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

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Overview

This document describes the procedure for 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. Reconstruction of the data into AFNI briks is described. Additional calibration scans are required in order to allow quantification of the perfusion signals via a MATLAB script.

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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, and the CSF and MinContrast are calibration scans that are needed for perfusion quantification. A GE 8-channal 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 the imaging slab. QUIPSSII saturation pulses are applied. Some important pulse sequence parameters are: TI1=600 msec, TI2=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** sequence 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 4:10 minutes (**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***, 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-FAIR scan).
5. Click ***Scan***
   *(**Note:** if you are using the old CSF protocol(scan time is 4sec for the old protocol, 36sec for the new protocol), please wait ~ 30 seconds to allow for full relaxation of signal and 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***

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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 usrname
   (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).*

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Data reconstruction using SENSErc program (v1.2)
- for multi-shot data only

Multi-shot data, such as that acquired using the **Brain_perfusion_4S** sequence, is sensitive to modulations between shots caused by physiological fluctuations or motion. This can lead to significant image artifacts. The use of a SENSE reconstruction rather than a simple Fourier transform (as performed in the automatic reconstruction described above) significantly reduces sensitivity to these modulations and produces cleaner images. The **SENSErc** program is designed to reconstruct fully-sampled multi-shot spiral data using the SENSE algorithm.

System Requirements
- **Redhat linux 8.0** or above (Windows and Mac OS not supported).
- **Matlab R14** service pack 1 or above**.**
- 512Mb or more available system memory recommended.
- **AFNI** v2.55j or above.
- **FSL** 3.x or **FS**L 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

Program Installation
- Download SENSErcv1.2_14x.tar from the cfmri website.
    (For data acquired before the 14x system upgrade, please download SENSErcv1.2.tar)
- Untar the file (in Linux: tar –xvf SENSErcv1.0.tar).
- Add the SENSErc folder to Matlab path.

(e.g. add the line "addpath yourpath/SENSErcv1.2_14x" in your startup.m)

Required Data
- ASL P-file
- If CBF quantification is required, a CSF P-file is also needed.

Reconstruction steps
- Start Matlab
- In Matlab command window, type:

  senserc({'Pfilename1',' Pfilename2'},{'AFNIprefix1',' AFNIprefix2'});
  e.g.
  senserc({'P02056.7','P03895.7'},{'senseASL','senseCSF'});

  Pfilenames are the names of the P files to be reconstructed
  AFNIprefixes are the prefixes of the AFNI briks that are output

Important Notes:
- If CBF quantification is required, **both** the ASL **and** the CSF scans should be reconstructed using the SENSErc program; the minimum contrast data does **not** require this, and the brik created automatically at the scanner console should be used.
- The reconstruction is slow and may take several hours depending on the size of the raw data and the speed of the computer.
- This data reconstruction approach is NOT necessary or advised for data acquired using the single shot sequence (Brain_perfusion_SS).

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Perfusion Quantification using CBF program (v3.2)

System Requirements
- **Redhat linux 8.0** or above (Windows and Mac OS not supported).
- **Matlab R14** service pack 1 or above, plus Matlab toolboxes.
  NOTE: If using Matlab release **R2006b**, you may encounter an incompatibility between Matlab's C++ libraries and your system's GCC. To solve this problem, force Matlab to use your system's libraries by deleting one of the Matlab libraries. Ask your system administrator (you need to be logged in as root) to execute the following commands:
  cd <matlab installation folder>/sys/os/glnx86
  mv libgcc_s.so.1 libgcc_s.so.1_backup
- **AFNI** v2.55j or above.
- **FSL** 3.x or **FS**L 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.
- Not tested with 64-bit version of Linux

Program Installation
- Download **CBFv3.2.tar** from the cfmri website.
- Untar the file (in Linux: tar –xvf CBFv3.2.tar).
- Add the CBFv3.2 folder to your Matlab path.
  (e.g. add the line "addpath yourpath/CBFv3.2" in your startup.m)

**Required Data**
- ASL-FAIR brik, CSF brik, MinContrast brik
- *Optional*: High resolution anatomical brik.
  <u>NOTE:</u> 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-FAIR','CSF','MinCon');

  OR, if anatomical is available:

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

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

- If the SENSE reconstruction was used, take care to pass the SENSE ASL and CSF briks to calcCBF, rather than the brik automatically transferred at the scanner console using 'aslgecopy'.

- *<u>If anatomical is supplied</u>*:
  o The anatomical is segmented into gray, white and CSF (takes ~6mins).
  o All brain slices will then pop up in a matlab figure window; select those containing ventricles by left-clicking.

- *<u>If anatomical is NOT supplied</u>*:
  o 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***
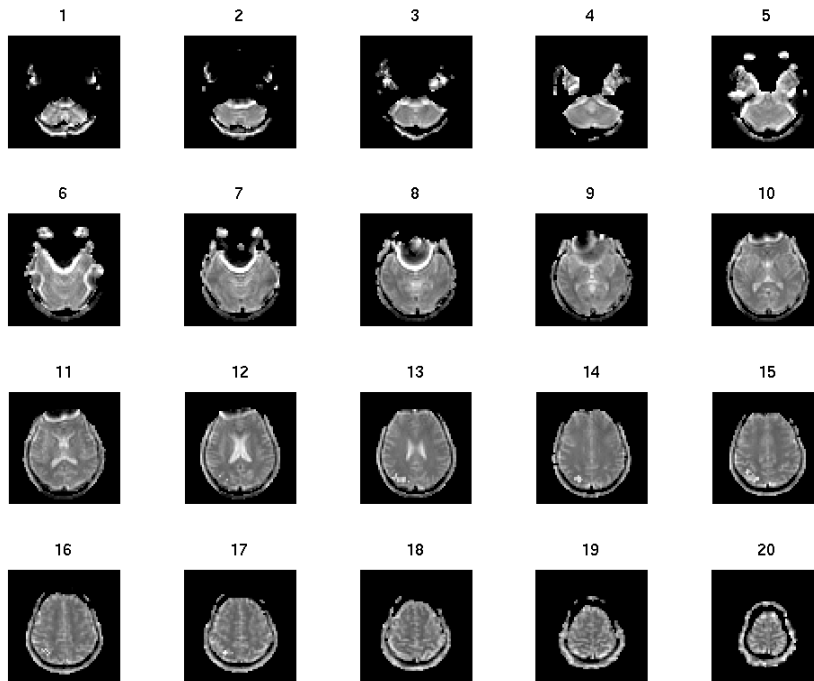
- Use left mouse button to carefully trace around the edge of CSF region and double click to finish. If anatomical is supplied, this is performed for all chosen slices. (You may find double click does not work for certain version of matlab. In this case, please refer to the help file for *roipoly* in your matlab.)
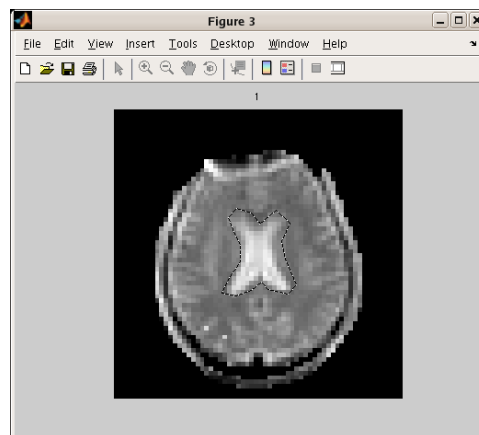
*Note: this step creates a new directory called '**processed**' under your current working directory. A text file called '**CSFvalue.txt**' is saved under the new directory. This file contains the calculated CSF value, which will be automatically retrieved should you process the same dataset again (you 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.*

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- 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.

CBF data, run 1
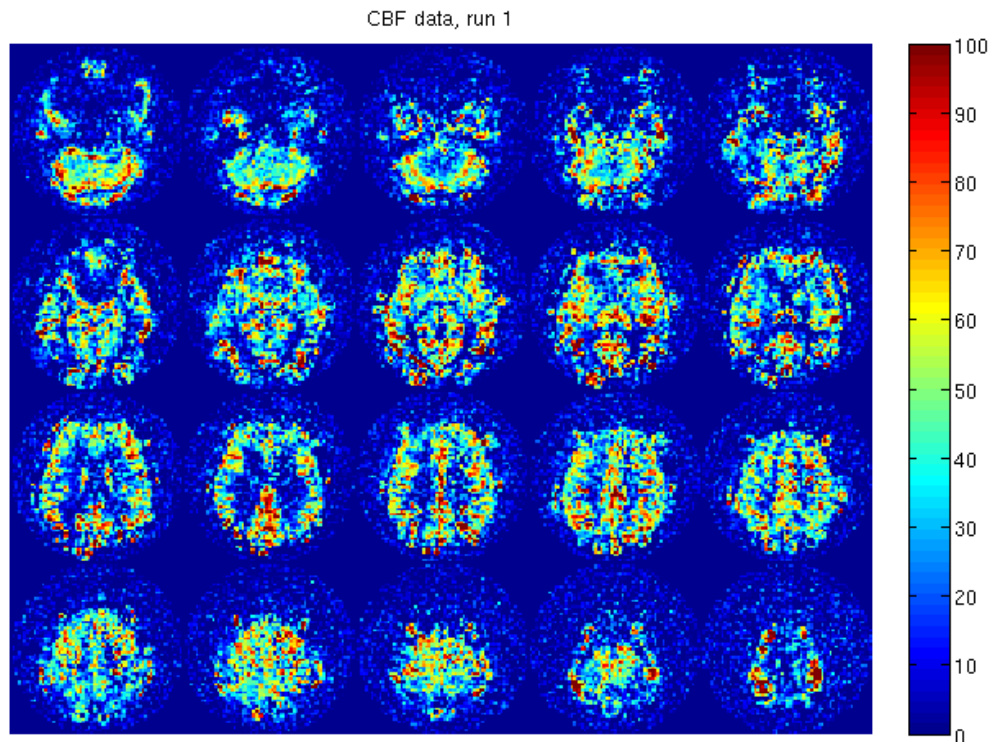
- An AFNI brik containing the calibrated CBF values is also saved. Look for the suffix '**_CBF**' in the brik name.

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Please contact kunlu@ucsd.edu with questions/comments