Information Extraction From Ischemic Stroke MR Images Using Independent Component Analysis Technique

S. Pourabdollah-Nejad[1,2], H. Bagher-Ebadian[1], Q. Jiang[1,3], D. C. Noll[2], D. C. Alexander[4], J. R. Ewing[1,3], K. Jafari-Khouzani[5], and M. Chopp[1,3]

[1]Department of Neurology, Henry Ford Health Sciences Center, Detroit, MI, United States, [2]Department of Biomedical Engineering, University of Michigan, Ann Arbor, MI, United States, [3]Department of Physics, Oakland University, Rochester, MI, United States, [4]Department of Computer Science, University College, London, United Kingdom, [5]Department of Radiology, Henry Ford Health Sciences Center, Detroit, MI, United States

Introduction

Independent Component Analysis (ICA) has recently become the focus of attention in MR imaging and medical signal processing for finding statistically independent signals that form a linear coordinate system [1]. ICA has been used in fMRI for detecting spatially and temporally task related components. In this study we introduce a new approach to extracting the white matter tract from the T1 and q-ball diffusion tensor images (DTI) using ICA. Of particular interest to us is extracting information from the MR images about the ischemic area in stroke patients at different stages of recovery. We have used this method to decompose these image sets to images that show the white matter tract and the ischemic area in the brain. The results show that our method can be an effective tool for this purpose.

Materials and Methods

MR images were acquired on a 3-Tesla GE Signa scanner (GE, Milwaukee, Wisconsin, USA) using an 8-channel coil. Each MRI study consisted of a set of T1-Weighted images and a set of q-ball images. For the T1 images, the FOV was 240×240mm and the matrix was 512×512 with a slice spacing of 5mm; also TR =2653ms, TE=6.356ms for these images. The q-ball images had an FOV of 240×240mm and slice spacing of 2.6mm with a 256×256 matrix with TR=8000ms and TE = 91.9ms. The configuration of the image acquisition scheme for these images was 6 B0 images and a spherical acquisition system with 55 diffusion directions. All the images were co-registered to one of the B0 images using the Eigentool software [2]. Also the T1W images were downsized to 256×256 to be consistent with the other images. The brain was then segmented from the images. The slice showing the largest lesion was selected for each patient and the corresponding images from all the datasets for that patient were extracted for further processing. We used the Camino software for processing the Q-ball images [3]. Using this software, the diffusion tensor was fit to each voxel to produce the xx, xy, yy, yz, zz and xz images. These were used along with the B0 and T1W images as inputs to the program. For preparing the data for the ICA program, we converted the 2D images to a 1D signal by reading the images row by row and concatenating the signals. This resulted in having a digital signal corresponding to each image. Each signal consisted of 65536 points. Next, these signals were centralized, whitened and normalized to the mean value of the brain tissue so that they have the same intensity range. Using the FastICA software (Adaptive Informatics research center, Helsinki University of Technology) we implemented a 5-input, 5-output ICA system to process our composed signals. The output signal for the images for one patient can be seen in Figure 1. As the last stage, each of these signals was converted back to the 2D image form.

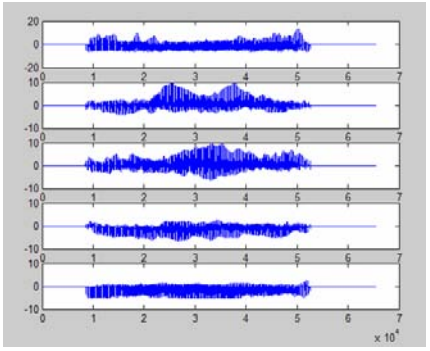

Figure 1: The 1D signals representing the independent components that form the 5 resulting images

Results

Figure 2 shows the images that correspond to the signals in Figure 1. These images belong to a stroke patient, two months after the onset of the disease. The images in the top row are the original images that have been used as the input to the ICA program. From left to right these are the T1, B0, DT-xx, DT-yy and DT-zz images. We initially included the xy, yz and xz images in the processing step but as they did not add new information we did not use them to get the final results. The bottom row shows the output images of the ICA program that have been sorted according to the correlation coefficient of the signals. The bright areas in images IC1 (Independent Component #1), IC3 and IC5 show the white matter tract in the x, z and y directions respectively. These are similar to the Fractional Anisotropy (FA) map of the images but in a decomposed form showing the fiber orientation in separate images. Image IC4 shows the ischemic area as a dark area over a bright background. The information about the lesion in this high contrast image matches that of the B0 image (image b) in the sense that the contrast between the white and gray matter is low however, the interesting point seen here is that the bright areas in image b that are related to the sulci are suppressed in IC#4 and are seen more clearly in IC2. By using these images, a clear picture of white matter remodeling can be observed over time: The reorganized neuronal fibers can be seen in IC1, IC3 and IC5 and the dead tissue can be observed in IC4.

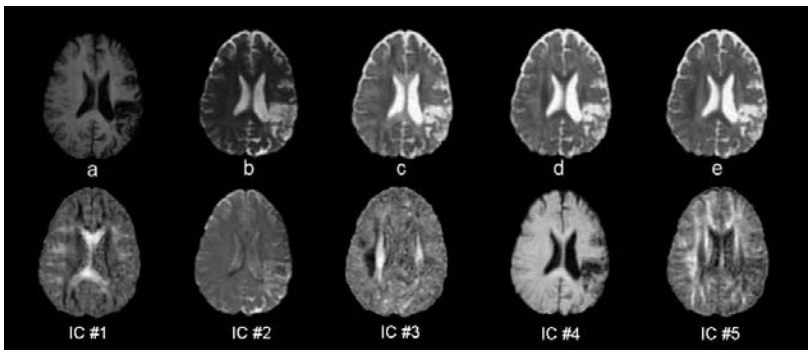

Figure 2: Images a-e show the original images that were to be decomposed. These are the T1W, B0, D-xx, D-yy and D-zz images. The second row shows the results of extracting the independent components from these images. Images IC1, IC3 and IC5 represent the white matter tract in the x, z and y directions respectively. Image IC4 shows the lesion as a dark area over a bright background.

Conclusion

The results from our study clearly shows the feasibility of using ICA for decomposing MR images for extracting the white matter tract and lesion information from q-ball and T1W images. For future work we will study the application of other image modalities for mapping white matter remodeling and the ischemic area using ICA.

References

1. Nakai et al, *Neuroimage*, 21 (2004) 251–260
2. Cook et al, *ISMRM* pp 2759 2006
3. Windham JP et al., J. *Computer Assist. Tomography* 1988; (12):1-9