Slice Dependent Time Shift Efficiently Corrected by Interpolation in Multi-Slice EPI fMRI Series

P. F. Van de Moortele, J. B. Poline, A. L. Paradis, E. Lobel and D. Le Bihan
CEA, SHFJ, Orsay, France

Introduction

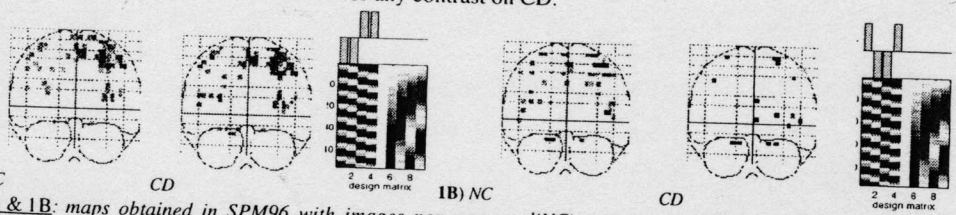
Data collected for fMRI studies with multi slice Echo Planar Imaging intrinsically present a Slice Dependent Time Shift (SDTS) resulting from slice by slice sampling of the brain along each Repetition Time [1]. This leads to a systematic phase error for BOLD responses collected on different slices. If not taken into account, this SDTS yields a loss of activation detection in regression analysis, and a bias to examine any true phase variations of the hemodynamic response across the brain. This problem can be addressed at the statistical analysis level using either some phase-independent algorithms (autocorrelation [2], Fourier analysis [3]), or taking into account the SDTS in the model (e.g. shifting the reference waveform [1,4] or correcting for slice dependent phases [5]). However, a Fourier analysis assumes a periodic paradigm, and shifting a reference waveform requires an additional dimension to describe the model. Finally, motion correction involves interpolation between slices sampled at different times and thus implies a certain loss of phase information for the observed BOLD response. We propose here to directly correct fMRI data for the SDTS by temporal interpolation, before any realignment and statistical analysis, and to examine the consequences of this correction on the activation maps generated by SPM96[6]. SPM96 offers a standard hemodynamic model based on two functions (early and late) allowing to detect BOLD responses presenting various temporal delays. One would expect that with this model, data non corrected for SDTS would exhibit some early/late contrast due to SDTS, and would not when corrected.

Method

Three volunteers performed a finger tapping task with 8 ON-OFF cycles of 30 sec in a whole-body 3T system. 48 blocks of 20 slices were acquired using a gradient-echo EPI interleaved multi-slice sequence with TR=5sec. Non corrected data (NC) were registred for movement, then analyzed in SPM96 with temporal smoothing and cut-off for frequencies lower than 1/120Hz. Data were not spatially smoothed to avoid temporal averaging between slices. We used the two-function (early/late) model proposed by the software, and we examined different contrasts showing main effect and interactions of the activation and the early/late factors. Corrected data (CD) were first interpolated to generate brain volumes resampled at unique sampling times. CD were then registred for motion and analyzed in SPM identically as NC.

Results

Strong activations were detected in cortical areas known to be related to motor tasks. For the main effect of activation (Fig. 1A), no noticeable differences in detected patterns were observed between NC and CD. However, a highly significant slice effect appeared clearly on NC for some contrasts between early/late functions, reflecting the SDTS. Fig1B shows an example of such a contrast. This slice effect (which exhibits as activated strips on only odd or even slices) was not observed for any contrast on CD.



1A) *NC* *CD* **1B)** *NC* *CD*

Fig1A & 1B: *maps obtained in SPM96 with images non corrected(NC) or corrected (CD) for SDTS. Note that images were not normalized into Talairach coordinate. Contrast coefficients were set as following :*
Fig1A: *(+1) during rest and (-1) during action for both early and late functions*
Fig1B: *(+1) during rest and (-1) during action for early function, (-1) during rest and (+1)during action for late function.*

Conclusion

We conclude that temporal data interpolation efficiently corrects for the SDTS, removing the slice effect visible in some early/late contrasts. It should then be possible to analyze residual early/late differences arising between activated regions, which could be of great physiological interest. It is very likely that this correction will be even more important in event-related fMRI, compared to block designs, as the BOLD response phase would be evaluated more accurately.

References : (1) Van de Moortele & al., NMR in Biom., 10, 230-236, 1997 (2) Paradis & al, IEEE-EMBS, abst, 3.2.2-2, 1996 (3) O. Joseph & al., Hum. Brain Map., 5, 1-6 1997 (4) Savoy & al., ISMRM, abst, 450, 1995 (5) Sereno & al., Science, 268,889-893, 1995 (6) Friston, NeuroImage, 2, 45-53, 1995