf{U}^{(n)} \) can be determined by minimizing the cost function as:

\[ C = \sum_{i=1}^{M} \left\| \mathcal{A}_i - \mathbf{b}_i \times_1 \mathbf{U}^{(1)} \times_2 \cdots \times_n \mathbf{U}^{(n)} \times_n \mathbf{U}^{(N)} \right\|_2. \]

Supposing the rank of the \( N \) matrices \( \mathbf{U}^{(n)} \) are known, we use an iteration algorithm to get the \( N \) optimal matrices, \( \mathbf{U}_{Opt}^{(1)} \times_1 \mathbf{U}_{Opt}^{(2)} \cdots \times_n \mathbf{U}_{Opt}^{(N)} \), which are able to minimize the cost function \( C \).

![Fig.1: Reconstruction of a three order tensor by the three orthogonal bases of mode subspace.](image)
Here each matrix $U^{(e)}$ contains a set of basis vectors. An input sample can be calculated as a core tensor with the benefit of $U^{(e)}$. This core tensor is the feature of the input sample.

Details about GND-PCA can be referred to [5].

3. Experimental Results

3.1. Datasets

The dataset we used to test the proposed method contains 23 abdominal CT-scans collected from 23 patients under similar conditions of illuminations and scanner settings. This dataset contains 19 cases with no radiological found (noted as normal) and 4 cases with radiological found (noted as abnormal). The dimension of each sample is $256 \times 256 \times 79$. Initially livers are segmented from the datasets manually. Then we apply a rigid-registration [10] for pose normalization. Such pre-treated datasets are noted as original datasets. As we mentioned in previous section, we also apply a non-rigid registration (3D morphing) to the dataset for both pose and shape normalization to remove shape variation. The shape-normalized volumes are noted as morphed datasets. Some original datasets and their morphed data are shown in Fig.2.

3.2. Statistical Modeling

The proposed GND-PCA is applied to both original and morphed datasets. The leave-one-out experiment is done to test the generalization ability of GND-PCA. As the small number of abnormal datasets of liver, we just use 15 datasets to learn the optimal subspaces and the left-untrained one of the others is used as an input. The typical results are shown in Fig.3 and Fig.4. The test volume is reconstructed from $10 \times 10 \times 4$ and $100 \times 100 \times 40$ mode-subspace basis by GND-PCA, respectively. It can be seen that the reconstructed images were improved by increasing the sub-space basis. In spite of very few samples, we still can obtain an almost perfect reconstruction with $100 \times 100 \times 40$ basis. In order to make a comparison, we also show the reconstructed results by conversional PCA (Eigenface) method in Figure 3(d) and Figure 4(d). It can be seen that the quality of the reconstructed results are not satisfied even though the entire 15 available basis are used for reconstruction because of overfitting.

The Normalized Correlations between the original volume and the reconstructed volume and are shown in Fig.5. Compared with in the case of original dataset, the datasets can be represented by a fewer number of
basis in the case of morphed dataset because the subspace contains only texture variations.

3.3. Features for Classification
Following we introduce a simple experiment to show that the features extracted by our methods have capability of discrimination. We just used 15 normal datasets for training and leave the other 8 datasets for testing. The testing samples contain 4 normal datasets and 4 abnormal datasets. After we got optimal subspace by GND-PCA method, each sample is represented by a core tensor. The core tensor is the feature of the sample and noted as \( B_i \). We also calculate the mean feature of all the training datasets and noted it as \( B_{Center} \). Here the dimension of core tensor is \( 100 \times 100 \times 40 \).

Euclidean distance (ED) is applied to calculate the distance between \( B_i \) and \( B_{Center} \). Fig.6 shows the ED for all the testing samples. Compared with the ones in original datasets, the distances decreased in the morphed datasets experiments. It demonstrated that shape variations are removed through 3D volume morphing.

![Fig.6: Euclidean distances of features.](image)

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<th>Table 1: Classification Result.</th>
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<td>Class</td>
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<tr>
<td>Original Data Experiment</td>
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<td>Morphed Data</td>
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Since we only use normal samples as training samples, we use the largest ED of training sample (LDT) which is also shown in Fig.6, as a boundary of normal data and abnormal for classification. Table 1 gives the classified results for two kinds of datasets experiments. It demonstrated that the features extracted by our method have better performance for discriminations between the normal class and abnormal class.

4. Conclusion
In this paper, we proposed a framework for statistical texture modeling using GND-PCA method and 3D volume morphing. Experiments on liver volume data show that our method can represent the data more efficient and the features extracted by our method have the capability of discrimination for different types of data. In future, we will test our method with more datasets for classification and focus on finding out the specific basis vectors of each optimal subspace which are mainly helpful for the judgment of normal or abnormal.

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References