

# Measuring baseline whole-brain perfusion on GE 3.0T using arterial spin labeling (ASL) MRI with MPPCASL Sequence

Revision date: 04/25/2010

## Overview

This document describes the procedure for measuring baseline whole-brain perfusion in humans using arterial spin labeling (ASL) MRI on GE 3.0T using the Multi Phase Pseudocontinuous ASL (MPPCASL) sequence with single-shot spiral read out.

Reconstruction of the data into AFNI BRIKs is described. Additional calibration scans are required in order to allow quantification of the perfusion signals via the MATLAB post processing program **CBFv3.4**.

A separate manual is available for measuring baseline whole-brain perfusion using a modified flow-sensitive inversion recovery (FAIR) sequence, which can be downloaded from:

<http://cfmriweb.ucsd.edu/Howto/asl.shtml>

## Acquiring ASL data

There is currently one protocol available for MPPCASL ASL acquisition, **MP\_Brain\_perfusion\_SS** saved in the **head** section of the protocol list. The protocol consists of 5 core scans, **ASSET Calibration**, **3D TOF**, **MPPCASL**, **CSF** and **MinContrast** and 2 optional but highly recommended field map scans, **fm\_TE1\_NFS**, and **fm\_TE2\_NFS**.

The 6-second ASSET calibration scan is done once during the scan session to enable the parallel imaging option in the 3D-TOF and field map scans. It should be noted that if a high-resolution anatomical scan is planned, this same ASSET scan can be utilized. With the default acceleration factor of 2, the scan time of each ASSET enabled acquisition can be reduced roughly by half.

Unlike a pulsed ASL sequence such as FAIR, manual definition of the tagging plane is required. The 3D TOF scan is used to define this tagging plane for continuous inversion of arterial blood. Since the selection of this plane can have a significant impact on the quality of ASL data, this step should be carried out with care. The next section is dedicated for the appropriate slab prescription during the 3D TOF and optimal selection of the tagging plane.

The MPPCASL scan collects perfusion-weighted data, and the CSF and MinContrast are calibration scans that are needed for perfusion quantification. A GE 8-channel phased array coil is used for all the scans excluding field map scans.

## 3D TOF

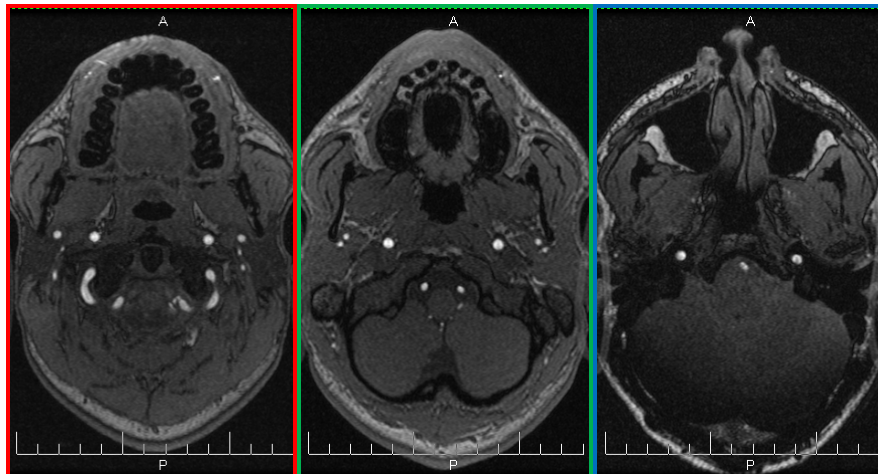
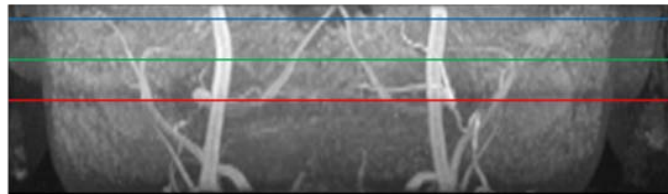
Below are the instructions on how to prescribe and acquire the 3D TOF scan.

1. Double click the 3D TOF series on the scanner console Task panel.
2. On the Graphical Rx window, align the midline of the graphic prescription slab to the bottom of cerebellum. Make sure to use the mid-sagittal slice from the 3-plane localizer series. An example prescription is shown in the figure below.



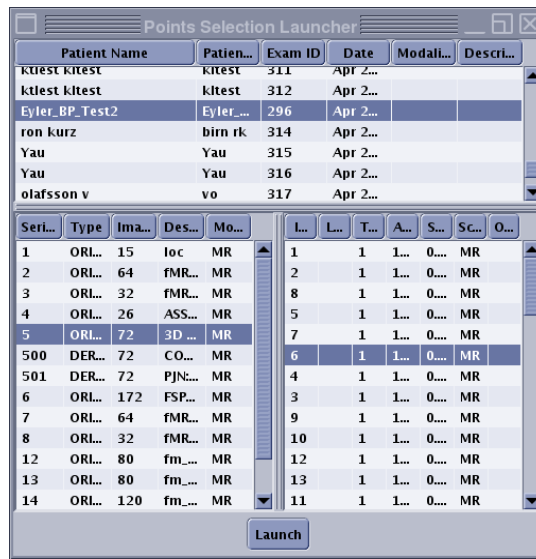
3. Click Scan.

Once the acquisition is complete, the TOF images are used to define the tagging plane, which is selected through the vertebral arteries *below* the confluence to the basilar artery and *above* the vertebral crossing into the brain. These upper (blue) and lower (red) limits as well as the preferred tagging location (green) are shown in the figure below. Choose a plane between these two limits and where all arteries are as perpendicular to the tagging plane as possible. This perpendicularity can be verified by inspecting the shape of the carotid and vertebral arteries (more circular, the better).

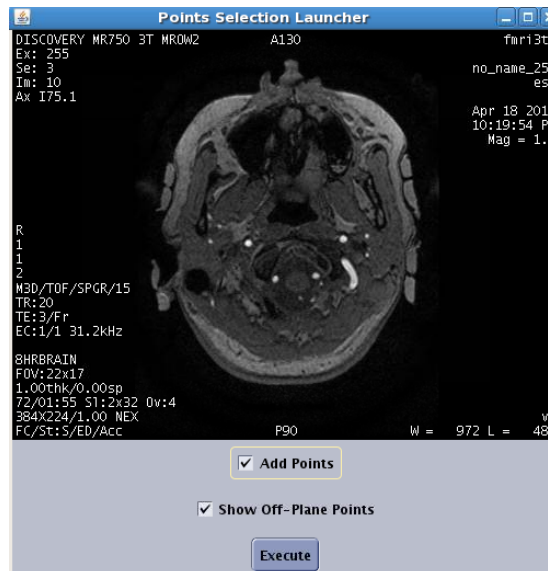


Once the tagging plane is determined, this information needs to be saved to a text file located at '/tmp/points.txt', which then can be read by the subsequent MPPCASL scan. This is done using a Java-based application called Points Selection Launcher available on the scanner.

4. Open a new command window and type 'vsigui'. Using the application browser, choose the current exam, your 3D TOF series and any one of the images on the bottom right panel.
5. Click Launch.



6. Uncheck the Add Points field and scroll through the TOF images using the Page Up and Page Down keys on the keyboard. Once the tagging plane you determined in Step 3 is located, recheck the Add Points field and mouse click on the right carotid, left carotid, and center of the two vertebral arteries.



7. Click Execute.

## MPPCASL

The MPPCASL acquisition uses a modified pseudocontinuous ASL sequence. The sensitivity of the tagging efficiency in PCASL can be greatly reduced with the MPPCASL acquisition, which translates to higher signal to noise ratio. Some important pulse sequence parameters are: tagging duration = 2 sec, TI=3.6 sec, TR=4.2 sec, TE=minimum, reps = 64, FOV=22x22cm.

The **MP\_Brain\_perfusion\_SS** sequence uses a single shot spiral acquisition, collecting 8 cycles where each cycle consists of 8 images acquired with unique phase offsets.

Below are the instructions on how to prescribe and acquire the MPPCASL scan.

1. *Double click* the MPPCASL series
2. Using the graphic Rx tool, prescribe slices (Default: 20x5mm with 1mm gap, axial slices)

*Considerations for slice prescription: The slice orientation is defaulted to axial and the slice number increments from bottom to top. Please make sure not to change these default settings when prescribing slices. The default 20x5mm (1mm gap) imaging slab will provide full brain coverage for most subjects. When prescribing, place the highest slice (i.e. slice No.20) at the very top edge of the brain region.*

3. *Save series*
4. *Click on the arrow at the right edge of the Scan button*  
*A small window appears.*
5. *Choose Research and Download*
6. *Click on the arrow again, then Research, and Display CVs*
7. *Enter the CVs as shown on the Protocol Notes*  
*Verify that the scan time is 4:46 minutes.*
8. *Click Scan*

## CSF

1. *Double click the CSF series*
2. **Copy Rx** from the MPPCASL run (Note: The FOV and slice thickness/gap have to match those of the ASL run in order to use Copy Rx.)
3. **Save series** and **Prepare to scan**
4. Click **Manual Prescan**, and once the clicking sound is heard, click **Done** (this step ensures that no prescan is performed and all the gain settings are preserved from the ASL scan).

5. Make sure that the scan time is 36 sec and Click **Scan**

## MinContrast

1. **Double click the MinContrast series**
2. **Copy Rx** from the ASL scan
3. **Save series** and **Prepare to scan**
4. Click **Manual Prescan**, once hearing clicking sound, click **Done**
5. **Scan**

## Data transfer and reconstruction

Unlike data acquired with GE product sequences, ASL data are stored as raw data in P-files in directory **/usr/g/mrraw**. Image reconstruction into AFNI BRIKs is done automatically offline after the scan. **Please allow time for reconstruction to finish** (~5 minutes after the scan finishes) before transferring your data. Open a command tool and follow the instructions below:

1. **cd /usr/g/mrraw**
2. **ls -ltr P\*** to find the latest P-files.
3. *To transfer the P-file and reconstructed BRIK:*

**aslgecopy -s server -r raid# -d datadir Pfilename brikname username**

(EXAMPLE: aslgecopy -s cfmri -r raid3 -d 060601Pilot P01208.7 scan1 guest)

### Important Notes:

*The P-files created during ASL scans are stored in directory /usr/g/mrraw. The space available in this directory is NOT reflected in the storage bar on the GE GUI. It is recommended that you check the space available before running any ASL scans to avoid possible loss of the P-files. Do this by typing `df -k .` in the command line after cd-ing to /usr/g/mrraw.*

*Some sequence information is stored in the header of the AFNI BRIKs. This information (including sequence parameters, ASL parameters and Rx info) can be accessed using the command from within the directory containing the BRIK: **3dNotes scan1brik+orig***

*The BRIKs can be viewed in AFNI. Running the **ASL a3/d3** plug-in on a BRIK will create three additional BRIKs, labeled as follows:*

**A3:** *running average of the data (using the 2 neighboring images)*

**D3:** *running subtraction of the data (using the 2 neighboring images)*

**avgD3:** *Average D3 (average perfusion image)*

## Perfusion Quantification using CBF program (v3.4)

### System Requirements

- **Redhat linux 8.0** or above (Windows and Mac OS not supported).
- **Matlab R2007a** or above, plus Matlab toolboxes.
- **AFNI v2.55j** or above.
- **FSL 3.x** or **FSL 4.0** (FSL 4.1 and above are not supported at this time).

**NOTE:** FSL output type needs to be set to **ANALYZE**. To do this, in a command terminal type:

```
setenv FSLOUTPUTTYPE ANALYZE
```

or, if using a bash shell:

```
export FSLOUTPUTTYPE=ANALYZE
```

You can check your environment variable settings by typing:

```
env
```

- 512Mb or more available system memory recommended.

### Program Installation

- Download **CBFv3.4.tar** from the cfmri website:  
<http://cfmriweb.ucsd.edu/Howto/asl.shtml>
- Untar the file (in Linux: `tar -xvf CBFv3.4.tar`).
- Add the CBFv3.4 folder to your Matlab path.  
(e.g. add the line “`addpath yourpath/CBFv3.4`” in your `startup.m` )

### Required Data

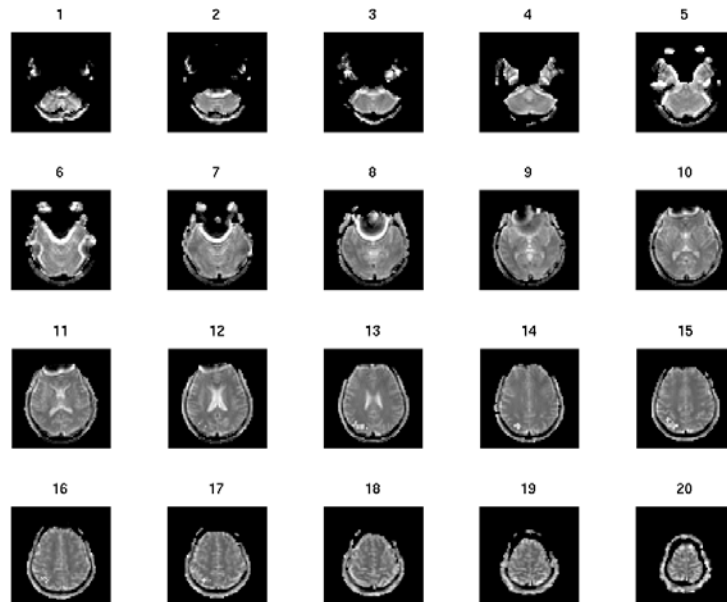
- MPPCASL-ASL BRIK, CSF BRIK, MinContrast BRIK
- *Optional:* High resolution anatomical BRIK

**NOTE:** The anatomical BRIK must be created from the DICOM files using the **d2afni** command rather than **to3d**. **d2afni** is available on the servers and simply calls **to3d**, additionally saving Rx information into the BRIK header.

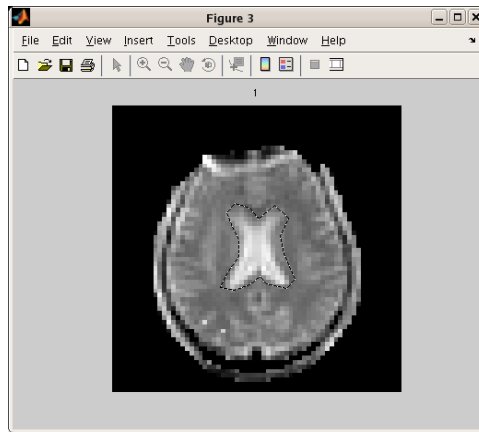
### CBF Quantification Steps

- Start Matlab
- In Matlab command window, type:  
***calcCBF('ASL-MPPCASL','CSF','MinCon');***  
***OR, if anatomical is available:***  
***calcCBF('ASL-MPPCASL','CSF','MinCon','anat');***
- **Note:** Pass only the prefix of the AFNI BRIK names (no '+orig' needed).
- *If anatomical is supplied:*
  - The anatomical is segmented into gray, white and CSF (takes ~6mins).
  - All brain slices will then pop up in a matlab figure window; select those containing ventricles by left-clicking.
- *If anatomical is NOT supplied:*
  - A matlab figure window will pop-up. Identify a slice that best defines a region of cerebral-spinal fluid (CSF) (e.g. slice No. 12 in the figure below). Type the slice # in the matlab command window when prompted. Another window pops up containing the chosen CSF slice.

Choose slice for CSF (beware partial-volumed slices!) ? : 12

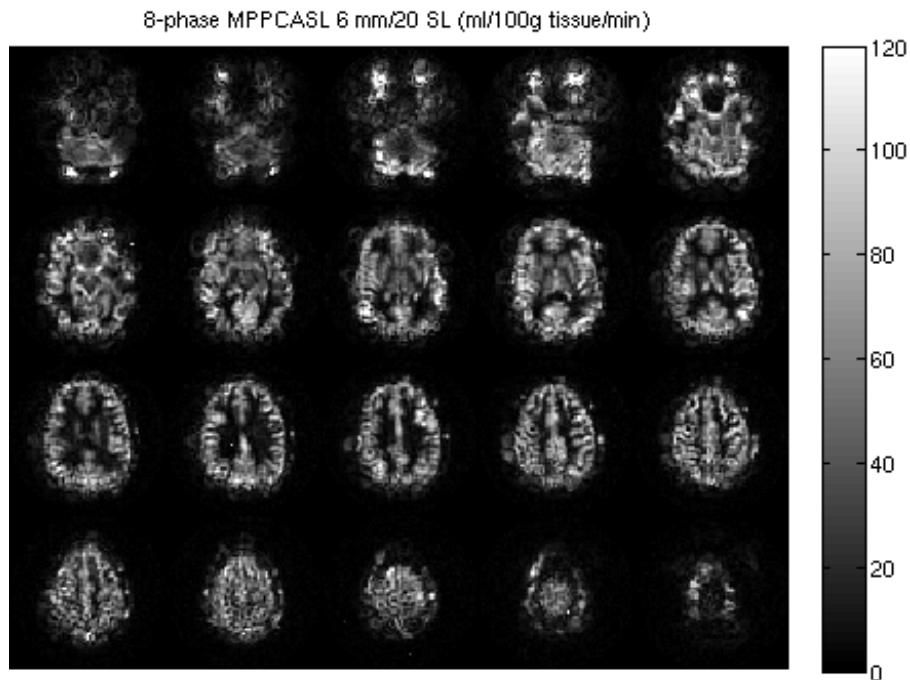


- Use left mouse button to carefully trace around the edge of CSF region and double click to finish. If anatomical is supplied, this is performed for all chosen slices. You may find double click does not work for certain version of matlab. In this case, please refer to the help file for *roiopoly* in your matlab.

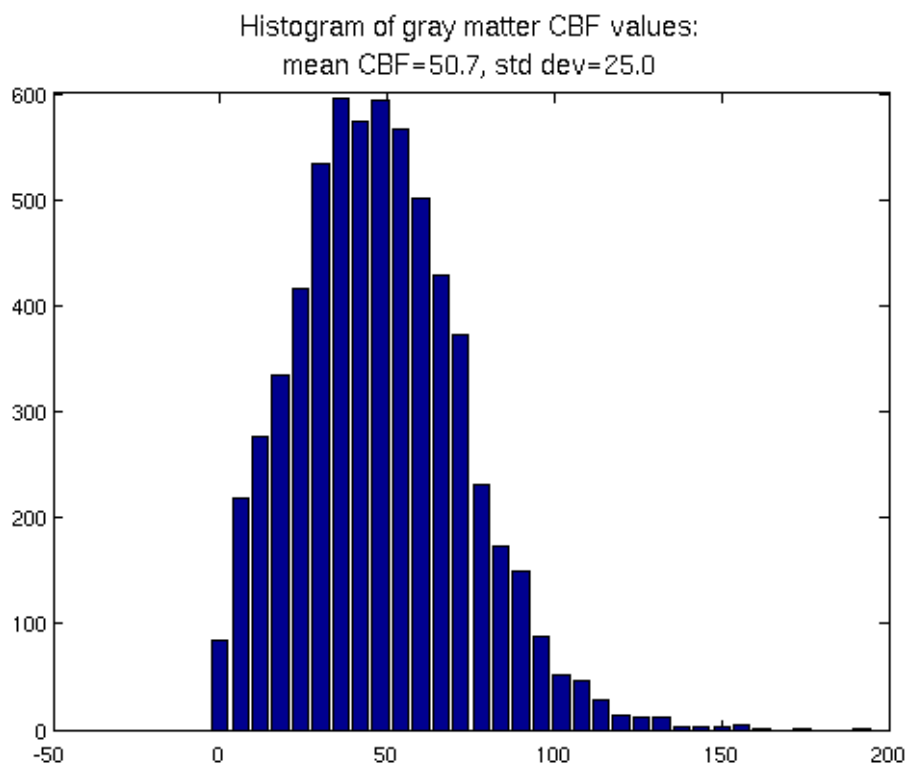


**Note:** this step creates a new directory called '**processed**' under your current working directory. A text file called '**CSFvalue.txt**' is saved under the new directory. This file contains the calculated CSF value, which will be automatically retrieved should you process the same dataset again (you will be prompted to choose whether or not to use this saved value in the repeated analysis). Note also that if the anatomical was supplied, this directory will also contain the rotated anatomical that aligns with the ASL slices, as well as partial volume maps created from the anatomical.

- The calculated CBF maps are displayed in a new figure. If the anatomical was supplied, a histogram showing the CBF values within gray matter voxels is also shown.







*Note: Unlike conventional ASL acquisitions where the perfusion-weighted images are generated from simple pair-wise subtraction of the tag from the control, the MPPCASL acquisition involves a curve-fitting procedure per voxel basis. Therefore, the CBF quantification process takes considerably longer. If your MATLAB environment has the MATLAB Parallel Computing Toolbox, CBFv3.4 automatically invokes this capability, which can significantly reduce the processing time.*

- An AFNI BRIK containing the calibrated CBF values is also saved. Look for the suffix '**\_CBF**' in the BRIK name.

Please contact David Shin at [ddshin@ucsd.edu](mailto:ddshin@ucsd.edu) with questions/comments.