MDL-based Estimation of the Hemodynamic Response Function for fMRI data

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Introduction

The Hemodynamic Response Function (HRF) varies between experiments, subjects and brain regions [1]. Estimating the HRF is important for statistical analysis of the fMRI data and for obtaining information about the temporal dynamics of the brain. HRF models commonly assume varying amounts of prior knowledge about the shape of the HRF. This ranges from assuming a fixed HRF shape to a completely flexible model with as many free parameters as the data points. Also, there exist some methods in between these two extremes. The main difficulty in the HRF estimation is to determine the variability and range of the models. Too little flexibility prohibits adaptation to brain regions or subjects, while too much flexibility produces unlikely HRF shapes [2]. Thus, in this work we use the minimum description length (MDL) principle to extract models from the data itself. We pursue a novel approach that goes beyond the known applications of MDL for model-order selection. The proposed algorithm provides a nonparametric approach to HRF estimation without any explicit assumptions. The estimated HRF is compared with a benchmark, the Gamma and Poisson HRF models. Statistical analysis based on the estimated HRF by the proposed method shows better estimates of the t-tests compared with that of fixed HRF models.

Methods

The MDL principle gives a guideline for model selection [3]. In MDL principle data are considered as sequences to be compressed by the model. Models are compared by their ability to compress a data set. The goal is to select a model that gives the most compact description of both the data and the model. In MDL there is no need to assume that a true model generates the data and this is important in cases where the underlying truth is unknown. Based on this principle we develop an algorithm that iteratively estimates the HRF and activation level for each region of interest (ROI). The HRF shape is assumed to be the same over a homogeneous region, but its amplitude can vary. We use a General Linear model (GLM) for each voxel time series. The vector y_j shows the demeaned and detrended time series of voxel j. There are M number of voxels in the ROI. X is a $N \times 1$ vector that includes the convolution of the Hemodynamic Response Function $h(t)$, with the stimulus time series $S(t)$. The HRF and activation levels are unknown and will be estimated. Activation level for voxel j is shown by the scalar α_j and e_j is the white Gaussian noise. First, the BOLD response X is estimated using the MDL principle [4]. Then by knowing the BOLD response, the least square estimation of the activation level is calculated. The steps will be done iteratively until convergence. The HRF is estimated by deconvolution of the final estimation of the BOLD response and the stimulus function.

Results

The synthetic time series are generated for a ROI containing 27 active voxels. The true HRF is the difference of two Gamma functions as in [5]. The HRF is convolved with an event-related paradigm to generate the BOLD response. The signal to noise ratio for each time series is 0.2 dB. The benchmark and estimated HRF are shown in Fig.1, together with the Poisson and Gamma HRF plots. The MDL-based algorithm can estimate the benchmark with good precision. The t-statistics are calculated for all the voxels in the ROI with each of the HRFs. These t-statistics are shown in Fig.2. The t-values with the proposed MDL-based method are better estimates of the t-values obtained with the benchmark HRF. The algorithm is also tested on a real data set. The real data is acquired from a healthy subject. The experiment is an event-related paradigm with 27 auditory stimuli with voxel size 3.125mmx3.125mmx4mm. The registration and detrending are the preprocessing steps done on the data. Active regions are determined by AFNI software and HRF estimation algorithm is applied to these defined active regions to check the variations of the HRF between different brain regions. This study shows that variations in the HRF can be captured by the proposed algorithm both on synthetic and real fMRI data.

Discussion

We propose a method based on MDL principle for the HRF estimation that can capture HRF variability. No model is assumed for the HRF shape. The results show the ability of the MDL-based algorithm to estimate the benchmark HRF with good approximation. Comparing the t-statistics of the voxels obtained with different HRF shapes, shows that t-values with the proposed MDL-based method are better estimates of the t-values obtained with the benchmark HRF.

References

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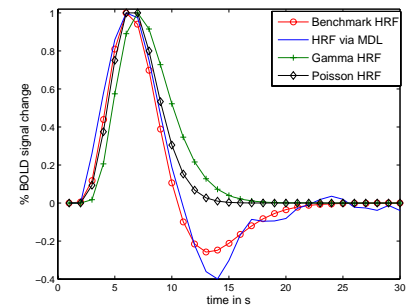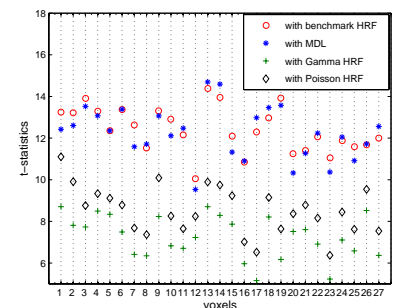
Fig.1: Measuring the precision of HRF estimate

Fig.2: Comparing t-statistics obtained by benchmark, Gamma, Poisson and estimated HRF