

## Defining Arterial Input Function (AIF) in DSC-MRI: From Global to Local

Q. Ji<sup>1</sup>, J. O. Glass<sup>1</sup>, and W. E. Reddick<sup>1</sup>

<sup>1</sup>Radiological Science, St.Jude Children's Research Hospital, Memphis, TN, United States

**INTRODUCTION:** Determination of an AIF is an important step in accessing cerebral blood flow in DSC-MRI. The AIF is usually manually measured in a major artery (e.g. internal carotid or middle cerebral artery) or automatically selected by computer algorithms<sup>[1]</sup>. An AIF obtained by these methods is a global AIF. Using a global AIF to calculate the cerebral blood flow can result in significant errors because the local AIF in the tissue of interest can be substantially different from the global AIF. To determine the local AIF, smaller arteries closer to the tissue of interest are usually chosen. Based on this idea, several techniques have been reported<sup>[2-3]</sup>. In this study, we proposed a new approach to extract a local AIF. Many studies have suggested that the local AIF is a convolution of the global AIF with a vascular transport function (VTF)<sup>[4]</sup>, which can be modeled as a single exponential function. In our study, we adapted this idea and incorporated it into a pharmacokinetic model, and then used the model to fit the concentration-time course for each image voxel. The local AIF can be obtained by convolving the fitted VTF with the measured global AIF. DSC perfusion images from ten pediatric brain tumor patients have been studied and the initial results will be demonstrated in this study.

**METHOD:** Ten pediatric patients treated for brain tumors were imaged by T2\* weighted DSC-MRI. For each patient's data, the image intensity-time course was first converted into a concentration-time course, and the global AIF was then identified by the iterative self-organizing map clustering algorithm<sup>[5]</sup>. The local AIF was defined as the global AIF convolved with a vascular transport function given in equation (1).  $C_p(t)$  is the global AIF and  $h(\beta, t)$  is the vascular transport function and can be modeled as a single exponential function (equation (2)) where the normalization factor  $\alpha$  can be expressed as shown in equation 3. Equation (1) can be incorporated into a pharmacokinetic model for describing the tracer concentration-time course in the tissue<sup>[6]</sup> as shown in equation (4). In equation (4) the  $v_p$  is the volume fraction of vascular space and  $k$  is the coefficient for recirculation and leakage. Three parameters ( $v_p$ ,  $k$  and  $\beta$ ) in equation (4) can be determined by fitting it with the concentration time-course of each voxel. An automatic procedure that aligns the global AIF with the voxel concentration-time course was applied before each fitting. The obtained parameter  $\beta$  can be used to determine the underlying AIF for that voxel.

**RESULTS:** After analyzing the ten patients' data, we found that most of the voxels in imaging data can be fitted very well by the model (chi-squares are below the fitting threshold) with the exception of very noisy and non-enhancing regions (such as CSF, which is about 15%-25% brain volume). In **Fig.1**, the top figure illustrates a single slice of T2\* weighted DSC perfusion data at one time point with two white arrows showing the positions of one white matter voxel and one gray matter voxel (right arrow points to a gray matter voxel and left arrow the white matter voxel). The bottom right figure shows the model fitting of the concentration time-courses for those two voxels. The bottom left figure shows the global AIF and local AIFs reconstructed for these white matter and gray matter voxels. In **Fig.1**, the time delay of the white matter voxel and the dispersion of gray matter can be appreciated. **Fig.2** illustrates three temporal images of the reconstructed concentration-time course for local AIFs from time points 50, 54 and 58 seconds relative to the start of acquisition. The left image shows that the tracer arrives in the blood vessels and gray matter first, the middle image shows that tracer concentration peaks at almost all the voxels with the exception of some white matter voxels, and the right image shows the delayed peaks on some white matter voxels. Our results on ten pediatric brain tumor patients suggested that the tracer bolus does not arrive at all voxels simultaneously even for the normal appearing brain. The bolus delay on some deep white matter voxels can be as long as five seconds.

**DISCUSSIONS AND CONCLUSION:** We have demonstrated a novel method for extracting a local AIF from T2\* weighted DSC perfusion MRI. Our approach does not directly search the blood vessels around the tissue of interest; instead, we start with the global AIF, which is relatively easy to measure, and use it with the local concentration-time course to calculate a local AIF. The local AIF obtained by our approach gives more detailed local blood flow information.

### REFERENCE

- [1] Kim Mouridsen et al. *MRM*, 55, 524-531, (2006)
- [2] Fernando Calamante et al. *MRM*, 52, 789-797, (2004)
- [3] Cory Lorenz et al. *JMRI*, 24, 57-65, (2006)
- [4] Fernando Calamante et al. *MRM*, 44, 466-473, (2000)
- [5] Jinesh Jain et al. *SPIE Med Imag Procs*, (2006)
- [6] Qing Ji et al. *ISMRM*, (2008)

$$C_{lp}(\beta, t) = \alpha \int_0^t C_p(\tau) h(\beta, \tau) d\tau \quad (1)$$

$$h(\beta, t) = \beta e^{-\beta t} \quad (2)$$

$$\alpha = \frac{\int_0^\infty C_p(\tau) d\tau}{\int_0^\infty C_{lp}(\beta, \tau) d\tau} \quad (3)$$

$$C(t) = v_p C_{lp}(\beta, t) + k \int_0^t C_{lp}(\beta, \tau) d\tau \quad (4)$$

