Adaptive fMRI Data Filtering Based on Tissue and Signal Similarities

J. Rydell[1], H. Knutsson[1], and M. Borga[1]
[1]Department of Biomedical Engineering, Linköping University, Linköping, Sweden

Introduction

Typically, the signal to noise ratio in fMRI data is very low, and therefore sensitive detection algorithms are needed to find neural activation. Usually, for example in SPM [1], the signal to noise ratio is enhanced by low-pass filtering, i.e. by averaging signals from several neighboring pixels or voxels before they are compared to a reference time-course to determine what regions of the brain are activated. While this approach increases the sensitivity in activated regions which span a sufficient number of voxels, the averaging causes the signals from small activated regions to be drowned in noise from surrounding inactive parts of the brain. Also, information about the exact size and shape of the activated regions is lost. To alleviate these problems, several different methods for adaptive data filtering have been proposed. Unlike low-pass filtering, adaptive filtering uses different filters in different parts of the data. The filters are adapted to the data to be filtered, or to some other description of the individual regions in the data set. One method for adaptive filtering of fMRI data is so called bilateral filtering, originally suggested for filtering of 2D images [2]. In the fMRI context, bilateral filtering averages signals if they are located close to each other and if the variation over time is similar. Different variations of this approach have been suggested and shown to work well for detecting activation with high accuracy [3, 4, 5]. Another variation of this theme is to instead average signals if they are located close to each other and if they reside in the same type of tissue (fat, cerebrospinal fluid (CSF), or gray or white matter) [6, 7]. Neural activation occurs in gray matter and has also been observed in white matter at high magnetic field strengths (4 T) [8]. However, no activation is present in fat or CSF. By only averaging signals from the same type of tissue, activation will not "leak" into parts of the brain where it is biologically implausible. Equally important, noise from regions in other tissue types will not degrade the signal from an activated part of the brain. Each of these methods for adaptive filtering has its own drawbacks. If only anatomical information is used to constrain the filters, activation may be smeared into adjacent voxels in the same type of tissue. If only the similarity between different time-series is considered, random noise variations may cause signals from active and inactive regions to be averaged, thereby degrading the detection accuracy. We propose a method which uses both of these types of information to guide the filter design and show that this increases the accuracy of the activity detection.

Theory and proposed method

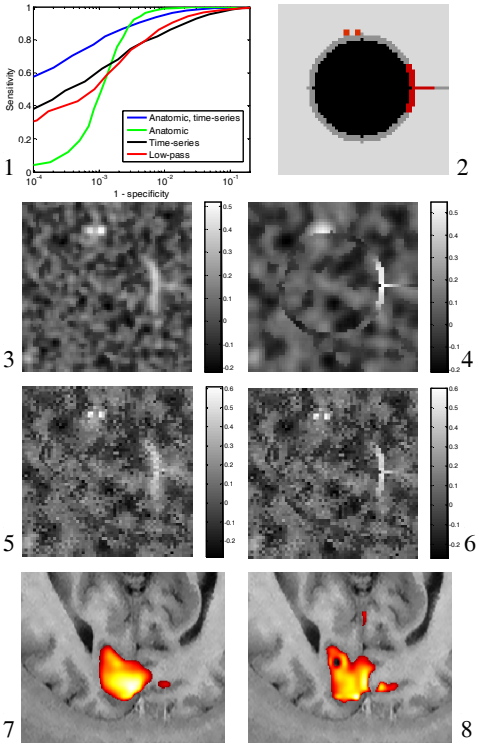
In bilateral filtering of images, the filter kernel in each neighborhood can be expressed as a product of two filter kernels: the domain filter F_d and the range filter F_r. The domain filter is based on spatial distance while the range filter is based on the difference in image intensity. That is, given an image $I(x, y)$, the bilateral filter kernel $F(i, j)$ at image coordinates (x, y) can be written $F(i, j) = F_d(i, j)\, F_r(i, j)$,where $F_d(i, j)$ is an ordinary spatial filter kernel $g(i, j)$ and the range filter is defined as $F_r(i, j) = h(I(x + i, y + j) - I(x, y))$. Thus, two pixels are averaged if they are located close to each other and if their values are similar. The range filter gives bilateral filtering the ability to preserves edges in the filtered image. A common choice of the filter kernels g and h is Gaussian functions. What we propose here is similar to bilateral filtering, but instead of creating a range filter from differences in image intensity, we use two range filters. One is based on the difference between the projections onto the BOLD model. This means that all signals with low correlation to the signal model are considered similar and can be averaged. Signals with high correlation are averaged if their projections on the model signals are similar. Thus, all noise time-series are averaged, while possible activated time-series are only averaged if they are similar to each other. The other range filter is based on intensity differences in a T1 weighted image. Since T1 values reflect different tissue types, this range filter precludes averaging of signals from parts of the brain with different types of tissue. The two range filters are multiplied, and thus we end up with $F(i, j) = F_d(i, j)\, Fr_1(i, j)\, F_{r2}(i, j)$, where $F_{r1}(i, j)$ is the range filter based on time-series similarity and $F_{r2}(i, j)$ is based on anatomical similarity. Each of the domain filter and the two range filters has its own standard deviation, which controls to what extent two signals are allowed to affect each other given a certain degree of similarity.

Results and discussion

We have used both synthetic and real fMRI data to evaluate the method. The synthetic data consist of an image describing the anatomy and a sequence of noisy images with biologically plausible BOLD signals embedded at known locations. The activated locations are chosen such that most of the activation is located within gray matter, while some activation is present in white matter. Neither the anatomy nor the activated locations have been designed to mimic real fMRI data, but rather to demonstrate how the detection of activation works. The anatomy and the activated regions are shown in figure 2, where light gray illustrates white matter, dark gray is gray matter, black is CSF and the red regions are activated. Figure 3 shows the activation map obtained by using ordinary low-pass filtering. Figures 4-6 show the activation maps obtained using only anatomical constraints, only constraints based on time-series similarity and the proposed combination of constraints respectively. The adaptive methods provide enhanced detection performance. When only anatomical information is used to constrain the filters, the activation "leaks" into surrounding areas with the same type of tissue. On the other hand, when only the similarity between the time-series themselves are used to constrain the filters, some boundaries between active and inactive regions are slightly blurred. The proposed method, where both types of constraints are used, provides an activation map with clear boundaries between active and inactive voxels. These visual results are confirmed by the ROC curves in figure 1. These curves show the sensitivity (ability to correctly classify active voxels) and specificity (ability to correctly classify inactive voxels) of the different methods, and it is clear that the proposed method provides the best overall performance, followed by the two other bilateral methods, and finally the low-pass filtering. ROC curves calculated from pseudo-real data (real data where signals from active regions have been embedded at known locations) indicate similar results, but are not shown here due to space constraints.

Figures 7 and 8 show activated regions detected in real data from an experiment where the visual cortex was stimulated using a flashing checkerboard pattern. A close-up of the visual cortex is shown. The activation shown in figure 7 was detected using low-pass filtering while that in figure 8 was detected using the proposed method. Since the ground truth is not known, no certain conclusions can be drawn from this data set. However, the regions detected as active using the proposed method seem to follow anatomical structures more closely than those detected using low-pass filtering. For example, the proposed method does not find activation in the CSF.

While the results shown here are all from two-dimensional filtering and analysis, an extension to three dimensions is trivial and expected to further improve the activity detection.



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