Bioengineering 208: Magnetic Resonance Imaging Laboratory
Winter 2007
Lab 8- Week of 2/26

1. **Compare pulsed and pseudocontinuous ASL**. In this exercise you will compare two ASL methods for quantitative measurement of CBF: PICORE tagging with QUIPSS II; and pseudocontinuous ASL with a post labeling delay. For the four scans described below, calculate the average ASL signal (all control images minus all tag images), and compare the relative ASL signals with those predicted from theory. For each of the two tagging methods, you will acquire one data set with a short delay between the end of the tag and image acquisition, and one with a long delay. In principle, if all of the tagged blood is delivered to the image slices, you should calculate the same relative CBF from each scan.
   a. **Acquire a 3D TOF angiogram**. This should span from the nose to about one inch below the chin, and will be used to choose a tagging location.
   b. **General ASL imaging parameters**. For ASL acquisition, use spep_product in gradient echo mode, with: FOV=24cm; 5 slices 8mm skip 2mm, centered in the middle of the brain; 64x64 resolution; min TE; TR=3000. Do an autoprescan before turning the tag on so that prescan will be adjusted for maximum signal intensity, and do not do any more prescans.
   c. **Collect 2 pasl and 2 casl scans according to the Table below**. The signal equation for pasl and casl are given below. pld in the casl expression stands for post labeling delay, and is equal to (prepti-pwpcasl). Check to see that these expressions match the cartoon of relative pasl and casl signals in slide 7 of the lecture. We will not worry about absolute quantification in this lab, so you can normalize all calculations assuming $(2M_{0b})=1$. For each scan, calculate a map of the relative CBF, and estimate the dominant source of the differences that you see between scans. Which scan(s) are most likely to reflect true CBF?

$$pasl : \Delta M = 2M_{0b}(TI_1)(cbf)e^{-TI/T_{1b}}$$

$$casl : \Delta M = 2M_{0b}(cbf) \int_{pld}^{pld+pwpcasl} e^{-t/T_{1b}} dt$$

Common CVs:
tagslgap -> from Angio. Gap in mm from top of tag slab to bottom of bottom imaging slice:
        Choose a tagging location where the carotids and vertebrals are relatively straight
reps -> 80   Number of images
bgs_on -> 0 This turns background suppression off
dda -> 2 Number of dummy scans for equilibration before data acquisition starts

Parameter	CV	Scan 1	Scan 2	Scan 3	Scan 4
Tagging type	tag	3 (PICORE)	3	9 (PCASL)	9
QUIPSS	q	2	2	0	0
Start of tag	prepti	2200ms	1200ms	2200ms	1200ms
Tag duration(pasl)	prepti1	1000ms	1000ms	-	-
Tag duration(casl)	pwpcasl	-	-	1000ms	1000ms

2. **Combined ASL and BOLD fMRI**. In this exercise, you will collect dual echo ASL data during the performance of a functional task. Using the parameters from Scans 3 and 4 above, collect 2 functional scans with task timing 8x(10s on, 20s off). Finger tapping will work well. For both scans, set the following 2 CVs:
    - opnecho->2 to prescribe a dual echo acquisition. This collects one minimum TE scan, followed immediately by a second scan at longer TE.
    - opte2->30ms – this sets the second echo time to 30ms

When you reconstruct this data, you will end up with 4 time series: one for each echo of each scan. To get a quick look at the data, you can look at it in afni to see the BOLD signal. Which echo should you be looking at? Recollect data if you don't see a clear activation. For each of the 4 image time series, go through the following processing steps:

a. Within afni, run the plugin a3/d3 to generate separate ASL and BOLD time series. This plugin subtracts from each image the average of the previous and the next image, creating a new time series of signal differences (the ASL signal), and it also adds to each image the average of the previous and the next image, creating a new time series with the ASL alternation removed (this can be used as a BOLD timecourse). You now have 8 time series (4 ASL and 4 BOLD).

b. From the short TE ASL data set (whichever TI looks better), look for functional activation and generate a mask for the activated ROI. You can start with a command line program called waver to generate an ideal functional waveform for the activation:

waver –GAM –dt 3 –numout 80 –tstim 0:10 30:40 60:70 90:100 120:130 150:160 180:190 210:220 > aslref

will generate a reference function file named aslref. A script with this call is in the guest account on cfmri. Within the FIM option of afni, you can read in this file, and cross correlate every pixel of your data with this reference function. Those pixels with the highest correlation will be the brightest in the resulting image. This image can then be read into matlab, and a threshold applied to generate a functionally activated ROI mask.

c. For each of your 8 time series, calculate a signal timecourse of the average signal over this ROI. *Hint: Your data is 4D (xyzt). In matlab, repmat is useful for replicating the mask from 3D to 4D, so you can just multiply your replicated mask with your data and average across (xyz) to arrive at a 1D timecourse of the average signal across the ROI.*

d. From each of your 8 timecourses, estimate the absolute and fractional signal increase with activation. If the SNR is low, it may help to average across functional cycles.

Questions:
1. Which ASL data set gives the largest absolute activation? Why?
2. Which ASL data set give the largest fractional activation? Why?
3. Which ASL data set is most likely to reflect the true fractional CBF increase? Why?
4. Should the first or second echo be used for the ASL measurement? Why?
5. Which BOLD data set gives the largest absolute activation? Why?
6. Which BOLD data set give the largest fractional activation? Why?
7. Should the first or second echo be used for the BOLD measurement? Why?
8. Should the TI of the tag affect the BOLD signal? Why?