

Measuring baseline whole-brain perfusion on GE 3.0T using arterial spin labeling (ASL) MRI (version 2.0)

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Overview

This document describes the procedure of measuring baseline whole-brain perfusion in humans using arterial spin labeling (ASL) MRI on GE 3.0T. ASL data are acquired using a modified flow-sensitive inversion recovery (**FAIR**) pulse sequence with interleaved **spiral** read out. The data can be reconstructed at the scanner console and viewed in AFNI. Additional calibration scans are required in order to allow quantification of the perfusion signals via a MATLAB script.

Acquiring ASL data

There are two protocols available: **Brain_perfusion_4S** and **Brain_perfusion_SS**, saved in the **head** section of the protocol list. The CMFRI webpage lists the pros and cons of these two protocols. Each of the protocols consists of 3 scans, **ASL-FAIR**, **CSF** and **MinContrast**. The ASL-FAIR scan collects perfusion-weighted data using FAIR. 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.

ASL-FAIR

The ASL-FAIR acquisition uses a modified FAIR sequence. The global inversion pulse in standard FAIR is replaced by a spatially selective inversion pulse, which extends 10cm in either direction outside of the imaging slab. QUIPSSII saturation pulses are also used. Some important pulse sequence parameters are: T11=600 msec, T12=1600 msec, TR=2.5sec, TE=minimum, FOV=22x22cm. The **Brain_perfusion_4S** sequence uses a spiral read out with 4 interleaves to reduce signal dropout due to susceptibility effects, and 20 tag+control image pairs are acquired. The **Brain_perfusion_SS** sequences uses a single shot spiral acquisition, collecting 50 tag+control image pairs. Below are the instructions on how to prescribe and acquire the ASL-FAIR scan.

1. **View Edit** the ASL-FAIR series.
2. Click **Graphical Rx** button and 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 lowest slice (i.e. slice No.1) at the very bottom edge of the brain region that you are interested in, and verify that the top slice covers the top edge of the desired region. If necessary, a few more slices can be added, but only to the **top** of the slab. We do not recommend to use more than 22 slices. It is fine if a few top slices fall outside of the brain.*

3. **Save series** and **Prepare to scan**
4. **Scan**
Verify that the scan time is 6:40 minutes (**Brain_perfusion_4S**) or 4:10minutes (**Brain_perfusion_SS**).

CSF

1. **View Edit**
2. **Copy Rx** from the ASL-FAIR run (Note: The FOV and slice thickness/gap have to match those of the ASL_FAIR run in order to use Copy Rx.)
3. **Save series** and **Prepare to scan**
4. Click **Manual Prescan**, once hearing clicking sound, click **Done**. (this step ensures that no prescan is performed and all the gain settings are preserved from the ASL-FAIR scan).
5. **Wait** ~30 seconds (for full relaxation of signal), then click **Scan**.

MinContrast

1. **View Edit**
2. **Copy Rx** from the ASL-FAIR 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 protocol finishes). 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. 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 (v2.1)

System Requirements

- **Redhat linux 8.0** or above recommended.
- **Matlab v.14** service pack 2 or above is required. **Afni v2.55j** or above and **FSL 3.1** or above are required. FSL output type needs to be set to **ANALYZE**.
- 512Mb or more available system memory recommended.

Program Installation

- Download CBFv2.1.tar from the cfmri website.
- Untar the file (in Linux: tar -xvf CBFv2.1.tar).
- Add the CBFv2.1 folder to Matlab path.
(e.g. add the line "addpath yourpath/CBFv2.1" in your startup.m)

Required Data

- ASL-FAIR brik
- CSF brik
- MinContrast brik
- *Optional:* High resolution anatomical brik

CBF quantification steps

- Start Matlab
- In Matlab command window, type:

CalcCBF('ASL-FAIR','CSF','MinCon');

OR, if anatomical is available:

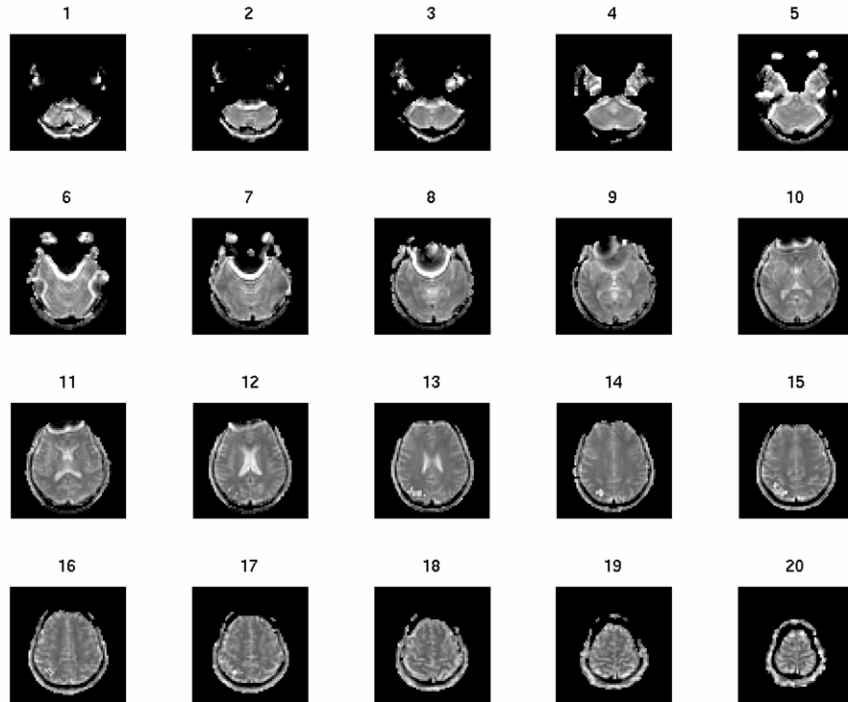
CalcCBF('ASL-FAIR','CSF','MinCon','anat');

Note: Pass only the prefix of the Afni brik names to calcCBF (no '+orig' needed).

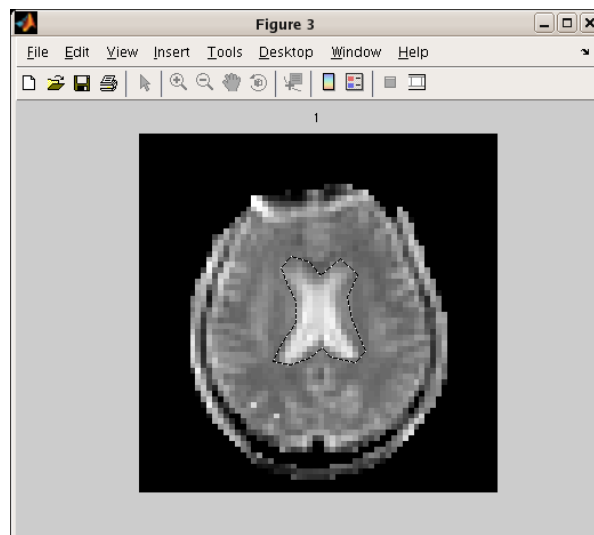
- *If anatomical is supplied:*
 - The anatomical is segmented into gray, white and CSF. This takes ~6mins.
 - Brain slices will then pop up in matlab figure windows one at a time.
- *If anatomical is NOT supplied:*

- 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 corresponding slice No. in the matlab command window. Another window pops up containing the chosen CSF slice.

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

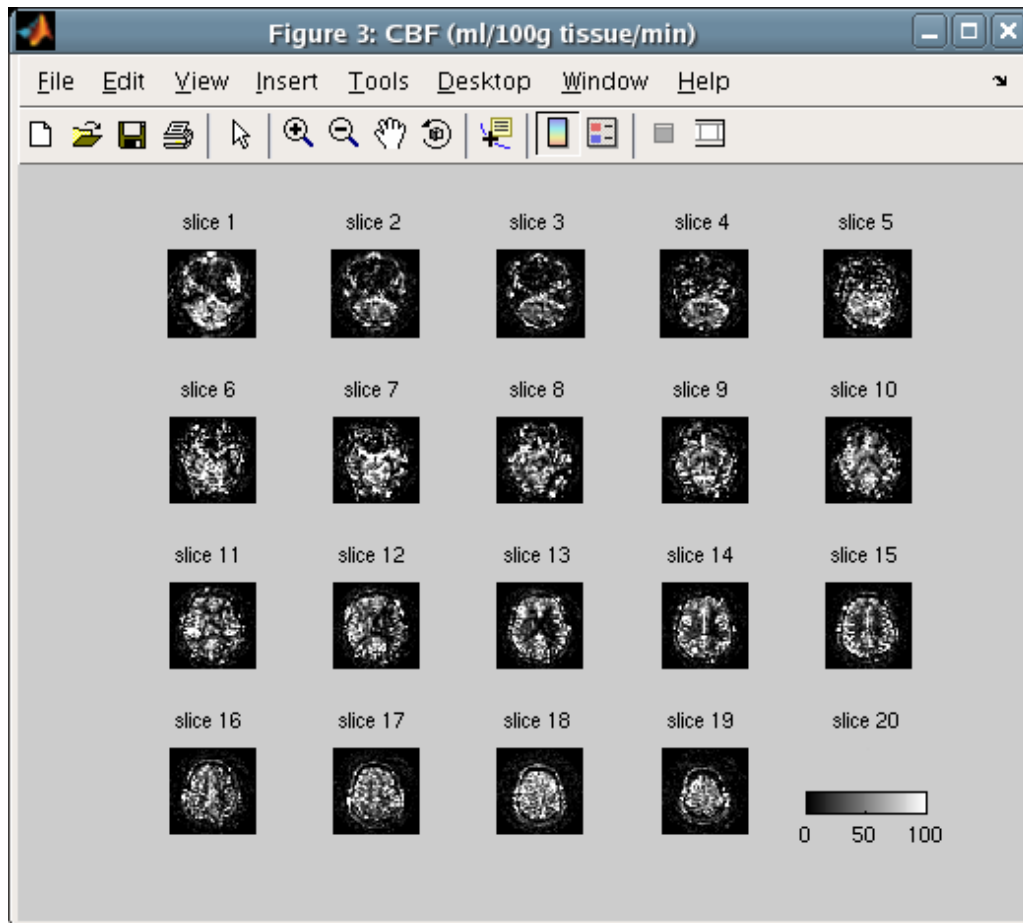


- Use left mouse button to carefully trace around the edge of CSF region, click right mouse button to finish. If anatomical is supplied, this is performed for **all** slices in turn (if no ventricles are visible on the current slice, double click to move to the next).



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).

- The calculated CBF maps are displayed in a new figure.



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

Please contact jperthen@ucsd.edu with questions