



Assimilation of functional magnetic resonance imaging data using the Extended Kalman Filter.

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Abstract

On this present work, the Extended Kalman Filter (EKF) was applied to make the data assimilation of Buxton-Friston hemodynamic model in Functional Magnetic Resonance Imaging (fMRI). From the typical values of the parameters of Buxton-Friston hemodynamic model (B-F) and input signals that can generate signals related to physiological changes at the time of brain activation. As the hemodynamic model has no analytical solution, was applied the 4th order of Runge-Kutta method for their numerical approximation. The assimilation of the parameters of the noisy signal by EKF has showed good results for some parameters of the model. It follows that the Extended Kalman Filter has reasonable efficiency for assimilation of fMRI data through the hemodynamic model of Buxton-Friston, therefore, the model has a strong nonlinearity.

Keywords: fMRI; Hemodynamic model; Kalman filter.

1.INTRODUCTION

The functional Magnetic Resonance Imaging (fMRI) is a neuroimaging technique that uses magnetic resonance technology (MR), applied to the monitoring of brain activity for the diagnosis and control of diseases, pre-surgical mapping, among others [3]. The fMRI is widely used because it is a noninvasive technique and good spatial and temporal resolution.

Image acquisition is performed through an examination with a volunteer/patient who receiving stimulus for the activation of brain part be studied. When there is stimulation, barter venous blood is performed by the arterial blood, and this natural contrast acts are termed as effect BOLD (Blood Oxygenation Level Dependent) [3].

Several studies in the literature are meant for the detection of active regions of the brain by applying methods such as Estimation Bayesian [6], Linear Model Generalized [4], among others. These methods were intended to make a qualitative analysis, in other words, only localize the regions of the brain responsible for performed stimulating.

Buxton, Friston [5,7] developed a hemodynamic dynamic model that describes the coupling of the synaptic activity of fMRI signals. The model seeks to estimate the physiological phenomena (represented by parameters models) that occurs in the brain during the stimulus activation, such as the increase of cerebral blood volume, blood flow and the amount of deoxyhemoglobin (dHb-deoxygenate hemoglobin) in the cerebral veins. From the Buxton-Friston model can then make a quantitative analysis of the BOLD signal. The Kalman filter was utilized for the assimilation of parameters generated from the BOLD signal.

For the application of Kalman filter, the model has to be linear and Gaussian residue. However, the hemodynamic model consists of a system of nonlinear equations. For these cases you can use a variation of the filter named: Extended Kalman filter (EKF). The technique consists of linearization model compound in two steps: the prediction step (previous estimate), and the correction step (predicted estimate) and integrating their comments to the correction of the estimation and covariance [1]. The EKF method is applied in real time, sequences and recursive [2], fitting the problem of non-linearity and estimation of parameters of the hemodynamic model of Buxton-Friston,

and thus, performing an evaluation of these variations of Kalman filter in the assimilation of the data of hemodynamic Buxton-Friston model.

2. FUNCTIONAL MAGNETIC RESONANCE IMAGING

Functional imaging technique for magnetic resonance imaging (fMRI) today is considered one of the main methods of monitoring brain for being safe, non-invasive and does not emit radiation. Another advantage is that, by having a good spatial and temporal resolution, this technique is able, in addition to producing images of CT slices, to map specific areas of brain activity. The objective of this technique is to detect areas of brain activation responsible for a stimulus or tasks/functions performed.

The brain activation is detected by the MRI machine through the BOLD effect. It is based on regional differences of blood flow [3]. When a region of the cerebral cortex increases its activity from a stimulus, there is a reduction in oxyhemoglobin and an increase of deoxyhemoglobin with carbon dioxide (CO₂). Then, the increased blood flow provides a surplus oxygenated hemoglobin, causing the brain tissues being filled of oxygen [3]. Because blood has different magnetic properties, deoxygenated blood is paramagnetic property and the oxygenated blood diamagnetic property, MR detects when they happen the blood flow changes which may generate the images. When the BOLD signal is detected over time, creating a time series, it is now called the hemodynamic response function (HRF).

The fMRI is the acquisition of quick images with functional regions when the patient, or volunteer, is in a stimulation or resting periods. Since there is no possibility to make a direct analysis of the images by the low signal to noise ratio (SNR), an image pre-processing is required using computer algorithms to identify active areas using statistical methods. These methods such as generalized linear model (GML), cross correlation, and the Student t test [3] seek to qualitative analyzes of HRF.

3. BUXTON-FRISTON HEMODYNAMIC MODEL

The Buxton-Friston hemodynamic model mediates between synaptic activity and the BOLD signal. This is a model consisting of three steps: system input, cerebral blood flow, state variables, cerebral blood volume, the amount of deoxyhemoglobin in brain veins and the output signal, BOLD signal [5,7]. The model-Buxton Friston is shown in equation system (1).

$$\left\{ \begin{array}{l} \ddot{f} = \epsilon u(t) - \frac{\dot{f}}{\tau_s} - \frac{f-1}{\tau_f} \\ \dot{v} = \frac{1}{\tau_0} \left(f - v^\alpha \right) \\ \dot{q} = \frac{1}{\tau_0} \left(f \frac{1 - (1 - E_0)^{\frac{1}{f}}}{E_0} - v^\alpha \frac{q}{v} \right) \\ y(t) = V_0 \left(k_1 (1 - q) + k_2 \left(1 - \frac{q}{v} \right) + k_3 (1 - v) \right) \end{array} \right. \quad (1)$$

where, f is the cerebral blood flow; v is the cerebral blood volume; q the veins deoxyhemoglobin content; $u(t)$ is the neuronal inputs; τ_s reflects signal decay; τ_f is the feedback autoregulation time constant; τ_0 is the transit time; ϵ is neuronal efficacy; E_0 represent the resting oxygen extraction fraction; α is the stiffness parameter, $k_1 = 7E_0$, $k_2 = 2$, $k_3 = 2E_0 - 0.2$, V_0 is the resting blood volume fraction.

In order to facilitate the resolution of the model's system, it has been introduced a new variable s . Thus, a system 1st-order four equations is obtained: $s = \dot{f}$. Table 1 shows typical values of the model parameters.

Table 1- Typical values of the hemodynamic model parameters

Parameters	ϵ	τ_s	τ_f	τ_0	α	E_0
Typical values	0,54	1/(1,54)	1/(2,46)	0,98	0,33	0,34

The model of Buxton-Friston and output of the BOLD signal can be written as the following vectors and their respective errors:

$$\begin{cases} \dot{x} = g(x, \beta, u, n) & n \sim N(0, R_n) \\ y = h(x, \beta, w) & w \sim N(0, R_w) \end{cases} \quad (2)$$

where g and h are nonlinear equations, $x(t) = [s, f, v, q]^T$ is the system of state variables, $\beta = \{\epsilon, \tau_s, \tau_f, \tau_0, E_0\}$ is the system parameters to the values set by the mean, u is system input, n is the noise process caused by disturbances and modeling errors, y is the observation vector and w is measurement noise.

4. EXTENDED KALMAN FILTER

In this case, it is used as an estimator to estimate parameters related to hemodynamic model of Buxton-Friston [1,2,8]. The EKF is composed of two stages. Given the following nonlinear system described by the difference equation and the noisy observation model:

$$\begin{cases} \dot{x}_k = M(x_{k-1}) + n_k \\ y_k = h(x_k) + w_k \end{cases} \quad (3)$$

x_0 is a random vector, where the expected value is $\hat{x} = m_0 = E[x_0]$ and the covariance is $P_0 = E[(x_0 - \hat{x}_0)(x_0 - \hat{x}_0)^T]$.

Prediction:

With some operations the approximate value of x , the predicted error and the error covariance are defined by equations (4), (5) and (6), respectively:

$$x_k^f \approx M(\hat{x}_{k-1}) \quad (4)$$

$$e_k^f \approx J_M(\hat{x}_{k-1})e_{k-1} + w_k \quad (5)$$

$$P_k^f \equiv J_M(\hat{x}_{k-1})P_{k-1}J_M^T(\hat{x}_{k-1}) + Q_k \quad (6)$$

where J_M is the Jacobian of the function.

Assimilation:

The estimated value of x , approximate error in the estimated value of x and the later covariance of the new estimate is defined by equations (7), (8) and (9) respectively:

$$\hat{x}_k = x_k^f + K_k(z_k - h(x_k^f)) \quad (7)$$

$$e_k \approx (I - K_k J_h(x_k^f))J_M(\hat{x}_{k-1})e_{k-1} + (I - K_k J_h(x_k^f))w_k - K_k n_k \quad (8)$$

$$P_k = (I - K_k J_h(x_k^f))P_k^f \quad (9)$$

where J_h is the Jacobian of the function.

5. RESULTS

From the typical values of the parameters of the Buxton-Friston hemodynamic model, shown in Table 1, the input signal (Figure 1) and the solution of the differential equations (1), (2) and (3) using the fourth-order Runge-Kutta method, it was generated blood flow changes, volume of venous blood and the quantity of deoxyhemoglobin in the cerebral veins shown in Figure 2.

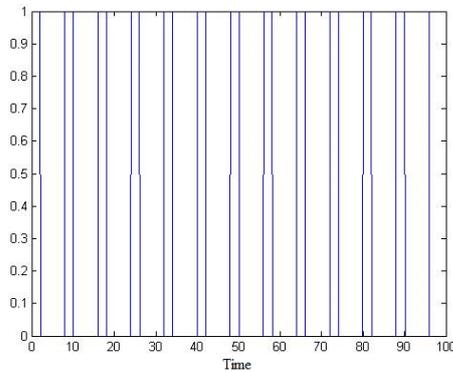


Figure 1 - Input signal.

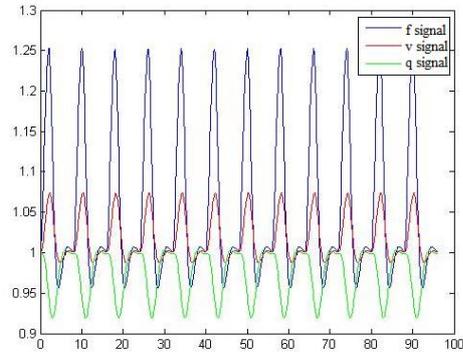


Figure 2 - Blood flow changes.

Upon obtaining f , v and q , the BOLD signal is generated in the course of time, which is called Hemodynamic Response Function - HRF (Figure 3). The HRF was contaminated with Gaussian white noise with mean 0 and standard deviation 0.316 as shown in Figure 4.

The assimilation of the parameters of the signals generated with noise was made with the Extended Kalman Filter with initial approximations of the parameters shown in Table 2. The assimilation of signal parameters with noise by EKF was good. The parameters are approximate as shown in Figures 5, 6 and 7. Therefore the estimation of HRF (Figure 8) from the noisy HRF generated was also good.

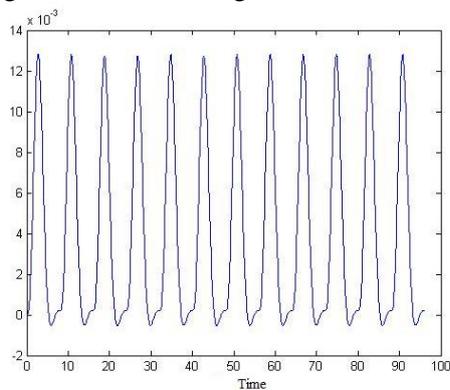


Figure 3 - Hemodynamic Response Function.

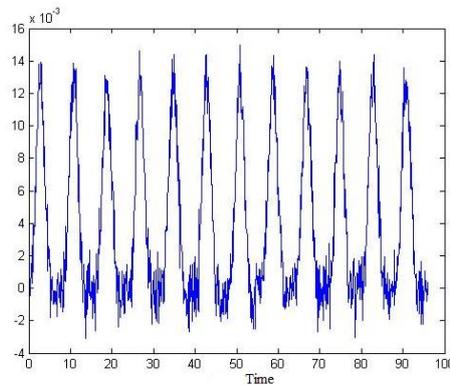


Figure 4 - Hemodynamic Response Function contaminated with Gaussian white noise with mean 0 and standard deviation 0,0316.

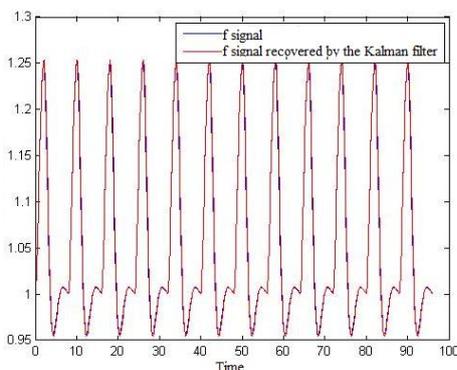


Figure 5 - Estimation of the parameter f by Extended Kalman filter in the contaminated hemodynamic function with Gaussian white noise.

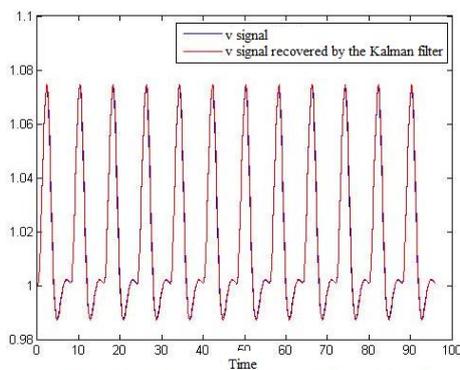


Figure 6 - Estimation of the parameter v by Kalman filter extended in the contaminated hemodynamic function with Gaussian white noise.

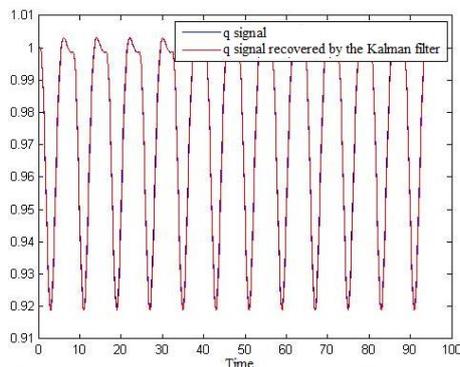


Figure 7 - Estimation of the parameter q by Kalman filter extended in the contaminated hemodynamic function with Gaussian white noise.

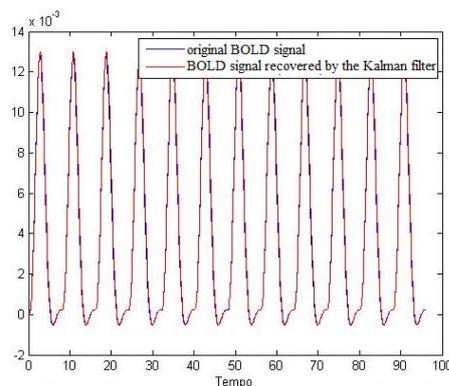


Figure 8 - Estimation of hemodynamic response function by Kalman filter extended from the contaminated hemodynamic function with Gaussian white noise.

However, the EKF recovers only the main parameters f , v and q . It cannot achieving other physiological parameters such as: transition time, neuronal efficiency or extraction and oxygen fraction. These parameters remained practically with the same values of the initial approach.

Table 2 – Initial approximation of the parameters values.

Parameters	s	f	v	q	ϵ	τ_s	τ_f	τ_0	E_0
Initial approximation	0	1,0000	1,0000	1,0000	0,5350	0,6601	0,4057	0,9900	0,3500

6. CONCLUSIONS

The solution of the hemodynamic model of Buxton-Friston (BF) was made using the fourth-order Runge-Kutta method for its numerical approximation thus generating the BOLD signal. With the resolution of the equations system and the input signal, the signals related to physiological changes at the time of brain activation were generated. Thus, the BOLD signal over time (HRF) was built.

The HRF signal was contaminated with Gaussian white noise with mean 0 and standard deviation 0.316. The assimilation of the parameters signals generated with and without noise was made with the Extended Kalman Filter.

The assimilation of signal parameters with by EKF was good. However, the EKF only recovered key parameters to estimate f , v and q achieving other physiological parameters such as: transition time, neuronal efficiency or extraction and oxygen fraction.

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