Assessing fMRI activation using maximum convoluted correlation

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A traditional and popular approach to assessing activation in functional neuroimages is to use the correlation between fMRI signal and reference stimulus or equivalently rely on a t-test between rest and activation scans. This approach has been extended to accomodate faster sampling rates available in fMRI by modelling the haemodynamic response with eg a Poisson filter [1]. A major drawback of this approach is that the filter parameters are estimated on the data and hence produce a positive bias in the resulting correlation. This effect is increased when parameters are estimated locally in order to account for the brain's inhomogeneity. In this contribution, we propose a novel method based on investigating the correlation over a whole range of parameter values. Important parameters like delay or activation strength can be estimated locally, without bias in the resulting statistics, leading to added flexibility, but correct significance levels.

Maximum Convoluted Correlation (MaCC)

For a stimulus $p(t)$ covering T images $1 \ldots T$, a signal $f(t,x,y,z)$, and a filter $h_w(\tau)$ parameterised by w, the convolved stimulus is: $r_w(t) = \sum_{\tau=0}^{+\infty} p(t-\tau) h_w(\tau)$, and the (unnormalised) signal correlation: $c_w(x,y,z) = \frac{1}{T} \sum_{t=1}^{T} f(t,x,y,z) r_w(t)$. Usual (linear) filters include Poisson, Gamma, Gaussian, delay or FIR. We consider the statistic $M(x,y,z) = \max_w c_w(x,y,z)$ where the maximum is taken over an admissible domain (eg positive delays between 5 and 10 s). The distribution of M under the null hypothesis is usually intractable and we resort to numercial approximation using a Monte Carlo sampling scheme. For Gaussian noise with covariance $\mathbf{\Sigma}_0$, the convoluted signal under H_0 can be sampled directly from a multivariate Gaussian with covariance $\mathbf{R}\mathbf{\Sigma}_0\mathbf{R}^\top$, where $\mathbf{R}$ is a matrix containing convolution coefficients $r_w(t)$.

The dataset was acquired at Hvidovre Hospital on a 1.5 T Magnetom Vision MR scanner, with a 2D gradient echo EPI (T2* weighted) scanning sequence with 66 ms echo time, 50 degrees RF flip angle, and a 128x128 matrix size, FOV of 230 mm, and 10 mm slice thickness. For 10 runs of 121 images in a para-axial orientation parallel to the calcarine sulcus were acquired at 3 images/s: 31 rest scans, 30 scans of full-field checkerboard reversing at 8Hz, and 60 rest scans. 29 prescans were performed at same rate to minimize saturation effects.

Results

These preliminary results use the delay filter $h_d(\tau) = \delta(\tau - d)$ such that the resulting c_d is the traditional cross-correlation function [2]. We test 4 methods: 1) standard correlation, 2) delayed correlation with globally estimated delay, 3) same with locally estimated delay and 4) MaCC method. We first use 4057 voxels pure noise images, to check false positives. The *correct* (in *italics*), and observed (method 1,2,3,4) amounts of false positives are, respectively: for $p < .01$: *40*, 36, 38, 3356, 32; for $p < .001$: *4*, 4, 1, 2295, 4. The local adaptation of the filter parameter leads as expected to an inacceptable increase in false positives. Figure 1 displays the results obtained on the actual dataset in the form of probability maps. White areas mean that H_0 is strongly rejected. As expected, the activation concentrates on the visual cortex, primarily V1 and V5. There is also activity in the area of the sagittal sinus. The standard correlation misses part of the activation, and the local estimation gives too many false positives. The MaCC method handles the delays well and noticeably gives a better resolution in regions that react with shorter delays.

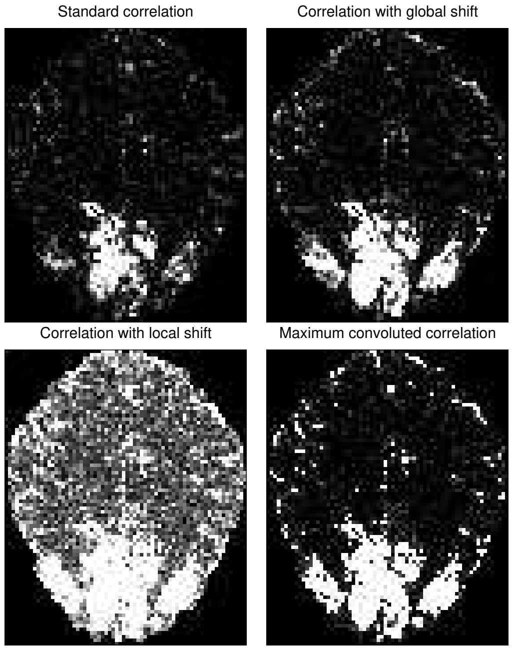

Fig 1: Probability maps (white=small p).

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References

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