

Measuring baseline whole -brain perfusion on GE 3.0T using arterial spin labeling MRI (version 1.0)

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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 is 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

A protocol called **Brain_Perfusion** is saved in the **head** section of the protocol list. This protocol 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 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. QUIPSSII¹ saturation pulses are also used. Some important pulse sequence parameters are: T11=600 msec, T12=1600 msec. A spiral read out with 4 interleaves is used to reduce signal dropout due to susceptibility effects. 20 tag+control image pairs are acquired. TR=2.5sec, TE=minimum, FOV=22cmx22cm. Below are the instructions on how to prescribe 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 using more than 22 slices. It is fine if a few of the top slices fall outside of the brain.*

3. **Save series** and **Prepare to scan**

¹Wong et al, Quantitative imaging of perfusion using a single subtraction (QUIPSS and QUIPSS II), Magn. Reson. Med. 39:702-8, 1998

4. **Scan**

Verify that the scan time is 6:40 minutes.

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**, and images need to be reconstructed off-line using the **gr** program. The **gr** command can be run from a unix shell on **cfmri** or **fmrserver** at the Center. The P-files should be transferred to a server immediately after acquisition as P-file filenames are reused.

Important Note: *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, as well as between scans to check it is not getting full. Do this by typing **< df -k >** in the command line after cd-ing to /usr/g/mrraw.*

1. Open a command tool and change directory: **cd /usr/g/mrraw**
2. Find the latest P-files using: **ls -ltr P***
3. Copy the P-files to a server using the secure copy command. For example, to copy one P-file to the **cfmri** server, use:
scp /usr/g/mrraw/P54159.7 username@cfmri.ucsd.edu:data/
(You will be prompted to enter a password).
4. Reconstruct the P-files using the program 'gr', for example by typing:
gr P5159.7 myscan

The program will produce an AFNI brik called **myscanbrik+orig.{HEAD, BRIK}**.

Note: *the reconstruction process may be rather lengthy depending on # images to be reconstructed. One brik per P-file is created. Some sequence information is stored in*

the header of the AFNI briks created by gr. This information (including sequence parameters, ASL parameters and Rx info) can be accessed using the command (from within the directory containing the brik): **3dNotes myscanbrik+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 (v1.0)

System Requirements

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

Program Installation

- Download CBF.tar from <http://cfmri.ucsd.edu/download/CBF.tar> .
- Untar the file (in Linux: tar -xvf CBF.tar).
- Add the CBFv1.0 folder to Matlab path.
(To do so, you can add a line "addpath yourpath/CBFv1.0" in your startup.m)

Required Data

- ASL-FAIR brik
- CSF brik
- MinContrast brik

CBF quantification steps

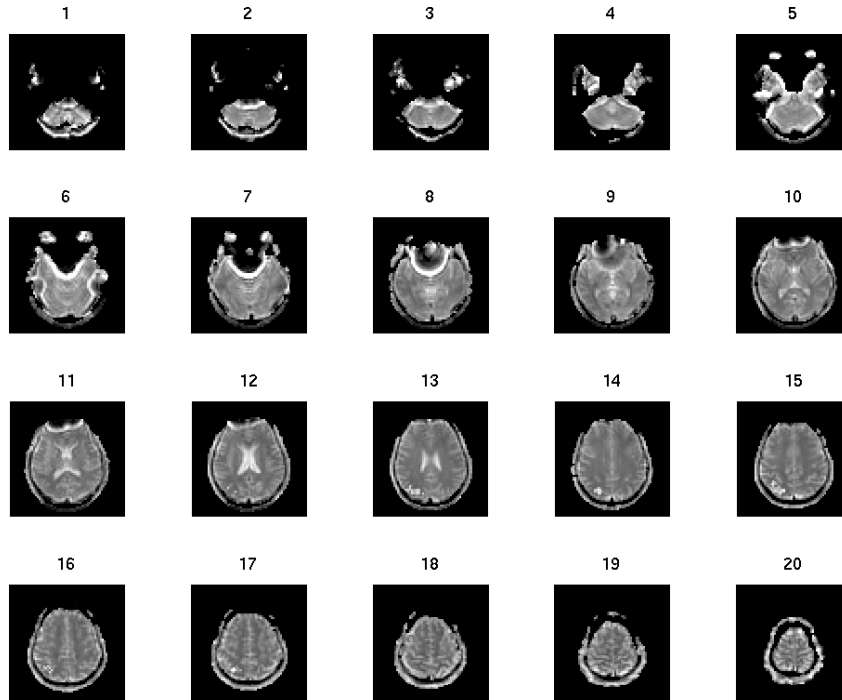
- Start Matlab
- In Matlab command window, type:

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

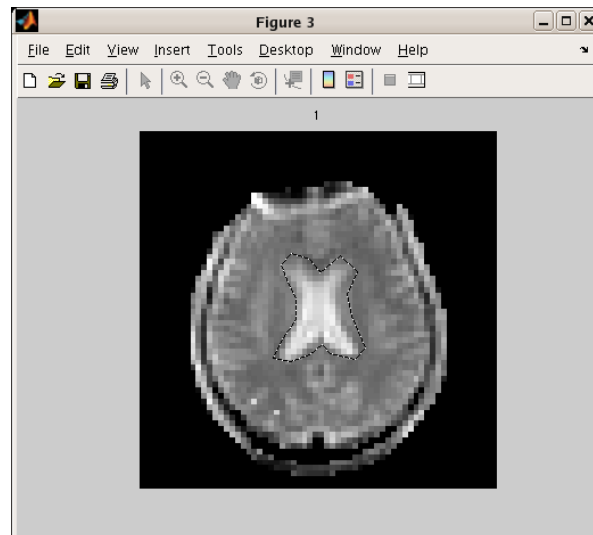
Note: Pass only the prefix of the Afni brik names to calcCBF (no '+orig' needed).

- In the pop-up matlab figure window, 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.

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



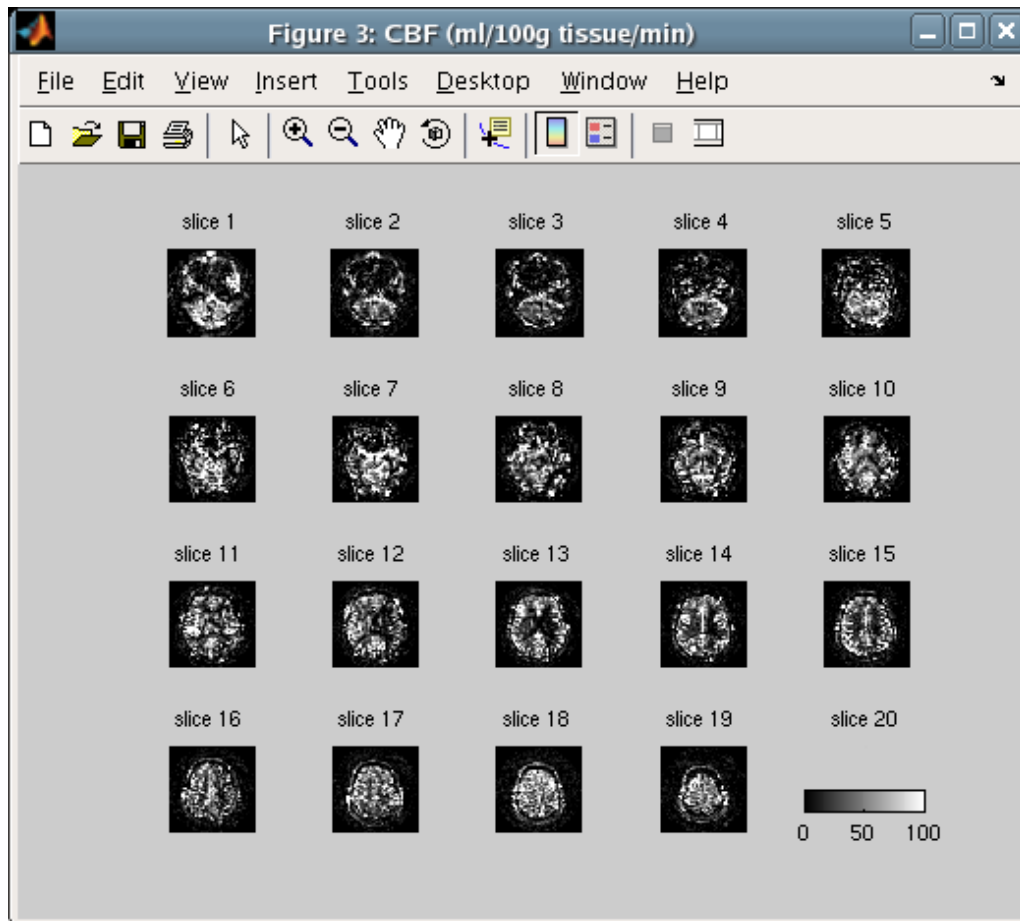
- Another window pops up containing only the chosen CSF slice from the step above. Use left mouse button to carefully trace around the edge of CSF region, click right mouse button to finish.



Note: this step creates a new directory called **'processed'** under your current working directory. A text file with suffix **'CSFvalue.txt'** is saved under the new directory. This file contains the calculated CSF value from the region you just draw. Should you want to process the same data again, the saved CSF value will

be automatically retrieved and you will be prompted to choose whether or not to use this saved value.

- Perfusion calibration will then be performed and the final calibrated CBF maps are displayed in a new figure.



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

Acknowledgements

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Please send questions and suggestions to kunlu@ucsd.edu or jperthen@ucsd.edu