Fast and accurate voxel-by-voxel perfusion imaging using convolution models

A. Mikheev[1], and H. Rusinek[1]

[1]Radiology, NYU School of Medicine, New York, NY, United States

Modeling of the perfusion using dynamic contrast-enhanced (DCE) imaging based on convolution models is gaining increasing attention. The time activity curve of i^{th} voxel is sampled at predefined time intervals, yielding a contrast concentration $C_i(t)$ evaluated at discrete times $t=t_1 \ldots t_{NT}$. Perfusion model is then specified to express $C_i(t)$ as the convolution of an impulse response function $IRF(t)$ and the arterial input function $A(t)$. For a given model, $IRF(t)$ is represented as a piecewise analytical function that is parametrized by tissue parameters such as flow rate, transit time, or distribution volume. These parameters $\{p_1, p_2, \ldots p_n\}$ are then used to fit the measured data $C_i(t)$ by minimizing the residual:

$$\delta = \sum_{t=1}^{NT} \left(C(t) - A \otimes IRF(t)\right)^2$$

Typically the convolution operator is invoked on the order of 10^4 times for each voxel's minimization, and the imaging volume of interest contains between 10^5 and 10^6 voxels. Thus, an efficient implementation of the convolution represents a significant computational challenge. The naive approach consists of a uniform sampling $t=t_1, \ldots t_N$ of the temporal domain, extrapolation of $A(t)$ and $IRF(t)$ over these samples, and calculation of convolution either by discrete integration or by multiplying corresponding Fourier transforms. Computational complexity is $O(N^2)$ and $O(N \log(N))$ respectively. In practice direct integration is often used due to its simplicity. Additionally, due to discrete sampling of IRF result in an error that is proportional to 1/N. To improve the computational speed and be able to control the convolution error due to discrete sampling of $IRF(t)$ we have developed and implemented the adaptive convolution algorithm. The method was tested for its speed and convolution accuracy on renal perfusion renography data using Gd-DTPA as the tracer.

METHODS

The method takes as an input parameter a user-specified tolerance τ measured in units of tracer concentration. The value

$$\varepsilon = \tau \Big/ \int_{t=0}^{T} A(t)dt$$

is then computed. For any given value of fitting parameters $\{p_1, p_2, \ldots p_n\}$ we approximate the $IRF(t)$ with a (possibly discontinuous) piecewise linear (PWL) function $IRF^*(t)$. To achieve this, we subdivide the domain [0,T] into subintervals $[t_j, t_{j+1}]$ where: (a) IRF is continuous, and (b) the modulus of its 2^{nd} derivative is non-strictly monotonic. For each such subinterval we apply the following procedure to calculate IRF^* with accuracy $|IRF(t)-IRF^*(t)| < \varepsilon$. Starting from the endpoint where the 2^{nd} derivative module is larger, we compute the longest step [u,v] towards the second endpoint, such that is guaranteed to satisfy $|IRF(t)-IRF^*(t)| < \varepsilon$ for all t in [u,v]. We are using the fact that module of the 2^{nd} derivative can only decrease in the direction of advance according to the subinterval constraints. The process is iterated (i.e u:=v or v:=u depending on the starting endpoint) until the entire subinterval $[t_j, t_{j+1}]$ is covered. The second task, the convolution of two PWL functions, $A(t)$ and IRF^* is then calculated precisely in analytical form. The computational complexity of this step is $O(N_1+N_2)$ where N1 is the number of samples for A(t) and N2 the number of samples for IRF^*. The result is guaranteed to differ by no more than τ from the exact convolution. The adaptive convolution algorithm was implemented using C++ language.

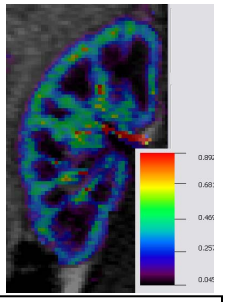

Fig.1. Aapplication of the adaptive convolution to renal flow mapping using the model from ref [1].

RESULTS AND DISCUSSION

The algorithm was tested on the kidney perfusion model [1] and MR renography acquisition that consisted of 17 dynamic frames acquired in a nonuniform fashion over 75 seconds. Each 3D volume consisted of 300K voxels. Calculation of renal plasma flow (Fig. 1) on the dual-core Intel T7200 2.3GHz mobile processor took about 3 minutes for τ = 0.001 mM. Figure 2 plots the execution time as a function of τ. For comparison, the naïve approach, when implemented using optimized C++ code, required sampling dt = 0.1 sec to attain a similar precision and took 400 times longer to execute. In conclusion, the adaptive convolution algorithm enables fast and accurate analysis of DCE MR datasets.

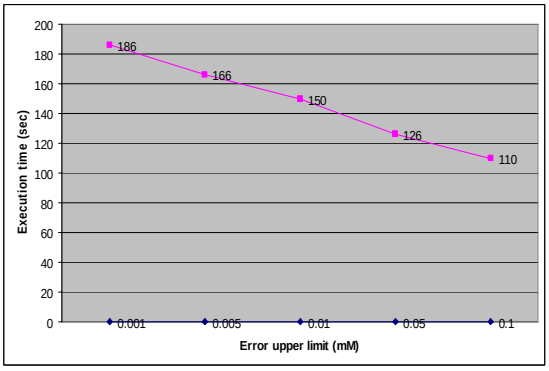

Fig.2. Execution time of the adaptive convolution as a function of tolerance τ.

REFERENCES

[1]. Zhang JL et al. Functional Assessment of the Kidney from MR and CT Renography: Impulse Retention Approach to a Multi-Compartment Model. MRM 2007 (in press).

[2] Functional CT imaging of prostate cancer. Henderson E et al. Phys. Med. Biol. 48 (2003) 3085-3100.

[3] Kershaw LE anf Buckley DL. Precision in Measurements of Perfusion and Microvascular Permeability with T1-Weighted Dynamic Contrast-Enhanced MRI. Magnetic Resonance In Medicine 56:986-992 (2006)