

Optimization of event-related fMRI design for BOLD deconvolution

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Introduction. Standard analysis methods of event related fMRI (er-fMRI) are based on convolving the timing sequence of stimuli with a BOLD model, and applying a multiple-regression analysis (MRA) to detect ‘active’ voxels. As the BOLD response function can vary across regions and subjects, alternative analysis methods have been proposed that allow for model free fMRI signal analysis through ‘deconvolution’ [1] (also called ‘finite impulse response models’, FIR, [2]) This method employs a number of delta-pulse regressors for each event type, that estimate the BOLD signal at specific time-points relative to stimulus presentation. A disadvantage of this method is that the increased number of regressors can increase multicollinearity (MC), or linear dependency between regressors. The effect of MC on the sensitivity and reliability of MRA-based deconvolution analysis is investigated in this work by using simulations and a fMRI experiment.

Method. We examined the effect of MC on the sensitivity and reliability of MRA-based deconvolution analysis using 128 different er-fMRI designs with a random stimulus distribution, and one pseudo-random design based on the m-sequence (e.g. [3,4]) which previously has been proposed as optimal. Each design consisted of 63 stimulus trials. The efficiency of each design was determined by averaging the ‘tolerance’ (aTOL) value of all regressors ($aTOL = (1-R^2)$, where R^2 is the result of a MRA with one regressor as a dependent variable and all other regressors as independent variables). Signals were simulated using a BOLD model (BOLD impulse response function: time-to-peak=4s, width=8s) in 10,000 voxels with different random Gaussian noise. Mean t-value and the standard deviation (SD) of relative signal change were determined by a standard multiple regression deconvolution analysis with 15 regressors. The average of these values over the 10,000 voxels was correlated against the aTOL value for each design. We selected 3 designs (low aTOL, high aTOL and m-sequence) to be applied in a fMRI experiment, to confirm the results of the simulation (3 healthy volunteers performed a simple visual comparison task based on [5]: 3T-GE scanner; 8 channel head coil; SENSE-EPI; TE/TR 25/2000; 3.5mm³ voxel size). Scans were registered to reduce effects of motion. Acquired and simulated were analysed using the same multiple regression analysis comprised of 15 deconvolution regressors. For comparison of the 3 designs we selected voxels with a $t > 3.0$ in any of the 3 designs and averaged the t-values in those voxels for each design.

Results. The aTOL value of the simulations varied from 0.57 to 0.92 for the 128 random sequences, with a value of 0.995 for the m-sequence. aTOL strongly correlates with the sensitivity (fig. 1a, $r=0.82$, $p<0.001$) and reliability (Fig. 1b, $r=-0.91$, $p<0.001$) of the design. T-values varied across random designs from $t=2.75$ to $t=3.96$, with a value of 4.16 for the m-sequence based design. The results of the fMRI experiment are illustrated in figures 2 and 3. Experimental fMRI results showed good correspondence with the simulation results. T-values in the selected voxels strongly correlated with the aTOL value in all three subjects with highest values for the m-sequence based design.

Conclusion. Multicollinearity strongly influences the reliability and sensitivity of a deconvolution design in er-fMRI, as was shown in a simulation and with experimental data. Experimental data verify that optimized er-fMRI design can be reached by basing the stimulus timing on a pseudo-random m-sequence, as previously shown in simulations by Buracas et Al. [3].

References

- [1] Ollinger JM, et al. 2001 NeuroImage 13 210-217
- [2] Manoach DS et al. Neuroimage. 2003 20(3) 1670-1684
- [3] Buracas, G.T et al., 2002. NeuroImage 16, 801– 813
- [4] Kellman P, et al. 2003 Neuroimage 19,190-199
- [5] Hariri AR et al, 2002 NeuroImage; 17, 317–323

figure 1

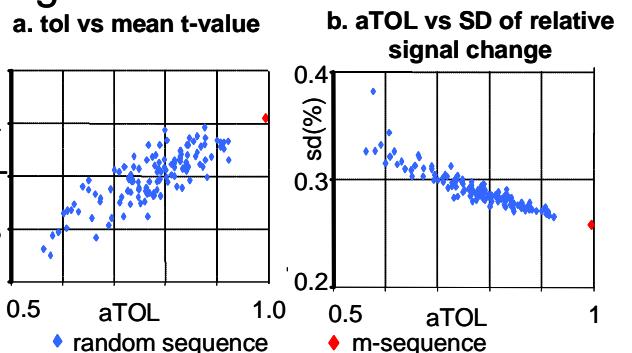


figure 2

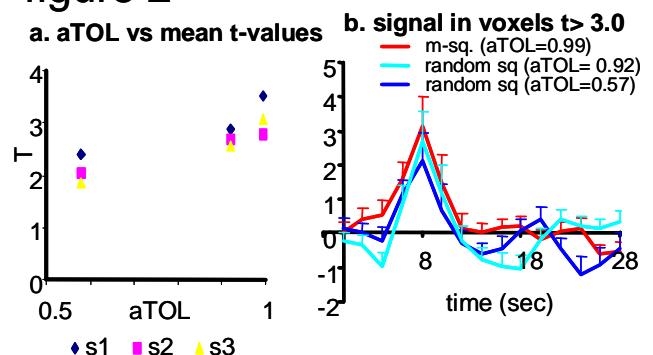


figure 3

