Slice-by-slice motion correction in spinal cord fMRI: SliceCorr

J. Cohen-Adad[1,2], S. Rossignol[2], and R. D. Hoge[3]

[1]INSERM, Univ Paris 6, Pitie Salpetriere Hospital, Paris, France, [2]GRSNC, Physiology department, Univ Montreal, Montreal, QC, Canada, [3]UNF, Univ Montreal, Montreal, QC, Canada
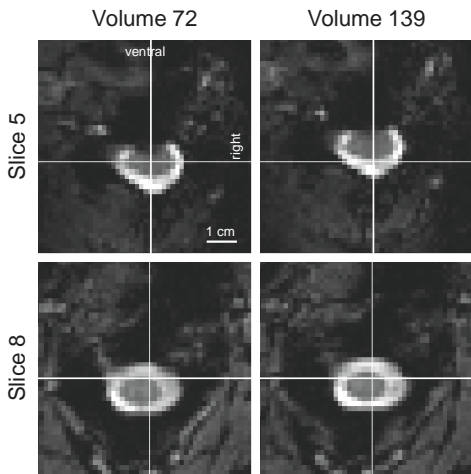
Introduction

Subject motion in functional magnetic resonance imaging (fMRI) is highly problematic for the detection of responses showing small effect size and/or spatially extent. To mitigate this problem, various methods have been proposed to correct this type of motion *a posteriori*. These methods correct each volume using a 3D rigid-body matrix having six parameters for translation and rotation (Tx, Ty, Tz, Rx, Ry, Rz). Although this approach is well adapted for brain time series, it is less efficient in the spinal cord due to its articulated geometry and the presence of susceptibility artifacts as well as physiological motions [1]. Hence, spinal cord time series are usually plagued with slice-independent motions in the antero-posterior and/or lateral directions, as illustrated in Fig 1. Previous studies addressed realignment in spinal cord fMRI by estimating a rigid-body transformation matrix within a mask [2,3]. However, issues related to slice-independent motion remain. In this study, we developed the 'SliceCorr' method, to correct motion for each axial slice independently. Although 2D alignment has already been implemented in packages such as AIR or AFNI, the SliceCorr method is purely dedicated to spinal cord data. Here, we demonstrate its usefulness in human data, and compare it with 3D-based methods.

Methods

We made the assumption that motion only occurred in the axial plane. Therefore we accounted for two translations (Tx,Ty) and one rotation (Rz). Estimation of these three parameters was done for each slice using the *fmeansearch* algorithm, with correlation criterion as the cost function. Each slice was registered to a reference slice made-up of an average of the whole dataset. Parameters for slice $t+1$ were initialized by parameters from slice t, allowing faster and more robust convergence of the algorithm. The SliceCorr method was validated on real data from six healthy volunteers, who were asked to stay 'relatively' still during 9 minutes and were allowed to swallow. Data were acquired at 3T (Siemens TIM Trio) using a 12-channel head coil and a neck coil combined. Ten axial slices covering the whole cervical spinal cord were positioned in the middle of each vertebral body to limit susceptibility artifacts [4]. The sequence used was a gradient echo EPI with acceleration factor 2 (TR/TE = 3000/30ms, alpha = 70°, slice thickness = 4 mm, matrix size = 128x72, in-plane resolution = 1.5×1.5 mm). To show the benefits of SliceCorr over 3D-based methods, the same data were corrected for motion using the SPM2 package [5], taking the mean volume as the target. We believe this implementation is representative of 3D-based correction methods, since most packages give similar results in terms of robustness and accuracy [6].

Results

As expected, transformation matrices were different between slices, highlighting the fact that each slice shows very different motion patterns within spinal cord time series. For instance, slices positioned close to the throat were subject to large motions due to swallowing, whereas slices close to the lungs had only small oscillatory displacements along the phase-encoding direction (left-right) due to variations of local B_0-field related to respiration [7]. To quantify the extent of motion between volumes, root mean square error (RMSE) was computed between each volume and the reference volume (Fig 2). The results show that the SliceCorr method exhibited the lowest residual motion in all subjects. In some subjects, the volume-based approach even introduced more variance than that in raw data. An example of single slice in one subject illustrates the type of motion pattern that are present in spinal cord time series, and how it is corrected by both methods (Fig 3).

Discussion

This study demonstrates the benefits of slice-by-slice correction of subject motion in spinal cord fMRI. The robustness of SliceCorr is counterbalanced by assuming subject motion is negligible along the rostro-caudal direction (Tz=0) and around X and Y axis (Rx=Ry=0). Although relatively strong, this assumption is realistic in standard spinal cord acquisition, as subjects are usually positioned supine therefore hardly move rostro-caudally. Notice that the SliceCorr method as implemented here is only suitable for axial acquisitions. To extend the method to other slice orientations, one solution would be to reconstruct the data in axial plane and subsequently apply the SliceCorr method. This will be addressed in future studies.

References

[1] Piché et al., *Magn Reson Imaging* (in press)
[2] Cohen-Adad et al., *Neuroimage* (in press)
[3] Stroman et al., *Spinal Cord*, 42:59-66 (2004)
[4] Brooks et al., *Neuroimage*, 39:680-692 (2008)
[5] Friston et al., *Hum Brain Map*, 2:165:89 (1995)
[6] Oakes et al., *Neuroimage*, 28:529-543 (2005)
[7] Van de Moortele et al., *Magn Reson Med*, 47:888-895 (2002)

Fig 1. Two slices in one subject recorded at two different times. In slice #5 the spinal cord is displaced dorsally by ~5 voxels whereas in slice #8 it moves by ~1 voxel. This type of motion is probably caused by a small tilting of the subject's head in the X,Y plane, inducing variable A-P displacement along the cord. This figure highlights the need for a slice-independent motion correction approach.
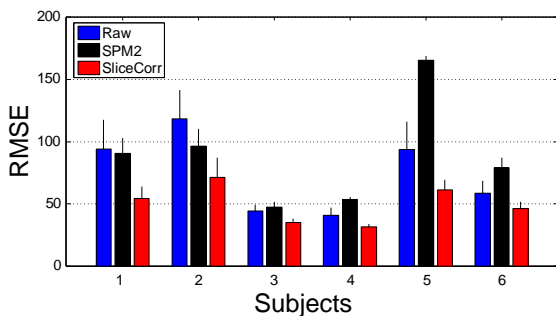

Fig 2. Root mean square error (RMSE) computed between each volume and an average volume. RMSE was computed within a mask covering the spinal cord. Standard deviation shows inter-slice variability.
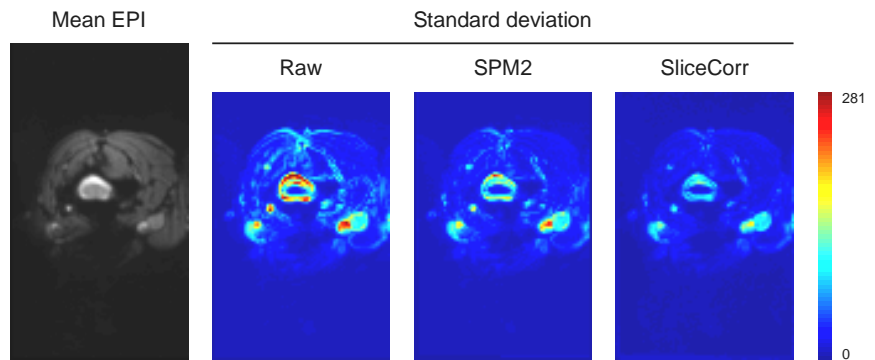

Fig 3. Typical standard deviation map for one subject and one slice located at C4. This figure shows the improvement of motion correction in axial plane for the SliceCorr method.