A Modified Version of Hrabe-Lewis Model to Account Dispersion of Labeled Bolus in Arterial Spin Labeling

O. Ozyurt¹, A. Dincer², and C. Ozturk¹

¹Bogazici University, Biomedical Engineering Institute, Istanbul, Turkey, ²Acibadem University, School of Medicine, Department of Radiology

Introduction

Standard arterial spin labeling (ASL) kinetic model [1] was based on the assumption that the arrival of labeled blood to the imaging slice is via plug flow. Later, Hrabe and Lewis [2] offered to convolve inverted bolus with Gaussian probability distribution function (in temporal domain) in order to relax this assumption. However, this approximation and having a Gaussian smoothing both at leading and trailing edges of the bolus, resulted in a non-zero signal at imaging slice even at t=0. To give a more realistic approach for the temporal dispersion effect, and -in addition- to correct the sharp increase of ASL signal for short arrival times, we propose here a modified version of Hrabe-Lewis model for pulsed ASL (pASL) signal and discuss its parameter estimation in a simulation with a realistic noise data coming from in vivo ASL measurements.

Background

The dispersion effect physically occurs in spatial domain. The dispersion of a spatial impulse (delta) function can be described using a Gaussian probability distribution with mean x and standard deviation, $N(x', x, \sigma_t)$. It describes the probability of particle, originated from impulse at position x,

being at position x' at time t. As the impulse moves towards the imaging slice, it is subject to Gaussian smoothing with time-dependent standard deviation $(\sigma_{c} = \sqrt{2Dt})$ (adopted from diffusion equation solution, D: diffusion constant) [Figure 1]. The inversion pulse produces an initial bolus shape as boxcar function. When the leading edge of bolus arrived to the position x, the fraction of particles arrived to the imaging slice is calculated integrating $N(x'; x, \sigma_1)$ between (x_2, x_1) $(x_1$: imaging slice-leading edge distance at the time of tagging, x_2 : imaging slice- trailing edge distance at

the time of tagging). If a linear transformation is used between spatial and temporal coordinates $(x = \overline{v}t, x_1 = \overline{v}\delta t, x_2 = \overline{v}(\delta t + \tau))$ where $\overline{v}, \delta t, \tau$ are the average velocity of bolus, transit time and temporal width of the bolus respectively), then the fraction of particles arrived to the imaging slice at time t can also be calculated as integrating $N(t';t,\sigma_t)$ between $(\delta t + \tau, \delta t)$ with $\sigma_t = \sqrt{2Dt}/\overline{v}$. When the last integral is written as error function and

convolved with the tissue response, the correspondent ASL (magnetization difference) signal can be written as:

$$\Delta M(t) = \int_{0}^{t} 2\alpha M_{0B} f e^{-t'/T_{IB}} \left(erf\left(\frac{\tau + \delta t - t'}{k\sqrt{t'}}\right) - erf\left(\frac{\delta t - t'}{k\sqrt{t'}}\right) \right) e^{-(t-t')/T_{I,app}} dt'$$
 (Eq. 1)

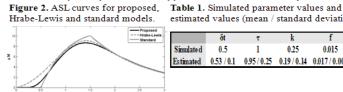
where α is tagging efficiency, M_{0B} is equilibrium magnetization of blood, f is flow, T_{1B} is T_1 of blood, $T_{1,app}$ is apparent T_1 of tissue and $k = \sqrt[2]{D} / \sqrt{1}$.

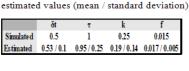
Methods

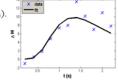
ASL signal is plotted for correspondent parameter values using Hrabe-Lewis model, Standard Model, and proposed model for initial check. Common parameters f, δt, τ are set to 0.015 ml/g.s, 0.5s and 1s respectively. When setting up non-common parameters in Hrabe model and proposed model, we assume that if we wait enough (say t=2 s) for inverted blood to distribute, the total labeled bolus arrived is expected to be very close for both models. σ_1 and σ_2 set to 0.2 and 0.35 respectively as offered in [2], we found the correspondent k as 0.25. Eq.1 is approached numerically in MATLAB and used to estimate the parameters $f, \tau, \delta t, k$. To check the accuracy of parameter estimation, we conducted a simulation. Eq.1 is used to produce synthetic data with the same parameters as above (20 simulations were performed with identical parameter values). Instead of adding noise from a mathematical model, we used the noise obtained from real data. One normal volunteer was imaged using a Siemens 3T Trio scanner, 5 axial slices were acquired; spatial resolution (4x4x10 mm), PICORE tagging scheme [3] is used with 10 uniformly distributed TI's between 200 and 2200 ms. For each TI, difference signals of selected voxels from background were added to the synthetic data. Curve fitting of our model was applied for synthetic ASL signals and from the gray matter (GM) voxels of real measurements from human brain. For comparison Hrabe-Lewis model is also fitted to the real data.

Results and Discussion

Both our proposed version and Hrabe-Lewis model itself use probability distribution functions to describe dispersion effect instead of exact physical modeling [4, 5]. Exact models are certainly more accurate if the assumed conditions were hold, but a physiological system has extensive complications; so we prefer probabilistic approaches to describe the system.







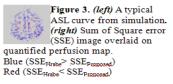


Figure 1. The dispersion of spatial impulse while moving to the imaging slice (D=0.5 taken). Velocity of impulse is 6cm/s.

t=0.4 s

Our proposed model, as summarized as Eq. 1, is identical with the ASL signal equation of Hrabe-Lewis model except the denominator of error function which is not constant in our model and includes a time parameter. The dispersion in our model is defined in spatial coordinates which is also easier to visualize (Figure 1), it is time dependent ($\sigma_{t=0}$ =0 and it changes over time) so is more realistic than constant dispersion. Thus, the initial fast rise of the Hrabe-Lewis model is corrected [Figure 2].

Table 1 summarizes the original and estimated model parameters in our simulation experiment that had realistic noise. High variations in k estimates are observed, but f values seem to be quantified well. Currently, we are not interested in interpretations of the parameter k, and use it only for correction term for quantification of f. Figure 3.b show that in overall our model gives better fits than Hrabe-Lewis model in real data (based on measured SSE's). Number of free parameters was also same for both models, since σ_2 taken dependent to σ_1 [2].

Acknowledgements: This work is supported by the Turkish State Planning Organization (DPT) under the Bogazici University TAM Project (2007K120610) and Life Sciences Research Center Project (2009K120520) References: [1] RB. Buxton et al., MRM, 40(3) 383-96, 1998 [2] J. Hrabe and DP. Lewis, JMRI, 167(1) 49-55, 2004 [3] EC. Wong et al., NMR Biomed., 10: 237-249, 1998 [4] D. Gallichan and P. Jezzard, MRM, 60(1), 53-63, 2008 [5] ME. Kelly, Phys Med Biol., 54(5) 1235-51, 2009