

정류된 부공간 해석을 이용한 PET 영상 분석

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Rectified Subspace Analysis of Dynamic Positron Emission Tomography

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ABSTRACT

Subspace analysis is a popular method for multivariate data analysis and is closely related to factor analysis and principal component analysis (PCA). In the context of image processing (especially positron emission tomography), all data points are nonnegative and it is expected that both basis images and factors are nonnegative in order to obtain reasonable result. In this paper we present a sequential EM algorithm for rectified subspace analysis (subspace in nonnegativity constraint) and apply it to dynamic PET image analysis. Experimental results show that our proposed method is useful in dynamic PET image analysis.

1. INTRODUCTION

In many application such as data analysis and pattern recognition, one often encounters into a set of huge dimensional data and wish to extract a small number of features which is able to represent the data as well as possible. Subspace analysis is a popular method for dimensionality reduction and feature extraction and is closely related to factor analysis and PCA.

The singular value decomposition (SVD) is a numerically robust method which calculates the eigenvectors of the covariance matrix, however, it is computationally expensive, especially for the case of data with high dimension. For adaptive computation of eigenvectors, a variety of PCA neural networks have been developed [3], most of which are gradient-based learning algorithms, so their convergence is very slow.

Recently probabilistic model-based methods for subspace analysis have been proposed. These include probabilistic PCA (PPCA), EM-PCA, mixture of factor analyzers [4], and mixtures of probabilistic principal component analyzers [13]. All these algorithms employ the EM learning which is an iterative maximum likelihood estimation method in the presence of hidden variables. PPCA and EM-PCA are batch algorithms thus, when a new data arrives, whole calculation should be carried out again. In order to overcome this drawback, a sequential EM subspace algorithm was developed [2].

In the context of image processing (especially positron emission tomography), all data points are nonnegative and it is expected that both basis images and factors are nonnegative in order to obtain reasonable results. Recently the nonnegative matrix factorization (NMF) was introduced [6]. It was demonstrated that the NMF gave parts-based representation [6] and was useful in dynamic positron emission tomography (PET) image analysis [9].

On the other hand, Oja's subspace algorithm in

nonnegative constraint was shown be useful for the identification of face orientation [5]. Motivated from these result [6,9,5], we present a sequential EM rectified subspace algorithm and apply it to dynamic PET images. Experimental results show that our proposed algorithm is very useful for dynamic PET analysis.

2. PROBABILISTIC PCA

The linear generative model assumes that the set of m dimensional observed vectors $\{x_i\}$ is generated from a corresponding set of latent variable $\{s_i\}$ by

$$x_i = A s_i + v_i \quad (1)$$

where $s_i \in \mathbb{R}^n$ ($n \leq m$) and v_i is Gaussian noise vector that is assumed to be statistically independent of s_i .

Assuming an isotropic noise model, $v_i \sim \mathcal{N}(0, \sigma^2 I)$, following EM algorithm is derived [14].

Algorithm Outline : PPCA

E-step Compute sufficient statistics

$$\langle s_i \rangle = M^{-1} A^T x_i \quad (2)$$

$$\langle s_i s_i^T \rangle = \sigma^2 M^{-1} + \langle s_i \rangle \langle s_i^T \rangle \quad (3)$$

where $M = \sigma^2 I + A^T A$

M-step Re-estimate the parameters A and σ^2 by

$$\hat{A} = \left(\sum_{i=1}^N x_i \langle s_i^T \rangle \right) \left(\sum_{i=1}^N \langle s_i s_i^T \rangle \right)^{-1} \quad (4)$$

$$\hat{\sigma}^2 = \frac{1}{m} (\text{tr}[R - R \hat{A} M^{-1} \hat{A}]) \quad (5)$$

Simple EM algorithm for PCA can be obtained by taking the zero noise limit ($\sigma^2 \rightarrow 0$) into account [10].

Algorithm Outline : PPCA(zero noise limit)

E-step Compute sufficient statistics

$$S = (A^T A)^{-1} A^T X \quad (6)$$

where

$$S = [s_1, \dots, s_M] \quad (7)$$

$$X = [x_1, \dots, x_N] \quad (7)$$

M-step Re-estimate the parameters A and σ^2 by

$$\hat{A} = X S (S S^T)^{-1} \quad (8)$$

$$R_{s,t} = \sum_{k=1}^M \beta^{t-k} s_k s_k^T \quad (16)$$

Define $P_t = R_{s,t}^{-1}$ and apply the matrix inversion lemma. Then we have a recursion equation for updating P_t

$$P_t = \frac{1}{\beta} \left\{ P_{t-1} - \frac{P_{t-1} s_t s_t^T P_{t-1}}{\beta + s_t^T P_{t-1} s_t} \right\} \quad (17)$$

Using the recursion (17), the adaptation for A is given by

$$A_t = A_{t-1} + [x_t - A_{t-1} s_t] \frac{s_t^T P_{t-1}}{\beta + s_t^T P_{t-1} s_t} \quad (18)$$

3. SEQUENTIAL EM FOR SUBSPACE ANALYSIS

3.1 Separable Least Squares

The PPCA algorithm for the case of zero noise limit can be also derived in the framework of separable LS method. Moreover sequential LS can be employed in order to develop an on-line algorithm which learns principal subspace of the observed variables.

As pointed out in [10], in the zero noise limit, the likelihood of a data point x is dominated solely by the squared distance between it and its reconstruction As . In such a case, ML estimation of both A and s becomes a separable LS minimization problem. The LS estimates, A and S are computed by

$$\hat{A}, \hat{S} = \min_{A, S} \|X - AS\|_F^2 \quad (9)$$

The separable LS minimization is carried out in two steps. First we minimize (9) with respect to A with S being fixed. It leads to

$$\hat{A} = X S (S S^T)^{-1} \quad (10)$$

which corresponds to the M-step in PPCA (for the case of zero noise limit).

The estimate \hat{A} is substituted back into (9), then we obtain a new criterion which is a function of S only

$$\min_S \|X P_S^\perp\|_F^2 \quad (11)$$

where P_S^\perp is the orthogonal projection matrix given by

$$P_S^\perp = (\hat{A}^T \hat{A})^{-1} \hat{A}^T X \quad (12)$$

which correspond to the E-step.

4.2 Sequential LS

For sequential estimation of A and s , we consider the weighted LS minimization problem where the objective function is given by

$$\epsilon = \sum_{k=1}^M \beta^{t-k} \|x_k - A s_k\|^2 \quad (13)$$

where $0 < \beta \leq 1$ is the forgetting factor.

Our objective is to compute A_t and s_t , assuming a good estimate of s_{t-1} (or equivalently A_{t-1}) is available. The exponential weighting is used to de-emphasize old data in a time-varying environment. Setting the derivative of ϵ with respect to A to be zero, then we have

$$A_t = R_{s,t} [R_{s,t}]^{-1} \quad (14)$$

where

$$R_{s,t} = \sum_{k=1}^t \beta^{t-k} x_k s_k^T \quad (15)$$

Algorithm Outline : Sequential EM

E-step Estimate s_t by the LS projection

$$s_t = (A_{t-1}^T A_{t-1})^{-1} A_{t-1}^T x_t \quad (19)$$

M-step estimate A_t by

$$A_t = A_{t-1} + [x_t - A_{t-1} s_t] \frac{s_t^T P_{t-1}}{\beta + s_t^T P_{t-1} s_t}$$

4. RECTIFIED SUBSPACE ANALYSIS

Subspace analysis in nonnegativity constrain seeks for LS estimates, A and S which are computed from (9) with all elements of A and S being nonnegative. In order to find a solution which satisfies a nonnegativity constraint, NMF introduced a multiplicative updating rule. On the other hand, Charles and Fyfe [1] used a simple rectification method with factor analysis network.

As in [1], we also use a rectifier defined by

$$[x]^+ = \begin{cases} x & \text{if } x \geq 0 \\ 0 & \text{if } x < 0 \end{cases} \quad (20)$$

The rectifier is operated in an elementwise fashion.

We call a subspace in nonnegativity constraint as rectified subspace. We incorporate the rectification into our sequential EM subspace algorithm described in previous section.

Algorithm Outline : Rectified Sequential EM

E-step Estimate s_t by the LS projection

$$s_t = [(A_{t-1}^T A_{t-1})^{-1} A_{t-1}^T x_t]^+ \quad (21)$$

M-step estimate A_t by

$$A_t = [A_{t-1} + (x_t - A_{t-1} s_t) \frac{s_t^T P_{t-1}}{\beta + s_t^T P_{t-1} s_t}]^+ \quad (22)$$

5. APPLICATION TO DYNAMIC PET IMAGES

5.1 PET Image Acquisition

We performed $H^{15}O$ PET scans on seven dogs at rest and after pharmacological stress using Adenosine or Dipyridamole. All the scans were acquired with an ECAT EXACT 47 scanner (SimensCTI, Knoxville, USA). Before $H^{15}O$ administration, transmission scanning was performed using three Ge-68 rod sources for attenuation correction. Dynamic emission scans (5sec \times 12,10sec \times 9,30sec \times 3) were initiated simultaneously with the injection of 555-740 MBq $H^{15}O$. Transaxial images were reconstructed by means of a filtered back-projection algorithm as $128 \times 128 \times 47$ matrices with a size of $2.1 \times 2.1 \times 3.4$ mm.

5.2 Experimental Result

The initial eighteen frames (two minutes) of PET images were used for analysis. The dynamic PET images were re-oriented to short axis and were re-sampled to produce 1cm thick slices in order to increase the signal to noise ratio. Only the cardiac regions were then masked to remove extra cardiac components and to reduce the quantity of data and hence the burden of computation. The resulting masked images with dimension of $32 \times 32 \times 6 \times 18$ (pixel \times pixel \times plane \times frame) were reformulated to 18×6144 data matrix X .

In the rectified subspace analysis algorithm, we used $\beta = .99$. In most of simulations, all the parameters converged within 500 iterations. For NMF, all the data points were re-used 100 times to ensue the convergence.

Each row of the matrix S corresponds to basis image which represent cardiac component. Fig.1 shows the basis images that we obtained using the rectified subspace analysis algorithm and the NMF. For both cases, three cardiac components (right ventricle, left ventricle, myocardium) were successfully extracted. Each column vector of the matrix A represent the time activity curve (TOC) which is useful, to calculate blood flow estimation[7]. Fig.2 shows the TOC for both algorithms. These TOC showed reasonable shape that we were familiar with (two peaks at each of right ventricle an left ventricle, more dispersion in left ventricle and myocardium). With the assumption of proper number of factors, both the rectified subspace analysis algorithm and NMF showed good results. The benefit of the rectified subspace analysis algorithm is a fast sequential algorithm, so will be useful for handling with high dimensional data matrix.

6. CONCLUSION

We have introduced a rectified subspace analysis method and presented a fast sequential EM algorithm which was able to find subspace in nonnegativity constrain. The rectified sequential EM algorithm extended our previous work [2] by incorporation with a simple rectification method. We have applied the rectified subspace analysis method to dynamic PET images and demonstrated its useful behavior.

7. ACKNOWLEDGMENT

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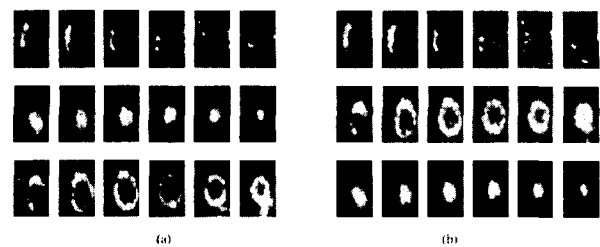


Fig. 1 basis images computed by (a) the rectified subspace analysis algorithm (b) NMF

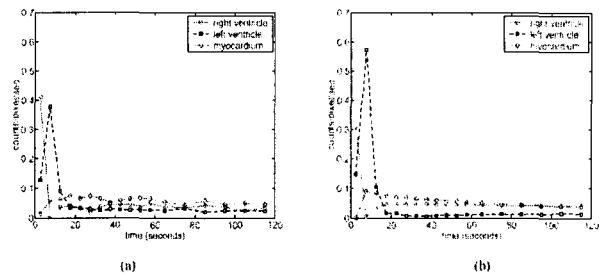


Fig. 2 Time activity curves obtained by (a) the rectified subspace analysis algorithm (b) NMF