

Semi-Supervised Affine Alignment of Manifolds

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Abstract

High dimensional data is usually produced by the source that only enjoys a limited number of degrees of freedom. Manifold learning technique plays an important part in finding the correlation among the high dimensional data datasets. By making use of manifold alignment, the paired mapping relationship can be explored easily. However, the common manifold alignment algorithm can only give the mapping result of the training set, and cannot deal with a new coming point. A new manifold alignment algorithm is proposed in this paper. The benefit of our algorithm is two fold: First, the method is a semi-supervised approach, which makes better use of the local geometry information of the unpaired points and improves the learning effect when the labeled proportion is very low. Second, an extended spectral aggression trick is used in the algorithm, which can produce a linear mapping between the raw data space and the aligned space. The experiments result shows that, the correlation mapping can be precisely obtained, the hidden space can be aligned effectively, and the cost of mapping a coming point is very low.

Keywords: manifold alignment, out of sample, affine transformation, spectral regression

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1. Prefix

High dimensional data is usually produced by the source that only enjoys a limited number of degrees of freedom (e.g. many head image sequence obtained only by changing light and pos parameters). This kind of data can be thought of as having a low-dimensional manifold embedded, and the degree of the freedom is the intrinsic dimensionality. By unfolding the manifold, the influential factor can be observed. In recent years, many techniques [1-6] are proposed to distill the embedded low-dimensional manifold. These algorithms avoid the curse of dimensionality and have been successfully applied to the fields of high-dimensional data visualization, data compression, data classification, correspondence learning [7].

Correspondence learning is primarily inspecting the inner correspondence between data sets, learning the shared latent structure, and finding the mapping relationship. Given some paired corresponding points, if the two high dimensional data sets can be mapped into a global low-dimensional space, the relationship between them can be inspected clearly. This procedure is something like aligning the manifolds together with some given information. There has been a body of work related to this problem. Ham et al [8] uses a global Laplace graph [2] to describe the local geometry structure of multiple high-dimensional data sets, and get their low-dimensional embedding by spectral decomposition. Verbeek et al [9] use Gaussian process regression to learn the shared latent structure among data sets. Shon et al [10] uses extended Gaussian process model to study the relationship between motion data and the robotic gesture data. Lafon et al [11] use Diffusion Maps to get the manifolds of different datasets separately, then use Nystrom algorithm to find an affine transformation to align them. The algorithm is successfully applied to the problems of lip-reading and image alignment. Bai et al's method is similar to Lafon's. He use ISOMAP [5] to transform the embed nodes of graphs into a metric space for graph-matching. However, all these techniques are non-linear, which can not give a clear mapping between the training data and the aligned data. As a result, they have to retrain all data when a new point is coming.

A linear manifold alignment algorithm based on affine transformation is proposed in this paper. In this algorithm, the clear transformation between original sample space and the hidden space can be obtained during the training step, which can be used to realize the fast and accurate out of sample transformation. Unlike some common linear subspace learning methods

(PCA, LPP et al.) which can reflect the character of only one data set, manifold alignment based on affine transformation can reflect the common character of multiple data sets. In our approach, the Laplacian eigenmaps [2] is used to get the nonlinear alignment result, then an extended spectral regression method [13, 14] is used to obtain the affine transformation parameters. The effect of our method is validated by image sequence alignment in the experiments.

2. The Principle of Semi-supervised Affine Alignment

Suppose, the two high-dimensional data sets to be align are $X = \{x_1, \dots, x_{n_x}\} \subset \square^{d_x}$, $Y = \{y_1, \dots, y_{n_y}\} \subset \square^{d_y}$, and they can be aligned together by applying two sets of affine transformation parameters T_x, T_y . The aligned low dimensional data set is noted by $Z = \{z_1, \dots, z_{n_z}\} \subset \square^{d_z}$ ($d_x \gg d_z, d_y \gg d_z$), where Z_x, Z_y respectively represent the low-dimensional mapping result of X, Y . In the ideal case, the labeled matching points should be mapped to the same point in the low-dimensional space, so we let $Z_l = Z_x \cap Z_y$ to represent the intersection of Z_x and Z_y . l is used to represent the number of matching points, and the number of points in Z is $n_z = n_x + n_y - l$. The principle of semi-supervised affine alignment is described as Figure 1.

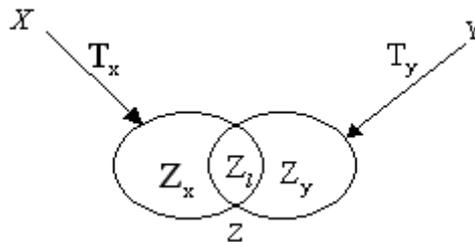


Figure 1. The Principle of the Semi-supervised Affine Alignment

3. Semi-supervised Affine Alignment Algorithm

3.1. The Constraint of Laplace Graph and Nonlinear Alignment

The Laplace graph is used here to describe the local geometrical information of the high-dimensional data. Though there are many methods to define Laplace graph, random walk is used here for its invariance of translation. Generally, let's make a graph to describe the high-dimensional data set X , the connection strength of x_i, x_j in X is defined by $w_x(i, j) = \exp(-\|x_i - x_j\|^2 / 2\sigma^2)$, where σ is a scale parameter. Let \square_i denote the collection of x_i 's k -close neighbors., $d_x(i) = \sum_{j \in \square_i} w_x(i, j)$ denote the density at the neighbor of x_i , then the approximate matrix could be written as $L_x = I - D_x^{-1}W_x$. Similarly, there is approximate matrix $L_y = I - D_y^{-1}W_y$ for Y . The approximate error for X and Y is described by e .

$$e = \|Z_x L_x\|_F^2 + \|Z_y L_y\|_F^2 \quad (1)$$

Where $\| \cdot \|_F$ denotes Frobenius norm. Let S_x, S_y as 0-1 selection matrix satisfying $Z_x = ZS_x, Z_y = ZS_y$, and let $S = \begin{bmatrix} S_x & S_y \end{bmatrix}, L = \text{diag}\{L_x, L_y\}, B = (SL)(SL)^T$, the formula (1) could be written as:

$$e = \|ZSL\|_F^2 = \text{trace}(ZBZ^T) \quad (2)$$

When minimizing formula (2), for the propose of ensuring the uniqueness of the solution, $ZZ^T = I_{d_z}$ is imposed as another restriction. The best solution for minimizing formula (2) can be obtained by calculating B 's 2nd to $(d_z + 1)$ nd smallest eigenvalue responding eigenvectors. Then the best non-linear solution is denoted as \tilde{Z}_x and \tilde{Z}_y .

3.2. Spectral Regression and Affine Alignment

\tilde{Z}_x, \tilde{Z}_y obtained above as the best solution can give the accurate coincidence of the matching points. However, the mapping is non-linear and cannot be applied to a new testing point. In our method, spectral regression [13] is used to preserve the affine transformation relationship when aligning the manifold.

For a normal point x_i in X , we want to find an affine transformation T_x , by applying which the result z_{xi} can mostly approximate to the best solution \tilde{z}_{xi} in \tilde{Z}_x , that is:

$$z_{xi} = T_x \begin{bmatrix} x_i \\ 1 \end{bmatrix} \rightarrow \tilde{z}_{xi} \quad (3)$$

The error of approximation is denoted as:

$$e_{xi} = a_{xi}^2 \left\| T_x \begin{bmatrix} x_i \\ 1 \end{bmatrix} - \tilde{z}_{xi} \right\|^2 \quad (4)$$

Where a_{xi} is the parameter influencing the coincidence accuracy of the matching points. In this paper, it's defined as:

$$a_{xi} = \begin{cases} 1 & \cdots & \tilde{z}_{xi} \notin Z_l \\ \gamma & \cdots & \tilde{z}_{xi} \in Z_l \end{cases} \quad (5)$$

Here γ is a const value to distinguish different influence between matching points and un-matching points. The total approximate error can be accumulated as:

$$e_x = \sum_i e_{xi} = \left\| (T_x \tilde{X} - \tilde{Z}_x) A_x \right\|_F^2 \quad (6)$$

Where $\tilde{X} = \begin{bmatrix} X \\ 1_{1 \times n_x} \end{bmatrix}, A_x = \text{diag}\{a_{x1}, \dots, a_{xn_x}\}$.

When minimizing formula (6), the optimal affine transformation can be obtained as:

$$T_x^* = Z_x^* A A^T \tilde{X}^T \left(\tilde{X} A A^T \tilde{X}^T + \lambda I \right)^{-1} \quad (7)$$

Here, $\lambda \in R^+$. Similarly,

$$T_y^* = Z_y^* A A^T \tilde{Y}^T (\tilde{Y} A A^T \tilde{Y}^T + \lambda I)^{-1} \quad (8)$$

By applying T_x^* , T_y^* to X and Y , the optimal affine transformation for them are $Z_x^* = T_x^* \begin{bmatrix} X \\ \mathbf{1}_{1 \times n_x} \end{bmatrix}$ and $Z_y^* = T_y^* \begin{bmatrix} Y \\ \mathbf{1}_{1 \times n_y} \end{bmatrix}$.

4. Experiments and Discussion

The experiment of image sequence alignment is used here to validate the effectiveness of our algorithm. COIL20 are data set about rotating toys, and CUbiC FacePix is data set about head pos. Two image sequences in COIL20 are showed in Figure 2, where each image is obtained by rotating the toy every 5 degree. It's clear that the embedded manifold is a circular. Two image sequences in CUbiC FacePix are showed in Figure 3, where each image is taken from different head pos. It's clear that the embedded manifold is half circle.

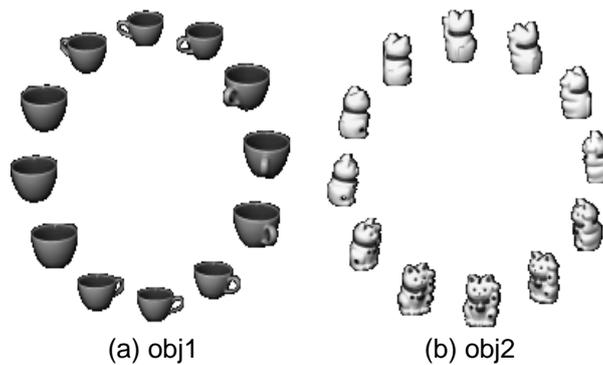


Figure 2. Two Image Sequences of COIL20

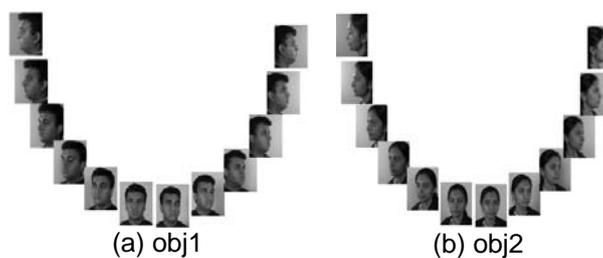


Figure 3. Two Image Sequences of CUbiC FacePix

In the experiment, every data set is randomly divided into two parts, one part for training denoted by small solid point, and another part for testing denoted by big hollow point. Then some matching points are taken from the training points denoted by big solid point. By applying the affine transformation obtained in training, the two high-dimensional datasets can be aligned in a global low-dimensional space. For the continuous linear character of affine transformation, the mapping result of training points and testing points are melted together.

The Figure 4 is the aligning result of two image sequences in COIL20. The affine align algorithm can find the embedded manifold of separate data set, and the low-dimensional data is

aligned approximately together. The Figure 5 is the aligning result of two image sequences in FacePix. The mapping result of testing points and training points are uniformly distributed, and the mating points are almost coincided.

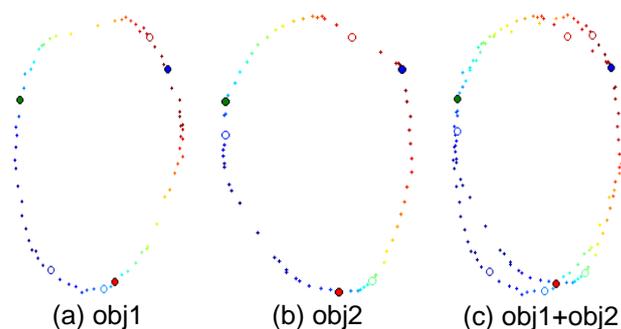


Figure 4. Affine Alignment of COIL20 Dataset

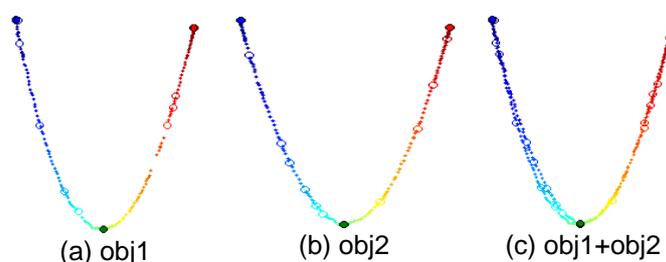


Figure 5. Affine Alignment of CUBiC FacePix Dataset

The cost time for projecting a new point between affine alignment and retraining is listed in Table 1. It's clear that the time for projecting a new point is largely cut off by our algorithm.

Table 1. The Cost Time for Projecting a New Point

Dataset	Affine alignment(s)	Retraining(s)
COIL20	$2.1e-4$	$1.4e-1$
CUBiC FacePix	$7.3e-5$	$3.1e-1$

4. Conclusion

Semi-supervised manifold alignment based on affine transformation proposed in this paper simultaneously fulfils the two requirements of manifold alignment and retaining the linear mapping. It obtains the clear mapping relationship between the original space and the aligned space, and the linear mapping can be used to give a fast and accurate out of sample mapping transformation.

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