Benefits of Short Bolus ASL

M. Günther[1]

[1]Neurology department, University Hospital Mannheim, University Heidelberg, Mannheim, Germany

Introduction: In dynamic susceptibility contrast perfusion MRI it is common to deconvolve the acquired data with an arterial input function to yield perfusion and other related hemodynamical parameters. The approach usually taken in ASL experiments differs in that a certain shape of the inflowing labeled blood bolus is assumed. Most often, a plug flow model is used but the influence of other bolus shapes on the ASL modeling was examined also [1-3].
As one of the only deconvolution approach in ASL, Petersen et al. [4] presented a clever technique to extract the tissue response curve from the measured ASL inflow data by deconvolution with a local arterial input function. However, using a rather short ASL bolus would allow to neglect the deconvolution step and no arterial input function has to acquired. In this work some aspects of ASL with a short labeled blood bolus is discussed.

Methods: The general kinetic model [5] considers the ASL signal as a convolution of the tissue response curve multiplied by a retention function (equals 1-outflow function) with the inflowing labeled blood bolus shape (arterial input function). Blood needs approximately 4-5 seconds to pass the microvasculature and reach the venous part of the vascular tree. Therefore, in a typical ASL experiment, where inflow times longer than 4 seconds are rarely used, the outflow function can be assumed to be zero. An (hypothetical) ASL inflow sampling experiment, which uses an infinitely short bolus (i.e. Dirac impulse), will thus yield the tissue response curve directly. The longer the bolus length is the more blurring occurs in the measured inflow curve compared to the original tissue response function. If the arterial input function is known, the measured inflow curve can be deconvolved to yield the tissue response curve (see [4]). Nonetheless, using a relatively short bolus, which is adequately close to the Dirac impulse, it might not be necessary to deconvolve the data with the bolus shape.
It is obvious that the original short bolus data set will have lesser signal than a data set with a longer bolus due to the amount of labeled blood spins. However, the short bolus ASL data set can be used for the reconstruction of ASL data sets with a virtually longer bolus. This can be achieved by adding the measured signal of successive time steps of the short bolus ASL data and correcting for the additional T1 relaxation. The length of the new virtual bolus can be selected in multiples of the original bolus length BL. Mathematically, this corresponds to:

$$dM(TI,\ n\cdot BL) = q(TI, R1,\ R1a,\ BL, BAT, f)\cdot\sum_{j=0}^{n-1} dM(TI - j\cdot BL,\ BL)\cdot e^{-j\cdot BL\cdot R1a} \qquad \text{(Eq.1)}$$

Here, BL is the bolus length, TI the inflow time and R1a the T1 relaxation rate of blood. The ratio q(TI, R1, R1a, BL, BAT, f) between the left and the right term in equation 1 above is very close to 1. For typical parameters (R1=1/800ms, R1a=1/1500ms, f=120ml/min/100g, BL=500ms) this ratio of the true and the calculated long bolus data is 0.996.
Measurements were performed on a 3T MR scanner (Tim Trio, Siemens, Erlangen). A 3D-GRASE sequence was used with FAIR preparation and modulated Q2TIPS saturation [6]. Inflow curves were sampled with 100ms temporal resolution starting at an inflow time TI starting at 300ms up to 3000ms. Two different bolus lengths were employed, BL=500ms and BL=1000ms. Apparent T2 relaxation time of the tissue response curve was estimated by fitting.

Results: Figure 2a shows the apparent T2 of the tissue response curve. Vessels appear darker (shorter apparent T2), some differentiation within the tissue can be seen. In Fig. 2b a virtual bolus length of 1000ms is simulated according to eq.1 and based on the measured BL=500ms data. For comparison, the measured BL=1000ms data is shown as well.

Discussion and Conclusions: Using a rather short bolus in ASL can be beneficial in several ways. The short bolus is an approximation of the Dirac impulse, which allows measuring the tissue response curve directly. In this work, a simple mono-exponentional decay was assumed. More complex models can be used to extract other parameters like permeability and exchange rate constants.
The short bolus ASL data can also be used to calculate any data set with a virtual bolus length of a multiple of the true bolus length. The deviation between true and calculated data is (at least theoretically) below one percent. Therefore, in case of low signal-to-noise ratio of the measured data useful information might be extracted from these virtual data sets with longer bolus length.
Another advantage of short bolus ASL is that the bolus can probe different properties along the arterial tree more precisely, since only a small portion of vessels is assessed. This includes diffusion, T2 and T2* measurements along the arterial tree, which might yield valuable information about exchange processes between vascular and extravascular compartment. Another application could be the measurement of dispersion of the bolus along the arterial tree (see other abstract submitted to this meeting).

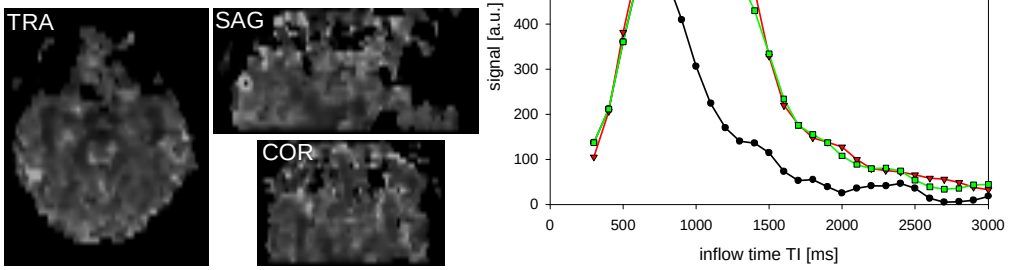

Fig.1: On the left side, the apparent T2 of the tissue response curve is shown fort he whole brain (transverse, sagittal and coronar view). On the right side, time course are given fort wo different bolus lengths [500ms (black) and 1000ms(red)] as well as a calculated virtual bolus length of 1000ms (green) based on the BL=500ms data.

Short bolus ASL can be used to measure properties, which vary along the vascular tree, including the vascular and the tissue response function. This might prove valuable in patients with neurodegenerative and small vessel diseases.

References: 1. Hrabe, J. and D.P. Lewis, JMR 2004. 167(1): p. 49-55. 2. Gallichan, D. and P. Jezzard, MRM 2008. 60(1): p. 53-63. 3. Wu, W.C., Y. Mazaheri, and E.C. Wong, IEEE Trans Med Imaging, 2007. 26(1): p. 84-92. 4. Petersen, E.T., T. Lim, and X. Golay, MRM 2006. 55(2): p. 219-32. 5. Buxton, R.B., et al., MRM 1998. 40(3): p. 383-96. 6. Gunther, M., K. Oshio, and D.A. Feinberg, MRM 2005. 54(2): p. 491-8.