Robust Independent Component Analysis for fMRI

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SUMMARY. Independent component analysis (ICA) is an effective exploratory tool for analyzing spatio-temporal data. It has been successfully applied in analyzing functional Magnetic Resonance Imaging (fMRI) data, to recover the interested source signals from different parts of the brain. Due to the high sensitivity of MR scanners, outliers are inevitable in acquiring fMRI datasets while they cause misleading effects for the analysis. In the current literature, no particular method exists yet to handle this problem. In this paper, we propose a robust ICA procedure that is less sensitive to outliers in fMRI analyses. Singular value decomposition (SVD) is commonly used prior to ICA for dimension reduction. We first motivate SVD from a low rank

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matrix approximation perspective. Regularization through basis expansion is then introduced to the corresponding minimization problem to achieve a regularized low rank approximation. Such regularization performs dimension reduction as well as trims the outlier effect. Our method makes use of the particular designs of fMRI experiments, and is shown very effective in reducing outlier effect in a spatio-temporal simulation study. We also compare our method with two existing ICA packages by analyzing a real fMRI dataset, and our method can detect extra underlying components.

**Key words:** Basis Expansion; Functional Magnetic Resonance Imaging (fMRI); Regularization; Robustness; Singular Value Decomposition (SVD); Independent Component Analysis (ICA); Spatio-Temporal Data.

## 1. Introduction

Functional Magnetic Resonance Imaging (fMRI) is a set of noninvasive techniques for functional brain mapping. By generating high quality “movies” of the brain in action, it helps us to determine which parts of the human brain are activated by different task performances (Jezzard et al., 2001; Huettel et al., 2004).

In a typical fMRI experiment, functional images of the brain are recorded every few seconds while the subject is performing a task sequence or receiving a certain stimulus. The images are taken using an Magnetic Resonance (MR) sequence which is sensitive to changes in local blood oxygenation levels; hence, during a certain activation or stimulation, the parts of the brain that are activated by the stimulation would correspond to the parts of the images that show a change of intensity.

A single MR image usually consists of a certain number of slices and
each slice is made up of individual cuboid elements called voxels. Hence an fMRI dataset can be considered as a three dimensional matrix of voxels that is repeatedly sampled over time. This 4D fMRI dataset can then be either thought of as \( N \) images, one taken every few seconds, or as \( M \) voxels, each with an associated time series of \( N \) time points. Mathematically an fMRI dataset is usually represented as a space-time matrix \( X \) which has dimension \( M \times N \), where \( M \) is the number of voxels on one image and \( N \) is the number of time points in the experiment. Thus each column of \( X \) represents an fMRI image with \( M \) voxels and each row of \( X \) is a time series for one voxel. In most fMRI experiments, the number of time points is far less than the number of voxels \( (N \ll M) \). For example, the fMRI data that we analyze in Section 4.2 have \( M = 153,594 \) voxels and \( N = 200 \) time points.

Independent component analysis (ICA) is an effective data-driven technique for extracting individual signals from mixtures of signals. It aims to solve the “blind source signal” problem by expressing a set of random variables (or observations) as linear combinations of statistically independent latent component variables (or source signals) (Hyvärinen et al., 2001; Stone, 2004). In the context of fMRI study, the recorded fMRI signals are mixtures of source signals coming from all parts of the brain. To recover these different source signals, ICA has been successfully applied to fMRI data as an exploratory data analysis technique (McKeown et al., 1998; Petersen et al., 2000; Calhoun et al., 2003).

ICA of fMRI usually involves various processing stages (Calhoun et al., 2003). Before applying any ICA algorithm to an fMRI dataset, a data reduction step is commonly taken first by making use of singular value de-
composition (SVD) (Petersen et al., 2000) or some other techniques. The idea behind this data reduction is to focus ICA decomposition on a feature subspace retained by SVD, instead of the whole space. This preprocessing step aims to make the ICA decomposition more efficient by reducing the data dimensionality. Section 2.2 gives more details about the data reduction step.

Due to the high sensitivity of MR scanners, outliers are inevitable when acquiring fMRI datasets. As an example, Figure 1 shows the recorded time series corresponding to three different voxels in our fMRI dataset, which are respectively indicated by the crossings of the two lines on the images in the left column. The big spikes around time points 110, 100 and 120 in the three time series plots are examples of many other outliers which can be commonly detected in fMRI data.

[Figure 1 about here.]

The conventional SVD method used for data reduction in ICA of fMRI, however, is known to be highly susceptible to outliers as a least squares method and hence the results from ICA procedures could be contaminated and misleading. No robust methods have been proposed in the literature to the best of our knowledge. In this paper, we propose a robust ICA (rICA) procedure to deal with the outliers in fMRI datasets. Our proposal is motivated by the observation that SVD can be interpreted as a low rank matrix approximation technique. The SVD components can then be obtained from solving a sequence of minimization problems. We then introduce some regularization through basis expansion in the corresponding optimization problems to achieve regularized low rank approximations. The basis expansion is
constructed using the information of the fMRI experiment designs, particularly the frequencies of the stimulus sequences. Such regularization makes the SVD more robust against outlier effects as illustrated in a spatio-temporal simulation study. Our rICA procedure uses the robust SVD (rSVD) to perform dimension reduction instead of the conventional SVD. In addition to being more robust, our method can actually detect interested components that otherwise can hardly be detected by existing ICA packages in a comparative study using real fMRI data.

The rest of the paper is organized as follows. Section 2 provides an overview of the ICA methodology as well as the conventional data reduction step before ICA. In Section 3, we introduce the proposed rICA procedure, in particular the rSVD technique through basis expansion. Section 4 illustrates the performance of our proposed method via a simulation study, as well as a comparative study with two existing ICA packages through analyzing a real fMRI dataset. Some discussion are given in Section 5 to close the paper.

2. Independent Component Analysis

The basic idea of ICA can be illustrated using the classic “cocktail party” problem (Hyvärinen et al., 2001; Stone, 2004). Suppose there are many people talking simultaneously in a party and several microphones are present in different locations. The signals recorded from these microphones are then mixtures of different voices. Using only these recorded mixtures as inputs, ICA aims at identifying the individual voices of different people. ICA has been the most widely used method for performing “blind source separation”, where “blind” means that no knowledge of the mixing coefficients is available when recovering the source signals from the mixtures (Stone, 2004).
To set up the general mathematical model of ICA, let \( \mathbf{x} \) be an \( M \)-dimensional vector variable, whose elements are signal mixtures recorded at one time point, and \( \mathbf{s} = (s_1, \ldots, s_K)^T \) be a \( K \)-dimensional vector variable with each element being a source signal. The typical ICA model is written as

\[
\mathbf{x} = \mathbf{A}\mathbf{s},
\]

where \( \mathbf{A} \) is an \( M \times K \) mixing matrix, \( M \) is the number of signal mixtures and \( K \) is the number of source signals. The independent source components \( s_1, \ldots, s_K \) are taken as latent variables in this model. With the mixing matrix \( \mathbf{A} \) unknown, we must estimate both \( \mathbf{A} \) and the source signals \( \mathbf{s} \) only using the observed vector variable \( \mathbf{x} \).

For estimation purpose, the source signals \( s_1, \ldots, s_K \) are assumed to be statistically independent and have non-Gaussian distributions. Hyvärinen et al. (2001) prove that, without non-Gaussianity of the independent components, the mixing matrix \( \mathbf{A} \) is not identifiable at all. In practice, most ICA methods also require at least the same number of simultaneously recorded signal mixtures (or microphones) as the source signals (or voices) (Stone, 2004), i.e. \( M \geq K \).

According to the Central Limit Theorem, the distribution of a sum of independent random variables goes to a Gaussian distribution under certain assumptions. This means that the distribution of the sum of several independent random variables is more Gaussian than any of the original random variables. Making use of this fact, ICA recovers the independent components by finding an unmixing matrix \( \mathbf{W} \) to maximize the non-Gaussianity of \( \mathbf{Wx} \). Then the mixing matrix \( \mathbf{A} \) is estimated as \( \mathbf{W}^{-1} \) and the source signals are re-
covered as $s = Wx$. There are several different measures of non-Gaussianity, including kurtosis, negentropy, mutual information and so on. Many different ICA algorithms have been developed accordingly. For more details about ICA theory, see Hyvärinen et al. (2001) and Stone (2004).

2.1 ICA for fMRI

As discussed earlier, fMRI data have a complicated spatio-temporal nature. An fMRI dataset is usually represented as a space-time matrix $X$ which has dimension $M \times N$. Each column of $X$ contains an fMRI image with $M$ voxels recorded at one time point and each row of $X$ consists of a time series for one voxel. To recover the source signals based on these repeatedly sampled mixture signals, ICA is used to decompose $X$ into a product of spatial patterns and corresponding temporal sequences. The generality of ICA resides in that the recovered source signals can be independent either spatially or temporally (Petersen et al., 2000).

Adopting Equation (1) in the context of fMRI, we can write the ICA decomposition model for fMRI data as:

$$X = AS,$$

where each column of the $M \times N$ matrix $X$ consists of $M$ signal mixtures recorded at one time point, $N$ is the number of time points in the experiment, $K$ is the number of underlying independent components. Each column of the $M \times K$ matrix $A$ holds a component map, and the rows of the $K \times N$ matrix $S$ are the time series corresponding to the component maps respectively.

Due to the spatio-temporal nature of fMRI signals, there are two distinct ICA decomposition options, spatial ICA (sICA) and temporal ICA (tICA). The sICA aims to find independent image components (the columns of $A$),
while tICA looks for independent time courses (the rows of $S$). In either sICA or tICA, a single ICA component, as in the model (2), can be interpreted as one spatially distributed set of voxels (one column of $A$) that are activated by one time course which corresponds to one row in $S$ (McKeown, Hansen and Sejnowski, 2003). As an example, Figure 8 shows one ICA component extracted from a real fMRI dataset analyzed in Section 4.2. The 46 image slices constitute one column of the matrix $A$ and they represent one image component extracted by ICA. The red and blue areas indicate the voxels that are activated by the experiment stimulus. The corresponding time component is shown subsequently. The activated voxels are known to follow this time course. The spectrum plot of the time component is also given in the end.

2.2 Data Reduction Step before ICA

When applying ICA to fMRI data, it’s common to first use either SVD or some other methods to perform a data reduction step. ICA algorithms are then applied in the reduced space.

Suppose $\text{rank}(X) = r \leq \min(M, N)$. The SVD decomposes $X$ as follows,

$$X = UDV^T,$$  \hspace{1cm} (3)

where $U$ is the $M \times r$ matrix of orthonormal left singular vectors, $V$ is the $N \times r$ matrix of orthonormal right singular vectors, and $D$ is the $r \times r$ diagonal matrix of positive singular values that are ordered decreasingly. Here $U$ and $V$ can be viewed as the basis vectors that span the spatial patterns and temporal sequences respectively.

As described in the previous section, ICA decomposition on the $M \times N$ matrix $X$ is modeled as in Equation (2). The sICA in this context then means
looking for independent image columns in \(A\), and tICA for independent time series rows in \(S\).

Hence, when performing tICA, we can then focus on the subspace spanned by \(Y \equiv DV^T\), which is of dimension \(r \times N\). Applying an ICA algorithm on the reduced data \(Y\), we can get \(Y = \tilde{A}S\), where \(S\) contains the independent time components. The original component maps in the model (2) can then be reconstructed as \(A = U\tilde{A}\).

Similarly, sICA can be performed by focusing on the subspace retained by \(Y^* \equiv UD\). An ICA decomposition on \(Y^*\) results in \(Y^* = \tilde{A}S\), where \(A\) consists of the component maps. The original time courses in the model (2) are then recovered as \(S = \tilde{S}V^T\).

In summary, the idea of the data reduction step before ICA decomposition is to reduce the dimension of the matrices that will be used as inputs to ICA algorithms. Considering the fact that most fMRI experiments have far less time points than the number of voxels, i.e. \(r \leq N \ll M\), this preprocessing step can improve the computational efficiency of the whole procedure.

3. Robust Independent Component Analysis

As mentioned earlier, outliers are frequently encountered in fMRI datasets and they cause misleading effects for the ICA in fMRI studies. To overcome the analysis challenges caused by their presence, we propose a robust procedure, rICA. The key idea is to reduce the outlier effect in the data reduction step by using a regularized SVD technique, which is more robust than the conventional SVD.
3.1 Low Rank Approximation via SVD

To motivate our approach, we need to look at SVD from the viewpoint of low rank approximation of matrices. In the SVD (3), let $U = [u_1, \ldots, u_r]$, $V = [v_1, \ldots, v_r]$ and $D = \text{diag}(d_1, \ldots, d_r)$. For an integer $l \leq r$, define

$$X^{(l)} \equiv \sum_{k=1}^{l} d_k u_k v_k^T.$$  

Then, $X^{(l)}$ is the closest rank-$l$ matrix approximation to $X$ (Harville, 1997). Here the term “closest” simply means that $X^{(l)}$ minimizes the squared Frobenius norm between $X$ and an arbitrary rank-$l$ matrix $X^*$, where the Frobenius norm is defined as

$$\|X - X^*\|_F^2 = \text{tr}\{(X - X^*)(X - X^*)^T\}.$$  

Suppose, for example, we seek the best rank-one matrix approximation of $X$ under the Frobenius norm. Note that any $M \times N$ rank-one matrix can be written as $uv^T$, where $u$ is a norm-1 $M$-vector and $v$ is a $N$-vector. The problem can be formulated as the following optimization problem,

$$\min_{u,v} \|X - uv^T\|_F^2. \quad (4)$$

Then the low rank approximation property of SVD implies that the solution is

$$u = u_1, \quad v = d_1 v_1.$$  

The subsequent pairs $(u_k, d_k, v_k), k > 1$, provide best rank one approximations of the corresponding residual matrices. For example, $d_2 u_2 v_2^T$ is the best rank one approximation of $X - d_1 u_1 v_1^T$.  

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3.2 Regularized Low Rank Approximation via Regularized SVD

However, the conventional SVD is highly susceptible to outliers as a least squares method. In block-design fMRI studies, experiment tasks or stimuli are typically applied in alternating blocks. Hence in the areas activated by these stimuli, we would observe time courses that are correlated with the experiment design. Figure 2 shows the time course (solid line) of a voxel that is activated by the experiment stimulus (dashed line) in the fMRI study reported below in Section 4.2. It is a rest-activate block-design experiment. The recorded signals are then blurred and delayed versions of the stimulus sequence due to the hemodynamic response. We note that the time components can usually be modeled as sinusoidal curves in such experiments. This observation motivates us to propose the following robust SVD procedure which is obtained through a regularized low rank approximation perspective.

[Figure 2 about here.]

Suppose the time component of interest, \( v = (v(t_1), \ldots, v(t_N))^T \), can be modeled as

\[
v(t_i) = a \sin(2\pi \omega t_i + \phi) = a \cos \phi \sin(2\pi \omega t_i) + a \sin \phi \cos(2\pi \omega t_i),
\]

where \( a \) is the amplitude, \( \phi \) is the phase, \( \omega \) is the frequency, \( t_i \) is the \( i \)th scanning time and \( N \) is the number of time points. Define \( b_1 = (\sin(2\pi \omega t_1), \ldots, \sin(2\pi \omega t_N))^T \), \( b_2 = (\cos(2\pi \omega t_1), \ldots, \cos(2\pi \omega t_N))^T \), \( B = (b_1, b_2) \) and \( \psi = (a \cos \phi, a \sin \phi)^T \).

Then, one can see that

\[
v = B \psi,
\]  

(5)
which suggests that $v$ is constrained to be in the linear space spanned by the bases $b_1$ and $b_2$.

To make use of the sinusoidal nature of $v$, we propose to impose the regularization constraint (5) on $v$ in the optimization problem (4), and formulate the problem as follows,

$$\min_{u, \psi} \|X - uv^T\|_F^2 \quad \text{subject to } v = B\psi. \quad (6)$$

The minimization problem (6) is automatically scale invariant in that

$$(cu)(v/c)^T = \{uc\}\{B(\psi/c)\}^T = (u)(B\psi)^T = uv^T,$$

where $c$ is a nonzero constant. For identifiability purpose, we can standardize $u$ and $v$ to unit length and introduce a slope parameter $d$. Hence, the problem can be rewritten as

$$\min_{d, u, \psi} \|X - duv^T\|_F^2 \quad \text{subject to } v = B\psi, u^Tu = 1, v^Tv = 1. \quad (7)$$

3.3 Practical Implementation

In this section, we derive the solution to the problem (7) using matrix algebra. Note that (7) is equivalent to minimizing

$$\text{tr}(XX^T) - 2d\psi^TB^TX^Tu + d^2(\psi^TB^TB\psi)(u^Tu), \quad (8)$$

subject to $u^Tu = 1$ and $v^Tv = 1$. For fixed $d$ and $u$, the minimizer is

$$\psi = (du^TuB^TB)^{-1}B^TX^Tu = (B^TB)^{-1}B^TX^Tu/d,$$

which we can plug back into (8) to obtain

$$\text{tr}(XX^T) - u^TXB(B^TB)^{-1}B^TX^Tu.$$
Hence the minimization problem (7) is reduced to

$$\max_u \ u^T XB (B^T B)^{-1} B^T X^T u \quad \text{subject to} \ u^T u = 1, \tag{9}$$

which is a generalized eigen-problem. Similarly, the \( \psi \) that solves (7) is the solution to the following generalized eigen-problem,

$$\max_{\psi} \ \psi^T B^T X^T X B \psi \quad \text{subject to} \ \psi^T B^T B \psi = 1. \tag{10}$$

According to (8), the \( d \) that solves (7) is given by \( d = \psi^T B^T X^T u \).

The generalized eigen-problems can be solved using standard methods. For example, to solve (9), consider the Cholesky decomposition \( B^T B = R_B^T R_B \) where \( R_B \) is a \( 2 \times 2 \) upper triangular matrix. The maximization problem (9) is then equivalent to

$$\max_u \ u^T X B R_B^{-1} (R_B^{-1})^T B^T X^T u \quad \text{subject to} \ u^T u = 1.$$ 

The solution to this problem, denoted as \( u^* \), is actually the first left eigenvector of the matrix \( X B R_B^{-1} \) (Harville, 1997).

Problem (10) can be solved similarly. Let \( \tilde{\psi} = R_B \psi \), then (10) is equivalent to

$$\max_{\tilde{\psi}} \ \tilde{\psi}^T (R_B^{-1})^T B^T X^T X B R_B^{-1} \tilde{\psi} \quad \text{subject to} \ \tilde{\psi}^T \tilde{\psi} = 1.$$ 

The maximizer \( \tilde{\psi}^* \) is the first right eigenvector of \( X B R_B^{-1} \). Consequently, the maximizer of the original problem (10) is \( \psi^* = R_B^{-1} \tilde{\psi}^* \).

The above derivation suggests that one only needs to perform a single SVD of \( X B R_B^{-1} \) to obtain both \( \psi^* \) and \( u^* \). Then the scale parameter \( d \) can be estimated as \( d^* = \psi^{*T} B^T X^T u^* \).
Note that the derivation relies on knowing the sinusoidal frequency $\omega$ or being able to estimate it using fMRI data. In most fMRI experiments, the experimenter is interested in finding activation areas responding to certain particularly designed experiment stimuli, which means the frequency $\omega$ is known. In certain cases, the experimenter might be interested in some underlying unknown signals. Then we propose to estimate $\omega$ through spectrum analysis on the $v$ component extracted from the conventional SVD. The effect of outliers is trimmed by the fact that outliers have a much smaller effect on the peak of the spectrum, or the frequency of the signal. This means that we can probably estimate $\omega$ reasonably accurate. See Section 4 for an illustration of the performance of this estimation method. Once we obtain an estimate for the frequency $\psi$, the amplitude $a$ and the phase $\phi$ can then be easily estimated.

Below we summarize the algorithm to obtain the first regularized time component as well as its corresponding spatial component. We focus our discussion on extracting the first pair of components. The same algorithm can be applied repeatedly on the residual matrices until the desired number of components is obtained.

1. Apply the conventional SVD on $X$ to obtain the first right singular vector $v_1$;
2. Obtain the corresponding $\omega$ from the experimenter, or estimate it through spectrum analysis of $v_1$;
3. Form the basis matrix $B$ and apply Cholesky decomposition on $B^TB$ to get $B^TB = R_B^TR_B$;
(4) Apply SVD on $XBR_B^{-1}$ to derive its first left singular vector $u^*$ and the first right singular vector $\tilde{\psi}^*$;

(5) Set $\psi^* \equiv R_B^{-1}\tilde{\psi}^*$ and $d^* \equiv \psi^*T B^T X^T u^*$, which leads to $v^* = B\psi^*$.

Hence we get the set of components $(u^*, d^*, v^*)$.

3.4 Robust Independent Component Analysis

Once we obtain the desired number of regularized SVD components, we propose to apply any ICA algorithm on them. As the SVD components are obtained using a regularization procedure that is robust to outliers, the analysis results from the follow-up ICA procedure should be robust as well (Section 4.1). In addition, because our procedure makes use of the nature of the fMRI experiment design, it appears to be more powerful in detecting activated brain areas of interest (Section 4.2).

4. Simulation Study and Real Data Analysis

In this section, we illustrate our proposed procedure using a simulated study and a real fMRI dataset.

4.1 A Simulation Study

4.1.1 Data Description

According to the ICA decomposition model (2), we can simulate an $M \times N$ fMRI data matrix $X$ by first simulating the $M \times K$ spatial component map matrix $A$ and the $K \times N$ time series matrix $S$ separately, where $K$ is the number of desired independent components, $M$ is the number of voxels on each component map and $N$ is the time points of each time series. The data matrix $X$ then can be obtained as $X = AS$.

In our simulation study, we set $K = 5$, $M = 900 \times 10$ and $N = 240$. The simulated data can be explained as follows: There are 5 underlying independent components; each column of the spatial component matrix $A$ is
a component map that consists of 10 slices and each slice contains $30 \times 30$ voxels, while each row of $\mathbf{S}$ is a time series of length 240 that corresponds to the five spatial components in $\mathbf{A}$ respectively.

We simulated the data based on a simple rest-activate block design (the dotted line in the time plot at each panel in Figure 3). Each rest or activate period held 30 scans. There were 4 rest-activate periods altogether. The repetition time (TR) was set to be 0.3 seconds. Hence each rest-activate period lasted for $60 \times 0.3 = 18$ seconds.

Out of the five time series in the matrix $\mathbf{S}$, the first four were simulated based on simple sinusoidal functions plus randomly generated Uniform noises, which are plotted in Figure 3 along with their corresponding spectrum plots highlighting the frequencies. The first time component stands for the stimulus of the experiment; hence it can be viewed as a delayed and blurred version of the block design with the same periodicity. The second and third time series correspond to the heart beat and breath with frequencies of 1Hz and 0.3Hz respectively. The fourth one is an artifact effect with a frequency of 0.7Hz. The last time component is pure noise. The amplitudes of the first four components are 0.5, 0.45, 0.35 and 0.45 respectively, while the corresponding phases are 15, 0, 0 and 10. When shown in Figure 3, the amplitudes of the time components were normalized to be 1. The noises are sampled from a Uniform distribution between -0.1 and 0.1. Note that the noise distribution has to be non-Gaussian in order for ICA to be well defined as discussed in Section 2.

Each one of the five spatial components contains 10 slices of $30 \times 30$-voxel images. All the voxels were given a numerical value of either 0 or 1.
The voxels with value 1 are those activated by the corresponding stimulus. Figure 3 plots the four spatial components corresponding to the first four time components mentioned above, and the dark red areas consist of the activated voxels.

After obtaining the data $X = AS$, we added outliers to it in the following way. Let $m_1$ be the minimum value of $X$, $m_2$ be the maximum value, and $IQR$ be the inter-quartile range of $X$. We randomly selected 10% of the cells from the simulated matrix $X$, and then replaced them with randomly generated values that are bigger than $(m_2 + 1.5 \times IQR)$ or less than $(m_1 - 1.5 \times IQR)$. Below we use the simulated data with outliers to illustrate the robustness of our method.

4.1.2 Analysis Before the analysis, we normalized the contaminated data matrix $X$ by column centering and row standardization. This normalization step is standard practice in ICA, which makes the independent components identifiable (Hastie and Tibshirani, 2002). Both the ordinary SVD and our proposed rSVD were applied to the normalized matrix. ICA was then employed on the reduced data matrices respectively. In this study, the fastICA algorithm was used because of its fast computation and popularity as discussed in Hyvärinen et al. (2001).

To effectively display the activated voxels in the resulting component maps, all the values of the cells in each component map were scaled to $z$-scores (McKeown et al., 1998). Voxels with $|z| \geq 1$ were then identified as
those activated by the corresponding stimulus and they were then given value 1 when plotting the image components as described in the following section. All the voxels with $|z| < 1$ were assigned as 0 when plotting.

4.1.3 Results The results from our proposed rICA procedure are shown in the first column of Figure 4. All the four components can be recovered reasonably well, although some noises do exist. We expect that the noises could be further reduced by imposing some regularization such as smoothing penalties on the spatial components. Investigation is currently under way to see the performance. Similar to Figure 3, dark areas here indicate the activated voxels. The time course plots in each panel show the corresponding time components. The spectrum plot for each time component is also provided. Components recovered by ICA algorithms are known to follow no particular order. For the sake of easy comparison, in Figure 4, the components are arranged to match the order of the simulated components in Figure 3.

The second column of Figure 4 show the results from the conventional ICA technique. When outliers exist in the dataset, only the dominant (i.e. the first) component can be recovered; and the result is much noisier than the corresponding one in the left column. As for the remaining components, the conventional method can hardly identify them. In the current simulation study, the dominant SVD component happens to be the component corresponding to the experiment stimulus, because of the magnitudes of various components used in the simulation. This may not be the case in real fMRI studies. Thus, the standard SVD has the risk of missing out the components
of interest if they were not the dominant ones.

4.2 One Real fMRI Dataset

4.2.1 Data Description  An fMRI dataset was obtained from our collaborator at Neurology Department in a research institute. Two hundred MR scans were acquired on a modified 3T Siemens MAGNETOM Vision system. Each acquisition consisted of 49 contiguous slices. Each slice contained 64 × 64 voxels. Hence there were 64 × 64 × 49 voxels from each scan. The size of each voxel is 3mm × 3mm × 3mm. Each acquisition took 2.9388 seconds, with the scan to scan repetition time (TR) set to be 3 seconds.

In the experiment, 200 acquisitions were made in blocks of 50 acquisitions. Each of the four blocks began with 10 scans when the subject was at rest. Then 40 scans followed when the subject performed different sequences of finger tapping. In the first and third blocks, the subject used the right hand for finger tapping, while in the second and fourth blocks the subject used the left hand. During the first 20 scans in each activated period, the subject did the finger tapping following video instructions (externally guided). During the last 20 scans in each activated period, the subject needed to finish the task according to their memory (internally guided). The experimental paradigm is described in Figure 5.

4.2.2 Analysis  The dataset was pre-processed using SPM5 (available at http://www.fil.ion.ucl.ac.uk/spm/). The pre-processing included realignment, coregister, segmentation, spatial normalization and smoothing.
the spatial normalization step, the dimension of the dataset was adjusted to be $53 \times 63 \times 46$.

We then used BIAC (http://www.biac.duke.edu/) to visually check the processed dataset, and we could easily see many spikes, three of which are plotted in Figure 1 as examples of outliers. This illustrates that outliers do exist in our fMRI dataset.

The processed dataset was then analyzed using two existing analyzers of fMRI data, including GIFT (Calhoun et al., 2001) and AnalyzeFMRI (Marchini, 2002). In addition, we applied our proposed method to the data using both the true frequencies and the estimated ones, respectively. For all the four methods, spatial ICA was carried out and the fastICA algorithm was used. The results from the methods are presented and discussed in the following section.

4.2.3 Results The most interested components extracted by the different methods are shown in Figures 6 to 9 respectively. For easy comparison, the numerical results from AnalyzeFMRI were exported and the image results were then generated using our color scheme.

When using GIFT, we extracted 20 components altogether. The component shown in Figure 6 appears to be mostly related to the left-hand movement, as indicated by the dark red areas in the slices in the first two rows. The primary motor cortex (PMC) areas activated by the left-hand movement (the red areas in Figure 6) were identified by the method. However, the corresponding cerebellum areas were not clearly shown. No other components showed any association with the right-hand movement.
We used the R version of AnalyzefRMI to acquire 30 components. The most related component aligned with the right-hand movement (the blue areas in Figure 7). This method also fails to detect any components corresponding to the left-hand movement, which is to the opposite of GIFT. The activated cerebellum areas were not clearly detected either, similar to GIFT.

Figure 8 shows the component extracted by our rICA method. Here we specify the experimental frequency of 0.0033Hz as an input to the rSVD procedure in the data reduction step. Hence only one component is needed. Since the left-hand movement and the right-hand movement shared the same frequency in this study, our method successfully identified all the activated areas (both PMC and cerebellum) corresponding to both the left-hand movement (the red areas in Figure 8) and the right-hand movement (the blue areas in Figure 8). It is clear to see that there is much less noise in Figure 8 than in Figures 6 and 7.

Instead of using the exact experiment frequency, we also estimated the frequencies of the first 30 SVD time components using spectrum analysis. We then extracted the rSVD components corresponding to the estimated frequencies, and identified the one that seemed to correspond to the two movements. Figure 9 plots the interested component. Both the left-hand and the right-hand movements are detected.
5. Discussion

In this paper, we introduced a new ICA procedure for fMRI study to improve the robustness against outliers which are common in fMRI datasets. The idea is to reduce the outlier effect at the data reduction step, using a regularized SVD procedure through basis expansion. Our method is proven to be powerful and advantageous for handling the situation with outliers.

Besides reducing the outlier effect, another advantage of our method is to save computing time. ICA procedures are known not to be able to order the components. Thus the components of interest do not necessarily come out first. Hence people usually acquire around 20 to 40 components when doing ICA on fMRI data, and then “eyeball” the most related components. In our method, we can decide on the number of components by specifying the experimental frequencies. This way the analysis procedure becomes more efficient, and it saves lots of computing time considering the huge size of fMRI data.

In conclusion, our method generates more robust results when we know the frequencies of interested components. In addition, by estimating the dominant frequencies instead of specifying them, we can expect to detect components that are not foreseen by experimenters. In either case, our method performs better than the conventional ICA under the presence of outliers.

For future work, we would extend our procedure to group ICA. We also noticed that in the real fMRI data study reported in Section 4.2, the components for internal-guided and external-guided movements could not be differentiated. The reason is that both of these components share the same
frequency as the left-hand and right-hand components. However, these components do have distinct phases when modeled as sinusoid curves (as shown in Figure 5). Hence, we believe that the problem could be addressed by estimating the phases of the components in addition to estimating the frequencies. This will be investigated in future as well.

REFERENCES


Figure 1. Examples of outliers in our fMRI dataset. The left column contains the images for three different slices of the brain. The time series corresponding to the voxels at the crossings of the two lines on the images are shown in the right column. The big spikes around time points 110, 100 and 120 show outliers which are examples of many others in the dataset.
Figure 2. The recorded time course (solid line) of a voxel that is activated by the experiment stimulus sequence (dashed line).
Figure 3. The first four components of the simulated data. In each panel, the first 10 images are the component maps, and the dark red areas stand for activated voxels. The solid line in the subsequent plot is the corresponding time series. The dotted line stands for the rest-active block design, 0 for “rest” and 1 for “active”. In this simulation study, Component 1 can be viewed as the one related to the experiment stimulus. Components 2 and 3 stand for heart beat and breath respectively. Component 4 could be an artifact effect. Component 5 is not shown here since it is pure noise.
Figure 4. Comparison of the results from the proposed rICA procedure (the left column) and the conventional ICA (the right column). The components are arranged to match the order of the simulated components.
Figure 5. The experimental design used in acquiring the fMRI data. Panel a. shows the complete design sequence. Panels b. and c. show the paradigms for right hand and left hand separately. Each rest block took 30 seconds (10 scans when TR = 3 seconds). Each activation block took 60 + 60 seconds (20 + 20 scans), the first half for externally-guided movement and the second for internally-guided movement.
Figure 6. The interested component extracted by GIFT. It matches the left-hand paradigm. The red areas correspond to the PMC areas that are activated by the left-hand movement. The time plot at the top shows the time series corresponding to this component.
Figure 7. The interested component extracted by AnalyzeFMRI in R. It matches the right-hand paradigm. The blue areas exhibit the PMC that are activated by the right-hand movement. The corresponding time course and the estimated periodogram are given as well.
Figure 8. The component extracted by our rICA procedure. This component was obtained by specifying the experimental frequency. The red and blue areas in the slices of the top two rows are the PMC areas activated by the subject’s movement. The red and blue areas in the slices of the bottom rows are the cerebellum areas activated by the movement. Red areas correspond to the left-hand movement and blue areas correspond to the right-hand movement. The corresponding time series and the estimated periodogram are given as well. The solid line in the time plot is the estimated time course and the dashed line shows the experimental paradigm.
Figure 9. The interested component extracted by our rICA procedure, estimating the component frequencies. The interpretation is the same as in Figure 8. The signals detected in the cerebellum area are not as strong as the ones in Figure 8