Generating CBF Map from single PLD pcASL MRI

Sunnybrook Neuroimaging summer school Perfusion Module Tutorial 1

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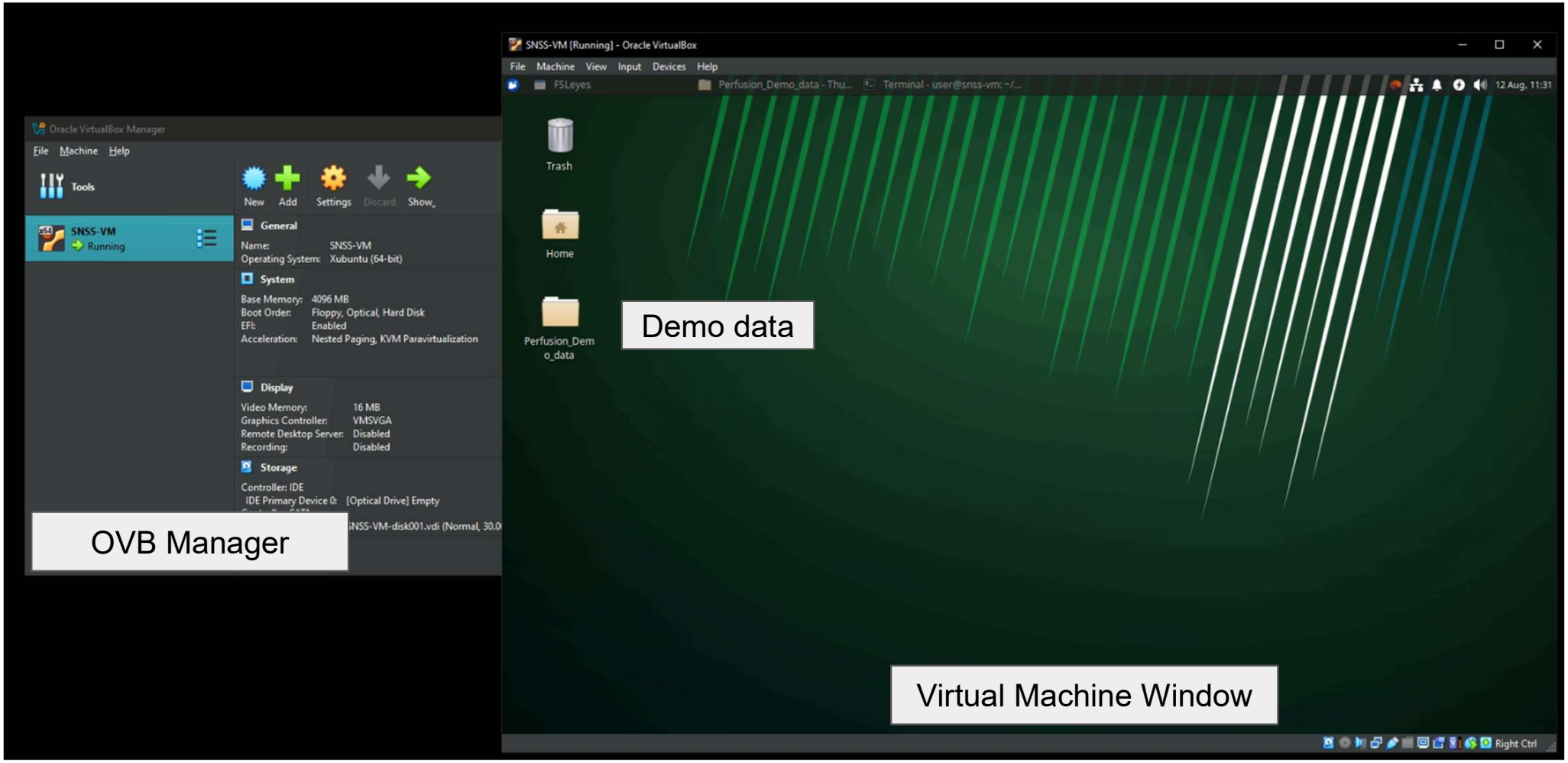
If you want to try creating a CBF map on your laptop but have not installed the software libraries:

VirtualBox

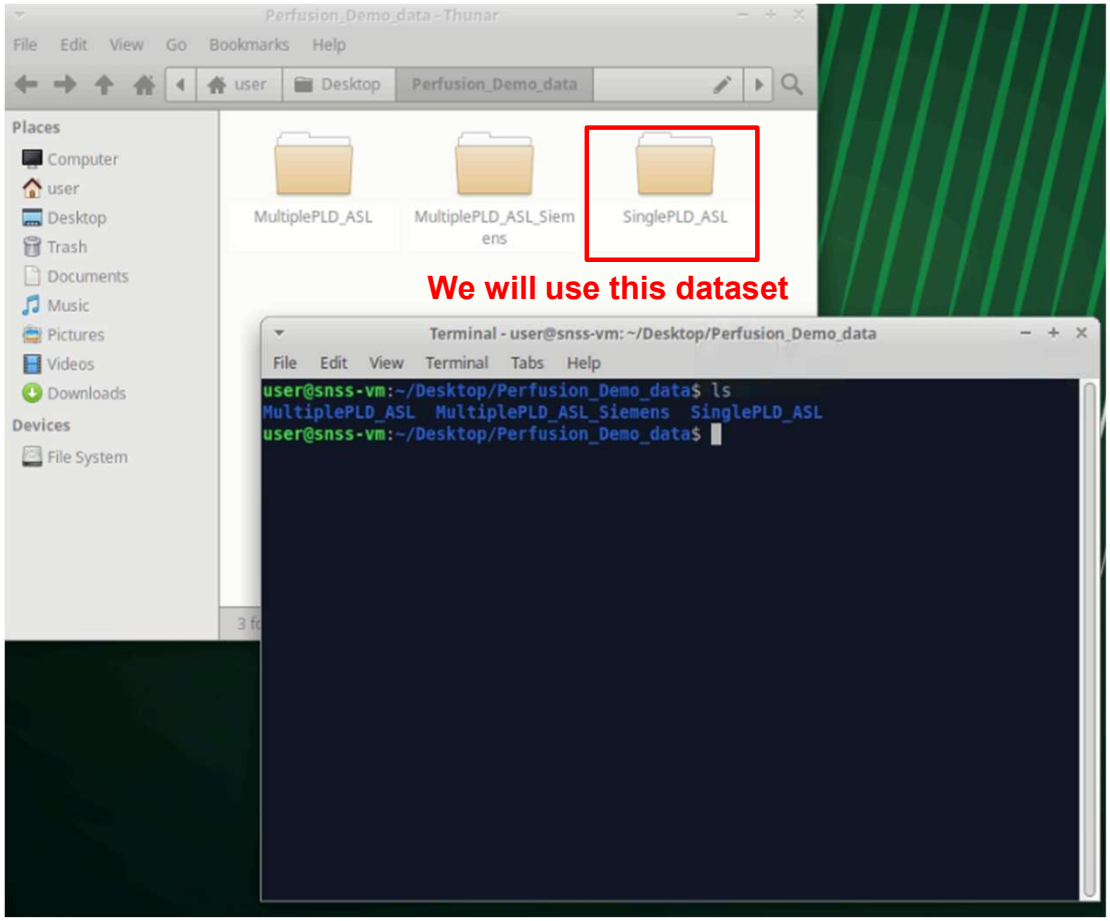
Windows Users need to download a virtual machine:
1. Install Virtualbox (www.virtualbox.org/wiki/Downloads)
2. Download the VM OVA file (http://bit.ly/3HrkpwC)
3. Open Virtualbox, and select “File—>Import Appliance”
4. Select the downloaded OVA file and press “Next—>Finish”

Mac and Linux users can directly download the FSL, no virtual machine is needed:
1. FSL (https://fsl.fmrib.ox.ac.uk/fsl/docs/#/install/index)
2. Perfusion Dataset (http://bit.ly/3J6H95K)

If your VM boots correctly it will look like this:



There is a demonstration dataset included in the virtual machine



Data from Sunnybrook Siemens Prisma 3T scanner and GE 3T scanner.

Mac and Linux users can download the dataset:
Perfusion Dataset (http://bit.ly/3J6H95K)

Linux Users Tips:

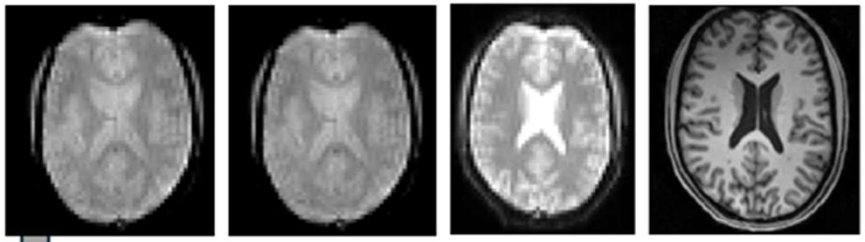
1. Right click on the window and select "Open Terminal Here" allows you to call out the command line terminal

2. Use "**ls**" to list files in the current folder;
   Use "**cd**" to move between directories;
   Use "**pwd**" to show the current path

Agenda: Creating an ASL-CBF map from single PLD pcASL data

DICOM

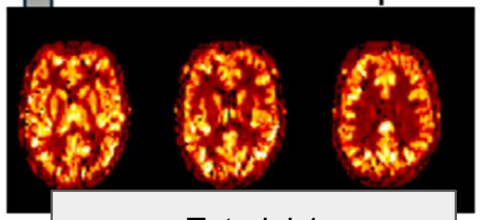
Tag-Control Pairs | PDw | T1w



Anatomical preprocessing
Brain extraction
Motion correction

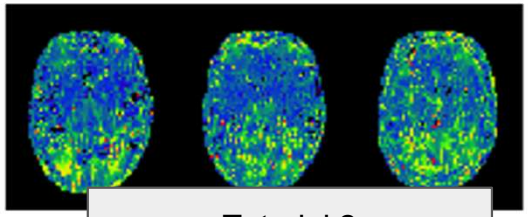
CBF Mapping using BASIL
- *Tag-control subtraction*
- *Output calibrated image*
- *Output ATT maps*

Calibrated CBF Map



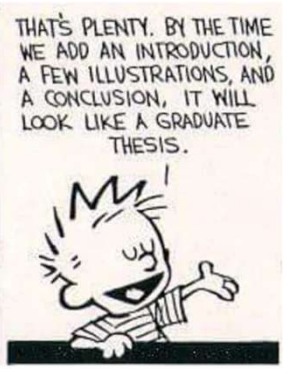
Tutorial 1

Arterial transit time map

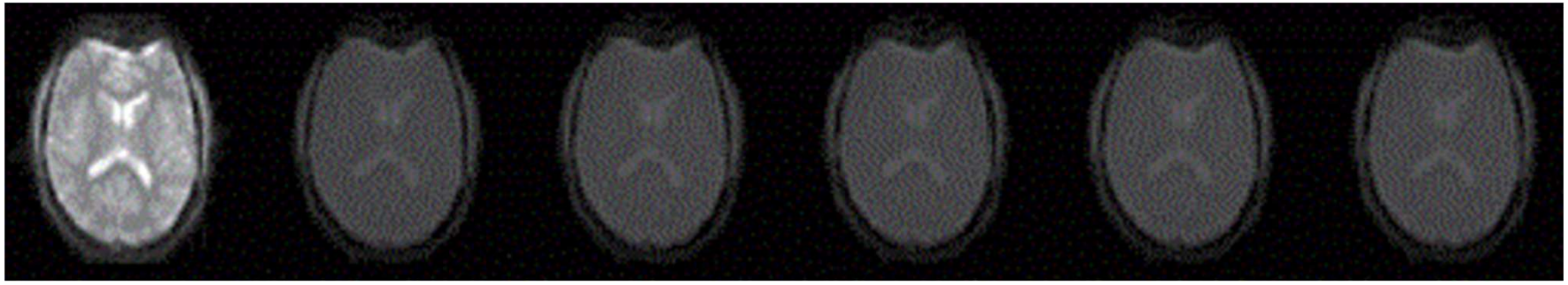


Tutorial 2

** Actually more works are needed in a real thesis



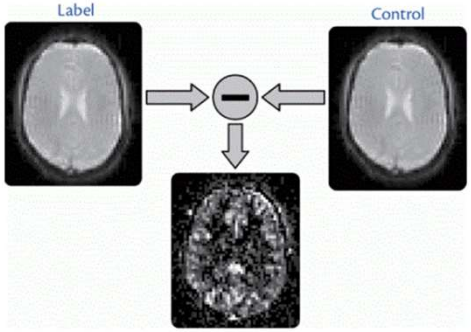
What does a typical single PLD pcASL dataset looks like?



Calibration image

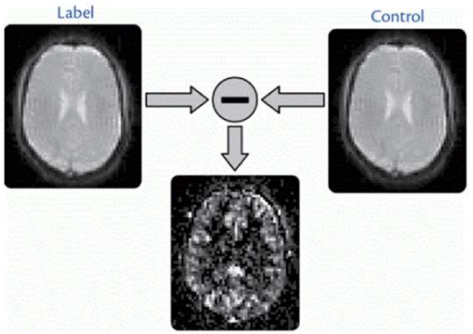
An extra image

Label-Control 1



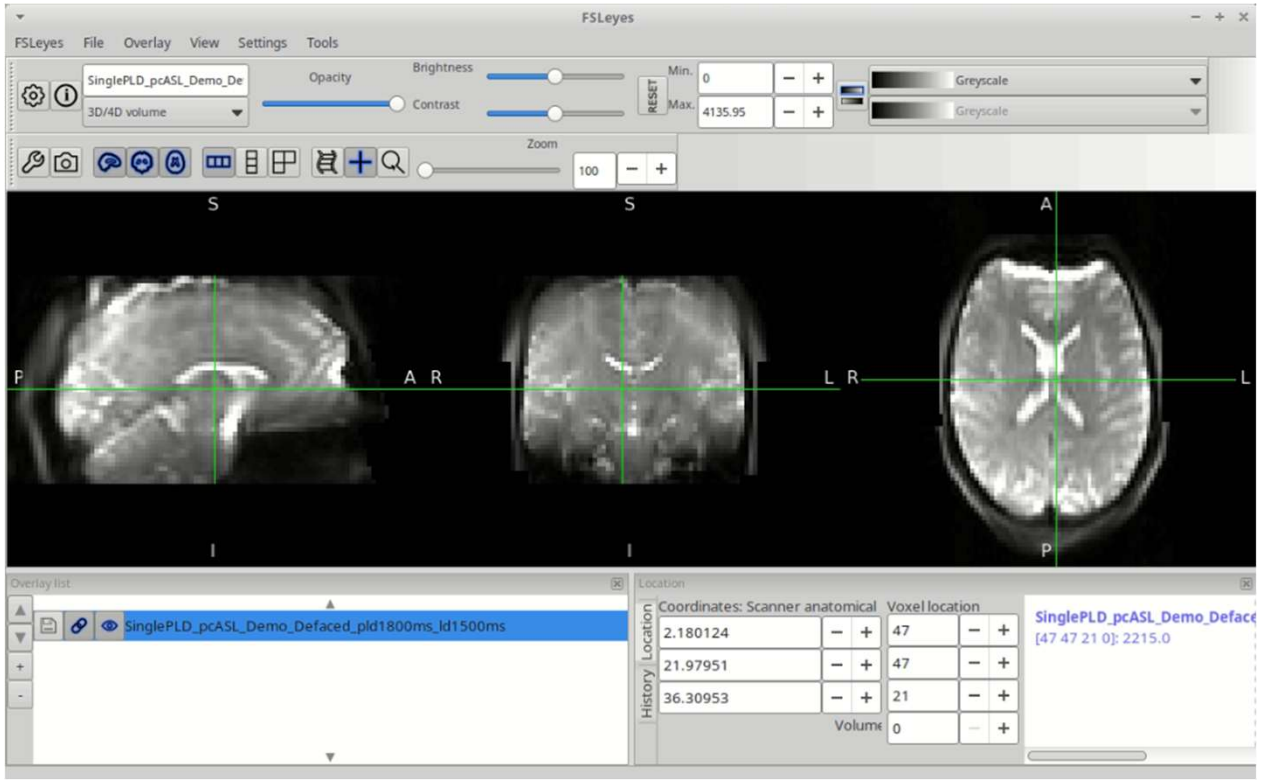
PWI 1

Label-Control 2



PWI 2

Exercise 1: Visualization of the pcASL dataset



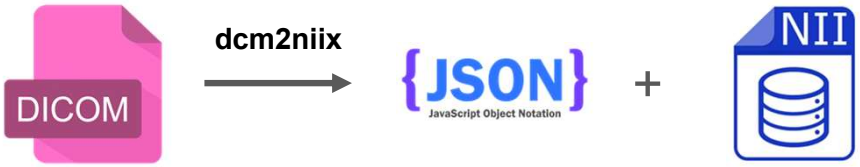
Linux Users Tips:

1. To start the FSLeyes program, start a terminal and type "**fsleyes**" and press enter.

To-discuss:

1. If you increase the volume number, what you will see?
2. Why the first volume is much brighter than the next few volumes?
3. Will label image show higher or lower signal intensity than the control image?

Exercise 2: Reading through the image data to identify ASL parameters




```
Series description: tgse_pcasl_PLD1800_2p5iso_48sl
Image type: ORIGINAL\PRIMARY\ASL\NONE\ND\MOSAIC
Manufacturer: SIEMENS
Model name: Prisma
Software version: syngo MR E11
Study id: 1
Series number: 8
Repetition time (ms): 4190
Echo time[1] (ms): 38.32
Flip angle: 120
```

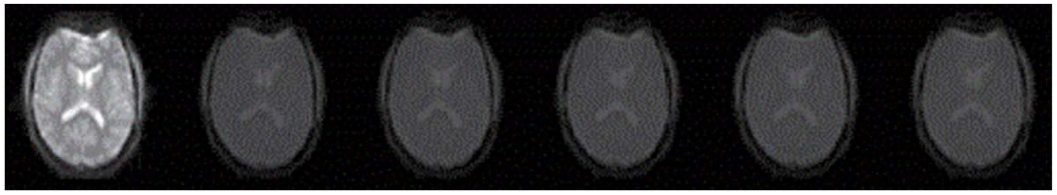
Modality: MR
MagneticFieldStrength: 3
Manufacturer: SIEMENS

Repetition time (ms): 4190
Echo time[1] (ms): 38.32

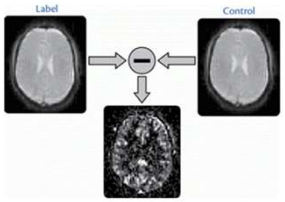
Slice thickness (mm): 2.5
Voxel size x (mm): 2.5
Voxel size y (mm): 2.5
Number of slices: 48

Image type: “Original”, “Primary”, “ASL”
LabelingDuration (s): 1.8
PostLabelDelay(InversionTime) (s): 1.6

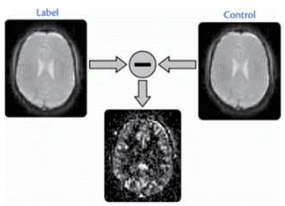
Exercise 3: Preparing the dataset for ASL analysis using fslsplit and fslmerge functions



Calibration image | An extra image | Label-Control 1 | Label-Control 2



PWI 1



PWI 2

Bash Users Tips:

To show help message in any fsl comments, you can just type the command and press enter.

To select all files with part of file names in common, you can use * sign (e.g. *.nii.gz selects all NIFTI images in the current directory)

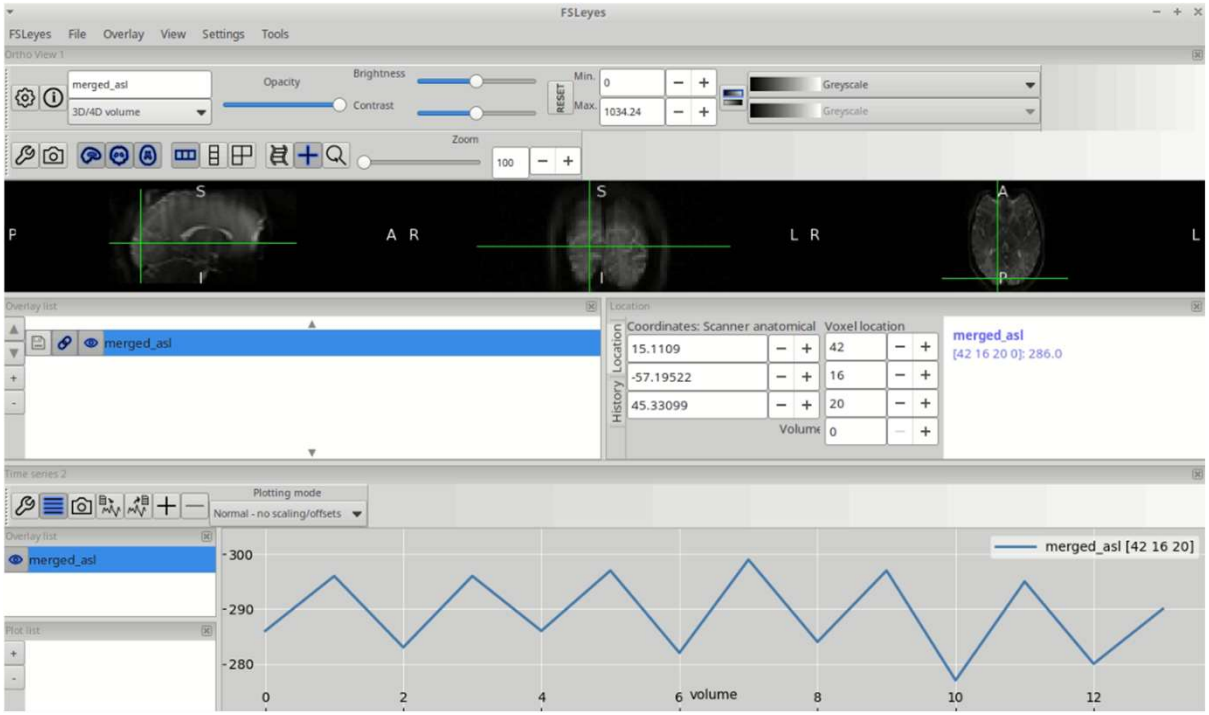
To-dos:

1. Use "**fslsplit**" command to split the 4D time series into 3D volumes.
2. Identify and rename the PDw image.
3. Use "**fslmerge**" command to merge the tag-control pairs back into the 4D time series.

Hints:

1. **fslsplit <input.nii.gz> -t**
2. Identify and rename PDw image
3. Identify the 7 label-control pairs
4. Remove the one extra unused image
5. **fslmerge -t <output name> <all inputs vol*.nii.gz>**

Exercise 4: Visual inspection of label-control sequence using time series plot in FSLeyes



To-dos:

1. Load the merged label-control images post “fslmerge” function to the fsleyes viewer.

2. Use green cursor to select a brain region of your interest.

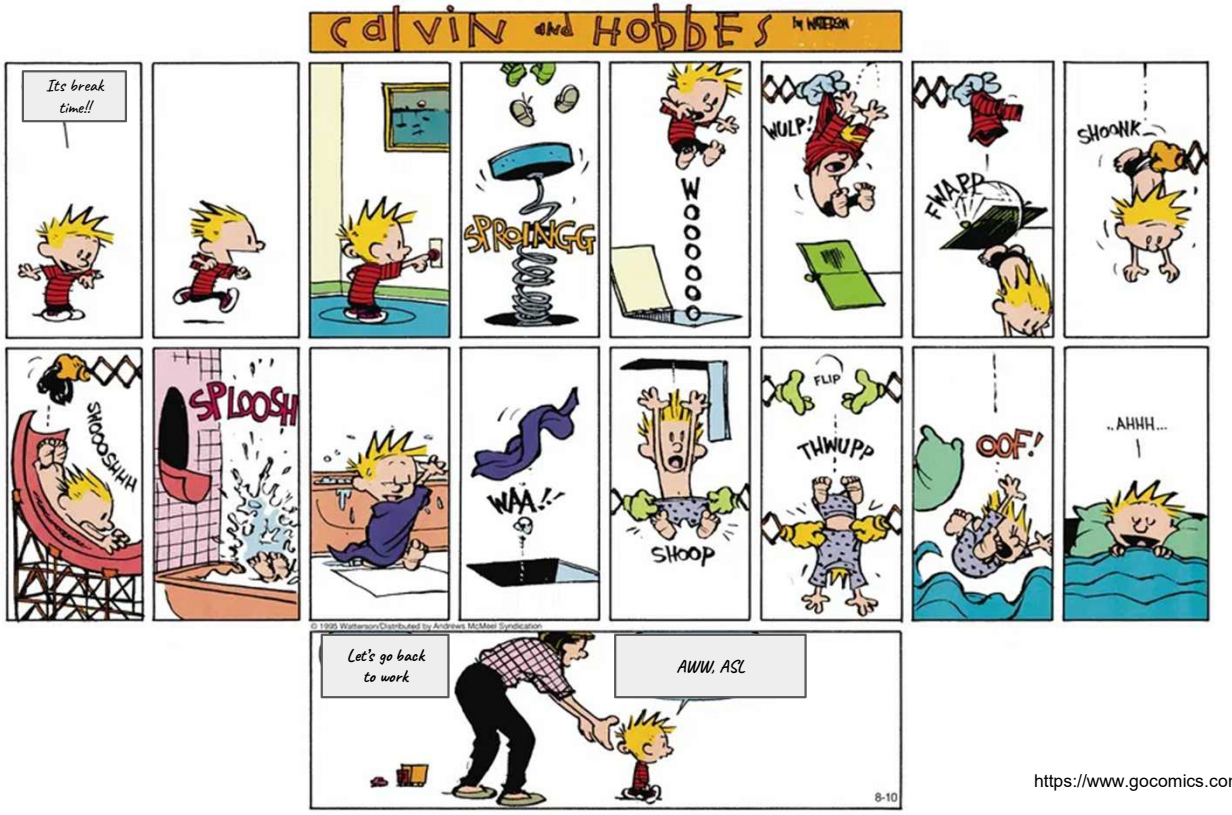
3. Create a time series plot using “view” menu > “Time Series”

Question:

1. Is the first image a control image or a tag image?

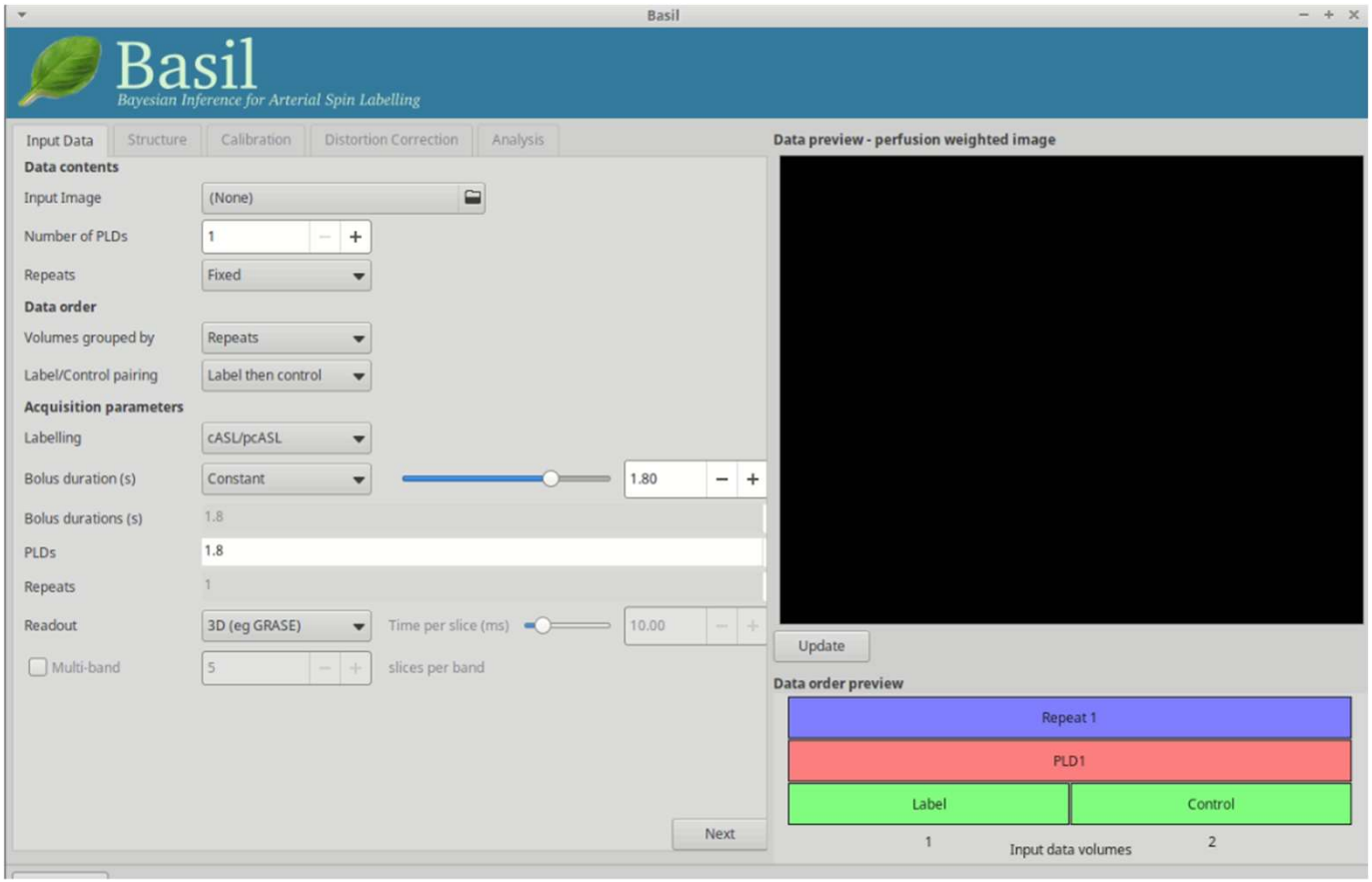
2. Which brain region showed higher ASL signal fluctuation?

Let’s take a break …



https://www.gocomics.com/calvinandhobbes/2025/08/10

Exercise 5: Introduction to the Oxford ASL GUI



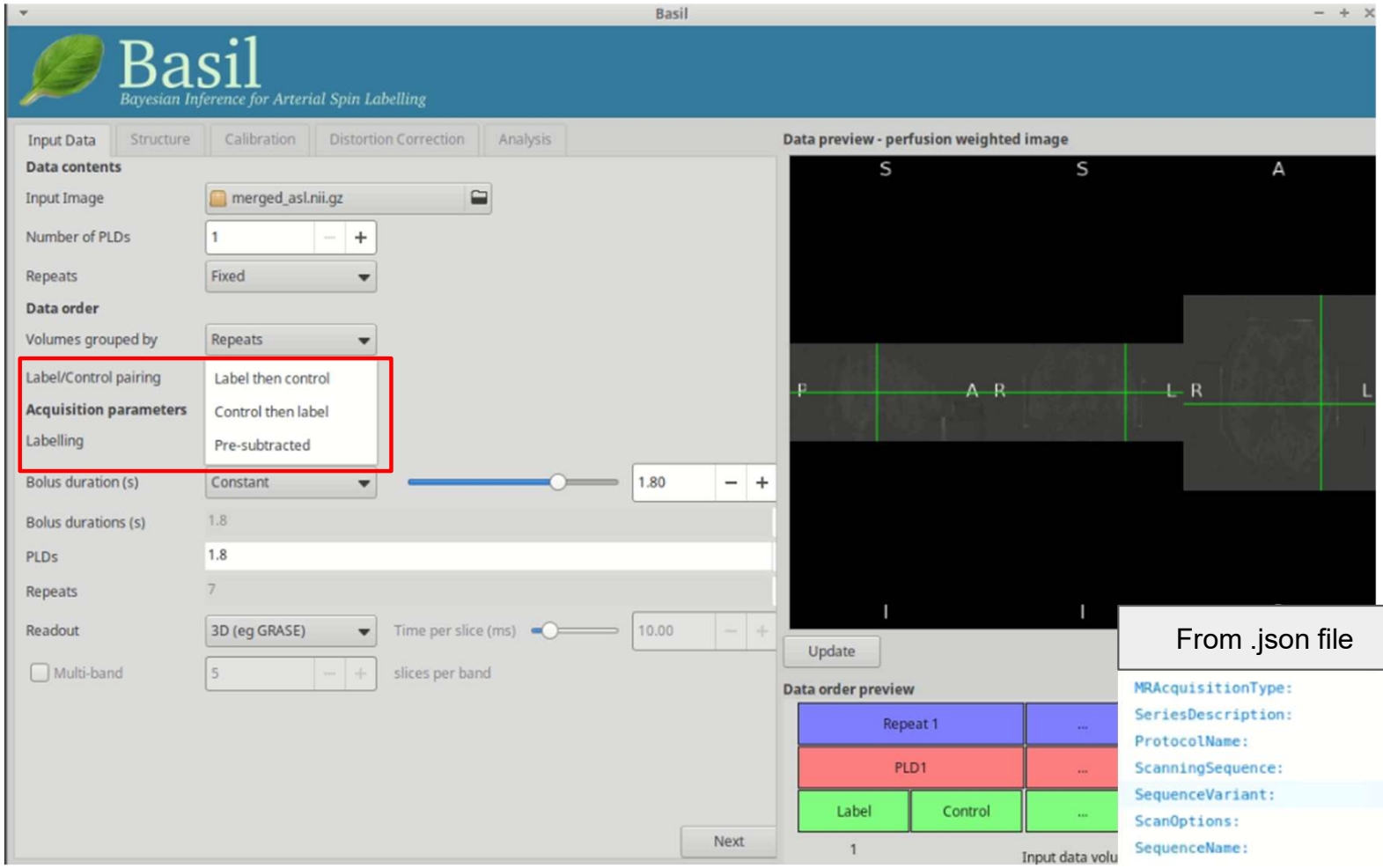
Linux Users Tips:

For programs like OxfordASL and Fsleyes with GUI, each terminal usually can only run one of such program. If you close the terminal or force run another task on the same terminal, the program will stop. Thus you want to create a new terminal everytime when running a new GUI-based program on top of another.

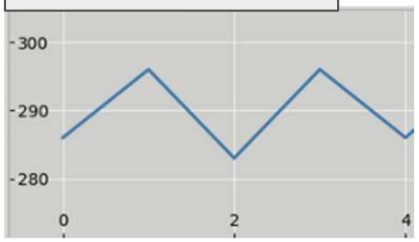
To-dos:

1. Call “asl_gui” in a new terminal to open up the OxfordASL-BASIL program
2. Input the label-control pairs to the **Data contents > Input Image** tab
3. Conduct a data preview by clicking the “Update” button

Exercise 5: The “Input Data” Tab



Time series plot



Question:
Is the first image a control image or a tag image?

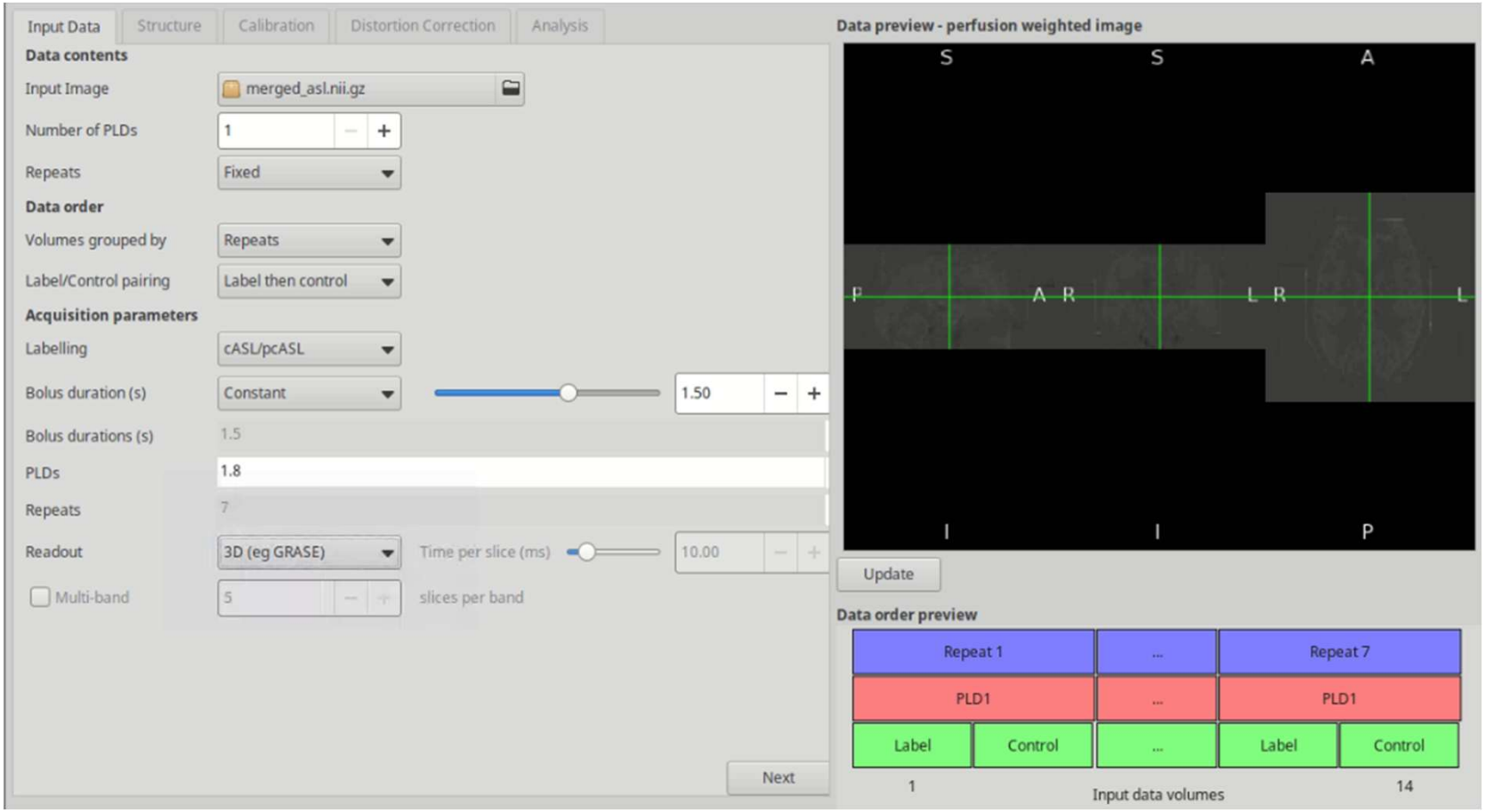
How many repeats do we have?

What is the bolus duration, PLD, readouts?

From .json file


```
MRAcquisitionType:          "3D"
SeriesDescription:          "tgse_pcasl_PLD1800_2p5iso_48sl"
ProtocolName:               "tgse_pcasl_PLD1800_2p5iso_48sl"
ScanningSequence:           "EP"
SequenceVariant:            "SK"
ScanOptions:                "FS"
SequenceName:               "tgse3d1_3528"
```

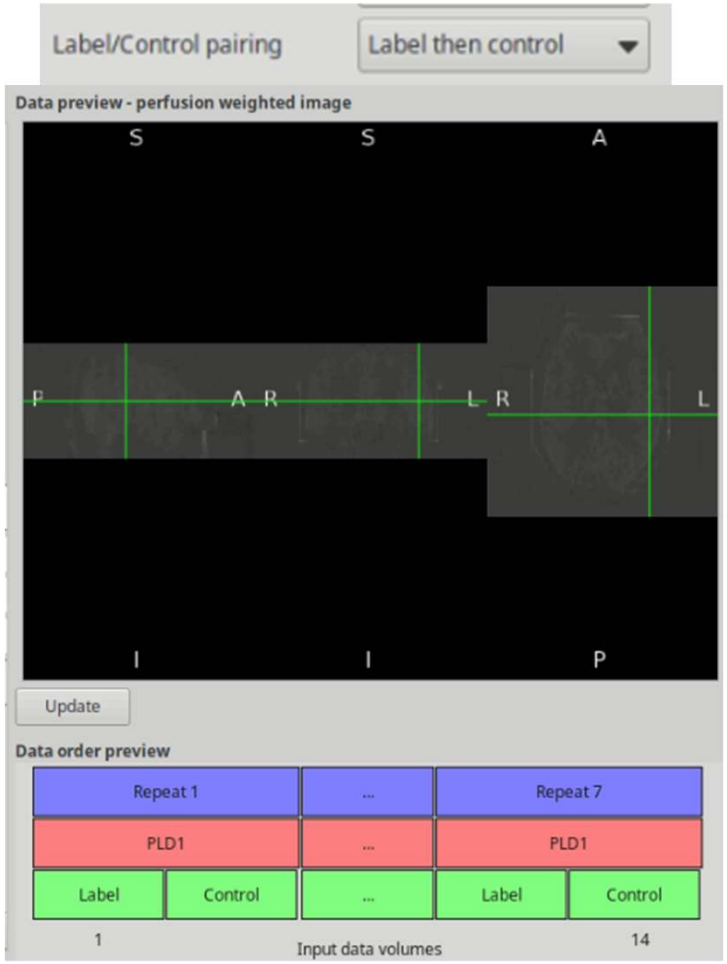
Exercise 5: The completed “Input Data” tab:

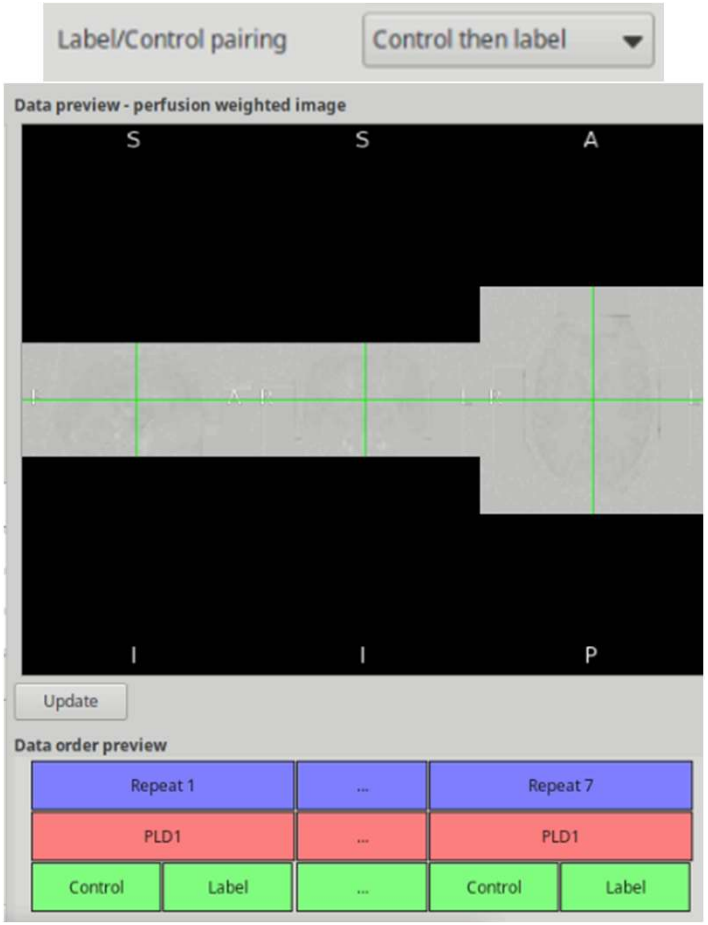


This scan:

1 PLD;
Fixed repeats;
pcASL imaging;
LD=1.5s;
PLD=1.8s;
3D readouts

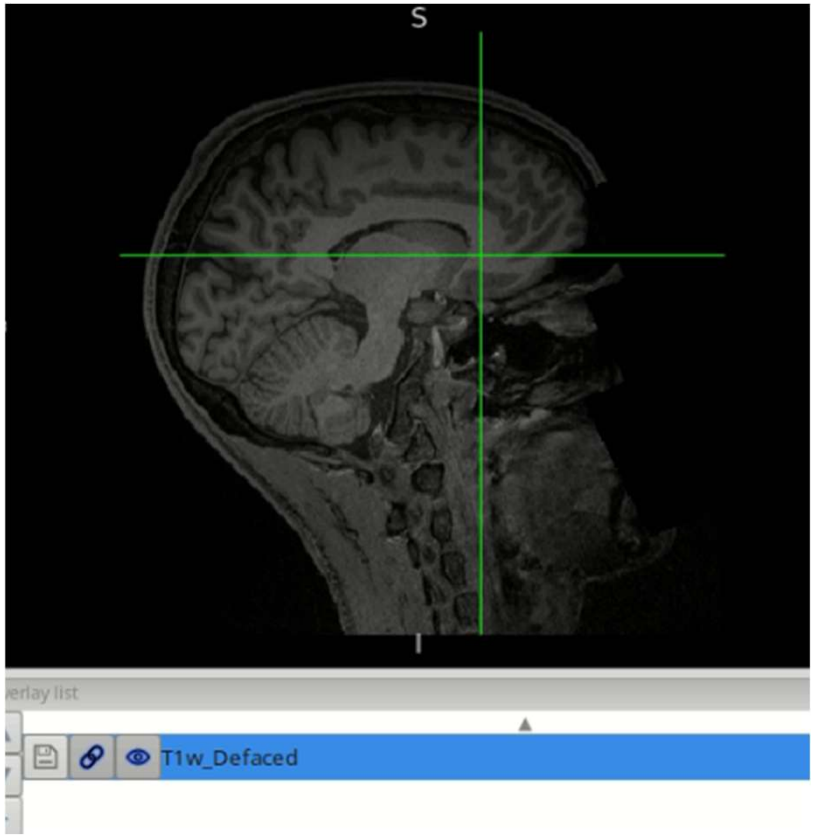
Exercise 5: What happens if you select the wrong label-control pair



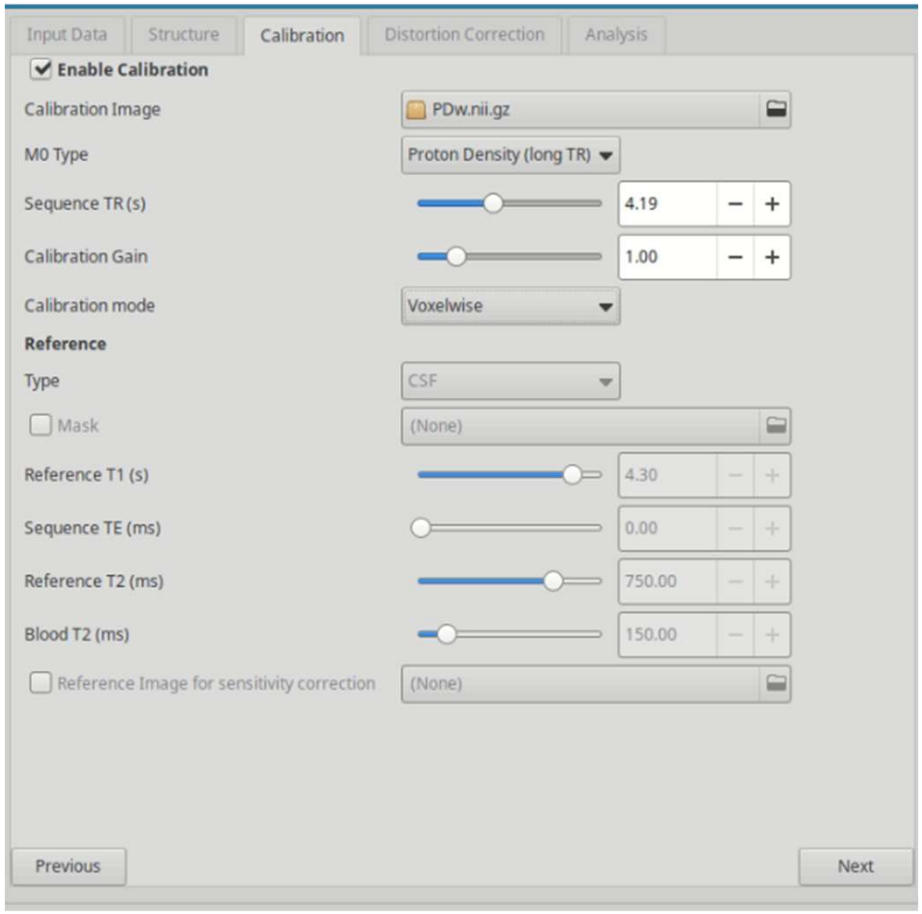


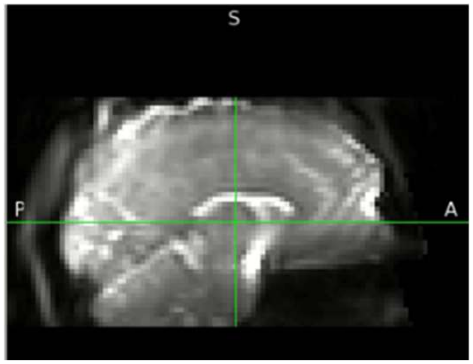
I was told my cerebral blood flow was negative 30 ml/100g/min ..?

Exercise 5: Loading the T1w image to the “Structural” tab



Exercise 5: Loading the PDw image to the “Calibration” tab





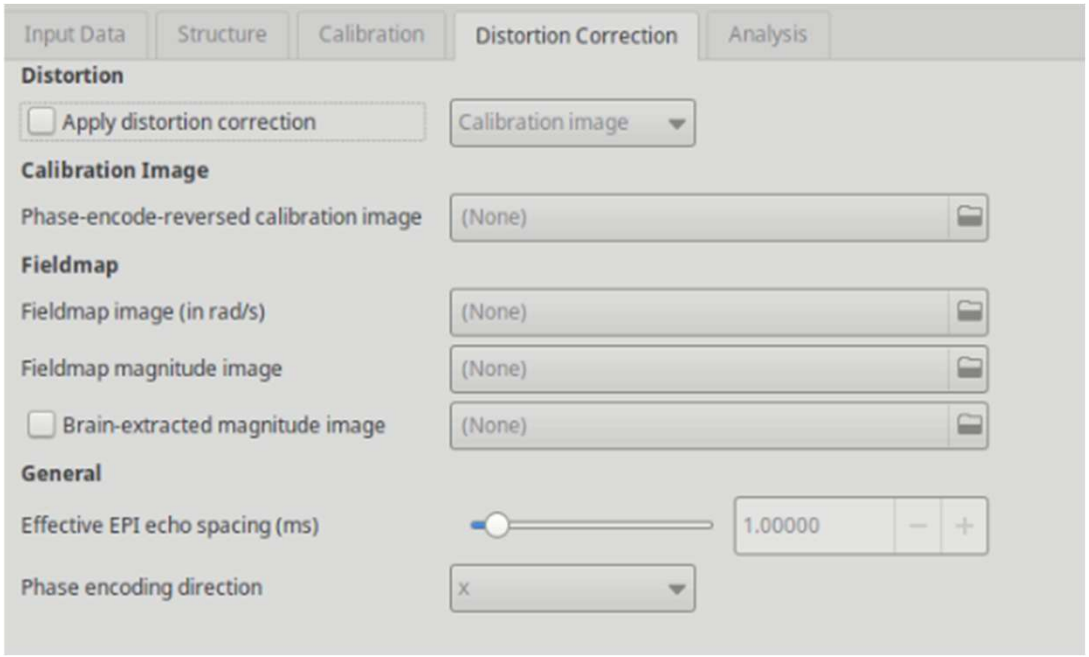
Question:

1. How will you find the sequence TR value?

2. Why we need a PDw image here?

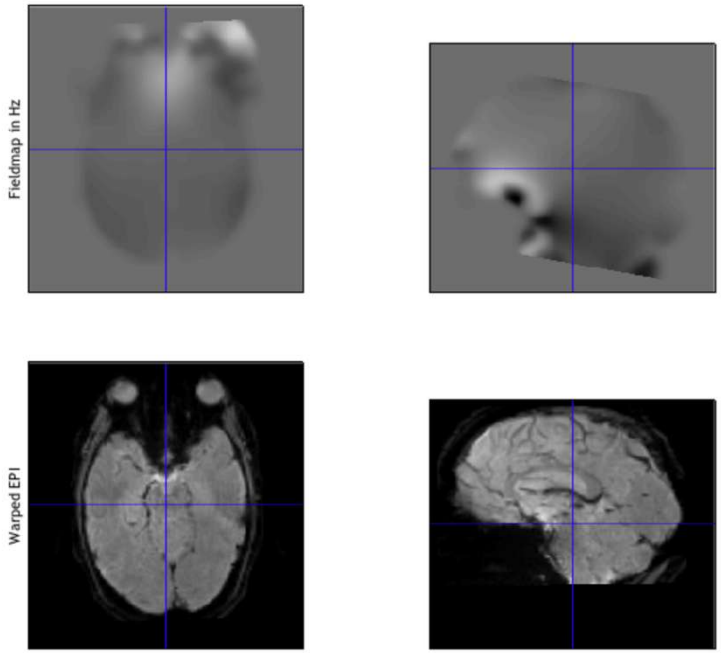
3. If you got an ASL scan, and the sequence TR was 1.5s, how would you comment on the acquisition? (Hint: Short TR makes PDw image look closer as a T1w image. What will happen on signals in GM, WM, and CSF? We also know from kinetic model: CBF $\propto$ (ΔM/M0)

Exercise 5: Introducing the “Distortion Correction” tab

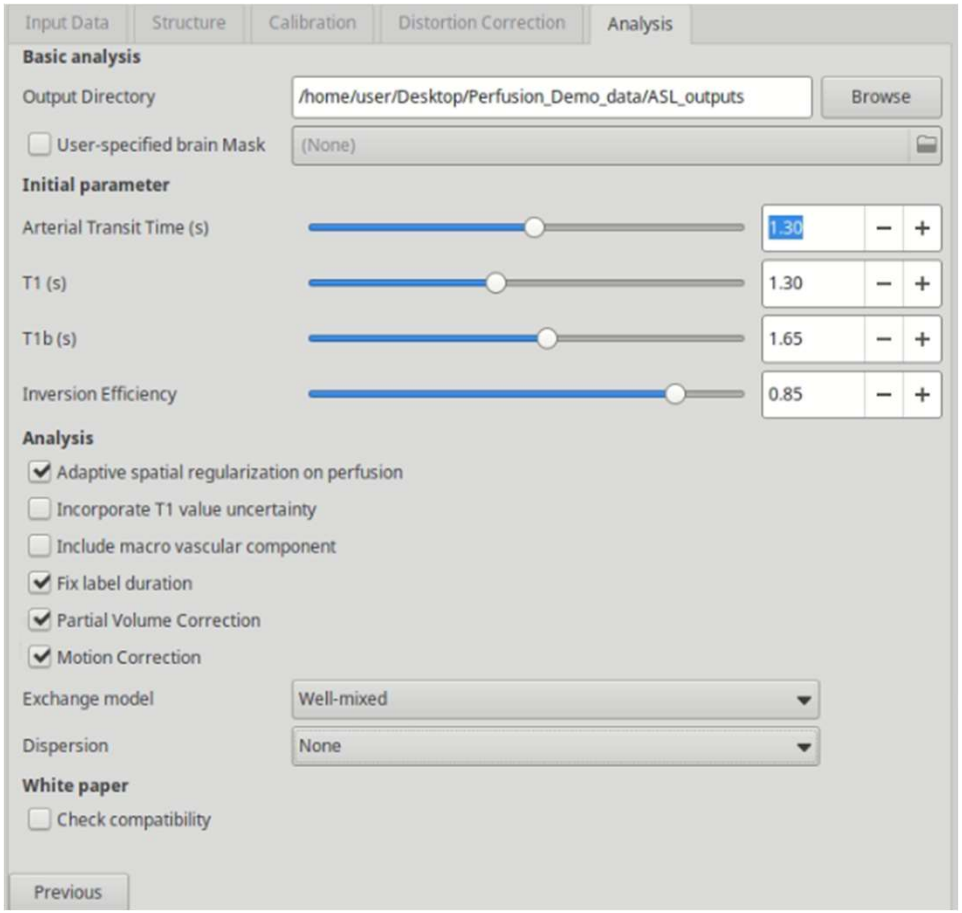


If you acquire ASL with **anterior–posterior (AP)** phase encoding, reversing the PE direction to **posterior–anterior (PA)** flips the sign.

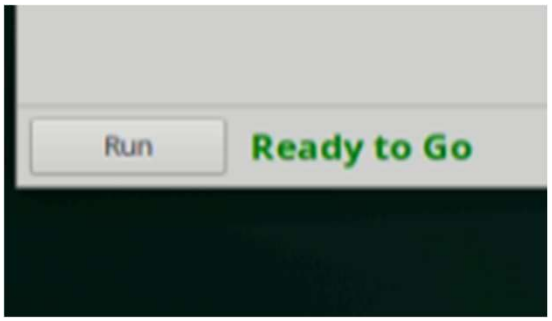
(Optional) The calibration image mode uses the two opposite-PE images to estimate a field map of displacements and applies this to correct distortions in ASL data.

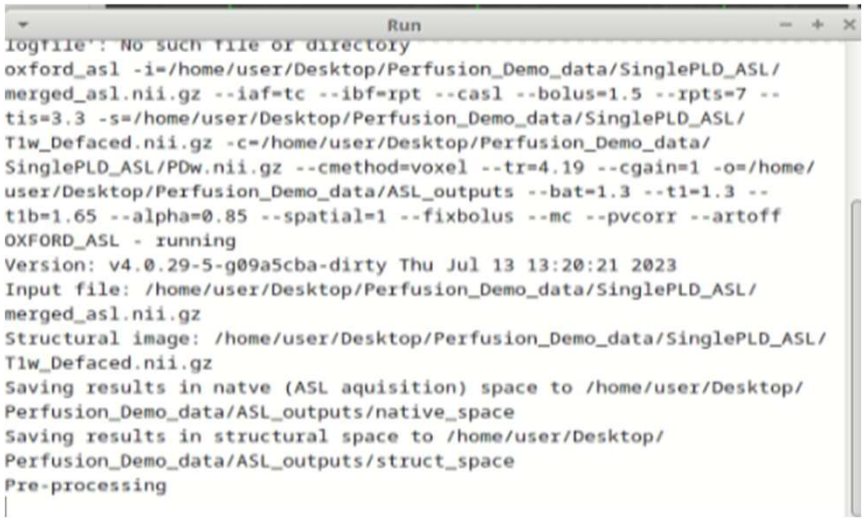


Exercise 5: Introducing the “Analysis” Tab



Exercise 5: Let's run the code - It will take some time.



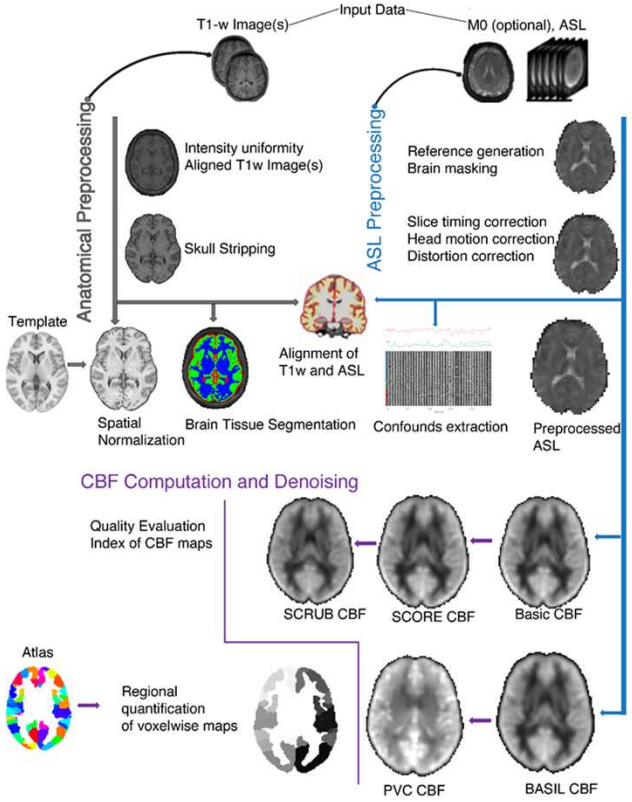


Linux Users Tips:

If you found the GUI is too large and you can't rescale it because buttons are outside the window, try increase the resolution of your virtual machine via: Settings > Display

Exercise 6: The CBF Mapper: Creating a pipeline to auto-run every cases for your future study

An example ASL processing pipeline



Raw ASL images> **ASLPipeline.sh** > CBF Map

```
#!/bin/bash

# Define the constants - Which should be consistent over your study
TC_Mark="tc"            # Input "tc" if 1st image is label.
LD=1.6                  # second
TR_PDw=4.21             # second
T1_tissue=1.3           # second
T1_blood=1.65           # second
InvEff=0.85             # Inversion Efficiency (%)
rpts=7                  # Number of repeats

# Define the image inputs:
Label_Ctrl=$1           # nii image of label-control pairs
T1w=$2                  # nii image of structural MRI
PDw=$3                  # nii image of calibration PDw MRI

# Run the ASL pipeline (Example):
oxford_asl -i ${Label_Ctrl} -o ASL_Analysis_xxxStudy        \
           -c ${PDw} --tr=TR_PDw --cmethod=voxel            \
           -s ${T1w}                                        \
           --t1=T1_tissue --t1b=${T1_blood} --alpha=${InvEff}  \
           --casl --bolus=${LD} --rpts=${rpts} --mc --pvcorr
           … # More costume arguments available
```

Exercise 6: The CBF Mapper: Creating a pipeline to auto-run every cases for your future study

The “**TIS**” matrix in oxford ASL = PLD + LD

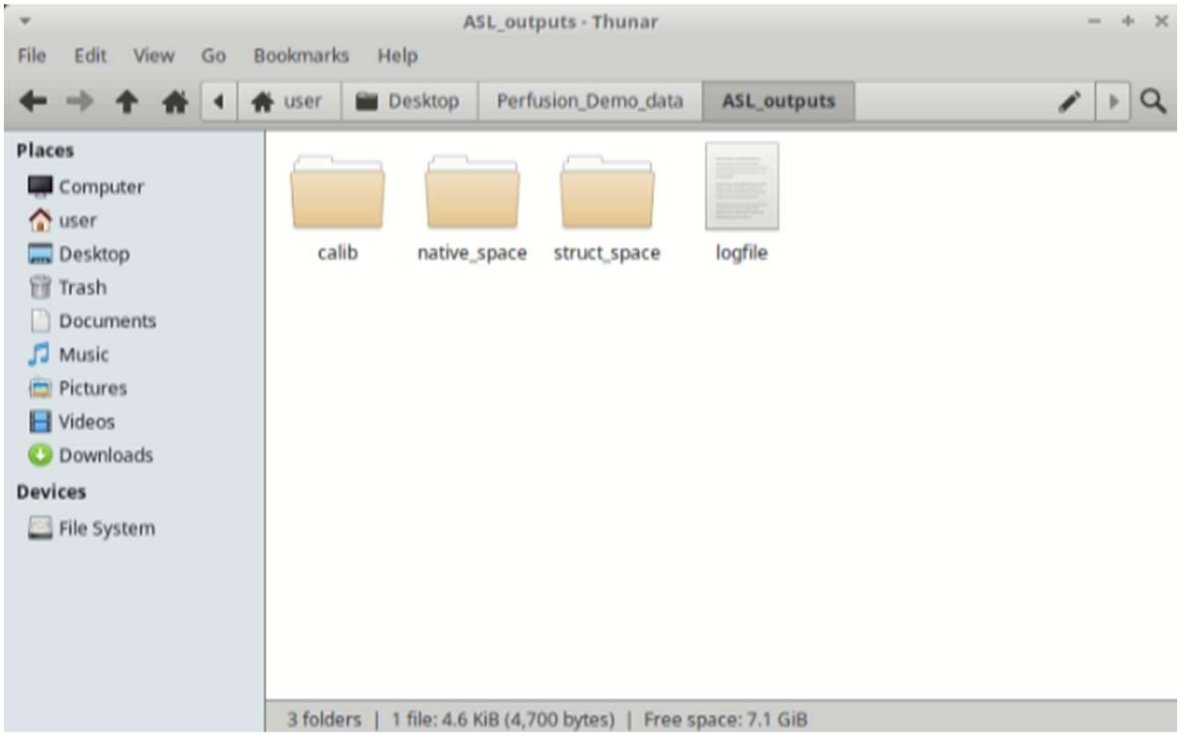
```
# Design matrix for the ASL timeseries:

repeats="2,2,2,2,2"
TISs="3.4,2.2,3.7,2.8,1.8"

# Tutorial: For example, we have 3 PLD, each PLD have two repeats:
#           For your ASL image sequence: PLD1(T,C,T,C); PLD2(T,C,T,C); PLD3(T,C,T,C)
#
# First input the repeat number matrix:
#                       repeats="2,2,2"  (2 repeats for each PLD)
#
# Then for the TIS calculation:
#                       TIS = PLD + Bolus time (Label duration)
#                  e.g. TIS1 = 1.8 sec + 1.6 sec = 3.4 sec for first PLD
#                       TIS2 = 1.0 sec + 1.6 sec = 2.6 sec for 2nd PLD
#                       TIS3 = 0.2 sec + 1.6 sec = 1.8 sec for 3rd PLD
#
# Finally input your TISs matrix:
#                       TISs="3.4,2.6,1.8"
```

- A good practice is to copy and save the code in the “Run” window for future use
- To learn more about Unix scripting: https://andysbrainbook.readthedocs.io/en/latest/unix/Unix_Intro.html

Exercise 7: Let us take a look at the CBF map you generated!



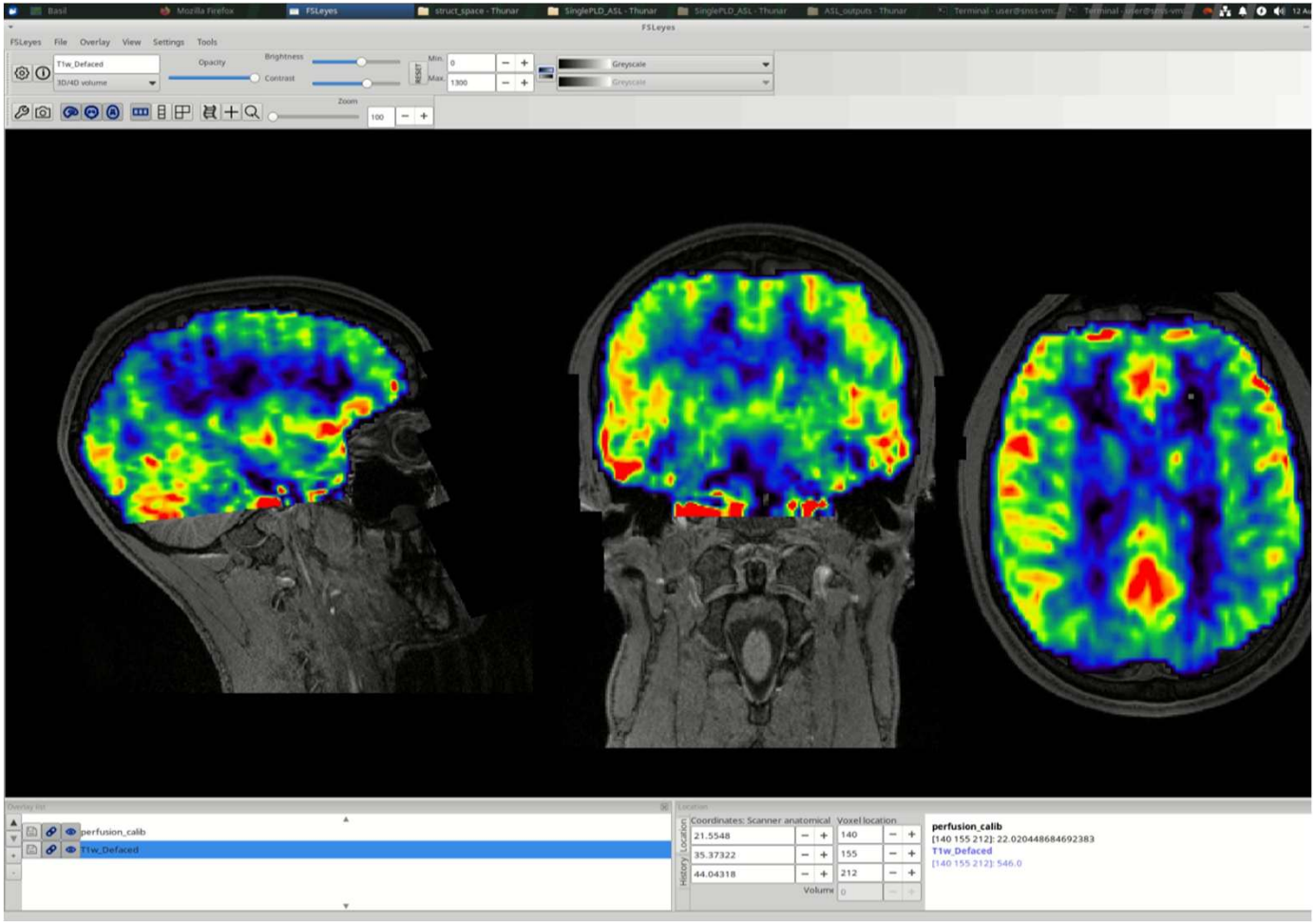
The **calib** tab contains the M0 image;

The **native space** contains the CBF image in its original ASL space (position).

The **struc_space** contains the CBF image that is co-registered to the T1w images.

** We will examine the CBF images in the **struc_space** folder.

Exercise 7: Let us take a look at the CBF map you generated!



To-dos:

1. Import **T1w** and **perfusion_calib** images to the fsleyes.

2. Select the **perfusion_calib** image and change the color bar to "**X-rain**"

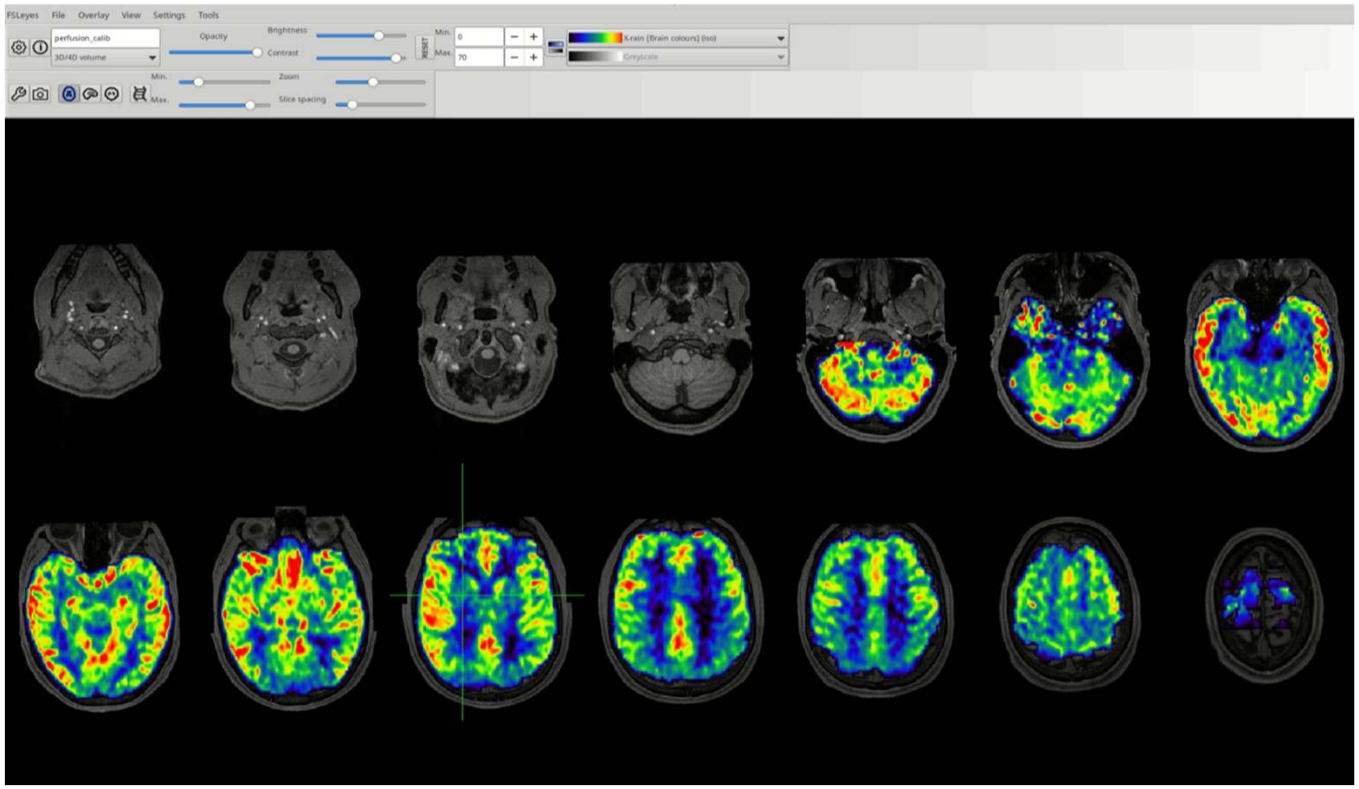
3. Make sure **perfusion_calib** image is on top of the **T1w_Defaced**

Questions:

1. What is the unit of each voxels in this CBF map?

2. Pick your favorite brain region and find an approximate CBF value.

Exercise 7: Visually-inspect the CBF image using “Lightbox” view



Summary of the workshop:

Method:

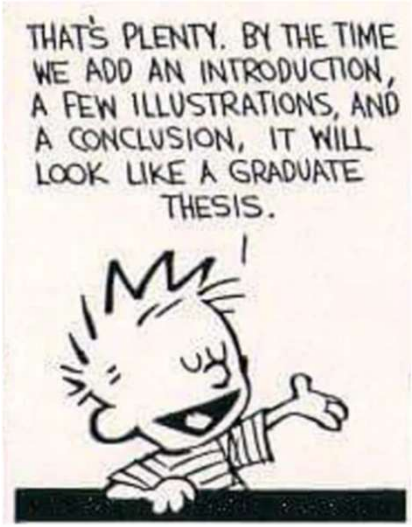
We recruited the healthy volunteer from University of Toronto (n=1). Neuroimaging was acquired using a _____(scanner name, field strength=___). We collected T1-weighted images were acquired using ___ sequence for anatomical registration.

Cerebral blood flow (CBF) was measured using (*pASL/cASL/pcASL*) sequence (TR=____, TE=____, Spatial resolution=____, Flip angle=____). The labeling duration was ____ms, and we selected a single post-label delay of ___ ms. In total, _____ pairs of label-control images were collected. A proton-density-weighted image (TR=___, TE=____) were acquired for calibration.

Oxford ASL (version____) were used for perfusion calibration and quantification…

Results:

Figure 1 shows the estimated CBF from pcASL experiment. The CBF in the _____ (Your ROI) was _____(unit).



** Actually more works are needed in a real thesis