

## Prospective motion correction reduces the number of false positive activations in an fMRI group study involving task-correlated motion

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**PURPOSE** – The aim of this study was to compare the rate of false positive activations in an fMRI group study at 7T with and without slice-by-slice prospective motion correction using an optical tracking system<sup>1,2</sup>. The paradigm chosen involved strong task-correlated motion, which is a major cause of false positive activations in fMRI<sup>3</sup>.

**METHODS** – An fMRI group study was conducted on 15 volunteers at 7T using an 8-channel head coil. The block design paradigm was a left-right motion of the lifted right leg for 20 s following a rest period of 20 s. Six blocks were acquired without and six blocks with prospective motion correction (NoPMC / PMC) using an embedded optical tracking system<sup>2</sup>. In six volunteers the PMC blocks were acquired before the NoPMC blocks. The acquisition parameters for the functional EPI scans were as follows: TR=2000 ms, TE=25 ms, 3.1×3.1×3 mm,  $\alpha=90$  deg, number of slices=30, BW=2056 Hz/pixel, 120 volumes, TA=4:04 min. The tracking system recorded the head motion during all scans, including the period without prospective motion correction. The motion curves for translations along the head-foot (z-) axis averaged over all volunteers [Fig.1] reveal a strong task-correlated head motion. Along with the functional data, a GRE field map to undistort the EPI scans was acquired, as well as anatomical data (MP2RAGE: TR=4130 ms, TE=4.04 ms, TI=1000 ms / 3300 ms, 0.9×0.9×0.9 mm,  $\alpha=5 / 7$  deg, number of slices=176, BW=240 Hz/pixel, Grappa 3, TA=5:41 min).

To undistort the PMC data within a time series, the method proposed by Ooi et al.<sup>4</sup> was applied. For the NoPMC data the SPM Realign&Unwarp function<sup>5</sup> was used. The PMC data were processed with and without additional retrospective realignment. For the analysis of false positive activations, the data were processed on a subject-by-subject level using GLM analysis in SPM without smoothing or normalizing the data to a template. Also, the default brain masking was deactivated.

The anatomical data were segmented using CBS Tools<sup>6</sup> and co-registered to the functional data. Grey matter masks were created covering all regions in the brain where BOLD activation may occur (grey matter, amygdala, caudate, hippocampus, putamen, thalamus, globus pallidus, brainstem) [Fig. 2]. Histograms of the T-value distributions of voxels outside of these masks were generated.

Additionally, the data were analyzed according to SPM convention using smoothing with 8 mm FWHM and normalization to the MNI space, to calculate a familywise error rate (FWE) corrected ( $p<0.05$ ) activation on the group level.

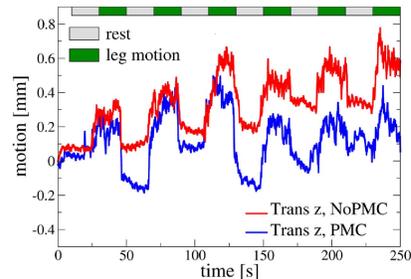
**RESULTS** – The standard deviations of the SPM realignment parameters were 0.19/0.30/0.17 mm / 0.16/0.13/0.07 deg (PMC) and 0.25/0.17/0.73 mm / 0.42/0.25/0.25 deg (NoPMC). The linear correlation coefficients between the SPM realignment parameters averaged over all volunteers and the block design for the most pronounced motions were reduced from 0.71 to 0.17 (translation along head-foot axis) and from 0.67 to 0.12 (rotation around left-right axis) by PMC.

Figure 3 shows a plot of the total number of activated voxels outside the grey matter masks with T-values above  $T_{\text{threshold}}$ . The number of falsely activated voxels was substantially lower when applying the prospective motion correction. For  $T_{\text{threshold}} = 5$ , the prospective motion correction reduced the amount of activated voxels outside grey matter to 52 % (no retrospective realignment) or to 56 % (additional retrospective realignment) of the number of falsely activated voxels in the NoPMC data. The conventional group analysis indicates that the peak T-value for the activation in the right leg motor region as well as the cluster size is larger in the PMC data [Fig. 4].

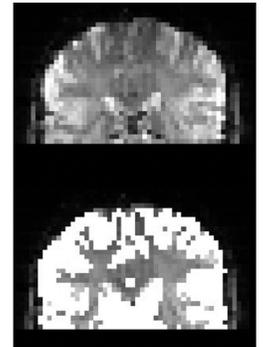
**DISCUSSION** – This study shows that the number of activated voxels that are obviously false positives is reduced when the functional data is acquired using slice-by-slice prospective motion correction. Additionally, the conventional analysis confirmed that prospective motion correction improves the statistical power in group fMRI<sup>4</sup>. It is unclear from our data if additional retrospective realignment of the PMC data is useful: In terms of false positive rate it seems slightly beneficial not to realign, whereas statistical significance is increased by retrospective realignment. A possible cause for this improvement is the blurring introduced into the images by the interpolation used in the retrospective realignment step. In general, it will depend on the amount of residual misalignment, i.e. the quality of the prospective motion correction, if a retrospective correction is favorable.

**CONCLUSION** – Prospective motion correction reduces the rate of false positive activations in fMRI experiments that include task-correlated motion and, additionally, increases the statistical power of the analysis. Therefore, we suggest that prospective correction techniques should be used whenever available.

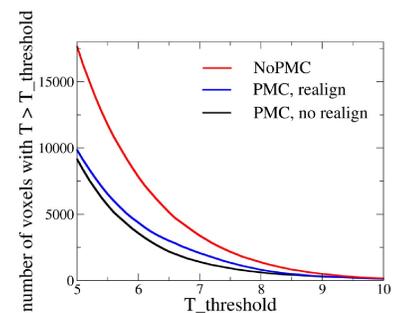
**REFERENCES** – 1. Speck O et al. Magma. 2006;19(2):55-61; 2. Schulz J et al. Magma. 2012 Jun 13. [Epub ahead of print]; 3. Hajnal JV et al. MRM 1994;31:283-291; 4. Ooi MB et al. MRM 2012 Apr 12. [Epub ahead of print]; 5. Andersson JLR et al. NeuroImage 2001;13:903-919; 6. Bazin P-L et al. Proceedings of the 18th Annual Meeting of the Organization for Human Brain Mapping, 2012



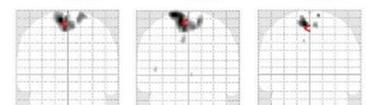
**Fig. 1:** To show the strong task-correlated motion, the translation along the z-axis (head-foot) with time, that was recorded with the optical tracking system, averaged over all volunteers is plotted for the PMC and NoPMC scans.



**Fig. 2:** EPI image (top) and the corresponding grey matter mask overlaid on it (bottom).



**Fig. 3:** Number of voxels with T-values larger than  $T_{\text{threshold}}$  outside the grey matter masks.



	PMC, no realign	PMC, realign	NoPMC
Voxels in cluster	869	1261	136
Peak T-value	13.8	14.8	11.7

**Fig. 4:** Results of the group analysis ( $p<0.05$  FWE corr): Coronal maximum intensity projections are shown and the number of voxels and the peak T-value in the cluster representing the activation of the motor region of the right leg are given.