A New General Linear Convolution Model for fMRI Data Process

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Abstract General linear model (GLM) is the most popular method for functional magnetic resource imaging (fMRI) data analysis. However, its theory is imperfect. The key of this model is how to constitute the design-matrix to model the interesting effects better and separate noises better. For the purpose of detecting brain function activation, according to the principle of GLM, a new convolution model is presented by a new dynamic function convolving with design-matrix, which combining with t-test can be used to detect brain active signal. The fMRI imaging result of visual stimulus experiment indicates that brain activities mainly concentrate among v1 and v2 areas of visual cortex, and also verified the validity of this technique.

Key words fMRI; general linear model; t-test; hemodynamic response function

1 Principia

1.1 GLM Theory

It will be assumed that the blood oxygenation level dependent (BOLD) response is 'boxcar'-like, i.e., follows a square wave function. This is a somewhat crude assumption to make. More realistic models will be explained later on. The general linear model (GLM) has the form

\[ y_i = \beta_0 + x_{i0}\beta_1 + \cdots + x_{ik}\beta_k + \cdots + x_{ip}\beta_p + \varepsilon_i \]

where \( y_i \) stands for the activation value of the voxel in scan \( i \) (i.e., at time point \( i \)). This value is assumed to consist of linear terms. \( \beta_k \) denotes the influence of the experimental condition \( k \) on scan \( i \), i.e., if at scan \( i \) condition \( k \) is measured, then \( x_{ik} \) equals to one and \( \beta_k \) denotes the activation change that is caused by condition \( k \). The terms \( x_{ik} \) of conditions \( k \) that do not exert an influence on scan \( i \) (but may have on other scans) are zero. Nevertheless, it is possible that more than one \( x_{ik} \) is one. The measurement error at scan \( i \) is denoted by \( \varepsilon \). \( \varepsilon \) is assumed to be independent and identically normally distributed with the expected value \( E(\varepsilon) \) being zero.

Overall, there are \( n \) Eq.(1), one for each scan \( i \). Therefore, matrix notation offers a simpler way to describe this system of linear equations

\[ y = X\beta + \varepsilon \]

In the above equation, \( y \) denotes the data vector containing \( n \) elements, \( X \) is the so-called design matrix...
(n(p+1)) that includes the x_{ij} (because x_{i0} is one, the first column of X contains ones exclusively), \( \beta \) is the parameter vector ((p+1) elements), and \( \varepsilon \) is the (n)-vector of errors. Generally, the first column of the design matrix model stimulation pattern, the second model brain activity on the condition of non-stimulation, the rest of columns model physiological noise which aroused by respiration and palpitation. Friston et al consider physiological noise as low-frequency artifacts, and modeled with discrete cosine function, essentially high-pass filter\(^5\).

In the above equation, \( y \) is known (measured), and the design matrix \( X \) is given. The vectors \( \beta \) and \( \varepsilon \), however, have to be estimated.

The aim of parameter estimation is to derive a prediction equation

\[
\hat{y} = X\hat{\beta}
\]

so that

\[
\sum \varepsilon_i^2
\]

is minimized. In the above equations, the symbol \( ^\top \) indicates variables that are estimators rather than measured. The ‘least-squares’ estimation of parameter is

\[
\hat{\beta} = (X^\top X)^{-1} X^\top y
\]

If \( X \) is independent to noise \( \varepsilon \), the estimate of \( \beta \) is unbiased. This is because

\[
E(\hat{\beta} - \beta) = E(\varepsilon) = 0
\]

In general, the matrix product \( X^\top X \) is rank deficient, so that the inverse \( (X^\top X)^{-1} \) does not exist, and the equation cannot be solved. Consequently, a generalized concept of the inverse of a matrix may be used for the estimation of \( \beta \) Now

\[
\hat{\beta} = X^+ y
\]

Some of these parameters will be of interest (e.g. the effect of particular sensorimotor or cognitive condition or the regression coefficient of hemodynamic responses on reaction time). The remaining parameters will be of no interest and pertain to confounding effects. Inferences about the parameter estimates are made using their estimated variance. The unbiased estimate of the variance of the noise is given by

\[
\hat{\sigma}^2 = \frac{1}{N-p} (y - X\hat{\beta})^\top (y - X\hat{\beta})
\]

where \( N \) is the number of the variance of observations, i.e., the dimensionality of the vector \( X \), and \( p \) is the number of elements in parameter \( \beta \). This allows one to test the null hypothesis by \( T \) or \( F \) statistic\(^5\). Here, a \( t \)-test is used to test whether the BOLD responses contribute to detected fMRI signal.

Null Hypothesis: the action of an interested biological effect (include the intrinsic signals and the out stimuli) is null in the brain activity, i.e., the contribution of a selected \( i \)-th column \( X \) is none. It is same to say the element in parameter vector which corresponding to the interested biological effect is equal to zero. An example of a contrast weight vector \( c \) would be \([1\ 0\ 0\ \cdots\ 0\ 0]\). Now let

\[
t = \frac{c^\top \hat{\beta}}{\text{Std}(c^\top \hat{\beta})}
\]

where \( t \) is of \( t \)-distribution with degrees of freedom \( N-p \). The denominator is the standard deviation of

\[
\text{Std}(c^\top \hat{\beta}) = \sqrt{c^\top X^\top \text{Std}(\varepsilon) X c}
\]

When the number of samples \( N \) is large enough and the number of \( n \) is small, typically when \( N-n\geq 45 \), this distribution is equivalent to normal distribution. Given \( t_{c,\alpha} = 1.96 \), find \( \alpha = 0.05 \).

If \[|t| > t_{c,\alpha} \], then it is said the voxel is significantly activated by the \( i \)-th biological effect. By plotting the absolute value of \( t \) in the location of the voxel which is dealing with and repeating the above process with every voxel in the image space, it have obtained the statistic parameter map of the \( i \)-th effect.

However, the design matrix is simply implemented to analyze fMRI data, its result is unsatisfactory.

### 1.2 Dynamics Convolution Model

It has been assumed that the BOLD response is ‘boxcar’-like. Practically, the detected BOLD response is incompletely consist with the stimuli which experiment attached to. The stimuli function is square wave function, but BOLD response is lag the stimuli 1~2 s, and waveform is somewhat difference\(^6\,\,7\). Friston et al imported time basic function to model fMRI evoked response, and Josephs et al applied it to event-related response\(^5\,\,8\). Along with understanding of the biophysical and physiological mechanisms that underpin the BOLD responses has grown considerably in the past few years, people gradually came into the define of hemodynamic impulse function (HRF). First of all, HRF is nonlinear function\(^6\,\,10\), peaking at about 5 s, transitorily descending baseline in the course of attenuation, being similar to the curve of...
electroencephalogram (EEG) post-synaptic electricity. The HRF, estimated in Friston resembled a Poisson or Gamma function.

So, to combine biology effects of brain better, instead of box-car stimuli series at the first column, we convolved a new HRF with design matrix to model experiment stimuli pattern, and gained the more realistic design matrix. The HRF is introduced as follow

$$h = \exp\left(-\frac{i + t}{m}\right)\cos\left(-\frac{j + t}{n}\right)$$

(11)

2 fMRI Data Analysis

2.1 Data Description

The fMRI data was collected from Peking Cognizant Science Open lab at Beijing hospital. The stimulus was a red illuminant point presenting at the center of the visual field with frequency 8 Hz, light intensity 200 cd/cm² and visual angle of 2 degrees. Each section is composed of 128×128 voxels. Each section map was completely collected in 160 s resulting in 80 sample images alternating between stimulation and non-stimulation conditions as illustrated in Fig.6. The sample time interval is 2 s.

2.2 Result of Data Analysis

Convolving design matrix with HRF, the first column of the design matrix is improved, as shown in Fig.1. BOLD response of brain activity is shown in Fig.3.

According to the principle of GLM, the cut-off condition $t$-test $>4$, gave approximately $P<0.0001$, and were considered to be the true active voxels. Then the fMRI result image is gained in Fig.2, where the black points denote those activity voxels aroused by stimuli. Result of experiment correspond to the physiology fact that activity voxels, aroused by vision stimuli, mainly distribute at visional function region which located at outboard of occipital lobe, and it consists with the result of independent component analysis (ICA)\[11]. Accordingly, we take principium testifying for the validity of this method.

3 Conclusions

MRI is a new technology to detect brain function activation and the GLM is one of the most popular technique for fMRI data analysis, but its theory is imperfect. In this paper, a new convolution model has been tested by the vivo experiment which successful detected fMRI activation. Nevertheless, GLM has many unresolved problem, for example, whether the autocorrelation of signal need be considered, whether the HRFs are varied in different brain regions or the same HRFs in different brain regions with different parameters, whether discrete cosine function model the effect perfectly, which is aroused by physiological effects such as respiratory and cardiac cycles, accordingly successfully separating the noise aroused by these facts. All of these problems are waiting for further study.

References


References


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