

Small scale functional activations using a non-linear, population-specific brain model and 3D EPI at 7 Tesla

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Introduction:

Due to the availability of high field scanners and novel imaging methods, high resolution, whole brain fMRI becomes feasible (Poser et al, 2010). However, for performing fMRI group analyses spatial smoothing is necessary to account for inter-individual anatomical variation. Here, we investigate the possibility to build a high resolution, group specific anatomical template (model) directly from the functional T2* weighted data acquired at 7 Tesla. The purpose of this model is two fold; first, spatial smoothing can be kept at a low level and second, misregistration between distorted functional and anatomical data is avoided.

Materials and Methods:

Data acquisition: An accelerated 3D EPI sequence (Poser et al, 2010) was used to acquire functional data of 8 subjects using 1 mm isotropic resolution, TE = 23 ms, TRslice = 50 ms, TRvolume = 3.2 s, AF = 3 x 3, BW = 2000 Hz / px, slice oversampling of 25%. A matrix size 180 x 180, and 104 or 112 (four subjects) slices in an axial orientation using a 32 channel head coil (Wiggins et al., 2006) were used. Measurements were performed on 8 subjects on a Magnetom 7 T scanner (Siemens Healthcare, Erlangen, Germany) in accordance with local ethics regulations. The fMRI task consisted of four blocks of different finger tapping tasks with a length of 20 s each: tapping of the left index (LI), left little (LL), right index (RI), and right little (RL) finger, and each was repeated four times in a pseudorandom order embedded in 10 s resting blocks. The total acquisition time for this functional run was 370 seconds. **Functional analysis:** fMRI data processing (preprocessing, first and second level analysis) was carried out using FEAT - part of FSL (FMRIB's Software Library, www.fmrib.ox.ac.uk/fsl). Motion correction, 2mm spatial smoothing and highpass temporal filtering (sigma = 20.0 s) were applied. **Model generation:** The symmetric EPI model of the 8 subjects was created by using the approach presented by (Grabner et al. 2006). This method involves linear and stepwise non-linear registration of EPI data, in both their original and left-right flipped version to an evolving model of averaged structure. The average, motion corrected functional image was used to create the non-linear subject-to-model transformation.

Results:

Figs.1 and 2 show group activation maps using a z-threshold of 6. The number of activated voxels (av) and the maximum z-values (mzv) in the ROIs defined by the activation clusters in the motor cortex for the different models are: LL-LI: av = 762, mzv = 10.7; LI-LL: av = 410, mzv = 10.9; RL-RI: av = 179, mzv = 8.82; RI-RL: av = 361, mzv = 11.20. The Euclidean distances between the center of gravity (CoG) between the activation clusters were calculated: between LL-LI and LI-LL = 12.8mm, and between RL-RI and RI-RL = 13.9mm.

Discussion and Conclusion:

Due to the high resolution and the excellent anatomical contrast of T2*-weighted functional images at 7 Tesla the functional data could be used directly to generate a group specific model without transforming fMRI data to an anatomical data set. Our approach improves localization of activation of group data as it provides high resolution and a more accurate normalization by providing a model specific for the group. Of course, the model can still be normalized to a standard anatomical atlas (e.g. non-linear MNI) which enables labeling of anatomical structures.

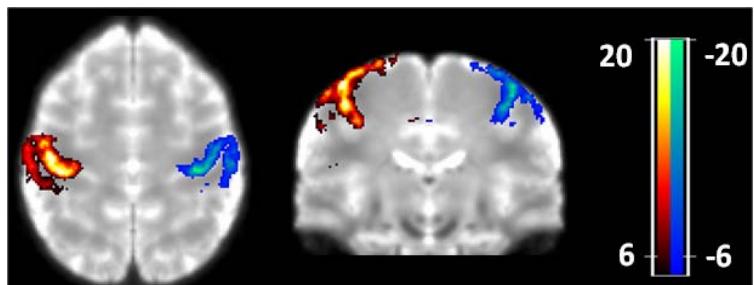


Figure 1: Group Activation (N=8), left hand versus right hand on the group specific model.

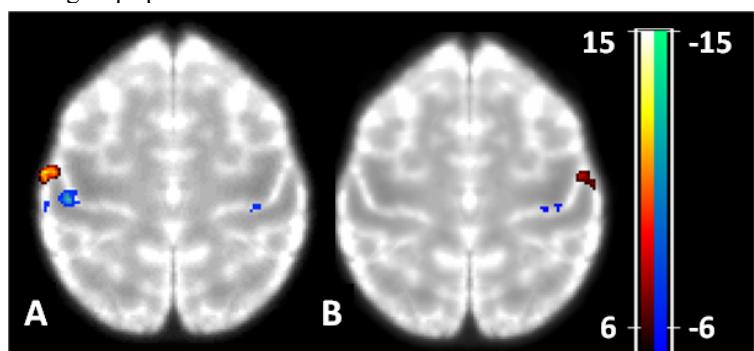


Figure 2: Group Activation (N=8), LL-LI (A) and RL-RI (B) on the group specific model.

References:

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- 3) Wiggins et al. Proc. ISMRM 2006:#415.

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