Procedure for Comparing Virtual Injection to PCASL:

Reconstruct and Background Phase Correct

1. Find a case in which both dynamic PCASL and PCVIPR are performed

* Find locations of PCASL/PCVIPR cases using “index\_pfiles” command.

1. Reconstruct PCVIPR data on CN machines (if not already reconstructed)

* Reconstruction should create a folder called *RECON\_######*,

1. Bin all PCASL dats and dicoms into a general *PCASL* folder
2. Pull *PATIENT* folder to personal machine

* Example: D:\\Patients\\PATIENT1

1. Open Matlab
2. Add ‘PCToolV2’ to Matlab path
3. Run ‘standalone\_background\_correction’ on PCVIPR .dat files

* Phase corrected .dat files should be output to a folder called *CORRECTED*, located in the directory in which the original .dat files are located.

1. Move ‘CD.dat’ and ‘MAG.dat’ files to *CORRECTED* from *dat*

Run virtual injection

1. Create folder named *inject\_data* in *RECON* folder

* If this folder already exists, there may be data in that folder. You can choose to save this data in a different folder, as it will be overwritten.

1. Open ‘new\_test.py’ with IDLE

* Right-click on the python file, an option “Edit with IDLE” should be available. If not, you may need to uninstall previous version of python.
* Check that PLoader (line 12) leads to the correct data folder (*dat* folder or *CORRECTED* folder if phase corrected)

1. Open command prompt terminal
2. Move to *RECON* directory in terminal

* ‘cd’ changes directory, ‘dir’ lists directories, ‘D:’ changes to D-drive
* Make sure the newly created *inject\_data* folder is in the *RECON* (along with *dat* and *DICOM*)

1. Ensure ‘new\_test.py’ is in Windows path

* If not, change path in environment variables in Windows (“Edit the System Environment Variables” 🡪 “Environment Variables …”)
* The path should lead to all python scripts in the Virtual Injection folder provided

1. Type “new\_test.py” in command line

* A pop-up window should appear with a MIP complex difference image of the brain.
* If there is noise in this image or the vessels are not seen clearly, close the image, kill the running process in the command prompt (ctrl+c), and then adjust the threshold value (as in step 15).

1. Adjust thresh1 variable in ‘new\_test.py’ until only vessels are seen in the pop-up image

* You may need to test a few values. Testing is done by closing the window, killing the script in the terminal, and entering new thresh1 values.

1. Run virtual injection

* Once image is satisfactory, close the image and let script run (1200 steps ~ 10 minutes)
* Information will be saved in the current directory in the command prompt

1. Run ‘new\_save\_pngs.py’ to save MIP images

NPY/DICOM to NIFTI

1. Open Matlab
2. Move to inject\_data folder
3. Run ‘sort\_output’

* This sorts the python output into different directories
  + *data* = output .npy files
  + *raw* = output .png images
  + *sqrt* = output .png images (sum of squared velocity)
* This also turns .npy files into .dat files

1. Run ‘dat2nii(dataFolder)’
2. Move to PCASL folder
3. Run ‘dcm2nii’
4. Copy TOA.nii and PCASL.nii file to COMPARE