MEASURING CEREBRAL BLOOD FLOW FROM PERFUSION MAGNETIC RESONANCE IMAGES BY WAVELET TRANSFORM

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Abstract

In this paper, we consider the problem of Measuring Cerebral Blood Flow (CBF) from Perfusion Magnetic Resonance Images (pMRI). CBF analysis is performed by observing the passage of a contrast agent through the desired tissue and through the relevant input artery. The concentration of the contrast agent in the volume of interest (brain tissue) and in the input artery, are related with a convolution integral. The convolution kernel is the Residue Function, that models the vasculature of the tissue. In model-independent methods, the Residue Function is unknown. Hence, CBF measurement becomes a deconvolution problem. The SNR of the images decreases due to the speed of the imaging system, which is required to have enough observed samples of the bolus passage. Deconvolution problems are sensitive to noise, because of the zeros of the convolution kernel that become the poles of the inverse system. Wavelet Transform is employed to suppress this noise while deconvolving the concentration-time curves of the volume of interest with that of the main cerebral artery, to measure the flow.

Keywords: perfusion Magnetic Resonance Imaging (pMRI), Cerebral Blood Flow (CBF), Deconvolution, Mirror Wavelet Basis

1. Introduction

Blood flow measurement and tissue perfusion assessment are of considerable clinical importance. Perfusion is the rate at which nutrient-supplying blood, passes through tissue, and it gives an impression of the functioning of tissue. Blood flow measurement, and assessment of tissue perfusion can be applied in tumor characterization, assessment of prognosis, and monitoring of cancer therapy, besides its applications in the fields of stroke and Alzheimer's disease. It is likely to become a powerful diagnostic tool in prediction of stroke outcome [3]. Currently three medical imaging modalities are used to image brain perfusion: Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET) and Single Photon Emission Computed Tomography (SPECT). Among these three, MRI has higher spatial resolution and superior anatomical imaging, with no patient exposure to ionizing radiation [5]. One of the expanding areas of MRI in brain research is high resolution determination of cerebral perfusion. With the development of rapid MR imaging methods, e.g. Echoplanar Imaging (EPI), dynamic imaging of the passage of intravascular contrast agents, e.g. Gd-DTPA has become possible [1].

2. Theory

Based on the assumption that for an intact blood brain barrier, the contrast agent remains intravascular, the concentration of the contrast agent within the tissue at time *t* after injection is given by [1] :

$$C_{VOI}(t) = \frac{\rho}{k_H} F \int_0^t C_{AIF}(\tau) R(t-\tau) d\tau \quad (1)$$

where ρ is the density of brain tissue (ρ=1.04g/ml), $k_H = (1-H_{art})/(1-H_{cap})$ is a correction factor that takes into account the difference between hematocrit of capillaries (H_{cap}) and that of large arterial vessels (H_{art}). F is the Cerebral Blood Flow (CBF), $C_{AIF}(t)$ is the Arterial Input Function (AIF), i.e. the concentration of the contrast agent at the feeding vessel of the volume of interest

(VOI) and $R(t)$ is the Residue Function which is the relative amount of contrast agent in the VOI at time *t* after an ideal perfusion experiment, where a unit area bolus is instantaneously injected and gradually washed out by perfusion. In model-independent methods the residue function is unknown and, $F \cdot R(t)$ has to be calculated from ρ/k_H, $C_{AIF}(t)$ and $C_{VOI}(t)$ by solving Eq.(1). The maximum value of the calculated curve, is equal to the CBF [1] and [5]. The concentration-time curves are obtained from the MR signals, i.e. image intensity of pixels, by the change in transverse relaxation rate, R_2 [1]:

$$C(t) = k \cdot \Delta R_2 = \frac{-k}{TE} \ln\left[\frac{S(t)}{S_0}\right] \quad (2)$$

3. Materials and Methods

In practice, only a limited number of samples of the MR signal is available from the two series of images taken simultaneously from the two slices containing the AIF region and the VOI. However the images of each set are equally spaced in time, with a sampling time usually equal to the repetition time (TR) of the scanner. Hence, the sequence of intensities for each pixel of any of the two slices is a sampled discrete-time signal of the MR signal of that pixel. With this motivation, Eq.(1) is dicretized as follows:

$$C_{VOI}(t_n) = AF \int_0^{t_n} C_{AIF}(\tau) R(t_n - \tau) d\tau$$

$$\approx AF\left[\sum_{m=0}^{n} C_{AIF}(t_m).R(t_n - t_m)\right].\Delta t$$

$$= AF\left[\sum_{m=0}^{n} C_{AIF}(m.\Delta t).R((n-m).\Delta t)\right].\Delta t$$

$$= AF \cdot \Delta t\left(\sum_{m=0}^{n} C_{AIF}[m].R[n-m]\right)$$

$$\Rightarrow C_{VOI}[n] = AF.\Delta t.C_{AIF}[n] \otimes R[n] \quad (3)$$

where $A=\rho / k_H$, *n = 0, 1, ..., N-1* and *N* is the number of images taken from each slice. Since the observations are noisy, due to the speed of the imaging system, we modify the above equation as follows:

$$C_{VOI}[n] = \frac{\rho}{k_H} \cdot F \cdot \Delta t \cdot C_{AIF}[n] \otimes R[n] + \eta[n] \quad (4)$$

where $\eta[n]$ is the noise, and the unknown sequence $F \cdot R[n]$, has to be estimated by deconvolution. Toward this end, we propose use of Deconvolution in Mirror Wavelet Basis [2]. This deconvolution method benefits from Thresholding Estimators and is performed as follows:

1) First the noisy observations (convolution output), i.e. $C_{VOI}[n]$ in the CBF problem, are passed through the inverse filter, i.e. $\left(k_H /(\rho \cdot \Delta t)\right) \cdot C_{AIF}^{-1}[n]$.

$$x[n] = C_{VOI}[n] \otimes \left(\frac{k_H}{\rho \cdot \Delta t} \cdot C_{AIF}^{-1}[n]\right) \quad (5)$$

This task enormously amplifies the noise, because of the poles of the inverse system.

2) Then, *x*[*n*] is decomposed in the Mirror Wavelet Basis [2] and the wavelet coefficients are soft thresholded by the thresholds given therein.

3) This deconvolved signal can be further denoised, by hard thresholding its first level wavelet coefficients, with a threshold proportional to the standard deviation of the finest scale wavelet coefficients.

4) The last step of the algorithm of deconvolution in mirror wavelet basis is to make the output shift-invariant, by averaging the results of applying the above steps to all possible shifts of the signal.

The final obtained sequence is an estimate of $F \cdot R[n]$ and its maximum value is the regional CBF corresponding to the pixel from which the concentration-time curves were measured.

4. Simulations

In simulations the AIF is modeled by the Gamma-Variate Function [4]:

$$C_{AIF}(t) = \begin{cases} K(t-t_0)^3 e^{-(t-t_0)/1.5} & t > 0 \\ 0 & t < 0 \end{cases} \quad (6)$$

For the residue function we have used the exponential function:

$$R(t) = e^{-t/MTT} \quad (7)$$

where the Mean Transit Time (MTT) was set to 4 sec . The above two functions were sampled with a sampling time of Δt = 1500ms. For simplicity, the flow, F was given a value of 1. The concentration-time curve of the VOI was calculated with these parameters using Eq.(3) and then Additive Gaussian White Noise was added to the corresponding MR signals of $C_{AIF}[n]$ and C_{VOI} [n], obtained by Eq.(2), and then they were taken back to concentration-time curves. The noise was chosen to generate single pixel SNRs of 5, 10 and 15. In real clinical data, a remaining MR signal drop exists after the main peak. This is due to the recirculation of the contrast agent, and it was modeled by adding a function of the form : $a(1-e^{-t/b})$, to the concentration-time curves. To avoid the effect of recirculation, the data after the initial concentration peak is not used. In Fig. 1, an outcome of simulated noisy AIF and VOI concentrations is shown.

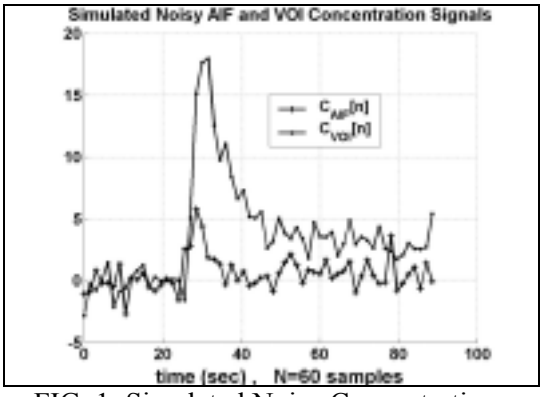

FIG. 1: Simulated Noisy Concentrations

5. Results

To evaluate this method, it was compared with the Fourier method, in which a ten point Hanning filter is applied to $C_{AIF}[n]$ and $C_{VOI}[n]$, before deconvolving their Fourier Transforms, using the convolution theorem. Preliminary results show that the Wavelet method, outperforms the Fourier method. Fig. 2 shows a result of applying both methods to an outcome of noisy concentrations (shown in Fig. 1).

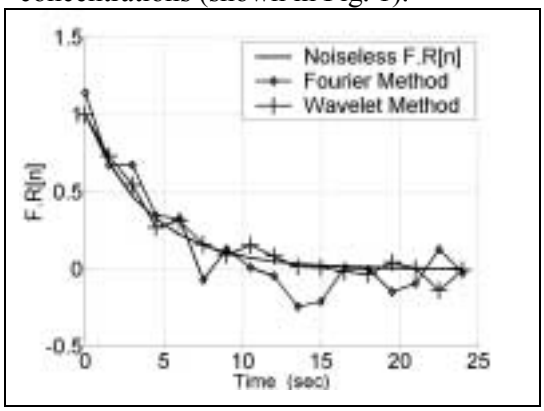

FIG. 2: Deconvolved Curves of F.R[n]

The wavelet method produced smaller mean square error (MSE) for the three SNRs of the simulations.

In conclusion, the method can be extended to clinical applications by choosing an appropriate thresholding parameter, i.e. the maximum amplitude of Mirror Wavelet Coefficients.

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